A Complete Bibliography of *IEEE/ACM Transactions on Computational Biology and Bioinformatics*

Nelson H. F. Beebe
University of Utah
Department of Mathematics, 110 LCB
155 S 1400 E RM 233
Salt Lake City, UT 84112-0090
USA

Tel: +1 801 581 5254
FAX: +1 801 581 4148

E-mail: beebe@math.utah.edu, beebe@acm.org,
beebe@computer.org (Internet)
WWW URL: https://www.math.utah.edu/~beebe/

26 September 2024
Version 1.86

Title word cross-reference

((1, 2)) [BJ13]. (∗, 2) [KO15]. (1.5 + ϵ) [CWZL08]. (L, d) [CW11, DBR07, Tan14]. + [ZSH21]. 1 [APPG18]. 1.375 [EH06]. 1β1β [LCH19]. 2 [BLR15, GKS+22, HZL19, KD15, LN21, LBQ+13, SSF18, YLW+24]. 2+ [LCOMG14]. 3 [ACSR21, ARP+16, BWRF12, CWT+19, CSW+23, CHC+21, CBF+18, GHZ+22, GPF+20, GH15, GJSB23, GKS+22, HS15, KL19, KSMT19, LQV+13, LHQ+18, NPK+07, RG16, RWH+10, Str11, SSF18, TB23, VMD+08, YLH+15, YCZ+18]. 4 [KHI+21, LBQ+13, MCRC17]. ^{13} [AAG+18]. ^{2} [LQJ+23, LWL+20]. ^{3} [PM20, YLY+12]. ^{7} [MZLL22]. $_{0}$ [GM22]. $_{\text{ATP}}$ [BMH+16]. α [GCGCP+23, MRB12]. β [AAE11, BMH+16, CNS+22b, DNS19, YXS16]. $\ell 1$ [CMR19]. ℓ_2 [JXN+16]. F^2 [BCS11]. G [LBQ+13]. K [CZ20, ARZ+14, PFJ+19, SC22a, WXY+23, ATX21, AC12, AFJ12, HC14a, IM14, LMZ14, PSC20, QZZ21b, RLRP23]. L_p [LLT10]. λ [SPA17]. M [ZWZ16]. μ [CPRC24]. N [LZGZ14, MRK18, SLL+19, KNTB18]. $O(m \log m)$ [SSS+15]. $O(N^2)$ [BHS+04]. $O(n \lg n)$ [WLY14]. $\Omega(n^2/\log n)$ [BE08]. P [VTGC16, UKV18]. q [CZX19]. R [MTNH17, Pol13]. S [SP11].

-Activation [LCH19]. **-Approximation** [CWZL08, EH06, HZL19]. **-ATPase** [BCFCC13]. **-Barrel** [YXS16]. **-bounded** [KO15]. **-Bulges** [CNS+22b]. **-Cell**

WS21, WDH08, WLC11, WMS09, XHQ+18, XCR21, XWC15, XYLL23, YWK+07, YCYC12, YXYC13, YLC+23, YC08, ZWL+12, ZZZC17, ZZH18a, ZWM+20, ZWLZ21, ZXZ+21, ZGW+24, ZFZL22, ZLJT17, ZW13, AMBK14, CFIS+15, DST+15b, FWY+15, GRDV14, GM14, GÁVRRL15, HLW15, ARZ+14, Nye14, PWZW15, PWC+15, RHH16, SHK14, SSKH15, STT+14, SSS+15, XXM+16, YHV+15, ZSY+14]. **Algorithm-Based** [DM22]. **Algorithmic** [LQV+13]. **Algorithmics** [BvBF+11]. **Algorithms** [AAKB22, AKS13, ASI+11, AAE11, BEW09, BAK06, BBK+07, BG17, BM13, CMR19, CEFBS06, CW09b, CW11, CW12, Che13, CAN+08, DBR07, GH08b, HK12, HCLS11, HYW08, HKM+18, JRSS18, Jia10, KB19, LNC+05, LCC+11, MJZY22, MO04, Mai09, MSP+19, MVVR19, MVVR20, MVVR23, MWSM12, NS19, NSNA19, PG18, PH10a, POS+18, Pol13, RZMC17, RAA10, SK08, Shi10, SHUP19, SLH+06a, SVE21, SDB+07, TS18, TRKRC13, WL11, Wan12, WL19, WBE13, WCLY12, XZG+18, YLCC13, YDM+08, ZD12, ZZ18, vIKKS08, vIJJ+20, PSK+16, Tan14, ZHL+14, MVVR21b, MVVR21a]. **Alignable** [PS11]. **Aligned** [LSTW+17, ZZW+22]. **Aligner** [EMK18]. **Aligning** [GTL+21, WL14, YlCW+15]. **Alignment** [AH11, Alt23, ANR+23, AKLJ17, AGMP09, BTTR11, BAK06, BKAV23, CWC04, COW20, CSE+21, CGPW06, DBZ12, DK17, DK13, DBN18, ECK16, FGKH11, FMD18, GPMH16, HT09, HGM18, HB11, IGM+07, JZW17, AKD17, KG20, KK08, LNR+09, LPR+08, MWL+12, MGK08, MTH22, MS21, MKH11, MGC19, MGKG17, NP13, NSZK15, PHX+08, Pol11, Pol12, Pol13, QZZ21b, RCM+19, RGN+09, SH11b, SLH+06a, SSFW12, TRKRC13, TDK13b, TED+12, TDA+09, TTWR13, VM18, WS08, WLMW+11, WHKK07, WAK13, WB11, WCLY12, Xu05, YLC+23, YLL+06, YH13, ZSW23, ZLS+21, ZLLS17, ZGB+12, CV14, FZM15, FSL+15, MG14, PSK+15, SHS15, SCC+15, SPWF14, XXM+16]. **Alignment-Based** [CSE+21]. **Alignment-Free** [ANR+23, BKAV23, MS21, QZZ21b, YH13, CV14]. **Alignments** [BDD+10, HVG04, HPL+13, PT09]. **All-Mapper** [CZX19]. **Allele** [BBSP08, DLM12]. **Allelic** [NT24]. **Allowing** [AGMP09]. **almost** [WLY14]. **along** [AGMP09]. **Alphabet** [SJNS19]. **Alphabet-Friendly** [SJNS19]. **Alphabetical** [FMD18]. **alphabets** [YHV+15]. **Alter** [JLW17]. **Alteration** [MW21]. **Altering** [Zha18]. **Alternating** [HYL+19]. **Alternations** [XLW20]. **Alternative** [NHTD17]. **Alternatively** [RLRH18]. **Always** [BBCP07]. **Alzheimer** [AKH+23, GT24, JHZL19, LWT+18, MT24, NLW+24, PZC+23, RNAR+24, SSK+20, WLA+13]. **Alzheimer#x0027** [GCC+22]. **AMAS** [TC16]. **Ambiguities** [ZZS07]. **Ambiguity** [GzS11]. **American** [FMA+20]. **Amino** [AHK+21, HLG10, JDHL20, Kar12a, LYL+17, NLGG12, TZWZ23, YH13]. **Amnioserosa** [DABV17]. **Among** [GCC+22, LZS23, PZWC20]. **AMP** [GM22]. **Amphipathic** [FXZS22]. **Amphiphilic** [JMCY23]. **Amyotrophic** [MGP+22]. **Analog** [Pre04]. **Analog-Spectrum** [Pre04]. **Analyses** [ATA+17, KPP19, SSD19, WYY+13]. **Analysis** [ACC+13, AAT20, APKP18, iAOSS16, AKS20, BB11, BRS18, BGS+12, BCY+22, BRB21, BKLS18, BSLR05, BCFCC13, CP13, CC21, CDBR21, CXW+13, CBM+20, CZCL23, Che10, CS24, CBK20, CWZ08, CZM+18, CMC+12, Dal16, DSHM08, DADF+10, DKDD10, DLY+21, DSVMM18, DKY21, DPW12, FZWS17, FM12, FWY19, FVP+20, GPZ20, GGH+13, GCZ18, GF10, Gos11, GPC+20, GM16, HCN+19, Han10, HB05, HYC12, HSTW06,

LBM+18, LLH+07, LN13, LWZ12, LLZ+20b, LNW20, MO04, MJPP20, MBGP12, MNND13, MSS+19b, MVS+13, MB16, MJ23, NM22, NAHT+20, NNM+12a, NNM+12b, PFJ+19, Pau18, PR18, PLCW17, PZWC20, PCK19, PPZ12, RYK+19, RA16, SFB+08, SdOD+12, Sef22, SDN+11, SJZ19, SZL+20, STS21, TV11, TDK13a, TDK13b, VBB18, WLWN17, WDL+17, WHW21, WCZ+23, Wig15, ZLF+21a, ZWZS16, ZKW19, ZGZ+20, ZSC+10, ZTY22, ED14, GTDK15, Gu16, HM15, HPH+15, HKLN14, Jam15, MZL15, WZC+15, ZSY+14]. **Biologically** [BB11, KP12, MTR+22, SMK+12, TNQ08]. **Biology** [ALWG18, Ano05b, Ano09c, Ano12b, BLP18, BU17, Cas06, Cas07, CSW11, CN12, FS12, FS13a, FJJ18, GCZ18, GTTR+17, GAH+21, GJH19, Gus04b, GZ22, HKK07, HSS18, Jam13, JFN11, MLFM22, MVVR19, MVVR20, MVVR23, Maz12, MCD+11, RZF07, SPK19, SYL19, SGH12, TS18, Tit16, TC13, VRHB23, WYWX16, WH11, WCXL18, Zha16, ZS19, KG15, TWZ+14, MVVR21b, MVVR21a]. **Biology-Based** [MLFM22]. **Biomarker** [ALQ17, BMSZ22, BYS+22, CBM+20, HLL+22, HSZ+23, IC23, KGF+14, LLT10, MSB19, MLZ18, PSIM17, PS19, TP18, WDS+12, ZZLH23, pD20, OFC+14]. **Biomarkers** [Bha23, DHCW18, GCC+22, LLR+23, SQZA14]. **Biomathematical** [GCGCP+23]. **Biomechanical** [JGBR15]. **Biomedical** [ACJ24, BYZ+23, BYW+23, BMHS13, CDAL22, DDZ+21, DYL+23, ELH24, GZB23, HLL+18a, HW07, HDS+18, JLH16, JZZ+21, KLCH22, LHLY11, LLQ+16, LLQ20, LJ20, LXZ+23, LTwG+11, LNC+05, LQY+20, MWH+23, MMG+22, MCC16, NCL+23, NAHT+20, OLZ11, Ozy12, QKÖ18, RGB+21, SLCZ22, SSZ+23, WCMZ15, WB17, WGX+17, XLL+18, XLL19, YRL+20, ZYC+22, ZBL+23, ZLWF24, ADTAQ16, GFG16, JZCZ15, MKARB16, Vog15]. **biomedicine** [YN14]. **Biomolecular** [Bi09, Gon13, GBB+11, HW07, LBL+10, RMV12, RJNN18, YB08, YCY+13]. **Biomolecule** [SMB12]. **Biopathways** [PAL+12]. **Biophysical** [MVS+13, SCM19]. **Biopolymer** [SLH+06a]. **Biopsy** [CYL+21]. **Bioreductive** [KHP12]. **Biosequences** [SK12]. **Bipartite** [KPK+17, PCK19, ZS18]. **Birth** [FMA+20]. **Bistability** [AKS20]. **bistable** [WLY15]. **Bit** [MCM22]. **BitMapper2** [CZX19]. **Black** [NQNT23]. **Blanket** [RC11]. **bLARS** [SV16]. **BLAST** [CWC04, CW07]. **BLASTP** [LSMW11]. **Blebs** [GBTW16]. **Blending** [AHK+21]. **Block** [GD22, HZL19, KPK+17, LJZ+24, LNW20, TGLP16, ZJ23]. **Block-Interchange** [LJZ+24]. **Block-Interchanges** [HZL19]. **Blockchain** [ACJ24]. **Blocking** [Bon07]. **Blood** [BYS+22, GRD+21, GSC17, ZZH+24]. **BLOSUM** [SCC+15]. **BlSSSA**} [GD22]. **BLSTM** [LJ20]. **BLSTM-CRF** [LJ20]. **BM** [XZY+14]. **BM-SNP** [XZY+14]. **BMExpert** [WCMZ15]. **Boltzmann** [TAI+19]. **Bone** [PLMV12, LLRZ15]. **Boolean** [AKMT12, AKS20, BHS+04, BD19, CPL+23, CMQ+16, CCN22, DT11, GAH22, HAH13, HMW+12, KH14, LT17, LLL16b, MSP+19, MPP+20, MPSY18, MPQY19, MDM13, PSPM20, PH10b, SRLR14, SPP21, TLSA18, VRK12, ZWL14a, ZWL15, ZZM17, ZK16, Zou13]. **Boost** [DZD+23]. **Boosted** [YMW+12]. **Boosting** [CMSE+15, HLZ+17, LZX20, MGSP22, SKS22, WYY+13, YL12]. **Bootstrap** [CBZ18]. **Borderline** [NZM22]. **Borderline-SMOTE** [NZM22]. **Both** [HC13, NSAH19, YLWS21]. **Botulinum** [MWLS18]. **Bound** [BFK17, CHC+21, MKS+17]. **Boundaries** [SCM19]. **Boundary** [Gon13, YPL+23]. **Bounded** [MZLL22, YCCY20, KO15]. **Boundedness** [HC19]. **Bounding** [NSNA19]. **Bounds**

PWZW15, XG14, ZZ15, ZWL+14b]. **Complexity** [BN06, BCF+07, BS10b, BLS12, CEFBS06, HKM+18, KB17, LLW10, PH10b, Pol12, RZMC17, TZP17]. **Complicated** [HWPE17]. **Component** [BKLS18, BSLR05, CXW+13, CZCL23, DSHM08, Gos11, GPC+20, Han10, HLGS21, JDCC12, KKP22, LWW+21, LXG+16, MZLL22, SDCW11, dCAR11, LLH+14]. **Component-Based** [Gos11]. **Components** [Wan16]. **Composable** [CKRS21]. **Composite** [LMPT15, MSS19a]. **Composition** [AHK+21, CCYW12, HHC+24, KAL+17, LLTC19, NLGG12, RST10]. **Compositions** [KNTB18]. **Compound** [CZW+18, HSF+23, LQW+23, QLZZ22, TZWZ23, ZYC+22, ZYYX23]. **Compound-Protein** [CZW+18, HSF+23, LQW+23, TZWZ23, ZYC+22, ZYYX23]. **Compounds** [ZAZ+22]. **Comprehensible** [FWA10]. **Comprehensive** [GSK13, JDHL20, QZD+22, SGH12, WWBZ19, YZG+19, YOGY11]. **Compress** [GDM12]. **Compressed** [CW07, GRS+13, MDM13]. **Compressing** [XZG15]. **Compression** [CGLF12, CWLS15, CLS19, How13, KT07, KBSCZ12, LN17, SN24, WL13a, WHWP12, Mat15]. **Computation** [ÅSWH22, CKRS21, CHNW20, KK19, SSK+20, TWG+12, Wu10, GFG16]. **Computational** [AJD+12, ANR11, ATA+17, ALWG18, Ano05b, Ano09c, Ano12b, BLP18, BBSP08, BRZ+17, BSR+21, BCF+07, BMZM15, Cas06, Cas07, CN12, DLO+23, DTA+23, DBN18, FS12, FS13a, GCZ18, GLL+18, GRD+21, GAH+21, GCJ+21, GCC+22, Gus04b, HKK07, HSS18, Jam13, JJH12, KZW+18, LHH13, LHL+19b, LHY+11, LWL+19, MTNH17, MVVR19, MVVR20, MVVR21b, MVVR21a, MVVR23, MBP+18, Maz12, MCM22, NSAH19, PLMV12, PM20, PH10b, QQD+21, QZD+22, QZA+23, RZF07, RG16, RCBB19, SK21, SK08, SBW15, SVG+24, SPK19, SHG+23, SXW+24, SYL19, SZGZ21, SWX+19, TS18, Tit16, WYWX16, WKSP21, WWT+20, YZC+23, YB08, ZDL+19, ZZ20, ZYC+22, ZSZ+22, MM14a]. **Computations** [ZXB11, ZSC+10, MKARB16]. **Computed** [ZZH+24]. **Computer** [GCJ+21, LQWP21, MVS+13, XJZS21, XTO+24]. **Computer-Aided** [MVS+13, XTO+24]. **Computerized** [XPH20]. **Computers** [TIA+11]. **Computing** [APPG18, BGS+12, BS07, BS09, BWRF12, BBH12, DB14, GLS+16, GZB23, GDWK+15, GSB+13, GJS11, HZR+19, HM13, HBG16, HBG17, HBG18, HBG19, HBG20, HBG21, HHA22, ME19a, MKS+17, MDH11, MJ23, OP11, PK13, RP13, RLRP23, SNM08, TLSA18, TS17, UAH16, WS08, WYWX16, WL19, WS21, WSB21, CFIS+15, GPScF15]. **Computing-Deep** [GZB23]. **Concentrations** [MKKS20]. **Concept** [TWZW16]. **Concepts** [BMT17]. **Concerning** [BvdGK+11]. **Concise** [Son06]. **Concurrent** [MTM+15]. **Concussion** [WNT+17]. **Condition** [Gon13, MSQ18, RB16, Son06]. **Condition-Specific** [MSQ18]. **Conditional** [BLR08, JZZ+21, LDM18, WWL+17, XYLL23, GGZZ14, LWG+14]. **Conditioning** [DBTB09]. **Conditioning-Based** [DBTB09]. **Conditions** [YLW+24]. **Conference** [BLP18, FJJ18, GJH19, HBG16, HBG17, HBG18, HBG19, HBG20, HBG21, HHA22, Kim18, MJ18, SPK19, STHA15, ZLZ20, ESW14, HC15, WLC18, YSC19, ZPC+21, ZC14]. **Conferences** [Kim18]. **Confidence** [CWCJ21, MC07, PA22]. **Confidence-Based** [CWCJ21]. **Configurations** [SLH06b]. **Conflict** [BB04]. **Confocal** [MCRC17, BLR15]. **Conformation** [BIDS23, LW18, YDM+08].

[MMH15, YLW+24]. **Cross** [AMGC16, HKS11, JGW+21, LSW+23, LPH+13, PBhL+11, SLRQ19, WCDM23, WYF+23, WGK16, WWL+23b, XNYC21, YGJZ23, ZWG+21, PS15]. **Cross-Attention** [WCDM23]. **Cross-Context** [SLRQ19]. **Cross-Domain** [JGW+21, XNYC21]. **Cross-Entropy** [PBhL+11, PS15]. **Cross-Hybridization** [HKS11]. **Cross-Laboratory** [LPH+13]. **Cross-Modality** [WYF+23]. **Cross-Ontology** [AMGC16]. **Cross-Sectional** [WGK16]. **Cross-Species** [WWL+23b, YGJZ23, ZWG+21]. **Crossing** [Gra04]. **cruzi** [GAR+09]. **Cryo** [BRZ+17, GHZ+22, LDS+07, ARZ+14, ZCR+17]. **Cryo-Electron** [GHZ+22]. **Cryo-EM** [BRZ+17, LDS+07, ARZ+14, ZCR+17]. **CryoEM** [ALR+13]. **Cryptographic** [JHW+19]. **Cryptographically** [BKLS18]. **Crystal** [DDS+17]. **Crystallization** [STB+20]. **Crystallography** [Str11]. **CSD** [Wil12]. **CSS** [AKS13]. **CT** [CSQ+22, CZL+22, JGW+21, LSW+23, LLMZ23, QZZ+21a, RHZ+24]. **CTLA4** [GCGCP+23]. **ctP** [LQJ+23]. **cuBLASTP** [ZWcF17]. **Cuckoo** [AKS13]. **CUDA** [BBH12, CNM11, LSMW11, ZWLZ21, ZLS+15]. **CUDA-BLASTP** [LSMW11]. **CUDA-Enabled** [LSMW11, ZLS+15]. **cumulative** [TYA15]. **Curatable** [HK15]. **Curated** [GTTR+17, PZC+23]. **CURatio** [KMSY20]. **Curation** [CDAL22, CCF+24, HLLO19]. **Current** [MSS+13a, SW17]. **Curvature** [MBF+13]. **Curves** [IGA18, KGK14]. **Custom** [MRB+24]. **Cut** [BFM13, NSNA19, SR06]. **Cutting** [NSZK15]. **cyber** [KSA16]. **cyberphysical** [AIS+16]. **Cycle** [BRF17, CAW+19, SSS20a, ZZM17, ZWW17, WZ14]. **Cycles** [Gru11]. **Cyclic** [ZLB24, ZHX+24]. **Cytogenetic** [LYK07]. **Cytometry** [PN17, Qiu14]. **cytoscape** [NCMCAR15, WZC+15]. **cytosolic** [LCOMG14].

D [CHC+21, ACSR21, ABS17, APPG18, ARP+16, BLR15, BWRF12, CWT+19, CSW+23, CBF+18, GHZ+22, GPF+20, GH15, GJSB23, GKS+22, HS15, KL19, KSMT19, KHI+21, KD15, LQV+13, LN21, LHQ+18, LBQ+13, MCRC17, NPK+07, RG16, RWH+10, Str11, SSF18, TB23, VMD+08, YLH+15, YCZ+18, ZHD+21]. **D-Map** [ABS17]. **D-pattern** [KD15]. **D-UNet** [ZHD+21]. **DAC** [Alt23]. **DAG** [BM15, TGP+15]. **DALI** [WAK13]. **DALIX** [WAK13]. **Damage** [ZLL+20]. **DAPD** [GJK15]. **Data** [AAKB22, AM22a, AKH+23, AGAS18, AAH+18, AFAAW+11, ABVD12, AN21, ASI+11, AAB22, ACWW05, ACWW07, BKP+19, BDD18, BMK11, BTTR11, BDP11, BZ10, BHMA06, BLP+12, BMHS13, BKLS18, BHHMCL16, Bon07, BMZM15, BLR08, CMR19, CCCY20, CMS12, CSSS16, CSZ+19, CKM+17, CW09a, CHL+12, CHWY19, CMMZ20, CBM+20, CWCJ21, CZCL23, Che10, CKWY12, CCE19, CWZ08, CKL+23, CCC+22, CZM+18, DNR15, DCHW17, DHCW18, DG19, DMJ+18, DLA+23, DLG+24, DWSB11, DYL+23, DPS22, EAS12, EAS13, ELH24, FSNF21, FHH+11, FJJ11, GZG17, GTX+23, GKPS11, GXSZ17, GMSD11, GC22, GZR+18, GJZH17, GZXH21, GYW+24, GTL+24, GBJ08, GLG10, GM16, HYW+17, HBH12, HYY11, HZW+17, HYL+20, HYC12, HAH13, HMW+12, How13, HLY+16, HC16, HW07, HLL18b, HDS+18, HHCY20, HTLL12, HL21, HWY+23, HSZ+23, HTZ+23, IGA18, IC23, IMA13, JCF13, JKC23, JLJC24, JXN+16, JHX17]. **Data** [JFN11, KCD+12, KBND19, KQD21, KHO+20, KB20, KNS+05, KCY+24, KKP22, KKP+21, KMG+05, KBSCZ12, KZ10, LTM+13, LHH13, LBM+18, LH10, LLW+11, LN13, LLHF15, LW18, LKW+19, LQJ+23,

LMW+24, LLCC21, LJL+15, LLZ+20a, LDGY21, LTLL23, LXG+16, LZHZ17, LW19b, LYY+19, LLZ+20b, LNW20, LSL22b, LLL+23, LLL15, LC10, LLA19, LGYW21, LTRW19, LBL+10, LTX21, LLY+23, LGL24, LP21, MSZ19a, MHHJ20, MWH+23, MMC+23, MO04, MTSCO10, dHMPFdM23, MP13, MP19, MMBC22, MJPP20, MWZ+20, ML18, MPM11, NRV22, NJMF19, NNSZ07, NVL22, NCL+23, NZM22, NSAH19, NNM+12b, OLZ11, OMWX09, OLS+13, OC13, PKM22, PLC+20, PSS09, PIPC18, PAS+11, PI09, PR18, PL17, PZH20, PYL+21, PH10b, PNP+18, PAAG07, POJ+22, PN17, QV17, QKÖ18, QBPEL12, RGB+21, RLR20, RCP+18, RTPM+19, RSK23, RKZ16, RM18, RBdlVMPG16, RGCB05, RWH+10, SN24, SBOA23, SSD19, SMK22]. **Data** [Sef22, SDN+11, Sen19, SBW15, SC11, SY09, SIM12, ST05, SDCW11, SND22, STB+20, SWSA21, SMK+12, SK12, SC22a, SWX+19, SGK12, SWL19, SPL+23, TWW+20, TZH07, TZ16, TGGF10, TDZ+19, TZY11, TBRS13, TTWR13, TK05, TC13, TWZW16, TOYHZ19, TBKH05, UC10, UKV18, VMC22, VBG+18, WZA07, WGP11, WYWX16, WLWN17, WFY+19, WHF+20, WSJ21, WMW+21, WZZ+22, WYF+23, WWY+24, WP08, WAG19, Wil09, WMS09, WDS+12, WGK16, WZHM23, XHQ+18, XLL+20, XSS17, XZC07, XAW07, XOYHZ18, XXW+23, YSC13, YHW+21, YM11, YWW20, YZP+21, YLXJ04, YC08, YNWC07, YNBM05, YLL+06, YHB12, YP13, YCY+13, YWW+18, YYY+22, YGY+19, YLWS21, YLBX21, YYX+21, YNN+18, ZZKW18, ZANN20, ZL24, ZLW+11, ZWSX12, ZDL12, ZXLZ18a, ZXLZ18b, ZZZW19, ZWHC19, ZZ20, ZXZ20, ZLC+21, ZFH+21, ZCL22, ZZGL24, ZC11, Zha16, ZKL18, ZY20, ZYC+22, ZHG20, ZWD+17, ZYW+13, ZYF+18, ZLWF24, ZGDH16, ZGB+12, ZM22]. **Data** [dCAR11, BMM14, CWZW15, CZWT15, FN14, GFG16, GMCB14, IM14, JZCZ15, JR14, KSM14, KGF+14, LLCZ15, LXZ+15, LHS16, MM14b, OFC+14, PS15, Qiu14, SHK14, Vog15, WLC+15, XZY+14, YN14, YCY+15]. **Data-Dependent** [XZC07, ZLC+21]. **Data-Driven** [AAKB22, CCE19, HLY+16, HSZ+23, PLC+20, RGB+21, Sef22, ZHG20, ZM22]. **Data-Enabled** [YHW+21]. **Data-Fusion** [KZ10]. **Database** [ANR11, GKPS11, LYK07, LLJ+23, PZC+23, SDN+11, SPD24, WNT+17, WQL+16, XPH12, dAc17, OSA+21]. **Databases** [Ano13b, Ano13c, HW07, Jam17, LTwG+11, SHG+23, SXW+24, ZSC+10, Ano13d, XHS15]. **Dataset** [HLY+22, LN17]. **Datasets** [CKM+17, FFT16, MB16, WDL+17, ZZH18a, ZWHH21, BCLC15]. **Day** [MSH+11]. **Day-to-Day** [MSH+11]. **DB** [WQL+16]. **DCHap** [LL22]. **DCNN** [WSJ21]. **DDE** [ZSY+14]. **De-Noising** [YFCM17]. **Deal** [GAH+21]. **Deciphering** [BSS+22]. **Decision** [ELH24, Smi09, TNQ08, YNBM05]. **Decisiveness** [PBFB22]. **declarative** [LV14]. **Decoding** [LLK+22, LDGY21, PV16, UJ09]. **Decomposition** [BMSZ22, FWXZ19, LLQ+16, LLZ+22, MJ23, QZJ+23, RGCB05, SK19, SPP21, WTM23, XL16, XLW20, YWK+07, ZZN+11b, ZGDH16, LYH+16, SB16]. **decompositions** [GMCB14]. **Decoupling** [LLL16b]. **Decoy** [MSS13b]. **Decoys** [LBL12a]. **Decrease** [TC13]. **Deep** [ALC22, AHN23, ACJP23, AHC+21, AKA+22, BMCY22, BP22, CZ20, CHL21, CWP+23, CGW+16, CZL+22, CCC+22, DN22, DH23, DSCM20, DPS22, FSX19, FYZ+19, FZM20, FXZS22, FMA+20, FPC20, GT24, GZB23, GPE17, GA23, GZWD23, GYW+24, GZ22, HLX+21, HWY+23, HWZ+23, IC23, JKC23, JLK+21, JCG+22, JHZL19, KCY+24, KBM21,

LLHW22, LFZ+19, LHCL20, LWZ+21a, LWL+21, LZW+22, LSZ+23, LLMZ23, LXS+24, LZQ+20, LWZ+21c, LJN+23, LZC+23, LGL24, MGSP22, MT24, MWZ+20, NLXS19, OLS+13, ÖBT21, PSA21, PLTG22, QRT+23, RFFB+20, RSK23, RNAR+24, RTC23, SKS22, SSV+19, SZHH22, SZD+23, SXW+24, SGP+20, SLCL22, SWL19, ST23, TDZ+24, TR13, TDZZ24, UKC+23, UBP+19, WCC+18, WYHZ20, WZZ+22, WZS+22, WQLL23, WWL+17, WCXL18, XLZW22, XXW+23, YCX+21, YGJZ23, YZP+21, YWCC22, YXL+23, YZL23, YYY+22, YZH+23, ZLH+20, ZLF+21b, ZLF+21a, Zha11, ZSZ+21, ZZZ+23, ZJ23, ZGW+24, ZG19, ZYC+22, ZDY+23, ZDN+23]. **Deep** [ZLWF24, ZLZW22, wTCAK+20, GE14, GE15, LLCZ15, SEC15]. **Deep-Learning** [FPC20, PLTG22]. **DeepBarcoding** [YWCC22]. **DeepCLD** [FHDU22]. **DeepCPPred** [AKA+22]. **DeepDRBP** [ZCL21]. **DeepDRBP-2L** [ZCL21]. **DeepDSC** [LWZ+21a]. **DeepFusionDTA** [PLTG22]. **DeepIDA** [YYY+22]. **DeepIII** [WZZ+22]. **DeePROG** [DPS22]. **DeepSeed** [LLQW21]. **DeepSeqPanII** [LJC+22]. **DeepSG2PPI** [ZZZ+23]. **DeepSide** [UKC+23]. **deepSOM** [SYKM17]. **Defects** [LUdSCH10]. **defines** [LHWL15]. **Defining** [LTLTS23, WS08]. **Definitions** [NRV09]. **Deformable** [WKZ+24, ZLB24]. **Deformation** [ASJ+07]. **degenerate** [CFIS+15]. **Degenerative** [GTL+24]. **Degradation** [WMWA12]. **Degree** [GF10, SS06a, TWZP14]. **deGSM** [GFG+21]. **Delay** [EAS13, JSS+18, WLMZ22]. **Delayed** [JZS+18, KCCC15, LCZN16, LLL15]. **Delays** [AGAS18, FZWS17, YLZW21, ZWZ16, ZWC15]. **Deletion** [ZLS+21]. **Deletions** [QLLX10, HZZT14]. **Delivery** [MWD11]. **Dementia** [ZWS+18]. **Demethylation** [AAB22]. **Dempster** [RGI13]. **Dendrogram** [NSZK15]. **Dengue** [DM22]. **Denoising** [DCW+24, JZYL24, NNM+12b, GH15]. **Dense** [DADF+10, GHZ+22, Wil09, YNWC07, ZHL+24]. **Dense-Core** [DADF+10]. **Densely** [LSW+23, LLQW21]. **Density** [BCY+22, GLG10, LXL+21, MRB12, QRT+23, QL16, SKD+07, XYYZ20]. **Dependence** [LGN+19]. **Dependences** [YP13]. **Dependencies** [KNS+05, SZL+20]. **Dependency** [CL08]. **Dependent** [AKV16, KKK19, KSB12, XZC07, ZLC+21, MZS+16, WDX+15]. **Depends** [LCH19]. **Depression** [LKL+23, QRT+23]. **Depth** [GAGM11, IMA13, KBBD+17]. **Derivative** [KSP22, NVSH18, XSS17]. **Derivative-Free** [XSS17]. **Derivatives** [NSMH19, KPB14]. **Derived** [HYR+19, JS12, WQL+16]. **Deriving** [PLH22]. **Descendant** [MTH22]. **Descent** [NGY+16]. **Describe** [RGVP24]. **Description** [FS18, GAGM11]. **Descriptor** [ADPH11, YFYW23, YCZ+18]. **Descriptors** [ARP+16, HZTP12, KAS21, WB11, YZG+19]. **Design** [AKS13, BPM21, CZZ+23a, Che16, GJZH17, mHB13, IL18, IYA12, JSS+18, JZS+18, LHDS18, MDD18, MM17, OMAdG+12, QZA+23, SK08, SB12, TRBK09, VDS+20, WLC11, YCYC12, DYD15, HPH+15, KH14, MG14, MM14a]. **Designer** [BPP+13]. **Designing** [CIZ+22, GBSB21, GBB+11, Jam13, MDM13, NTCO07, SB09, SBY12, THH+19]. **Designs** [GK08]. **desired** [HPH+15]. **Detect** [HK12, YLC20, YWW20, YBGB10, ZSZ+22, ZYF+18, LLL16a, SSML15]. **detected** [AAG+18]. **Detecting** [ALQ17, ABVD12, AALD17, FSP23, GZYL22, HLHAJ20, HYL+19, JLYZ16, KSM14, LZ18b, NNW24, NVSH18, OYDZ15, RH05, SXW+24, SVE21, TWG+12, TBRS11, UJ09, WZR+22, YSGZ20, ZXLZ18a, ZXLZ18b, ZRK19, ZWL+14b, ZJW+22, SSS+15, ZZ15]. **Detection** [ARM+19, ACP22, AHN23, ACJP23, ACJ24, AGGM11, AAT20, BBN18,

CW09a, CWL12, DSM23, DADF+10, FYZ+19, FMD18, GLL+18, GAH22, GDWK+15, GZN21, GAX+23, GPC+20, HLL+18a, HGC+20, HTLL12, IGM+07, IC23, JGKP21, KHI+21, LGW20, LWW+21, LZM22, LXC+24, LL19, LCGW19, LYY+19, LZW23b, LGB15, LCB17, LTX21, MYCW12, MLZ+24, MMBC22, MB20, MGP+23, MPQY19, NSC17, PCK19, PFGDCRM22, QDZ+21, QZD+22, RHAK13, RNAR+24, RHZ+24, RB14, Shi10, SIK20, SCM19, SLCL22, TWW+20, TP18, WS12, WWF+21, WHW21, WZS+22, Wer06, WOYL17, WKZ+24, XGWW19, XDZ+23, YYLL22, YXL+23, YC08, YXZD21, YLBX21, YYX+21, ZANN20, ZLW+11, ZmCXS17, ZLS+21, ZZLH23, ZGW+24, ZHX+24, dNG17, CBN15, DGRC15, GBTL14, HWK14, LWM14, MMFD14, PS15, SB16, SXL+14, Vog15]. **Determination** [BRZ+17, BKR11, JS23b, WL07, DST+15b]. **Determine** [GCC+22]. **Determining** [AAF+13, HHC+24, Tah14]. **Developing** [SWX+19, XYYZ20, XLX+21]. **Development** [AM22b, Che12, HSS18, MMH15, TZH07, YJJW21]. **Devices** [GTTR+17, ZSZ23, MKARB16]. **DFseq** [YWW20]. **DFT** [NSMH19]. **DFTNet** [CXY+23]. **DGANDDI** [YLS23]. **diabetes** [GJK15]. **DiaDeL** [ALC22]. **Diagnosing** [HC16, WW19, XTO+24]. **Diagnosis** [BBN18, CZL+22, GT24, GYW+24, GTL+24, HSZ+23, HWZ+23, JWW+24, JHZL19, MT24, OW20, PTH+18, QRT+23, WSJ21, YGJZ23, YOKI09, ZHSS07, ZLL21, GJY+14]. **Diagnostic** [WQLL23]. **Diagnostics** [Ano12a, BDP11, YZL+22]. **Diagonal** [YHCS19]. **Diagrams** [YNBM05]. **Diameter** [HZR+19, HSlSM11, GE15]. **Diameters** [GPE17, GE18, GET21]. **Diazoxide** [WLCX18]. **dibenzopyrrole** [KPB14]. **DICLENS** [MA12]. **Dictionary** [KBSCZ12, PYL+21, TDZZ24]. **Difference** [CKL+23, JRSS18, ME19a, ME19c, WL19, DWZ+15]. **Differences** [vBdRD+11]. **Different** [DPS+13, HLL+22, RTC23, ZWL14a]. **Differential** [CHW+18, CBK20, CZM+18, HWY+23, LEAK11, LL11, LW19a, LYY+19, MSS19a, NI07, PZC+23, RCP+18, SdOD+12, WW22, YWW20, ZZY+17, dJP08, ABS17, BMM14, HLW15, ZSY+14]. **Differentially** [AAP06, EAS12, HHSC13, LLCC21, LXG+16, LWG+18, PS19, SDTK19, WS12, KSM14]. **Differentiating** [JLJC24, MTR+22, ZLXL19]. **Differentiation** [CBM+20, NGZ+22, ZRK19]. **Difficult** [BBCP07]. **Diffused** [WWC18]. **Diffusion** [Alt23, FZWS17, SHJL10, SWSA21, YD24]. **Digest** [BBK+07, JR14]. **Digestive** [YHW+21]. **Digital** [CCL+24, LGL24, WQLL23, ZLWF24, AIS+16]. **Dilated** [GHZ+22, LXL+21]. **Dimension** [ST05, ZHD+21, YTLL15]. **Dimension-Fusion** [ZHD+21]. **Dimensional** [AAKB22, Che10, CHC+05, DZA+06, GC22, GAX+23, HDS+18, HL21, LHL+19a, LTaS13, LN13, NPBD16, PL17, SWL19, VJRPNVJG24, WWLL16, WRH+09, WWL+17, ZMT13, ZD17, ZZZW19, ZWLZ21, ZZGL24, ZKL18, BF14, Qiu14, YN14, ZMC+14]. **Dimensionality** [LRM08, YLC20]. **DinoKnot** [NCJ24]. **DipC** [WCLY20]. **Diploid** [KWL07]. **Direct** [SZL+20]. **Directed** [ARS17, PPZ12, Zha18]. **Direction** [HYL+19]. **Directional** [ZS19]. **Directions** [SXW+24]. **Directly** [GJSB23]. **Dirichlet** [CGZ15, PRZ+14, RdlCGW09]. **Disagreement** [MW20]. **Disambiguation** [HVD18, HWK14]. **Discloses** [AAB22]. **DiscMLA** [ZZH18a]. **Discordance** [PT09]. **Discover** [MSZ19a]. **Discovering** [AOSN+18, ACP10, BHS+04, KN05, LSTW+17, LLH+07, LNC+05, MPF12, NTL+22, OHK+21, RB16, RM18, RA16, SLCZ22, SC22a, VJRPNVJG24, WHWP12,

WSTL+15, XL16, YSBB22, YJ22, YNBM05]. **Discovery** [ANR11, ABS17, BMSZ22, Bha23, Bi09, BD19, BVN+11, CZW+23a, CLST+13, CHK17, GXSZ17, GCB+18, Han10, HSZ+23, JL10, KL19, KC11, KZ10, LDS+07, LHL+19a, LMPT15, LCLL10, LCW+18, LT07, MYLS24, MLZ18, PWT10, PZH20, RLV04, RSV+22, SKDA19, SS04, SGP+20, SLCL22, TP18, UBP+19, WLCP11, YAB13, YYG+21, YLY+12, YFY+22, YNN+18, ZDL12, ZZ18, ZZN+11b, ZMC+14, ZAZ11, pD20, CWDS15, CA14, FWY+15, JZCZ15, KGF+14, OFC+14]. **Discrete** [CWZ08, ED15, GPZ20, HGM18, LCW+18, PTM+19, SH11a, WZ13b]. **Discrete-State** [SH11a]. **Discriminant** [FWY19, NO09, OG11, PYL+21, WYHD17, YLXJ04]. **Discriminate** [HXS+21, THH+19]. **discriminating** [SQZA14]. **Discrimination** [AKA+22, KCY+24, KBM21, DI15]. **Discriminative** [CGL+23b, GZN21, KC11, hLMBJ11, LZS23, SC22a, YFYW23, ZZH18a]. **Disease** [AHN23, AKH+23, BKKG19, CLL+21, CZW+23b, DHCW18, DMK22, GT24, GWW+22, GRK23, GSC17, GZYL22, GCC+22, GTL+24, HZW+17, JBgLS19, JY21, JZZQ19, JQGY21, JHZL19, LWL+18, LRR08, LTP22, LWW+21, LZX+21, LXWL22, LWXX22, LDZL23, LXS+24, LZHZ17, LWT+18, LWZ+21c, LJN+23, LLZ+22, LDL+17, LTRW19, MZLL22, MS17, MT24, MSB19, MLFM22, MGP+22, MCM22, NLW+24, NWZ+20, OW20, PSA21, PZC+23, PLD+23, PCD+23, PBV+20, QLZ16, QDZ+21, QQD+21, QBPEL12, RNAR+24, SSK+20, SZD+23, SXW+24, VBG+18, WLCX18, WXY+23, WLP23, WHL+24, WCMB19, WLA+13, WCX+22, XZG+23, XPH12, XW16, XDZ+23, YDW+20, YDW+21, YGJZ23, YG19, YYY+22, YWL+24, ZLLZ17, ZLH+20, ZLF+21b, ZWS+18, ZZCD19, ZZRPZ19, ZLG+21, ZCL22, ZZY+22, ZLZZ23, ZYW+21, ZYN+19, ZYZ+23, JWG+22, LWY+23, LKD23, YWN+19, YD24]. **Disease-Associated** [GWW+22, GZYL22, LDZL23, LDL+17]. **Disease-Gene** [ZCL22]. **Disease-Related** [JZZQ19]. **Diseased** [DPS22]. **Diseases** [AHC+21, BMR21, CC21, GZC+17, HC16, LTLL23, TP18, YWN+19, DWZ+15, LLRZ15, TYL+16]. **Disequilibrium** [LLC+13]. **Disjoint** [DNS19]. **Disorder** [LTW+22]. **Disordered** [FHDU22]. **Disorders** [GSC17, SVdSS+18]. **Disparate** [QKÖ18]. **Displacement** [SJWW23, ZWZZ22]. **Disrupt** [GED+17]. **Disruption** [HK20]. **Dissect** [WLHY19]. **Dissecting** [KDS+20]. **Dissimilarity** [FB19]. **Dissipativity** [YLZW21]. **Dissipativity-Based** [YLZW21]. **Distance** [AKNB07, ABO+23, AS05, ANR+23, BFK17, BG12, BS10b, BHP19, BODD20, BAO+23, BJ13, CZW+23a, CHNW20, CWZL08, DS14, FM11, GRS+13, Lab06, LTM+13, LTT+22, LJZ+24, MTH22, Pol12, RFB20, SGC07, SBDD21, SWH+12, WM19b, WSB21, WZ13b, XCR21, YPL+23, ZOMC24, ZZY+17, ZWM+20, ZSC+10, ZW13, dSMDB17, DNR15, TSM14]. **Distance-based** [DS14]. **Distances** [BPV+11, GJSB23, JZSZ12, LTLTS23, OP11, WL19]. **Distant** [JZF+21, VSKJ11]. **Distillation** [BYZ+23]. **Distinguishing** [AD12]. **Distorted** [Mos07]. **Distributed** [BHP19, GZR+18, LBL+10, PFJ+19, PNA20, PSN+15, RTPM+19, SSD19, WWC18, GFG16]. **Distribution** [ASI+11, BS09, DADF+10, Gru11, LKK+23, LLH+17, MT12a, WLL+20, YWW20, ZLS+21, ZZP+21b, ZXJ+23, DWZ+15]. **Distribution-Free** [YWW20]. **Distributions** [APPG18, LTM+13, PPFG20, SZZ+19, SHUP19, WM19a]. **Disturbance** [LL11, LLL16b, YM20]. **Disturbances** [YLZW21]. **Disulfide**

[YLH+15]. **Disunited** [SSS20b]. **Diurnal** [KM20, WGP11]. **Divergence** [EW04, ZZS18]. **Diverse** [LSB+11, PKM22]. **Diversity** [ATO22, DZMB22, FWY19, MPKvH09, SNM08]. **Divide** [KD15, LL22, OC13, SR10]. **Divide-and-Conquer** [LL22]. **Dividing** [SWSA21]. **Division** [XSL+21]. **Divisive** [MA12]. **DL** [RTC23]. **DL-m6A** [RTC23]. **DLBCL** [WWC18]. **DMBIH** [YGFC20]. **DMFLDA** [ZLF+21b]. **DMFMDA** [LWZ+21c]. **DMVO** [CIZ+22]. **DNA** [ASJ+07, AAB22, BMCY22, BAO22, BTYC13, CIZ+22, CFOS06, CLST+13, CW09a, CH11, CLZ+18, CWLS15, CLS19, CL08, CAN+08, DCHW17, DH23, DSVMM18, DPW12, FPC20, GZGX14, GKPS11, GZWD23, HEK18, HHSC13, HG16, HLZ+17, HLH11, KCD+12, KC11, KBSCZ12, LSTW+17, LPH18, LLH23, LLW+11, LZL+20, LZL+22, cLWA07, MGL+12, MRK18, MS21, MMSH14, NNW24, NVSH18, NTL+22, PKRD12, PG12, PGF18, RLV04, RG16, SSS20b, SLRQ19, SIK20, SJWW23, TDA+09, TSM14, UJ09, WZZ+18, WP08, WSTL+15, WLPW16, WW19, YWCC22, YF23, YZH+23, ZZH19, ZLL+20, ZZBH20, ZCL21, ZYH+21, ZWHH21, ZSH21, ZZW+22, ZXW+23, ZSZ23, ZLX+20, ZZDY13, ZWZZ22, ZL15]. **DNA-Binding** [DH23, MGL+12, ZCL21, ZLX+20, ZZDY13]. **DNA-Protein** [ZYH+21, WP08, ZZH19]. **DNA-Sequences** [MS21]. **DNA-Versus-Protein** [YF23]. **DNAzyme** [EES14]. **Dnmt3a** [LGN+19]. **DNN** [QZL+22]. **DNNs** [CZDZ22]. **DNRLMF** [YWN+19]. **Do** [RRTB12]. **Dock** [ADPH13, BCS11]. **Docking** [ADPH11, ADPH13, BCS11, GED+17, LSL+22a, LSB+11, PSN+15, SZ11]. **Document** [ZZY+22]. **Document-Level** [ZZY+22]. **Documents** [AC12, KAHK+10]. **Does** [BCVS19]. **Domain** [CYJ+19, JGW+21, JGKP21, KCP19, LB19, LNW20, LLL+23, MB23, SDP+21, WZC+21, WWT+20, XNYC21, YPL+23, ZJW+22]. **Domain-Gene-Species** [MB23]. **Domain-Residue** [YPL+23]. **Domains** [HMK+07, LDS+07, MB23, QLZ16, WCMZ15, ZHZ+20, DC15, PWC+15]. **DomBpred** [YPL+23]. **Dominating** [ZWW17]. **donovani** [SSP+17]. **DORMAN** [OSA+21]. **Dose** [SWX+19]. **Double** [HLGS21, SZCX19, YCY+14, YLS23]. **Double-Sparse** [HLGS21]. **Downhill** [SS04]. **Downstream** [SPW22]. **DP1** [IDD13]. **DPNuc** [CGZ15]. **Drawing** [Hus09, SNM12]. **Drawings** [VASG10]. **drift** [SPWF14]. **Driven** [AAKB22, CSW11, CCE19, FMA+20, HLY+16, HSZ+23, JQGY21, MRB+24, PLC+20, RGB+21, RRD+23, Sef22, YCCM12, ZHG20, ZM22, GBTL14, KG15]. **Driver** [LGW20, LDYZ22, LWD+21, SPW20, SPW22, YYG+21, ZZ18, ZW19, LP15, LWM14]. **Driving** [WHW21]. **DRLM** [FZNZ23]. **Drone** [JQGY21]. **Dropfeature** [CZDZ22]. **Dropfeature-DNNs** [CZDZ22]. **Drosophila** [GGH+13, LK11, LJK+12, LLYS21, LLDÁ21, MBJ19]. **DrPOCS** [WCQ+19]. **Drug** [Ale22, BD19, CCCY20, CNO+23, CLYR23, CZC+23, CYWW22, CCN22, CNH+23, DLO+23, DTA+23, DCM20, EZW+17, FZNZ23, HLN20, HXS+21, JQH+20, JZYL24, KCP19, KHP12, KS18, LC19, LWZ+21a, LWL+22, LXS+24, LZC+23, LWL+19, LWY+21, MWZY17, MYLS24, MCM22, NNNL22, NNLT22, NVL22, NQNT23, PRP21, PKM22, PSIM17, PCCM22, PLTG22, QZD+22, QZA+23, RV13, SK21, SZ11, SYKS15, SSP+17, SWX+19, UKC+23, UBP+19, UKV18, WLCX18, WCQ+19, WXWL20, WDL+22, WLWJ22, WLP23, WLW+23a, WYS+24, XYZ19, XHW+22, YDZ+22, YZC+23, YSBB22, YZL23, YJ22, YLJY21, YLS23,

DWSB11, FVP+20, FSB+11, GZG17, GK19, GD22, GAGM11, LHL+19a, LLK+21, MW16, OG11, OP11, PNA20, PVB+12, RMV12, RSJK13, Shi10, SBY12, TGLP16, WYY+13, WLCP11, WL19, WXS+19, XWC15, YXYC13, ZCG+18, ZLG+21, ZS19, ZL15, dAc17, GJY+14, ZLLS17]. **Fast-Adaptive** [ZCG+18]. **Fast-Known** [SBY12]. **Faster** [BAK06, CW07, CHNW20, HC16, SN12, SB09, WS21]. **FastEtch** [GK19]. **FASTQ** [How13, GDM12]. **FastR** [ZHEB05]. **Fatal** [CDBR21]. **Fatigue** [WHW21]. **Fault** [BBN18]. **Faults** [CCN22]. **FC** [YWW+18]. **FEAST** [HB11]. **Feature** [AWW18, AMHH16, AAT20, BM17, BMSZ22, BHP19, CXY+23, CZ20, CWCJ21, DPS+13, DM22, DPA+17, GZG17, GCB+18, GZWD23, HZZY16, HLL+18a, HBC+11, HDS+18, HLGS21, HLX+21, KCD+12, KWP+23, LTM+12, LHLY11, LSY+20, LJL+15, LLZ+20a, LZX+19, LZX20, LPH+13, LHH19, LTW+22, LLZ+22, MP22, MLFM22, MCHT17, NO09, PGHT12, PWY+21, PLD+23, PBhL+11, RSK23, SLX+18, SIM12, SDH20a, SGP+20, SZLL11, TZ16, TRKRC13, WZA07, WYHZ20, WCLY20, WZS+22, WCDM23, WZJS23, WXS+19, YSC13, YM11, YZG+19, YXS16, YH13, ZHL+24, ZWSX12, ZLPW16, ZwGC17, ZZZW19, ZWM+20, ZYJ+23, ZLZZ23, ZWY+10, ZCWW19, dSPFF21, BCLC15, GMCB14, HRHP16, LZGZ14, WFD15]. **Feature-based** [ZWM+20]. **Feature-Integrated** [LZX+19]. **Feature-Sensitive** [WZS+22]. **Featured** [CLW13]. **Features** [AD12, AHK+21, BYZ+18, BOSF24, BS10a, CZCL23, CZL+22, CHW+18, FLW12, FW20, HC17, HLZ+17, JY21, KTLM15, KKPP22, KAHK+10, LLX+16, LHZ+19, LZQ+20, NBGL19, QZL+22, QWC+16, SKS22, SPL+23, TZWZ23, VF09, WB11, ZZCY10, ZKW19, ZMKL22, ZZDY13, dSPFF21, DPL+14, GJPSV14]. **Federated** [LXC+24, MYLS24, SAM+19, SAS+23]. **Feedback** [BSV10]. **Feedbacks** [LCH19]. **Feedforward** [BHS21]. **Few** [CJH+21, GM22, LCTW24, TGP+15, WCX07, WLL+24]. **Few-Shot** [CJH+21, LCTW24, WLL+24]. **FGFICA** [CZCL23]. **FHAST** [FVLN15]. **fibers** [SXL+14]. **Fibrosis** [HEE+18]. **Field** [WWL+17]. **Fields** [RXAH+23, ZHE19, DGRC15, GGZZ14]. **Fifth** [MVVR20]. **Filaments** [CMC+12, BLR15]. **Files** [GDM12]. **Filling** [JZSZ12, LJZZ13, LHH19, LWS+20, MJZY22, ST19]. **Filter** [FLAM15, HKT+18, JSS+18, LTM+12, LH10, LHQ+18, MNND13, HPH+15]. **Filtering** [GMAS22, KAP+12, LX21, MJPP20, SP11, WLL+09, XSL+21, YLZW21, ZLH+20, pD20, HPH+15, SB16]. **Filters** [BHHMCL16, SBY12, WZJH12, XLZ+15]. **Filtration** [GBSB21, KNR05, TC16, LMZ14]. **Final** [Gus09a]. **Find** [ZSZ+22]. **Finder** [CXS15]. **Finding** [AAP06, AKMT12, ATX21, BvBF+11, BLS12, CMR19, DT11, GÁVRRL15, HLH11, HKM+18, IVA11, KVX12, LLR+23, hLMBJ11, LHL+19b, MIC+07, MDMR+22, NYOL15, PG06, PRU11, RHH16, RSJK13, SPW22, VSKJ11, WL11, Wan12, WCMZ15, XCR21, ZSC+10, SSKH15]. **Findings** [WWC18]. **Fine** [DSHM08, YWL+24, ZWcF17]. **Fine-Grained** [YWL+24, ZWcF17]. **Fine-Scale** [DSHM08]. **Fingerprint** [KKI20]. **Fingerprinting** [LZ18a, dAc17]. **Fingerprints** [KAS21, ST23]. **Finite** [FZWS17, JKNE21, EES14]. **Finite-Set** [JKNE21]. **Finite-Time** [FZWS17]. **Fireworks** [ZZZC17, ZLJT17]. **First** [Tho16]. **Fish** [LYW20, WWF+21]. **Fisher** [NT24]. **Fitted** [KSLW23]. **Fitting** [FKLS07, SHUP19, TSMMG+13, SXL+14].

RTD23, SZCX19, TDZ+24, VTMG22, Val11, WYHD17, WLG+21, WWL+23b, XWQ+24, YRD+13, YFWZ16, YWF+20, ZD12, ZWG+21, TYA15, WHZ14, XG14, YRD+14a, YRD+14b, YRD+15].

Functional [BCY+22, CNM11, CHL+12, CM16, DSZ+06, GT24, GLW12, GPC+20, JLYZ16, JZW+22, Kar12a, KNS+05, KL11a, KCY+24, KKPP22, KK12, LFK16, LLH+07, LHHL19, LKL+23, LWD+21, MS17, MFS+15, MFF+18, MBB+17, SKDA19, SNK+22, Tah18, TFTY23, WMK16, WLCP11, WWL19, WLHY19, WWBZ19, YNN+18, ZD12, ZZN15, ZZGL24, ZS19, DC15, JC15, LLL16a].

functionality [WL14].

Functionally [MP13, PB19, Yan22, SFH+14].

Functions [AM12, DTA+23, DLA+23, DM09, LSZ+23, MSKC19, MPM11, PLCW17, RMV12, Tah18, WP08, YSGZ20, ZZF+19, AM15].

Furious [LLK+21].

Fusarium [KZW+18].

Fused [ACP22].

Fusing [DPS22, NLGG12].

Fusion [CMMZ20, CLL+21, CGL+23b, CZCL23, GTL+24, HLX+21, HTZ+23, JXN+16, KZ10, LLZ+20a, LZW+23a, NNLT22, PLTG22, QWC+16, WZZ+22, WCDM23, WYS+24, WWT+20, YM11, YZP+21, YYY+22, ZHL+24, ZHJ17, ZZW+22, ZXJ+23, ZHD+21, ZYZ+23].

Future [QZA+23, SXW+24].

Fuzzy [AGAS18, AFAAW+11, BMZM15, JXN+16, JGW+21, LHKL17, MP13, NPD+17, NNM+12a, PKM06, SY09, SKD+07, SBM15, TNQ08, YCCY20, YCY+13, ZZP+21b, GRDV14, HC14a, YCY+15].

Fuzzy-Adaptive-Subspace-Iteration-Based [SY09].

FVS [GAH22].

FVS-Based [GAH22].

G [BAO22, JCG+22, LBQ+13, MZLL22, WCLY20, WLG+21].

G-DipC [WCLY20].

G-Quadruplexes [BAO22].

G4detector [BAO22].

GA [MWSM12].

Gabor [MCCZC08].

Gabor-Wavelet [MCCZC08].

Gain [AC12].

Gait [WFY21].

Galled [CLRV11, Son06].

Galled-Tree [Son06].

Game [LQV+13, MEOL14].

Game-Theory [LQV+13].

GaMRed [MJPP20].

GaMRed-Adaptive [MJPP20].

GAN [YCX+21].

Gap [LNR+09, LWS+20].

Gapped [CWC04, CZ20, WS08].

GapReduce [LWS+20].

Gaps [COW20, GGP08, ST19].

Gastric [HSZ+23, MBP+19].

Gate [Kar12b, LJ20].

Gated [SDH20b, ZJ23].

Gating [JLW17, Qiu14].

Gaussian [BEQD19, KDS+20, LLDÁ21, NFM+12, RXAH+23, YBGB10, ZFH+21, ZZLH23, ZC11].

GBM [PL17].

GBM-Related [PL17].

GC [RKDR10, TSM14, WLL+20].

GC-content [TSM14].

GC-contents [WLL+20].

GCNA [YLC+23].

GCNA-Cluster [YLC+23].

GCNPCA [LKD23].

GCNs [LLW+22].

GECC [RHK14].

GEFA [NNLT22].

gEFM [UAH16].

Gelsius [AAF+13].

GenCoder [SN24].

Gender [YCZ+18].

Gene [AAKB22, AJD+12, ASP20, AMGC16, AKNB07, ARK20, AM22a, AOSN+18, ADR18, AWW18, AKV16, AMHH16, ABS17, ACWW05, ACWW07, APPG18, BGHC20, BM17, BE08, BEW09, BS11, BVS+22, BGS+12, BDP11, BHMA06, BCL+13a, BA18, BHS21, Bon07, BLR08, BIBD21, CCCY20, CDB+16, CDW12, CHWY19, CMMZ20, Che10, CM16, CPM18, CWZ08, CKL+23, CHZ+21, DLT10, DGH+06, DRS12, DZH16, DCHW17, DLA+23, DYZC22, DKDD10, DHC12, DBK18, DSCM20, DPS22, EAS13, ED15, FWXZ19, FKB19, FLAM15, GZG17, GTX+23, GMSD11, GDM18, GE15, GE18, GSC17, GHL05, HL16, HYW+17, HBH12, HXXJ18, HRAGS+23, HHYH07, HMW+12, HWK14, HLY+16, HC16, HC07, HF12, HTLL12, HWY+23, INT11, IGM+07, IQA18, IBN19, IL18, JCF13, JZS+18, JS23b, KBNHD18, KBND19, KSN+12, KN05, KP12, KSP22, KG12, KCCC15, KCP18, KKK19, KB17].

Gene [KB19, KK12, KKP+21, LCEMO18, LEAK11, LTM+12, LTM+13, LSM+21, LBM+18, LRM08, LLH23, LH10, LJK+12, LLHF15, LCZN16, LW17, LDM18, LB19, LPH+21, LWXX22, LDZL23, LZH18, LJL+14, LX21, LNC+05, LHDS18, LW19b, LYY+19, LLK+21, LDYZ22, LZS23, LLL15, LLA19, LGYW21, LLT+19, LHY+11, LCC+11, LTRW19, MNR09, MLZ+24, MTSCO10, MSS19a, MSJP19, MB20, MPP+20, MT11, MWZ+20, MNLF+22, MZL15, MPM11, MDD18, MB23, MW21, MBF+11, MSG18, MG19, NRV09, NPK+07, NGZ+22, NI07, NSNN12, OHK+21, ÖBT21, PGHT12, PLH22, PI09, PA22, PYL+21, PCD+23, PBV+20, PCDP18, PG06, PAAG07, PKM06, PKA20, QD12, RM13, RC11, RdlCGW09, RXAH+23, RMV12, RRTB12, RWH+10, RMS15, SBOA23, SSS+11, SSK+20, SMK22, SCSS05, SMRP15, SSP+05, STO06, SIM12, SDCW11, SV16, STB+19, SPA17, SKD+07, SPW22, SZGZ21, SW09, SGK12, SPL+23, TIA+11, TAAP11].
Gene [TZH07, TGGF10, TFTY23, THL11, TK05, TWZW16, TOYHZ19, UC10, UKV18, Val11, VRK12, VRJ+10, VF09, WZA07, WLL+09, WL11, WKLL12, WLG+16, WLCX18, WWL19, WLHY19, WW22, WDL+22, WRH+09, WP08, WWC18, XHQ+18, XWQ+24, XAW07, XOYHZ18, XLP+21, XYLL23, YLC20, YWW20, YLC+23, YLXJ04, YNBM05, YHB12, YLY+12, YWF+20, YLW+24, YCCM12, YGY+19, YNN+18, YOKI09, ZZKW18, ZLZ06, ZHSS07, Zha11, ZWSX12, ZZN15, ZLH+17, ZXLZ18a, ZXLZ18b, ZZS18, ZWHC19, ZXZ20, ZSZ+21, ZCL22, ZYX+23, ZZLH23, ZGW+24, ZACS09, ZWY+10, dCAR11, vBdRD+11, BM14, CZWT15, CM15, DYD15, DR14, FN14, HZZT14, JR14, JC15, LXZ+15, LLH+14, MM14a, MM14b, PJN+14, RHK14, RHH16, WLY14, WDX+15, XLC+15, YCY+14, ZZ14].
Gene-Duplication [BE08, BEW09, BS11].
gene-environment [LLH+14].
Gene-Expression [CCCY20, UKV18].
Gene-Gene [ASP20].
Gene-Mediated [LWXX22].
Gene-Module [MB20].
Gene-Species [MSG18].
Gene-Specific [SZGZ21].
Gene-Team [WKLL12].
Gene-to-Class [HYW+17].
Gene-to-Gene [GHL05, LNC+05].
Gene/Protein [ED15].
Genecast [GTTR+17].
GeneChip [MSH+11].
GeneChips [LUdSCH10].
GeneNetFinder2 [HL16].
GeneOnEarth [TSMMG+13].
General [AHK+21, BCY+22, SC11, WKLL12, Wan12, YP13].
Generalizable [YZL+22, TAL+15].
Generalizations [CLRV09a].
Generalized [AAT20, BBN19, BSLR05, HHSC13, JMA17, ZACS09, ZAZ11, FN14].
Generalizing [MB23].
Generate [YLCC13].
Generated [ZZS18].
Generating [GLYZ21, PCGS05].
Generation [BBN18, FS13b, KCD+12, KMS+21, AKD17, LHLY11, LL22, PNP+18, PSC20, WPL15, YSC13, YWW+18, CWLZ14, KD16].
Generative [MYLS24, XWP+24, YLS23, ZDL12, ZZDW13].
Generator [HLG10].
Generators [ZWZS16].
Generic [BVN+11].
Genes [AAF+13, AAP06, BGHC20, BRF17, BSS+22, CZF+05, CHN+18, DZH16, DG19, EAS12, EFLA08, FFT16, GRK23, HAH13, JZZQ19, KCP18, KM20, LFK16, LTM+13, LLX+11, LGW20, LDZL23, LLCC21, LZX+19, LXG+16, LWG+18, MP13, MS17, MMH15, MB23, MTR+22, PS19, PWT10, PL17, PZH20, RYK+19, SSS+11, SBW15, SRM18, SBDD21, SPW20, SDTK19, TFTY23, TZY11, WS12, WCX07, WGP11, WZC+21, XPH12, XZS+21, YFY+22, YLW+24, ZLLZ17, ZLH+20, ZOZ10, dSPFF21, CBN15, DI15, KSM14, KKC+14, LWM14, MFS+15, SKK14, Tah14, WFD15].
GENESHIFT [LTM+13].
Genetic [AGAS18, BMK11, BvdGK+11, CSW11, CL15, CAN+08, DSHM08, DM22, FZWS17, GPZ20, GZFT15, Gos11, GJZH17, GTL+24,

HYR+19, HCLS11, JSA08, JSS+18, JZS+18, KSMT19, KB20, KN05, LL11, LLZC12, LTLL23, LWZ12, LGYW21, MTNH17, MLFM22, MIC+07, MDH11, MWSM12, MVW+13, NJMF19, OMAdG+12, PB12a, PI09, PWY+21, RKDR11, Sen19, SWSA21, SVE21, Tho16, TSMMG+13, TED+12, TBRS13, VMZM17, VKS17, VBG+18, WFY+19, WAG19, WCL11, XWF07, YCYC12, YLCC13, YAB13, YLZW21, ZLH12, ZWZ16, ZZGL24, ZSD08, dJP08, ADTAQ16, CL14, HRHP16, PV16, RHH16, TYL+16, WLY15, ZWC15]. **Genetics** [DLY+21, SLH06b, ZFH+21]. **Genome** [AKH+23, AP07, AJM18, ANT19, BGS+12, BMM06, Bha23, BAO+23, CZF+05, CHN+18, CCF+24, DGV+17, DWSB11, FLW12, FM13, FMA+20, FS13b, GZFT15, GSK13, GJZH17, GZC+17, GCY+21, HKS11, HWS+18, HBM19, KMSY20, Kim18, KSLW23, LN17, LW19a, LZW20, MSS+13a, MPA15, NPK+07, NTL+22, PIPC18, PS11, RZMC17, SKS+19, STHA15, SBDD21, SSS13b, TGLP16, TIA+11, TGP+15, Val11, VTGC16, WYY+13, WGL+21, WHZ14, XLX+21, XHY+18, YFY+22, ZZCY10, ZZS18, ZCL21, ZLZ20, ZAZ11, ESW14, LHS16, SVM14, TYL+16, WLC+15]. **Genome-Based** [KSLW23]. **Genome-Guided** [FS13b, TGP+15]. **Genome-Scale** [CCF+24, DWSB11, GJZH17, MPA15]. **Genome-Wide** [BGS+12, DGV+17, FLW12, GZC+17, KMSY20, LW19a, LZW20, NPK+07, NTL+22, PIPC18, SKS+19, TIA+11, Val11, VTGC16, WYY+13, ZZCY10, ZAZ11, WHZ14, TYL+16]. **Genomes** [BCF+07, DS21, GK19, HCMB18, LHL+19b, LSL22b, MS10, NLHL17, QLLX10, QTZ15, XZG15, YBGB10, ZOMC24, ZHEB05, BS15, CA14, RB14]. **GenomeTools** [GSK13]. **Genomic** [BBH+18, BKP+19, BOSF24, BKLS18, CKM+17, CHL+12, CZCL23, CHW+18, CBZ18, CRK+19, DHCW18, DMJ+18, DBTB09, FM12, FLM+16, GRS+13, GC22, HYL+20, HYC12, HCQ14, HL21, KPK+17, LTX21, LLY+23, MWL+12, MCC16, OLS+13, PHX+08, PG18, PWT10, RCP+18, RTPM+19, RH05, SN24, SHUP19, WMWA12, ZZZW19, dSMDB17, GMCB14, SSKH15, XLWL15, ZMP+14]. **genomic-range** [SSKH15]. **Genomics** [AN21, DN22, KNS+05, PR18, RCM+19, SNK+22, SPD24, WHF+20, WKSP21, YNN+18, CW22]. **GenoPri'16** [AJM18]. **GenoPri'17** [ANT19]. **Genotype** [CCE19, DLM12, GMP08, MRB+24, PVB+12, YLCC13, ZPW+19]. **Genotype-Phenotype** [ZPW+19]. **Genotypes** [HYL+20]. **Genotypic** [HXXJ18]. **Genotyping** [Che16, QBPEL12, YCYC12]. **GenSeq** [WGL+21]. **GENSIPS** [HCQ14]. **Genus** [AM22b]. **Geodesic** [BPV+11, OP11]. **geodesics** [Nye14]. **Geographical** [DZMB22]. **Geometric** [DM09, FSDR16, BCLC15]. **Geometrically** [KL19]. **Geometry** [LLES18]. **Germ** [AAB22]. **GeRNAMo** [MIC+07]. **GERWR** [ZJZ+24]. **GEVD** [TDD14]. **Gibbs** [AM19]. **Gibbs/MCMC** [AM19]. **GIFDTI** [ZDZ+23]. **Gillespie** [BU17]. **Give** [BCVS19]. **Given** [WMS09]. **GIW** [ESW14, Kim18, STHA15, ZLZ20]. **GIW/InCoB** [Kim18]. **GIW/ISCB** [STHA15]. **GIW/ISCB-Asia** [STHA15]. **GLAlign** [MGC19]. **GLassonet** [LZS23]. **GLBIO** [MJ18]. **Gleason** [XPH20]. **Glioblastoma** [CHW+18, ZLPW16]. **Glioma** [TB23]. **Global** [ARP+16, DBN18, ECK16, FZM15, GPMH16, HSS18, HOS+12a, HOS+12b, HGM18, LLL+21a, MQOH21, ST23, Tsa12, WQY18, WLWJ22, ZKW19, ZDZ+23, ZYF+18, XXM+16]. **Global-Local** [ST23]. **Globally** [ZWZ16]. **Globe** [TSMMG+13]. **GLProbs** [YlCW+15]. **Glucose** [RTA+16].

[XXW+23]. **Hyper** [PTH+18]. **Hyper/Hypocalcemia** [PTH+18]. **Hyperflows** [AFMS19]. **Hypergeometric** [KPW13]. **Hypergraph** [LCW+18, LLZ+23]. **Hypergraphs** [RPB+13, RAM17]. **Hyperplasia** [ZLXL19]. **Hypertensive** [ZLZW22]. **Hypocalcemia** [PTH+18]. **Hypothesis** [BZ07].

I-Health [SRM+24]. **I/O** [HPH+15]. **i2b2** [RCP+18]. **IAS** [YKWK18]. **ICD** [HXXJ18, LFZ+19]. **ICD-9** [LFZ+19]. **ICGA** [SSS+11]. **ICGA-PSO-ELM** [SSS+11]. **ICIC** [HBG16, HBG20, HBG21, HHA22, HBG17, HBG18, HBG19]. **ID** [Jam15]. **Identifiability** [AR09, APRS11, Wig15]. **Identifiable** [PW21]. **Identification** [ALQ17, AGGM11, AN21, BBN19, BGHC20, BVS+22, Bha23, CWZW15, CFOS06, CYJ+19, CDW12, CMQ+16, DMD13, DABV17, EAS12, FJJ11, GGJ+06, GRK23, HYY11, HC18, HC19, HZL+20, HHYH07, HC13, JXN+16, JRN+18, KCCC15, KKPP22, KSK+18, LLNW17, LZ18a, LHHL19, LMZ+20, LPH+21, LWL+21, LLX+23, LLT10, LMZL17, LSL22b, LWD+21, MRB12, MMC+23, MTSCO10, MP22, MS17, MSB19, MCCZC08, NRV22, NZM22, NWW19, Ozy12, PB19, PS19, PM20, PWZW15, RBB+19, RTA+16, RTC23, RYK+19, SSS20b, SSP+17, SFH+14, SBY12, SLL+19, TGK13, THL11, WGP11, WLWP12, WZJS23, WLW23b, WCMB19, WDS+12, XLWL15, YMW+12, YFYW23, YFCM17, YCZ+18, ZLC+21, ZYX+23, ZOZ10, ZZDY13, GM14, WLG+14]. **Identifies** [LLCC21]. **Identify** [AHK+21, HHSC13, KM20, LYW20, LXG+16, LHC18, MMH15, NHH+17, TWZW16, XLW20, Yan22, YLW+24, ZZP+21a, KKC+14, SQZA14]. **Identifying** [BRS18, BCC+23, CCCY20, CSK+11, CGZ15, CWP+23, CZW+18, DCHW17, DG19, DKS+15, FSNF21, FWW+22, GGZZ14, HYR+19, HXXJ18, HSZ+23, IMA13, JWZ+20, JZW+22, KSN+12, LW18, LZL+20, LZX+19, LLTC19, LQW+23, LP15, LWG+18, LLK+21, LZS23, MSQ18, MM14b, NLGG12, PRP21, PCL+22, PL17, PN17, QLZ16, RKZ16, SAE+20, SDN+11, SDP+21, SBW15, SPW20, SPW22, UWLH15, WDL+22, XLL+20, XOYHZ18, YAB13, YLC+23, YNWC07, ZLF+21a, ZW19, ZCL21, ZJ23, ZJZ+24, ZMKL22, ZSZ23, ZZDW13, ZDYH17, ZLZW22, BMM14, LLW+15, PWC+15]. **Identity** [NGY+16]. **Idf** [RFBTD22]. **IEEE** [HCQ14, Ano12b, Ano13e, Gus04b, Tit16]. **IEEE/ACM** [Ano12b, Gus04b, Tit16]. **IEF** [KBBD+17]. **IEF-LC** [KBBD+17]. **IEF-LC/MS** [KBBD+17]. **IFN** [ZZ13]. **IGPRED** [GA23]. **IGPRED-MultiTask** [GA23]. **II** [CLRV09b, EMDH11, FLW+14, KJ05, LJC+22, Zha11]. **II.5** [Ano09c, gCLL+10, CLM10, LS10, LMK+10, RSK+10]. **IIoT** [SRM+24]. **IL-** [LCH19]. **ILDMSF** [CLL+21]. **Illicit** [ZSZ+22]. **ILP** [BCVS19, HWS+18, KH14, WHBM15]. **ILP-Based** [BCVS19]. **ILP/SMT** [KH14]. **ILP/SMT-based** [KH14]. **Image** [CXY+23, CSW+23, DCW+24, DZD+23, DQZ+23, JGW+21, JS23b, KHI+21, LYK07, LLK+22, LLYS21, LCTW24, MCD+11, MCRC17, NU06, RRD+23, RGZ+23, WCDM23, WYF+23, WQLL23, WLL+24, XZG15, XLZW22, XWP+24, YCZ+18, ZLB24]. **Image-Based** [MCD+11]. **Image-to-Image** [WYF+23]. **Images** [ACJ24, ALR+13, BRZ+17, BdOS+18, CSQ+22, CYL+21, CZL+22, DDS+17, FZM20, GKS+22, JWW+24, LWW+21, LSW+23, LLMZ23, LXC+24, LLY+23, QZZ+21a, RHZ+24, RV06, SKS22, SYZ+13, SLX+18, SSD+16, SLCL22, SSF18, TDZZ24, UBP+19, WKZ+24, XPH20, ZHL+24, ZZH+24, ZHX+24, BLR15]. **Imaging** [BMT17, BWRF12, DHCW18, DLY+21, GTL+24, HTZ+23, IGA18, LZW21,

YHY13, YFCM17, YGY+19, ZZKW18, Zha11, ZPW+19, ZZCD19, ZLG+21, ZCT22, ZCL22, ZWDR20, ZWD+17, vIJJ+20, DNR15, PRZ+14, ZZ14]. **Inferential** [SVZ09]. **Inferring** [CLL+21, FWXZ19, FSD+11, KCZ+15, LBM+18, LTP22, LWXX22, LZHZ17, LLL15, MSG18, NI07, NSNN12, PKRD12, PNP+18, PAAG07, RGVP24, SSS13b, Tah18, TDZ+19, TOYHZ19, WLCX18, WGK16, XW16, XYLL23, ZHZ+20, ZSD08, ZAZ+22, CZWT15, LAI+14]. **Infinite** [BCVS19, Wu10, ZMT13]. **Infinite-Dimensional** [ZMT13]. **Inflammasome** [LCH19]. **Inflammatory** [WCMB19, ZZP+21a]. **Influence** [FMRS18, RSCX18, STS21, TAAP11]. **Influential** [ATA+17, BTYC13]. **Influenza** [BPJ12, ZYF+18]. **Informatics** [AM22b, HRAGS+23, Kim18, LZW21, MZ17, STHA15, ZLZ20, ESW14, SPK19]. **Information** [ABO+23, AC12, AL12, BLR08, CLYR23, CKWY12, CAN+08, DDZ+21, DGH+06, DMJ+18, DBK18, DSCM20, FPC20, GT24, GKPS11, GBS11, HYW+17, HXXJ18, HC13, HHL+20, HLG10, LLH+17, LDM18, LSY+20, LXG+16, LLW+22, MGL+12, MPA15, NLGG12, NGZ+22, PVB+12, PLTG22, RSG18, SMRP15, STY+23, SWH+12, TZ16, VTMG22, VRK12, WL07, WDL+17, XTL12c, XLL+18, XLL19, XDZ+23, XYLL23, YCX+21, YHYY12, YCCY20, YHZ+19, YLJY21, ZLF+21a, ZL24, ZM12, ZXLZ18a, ZXLZ18b, ZXZ20, ZSZ+21, ZXZ+21, ZXW+23, ZSD08, ZYJ+23, ZYZ+23, ZGB+12, BDBH15, CA14, GZGX14, HRHP16, MM14a, SLS+14, TAL+15, YLH+15]. **Information-Theoretic** [GBS11, ZL24, ZSD08]. **Informative** [LLC+13, LLZC12, LLRZ15, LLC+15]. **Informed** [MLFM22]. **infrastructures** [MKARB16]. **Inheritance** [HWPE17]. **Inhibition** [SYKS15]. **Inhibitor** [JKNE21]. **Inhibitors** [AFAAW+11, KAS21, RAA20, SDP+21, SB12, KPB14]. **Initializing** [Mai09]. **Initiation** [MVW+13]. **Initio** [HZZY16, MSS13b, WLG+21, SEC15, FXZS22]. **iNJclust** [LAI+14]. **Injection** [HC07, STY+23]. **Inner** [LTM+13]. **inorganic** [DKS+15]. **Insert** [LLH+17, ZLS+21]. **Insertion** [YXZD21, DI15]. **Insertions** [QLLX10, HZZT14]. **Insights** [BOSF24, BIBD21]. **Inspection** [MBP+19]. **Inspired** [BB11, GLL+18, LZW20, LLDÁ21, SSS20a, SMK+12, TNQ08, TS17, ZD17, PV16]. **Instability** [WQY18]. **Instance** [EMDH11, HLY+22, LJK+12, RLR20, WZS+22, WHZ14]. **Instances** [Lab06]. **Instantaneous** [ZYW17]. **Instruction** [XLZ+15]. **Integer** [AFMS19, BH06, CLH13, CSSS16, SLB+08, WCL11, YYG+21, YYLL22, ZFZL22, ZAZ+22]. **Integral** [KSP22, ZWC15]. **Integrated** [BMSZ22, CZW+23a, DS19, HXXJ18, Jam13, LB19, LDZL23, LXC+24, LZX+19, LBL+10, MZ17, PB19, RGB+21, SDCW11, TV11, Tsa12, VF09, YDZ+22, ZW19, BHW+14, DC15, MZL15, OFC+14, PSK+15]. **Integrating** [DHCW18, HZW+17, HLL+18a, HLG10, LTM+13, LLQ+16, LJ20, LHL+19b, LQY+20, LTRW19, LLY+23, MHHJ20, MB20, NVL22, PL17, RM18, RWH+10, SWL19, XOYHZ18, YZP+21, YHZ+19, YLJY21, ZLF+21a, ZZCD19, ZXZ20, ZY20, ZYYX23]. **Integration** [CKWY12, GJZH17, Kar12b, LBM+18, MSJP19, MCC16, STB+20, TWZ+14, WHF+20, WOYL17, YFWZ16, YGY+19, ZZN15, ZWD+17, Jam15]. **Integrative** [BMSZ22, GXSZ17, KPK+17, LLR+23, LLCZ15, MSZ19a, POJ+22, UKV18, XDZ+23, ZL24, GMCB14, LYH+16, TYL+16, PKM22]. **Integrity** [NFM+12]. **Intel** [MPA15]. **Intelligence** [ACJ24,

CNS22a, CLSW23, Cas06, Cas07, Cat17, CZ12, FS12, FS13a, GH08b, Gus04b, Gus04a, Gus06a, HMZ17, LCTS08, LNY05b, LNY05a, MPZ07, MPZ08, MPSZ09, MWZ13, MSZ19b, MNPZ10, MKARB16, RZF07, Wil04a, AS15, CEG14, XHS15]. **Intron** [SSS20b]. **Intronless** [CHN+18]. **Invariant** [LSY+20]. **Invariants** [JS12]. **Invasion** [JLK+21]. **Invasive** [MGP+22, WCMB19]. **Inverse** [HBM21, IBN19]. **Inversion** [WSB21]. **Inversion-Indel** [WSB21]. **Inversions** [dDD18]. **Invertibility** [ZZM17]. **Investigating** [BLP+12, BJ10, CCC+22, IQA18, LRM08]. **Investigations** [LS10]. **Involving** [vIJJ+20, DB14]. **Ion** [JLW17, KL11c, WM19a]. **Ionizing** [ZLL+20]. **Ionotropic** [KAL+17]. **Ions** [ZGC+05]. **IoT** [BVCD24]. **IPED2** [HWPE17]. **iPFPi** [TYA15]. **iPhosH** [AHK+21]. **iPhosH-PseAAC** [AHK+21]. **IR** [gCLL+10, NSC17]. **IR-Aided** [gCLL+10]. **IR-Based** [NSC17]. **IsAProteinDB** [dAc17]. **ISB** [ZC15]. **ISB/TBC** [ZC15]. **ISBRA** [BPW17]. **ISCB-Asia** [STHA15]. **Ischemic** [MFF+18]. **ISEA** [LLH+17]. **Island** [XYYZ20]. **Islands** [SHI06, SKD+07, vIKKS08]. **ISLMI** [STY+23]. **Isoform** [WZZ+22, YYY+22]. **Isoform-Disease** [YYY+22]. **Isoform-Isoform** [WZZ+22]. **Isoforms** [RLRH18]. **isolated** [SXL+14]. **Isolating** [BTYC13, RKDR11]. **Isolation** [RKDR10, YYX+21]. **isomerization** [AJYT+15, YMT+14]. **Isomorphism** [BG17]. **Isotope** [MGS17, ZGC+05]. **IsoTree** [ZFZ+20]. **ISP** [LQJ+23]. **Issue** [Ano05b, Ano09c, Ano12a, Ano13b, Ano13c, Cas06, GZB23, LNY05b, LNY05a, Ano13d]. **itemsets** [ZMC+14]. **Iteration** [SY09, FWY+15]. **iterations** [TYA15]. **Iterative** [KBSCZ12, LLH+17, PGHT12, STB+19, LAI+14]. **IVOCT** [HLX+21].

JigCell [VSR+06]. **jobs** [VPB15]. **Join** [BFM13]. **joining** [HS15, LAI+14]. **Joint** [BWS05, CYL+21, CSW+23, DH23, HLN20, JHX17, LYY+19, MHHJ20, SMRP15, SMPS20, WHXS17, WHF+20, ZWL+12, ZZP+21b, Kim18]. **Jointly** [BHMA06, HWM22, LQY+20, QZZ+21a]. **Journal** [Gus06b, Gus07c]. **Jump** [ZM22]. **Jumping** [LWY+23]. **Junction** [SN12]. **junctions** [LKLB14]. **Just** [PTH+18]. **Just-in-Time** [PTH+18].

K* [STT+14]. **K2Mem** [SC22a]. **Kalman** [MNND13, WLL+09]. **KAMI** [HLLO19]. **KATZ** [ZZF+19]. **KATZLGO** [ZZF+19]. **Kemeny** [SPMB13]. **KenDTI** [YLJY21]. **Kernel** [ASK+23, DYZC22, GLW12, HRdR09, IGM+07, JXN+16, LLMZ23, LXS+24, OG11, QL09, SLRQ19, SHJL10, SCPS12, WS21, WYS+24, WB11, XZC07, ZLY+12, ZLPW16, ZXJ+23, ZC11, LLC+15]. **Kernel-Imbedded** [ZC11]. **Kernel-Target** [IGM+07]. **Kernels** [BMHS13, IGM+07, Kuk13, WYH17, YRD+15]. **Key** [BSS+22, CHZ+21, DG19, KSK+18, YFCM17, ZJZ+24]. **KG** [JJZ+22]. **KG-Enhanced** [JJZ+22]. **Kidney** [CSQ+22, DCHW17, OW20]. **Kimura** [HS08]. **Kinase** [KAS21]. **Kinetic** [BMZM15, BCD+21, WBP+12]. **Kinship** [DMJ+18]. **Kit** [OLS+13]. **Kmerind** [PFJ+19]. **KNN** [HLSR18]. **Know** [RRTB12]. **Knowledge** [AAKB22, ASP20, BYZ+23, BMR21, CSW11, CHL21, DZ11, ED15, HLY+16, JZCZ15, JZZ+21, KDS+20, KB20, LWY+23, Mam05, MCC16, NP13, QZZ+21a, SLCZ22, TAAP11, WBE13, XNYC21, XHW+22, YSBB22, ZXJ+23, ZLZZ23, ZYN+19, ED14, MZL15]. **Knowledge-Based** [AAKB22, DZ11, HLY+16, NP13]. **Knowledge-Driven** [CSW11]. **Knowledge-Enhanced** [WBE13]. **Knowledge-Powered** [CHL21].

MSKC19, MFF+18, MW21, NNW24, NLW+24, NLXS19, NTL+22, NHTD17, NFM+12, OLZ11, PKM22, PTH+18, PYL+21, PH10b, PAAG07, PLTG22, QDZ+21, RLR20, RNAR+24, RTC23, RGZ+23, SBOA23, SFMS18, SDN+11, SKS+19, SSV+19, SZHH22, SZD+23, SXW+24, SSZ+23, SAK+21, SGP+20, SLCL22, ST23, TNQ08, TAAP11, TDZ+24, TBRS13, TDZZ24, UKC+23, UBP+19, VKS17, VMC22, WMK17, WL13b, WHXS17, WCC+18, WLHY19, WCA+19, WYHZ20, WQLL23, WZJS23, WWL+23a, WLL+24, WWBZ19, WCXL18, WZHM23, XJZS21, XZS+21, XPXY11, XLL+18, XLL19, XXW+23, YJJW21, YCX+21, YDZ+22, YGJZ23, YWCC22, YXL+23, YFYW23, YXS16, YHZ+19, YZH+23, ZLF+21b, ZLF+21a, ZL24, ZHSS07, ZLPW16, ZZH18a, ZCG+18, ZLXL19, ZSZ+21, ZWHH21, ZZZ+23, ZXJ+23, ZG19, ZYC+22, ZZY+22, ZMKL22, ZDY+23, ZYJ+23, ZDZ+23, ZDN+23, ZYW+21, ZLX+20, ZPW+21, ZLWF24, ZL19, wTCAK+20, AJYT+15, AM15, BCLC15, CR14, GJPSV14]. **learning** [GÁVRRL15, LLCZ15, SLW15, SEC15, SFH+14, WHZ14, YN14]. **Learning-Based** [ALC22, LWL+21, SLCL22, WQLL23, XXW+23, YXL+23, ZDN+23, ZYW+21]. **Learning-Empowered** [LGL24, ZLWF24]. **learning-to-rank** [SFH+14]. **Least** [DYZC22, FYSM12, LN13, WWC18, MBS15]. **Least-Squares** [LN13]. **Leishmania** [SSP+17]. **Length** [HYW08, LPH18, RFFB+20, RW07, SSS13a, YZH+23, dDD18, MM14b, SSKH15]. **Length-Weighted** [dDD18]. **Lengths** [KMSY20, FWY+15]. **Lesion** [LZZ+24, ZHD+21]. **Less** [ZSC+10]. **Lethality** [LWL+20, LCL+23]. **Leukemia** [BMSZ22, DSM23]. **Leukemogenesis** [SZGZ21]. **Level** [AS05, AV12, BU17, CSW+23, HvIKS11, JZF+21, KCP19, LLHW22, LB19, LLBL20, MZSL19, NRV22, PSC20, SPD24, TDZ+24, WGK16, ZZY+22, vIKK+09, LHWL15, UKV18, WLW23b]. **Level-** [PSC20]. **Level-1** [HvIKS11, LLHW22]. **Level-2** [vIKK+09]. **Leveraging** [AKLJ17, LLW+22, QZZ+21a]. **LGE** [WYF+23]. **LGE-CMR** [WYF+23]. **LGH** [XWC15]. **LGT** [PSC20]. **Liability** [QBPEL12]. **Libraries** [VGBK19, HPH+15]. **Library** [GSK13, PFJ+19, UJ09, ZLC+21]. **Life** [HGC+20, SNK+22, IM14]. **Ligand** [AM12, CHZ+16, FVP+20, GLW12, HF07, LSL+22a, STT+14, WLL13, ZCG+18, AM15]. **Ligand-Binding** [CHZ+16]. **Ligand-K*** [STT+14]. **Ligand-Specific** [ZCG+18]. **light** [GCC+14, VPB15]. **light-induced** [GCC+14]. **light-weight** [VPB15]. **Like** [DR16, FM11, GAR+09, GCY+21, HEF17, KG12, NSNA19, Ros13]. **Likelihood** [ACPR10, LCWZ13, MRS09, Roc06, Wu10, TDD14]. **Limb** [BMT17]. **Limits** [SLGK17]. **LincRNAs** [BKKG19]. **Line** [ZWL11]. **Lineage** [LP21, MR10, XYYZ20, ZZ14]. **Lineage-Associated** [XYYZ20]. **Linear** [BEW09, BFK17, CSSS16, CWG+18, FM13, HSS18, JNST09, LTT+22, LCC+11, MTSCO10, NRV22, NO09, OC13, PRU11, RBdJ11, SHUP19, SLB+08, UC10, WGX+17, WYHD17, Wig15, WCL11, YYG+21, YYLL22, ZLG+21, ZYX+23, ZFZL22, ZWZZ22, dJP08, BS15, KGK14]. **Linear-Time** [JNST09, LCC+11, NRV22]. **Linearization** [CC09]. **Lines** [LWZ+21a, NVL22, MFS+15]. **Link** [GT24, JZW+22, ZLG+21]. **Linkage** [BKP+19, LLC+13, XWC15, Jam15]. **Linked** [GGM21, LLW+22, SLL+19, WRH+09]. **Links** [DKY21, NZM22]. **Lipid** [HBRU13]. **List** [Ano06a, Ano08b, Ano09a, Ano10a, Ano13a, KL11b, RSJK13, IEE05, IEE07, XTL12b, Ano16]. **List-Colored** [RSJK13]. **Literature** [AAF+13, CDAL22, CLH+15, HW07, LHLY11, LNC+05, Ozy12, SLCZ22, XYZ19, XTL12c, ADTAQ16, TAL+15].

HYW+17, HZZY16, HLL+18a, HYL+19, HLGS21, HC07, HGM18, HLL+22, JWG+22, JLH16, KMSY20, KTLM15, LYW20, LZL+19, LWZ+21a, LWL+21, LLX+23, LXS+24, LLZC12, LZX+19, LHG+16, LWZ12, LXG+16, LZZ+16, LHKL17, LLH18, LTW+22, LZW23b, LGX10, MWZY17, MK16, MNLF+22, MBJ19, MKKS20, MW21, NGY+16, NZM22, PM20, PL17, PTH+18, RGI13, RLV04, SH11a, SZ11, SLCZ22, SNC+16, SIK20, SPW20, SSFW12, SPL+23, TWG+12, TZWZ23, TBRS13, TK05, USMS19, VTGC16, WBP+12, WZJH12, WHWP12, WCA+19, WLZ+19, WCLY20, WWF+21, WLW23b, WLW+23a, WWY+24, WGK16, WW19, WCX+22, XLW20, XXW+23, YCX+21, YWW20, Yan22, YCCY20, YM20, YH13, YZH+23, ZWSX12, ZCR+17, ZLS+21]. **Method** [ZLG+21, ZZZ+23, ZJ22, ZY20, ZYF+18, ZTY22, ZYZ+23, ZAZ+22, dSPFF21, DNR15, DPL+14, GCC+14, GH15, IM14, KKC+14, KH14, LLW+15, LLL16a, LLC+15, PS15, SYV14, YTLL15, YN14, ZSY+14, ZZ15]. **methodological** [BF14]. **Methodology** [JCF13, MS21, KG15]. **Methods** [ARK20, AV17, ADR18, BLP18, CSK+11, CYL+21, CCE19, DLRW18, DPS+13, DPA+17, FS12, FS13a, FYSM12, HTZ+23, JDCC12, JDHL20, KSN+12, LN13, LJL+15, LPH+13, LL19, LZW21, LQWP21, MBF+11, NLXS19, PFGDCRM22, QZD+22, QZA+23, RG16, Rho20, SHG+23, SXW+24, SMK+12, TV11, TAI+19, VRHB23, WNT+17, WWBZ19, WCZ+23, Wil09, Wu11, XJZS21, XLL+18, ZZRPZ19, ZZ20, ZCT22, DS14, SQZA14, SFH+14, WFD15]. **Methyladenosine** [FSP23, RTC23]. **Methylated** [HHSC13]. **Methylation** [CZM+18, DCHW17, FPC20, LLH23, LZL+20, LZL+22, MSZ19a, MB20, ML18, PZC+23, SKD+07, WXS+19]. **Methylcytosine** [NTL+22]. **Methylguanosine** [MZLL22]. **Metric** [Alt23, BS09, CLRV09a, CLRV09c, CAN+08, HEF17, HYZ16, LTT+22, LLMZ23, LRM12, LWY+21, Nak10]. **Metrics** [CLRV09a, CLRV09b, HSlSM11, Mos07]. **Metrizations** [Rho20]. **Metropolized** [MMS10]. **MF** [LWL+20]. **MGATRx** [YJ22]. **MGRFE** [PWY+21]. **MGT** [LZL+19]. **MHC** [EMDH11, FLW+14]. **MHC-II** [EMDH11]. **MIC** [PCY+19]. **Microalgae** [BdOS+18]. **Microarray** [ABVD12, BDP11, BZ10, BLP+12, BHHMCL16, BLR08, CLVT+20, Che10, EAS12, EAS13, EFLA08, FJJ11, GK08, HYW+17, HC16, IVA11, JCF13, JS23b, KZ10, LTM+12, LTM+13, LH10, LPH+13, LTL+07, MP13, MC07, NU06, PSS09, RGCB05, RV06, SBOA23, SVZ09, SBW15, SC11, SY09, SYZ+13, SIM12, ST05, TZH07, TZ16, TGGF10, TZY11, TC13, TBKH05, WGP11, WCA+19, WLPW16, WDS+12, WWC18, WW19, XZC07, YM11, YC08, YNWC07, YPS11, YHB12, ZLZ06, ZHSS07, ZWHC19, ZC11, BMM14, CZWT15, MM14b]. **Microarray-Based** [CLVT+20]. **Microarrays** [BHP19, CD08, PBhL+11]. **Microbe** [CZW+23b, LWZ+21c, PLD+23, WLP23, YDW+20, YDW+21]. **Microbe-Disease** [CZW+23b, LWZ+21c, PLD+23, WLP23, YDW+20, YDW+21]. **Microbe-Drug-Disease** [WLP23]. **Microbial** [HHC+24, KKPP22, MB23, NS19, SNK+22, TAI+19, WCMB19, GM22, JHXP15]. **Microbiome** [JHX17, KKP22, MHHJ20, ZHJ17, ZWDR20]. **Microbiota** [AAT20, BSR+21]. **microfluidic** [AIS+16]. **Microglia** [DPA+17]. **microhomology** [SSML15]. **microhomology-mediated** [SSML15]. **Micron** [RA16]. **MicroRNA** [BHS21, GZR+18, LWL+18, LWXX22, LZHZ17, WLW23b, ZLG+21, LLL16a, MKG20, RPBP18, SPMB13, WZ13a, YWN+19]. **microRNA-Binding** [WZ13a]. **MicroRNA-Disease**

[HWK14]. **Multi-Similarity** [CLL+21]. **Multi-Site** [JFR+19]. **Multi-Source** [YSW+17, YLJY21]. **multi-state** [Gu16]. **Multi-Subspace** [YZL23]. **Multi-Swarm** [NHTD17]. **Multi-Task** [ATO22, DLY+21, SSZ+23, CR14]. **Multi-Thread** [LZL+20]. **Multi-View** [CZL+22, LC19, LXL+21, PLD+23, SND22, SSF18, TDZ+24, WZHM23, YJ22, ZL24, ZHJ17]. **Multi-Zoom** [TDZZ24]. **Multicategory** [ZHSS07]. **Multiclass** [RM13, SSS+11, XAW07, YOKI09, ZC11]. **Multicore** [GDM18, MTM+15]. **Multicriterion** [YM11]. **Multidimensional** [DCW+24, HCA+10]. **Multidomain** [JJH12, WKE11]. **Multidrug** [NTCO07]. **Multiexpressions** [Zou13]. **Multifaceted** [AL12]. **Multifactor** [YLC20]. **Multiforme** [CHW+18, ZLPW16]. **Multifractal** [DSVMM18]. **Multigenomic** [GXSZ17]. **Multilabel** [WL13b, XXW+23, YRD+14a]. **Multilabeled** [GJS11, HSlSM11]. **Multilayer** [LPH+21, PWY+21, RSV+22]. **Multilevel** [PLMV12]. **Multilocations** [WL13b]. **Multilocus** [LLC+13, MWSM12]. **MultiMAGNA** [VM18]. **Multimeme** [NTCO07]. **Multimodal** [CGL+23b, DZD+23, GCZ18, GLX+22, HS09a, HS09b, HHCY20, LZW+23a, LGB15, NLW+24, SWL19, XHW+22, YLWS21, LLCZ15]. **Multimodal-Boost** [DZD+23]. **Multimodality** [JSM+22]. **Multimodality-Contribution-Aware** [JSM+22]. **MultiMotifMaker** [LZL+20]. **Multinomial** [LW13a]. **Multiobjective** [HKK07, LZW20, LZW23b, MPF12, MMB+13, TGK13, TGD+16, GÁVRRL15, MM14b, SB12]. **Multiomics** [POJ+22]. **Multiparameter** [SSDN12]. **Multipartite** [VKM07]. **Multiple** [AM19, AAH+18, ALWG18, ABS15, BAK06, BRZ+17, BLS12, BHHMCL16, Bro05, CPL+23, CW12, CHL21, CWLS15, CCN22, CGPW06, DBZ12, DK17, DG19, DBN18, DOK+21, EMDH11, GTL+21, GZC+17, HL16, HKT+18, HVG04, HS15, HPL+13, HLZ+17, HB11, JLYZ16, JXN+16, KG20, KKC16, LH10, LZHZ17, LWT+18, LCL+23, LCC+11, LW13b, MSQ18, MMH15, MR10, NP13, NVL22, NTR16, OHK+21, PS11, PZWC20, PT09, PS15, QZZ21b, QL09, QWC+16, RLR20, RM18, SHUP19, SIK20, SK12, SSFW12, SPWF14, TDY+18, TDA+09, VM18, WS08, WLMW+11, WB17, WGX+17, WZR+22, WYS+24, WHKK07, WPL15, WLA+13, YHCS19, YLL+06, YFWZ16, ZSW23, ZLF+21a, ZLPW16, ZZCD19, ZZF+19, ZLLS17, DNR15, MW16, PJN+14, YlCW+15, YRD+15]. **Multiple-Filter-Multiple-Wrapper** [LH10]. **Multiple-Filters** [BHHMCL16]. **Multiple-Grain** [JLYZ16]. **Multiple-Sequence** [NP13]. **Multiple-Structure** [WS08]. **Multiple-Swarm** [ALWG18]. **Multiple-Valued** [LW13b]. **Multiplex** [LXWL22]. **Multiplexing** [LWXX22]. **multiplier** [CL14]. **Multipliers** [HYL+19]. **Multipositional** [GLW12]. **Multiprotein** [HK12]. **Multiresolution** [CSZT19, HYC12, RNAR+24, ZKL18]. **Multisample** [PR18, SSS13b, ZYW+13]. **Multiscale** [GGH+13, GCZ18, HMW+12, NNM+12b, SZL+20, SCCDK09, ZLW+11]. **Multiseed** [KNR05]. **Multistage** [DLT10]. **Multistate** [GG11]. **Multitask** [DMK22, FB19, LZH18, XPXY11, GA23]. **MultiTrans** [ZFZL22]. **Multitype** [WLW+23a]. **Multivariate** [KPW13, Kuk13, PPFG20, ZAZ11, CBN15]. **Multiview** [ZJ22]. **Muscle** [BMT17, SXL+14]. **Muscular** [BCL+13a]. **Mutagenesis** [VGBK19]. **Mutagenic** [Che16, YCYC12]. **Mutant** [HLG10]. **Mutants** [DSZ+06, GCC+14]. **Mutated** [LGW20, QZA+23, SAE+20, ZZ18, ZW19]. **Mutation** [DSZ+06, KKI20, LHDS18,

WWF+21, WZC+21, WZS+22, WLWJ22, WLP23, WHL+24, WSL+24, WYS+24, Wer06, WGK16, WW19, WWL+23b, XLZW22, XWQ+24, XWF07, XW16, XOYHZ18, XDZ+23, XWP+24, YD24, YXYC13, YYLL22, YLC+23, YWW+24, YFCM17, YG19, YWL+24, YCCM12, YGY+19, ZZKW18, ZHL+24, ZDL12, ZZN15, ZWL15, ZHJ17, Zha18, ZXLZ18a, ZXLZ18b, ZPW+19, ZZH19, ZXZ20, ZZBH20, ZSZ+21, ZCL21, ZLG+21, ZYH+21, ZCL22, ZZLH23, ZXW+23, ZGW+24, ZK16, ZYYX23, ZYJ+23, ZS18, ZHD+21, ZPW+21, ZYZ+23, ZLB24, ZZDW13, ZWZZ22, ADTAQ16, BDBH15, FZM15, HLW15, LP15, MMFD14, MG14, SEC15, TWZ+14, WZC+15, XLC+15, XXM+16].

Network-Based [BSS+22, CDBR21, GTX+23, GSC17, KKPP22, PSS09, POJ+22, RV13, SMPS20, WGK16, ZSZ+21, FHRG14, SQZA14].

Network-Lasso-Constrained [GHL05].

Network-Regularized [MLZ18].

Networking [DG19].

Networks [ÅSWH22, AVD+12, AHN23, ARK20, AGAS18, AAH+18, AFJ12, AHC+21, ARS17, AAT20, ABS15, APPG18, AKS20, BBW18, BMCY22, BGHC20, BGS+12, BZ07, BCL+13a, BvBF+11, BD19, BSV10, BJ10, BPJ12, BVN+11, BCD+21, CZ20, CPL+23, CRV09, CLRV09a, CLRV09b, CLRV09c, CPRC24, CKRS21, CDB+16, CC07, CW12, CXW+13, CHW+18, CCN22, CW22, CWG+18, DZH16, DS19, DBN18, DT11, EAS13, ECK16, EMK18, FMRS18, FZWS17, FWXZ19, FSDR16, FSX19, FXZS22, FPPR11, FKB19, FSD+11, GH08a, GPZ20, GTL+21, GD22, GAH22, GDM18, Gos11, GBB+11, HK20, HLM+13, HB05, HC19, HS09a, HF07, HM13, HAH13, HMW+12, HLY+16, HC13, HYL+19, HHCY20, HWM22, HWY+23, HvIKS11, HDKS04, Hus09, INT11, IBN19, IL18, JvI18, JBgLS19, JLYZ16, JZW+22, JSS+18, JZS+18, JNST09, JFN11, JHZL19, KLCH22, KBNHD18, KN05, KP12, KCCC15, KBM21].

Networks [KSB12, KKC16, LFS06, LCTS08, LSMF08, LLHW22, LLR+23, LTP22, LLH+07, LL11, LCZN16, LT17, LLNW17, LZL+19, LHCL20, LLQ20, LPH+21, LZL+22, LZM22, LWL+22, LWY+23, LTLL23, LLL16b, LZQ+20, LNW20, LLK+21, LJN+23, LZC+23, LKD23, LLYS21, LCL+23, LW13b, LTRW19, MSQ18, MQOH21, MSP+19, MPP+20, MGP+23, MBGP12, MPA15, MDH11, MPSY18, MPQY19, MDD18, MNW+04, MDPR18, Nak10, NRV09, NNNL22, NWZ+20, NCL+23, NI07, NSNN12, OMAdG+12, OYDZ15, OC13, PB12a, PAL+12, PLH22, PSPM20, Pau18, PLCW17, PZWC20, PH10b, PCK19, PNP+18, Pha23, PB12b, PPZ12, PR12, PSC20, PKA20, QD12, QLZZ22, QZJ+23, RST10, RSK23, RXAH+23, RMV12, RHZ+24, RSV+22, RRTB12, RMS15, SdOD+12, SREK19, Sef22, SS06b, SSV+19, SDH20b, SZL+20, SV16, SPA17, SWSA21, SNM12, STS21, SPP21, SPL+23, TIA+11, TAAP11, TWG+12, TGK13, TGD+16, TV11, TGGF10, TZP17, TR07, TDK13a].

Networks [UWLH15, VRK12, VBB18, WLL+09, WLCP11, WWLL16, WZZ+22, WW22, WP08, Wil11, Wil12, XWF07, XGWW19, XYLL23, YDW+20, YZL23, YKWK18, YFWZ16, YLZW21, YYY+22, YLS23, ZM12, ZLY+13, ZZN15, ZWZ16, ZZM17, ZZCD19, ZZF+19, ZWHC19, ZD21, ZZGL24, ZSD08, ZWW17, ZWDR20, ZWD+17, ZZH+24, ZZDW13, ZDYH17, Zou13, dJP08, vIKK+09, CZWT15, CXS15, DYD15, GTDK15, HKLN14, KH14, KD15, LLW+15, MW16, MM14a, NCMCAR15, PWC+15, RHH16, SRLR14, XG14, ZWL14a, ZWC15, OSA+21].

Neural [ÅSWH22, AHC+21, AAT20, BMCY22, BP22, BAO22, BCC+23, CZ20, CC07, FSX19, FXZS22, GLX+22, GTX+23, GAX+23, HB05, HF07, HLL18b, HXS+21,

SBM15, SYKM17, SSS13b, TNQ08, TDZ+24, TDA+09, TK05, WWC18, XLW20, YLXS17, YXYC13, YM20, YC08, YH13, YSW+17, YZZ+24, YCZ+18, YXZD21, ZZCD19, ZY20, ZPW+21, ZAZ+22, ZWZZ22, dSPFF21, CL14, GZGX14, KPB14, LLL16a, STT+14]. **Novelty** [CPM18]. **Novo** [Bi09, SB12, AKR12, DST+15b, HG16, KSS15, ARZ+14, YKW17, ZFZ+20, CLVT+20, LLL+20, LLL+21b, LMW+24, GAJ+18, GCY+21, LLH+17, LMZL17, ZWM+20]. **NovoExD** [YKW17]. **NP** [LGZ+17]. **NP-Hard** [LGZ+17]. **NPPC** [GMSD11]. **NR** [ISK18]. **NS1** [RAA20]. **Nsp3** [SDP+21]. **nsSNPs** [GED+17]. **Nuclear** [HCA+10, ISK18, CZB+16]. **Nucleic** [NCJ24]. **Nucleosome** [CGZ15, CHN+18, GZGX14]. **Nucleotide** [CW07, CL08, KT07, LLTC19, SPD24]. **null** [LWM14]. **Number** [BB04, BHMA06, BFK17, BS07, CW09a, DR16, Gru11, MA12, MW21, NVSH18, PKRD12, PK13, QSJ+20, SDCW11, TWW+20, WHXS17, XL16, XLW20, YCCM12, YLBX21, ZANN20, ZmCXS17, ZRK19, dNG17, DR14, LWM14, MMSH14, SB16]. **Numbers** [YH13]. **Numerical** [FMD18, SCCDK09]. **NURBS** [IGA18]. **NURECON** [HHC+24]. **Nussinov** [TYDZ23]. **Nutrition** [HHC+24].

O [HPH+15]. **Object** [GAH+21, YXL+23]. **Objective** [BA18, CZZ+23a, CCF+24, GSC+18, GCL+18, MDD18, XZG+18, ZwGC17, RHH16, UKV18]. **Objective-Based** [MDD18]. **Objective-Oriented** [CCF+24]. **Objects** [AAB22, Str11]. **Oblivious** [CLR10]. **Observable** [SPA17]. **Obstructive** [ZLZZ23]. **Occurrence** [LSZ+23, ZWDR20]. **OCT** [WCDM23, ZHL+24]. **odd** [EES14]. **Odds** [Roc11]. **ODE** [ZSY+14]. **ODE/DDE** [ZSY+14]. **Off** [PH10b]. **Offloading** [NCL+23]. **Oligomeric** [SKDA19]. **Oligonucleotide** [HKS11, LEAK11]. **Omic** [Ano12a, CCC+22, NVL22, SND22, YZP+21, BCLC15]. **Omicron** [SCU+24]. **Omics** [DPS22, HTZ+23, MZ17, MMBC22, VMC22, YGY+19, ZL24, ZY20, PZH20]. **OMIM** [LTRW19]. **Oncogenes** [PG12, YCCM12]. **Oncology** [BVS+22]. **One** [CHZ+21, LX21, MCM22, MCHT17, QSJ+20]. **One-Class** [LX21]. **One-Sided** [QSJ+20]. **Online** [HHC+24, SNC+16, ZZP+21b, ZLL21]. **Onset** [GCC+22]. **Onto** [WCQ+19]. **OntoGene** [RSK+10]. **Ontologies** [HXXJ18, LQY+20, MSJP19]. **Ontology** [ASP20, AMGC16, BM17, CM16, CPM18, DLA+23, DKDD10, DBK18, FLM+16, HXXJ18, IQA18, MPM11, NGZ+22, PA22, PKM06, QDZ+21, TFTY23, YWF+20, ZLY+13, ZXLZ18a, ZXLZ18b, ZSZ+21, BM14, JC15]. **Ontology-Based** [CM16, FLM+16]. **Ontology-Independent** [QDZ+21]. **Open** [Ano13e, ZJW+22]. **OpenCL** [MGS+21]. **Operation** [BFM13, OLS+13]. **Operational** [WLA+13]. **Operations** [HS09a, LTLTS23, OJF+21]. **Operators** [GSC17]. **Operon** [CYTY13]. **Optimal** [AM19, BBN18, BHS+04, BAK06, BFK17, Dal16, DK13, DS21, DYD15, DFM+11, DOK+21, HYW08, KQD21, MCRC17, Mne09, MDD18, SK08, SPMB13, SPP21, THH+19, WAK13, YOKI09, pD20, ED14]. **Optimality** [ACC+13]. **Optimization** [AKS13, BIDS23, CZZ+23a, CCL+24, CAW+19, Che16, CYTY13, DMD13, ED15, GK08, GSX+18, GCL+18, HKK07, HSS18, HOS+12a, HOS+12b, mHB13, HGM18, HRdR09, IGM+07, JDCC12, KWP+23, LYW20, LPH+21, LSL+22a, LZH18, LZW23b, MPF12, Mai09, Mat07, MLZ17, NPD+17, NHTD17, NLW+18, ORCJ13, OHK+21, PAAG07, RKDR11, SdOD+12, SDS18, SB12, SIK20, SMSZ17, SB16, VGBK19, WWLL16, WB17, WZZ+18, XSS17, XWF07, XAW07, XZG+18,

POS+18, QV17, SPD24, SPW22, SSS13b, SB09, WPL15, YLY+12, YOKI09, YCY+14]. **Profiling** [CZCL23, FSMJ05, HCA+10, KKK19, NS19]. **Profitable** [UWLH15]. **Prognosis** [DPS22, HL21, MCHT17, SZLL11, SWL19, ZLPW16]. **Prognostic** [LLR+23, MGP+22, PLH22]. **Programming** [BRB21, BBK+07, BCD+21, BH06, CLH13, CSSS16, CLR10, HT09, MIC+07, OC13, PI09, SLB+08, VKS17, VBG+18, WYL07, WCL11, YYG+21, YYLL22, ZFZL22, ZAZ+22, LV14]. **Programs** [DKY21]. **Progression** [CSSS16, MGP+22, PSS09, RB16, RM18, SSK+20, WGK16, ZLH+17, ZW19]. **Progressive** [GRH08, GZYL22, HVG04, SLCL22, ZHL+24]. **Project** [HLLO19]. **Projection** [PYL+21, RLV04, WCQ+19]. **Projective** [SJWW23]. **prokaryotes** [MBS15]. **proline** [AJYT+15, YMT+14]. **Promising** [MKKS20, YJJW21, WLG+14]. **Promoter** [CFOS06, FLW12, NNW24, WLW23b, ZZCY10, HPH+15]. **promoter-RBS** [HPH+15]. **Promoters** [LLTC19, LHL+19b, NTL+22]. **promSEMBLE** [NNW24]. **Proof** [HS08, Roc06]. **propagating** [PRZ+14]. **Propagation** [HM13, JZW+22, NM22, WWL+23b, GBLZ14]. **Properties** [AGGM11, DTA+23, DGY05, DR16, DBK18, KS18, NRV09, RBdJ11, TZWZ23, TR13, WLL13]. **property** [KG15]. **property-driven** [KG15]. **Proportional** [HL21, KSP22]. **Proportional-Integral-Derivative** [KSP22]. **Proposal** [Pre04]. **Prospects** [QZA+23]. **Prostate** [FYZ+19, KCP18, XPH20, ZLXL19]. **Prostatic** [ZLXL19]. **Prosthetics** [XLZ+15]. **Prot2GO** [ZWL+23]. **ProtDet** [LL19]. **ProtDet-CCH** [LL19]. **Protease** [AFAAW+11, HHL+20]. **Protecting** [RCP+18]. **Protection** [MZSL19, YCX+21]. **Protein** [ACP22, ASJ+07, Alt23, AC12, ACSR21, AM12, ADPH13, AAE11, BCS11, BM17, BPM21, BP22, BWC17, BYZ+18, BIDS23, BSV10, BTYC13, BM12, BVN+11, BNV+13, Bro05, CCBR+21, CCA12, CLST+13, CC07, CWL12, CHZ+16, CZW+18, CHC+21, CHH+22, CDKT09, CGPW06, CBF+18, CHK17, DLT10, DKCM12, DZA+06, DNS19, DPS+13, DM22, DDS+17, DS19, DCVC11, DSCM20, ECK16, EMK18, ED15, FSDR16, FSX19, FJJ11, FXZS22, FMD18, FB19, FWA10, GSC+18, GBS11, GLF+23, GJSB23, GED+17, GA23, HBRU13, HK20, HLV+10, HCN+19, HZZY16, HYY11, HC18, HC19, HZL+20, HCLS11, HC13, HC17, HLDZ17, HLZ+17, HYL+19, HSF+23, HMK+07, mHB13, HRdR09, IQA18, IDD13, JJH12, JLwC11, JS23a, JLYZ16, JMCY23, JM12, JCG+22, JZW+22, JDHL20, JGKP21, KCP19, KL19, KKI20, KAHK+10, KAP+12, KSK+18, LS10, LDS+07, LRE+22, LRM08, LSTW+17, LH20]. **Protein** [LFF18, LLH+07, LBL12a, LZ18a, LNC+19, LW19a, LMZ+20, LSY+20, LQJ+23, LSZ+23, hLMBJ11, LZX20, LQW+23, LLW10, LLZ+13, LL19, LCGW19, LZQ+20, LDYZ22, LCH19, LGB15, LCB17, LWD+21, MSZ19a, MHTJ22, MGSP22, MGK08, MSJP19, MB20, Mam05, MGP+23, MK16, MMB+13, MPS18, MCCZC08, MKH11, MCDD12, MSKC19, MPM11, MSS13b, MDM13, NZR11, NHH+17, NLXS19, NWW19, ORCJ13, OM07, OYDZ15, PCL+22, PLF12, PA22, PLCW17, PR12, Pol11, Pol12, Pol13, PSN+15, QLZZ22, QLZ16, QZL+22, RFFB+20, RFBTD22, RTD23, RSK23, Roc11, dSRCT+11, RSG18, RSP08, RGN+09, SZ11, SYM+10, SDS18, SN12, SDH20a, SZHH22, SH11b, Shi10, STB+20, SLRQ19, SBM15, Str11, SSFW12, SPL+23, SSF18, TZWZ23, TRBK08, TRBK09, Tsa12, VMD+08, VBG+18, WMK17, WLYZ+09, WLCP11, WSX11, WLMW+11, WL13b, WYHD17, WMW+21, WZC+21, WP08, WXS+19,

WHKK07, WAK13, WLL13, WLPW16]. **Protein** [WOYL17, WLG+21, WWL+23b, WZ13b, XHY+18, XPXY11, XTL12c, XGWW19, YHYY12, YHY13, YDM+08, YSGZ20, YF23, YKWK18, YJS+24, YHZ+19, YRD+13, YRD+14a, YRD+14b, YFWZ16, YPL+23, ZD12, ZLY+12, ZDL12, ZLY+13, ZWcF17, ZZY+17, Zha18, ZZH19, ZWXL20, ZWM+20, ZZBH20, ZXZ+21, ZZQ22, ZZW+22, ZZZ+23, ZWL+23, ZG19, ZWG+21, ZYC+22, ZYYX23, ZWD+17, ZLX+20, ZZDY13, ZZDW13, ZDYH17, ZLZW22, AM15, BDBH15, BF14, CWZW15, CR14, CM15, CXS15, DPL+14, DC15, GJPSV14, GÁVRRL15, HLW15, KGK14, KD15, LMZ14, LHWL15, NYOL15, PSK+15, PWZW15, PWC+15, SCC+15, SEC15, TYA15, TAL+15, WL14, WHZ14, XG14, YTLL15, YLH+15, YRD+15, ZMT14, ZZ15, ZWL+14b, ZMC+14, GZWD23, SDH20b, WYHZ20, WSL+24, WSTL+15, ZYH+21]. **Protein-Binding** [ZZDY13]. **Protein-Coupled** [JCG+22, WLG+21]. **Protein-DNA** [ASJ+07, CLST+13, HLZ+17, LSTW+17, GZWD23]. **Protein-Ligand** [AM12, WLL13]. **Protein-Peptide** [YHYY12]. **Protein-Protein** [Alt23, AC12, ADPH13, BCS11, BSV10, BVN+11, BNV+13, DSCM20, ECK16, FSDR16, GLF+23, GED+17, HLV+10, HMK+07, JS23a, JLYZ16, KAHK+10, LSY+20, MGSP22, MB20, Mam05, MDM13, NWW19, OYDZ15, PR12, RSG18, SBM15, Tsa12, YKWK18, YHZ+19, ZLY+12, ZDL12, ZLY+13, ZZZ+23, ZZDW13, ZDYH17]. **Protein-RNA** [KSK+18, LW19a, WYHZ20]. **protein-to-protein** [XG14]. **Protein2Vec** [GTL+21, ZZQ22]. **Proteins** [AM22b, AHK+21, CYJ+19, CZZ+23b, DH23, DBK18, FHDU22, FWW+22, FL18, GAR+09, HCA+10, HLG10, KNTB18, LYW20, LCWZ13, LLX+16, LYL+17, LLNW17, LNC+19, LZW+22, MGL+12, MGXS15, NLGG12, QL16, QWC+16, SKDA19, SP11, SSS+11, SSP+17, Tah18, TR07, VJRPNVJG24, WMK16, WBP+12, WLWP12, WKE11, WZ13a, YFWZ18, ZLF+21a, Zha18, ZXLZ18a, ZXLZ18b, ZXZ20, ZCL21, ZZDY13, ZBFK10, dAc17, DGRC15, GJK15, LLW+15, PWC+15, TWZP14]. **Proteome** [MSJP19]. **Proteomic** [MCC16, RLRH18]. **Proteomics** [IC23, KBBD+17, PH10a]. **Protocol** [JHW+19]. **Protocols** [YFY+22]. **prototype** [EES14]. **Protozoan** [GAR+09]. **Proximity** [ASP20, JCF13]. **Prune** [WM19b]. **Prune-and-Regraft** [WM19b]. **PSAD** [ZLXL19]. **PseAAC** [AHK+21]. **Pseudo** [AHK+21, LLTC19, NLGG12]. **Pseudogene** [JZW17]. **Pseudoknot** [CC11]. **Pseudoknots** [Jia10, MWL+12, RAA10, SW17, WHS04, WCLY12, NCJ24]. **Pseudomonas** [AM22b]. **PSO** [SSS+11, AV17, HYW+17, MM14b, ZWL+12]. **PSO-based** [MM14b]. **PSPEL** [LYL+17]. **PSPGO** [WWL+23b]. **PSSM** [LN21]. **Psychological** [XLX+21]. **Psychologically** [TNQ08]. **Pubcast** [GTTR+17]. **Publications** [GTTR+17]. **Publishing** [Ano13e]. **Pull** [GZS12]. **Pulmonary** [ACJP23, ZLZZ23, ZZH+24]. **Pure** [BVD+10, BH06, HVG04, ICL11]. **Purely** [MSKC19]. **purification** [CWZW15]. **purification/mass** [CWZW15]. **Push** [HLN20]. **Putative** [CAN+08, LPH18, SSP+17, YCCM12]. **PyMut** [LHDS18]. **Python** [AAB22, CSZ+19, CS24].

QoS [CCL+24]. **QSAR** [NSMH19, WB11]. **Quadratic** [FWY19, RFB20, RB14]. **Quadruplexes** [BAO22, LBQ+13]. **quadrupole** [CZB+16]. **Qualitative** [BDS12, INT11, Pau18]. **Quality** [ANR11, BZ10, CLVT+20, GAJ+18, PvRV+20, SGR+17, WLG+14].

Quantification
[RCBB19, VRHB23, LCOMG14].
Quantifying
[FLW$^+$14, GF10, HC24, SZL$^+$20, ZLH12].
Quantitative
[AAF$^+$13, ARM$^+$19, BCMW15, BMZM15, CCBR$^+$21, CMC$^+$12, FYSM12, IDD13, MVS$^+$13, PLMV12, TRKRC13, RTWR15].
Quantum [Kar12b, SDP$^+$21]. **Quarantine**
[HC24]. **Quartet**
[BLS12, DLRW18, Rho20, WYL07].
Quartet-Based [WYL07]. **Quartets**
[GSB$^+$13, SR10]. **Quasi**
[CAW$^+$19, Kar12a, LLW10, MMB$^+$13].
Quasi-Bicliques [LLW10, MMB$^+$13].
Quasi-Newton [CAW$^+$19].
Quasi-Supervised [Kar12a]. **Queries**
[Jam18, SVM14]. **Query**
[HHSC13, NSC17, PHX$^+$08]. **Query-Based**
[HHSC13]. **Querying**
[BSV10, FPPR11, Jam17, MCC16, QKÖ18].
Quest [DHCW18]. **Question**
[BYZ$^+$23, DYL$^+$23, MKS$^+$17]. **QuickVina**
[HOS$^+$12a, HOS$^+$12b]. **Quorum**
[CZJ17, Kar12b].

r [SIM12, BBH12, VPB15]. **R-based**
[VPB15]. **R5** [LSMF08]. **R5X4** [LSMF08].
Radial [DM09]. **Radiation**
[ZLL$^+$20, SDAA$^+$14].
Radioimmunotherapy [GCGCP$^+$23].
Radiology [PvRV$^+$20]. **Radiomics**
[JLK$^+$21]. **RAFP** [KNTB18]. **RAFP-Pred**
[KNTB18]. **Rafts** [HBRU13]. **Random**
[ALQ17, ABS17, CNO$^+$23, CMSE$^+$15, CSK$^+$11, Cza18, GT24, GC22, GAH22, Gru11, HCMB18, HBM21, HBC$^+$11, HLHAJ20, ISK18, LZX$^+$21, LZHZ17, LWL$^+$19, MGXS15, PGHT12, PLCW17, RXAH$^+$23, RW07, WL13b, WFY$^+$19, WWL$^+$17, XW16, XGWW19, YDW$^+$20, YSW$^+$17, YFWZ18, ZLZ$^+$19, ZJZ$^+$24, ZWG$^+$21, ZHE19, CWZW15, DGRC15, GGZZ14, SHK14, SPWF14, YLH$^+$15].
Randomized [AJYT$^+$15, FWXZ19, MT24].
Range [HYW08, KL19, MK16, SSKH15].
RANGI [RSJK13]. **Rank**
[CDB$^+$16, DCW$^+$24, HLN20, LC19, LCW$^+$18, SBOA23, SND22, WLCX18, WLZ$^+$19, WWY$^+$24, XHQ$^+$18, XLL$^+$18, XLP$^+$21, YDW$^+$21, YZG$^+$17, ZOMC24, ZJ22, SFH$^+$14]. **Ranked** [DRS12, DR14].
Ranking [AM12, CJH$^+$21, DLT10, EFLA08, LXWL22, LJL$^+$15, LL19, LWZ$^+$21c, LGX10, PRP21, RMV12, RV13, SPMB13, Tsa12, ZLZ06, ZWSX12]. **Rapid**
[BPM21, PKA20, XLC$^+$15]. **Rare**
[BIBD21, SVE21, LLH$^+$14]. **Rarely**
[LGW20]. **Rate**
[AGMP09, CKRS21, GGP08, GCB$^+$18, HLM$^+$13, HZL$^+$20, JS12, LKY$^+$11, SS04, XSS17, YAB13, ZMT13, CWDS15, ZMT14].
Rate-Independent [CKRS21]. **Rates**
[EW04, HB11, GJY$^+$14].
Rates-across-Sites [EW04]. **Ratio**
[SBW15, WM19a]. **Ratios**
[JS23b, KMSY20]. **Raw** [STB$^+$19]. **Ray**
[LXC$^+$24, Str11, WKZ$^+$24]. **Rays**
[ZJW$^+$22, WSJ21]. **RBioCloud** [VPB15].
RBP [LZW$^+$23a]. **RBS** [HPH$^+$15].
RDCurve [LGX10]. **Re** [YLXS17].
Re-Mapping [YLXS17]. **Reachability**
[GTDK15, Gos11, LT17]. **Reaction**
[BBW18, CKRS21, FMRS18, FZWS17, HLM$^+$13, HM13, LR20, MKKS20, MDPR18, SWSA21, TLSA18, TZP17, VSR$^+$06, ZWZZ22, SYV14]. **Reaction-Based** [LR20].
Reaction-Diffusion [FZWS17]. **Reactions**
[BCFCC13, DB14, XLC$^+$15]. **Reactive**
[GLS$^+$16]. **Read**
[AKLJ17, GMAS22, JZW17, AKD17, LKW$^+$19, LLL$^+$20, LSL22b, LWS$^+$20, MGS$^+$21, MTM$^+$15, ML18, TED$^+$12, TC16, YZZ$^+$24, YYX$^+$21, CWLZ14, FSL$^+$15].
Readable [HLG10]. **Reading**
[GGP08, LJ20]. **Readmission** [WCC$^+$18].
Reads [CBK20, KK19, LZL$^+$20, LLL$^+$21b, LLBL20, PS11, STB$^+$19, SC22a, WLL$^+$20,

WGL+21, SDAA+14]. **Scale** [ALR+13, BBH+18, CCF+24, DSHM08, DWSB11, FWXZ19, GJZH17, GSX+18, GFG+21, GHL05, HAK+12, HZW+17, HLX+21, HXX21, JGBR15, JLYZ16, LFK16, LSM+21, LSY+20, LDGY21, LJZY24, MPA15, MKKS20, OHK+21, OC13, PZS+20, QBPEL12, RNAR+24, SNK+22, SSS20a, SDH20b, TBRS13, YLL+06, ZSW23, ZZF+19, ZYH+21, IM14, SHK14]. **Scale-Invariant** [LSY+20]. **Scale-Space-Based** [YLL+06]. **Scaled** [AC12]. **Scales** [SHUP19]. **scaling** [AMBK14]. **Scalogram** [NVSH18]. **Scan** [RHZ+24]. **Scans** [TB23]. **Scattered** [MZ17]. **scCAN** [DLG+24]. **SCDA** [YKG+21]. **Scenario** [NCL+23]. **Scenarios** [ZOMC24]. **Schafer** [RGI13]. **Schedule** [NCL+23]. **Schema** [STB+20]. **Scheme** [CWCJ21, HZL19, NHH+17, PPM+13, SSS13b, ZCG+18, ZWHH21]. **Schemes** [KK08, LRM08, OM07, RTC23, ZWL14a]. **Schizophrenia** [DHCW18, WHF+20]. **Schmidt** [GZG17]. **scICML** [ZL24]. **Science** [MMC+23, IM14]. **Scientific** [HVD18]. **SCJ** [FM11, LLT+19]. **Sclerosis** [MGP+22]. **SCOP** [AV12]. **scope** [HWK14]. **Score** [JNST09, Roc11, Tsa12, XWQ+24, LJL+14]. **Scores** [CLST+13, SSK+20, WOYL17, XPH20, ZLLZ17]. **Scoring** [AM12, Csu04, GZFT15, JLwC11, JBgLS19, KK08, LLZ+20a, MSKC19, PA22, PSN+15, AM15, OFC+14, RB14]. **Screening** [CHW21, GZYL22, HF07, RAA20, SDP+21, SDTK19, UJ09, ZPW+21, GCC+14, KKC+14]. **Screens** [STB+20]. **scRNA** [FSNF21, WZHM23]. **scRNA-Seq** [WZHM23, FSNF21]. **SCS** [FLW12, ZZCY10]. **SDE** [MCH+15]. **SDMF** [SB16]. **SDN** [SRM+24]. **SDN-Based** [SRM+24]. **Search** [AKS13, ARP+16, BPM21, BG05, Bro05, CCA12, CBFB12, CZZ+23b, DBR07, FLM+16, FS18, GD22, GDRLH21, HZZY16, LFS06, LTaS13, ME19a, ME19c, MSS13b, MWSM12, NI07, PG12, SZ11, SS04, Smi09, SMSZ17, SJNS19, SB09, TDY+18, YF23, Zha07, ZWcF17, ZKW19, ZLC+21, dJP08, CM15, DGRC15, KFHK14, LMZ14, SHK14, SSKH15, Tan14, YHV+15]. **Searches** [BEW09, CW07, CWDS15]. **Searching** [DWZ+15, GZC+17, KP12, MWL+12, RBdlVMPG16, TZY11, ZHEB05]. **Second** [LLH23, STY+23, BCMW15]. **Second-Order** [LLH23, STY+23]. **Secondary** [AS05, AL12, BRZ+17, CC07, CGPW06, GA23, HVG04, Jia10, KAP+12, LZZ+16, LBQ+13, NA11, NZR11, NSAH19, RSK23, RP13, ST23, TW10, WDH08, WHS04, Yan22, ARZ+14, SEC15]. **Secreted** [SSS+11]. **Secretion** [RSCX18, SZCX19]. **Secretory** [DADF+10, FWW+22]. **Section** [BLP18, BPW17, BPRZ11, CLS22, CNS22a, CLSW23, Cas07, CZ12, FS12, FS13a, FJJ18, GH08b, GJH19, Gus09b, GM16, HMZ17, HBG16, HBG17, HBG18, HBG19, HBG20, HBG21, HHA22, HMS09, KJ04, KJ05, MPZ07, MPZ08, MPSZ09, MWZ13, MSZ19b, MNPZ10, MJ18, RZF07, TS17, TS18, TH18, WYWX16, WLWN17, YS17, ZC15, dSK13, CEG14, LW15, MKARB16, PR14, SA15, XHS15]. **Sectional** [WGK16]. **Secure** [DBSL24, JHW+19, RTPM+19, SAM+19, SJNS19, ZGW+24]. **SecureLR** [JHW+19]. **Security** [AIS+16, AJM18, RCP+18, Sen19, KSA16, MKARB16, ANT19]. **Seed** [HAH13, LLH+17]. **Seed-Extension** [LLH+17]. **Seeded** [LPR+08]. **Seeds** [Bro05, RGN+09, TC16, Zha07]. **Seeks** [Ano12b]. **SeeSite** [LKLB14]. **SEGA** [MKH11]. **Segment** [Csu04, ZCWW19]. **Segmental** [CGPW06, FM12]. **Segmentation** [ALR+13, CXY+23, CSQ+22, CSW+23, DPA+17, DQZ+23, HLX+21, HLY+22, JGW+21, LSW+23, LLL+21a, LZZ+24, MWH+23, PWT10, RFBTD22, TB23,

PS11, POS+18, PT09, QZZ21b, RFBTD22, RTD23, RW07, RCM+19, dSRCT+11, SN24, SLH+06a, SLCL22, WLMW+11, WYHD17, WXS+19, WCZ+23, WZ13a, WCXL18, XHY+18, YZG+19, YHZ+19, YH13, YXZD21, ZSW23, ZANN20, ZWcF17, ZSZ+21, ZSH21, ZZW+22, ZXW+23, ZDY+23, ZLX+20, CV14, GJPSV14, MBS15, PSK+15, STT+14, SPWF14, YTLL15]. **Sequence-** [ZSZ+21]. **Sequence-Based** [CHZ+16, DM22, FHDU22, HLZ+17, LPH18, MGL+12, MHTJ22, WXS+19, WZ13a, ZDY+23]. **sequence-independent** [PSK+15]. **Sequence-Order** [LCGW19]. **Sequence-Specific** [AH11]. **Sequences** [BMCY22, Bi09, CW07, CZ20, CFOS06, CWLS15, CLS19, CAN+08, CHK17, DSVMM18, FM12, HC17, HLDZ17, HLH11, JDHL20, Kar12a, KWL07, KC11, KT07, LPH18, LLW+11, LYL+17, LL22, MRK18, MS21, MIC+07, NNW24, PFJ+19, RH05, RFFB+20, RLV04, RA16, SIK20, SLH06b, ST23, TED+12, WL13a, WKLL12, Wan12, WCLY20, WL22, Wu11, XLZW22, ZWZS16, ZGZ+20, ZWL+23, CR14, DKS+15, GÁVRRL15, LZGZ14, WL14, YlCW+15]. **Sequencing** [AKR12, BBN18, CH11, FS13b, HG16, JKC23, AKD17, KSS15, Kur13, LMW+24, LLL+21b, LMZL17, LSL22b, MMC+23, ML18, OLS+13, PNP+18, Pre04, SC22a, TWW+20, WM19a, WGL+21, WPL15, YKW17, YWW20, YWW+18, YYX+21, ZZ20, FSL+15, WLC+15, XZY+14]. **Sequencing-by-Hybridization** [Pre04]. **Sequential** [AKV16, KCZ+15, LLW+22, MSP+19, SSZ+23, WL07, YLL+06, ZWZS16, ZCT22]. **Serial** [WZA07]. **Series** [AM22a, BMK11, EAS13, GTX+23, HAH13, KSB12, KMG+05, LLL15, MTSCO10, ÖBT21, PH10b, RMS15, SMK22, SC11, WLL+09, WGP11, ZZKW18]. **Serum** [RTA+16]. **Server** [XYYZ20, LBL+10]. **Service** [XLX+21]. **Services** [KPP19, YJJW21, ZBY+21]. **Set** [AFAAW+11, BGHC20, BSV10, DRS12, FLAM15, HYY11, HMK+07, JKNE21, LDZL23, LZH18, NLGG12, SMSZ17, WYL07, XLZ+15, YSC13, YNN+18, ZJW+22, BM15, DB14, MZL15, WLG+14]. **Set-Integrated** [LDZL23]. **Sets** [AJD+12, ANR+23, BKP+19, BMHS13, BNV+13, Csu04, Cza18, DK17, DG19, GLG10, HS08, HC07, KNS+05, KBSCZ12, LZS23, LWS+20, OMWX09, PAS+11, Pol13, RBdlVMPG16, RGCB05, SSS+11, SMK+12, UC10, WZZ+18, WCQ+19, YC08, ZWW17]. **Seventh** [MVVR21a]. **Several** [FM11]. **Severity** [LZZ+24]. **Sex** [GGM21]. **Shaking** [CNS+22b]. **Shannon** [DGH+06]. **Shape** [ADPH11, ADPH13, ARP+16, DZA+06, GAGM11, Mat07, Str11, YFYW23, ZSH21, ZZW+22, ZHD+21]. **Shape-Structure** [DZA+06]. **Shaped** [AKS20, BG13]. **Share** [LBL12b]. **Shared** [JGW+21, PYL+21]. **Sharing** [NGY+16, WAG19]. **Shaving** [GLG10, SDCW11]. **Sheet** [AAE11, DNS19]. **Shewanella** [DS19]. **Shifting** [AMBK14]. **Shifting-and-scaling** [AMBK14]. **Shock** [CRP12]. **Shoot** [GPF+20, TRKRC13]. **Shorelines** [vIKKS08]. **Short** [AKLJ17, GBD17, JL10, KK19, LEAK11, LKW+19, LL19, LSL22b, MTM+15, Pha23, Roc06, SC11, SSS20b, TR07, TED+12, WLL+09, WCLY20, WHW21, YYX+21, ZCL21, ZMKL22, ZYYX23, ZLX+20, FSL+15]. **Short-Read** [LKW+19, TED+12, YYX+21, FSL+15]. **Short-Term** [LL19, Pha23, TR07, WHW21, ZCL21, ZYYX23, ZLX+20]. **Shortest** [ATX21, ARZ+14]. **Shot** [CJH+21, GM22, LCTW24, WLL+24]. **Shotgun** [YFY+22, ZKP+07]. **Show** [SYKS15]. **Shrinkage** [MRS09, WDS+12]. **Shuffled** [HDS+18]. **Siamese** [XWP+24]. **Siamese-Based** [XWP+24]. **Side** [AD12, JQH+20, LBL12b, UKC+23, ZYJ+23, GBLZ14]. **Side-Chain** [LBL12b, GBLZ14].

[OW20]. **XlnR** [OMAdG+12]. **XML** [LLZ+20b]. **XML-Based** [LLZ+20b]. **Xor** [BVD+10]. **Xylanase** [ZD21].

Y-Ion [WM19a]. **Y-Linked** [GGM21]. **YamiPred** [KTLM15]. **Year** [Gus09a]. **Yeast** [CAW+19, CS15, ZACS09].

Zassenhaus [CP13]. **zebrafish** [GCC+14]. **Zero** [GM22, YNBM05, ZW13]. **Zero-Suppressed** [YNBM05]. **Zika** [RAA20]. **Zoom** [TDZZ24]. **ZoomOut** [ABS15].

References

Ascension:2022:BPM

[AAB22] Alex M. Ascensión and Marcos J. Araúzo-Bravo. BigMPI4py: Python module for parallelization of big data objects discloses germ layer specific DNA demethylation motifs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1507–1522, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3043979`.

Aydin:2011:BMA

[AAE11] Zafer Aydin, Yucel Altunbasak, and Hakan Erdogan. Bayesian models and algorithms for protein β-sheet prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):395–409, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Abate:2013:GLB

[AAF+13] Francesco Abate, Andrea Acquaviva, Elisa Ficarra, Roberto Piva, and Enrico Macii. Gelsius: a literature-based workflow for determining quantitative associations between genes and biological processes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):619–631, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Alazmi:2018:SBD

[AAG+18] Meshari Alazmi, Ahmed Abbas, Xianrong Guo, Ming Fan, Lihua Li, and Xin Gao. A slice-based ^{13}c-detected NMR spin system forming and resonance assignment method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1999–2008, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Alim:2018:CSP

[AAH+18] Md Abdul Alim, Ahmet Ay, Md Mahmudul Hasan, My T. Thai, and Tamer Kahveci. Construction of signaling pathways with RNAi data and multiple reference networks.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 15(4):1079–1091, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Abbaszadeh:2022:DDK

[AAKB22] Omid Abbaszadeh, Ali Azarpeyvand, Alireza Khanteymoori, and Abbas Bahari. Data-driven and knowledge-based algorithms for gene network reconstruction on high-dimensional data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (3):1545–1557, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3034861`.

Azofeifa:2017:AAA

[AALD17] Joseph G. Azofeifa, Mary A. Allen, Manuel E. Lladser, and Robin D. Dowell. An annotation agnostic algorithm for detecting nascent RNA transcripts in GRO-Seq. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1070–1081, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Abul:2006:PAE

[AAP06] Osman Abul, Reda Alhajj, and Faruk Polat. A powerful approach for effective finding of significantly differentially expressed genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):220–231, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Arabameri:2020:DCC

[AAT20] Abazar Arabameri, Davud Asemani, and Pegah Teymourpour. Detection of colorectal carcinoma based on microbiota analysis using generalized regression neural networks and nonlinear feature selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):547–557, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2870124`.

Amit:2014:LEP

[ABH+14] Mika Amit, Rolf Backofen, Steffen Heyne, Gad M. Landau, Mathias Möhl, Christina Otto, and Sebastian Will. Local exact pattern matching for non-fixed RNA structures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):219–230, January 2014. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic).

Alexandrino:2023:RID

[ABO+23] Alexsandro Oliveira Alexandrino, Klairton Lima Brito, Andre Rodrigues Oliveira, Ulisses Dias, and Zanoni Dias. Reversal and indel distance with intergenic region information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1628–1640, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215615`.

Athanasiadis:2015:ZAM

[ABS15] Emmanouil I. Athanasiadis, Marilena M. Bourdakou, and George M. Spyrou. ZoomOut: Analyzing multiple networks as single nodes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1213–1216, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Athanasiadis:2017:DMR

[ABS17] Emmanouil Athanasiadis, Marilena Bourdakou, and George Spyrou. D-Map: Random walking on gene network inference maps towards differential avenue discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):484–490, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ansari:2012:DPS

[ABVD12] Nadeem A. Ansari, Riyue Bao, Calin Voichita, and Sorin Draghici. Detecting phenotype-specific interactions between biological processes from microarray data and annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1399–1409, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ambert:2012:IGS

[AC12] Kyle H. Ambert and Aaron M. Cohen. k-information gain scaled nearest neighbors: a novel approach to classifying protein-protein interaction-related documents. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):305–310, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Angione:2013:POO

[ACC+13] Claudio Angione, Giovanni Carapezza, Jole Costanza, Pietro Lio, and Giuseppe Nicosia. Pareto optimality in organelle energy metabolism

analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1032–1044, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Alden:2020:UEE

[ACCT20] Kieran Alden, Jason Cosgrove, Mark Coles, and Jon Timmis. Using emulation to engineer and understand simulations of biological systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (1):302–315, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2843339`.

Ahmed:2024:AIB

[ACJ24] Imran Ahmed, Abdellah Chehri, and Gwanggil Jeon. Artificial intelligence and blockchain enabled smart healthcare system for monitoring and detection of COVID-19 in biomedical images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):814–822, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3294333`.

Ahmed:2023:APN

[ACJP23] Imran Ahmed, Abdellah Chehri, Gwanggil Jeon, and Francesco Piccialli. Automated pulmonary nodule classification and detection using deep learning architectures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (4):2445–2456, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3192139`.

Apostolico:2010:VDE

[ACP10] Alberto Apostolico, Matteo Comin, and Laxmi Parida. VARUN: Discovering extensible motifs under saturation constraints. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):752–762, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Acharya:2022:RFP

[ACP22] Sudipta Acharya, Laizhong Cui, and Yi Pan. A refined 3-in-1 fused protein similarity measure: Application in threshold-free hub detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):192–206, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2973563`.

Alon:2010:AMP

[ACPR10] Noga Alon, Benny Chor, Fabio Pardi, and Anat Rapoport. Approximate maximum parsimony and ancestral maximum likelihood. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (1):183–187, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Angadi:2021:NWC

[ACSR21] Ulavappa B. Angadi, Krishna Kumar Chaturvedi, Sudhir Srivastava, and Anil Rai. A novel way of comparing protein 3D structure using graph partitioning approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1361–1368, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2938948`.

Au:2005:ACG

[ACWW05] Wai-Ho Au, Keith C. C. Chan, Andrew K. C. Wong, and Yang Wang. Attribute clustering for grouping, selection, and classification of gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):83–101, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Au:2007:CAC

[ACWW07] Wai-Ho Au, Keith C. C. Chan, Andrew K. C. Wong, and Yang Wang. Correction to "Attribute Clustering for Grouping, Selection, and Classification of Gene Expression Data". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):157, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ashlock:2012:DER

[AD12] Wendy Ashlock and Suprakash Datta. Distinguishing endogenous retroviral LTRs from SINE elements using features extracted from evolved side effect machines. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1676–1689, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Axenopoulos:2011:SDF

[ADPH11] Apostolos Axenopoulos, Petros Daras, Georgios Papadopoulos, and Elias Houstis. A shape descriptor for fast complementarity matching in molecular docking. *IEEE/ACM Transactions on Computational Biology*

and Bioinformatics, 8(6): 1441–1457, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Axenopoulos:2013:SDP

[ADPH13] Apostolos Axenopoulos, Petros Daras, Georgios E. Papadopoulos, and Elias Houstis. SP-Dock: Protein-protein docking using shape and physicochemical complementarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):135–150, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Allman:2018:STI

[ADR18] Elizabeth S. Allman, James H. Degnan, and John A. Rhodes. Species tree inference from gene splits by unrooted STAR methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):337–342, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Al-Dalky:2016:AMC

[ADTAQ16] Rami Al-Dalky, Kamal Taha, Dirar Al Homouz, and Murad Qasaimeh. Applying Monte Carlo simulation to biomedical literature to approximate genetic network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):494–504, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Andonie:2011:FAP

[AFAAW+11] Razvan Andonie, Levente Fabry-Asztalos, Christopher B. Abdul-Wahid, Sarah Abdul-Wahid, Grant I. Barker, and Lukas C. Magill. Fuzzy ARTMAP prediction of biological activities for potential HIV-1 protease inhibitors using a small molecular data set. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):80–93, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Amin:2012:TSG

[AFJ12] Mohammad Shafkat Amin, Russell L. Finley, Jr., and Hasan M. Jamil. Top-k similar graph matching using TraM in biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1790–1804, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Andersen:2019:CTM

[AFMS19] Jakob L. Andersen, Christoph

Flamm, Daniel Merkle, and Peter F. Stadler. Chemical transformation motifs — modelling pathways as integer hyperflows. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):510–523, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2781724`.

Ali:2018:SDS

[AGAS18] M. Syed Ali, N. Gunasekaran, Choon Ki Ahn, and Peng Shi. Sampled-data stabilization for fuzzy genetic regulatory networks with leakage delays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):271–285, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ambroise:2011:IRP

[AGGM11] Jerome Ambroise, Joachim Giard, Jean-Luc Gala, and Benoit Macq. Identification of relevant properties for epitopes detection using a regression model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1700–1707, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Arribas-Gil:2009:SAS

[AGMP09] Ana Arribas-Gil, Dirk Metzler, and Jean-Louis Plouhinec. Statistical alignment with a sequence evolution model allowing rate heterogeneity along the sequence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):281–295, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Agrawal:2011:PSS

[AH11] Ankit Agrawal and Xiaoqiu Huang. Pairwise statistical significance of local sequence alignment using sequence-specific and position-specific substitution matrices. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):194–205, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

An:2021:HRP

[AHC+21] Ying An, Nengjun Huang, Xianlai Chen, Fangxiang Wu, and Jianxin Wang. High-risk prediction of cardiovascular diseases via attention-based deep neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):1093–1105, May/June 2021. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2935059.

Awais:2021:PIP

[AHK+21] Muhammad Awais, Waqar Hussain, Yaser Daanial Khan, Nouman Rasool, Sher Afzal Khan, and Kuo-Chen Chou. iPhosH-PseAAC: Identify phosphohistidine sites in proteins by blending statistical moments and position relative features according to the Chou's 5-step rule and general pseudo amino acid composition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):596–610, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2919025.

Adhikari:2023:DTL

[AHN23] Mainak Adhikari, Abhishek Hazra, and Sudarshan Nandy. Deep transfer learning for communicable disease detection and recommendation in edge networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2468–2479, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3180393.

Anders:2018:IPR

[AHT+18] Gerd Anders, Ulrich Hassiepen, Stephan Theisgen, Stephan Heymann, Lionel Muller, Tania Panigada, Daniel Huster, and Sergey A. Samsonov. The intrinsic pepsin resistance of interleukin-8 can be explained from a combined bioinformatical and experimental approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):300–308, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ali:2016:SAC

[AIS+16] Sk Subidh Ali, Mohamed Ibrahim, Ozgur Sinanoglu, Krishnendu Chakrabarty, and Ramesh Karri. Security assessment of cyberphysical digital microfluidic biochips. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):445–458, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Acharya:2012:GCA

[AJD+12] Lipi Acharya, Thair Judeh, Zhansheng Duan, Michael Rabbat, and Dongxiao Zhu. GSGS: a computational ap-

proach to reconstruct signaling pathway structures from gene sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):438–450, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ayday:2018:GIW

[AJM18] Erman Ayday, Xiaoqian Jiang, and Bradley Malin. GenoPri'16: International workshop on genome privacy and security. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1403–1404, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Al-Jarrah:2015:RSL

[AJYT+15] Omar Y. Al-Jarrah, Paul D. Yoo, Kamal Taha, Sami Muhaidat, Abdallah Shami, and Nazar Zaki. Randomized subspace learning for proline cis–trans isomerization prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):763–769, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Arif:2022:DDL

[AKA+22] Muhammad Arif, Muhammad Kabir, Saeed Ahmed, Abid Khan, Fang Ge, Adel Khelifi, and Dong-Jun Yu. DeepCPPred: a deep learning framework for the discrimination of cell-penetrating peptides and their uptake efficiencies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2749–2759, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3102133`.

Kawam:2017:SSH

[AKD17] Ahmad Al Kawam, Sunil Khatri, and Aniruddha Datta. A survey of software and hardware approaches to performing read alignment in next generation sequencing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1202–1213, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Alatrany:2023:TLC

[AKH+23] Abbas Saad Alatrany, Wasiq Khan, Abir J. Hussain, Jamila Mustafina, and Dhiya Al-Jumeily. Transfer learning for classification of Alzheimer's disease based on genome wide data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2700–2711, 2023.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3233869`.

Arram:2017:LFA

[AKLJ17] James Arram, Thomas Kaplan, Wayne Luk, and Peiyong Jiang. Leveraging FPGAs for accelerating short read alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):668–677, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Akutsu:2012:FPA

[AKMT12] Tatsuya Akutsu, Sven Kosub, Avraham A. Melkman, and Takeyuki Tamura. Finding a periodic attractor of a Boolean network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1410–1421, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Agius:2007:TSA

[AKNB07] Phaedra Agius, Barry Kreiswirth, Steve Naidich, and Kristin Bennett. Typing *Staphylococcus aureus* using the spa gene and novel distance measures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):693–704, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Andreotti:2012:ALR

[AKR12] Sandro Andreotti, Gunnar W. Klau, and Knut Reinert. Antilope — a Lagrangian relaxation approach to the de novo peptide sequencing problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (2):385–394, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ahirwal:2013:EEA

[AKS13] M. K. Ahirwal, A. Kumar, and G. K. Singh. EEG/ERP adaptive noise canceller design with Controlled Search Space (CSS) approach in cuckoo and other optimization algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1491–1504, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Azuma:2020:SBA

[AKS20] Shun-Ichi Azuma, Toshimitsu Kure, and Toshiharu Sugie. Structural bistability analysis of flower-shaped and chain-shaped Boolean networks. *IEEE/ACM Transactions on Computa-*

tional Biology and Bioinformatics, 17(6):2098–2106, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2917196`.

Ancherbak:2016:TDG

[AKV16] Sergiy Ancherbak, Ercan E. Kuruoglu, and Martin Vingron. Time-dependent gene network modelling by sequential Monte Carlo. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6): 1183–1193, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Armano:2012:EII

[AL12] Giuliano Armano and Filippo Ledda. Exploiting intrastructure information for secondary structure prediction with multifaceted pipelines. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):799–808, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Abdollahi:2022:DAD

[ALC22] Sina Abdollahi, Peng-Chan Lin, and Jung-Hsien Chiang. DiaDeL: an accurate deep learning-based model with mutational signatures for predicting metastasis stage and cancer types. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1336–1343, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3115504`.

Aleb:2022:MAM

[Ale22] Nassima Aleb. A mutual attention model for drug target binding affinity prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3224–3232, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3121275`.

Adl:2017:DPI

[ALQ17] Amin Ahmadi Adl, Hye-Seung Lee, and Xiaoning Qian. Detecting pairwise interactive effects of continuous random variables for biomarker identification with small sample size. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6): 1265–1275, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

AlNasr:2013:IBS

[ALR+13] Kamal Al Nasr, Chunmei

Liu, Mugizi Rwebangira, Legand Burge, and Jing He. Intensity-based skeletonization of CryoEM gray-scale images using a true segmentation-free algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5): 1289–1298, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Altuntas:2023:DAC

[Alt23] Volkan Altuntas. Diffusion alignment coefficient (DAC): a novel similarity metric for protein-protein interaction network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):894–903, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3185406`.

Aluru:2021:ENE

[Alu21] Srinivas Aluru. Editorial: From the new Editor-in-Chief. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2058, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3108133`.

Alves:2018:MSE

[ALWG18] Pedro Alves, Shuang Liu, Daifeng Wang, and Mark Gerstein. Multiple-swarm ensembles: Improving the predictive power and robustness of predictive models and its use in computational biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):926–933, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ashtawy:2012:CAR

[AM12] Hossam M. Ashtawy and Nihar R. Mahapatra. A comparative assessment of ranking accuracies of conventional and machine-learning-based scoring functions for protein-ligand binding affinity prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1301–1313, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ashtawy:2015:CAP

[AM15] Hossam M. Ashtawy and Nihar R. Mahapatra. A comparative assessment of predictive accuracies of conventional and machine learning scoring functions for protein–ligand binding affinity prediction. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 12(2):335–347, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ahmed:2019:GMS

[AM19] Syed Ali Ahmed and Saad Mneimneh. Gibbs/MCMC sampling for multiple RNA interaction with sub-optimal solutions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):703–712, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ajmal:2022:DBN

[AM22a] Hamda B. Ajmal and Michael G. Madden. Dynamic Bayesian network learning to infer sparse models from time series gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2794–2805, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3092879`.

Alazmi:2022:IIB

[AM22b] Meshari Alazmi and Olaa Motwalli. Immuno-informatics based peptides: an approach for vaccine development against outer membrane proteins of *Pseudomonas* genus. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):966–973, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3032651`.

Ahmed:2014:SSC

[AMBK14] Hasin Afzal Ahmed, Priyakshi Mahanta, Dhruba Kumar Bhattacharyya, and Jugal Kumar Kalita. Shifting-and-scaling correlation based biclustering algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1239–1252, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Agapito:2016:ECO

[AMGC16] Giuseppe Agapito, Marianna Milano, Pietro Hiram Guzzi, and Mario Cannataro. Extracting cross-ontology weighted association rules from gene ontology annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):197–208, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ang:2016:SUS

[AMHH16] Jun Chin Ang, Andri Mirzal,

Habibollah Haron, and Haza Nuzly Abdull Hamed. Supervised, unsupervised, and semi-supervised feature selection: a review on gene selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):971–989, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Araghi:2021:HSA

[AN21] Sahar Araghi and Thanh Nguyen. A hybrid supervised approach to human population identification using genomics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):443–454, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2919501`.

Anonymous:2004:AI

[Ano04a] Anonymous. Annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(4):191–192, October 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2004:INA

[Ano04b] Anonymous. Introduction of new Associate Editor. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(2):65, April 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2005:AI

[Ano05a] Anonymous. 2005 annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(4):380–384, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2005:CPS

[Ano05b] Anonymous. Call for papers for Special Issue on Computational Intelligence Approaches in Computational Biology and Bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):271, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2006:RL

[Ano06a] Anonymous. 2005 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):95–96, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2006:AI

[Ano06b] Anonymous. Annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(4):??, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2008:AI

[Ano08a] Anonymous. 2007 annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5 (1):148–158, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2008:RL

[Ano08b] Anonymous. 2007 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5 (1):146–147, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2008:CAE

[Ano08c] Anonymous. Call for applications for Editor-in-Chief. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1): 159, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2009:RL

[Ano09a] Anonymous. 2008 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (1):171–173, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2009:TAI

[Ano09b] Anonymous. 2009 TCBB annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):Not in Print, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2009:CPS

[Ano09c] Anonymous. Call for papers: Special issue of transactions in computational biology and bioinformatics: Special issue on BioCreative II.5. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):703, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2010:RL

[Ano10a] Anonymous. 2009 reviewer's list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (1):188–190, January 2010. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Anonymous:2010:TAI

[Ano10b] Anonymous. 2010 TCBB annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):763–767, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2010:EN

[Ano10c] Anonymous. Editor's note. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1): 1, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2012:CPS

[Ano12a] Anonymous. Call for papers: Special issue on '-omics' based companion diagnostics for personalized medicine. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1855, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2012:IAT

[Ano12b] Anonymous. IEEE/ACM Transactions on Computational Biology and Bioinformatics seeks new Editor in Chief for 2013–2014 terms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):942, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2013:RL

[Ano13a] Anonymous. 2012 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (1):240–243, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2013:CPSb

[Ano13b] Anonymous. Call for papers: Special issue on software and databases in TCBB. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):816, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2013:CPSc

[Ano13c] Anonymous. Call for papers: Special issue on software and databases in TCBB. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1086, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2013:CPSa

[Ano13d] Anonymous. Call for papers: Special issue on sofware and databases in TCBB. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):544, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2013:IOA

[Ano13e] Anonymous. IEEE open access publishing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1344, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anonymous:2016:RL

[Ano16] Anonymous. 2015 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13 (1):168–171, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Aharoni:2011:QPD

[ANR11] Ehud Aharoni, Hani Neuvirth, and Saharon Rosset. The quality preserving database: a computational framework for encouraging collaboration, enhancing power and controlling false discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1431–1437, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Anjum:2023:CMA

[ANR+23] Naser Anjum, Raian Latif Nabil, Rakibul Islam Rafi, Md. Shamsuzzoha Bayzid, and M. Saifur Rahman. CD-MAWS: an alignment-free phylogeny estimation method using cosine distance on minimal absent word sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):196–205, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3136792`.

Ayday:2019:GIW

[ANT19] Erman Ayday, Muhammad Naveed, and Haixu Tang. GenoPri'17: International Workshop on Genome Privacy and Security. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1322–1323, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Al-Ouran:2018:DGR

[AOSN+18] Rami Al-Ouran, Robert Schmidt, Ashwini Naik, Jef-

frey Jones, Frank Drews, David Juedes, Laura Elnitski, and Lonnie Welch. Discovering gene regulatory elements using coverage-based heuristics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1290–1300, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Alekseyev:2007:CBG

[AP07] Max A. Alekseyev and Pavel A. Pevzner. Colored de Bruijn graphs and the genome halving problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (1):98–107, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Awdeh:2018:DEA

[APKP18] Aseel Awdeh, Hilary Phenix, Mads Karn, and Theodore J. Perkins. Dynamics in epistasis analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):878–891, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Avcu:2018:ACM

[APPG18] Neslihan Avcu, Nihal Pekergin, Ferhan Pekergin, and Cuneyt Guzelis. Aggregation for computing multi-modal stationary distributions in 1-D gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):813–827, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Allman:2011:ITT

[APRS11] Elizabeth S. Allman, Sonja Petrović, John A. Rhodes, and Seth Sullivant. Identifiability of two-tree mixtures for group-based models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):710–722, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Allman:2009:ICM

[AR09] Elizabeth S. Allman and John A. Rhodes. The identifiability of covarion models in phylogenetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):76–88, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ahmed:2020:AEC

[ARK20] Syed Sazzad Ahmed, Swarup Roy, and Jugal Kalita. Assessing the effectiveness of causality inference methods for gene regulatory net-

works. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):56–70, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2853728`.

Abbas:2019:QRE

[ARM+19] Houssam Abbas, Alena Rodionova, Konstantinos Mamouras, Ezio Bartocci, Scott A. Smolka, and Radu Grosu. Quantitative regular expressions for arrhythmia detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1586–1597, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Axenopoulos:2016:SSF

[ARP+16] Apostolos Axenopoulos, Dimitrios Rafailidis, Georgios Papadopoulos, Elias N. Houstis, and Petros Daras. Similarity search of flexible 3D molecules combining local and global shape descriptors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):954–970, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Aparicio:2017:EAG

[ARS17] David Aparicio, Pedro Ribeiro, and Fernando Silva. Extending the applicability of graphlets to directed networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1302–1315, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nasr:2014:SSS

[ARZ+14] Kamal Al Nasr, Desh Ranjan, Mohammad Zubair, Lin Chen, and Jing He. Solving the secondary structure matching problem in cryo-EM de novo modeling using a constrained K-shortest path graph algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (2):419–430, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Allali:2005:NDH

[AS05] Julien Allali and Marie-France Sagot. A new distance for high level RNA secondary structure comparison. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):3–14, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Aluru:2015:GEI

[AS15] Srinivas Aluru and Donna K. Slonim. Guest Editors' introduction: selected papers from ACM-BCB 2013. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):2–3, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Armananzas:2011:PSM

[ASI+11] Ruben Armananzas, Yvan Saeys, Inaki Inza, Miguel Garcia-Torres, Concha Bielza, Yves van de Peer, and Pedro Larranaga. Peakbin selection in mass spectrometry data using a consensus approach with estimation of distribution algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 760–774, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Aeling:2007:DDE

[ASJ+07] Kimberly A. Aeling, Nicholas R. Steffen, Matthew Johnson, G. Wesley Hatfield, Richard H. Lathrop, and Donald F. Senear. DNA deformation energy as an indirect recognition mechanism in protein-DNA interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):117–125, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ali:2023:EAK

[ASK+23] Sarwan Ali, Bikram Sahoo, Muhammad Asad Khan, Alexander Zelikovsky, Imdad Ullah Khan, and Murray Patterson. Efficient approximate kernel based spike sequence classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3376–3388, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3206284`.

Acharya:2020:MFG

[ASP20] Sudipta Acharya, Sriparna Saha, and Prasanna Pradhan. Multi-factored gene-gene proximity measures exploiting biological knowledge extracted from gene ontology: Application in gene clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):207–219, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2849362`.

Aakesson:2022:CNN

[ÅSWH22] Mattias Åkesson, Prashant

Singh, Fredrik Wrede, and Andreas Hellander. Convolutional neural networks as summary statistics for approximate Bayesian computation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3353–3365, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3108695`.

Alden:2017:EAS

[ATA+17] Kieran Alden, Jon Timmis, Paul S. Andrews, Henrique Veiga-Fernandes, and Mark Coles. Extending and applying Spartan to perform temporal sensitivity analyses for predicting changes in influential biological pathways in computational models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (2):431–442, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Aoki:2022:HMT

[ATO22] Raquel Aoki, Frederick Tung, and Gabriel L. Oliveira. Heterogeneous multi-task learning with expert diversity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3093–3102, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3175456`.

Allen:2021:UFP

[ATX21] Daniel R. Allen, Sharma V. Thankachan, and Bojian Xu. An ultra-fast and parallelizable algorithm for finding k-mismatch shortest unique substrings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):138–148, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2968531`.

Angadi:2012:SSS

[AV12] Ulavappa B. Angadi and M. Venkatesulu. Structural SCOP superfamily level classification using unsupervised machine learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (2):601–608, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Akkasi:2017:IBN

[AV17] Abbas Akkasi and Ekrem Varoglu. Improving biochemical named entity recognition using PSO classifier selection and Bayesian combination methods. *IEEE/ACM Transactions on Computational Biology and Bioin-*

formatics, 14(6):1327–1338, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Abate:2012:MMS

[AVD+12] Alessandro Abate, Stephane Vincent, Roel Dobbe, Alberto Silletti, Neal Master, Jeffrey D. Axelrod, and Claire J. Tomlin. A mathematical model to study the dynamics of epithelial cellular networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1607–1620, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

An:2018:LNN

[AWW18] Shuai An, Jun Wang, and Jinmao Wei. Local-nearest-neighbors-based feature weighting for gene selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1538–1548, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Adnan:2022:CER

[AZHR22] Nahim Adnan, Maryam Zand, Tim H. M. Huang, and Jianhua Ruan. Construction and evaluation of robust interpretation models for breast cancer metastasis prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1344–1353, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3120673`.

Biswas:2018:BOR

[BA18] Surama Biswas and Sriyankar Acharyya. A bi-objective RNN model to reconstruct gene regulatory network: a modified multi-objective simulated annealing approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):2053–2059, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bilu:2006:FAO

[BAK06] Yonatan Bilu, Pankaj K. Agarwal, and Rachel Kolodny. Faster algorithms for optimal multiple sequence alignment based on pairwise comparisons. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(4):408–422, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Barshai:2022:GCN

[BAO22] Mira Barshai, Alice Aubert, and Yaron Orenstein. G4detector: Convolutional neural net-

work to predict DNA G-quadruplexes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):1946–1955, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3073595`.

Brito:2023:GRD

[BAO+23] Klairton Lima Brito, Alexsandro Oliveira Alexandrino, Andre Rodrigues Oliveira, Ulisses Dias, and Zanoni Dias. Genome rearrangement distance with a flexible intergenic regions aspect. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1641–1653, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3165443`.

Bafna:2004:NRE

[BB04] Vineet Bafna and Vikas Bansal. The number of recombination events in a sample history: Conflict graph and lower bounds. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(2):78–90, April 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bandyopadhyay:2011:BIM

[BB11] Sanghamitra Bandyopadhyay and Malay Bhattacharyya. A biologically inspired measure for coexpression analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):929–942, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Berard:2007:PSR

[BBCP07] Severine Bérard, Anne Bergeron, Cedric Chauve, and Christophe Paul. Perfect sorting by reversals is not always difficult. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):4–16, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bustamam:2012:FPM

[BBH12] Alhadi Bustamam, Kevin Burrage, and Nicholas A. Hamilton. Fast parallel Markov clustering in bioinformatics using massively parallel computing on GPU with CUDA and ELLPACK-R sparse format. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):679–692, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Backes:2018:SLS

[BBH+18] Michael Backes, Pascal Berrang, Mathias Humbert, Xiaoyu Shen, and Verena Wolf. Simulating the large-scale erosion of genomic privacy over time. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1405–1412, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Blazewicz:2007:SPD

[BBK+07] Jacek Blazewicz, Edmund Burke, Marta Kasprzak, Alexandr Kovalev, and Mikhail Kovalyov. Simplified partial digest problem: Enumerative and dynamic programming algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):668–680, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Barnat:2012:PSP

[BBK+12] Jiri Barnat, Lubos Brim, Adam Krejci, Adam Streck, David Safranek, Martin Vejnar, and Tomas Vejpustek. On parameter synthesis by parallel model checking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):693–705, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bahadorinejad:2018:OFD

[BBN18] Arghavan Bahadorinejad and Ulisses M. Braga-Neto. Optimal fault detection and diagnosis in transcriptional circuits using next-generation sequencing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):516–525, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bai:2019:SGM

[BBN19] Wenruo Bai, Jeffrey Bilmes, and William S. Noble. Submodular generalized matching for peptide identification in tandem mass spectrometry. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1168–1181, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Barzuza:2008:CPP

[BBSP08] Tamar Barzuza, Jacques S. Beckmann, Ron Shamir, and Itsik Pe'er. Computational problems in perfect phylogeny haplotyping: Typing without calling the allele. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5

(1):101–109, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Backenkohler:2018:MBP

[BBW18] Michael Backenkohler, Luca Bortolussi, and Verena Wolf. Moment-based parameter estimation for stochastic reaction networks in equilibrium. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1180–1192, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bian:2023:IEA

[BCC+23] Yuexin Bian, Jintai Chen, Xiaojun Chen, Xiaoxian Yang, Danny Z. Chen, and Jian Wu. Identifying electrocardiogram abnormalities using a handcrafted-rule-enhanced neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2434–2444, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3140785`.

Breik:2021:PSI

[BCD+21] Keenan Breik, Cameron Chalk, David Doty, David Haley, and David Soloveichik. Programming substrate-independent kinetic barriers with thermodynamic binding networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):283–295, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2959310`.

Blin:2007:CGD

[BCF+07] Guillaume Blin, Cedric Chauve, Guillaume Fertin, Romeo Rizzi, and Stephane Vialette. Comparing genomes with duplications: a computational complexity point of view. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):523–534, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Braz:2013:PMC

[BCFCC13] Fernando A. F. Braz, Jader S. Cruz, Alessandra C. Faria-Campos, and Sergio V. A. Campos. Probabilistic model checking analysis of palytoxin effects on cell energy reactions of the Na+/K+-ATPase. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1530–1541, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bernardini:2013:GRN

[BCL+13a] Camilla Bernardini, Federica Censi, Wanda Lattanzi, Giovanni Calcagnini, and Alessandro Giuliani. Gene regulation networks in early phase of Duchenne muscular dystrophy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):393–400, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bozdag:2013:GTA

[BCL13b] Serdar Bozdag, Timothy J. Close, and Stefano Lonardi. A graph-theoretical approach to the selection of the minimum tiling path from a physical map. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):352–360, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boareto:2015:SVR

[BCLC15] Marcelo Boareto, Jonatas Cesar, Vitor B. P. Leite, and Nestor Caticha. Supervised variational relevance learning, an analytic geometric feature selection with applications to omic datasets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):705–711, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Barma:2015:QMS

[BCMW15] Shovan Barma, Bo-Wei Chen, Ka Lok Man, and Jhing-Fa Wang. Quantitative measurement of split of the second heart sound (S2). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):851–860, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bajaj:2011:FFP

[BCS11] Chandrajit L. Bajaj, Rezaul Chowdhury, and Vinay Siddahanavalli. F^2Dock: Fast Fourier protein-protein docking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):45–58, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bonizzoni:2019:DRI

[BCVS19] Paola Bonizzoni, Simone Ciccolella, Gianluca Della Vedova, and Mauricio Soto. Does relaxing the infinite sites assumption give better tumor phylogenies? An ILP-based comparative approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1410–1423, September

2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bi:2022:RSF

[BCY+22] Hui Bi, Shumei Cao, Hanying Yan, Zhongyi Jiang, Jun Zhang, and Ling Zou. Resting state functional connectivity analysis during general anesthesia: a high-density EEG study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):3–13, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3091000`.

Biane:2019:CRB

[BD19] Celia Biane and Franck Delaplace. Causal reasoning on Boolean control networks based on abduction: Theory and application to cancer drug discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1574–1585, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Birlutiu:2015:BFC

[BDBH15] Adriana Birlutiu, Florence D'Alché-Buc, and Tom Heskes. A Bayesian framework for combining protein and network topology information for predicting protein–protein interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):538–550, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Blin:2010:ARS

[BDD+10] Guillaume Blin, Alain Denise, Serge Dulucq, Claire Herrbach, and Heleene Touzet. Alignments of RNA structures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):309–322, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bao:2018:AAC

[BDD18] Feng Bao, Yue Deng, and Qionghai Dai. ACID: Association correction for imbalanced data in GWAS. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):316–322, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Borges:2018:RGS

[BdOS+18] Vinicius R. P. Borges, Maria Cristina F. de Oliveira, Thais Garcia Silva, Armando Augusto Henriques Vieira, and Bernd Hamann. Region growing for segment-

ing green microalgae images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):257–270, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Benso:2011:CMG

[BDP11] Alfredo Benso, Stefano Di Carlo, and Gianfranco Politano. A cDNA microarray gene expression data classifier for clinical diagnostics based on graph theory. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 577–591, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Badaloni:2012:QRB

[BDS12] Silvana Badaloni, Barbara Di Camillo, and Francesco Sambo. Qualitative reasoning for biological network inference from systematic perturbation experiments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1482–1491, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bansal:2008:STH

[BE08] Mukul S. Bansal and Oliver Eulenstein. An $\Omega(n^2/\log n)$ speed-up of TBR heuristics for the gene-duplication problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):514–524, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boluki:2019:CPB

[BEQD19] Shahin Boluki, Mohammad Shahrokh Esfahani, Xiaoning Qian, and Edward R. Dougherty. Constructing pathway-based priors within a Gaussian mixture model for Bayesian regression and classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):524–537, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2778715`.

Bansal:2009:GDP

[BEW09] Mukul S. Bansal, Oliver Eulenstein, and André Wehe. The gene-duplication problem: Near-linear time algorithms for NNI-based local searches. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):221–231, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bitar:2014:BPC

[BF14] Mainá Bitar and Glória Regina Franco. A basic protein comparative three-dimensional modeling methodological workflow theory and practice. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1052–1065, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boes:2017:LBN

[BFK17] Olivier Boes, Mareike Fischer, and Steven Kelk. A linear bound on the number of states in optimal convex characters for maximum parsimony distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):472–477, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Biller:2013:RBP

[BFM13] Priscila Biller, Pedro Feijao, and Joao Meidanis. Rearrangement-based phylogeny using the single-cut-or-join operation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):122–134, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bertrand:2005:TRL

[BG05] Denis Bertrand and Olivier Gascuel. Topological rearrangements and local search method for tandem duplication trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):15–28, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bogdanowicz:2012:MSD

[BG12] Damian Bogdanowicz and Krzysztof Giaro. Matching split distance for unrooted binary phylogenetic trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):150–160, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Baya:2013:HMC

[BG13] Ariel E. Baya and Pablo M. Granitto. How many clusters: a validation index for arbitrary-shaped clusters. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (2):401–414, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bonnici:2017:VOS

[BG17] Vincenzo Bonnici and Rosalba Giugno. On the

variable ordering in subgraph isomorphism algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):193–203, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bakhteh:2020:IMS

[BGHC20] Somayeh Bakhteh, Alireza Ghaffari-Hadigheh, and Nader Chaparzadeh. Identification of minimum set of master regulatory genes in gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):999–1009, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2875692`.

Bordewich:2009:CTM

[BGHM09] Magnus Bordewich, Olivier Gascuel, Katharina T. Huber, and Vincent Moulton. Consistency of topological moves based on the balanced minimum evolution principle of phylogenetic inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (1):110–117, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Belcastro:2012:REA

[BGS+12] Vincenzo Belcastro, Francesco Gregoretti, Velia Siciliano, Michele Santoro, Giovanni D'Angelo, Gennaro Oliva, and Diego di Bernardo. Reverse engineering and analysis of genome-wide gene regulatory networks from gene expression profiles using high-performance computing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):668–678, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Brown:2006:IPA

[BH06] Daniel G. Brown and Ian M. Harrower. Integer programming approaches to haplotype inference by pure parsimony. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):141–154, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bhattacharyya:2023:BAD

[Bha23] Ramkishore Bhattacharyya. Bidirectional association discovery leads to precise identification of lung cancer biomarkers and genome taxa class. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1783–1794, May 2023. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215630`.

Bonilla-Huerta:2016:HFU

[BHHMCL16] Edmundo Bonilla-Huerta, Alberto Hernandez-Montiel, Roberto-Morales Caporal, and Marco Arjona Lopez. Hybrid framework using multiple-filters and an embedded approach for an efficient selection and classification of microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):12–26, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Berger:2006:JAG

[BHMA06] John A. Berger, Sampsa Hautaniemi, Sanjit K. Mitra, and Jaakko Astola. Jointly analyzing gene expression and copy number data in breast cancer using data reduction models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):2–16, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Brankovic:2019:DFS

[BHP19] Aida Brankovic, Marjan Hosseini, and Luigi Piroddi. A distributed feature selection algorithm based on distance correlation with an application to microarrays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1802–1815, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2833482`.

Bannai:2004:ADO

[BHS+04] Hideo Bannai, Heikki Hyyro, Ayumi Shinohara, Masayuki Takeda, Kenta Nakai, and Satoru Miyano. An $O(N^2)$ algorithm for discovering optimal Boolean pattern pairs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1 (4):159–170, October 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bokes:2021:MBF

[BHS21] Pavol Bokes, Michal Hojcka, and Abhyudai Singh. MicroRNA based feedforward control of intrinsic gene expression noise. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):272–282, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2938502`.

Berlow:2014:IAA

[BHW+14] Noah Berlow, Saad Haider, Qian Wan, Mathew Geltzeiler, Lara E. Davis, Charles Keller, and Ranadip Pal. An integrated approach to anti-cancer drug sensitivity prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):995–1008, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bi:2009:MCE

[Bi09] Chengpeng Bi. A Monte Carlo EM algorithm for De Novo Motif discovery in biomolecular sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):370–386, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bouasker:2021:PAB

[BIBD21] Souad Bouasker, Wissem Inoubli, Sadok Ben Yahia, and Gayo Diallo. Pregnancy associated breast cancer gene expressions: New insights on their regulation based on rare correlated patterns. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 1035–1048, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3015236`.

BinZaman:2023:ASO

[BIDS23] Ahmed Bin Zaman, Toki Tahmid Inan, Kenneth De Jong, and Amarda Shehu. Adaptive stochastic optimization to improve protein conformation sampling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5): 2759–2771, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3134103`.

Bokhari:2010:RNI

[BJ10] Shahid H. Bokhari and Daniel Janies. Reassortment networks for investigating the evolution of segmented viruses. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):288–298, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bulteau:2013:IED

[BJ13] Laurent Bulteau and Minghui Jiang. Inapproximability of $((1, 2))$-exemplar distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1384–1390, November 2013. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Bohnsack:2023:AFS

[BKAV23] Katrin Sophie Bohnsack, Marika Kaden, Julia Abel, and Thomas Villmann. Alignment-free sequence comparison: a systematic survey from a machine learning perspective. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):119–135, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3140873`.

Biswas:2019:RIM

[BKKG19] Ashis Kumer Biswas, Dong-Chul Kim, Mingon Kang, and Jean X. Gao. Robust inductive matrix completion strategy to explore associations between LincRNAs and human disease phenotypes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 2066–2077, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2844816`.

Bogdanov:2018:IEA

[BKLS18] Dan Bogdanov, Liina Kamm, Sven Laur, and Ville Sokk. Implementation and evaluation of an algorithm for cryptographically private principal component analysis on genomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1427–1432, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Baker:2019:PPL

[BKP+19] Dixie B. Baker, Bartha M. Knoppers, Mark Phillips, David van Enckevort, Petra Kaufmann, Hanns Lochmuller, and Domenica Taruscio. Privacy-preserving linkage of genomic and clinical data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1342–1348, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bocker:2011:DGS

[BKR11] Sebastian Bocker, Birte Kehr, and Florian Rasche. Determination of glycan structure from tandem mass spectra. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):976–986, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bicego:2012:ITM

[BLP+12] Manuele Bicego, Pietro Lovato, Alessandro Perina, Marianna Fasoli, Massimo

Delledonne, Mario Pezzotti, Annalisa Polverari, and Vittorio Murino. Investigating topic models' capabilities in expression microarray data classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1831–1836, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bartocci:2018:GEI

[BLP18] Ezio Bartocci, Pietro Lio, and Nicola Paoletti. Guest editors' introduction to the special section on the 14th International Conference on Computational Methods in Systems Biology CMSB 2016. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1122–1123, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boscolo:2008:ITE

[BLR08] Riccardo Boscolo, James C. Liao, and Vwani P. Roychowdhury. An information theoretic exploratory method for learning patterns of conditional gene coexpression from microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):15–24, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Basu:2015:EIF

[BLR15] Saurav Basu, Chi Liu, and Gustavo Kunde Rohde. Extraction of individual filaments from 2D confocal microscopy images of flat cells. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):632–643, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bonet:2012:CFM

[BLS12] Maria Luisa Bonet, Simone Linz, and Katherine St. John. The complexity of finding multiple solutions to betweenness and quartet compatibility. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):273–285, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bocker:2008:CAM

[BM08] Sebastian Bocker and Veli Makinen. Combinatorial approaches for mass spectra recalibration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):91–100, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bonnel:2012:LFP

[BM12] Nicolas Bonnel and Pierre-François Marteau. LNA: Fast protein structural comparison using a Laplacian characterization of tertiary structure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1451–1458, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bordewich:2013:AGP

[BM13] Magnus Bordewich and Radu Mihaescu. Accuracy guarantees for phylogeny reconstruction algorithms based on balanced minimum evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):576–583, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bandyopadhyay:2014:NPB

[BM14] Sanghamitra Bandyopadhyay and Koushik Mallick. A new path based hybrid measure for gene ontology similarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1):116–127, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bhattacharyya:2015:CCS

[BM15] Sourya Bhattacharyya and Jayanta Mukherjee. COSPEDTree: couplet supertree by equivalence partitioning of taxa set and DAG formation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):590–603, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bandyopadhyay:2017:NFV

[BM17] Sanghamitra Bandyopadhyay and Koushik Mallick. A new feature vector based on gene ontology terms for protein–protein interaction prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):762–770, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boukari:2020:ACT

[BM20] Fatima Boukari and Sokratis Makrogiannis. Automated cell tracking using motion prediction-based matching and event handling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):959–971, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2875684`.

Bae:2022:DPA

[BMCY22] Ho Bae, Seonwoo Min, Hyun-Soo Choi, and Sungroh Yoon. DNA privacy: Analyzing malicious DNA sequences using deep neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):888–898, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3017191`.

Bahlouli:2016:FBP

[BMH+16] S. Bahlouli, A. Mokaddem, F. Hamdache, H. Riane, and M. Kameche. Fractal behavior of the pancreatic β-cell near the percolation threshold: Effect of the K_{ATP} channel on the electrical response. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):112–121, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bleik:2013:TCB

[BMHS13] Said Bleik, Meenakshi Mishra, Jun Huan, and Min Song. Text categorization of biomedical data sets using graph kernels and a controlled vocabulary. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1211–1217, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Barker:2011:LGR

[BMK11] Nathan A. Barker, Chris J. Myers, and Hiroyuki Kuwahara. Learning genetic regulatory network connectivity from time series data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):152–165, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bernt:2006:GRB

[BMM06] Matthias Bernt, Daniel Merkle, and Martin Middendorf. Genome rearrangement based on reversals that preserve conserved intervals. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):275–288, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bernt:2008:SPR

[BMM08] Matthias Bernt, Daniel Merkle, and Martin Middendorf. Solving the preserving reversal median problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):332–347, July 2008. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Bandyopadhyay:2014:SCS

[BMM14] Sanghamitra Bandyopadhyay, Saurav Mallik, and Anirban Mukhopadhyay. A survey and comparative study of statistical tests for identifying differential expression from microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1):95–115, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Biswas:2021:RPC

[BMR21] Saikat Biswas, Pabitra Mitra, and Krothapalli Sreenivasa Rao. Relation prediction of co-morbid diseases using knowledge graph completion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):708–717, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2927310`.

Bhadra:2022:UFS

[BMSZ22] Tapas Bhadra, Saurav Mallik, Amir Sohel, and Zhongming Zhao. Unsupervised feature selection using an integrated strategy of hierarchical clustering with singular value decomposition: an integrative biomarker discovery method with application to acute myeloid leukemia. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1354–1364, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3110989`.

Becker:2017:MTL

[BMT17] Matthias Becker and Nadia Magnenat-Thalmann. Muscle tissue labeling of human lower limb in multichannel mDixon MR imaging: Concepts and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (2):290–299, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bordon:2015:FLC

[BMZM15] Jure Bordon, Miha Moskon, Nikolaj Zimic, and Miha Mraz. Fuzzy logic as a computational tool for quantitative modelling of biological systems with uncertain kinetic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1199–1205, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Berry:2006:IPC

[BN06] Vincent Berry and François Nicolas. Improved parameterized complexity of the maximum agreement subtree and maximum compatible tree problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):289–302, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boyen:2013:MMM

[BNV+13] Peter Boyen, Frank Neven, Dries Van Dyck, Felipe Valentim, and Aalt van Dijk. Mining minimal motif pair sets maximally covering interactions in a protein-protein interaction network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):73–86, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boucher:2012:HCS

[BO12] Christina Boucher and Mohamed Omar. On the hardness of counting and sampling center strings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1843–1846, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Brito:2020:HRT

[BODD20] Klairton Lima Brito, Andre Rodrigues Oliveira, Ulisses Dias, and Zanoni Dias. Heuristics for the reversal and transposition distance problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):2–13, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2019.2945759`.

Bontempi:2007:BSI

[Bon07] Gianluca Bontempi. A blocking strategy to improve gene selection for classification of gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):293–300, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Barnett:2024:GML

[BOSF24] Eric J. Barnett, Daniel G. Onete, Asif Salekin, and Stephen V. Faraone. Genomic machine learning meta-regression: Insights on associations of study features with reported model performance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):169–177, 2024. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3343808`.

Bankapur:2022:EML

[BP22] Sanjay Bankapur and Nagamma Patil. An effective multi-label protein sub-chloroplast localization prediction by skipped-grams of evolutionary profiles using deep neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1449–1458, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3037465`.

Bokhari:2012:RNE

[BPJ12] Shahid H. Bokhari, Laura W. Pomeroy, and Daniel A. Janies. Reassortment networks and the evolution of pandemic H1N1 swine-origin influenza. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):214–227, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Banerjee:2021:EPG

[BPM21] Anupam Banerjee, Kuntal Pal, and Pralay Mitra. An evolutionary profile guided greedy parallel replica-exchange Monte Carlo search algorithm for rapid convergence in protein design. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):489–499, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2928809`.

Bach:2013:SND

[BPP+13] Christian Bach, Prabir Patra, Jani M. Pallis, William Sherman, and Hassan Bajwa. Strategy for naturelike designer transcription factors with reduced toxicity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5): 1340–1343, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Borodovsky:2011:GEI

[BPRZ11] Mark Borodovsky, Teresa M. Przytycka, Sanguthevar Rajasekaran, and Alexander Zelikovsky. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):865–866, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Battagliero:2011:EAA

[BPV+11] Simone Battagliero, Giu-

seppe Puglia, Saverio Vicario, Francesco Rubino, Gaetano Scioscia, and Pietro Leo. An efficient algorithm for approximating geodesic distances in tree space. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1196–1207, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Basu:2017:GEI

[BPW17] Mitra Basu, Yi Pan, and Jianxin Wang. Guest Editors introduction to the special section on ISBRA 2014. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (2):314–315, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Biswas:2021:CNM

[BRB21] Sourav Biswas, Sumanta Ray, and Sanghamitra Bandyopadhyay. Colored network Motif analysis by dynamic programming approach: an application in host pathogen interaction network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):550–561, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2923173`.

Barragan:2017:COA

[BRF17] Sandra Barragan, Cristina Rueda, and Miguel A. Fernandez. Circular order aggregation and its application to cell-cycle genes expressions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):819–829, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Brown:2005:OMS

[Bro05] Daniel G. Brown. Optimizing multiple seeds for protein homology search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):29–38, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Behinaein:2018:PNS

[BRS18] Behnam Behinaein, Karen Rudie, and Waheed Sangrar. Petri net siphon analysis and graph theoretic measures for identifying combination therapies in cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):231–243, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Biswas:2017:ECM

[BRZ+17] Abhishek Biswas, Desh Ranjan, Mohammad Zubair, Stephanie Zeil, Kamal Al Nasr, and Jing He. An effective computational method incorporating multiple secondary structure predictions in topology determination for cryo-EM images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):578–586, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bordewich:2007:CHN

[BS07] Magnus Bordewich and Charles Semple. Computing the hybridization number of two phylogenetic trees is fixed-parameter tractable. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):458–466, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bordewich:2008:NRS

[BS08] Magnus Bordewich and Charles Semple. Nature reserve selection problem: a tight approximation algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):275–280, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bryant:2009:CDT

[BS09] David Bryant and Mike Steel. Computing the distribution of a tree metric. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):420–426, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bogdanov:2010:MFP

[BS10a] Petko Bogdanov and Ambuj K. Singh. Molecular function prediction using neighborhood features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):208–217, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bonet:2010:CUD

[BS10b] Maria Luisa Bonet and Katherine St. John. On the complexity of uSPR distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):572–576, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bansal:2011:NFP

[BS11] Mukul S. Bansal and Ron Shamir. A note on the fixed

parameter tractability of the gene-duplication problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 848–850, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Braga:2015:SLG

[BS15] Marília D. V. Braga and Jens Stoye. Sorting linear genomes with rearrangements and indels. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):500–506, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boscolo:2005:GFN

[BSLR05] Riccardo Boscolo, Chiara Sabatti, James C. Liao, and Vwani P. Roychowdhury. A generalized framework for network component analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2 (4):289–301, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Blanco:2021:CAS

[BSR+21] Guillermo Blanco, Borja Sánchez, Lorena Ruiz, Florentino Fdez-Riverola, Abelardo Margolles, and Anália Lourenço. Computational approach to the systematic prediction of glycolytic abilities: Looking into human microbiota. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (6):2302–2313, November/ December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2978461`.

Bhatt:2022:DKG

[BSS+22] Sachin Bhatt, Prithvi Singh, Archana Sharma, Arpita Rai, Ravins Dohare, Shweta Sankhwar, Akash Sharma, and Mansoor Ali Syed. Deciphering key genes and miRNAs associated with hepatocellular carcinoma via network-based approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):843–853, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3016781`.

Braga:2008:ESS

[BSST08] Marília D. V. Braga, Marie-France Sagot, Celine Scornavacca, and Eric Tannier. Exploring the solution space of sorting by reversals, with experiments and an application to evolution. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 5(3):348–356, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Blin:2010:QGP

[BSV10] Guillaume Blin, Florian Sikora, and Stephane Vialette. Querying graphs in protein-protein interactions networks using feedback vertex set. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (4):628–635, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Befekadu:2011:PMR

[BTTR11] Getachew K. Befekadu, Mahlet G. Tadesse, Tsung-Heng Tsai, and Habtom W. Ressom. Probabilistic mixture regression models for alignment of LC-MS data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1417–1424, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Blumenthal:2013:IIR

[BTYC13] Seth Blumenthal, Yisheng Tang, Wenjie Yang, and Brian Chen. Isolating influential regions of electrostatic focusing in protein and DNA structure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1188–1198, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bittig:2017:MSH

[BU17] Arne T. Bittig and Adelinde M. Uhrmacher. ML-Space: Hybrid spatial Gillespie and particle simulation of multi-level rule-based models in cell biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1339–1349, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Betzler:2011:PAF

[BvBF+11] Nadja Betzler, Rene van Bevern, Michael R. Fellows, Christian Komusiewicz, and Rolf Niedermeier. Parameterized algorithmics for finding connected motifs in biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1296–1308, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bhavani:2024:SCV

[BVCD24] T. Bhavani, P. VamseeKrishna, Chinmay Chakraborty, and Priyanka Dwivedi. Stress classification and vital signs

forecasting for IoT–Health monitoring. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):652–659, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3196151`.

Bonizzoni:2007:ELC

[BVD+07] Paola Bonizzoni, Gianluca Della Vedova, Riccardo Dondi, Guillaume Fertin, Raffaella Rizzi, and Stephane Vialette. Exemplar longest common subsequence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):535–543, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bonizzoni:2010:PPX

[BVD+10] Paola Bonizzoni, Gianluca Della Vedova, Riccardo Dondi, Yuri Pirola, and Romeo Rizzi. Pure parsimony xor haplotyping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (4):598–610, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Buhrman:2011:SMR

[BvdGK+11] Harry Buhrman, Peter T. S. van der Gulik, Steven M. Kelk, Wouter M. Koolen, and Leen Stougie. Some mathematical refinements concerning error minimization in the genetic code. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1358–1372, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Boyen:2011:SGM

[BVN+11] Peter Boyen, Dries Van Dyck, Frank Neven, Roeland C. H. J. van Ham, and Aalt D. J. van Dijk. SLIDER: a generic metaheuristic for the discovery of correlated motifs in protein-protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1344–1357, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Battistella:2022:CCO

[BVS+22] Enzo Battistella, Maria Vakalopoulou, Roger Sun, Théo Estienne, Marvin Lerousseau, Sergey Nikolaev, Émilie Alvarez Andres, Alexandre Carré, Stéphane Niyoteka, Charlotte Robert, Nikos Paragios, and Éric Deutsch. COMBING: Clustering in oncology for mathematical and biological identification of novel gene sig-

natures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3317–3331, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3123910`.

Bao:2017:CPS

[BWC17] Wenzheng Bao, Dong Wang, and Yuehui Chen. Classification of protein structure classes on flexible neutral tree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1122–1133, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Burkitt:2012:CCB

[BWRF12] Mark Burkitt, Dawn Walker, Daniella M. Romano, and Alireza Fazeli. Constructing complex 3D biological environments from medical imaging using high performance computing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):643–654, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Biyani:2005:JCP

[BWS05] Pravesh Biyani, Xiaolin Wu, and Abhijit Sinha. Joint classification and pairing of human chromosomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):102–109, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bui:2022:HBB

[BYS+22] Lien A. Bui, Dacosta Yeboah, Louis Steinmeister, Sima Azizi, Daniel B. Hier, Donald C. Wunsch, Gayla R. Olbricht, and Tayo Obafemi-Ajayi. Heterogeneity in blood biomarker trajectories after mild TBI revealed by unsupervised learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1365–1378, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3091972`.

Bai:2023:IBR

[BYW+23] Jun Bai, Chuantao Yin, Zimeng Wu, Jianfei Zhang, Yanmeng Wang, Guanyi Jia, Wenge Rong, and Zhang Xiong. Improving biomedical ReQA with consistent NLI-transfer and post-whitening. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1864–1875, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL

https://dl.acm.org/doi/10.1109/TCBB.2022.3219375.

Bao:2018:MFP

[BYZ+18] Wenzheng Bao, Chang-An Yuan, Youhua Zhang, Kyungsook Han, Asoke K. Nandi, Barry Honig, and De-Shuang Huang. Mutli-features prediction of protein translational modification sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1453–1460, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bai:2023:AKD

[BYZ+23] Jun Bai, Chuantao Yin, Jianfei Zhang, Yanmeng Wang, Yi Dong, Wenge Rong, and Zhang Xiong. Adversarial knowledge distillation based biomedical factoid question answering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):106–118, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3161032.

Bereg:2007:PNB

[BZ07] Sergey Bereg and Yuanyi Zhang. Phylogenetic networks based on the molecular clock hypothesis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):661–667, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Brinza:2008:SPM

[BZ08] Dumitru Brinza and Alexander Zelikovsky. 2SNP: Scalable phasing method for trios and unrelated individuals. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):313–318, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bergemann:2010:SQM

[BZ10] Tracy L. Bergemann and Lue Ping Zhao. Signal quality measurements for cDNA microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):299–308, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Bi:2022:ABB

[BZWD22] Jingshu Bi, Yuanjie Zheng, Chongjing Wang, and Yanhui Ding. An attention based bidirectional LSTM method to predict the binding of TCR and epitope. *IEEE/ACM Transactions on Computational Biology*

and Bioinformatics, 19(6): 3272–3280, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3115353`.

Comin:2014:FEP

[CA14] Matteo Comin and Morris Antonello. Fast entropic profiler: an information theoretic approach for the discovery of patterns in genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):500–509, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Congdon:2008:EIC

[CAN+08] Clare Bates Congdon, Joseph C. Aman, Gerardo M. Nava, H. Rex Gaskins, and Carolyn J. Mattingly. An evaluation of information content as a metric for the inference of putative conserved noncoding regions in DNA sequences using a genetic algorithms approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):1–14, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Casadio:2006:GEI

[Cas06] Rita Casadio. Guest Editor's introduction to the special issue on computational biology and bioinformatics – part 1. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3 (4):321–322, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Casadio:2007:GEI

[Cas07] Rita Casadio. Guest Editor's introduction to the Special Section on Computational Biology and Bioinformatics (WABI) – part 2. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1): 3, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Catalyurek:2017:GEI

[Cat17] Umit V. Catalyurek. Guest Editor's introduction: Selected papers from ACM-BCB 2014. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1000–1001, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2019:QNS

[CAW+19] Minghan Chen, Brandon D. Amos, Layne T. Watson, John J. Tyson, Young Cao, Clifford A. Shaffer, Michael W. Trosset, Cihan

Oguz, and Gisella Kakoti. Quasi-Newton stochastic optimization algorithm for parameter estimation of a stochastic model of the budding yeast cell cycle. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):301–311, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cortes:2011:EMM

[CBES11] Juan Cortes, Sophie Barbe, Monique Erard, and Thierry Simeon. Encoding molecular motions in voxel maps. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):557–563, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Correa:2018:MAP

[CBF+18] Leonardo Correa, Bruno Borguesan, Camilo Farfan, Mario Inostroza-Ponta, and Marcio Dorn. A memetic algorithm for 3D protein structure prediction problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):690–704, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chaudhary:2012:FLS

[CBFB12] Ruchi Chaudhary, J. Gordon Burleigh, and David Fernandez-Baca. Fast local search for unrooted Robinson–Foulds supertrees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1004–1013, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chowdhury:2020:DEA

[CBK20] Hussain Ahmed Chowdhury, Dhruba Kumar Bhattacharyya, and Jugal Kumar Kalita. Differential expression analysis of RNA-seq reads: Overview, taxonomy, and tools. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):566–586, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2873010`.

Chen:2020:BPD

[CBM+20] Ziwei Chen, Xiangqi Bai, Liang Ma, Xiawei Wang, Xiuqin Liu, Yuting Liu, Luonan Chen, and Lin Wan. A branch point on differentiation trajectory is the bifurcating event revealed by dynamical network biomarker analysis of single-cell data. *IEEE/ACM Transactions on*

Computational Biology and Bioinformatics, 17(2):366–375, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2847690`.

Chen:2015:SDI

[CBN15] Ting Chen and Ulisses M. Braga-Neto. Statistical detection of intrinsically multivariate predictive genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):951–963, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chlis:2018:ISB

[CBZ18] Nikolaos-Kosmas Chlis, Ekaterini S. Bei, and Michalis Zervakis. Introducing a stable bootstrap validation framework for reliable genomic signature extraction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):181–190, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2007:CBR

[CC07] Jinmiao Chen and Narendra Chaudhari. Cascaded bidirectional recurrent neural networks for protein secondary structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):572–582, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2009:AAM

[CC09] Xin Chen and Yun Cui. An approximation algorithm for the minimum breakpoint linearization problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):401–409, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2011:FAP

[CC11] Qingfeng Chen and Yi-Ping Phoebe Chen. Function annotation for pseudoknot using structure similarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1535–1544, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cakmak:2021:PMA

[CC21] Ali Cakmak and M. Hasan Celik. Personalized metabolic analysis of diseases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):1014–1025, May/June 2021. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2020.3008196.

Cavuslar:2012:TSA

[CCA12] Gizem Cavuslar, Bulent Catay, and Mehmet Serkan Apaydin. A tabu search approach for the NMR protein structure-based assignment problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1621–1628, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Carrillo-Cabada:2021:GEM

[CCBR+21] Hector Carrillo-Cabada, Jeremy Benson, Asghar M. Razavi, Brianna Mulligan, Michel A. Cuendet, Harel Weinstein, Michela Taufer, and Trilce Estrada. A graphic encoding method for quantitative classification of protein structure and representation of conformational changes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1336–1349, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2945291.

Cristovao:2022:IDL

[CCC+22] Francisco Cristovao, Silvia Cascianelli, Arif Canakoglu, Mark Carman, Luca Nanni, Pietro Pinoli, and Marco Masseroli. Investigating deep learning based breast cancer subtyping using pan-cancer and multi-omic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):121–134, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2020.3042309.

Cai:2020:IMM

[CCCY20] Jiulun Cai, Hongmin Cai, Jiazhou Chen, and Xi Yang. Identifying "many-to–many" relationships between gene-expression data and drug-response data via sparse binary matching. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):165–176, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2849708.

Choudhury:2019:HAE

[CCE19] Olivia Choudhury, Ankush Chakrabarty, and Scott J. Emrich. Highly accurate and efficient data-driven methods for genotype imputation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1107–1116, July 2019.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cruz:2024:BOO

[CCF+24] Fernando Cruz, João Capela, Eugénio C. Ferreira, Miguel Rocha, and Oscar Dias. BioISO: an objective-oriented application for assisting the curation of genome-scale metabolic models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):215–226, March 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3339972`.

Cao:2024:CGC

[CCL+24] Kun Cao, Yangguang Cui, Liying Li, Junlong Zhou, and Shiyan Hu. CPU-GPU cooperative QoS optimization of personalized digital healthcare using machine learning and swarm intelligence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):521–533, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3207509`.

Caceres:2013:WSN

[CCLS13] Alan Joseph J. Caceres, Juan Castillo, Jinnie Lee, and Katherine St. John. Walks on SPR neighborhoods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (1):236–239, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chowdhury:2022:GAD

[CCN22] Tapan Chowdhury, Susanta Chakraborty, and Argha Nandan. GPU accelerated drug application on signaling pathways containing multiple faults using Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):927–939, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3014172`.

Chan:2012:CVM

[CCYW12] Raymond H. Chan, Tony H. Chan, Hau Man Yeung, and Roger Wei Wang. Composition vector method based on maximum entropy principle for sequence comparison. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):79–87, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cho:2008:CHC

[CD08] Hyuk Cho and Inderjit S. Dhillon. Coclustering of

human cancer microarrays using minimum sum-squared residue coclustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):385–400, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2022:LBT

[CDAL22] Qingyu Chen, Jingcheng Du, Alexis Allot, and Zhiyong Lu. LitMC-BERT: Transformer-based multi-label classification of biomedical literature with an application on COVID-19 literature curation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2584–2595, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3173562`.

Chang:2016:RGR

[CDB+16] Young Hwan Chang, Roel Dobbe, Palak Bhushan, Joe W. Gray, and Claire J. Tomlin. Reconstruction of gene regulatory networks based on repairing sparse low-rank matrices. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4): 767–777, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chakrabarty:2021:NBA

[CDBR21] Broto Chakrabarty, Dibyajyoti Das, Gopalakrishnan Bulusu, and Arijit Roy. Network-based analysis of fatal comorbidities of COVID-19 and potential therapeutics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1271–1280, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3075299`.

Chowriappa:2009:PSC

[CDKT09] Pradeep Chowriappa, Sumeet Dua, Jinko Kanno, and Hilary W. Thompson. Protein structure classification based on conserved hydrophobic residues. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):639–651, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2012:SID

[CDW12] Zhi-Zhong Chen, Fei Deng, and Lusheng Wang. Simultaneous identification of duplications, losses, and lateral gene transfers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1515–1528,

September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2006:MFS

[CEFBS06] Duhong Chen, Oliver Eulenstein, David Fernandez-Baca, and Michael Sanderson. Minimum-flip supertrees: Complexity and algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):165–173, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cai:2014:GEI

[CEG14] Zhipeng Cai, Oliver Eulenstein, and Cynthia Gibas. Guest editors introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):453–454, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cickovski:2015:GPI

[CFIS+15] Trevor Cickovski, Tiffany Flor, Galen Irving-Sachs, Philip Novikov, James Parda, and Giri Narasimhan. GPUDePiCt: a parallel implementation of a clustering algorithm for computing degenerate primers on graphics processing units. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):445–454, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Carvalho:2006:EAI

[CFOS06] Alexandra M. Carvalho, Ana T. Freitas, Arlindo L. Oliveira, and Marie-France Sagot. An efficient algorithm for the identification of structured motifs in DNA promoter sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):126–140, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2023:AAM

[CGL+23a] Jiamin Chen, Jianliang Gao, Tengfei Lyu, Babatounde Moctard Oloulade, and Xiaohua Hu. AutoMSR: Auto molecular structure representation learning for multi-label metabolic pathway prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3430–3439, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3198119`.

Chen:2023:EDM

[CGL+23b] Nan Chen, Man Guo, Yongchao Li, Xiping Hu, Zhijun Yao, and Bin Hu. Estimation of discriminative multimodal brain network connectivity using message-passing-based nonlinear network fusion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2398–2406, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3137498`.

Cheng:2012:MDT

[CGLF12] Yi-Ming Cheng, Srinivasa Murthy Gopal, Sean M. Law, and Michael Feig. Molecular dynamics trajectory compression with a coarse-grained model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):476–486, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chu:2006:BSM

[CGPW06] Wei Chu, Zoubin Ghahramani, Alexei Podtelezhnikov, and David L. Wild. Bayesian segmental models with multiple sequence alignment profiles for protein secondary structure and contact map prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):98–113, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2016:MDL

[CGW+16] Shuang Cheng, Maozu Guo, Chunyu Wang, Xiaoyan Liu, Yang Liu, and Xuejian Wu. MiRTDL: a deep learning approach for miRNA target prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1161–1169, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2015:DIN

[CGZ15] Huidong Chen, Jihong Guan, and Shuigeng Zhou. DPNuc: Identifying nucleosome positions based on the Dirichlet process mixture model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1236–1247, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2011:ARD

[CH11] Yang Chen and Jinglu Hu. Accurate reconstruction for DNA sequencing by hybridization based on a constructive heuristic. *IEEE/ACM Transac-*

tions on Computational Biology and Bioinformatics, 8 (4):1134–1140, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cickovski:2005:FTD

[CHC+05] Trevor M. Cickovski, Chengbang Huang, Rajiv Chaturvedi, Tilmann Glimm, H. George E. Hentschel, Mark S. Alber, James A. Glazier, Stuart A. Newman, and Jesus A. Izaguirre. A framework for three-dimensional simulation of morphogenesis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2 (4):273–288, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chou:2021:NBB

[CHC+21] Hsin-Hung Chou, Ching-Tien Hsu, Li-Hsuan Chen, Yue-Cheng Lin, and Sun-Yuan Hsieh. A novel branch-and-bound algorithm for the protein folding problem in the 3D HP model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):455–462, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2934102`.

Cheng:2010:SLM

[Che10] Qiang Cheng. A sparse learning machine for high-dimensional data with application to microarray gene analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):636–646, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2012:GEA

[Che12] Yi-Ping Phoebe Chen. Guest editorial: Application and development of bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (5):1265, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2013:GEA

[Che13] Yi-Ping Phoebe Chen. Guest editorial: Advanced algorithms of bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2): 273, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2016:NTL

[Che16] Yu-Huei Cheng. A novel teaching-learning-based optimization for improved mutagenic primer design in

mismatch PCR-RFLP SNP genotyping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):86–98, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chou:2022:NAI

[CHH+22] Hsin-Hung Chou, Ching-Tien Hsu, Chin-Wei Hsu, Kai-Hsun Yao, Hao-Ching Wang, and Sun-Yuan Hsieh. Novel algorithm for improved protein classification using graph similarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3135–3143, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3125836`.

Czeizler:2017:GTA

[CHK17] Elena Czeizler, Tommi Hirvola, and Kalle Karhu. A graph-theoretical approach for Motif discovery in protein sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):121–130, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2012:EFT

[CHL+12] Xin Chen, Xiaohua Hu, Tze Yee Lim, Xiajiong Shen, E. K. Park, and Gail L. Rosen. Exploiting the functional and taxonomic structure of genomic data by probabilistic topic modeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):980–991, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2021:KPD

[CHL21] Dehua Chen, Meihua Huang, and Weimin Li. Knowledge-powered deep breast tumor classification with multiple medical reports. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):891–901, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2955484`.

Cheng:2018:NPI

[CHN+18] Xiangfei Cheng, Yue Hou, Yumin Nie, Yiru Zhang, Huan Huang, Hongde Liu, and Xiao Sun. Nucleosome positioning of intronless genes in the human genome. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1111–1121, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2020:FEC

[CHNW20] Zhi-Zhong Chen, Youta Harada, Yuna Nakamura, and Lusheng Wang. Faster exact computation of rSPR distance via better approximation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):916–929, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2878731`.

Chiu:2018:ADR

[CHW+18] Yu-Chiao Chiu, Tzu-Hung Hsiao, Li-Ju Wang, Yidong Chen, and Eric Y. Chuang. Analyzing differential regulatory networks modulated by continuous-state genomic features in glioblastoma multiforme. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1754–1764, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2021:CMC

[CHW21] Junyi Chen, Junhui Hou, and Ka-Chun Wong. Categorical matrix completion with active learning for high-throughput screening. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (6):2261–2270, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2982142`.

Chen:2019:SWC

[CHWY19] Xiaojun Chen, Joshua Z. Huang, Qingyao Wu, and Min Yang. Subspace weighting co-clustering of gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):352–364, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2705686`.

Chen:2016:SBD

[CHZ+16] Peng Chen, ShanShan Hu, Jun Zhang, Xin Gao, Jinyan Li, Junfeng Xia, and Bing Wang. A sequence-based dynamic ensemble learning system for protein ligand-binding site prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 901–912, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cui:2021:IAI

[CHZ+21] Chunmei Cui, Chuanbo Huang, Wanlu Zhou, Xiangwen Ji, Fenghong Zhang, Liang Wang, Yuan Zhou,

and Qinghua Cui. AGTR2, one possible novel key gene for the entry of SARS-CoV-2 into human cells. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1230–1233, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3009099`.

Cao:2022:DUA

[CIZ+22] Ben Cao, Xue Ii, Xiaokang Zhang, Bin Wang, Qiang Zhang, and Xiaopeng Wei. Designing uncorrelated address constrain for DNA storage by DMVO algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):866–877, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3011582`.

Chen:2021:FSB

[CJH+21] Jiaojiao Chen, Jianbo Jiao, Shengfeng He, Guoqiang Han, and Jing Qin. Few-shot breast cancer metastases classification via unsupervised cell ranking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1914–1923, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2960019`.

Chu:2023:NBB

[CKL+23] He-Ming Chu, Xiang-Zhen Kong, Jin-Xing Liu, Chun-Hou Zheng, and Han Zhang. A new binary biclustering algorithm based on weight adjacency difference matrix for analyzing gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2802–2809, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3283801`.

Ceri:2017:DMH

[CKM+17] Stefano Ceri, Abdulrahman Kaitoua, Marco Masseroli, Pietro Pinoli, and Francesco Venco. Data management for heterogeneous genomic datasets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1251–1264, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chalk:2021:CRI

[CKRS21] Cameron Chalk, Niels Kornerup, Wyatt Reeves, and David Soloveichik. Composable rate-independent computation in continuous

chemical reaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):250–260, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2952836`.

Choi:2012:HAS

[CKWY12] Ickwon Choi, Michael W. Kattan, Brian J. Wells, and Changhong Yu. A hybrid approach to survival model building using integration of clinical and molecular information in censored data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (4):1091–1105, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chin:2008:DMR

[CL08] Francis Chin and Henry C. M. Leung. DNA motif representation with nucleotide dependency. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):110–119, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chuang:2014:NSG

[CL14] Chia-Hua Chuang and Chun-Liang Lin. A novel synthesizing genetic logic circuit: frequency multiplier. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):702–713, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2015:SGC

[CL15] Po-Kuei Chen and Chun-Liang Lin. Synthesis of genetic clock with combinational biologic circuits. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5): 1206–1212, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2017:ECR

[CLC+17] Qingfeng Chen, Chaowang Lan, Baoshan Chen, Lusheng Wang, Jinyan Li, and Chengqi Zhang. Exploring consensus RNA substructural patterns using subgraph mining. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1134–1146, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Catanzaro:2013:IPF

[CLH13] Daniele Catanzaro, Martine Labbe, and Bjarni V. Halldorsson. An integer

programming formulation of the parsimonious loss of heterozygosity problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1391–1402, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2015:USA

[CLH+15] Liang Cheng, Jie Li, Yang Hu, Yue Jiang, Yongzhuang Liu, Yanshuo Chu, Zhenxing Wang, and Yadong Wang. Using semantic association to extend and infer literature-oriented relativity between terms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1219–1226, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2021:IIA

[CLL+21] Qingfeng Chen, Dehuan Lai, Wei Lan, Ximin Wu, Baoshan Chen, Jin Liu, Yi-Ping Phoebe Chen, and Jianxin Wang. ILDMSF: Inferring associations between long non-coding RNA and disease based on multi-similarity fusion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):1106–1112, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2936476`.

Chen:2010:BSI

[CLM10] Yifei Chen, Feng Liu, and Bernard Manderick. BioLMiner system: Interaction normalization task and interaction pair task in the BioCreative II.5 challenge. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):428–441, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chowdhury:2010:COD

[CLR10] Rezaul Alan Chowdhury, Hai-Son Le, and Vijaya Ramachandran. Cache-oblivious dynamic programming for bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):495–510, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cardona:2009:MPNa

[CLRV09a] Gabriel Cardona, Mercè Llabrés, Francesc Rosselló, and Gabriel Valiente. Metrics for phylogenetic networks I: Generalizations of the Robinson–Foulds metric. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

6(1):46–61, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cardona:2009:MPNb

[CLRV09b] Gabriel Cardona, Merce Llabres, Francesc Rossello, and Gabriel Valiente. Metrics for phylogenetic networks II: Nodal and triplets metrics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):454–469, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cardona:2009:NMR

[CLRV09c] Gabriel Cardona, Merce Llabres, Francesc Rossello, and Gabriel Valiente. On Nakhleh's metric for reduced phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (4):629–638, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cardona:2011:CGT

[CLRV11] Gabriel Cardona, Merce Llabres, Francesc Rossello, and Gabriel Valiente. Comparison of galled trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):410–427, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2019:CBC

[CLS19] Kin-On Cheng, Ngai-Fong Law, and Wan-Chi Siu. Clustering-based compression for population DNA sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):208–221, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cai:2022:GEIa

[CLS22] Zhipeng Cai, Min Li, and Pavel Skums. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):166–167, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3123699`.

Chan:2013:MAP

[CLST+13] Tak-Ming Chan, Leung-Yau Lo, Ho-Yin Sze-To, Kwong-Sak Leung, Xinshu Xiao, and Man-Hon Wong. Modeling associated protein-DNA pattern discovery with unified scores. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):696–707, May 2013.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cai:2023:GEI

[CLSW23] Zhipeng Cai, Min Li, Pavel Skums, and Yanjie Wei. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6): 3329–3331, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3325032`.

Carvajal-Lopez:2020:MBQ

[CLVT+20] Patricia Carvajal-López, Fernando D. Von Borstel, Amada Torres, Gabriella Rustici, Joaquín Gutiérrez, and Eduardo Romero-Vivas. Microarray-based quality assessment as a supporting criterion for *de novo* transcriptome assembly selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (1):198–206, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2860997`.

Chen:2013:MFP

[CLW13] Qingfeng Chen, Wei Lan, and Jianxin Wang. Mining featured patterns of MiRNA interaction based on sequence and structure similarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):415–422, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liang:2007:BBD

[cLWA07] Kuo ching Liang, Xiaodong Wang, and Dimitris Anastassiou. Bayesian basecalling for DNA sequence analysis using hidden Markov models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):430–440, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2023:DCP

[CLYR23] Hegang Chen, Yuyin Lu, Yuedong Yang, and Yanghui Rao. A drug combination prediction framework based on graph convolutional network and heterogeneous information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1917–1925, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3224734`.

Chen:2018:SCF

[CLZ+18] Shifu Chen, Ming Liu, Xiaoni Zhang, Renwen Long, Yixing Wang, Yue Han, Shiwei Zhang, Mingyan Xu, and Jia Gu. A study of cell-free DNA fragmentation pattern and its application in DNA sample type classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1718–1722, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Christinat:2013:TPE

[CM13] Yann Christinat and Bernard M. E. Moret. A transcript perspective on evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1403–1411, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chicco:2015:SSG

[CM15] Davide Chicco and Marco Masseroli. Software suite for gene and protein annotation prediction and similarity search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):837–843, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chicco:2016:OBP

[CM16] Davide Chicco and Marco Masseroli. Ontology-based prediction and prioritization of gene functional annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13 (2):248–260, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Czeizler:2012:QAS

[CMC+12] Eugen Czeizler, Andrzej Mizera, Elena Czeizler, Ralph-Johan Back, John E. Eriksson, and Ion Petre. Quantitative analysis of the self-assembly strategies of intermediate filaments from tetrameric Vimentin. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):885–898, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2020:BDF

[CMMZ20] Haifen Chen, D. A. K. Maduranga, Piyushkumar A. Mundra, and Jie Zheng. Bayesian data fusion of gene expression and histone modification profiles for inference of gene regulatory network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):516–525, March 2020. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2869590.

Cheng:2016:EIS

[CMQ+16] Xiaoqing Cheng, Tomoya Mori, Yushan Qiu, Wai-Ki Ching, and Tatsuya Akutsu. Exact identification of the structure of a probabilistic Boolean network from samples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1107–1116, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cai:2019:EAF

[CMR19] Xingyu Cai, Abdullah-Al Mamun, and Sanguthevar Rajasekaran. Efficient algorithms for finding the closest ℓ1-mers in biological data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1912–1921, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2843364.

Campello:2012:SMA

[CMS12] Ricardo J. G. B. Campello, Davoud Moulavi, and Joerg Sander. A simpler and more accurate AUTO–HDS framework for clustering and visualization of biological data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1850–1852, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chaudhuri:2022:PMA

[CMS22] Anik Chaudhuri, Anwoy Kumar Mohanty, and Manoranjan Satpathy. A parallelizable model for analyzing cancer tissue heterogeneity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2039–2048, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3085894.

Chacon:2015:BFI

[CMSE+15] Alejandro Chacon, Santiago Marco-Sola, Antonio Espinosa, Paolo Ribeca, and Juan Carlos Moure. Boosting the FM-Index on the GPU: Effective techniques to mitigate random memory access. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1048–1059, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2012:GEB

[CN12] Luonan Chen and Michael K. Ng. Guest editorial: Bioin-

formatics and computational systems biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):945–946, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chu:2023:GTD

[CNH+23] Thang Chu, Thuy Trang Nguyen, Bui Duong Hai, Quang Huy Nguyen, and Tuan Nguyen. Graph transformer for drug response prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1065–1072, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3206888`.

Chalkidis:2011:HPH

[CNM11] Georgios Chalkidis, Masao Nagasaki, and Satoru Miyano. High performance hybrid functional Petri net simulations of biological pathway models on CUDA. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1545–1556, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Castiglione:2023:EDR

[CNO+23] Filippo Castiglione, Christine Nardini, Elia Onofri, Marco Pedicini, and Paolo Tieri. Explainable drug repurposing approach from biased random walks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1009–1019, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3191392`.

Cai:2022:GEIb

[CNS22a] Zhipeng Cai, Giri Narasimhan, and Pavel Skums. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):207–208, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3121736`.

Craveur:2022:SB

[CNS+22b] Pierrick Craveur, Tarun J. Narwani, Narayanaswamy Srinivasan, Jean-Christophe Gelly, Joseph Rebehmed, and Alexandre G. de Brevern. Shaking the β-bulges. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):14–18, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (elec-

tronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3088444.

Carroll:2020:SSA

[COW20] Thomas C. Carroll, Jude-Thaddeus Ojiaku, and Prudence W. H. Wong. Semiglobal sequence alignment with gaps using GPU. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2086–2097, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2914105.

Caglar:2013:SMS

[CP13] Mehmet Umut Caglar and Ranadip Pal. Stochastic model simulation using Kronecker product analysis and Zassenhaus formula approximation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1125–1136, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cao:2023:CAM

[CPL+23] Yu Cao, Wenya Pi, Chun-Yu Lin, Ulrike Münzner, Masahiro Ohtomo, and Tatsuya Akutsu. Common attractors in multiple Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2862–2873, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3268795.

Chicco:2018:NIE

[CPM18] Davide Chicco, Fernando Palluzzi, and Marco Masseroli. Novelty indicator for enhanced prioritization of predicted gene ontology annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):954–965, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ciocchetta:2008:ATS

[CPQ08] Federica Ciocchetta, Corrado Priami, and Paola Quaglia. An automatic translation of SBML into beta-binders. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):80–90, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cardona:2024:CON

[CPRC24] Gabriel Cardona, Joan Carles Pons, Gerard Ribas, and Tomás Martínez Coronado. Comparison of orchard networks using their extended μ-representation. *IEEE/ACM Transactions on*

Computational Biology and Bioinformatics, 21(3):501–507, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3361390`.

Charuvaka:2014:CPS

[CR14] Anveshi Charuvaka and Huzefa Rangwala. Classifying protein sequences using regularized multi-task learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1087–1098, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cleary:2019:EFR

[CRK+19] Alan Cleary, Thiruvarangan Ramaraj, Indika Kahanda, Joann Mudge, and Brendan Mumey. Exploring frequented regions in pangenomic graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1424–1435, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Czeizler:2012:PHS

[CRP12] Eugen Czeizler, Vladimir Rogojin, and Ion Petre. The phosphorylation of the heat shock factor as a modulator for the heat shock response. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1326–1337, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cardona:2009:CTC

[CRV09] Gabriel Cardona, Francesc Rossello, and Gabriel Valiente. Comparison of tree-child phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):552–569, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chu:2015:EPY

[CS15] Dominique Chu and Anton Salykin. Evolutionary pressures on the yeast transcriptome. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1087–1093, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Choudhuri:2024:CPP

[CS24] Souradipto Choudhuri and Keya Sau. CodonU: a Python package for codon usage analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):36–44, 2024. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3335823.

Chow:2021:PAA

[CSE+21] Kevin Chow, Aisharjya Sarkar, Rasha Elhesha, Pietro Cinaglia, Ahmet Ay, and Tamer Kahveci. ANCA: Alignment-based network construction algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):512–524, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2923620.

Chen:2011:MIS

[CSK+11] Carla C. M. Chen, Holger Schwender, Jonthan Keith, Robin Nunkesser, Kerrie Mengersen, and Paula Macrossan. Methods for identifying SNP interactions: a review on variations of logic regression, random forest and Bayesian logistic regression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1580–1591, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Causey:2022:EUN

[CSQ+22] Jason Causey, Jonathan Stubblefield, Jake Qualls, Jennifer Fowler, Lingrui Cai, Karl Walker, Yuanfang Guan, and Xiuzhen Huang. An ensemble of U-Net models for kidney tumor segmentation with CT images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (3):1387–1392, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3085608.

Cobanoglu:2011:CGU

[CSS11] Murat Can Cobanoglu, Yucel Saygin, and Ugur Sezerman. Classification of GPCRs using family specific motifs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1495–1508, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Catanzaro:2016:CPD

[CSSS16] Daniele Catanzaro, Stanley E. Shackney, Alejandro A. Schäffer, and Russell Schwartz. Classifying the progression of ductal carcinoma from single-cell sampled data via integer linear programming: a case study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):643–655, 2016. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Csuros:2004:MSS

[Csu04] Miklos Csuros. Maximum-scoring segment sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(4):139–150, October 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chang:2011:NKD

[CSW11] Rui Chang, Robert Shoemaker, and Wei Wang. A novel knowledge-driven systems biology approach for phenotype prediction upon genetic intervention. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1170–1182, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2023:SSM

[CSW+23] Qi-Qi Chen, Zhao-Hui Sun, Chuan-Feng Wei, Edmond Q. Wu, and Dong Ming. Semi-supervised 3D medical image segmentation based on dual-task consistent joint learning and task-level regularization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (4):2457–2467, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3144428`.

Caudai:2019:LSC

[CSZ+19] Claudia Caudai, Emanuele Salerno, Monica Zoppè, Ivan Merelli, and Anna Tonazzini. ChromStruct 4: a Python code to estimate the chromatin structure from Hi-C data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1867–1878, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2838669`.

Caudai:2019:ESC

[CSZT19] Claudia Caudai, Emanuele Salerno, Monica Zoppè, and Anna Tonazzini. Estimation of the spatial chromatin structure based on a multiresolution bead-chain model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):550–559, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2791439`.

Comin:2014:BFR

[CV14] Matteo Comin and Davide Verzotto. Beyond fixed-resolution alignment-free

measures for mammalian enhancers sequence comparison. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):628–637, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cameron:2007:CCS

[CW07] Michael Cameron and Hugh Williams. Comparing compressed sequences for faster nucleotide BLAST searches. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):349–364, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2009:SCP

[CW09a] Jie Chen and Yu-Ping Wang. A statistical change point model approach for the detection of DNA copy number variations in array CGH data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (4):529–541, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2009:IAA

[CW09b] Zhi-Zhong Chen and Lusheng Wang. Improved approximation algorithms for reconstructing the history of tandem repeats. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):438–453, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2011:FEA

[CW11] Zhi-Zhong Chen and Lusheng Wang. Fast exact algorithms for the closest string and substring problems with application to the planted (L, d)-motif model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1400–1410, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2012:ARN

[CW12] Zhi-Zhong Chen and Lusheng Wang. Algorithms for reticulate networks of multiple phylogenetic trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):372–384, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Clauwaert:2022:NTN

[CW22] Jim Clauwaert and Willem Waegeman. Novel transformer networks for improved sequence labeling in genomics. *IEEE/ACM Transactions on Computational Biology and Bioin-*

formatics, 19(1):97–106, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3035021`.

Cameron:2004:IGA

[CWC04] Michael Cameron, Hugh E. Williams, and Adam Cannane. Improved gapped alignment in BLAST. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(3):116–129, July 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2021:CCB

[CWCJ21] Yiyuan Chen, Yufeng Wang, Liang Cao, and Qun Jin. CCFS: a confidence-based cost-effective feature selection scheme for healthcare data classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 902–911, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2903804`.

Carroll:2015:IRE

[CWDS15] Hyrum D. Carroll, Alex C. Williams, Anthony G. Davis, and John L. Spouge. Improving retrieval efficacy of homology searches using the false discovery rate. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):531–537, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Czeizler:2018:STC

[CWG+18] Eugen Czeizler, Kai-Chiu Wu, Cristian Gratie, Krishna Kanhaiya, and Ion Petre. Structural target controllability of linear networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1217–1228, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2012:DOR

[CWL12] Peng Chen, Limsoon Wong, and Jinyan Li. Detection of outlier residues for improving interface prediction in protein heterocomplexes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1155–1165, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2015:CMD

[CWLS15] Kin-On Cheng, Paula Wu, Ngai-Fong Law, and Wan-Chi Siu. Compression of multiple DNA sequences using intra-sequence and inter-sequence similarities.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 12(6): 1322–1332, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2014:ANG

[CWLZ14] Peng Chen, Chao Wang, Xi Li, and Xuehai Zhou. Accelerating the next generation long read mapping with the FPGA-based system. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5): 840–852, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2023:TIT

[CWP+23] Taoning Chen, Tingfang Wu, Deng Pan, Jinxing Xie, Jin Zhi, Xuejiao Wang, Lijun Quan, and Qiang Lyu. TransRNAm: Identifying twelve types of RNA modifications by an interpretable multi-label deep learning model based on transformer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6): 3623–3634, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3307419`.

Chaudhury:2019:MVS

[CWT+19] Ayan Chaudhury, Christopher Ward, Ali Talasaz, Alexander G. Ivanov, Mark Brophy, Bernard Grodzinski, Norman P. A. Hüner, Rajnikant V. Patel, and John L. Barron. Machine vision system for 3D plant phenotyping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):2009–2022, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2824814`.

Christinat:2008:GED

[CWZ08] Yann Christinat, Bernd Wachmann, and Lei Zhang. Gene expression data analysis using a novel approach to biclustering combining discrete and continuous data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):583–593, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cui:2008:AAU

[CWZL08] Yun Cui, Lusheng Wang, Daming Zhu, and Xiaowen Liu. A $(1.5 + \epsilon)$-approximation algorithm for unsigned translocation distance. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 5(1):56–66, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cai:2015:IPC

[CWZW15] Bingjing Cai, Haiying Wang, Huiru Zheng, and Hui Wang. Identification of protein complexes from tandem affinity purification/ mass spectrometry data via biased random walk. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):455–466, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cho:2015:PFR

[CXS15] Young-Rae Cho, Yanan Xin, and Greg Speegle. P-Finder: reconstruction of signaling networks from protein–protein interactions and GO annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):309–321, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2013:RTR

[CXW+13] Xi Chen, Jianhua Xuan, Chen Wang, Ayesha N. Shajahan, Rebecca B. Riggins, and Robert Clarke. Reconstruction of transcriptional regulatory networks by stability-based network component analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1347–1358, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cai:2023:DDP

[CXY+23] Wentian Cai, Linsen Xie, Weixian Yang, Yijiang Li, Ying Gao, and Tingting Wang. DFTNet: Dual-path feature transfer network for weakly supervised medical image segmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (4):2530–2540, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3198284`.

Chai:2019:HWT

[CYJ+19] Guoshi Chai, Min Yu, Lixu Jiang, Yaocong Duan, and Jian Huang. HMMCAS: a Web tool for the identification and domain annotations of CAS proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1313–1315, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2021:TLB

[CYL+21] Jintai Chen, Haochao Ying, Xuechen Liu, Jingjing Gu, Ruiwei Feng, Tingting Chen, Honghao Gao, and Jian Wu. A transfer learning based super-resolution microscopy for biopsy slice images: The joint methods perspective. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):103–113, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2991173`.

Chuang:2013:OPU

[CYTY13] Li-Yeh Chuang, Cheng-Huei Yang, Jui-Hung Tsai, and Cheng-Hong Yang. Operon prediction using chaos embedded particle swarm optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1299–1309, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2022:DTI

[CYWW22] Zhongjian Cheng, Cheng Yan, Fang-Xiang Wu, and Jianxin Wang. Drug-target interaction prediction using multi-head self-attention and graph attention network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2208–2218, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3077905`.

Chen:2012:GEI

[CZ12] Jianer Chen and Alexander Zelikovsky. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (4):1002–1003, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cao:2020:PEF

[CZ20] Zhen Cao and Shihua Zhang. Probe efficient feature representation of gapped K-mer frequency vectors from sequences using deep neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):657–667, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2868071`.

Czapla:2018:RSS

[Cza18] Roman Czapla. Random sets of stadiums in square and collective behavior of bacteria. *IEEE/ACM Transac-*

tions on Computational Biology and Bioinformatics, 15 (1):251–256, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2016:AMU

[CZB+16] Cheng Chen, Fengchao Zhang, Jamie Barras, Kaspar Althoefer, Swarup Bhunia, and Soumyajit Mandal. Authentication of medicines using nuclear quadrupole resonance spectroscopy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):417–430, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Chen:2023:PDT

[CZC+23] Jiatao Chen, Liang Zhang, Ke Cheng, Bo Jin, Xinjiang Lu, and Chao Che. Predicting drug-target interaction via self-supervised learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2781–2789, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3153963`.

Chen:2023:FIC

[CZCL23] Shutao Chen, Lin Zhang, Xiangzhi Chen, and Hui Liu. FGFICA: Independent component analysis of fusion genomic features for mining epi-transcriptome profiling data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1842–1853, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3220552`.

Chen:2022:ECS

[CZDZ22] Zhong Chen, Wensheng Zhang, Hongwen Deng, and Kun Zhang. Effective cancer subtype and stage prediction via dropfeature-DNNs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):107–120, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3058941`.

Chen:2005:AOG

[CZF+05] Xin Chen, Jie Zheng, Zheng Fu, Peng Nan, Yang Zhong, Stefano Lonardi, and Tao Jiang. Assignment of orthologous genes via genome rearrangement. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(4):302–315, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2017:EAB

[CZJ17] Shan Cheng, Long-Long Zhao, and Xiao-Yu Jiang. An effective application of bacteria quorum sensing and circular elimination in MOPSO. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):56–63, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2022:ADC

[CZL+22] Jianhong Cheng, Wei Zhao, Jin Liu, Xingzhi Xie, Shangjie Wu, Liangliang Liu, Hailin Yue, Junjian Li, Jianxin Wang, and Jun Liu. Automated diagnosis of COVID-19 using deep supervised autoencoder with multi-view features from CT images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2723–2736, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3102584`.

Cui:2018:MND

[CZM+18] Xiaodong Cui, Lin Zhang, Jia Meng, Manjeet K. Rao, Yidong Chen, and Yufei Huang. MeTDiff: a novel differential RNA methylation analysis for MeRIP-Seq data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (2):526–534, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2018:EIC

[CZW+18] Zhanzhan Cheng, Shuigeng Zhou, Yang Wang, Hui Liu, Jihong Guan, and Yi-Ping Phoebe Chen. Effectively identifying compound-protein interactions by learning from positive and unlabeled examples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1832–1843, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cao:2023:IMB

[CZW+23a] Qingqing Cao, Jianping Zhao, Haiyun Wang, Qi Guan, and Chunhou Zheng. An integrated method based on Wasserstein distance and graph for cancer subtype discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3499–3510, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3293472`.

Cheng:2023:DNC

[CZW+23b] Enhao Cheng, Jun Zhao, Hong Wang, Shuguang Song,

Shuxian Xiong, and Yanshen Sun. Dual network contrastive learning for predicting microbe-disease associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3469–3481, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3228617`.

Chan:2015:MPP

[CZWT15] Shing-Chow Chan, Li Zhang, Ho-Chun Wu, and Kai-Man Tsui. A maximum a posteriori probability and time-varying approach for inferring gene regulatory networks from time course gene microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):123–135, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cheng:2019:BGA

[CZX19] Haoyu Cheng, Yong Zhang, and Yun Xu. BitMapper2: a GPU-accelerated all-mapper based on the sparse q-gram index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):886–897, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cao:2023:MMP

[CZZ+23a] Yahui Cao, Tao Zhang, Xin Zhao, Xue Jia, and Bingzhi Li. MooSeeker: a metabolic pathway design tool based on multiobjective optimization algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3609–3622, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3307363`.

Chen:2023:CAS

[CZZ+23b] Cheng Chen, Yuguo Zha, Daming Zhu, Kang Ning, and Xuefeng Cui. ContactLib-ATT: a structure-based search engine for homologous proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3421–3429, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3197802`.

Dureau:2017:MIA

[DABV17] Maxime Dureau, Angelo Alessandri, Patrizia Bagnerini, and Stephane Vincent. Modeling and identification of amnioserosa cell mechanical behavior by using mass-spring lattices. *IEEE/ACM Transactions on Computational Biology and Bioin-*

formatics, 14(6):1476–1481, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

dAcierno:2017:IID

[dAc17] Antonio dAcierno. IsAProteinDB: an indexed database of trypsinized proteins for fast peptide mass fingerprinting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1195–1201, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Diaz:2010:ADL

[DADF+10] Ester Diaz, Guillermo Ayala, Maria Diaz-Fernandez, Liang Gong, and Derek Toomre. Automatic detection of large dense-core vesicles in secretory cells and statistical analysis of their intracellular distribution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):2–11, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dalton:2016:ORB

[Dal16] Lori A. Dalton. Optimal ROC-based classification and performance analysis under Bayesian uncertainty models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):719–729, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

David:2014:CEF

[DB14] Laszlo David and Alexander Bockmayr. Computing elementary flux modes involving a set of target reactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6): 1099–1107, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dutta:2018:ASS

[DBK18] Pritha Dutta, Subhadip Basu, and Mahantapas Kundu. Assessment of semantic similarity between proteins using information content and topological properties of the gene ontology graph. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):839–849, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Djeddi:2018:NCA

[DBN18] Warith Eddine Djeddi, Sadok Ben Yahia, and Engelbert Mephu Nguifo. A novel computational approach for global alignment for multiple biological networks. *IEEE/ACM Transactions*

on Computational Biology and Bioinformatics, 15(6): 2060–2066, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Davila:2007:FPA

[DBR07] Jaime Davila, Sudha Balla, and Sanguthevar Rajasekaran. Fast and practical algorithms for planted (l, d) motif search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):544–552, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Djenouri:2024:SPP

[DBSL24] Youcef Djenouri, Asma Belhadi, Gautam Srivastava, and Jerry Chun-Wei Lin. A secure parallel pattern mining system for Medical Internet of Things. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):631–643, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3233803`.

Dougherty:2009:CBM

[DBTB09] Edward R. Dougherty, Marcel Brun, Jeffrey M. Trent, and Michael L. Bittner. Conditioning-based modeling of contextual genomic regulation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):310–320, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

DeBlasio:2012:MEM

[DBZ12] Daniel DeBlasio, Jocelyne Bruand, and Shaojie Zhang. A memory efficient method for structure-based RNA multiple alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):1–11, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Deng:2015:IFF

[DC15] Lei Deng and Zhigang Chen. An integrated framework for functional annotation of protein structural domains. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):902–913, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

daCosta:2011:WPC

[dCAR11] Joaquim F. Pinto da Costa, Hugo Alonso, and Luis Roque. A weighted principal component analysis and its application to gene expression data. *IEEE/ACM Transactions on Computa-*

tional Biology and Bioinformatics, 8(1):246–252, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Deng:2017:ISK

[DCHW17] Su-Ping Deng, Shaolong Cao, De-Shuang Huang, and Yu-Ping Wang. Identifying stages of kidney renal cell carcinoma by combining gene expression and DNA methylation data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1147–1153, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Delgado:2020:STR

[DCM20] Ramón A. Delgado, Zhiyong Chen, and Richard H. Middleton. Stepwise Tikhonov regularisation: Application to the prediction of HIV-1 drug resistance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):292–301, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2849369`.

Dotu:2011:LPS

[DCVC11] Ivan Dotu, Manuel Cebrian, Pascal Van Hentenryck, and Peter Clote. On lattice protein structure prediction revisited. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1620–1632, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Deng:2024:MTL

[DCW+24] Lizhen Deng, Yuxin Cao, Zhongyang Wang, Xiaokang Wang, and Yu Wang. A multidimensional tensor low rank method for magnetic resonance image denoising. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):596–606, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3272893`.

daSilvaArruda:2018:GBH

[dDD18] Thiago da Silva Arruda, Ulisses Dias, and Zanoni Dias. A GRASP-based heuristic for the sorting by length-weighted inversions problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):352–363, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dinc:2017:STS

[DDS+17] Imren Dinc, Semih Dinc, Madhav Sigdel, Madhu S. Sigdel, Marc L. Pusey, and Ramazan S. Aygun. Superthresholding: Supervised thresholding of protein crystal images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):986–998, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dai:2021:GAG

[DDZ+21] Suyang Dai, Yuxia Ding, Zihan Zhang, Wenxuan Zuo, Xiaodi Huang, and Shanfeng Zhu. GrantExtractor: Accurate grant support information extraction from biomedical fulltext based on Bi-LSTM-CRF. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (1):205–215, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2939128`.

Dematte:2012:SGP

[Dem12] Lorenzo Dematte. Smoldyn on graphics processing units: Massively parallel Brownian dynamics simulations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):655–667, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

DiLena:2011:TOS

[DFM+11] Pietro Di Lena, Piero Fariselli, Luciano Margara, Marco Vassura, and Rita Casadio. Is there an optimal substitution matrix for contact prediction with correlated mutations? *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):1017–1028, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

DiCamillo:2012:SSB

[DFTC12] Barbara Di Camillo, Marco Falda, Gianna Toffolo, and Claudio Cobelli. SimBioNeT: a simulator of biological network topology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):592–600, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Deng:2019:IKG

[DG19] Su-Ping Deng and Wei-Li Guo. Identifying key genes of liver cancer by networking of multiple data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):792–800, May 2019. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dawy:2006:GMM

[DGH+06] Zaher Dawy, Bernhard Goebel, Joachim Hagenauer, Christophe Andreoli, Thomas Meitinger, and Jakob C. Mueller. Gene mapping and marker clustering using Shannon's mutual information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):47–56, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Daniels:2015:MRH

[DGRC15] Noah M. Daniels, Andrew Gallant, Norman Ramsey, and Lenore J. Cowen. MRFy: remote homology detection for beta-structural proteins using Markov random fields and stochastic search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):4–16, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dias:2017:GWS

[DGV+17] Oscar Dias, Daniel Gomes, Paulo Vilaca, Joao Cardoso, Miguel Rocha, Eugenio C. Ferreira, and Isabel Rocha. Genome-wide semi-automated annotation of transporter systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):443–456, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Demir:2005:LTP

[DGY05] Cigdem Demir, S. Humayun Gultekin, and Bulent Yener. Learning the topological properties of brain tumors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):262–270, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dress:2004:CSG

[DH04] Andreas W. M. Dress and Daniel H. Huson. Constructing splits graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(3):109–115, July 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Du:2023:DML

[DH23] Xiuquan Du and Jiajia Hu. Deep multi-label joint learning for RNA and DNA-Binding proteins prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):307–320, 2023.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3150280`.

Doyon:2012:EME

[DHC12] Jean-Philippe Doyon, Sylvie Hamel, and Cedric Chauve. An efficient method for exploring the space of gene tree/species tree reconciliations in a probabilistic framework. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):26–39, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Deng:2018:IIG

[DHCW18] Su-Ping Deng, Wenxing Hu, Vince D. Calhoun, and Yu-Ping Wang. Integrating imaging genomic data in the quest for biomarkers of schizophrenia disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1480–1491, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maia:2023:IEC

[dHMPFdM23] Marcelo Rodrigues de Holanda Maia, Alexandre Plastino, Alex Freitas, and João Pedro de Magalhães. Interpretable ensembles of classifiers for uncertain data with bioinformatics applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1829–1841, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3218588`.

DeJesus:2015:CUM

[DI15] Michael A. DeJesus and Thomas R. Ioerger. Capturing uncertainty by modeling local transposon insertion frequencies improves discrimination of essential genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):92–102, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

deJong:2008:SSS

[dJP08] Hidde de Jong and Michel Page. Search for steady states of piecewise-linear differential equation models of genetic regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):208–222, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

DeRonne:2013:POP

[DK13] Kevin W. DeRonne and George Karypis. Pareto opti-

mal pairwise sequence alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):481–493, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

DeBlasio:2017:LPA

[DK17] Dan DeBlasio and John Kececioglu. Learning parameter-advising sets for multiple sequence alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1028–1041, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Daniels:2012:TPS

[DKCM12] Noah Daniels, Anoop Kumar, Lenore Cowen, and Matt Menke. Touring protein space with Matt. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):286–293, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Done:2010:PNH

[DKDD10] Bogdan Done, Purvesh Khatri, Arina Done, and Sorin Draghici. Predicting novel human gene ontology annotations using semantic analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):91–99, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Du:2015:IAC

[DKS+15] Nan Du, Marc R. Knecht, Mark T. Swihart, Zhenghua Tang, Tiffany R. Walsh, and Aidong Zhang. Identifying affinity classes of inorganic materials binding sequences via a graph-based model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):193–204, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dunn:2021:FAN

[DKY21] Sara-Jane Dunn, Hillel Kugler, and Boyan Yordanov. Formal analysis of network motifs links structure to function in biological programs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):261–271, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2948157`.

DiPersia:2023:EIP

[DLA+23] Leandro Di Persia, Tiago Lopez, Agustin Arce, Diego H. Milone, and Georgina Stegmayer.

exp2GO: Improving prediction of functions in the gene ontology with expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (2):999–1008, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3167245`.

Dong:2024:SCA

[DLG+24] Shujie Dong, Yuansheng Liu, Yongshun Gong, Xiangjun Dong, and Xiangxiang Zeng. scCAN: Clustering with adaptive neighbor-based imputation method for single-cell RNA-Seq data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1): 95–105, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3337231`.

DeFrancesco:2012:EGE

[DLM12] Nicoletta De Francesco, Giuseppe Lettieri, and Luca Martini. Efficient genotype elimination via adaptive allele consolidation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1180–1189, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dang:2023:ICD

[DLO+23] Qi Dang, Yong Liang, Dong Ouyang, Rui Miao, Caijin Ling, Xiaoying Liu, and Shengli Xie. Improved computational drug-repositioning by self-paced non-negative matrix trifactorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1953–1962, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3225300`.

Davidson:2018:EQR

[DLRW18] Ruth Davidson, MaLyn Lawhorn, Joseph Rusinko, and Noah Weber. Efficient quartet representations of trees and applications to supertree and summary methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (3):1010–1015, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dai:2010:MGN

[DLT10] Hong-Jie Dai, Po-Ting Lai, and Richard Tzong-Han Tsai. Multistage gene normalization and SVM-based ranking for protein interactor extraction in full-text articles. *IEEE/ACM Transactions on Computational Biology and Bioinformat-*

ics, 7(3):412–420, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Du:2021:MTS

[DLY+21] Lei Du, Kefei Liu, Xiaohui Yao, Shannon L. Risacher, Junwei Han, Andrew J. Saykin, Lei Guo, and Li Shen. Multi-task sparse canonical correlation analysis with application to multimodal brain imaging genetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (1):227–239, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2947428`.

Diago:2009:EGC

[DM09] Luis A. Diago and Ernesto Moreno. Evaluation of geometric complementarity between molecular surfaces using compactly supported radial basis functions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (4):689–694, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dey:2022:CGA

[DM22] Lopamudra Dey and Anirban Mukhopadhyay. Compact genetic algorithm-based feature selection for sequence-based prediction of dengue–human protein interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2137–2148, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3066597`.

Das:2013:ORS

[DMD13] Mouli Das, C. A. Murthy, and Rajat K. De. An optimization rule for in silico identification of targeted overproduction in metabolic pathways. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):914–926, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Deznabi:2018:IAG

[DMJ+18] Iman Deznabi, Mohammad Mobayen, Nazanin Jafari, Oznur Tastan, and Erman Ayday. An inference attack on genomic data using kinship, complex correlations, and phenotype information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1333–1343, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dong:2022:MBM

[DMK22] Ngan Dong, Stefanie Mücke,

and Megha Khosla. MuCoMiD: a multitask graph convolutional learning framework for MiRNA-disease association prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3081–3092, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3176456`.

DiCamillo:2022:GED

[DN22] Barbara Di Camillo and Giuseppe Nicosia. Guest editorial: Deep learning for genomics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):95–96, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3080094`.

doNascimento:2017:CNV

[dNG17] Francisco do Nascimento and Katia S. Guimaraes. Copy number variations detection: Unravelling the problem in tangible aspects. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1237–1250, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dasarathy:2015:DRP

[DNR15] Gautam Dasarathy, Robert Nowak, and Sebastien Roch. Data requirement for phylogenetic inference from multiple loci: a new distance method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):422–432, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dehghani:2019:EPA

[DNS19] Toktam Dehghani, Mahmoud Naghibzadeh, and Javad Sadri. Enhancement of protein β-sheet topology prediction using maximum weight disjoint path cover. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1936–1947, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2837753`.

Du:2021:MOR

[DOK+21] Haoxing Du, Yi Sheng Ong, Marina Knittel, Ross Mawhorter, Nuo Liu, Gianluca Gross, Reiko Tojo, Ran Libeskind-Hadas, and Yi-Chieh Wu. Multiple optimal reconciliations under the duplication-loss-coalescence model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2144–2156, November/December 2021. CO-

DEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2922337`.

Ding:2017:NMM

[DPA+17] Yuchun Ding, Marie Christine Pardon, Alessandra Agostini, Henryk Faas, Jinming Duan, Wil O. C. Ward, Felicity Easton, Dorothee Auer, and Li Bai. Novel methods for microglia segmentation, feature extraction, and classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6): 1366–1377, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dehzangi:2014:SBM

[DPL+14] Abdollah Dehzangi, Kuldip Paliwal, James Lyons, Alok Sharma, and Abdul Sattar. A segmentation-based method to extract structural and evolutionary features for protein fold recognition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):510–519, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dehzangi:2013:CFE

[DPS+13] Abdollah Dehzangi, Kuldip Paliwal, Alok Sharma, Omid Dehzangi, and Abdul Sattar. A combination of feature extraction methods with an ensemble of different classifiers for protein structural class prediction problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):564–575, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dutta:2022:DDA

[DPS22] Pratik Dutta, Aditya Prakash Patra, and Sriparna Saha. DeePROG: Deep attention-based model for diseased gene prognosis by fusing multi-omics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2770–2781, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3090302`.

Dwight:2012:UWB

[DPW12] Zachary L. Dwight, Robert Palais, and Carl T. Wittwer. uAnalyze: Web-based high-resolution DNA melting analysis with comparison to thermodynamic predictions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1805–1811, November 2012. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic).

Ding:2023:RMI

[DQZ+23] Yi Ding, Xue Qin, Mingfeng Zhang, Ji Geng, Dajiang Chen, Fuhu Deng, and Chunhe Song. RLSegNet: an medical image segmentation network based on reinforcement learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2565–2576, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3195705`.

Disanto:2014:NRS

[DR14] Filippo Disanto and Noah A. Rosenberg. On the number of ranked species trees producing anomalous ranked gene trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1229–1238, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Disanto:2016:APN

[DR16] Filippo Disanto and Noah A. Rosenberg. Asymptotic properties of the number of matching coalescent histories for caterpillar-like families of species trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):913–925, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Degnan:2012:CSS

[DRS12] James H. Degnan, Noah A. Rosenberg, and Tanja Stadler. A characterization of the set of species trees that produce anomalous ranked gene trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1558–1568, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Davidson:2014:DBP

[DS14] Ruth Davidson and Seth Sullivant. Distance-based phylogenetic methods around a polytomy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):325–335, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ding:2019:CSN

[DS19] Dewu Ding and Xiao Sun. A comparative study of network motifs in the integrated transcriptional regulation and protein interaction networks of *Shewanella*. *IEEE/ACM Transactions on*

Computational Biology and Bioinformatics, 16(1):163–171, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Debnath:2021:FOC

[DS21] Tathagata Debnath and Mingzhou Song. Fast optimal circular clustering and applications on round genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2061–2071, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3077573`.

Dutta:2020:EGC

[DSCM20] Pratik Dutta, Sriparna Saha, Saraansh Chopra, and Varnika Miglani. Ensembling of gene clusters utilizing deep learning and protein-protein interaction information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2005–2016, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2918523`.

Dawy:2008:FSG

[DSHM08] Zaher Dawy, Michel Sarkis, Joachim Hagenauer, and Jakob C. Mueller. Fine-scale genetic mapping using independent component analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):448–460, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

deSouto:2013:GES

[dSK13] Marcilio C. P. de Souto and Maricel Kann. Guest editorial for special section on BSB 2012. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):817–818, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Das:2023:EDC

[DSM23] Pradeep Kumar Das, Biswajeet Sahoo, and Sukadev Meher. An efficient detection and classification of acute leukemia using transfer learning and orthogonal softmax layer-based model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1817–1828, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3218590`.

daSilva:2017:GDH

[dSMDB17] Poly H. da Silva, Raphael Machado, Simone Dantas,

and Marilia D. V. Braga. Genomic distance with high indel costs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):728–732, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

daSilva:2021:NFS

[dSPFF21] Pablo Nascimento da Silva, Alexandre Plastino, Fabio Fabris, and Alex A. Freitas. A novel feature selection method for uncertain features: an application to the prediction of Pro-/ anti-longevity genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2230–2238, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2988450`.

Rodrigues:2011:PCE

[dSRCT+11] Thiago de Souza Rodrigues, Fernanda Caldas Cardoso, Santuza Maria Ribeiro Teixeira, Sergio Costa Oliveira, and Antonio Padua Braga. Protein classification with extended-sequence coding by sliding window. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1721–1726, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Diekmann:2007:EUR

[DST07] Yoan Diekmann, Marie-France Sagot, and Eric Tannier. Evolution under reversals: Parsimony and conservation of common intervals. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):301–309, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dellen:2015:GSR

[DST15a] Babette Dellen, Hanno Scharr, and Carme Torras. Growth signatures of rosette plants from time-lapse video. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1470–1478, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dong:2015:ANA

[DST+15b] Liang Dong, Bing Shi, Guangdong Tian, YanBo Li, Bing Wang, and MengChu Zhou. An accurate de novo algorithm for glycan topology determination from mass spectra. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):568–578, May 2015. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Duarte-Sanchez:2018:HAM

[DSVMM18] Jorge E. Duarte-Sanchez, Jaime Velasco-Medina, and Pedro A. Moreno. Hardware accelerator for the multifractal analysis of DNA sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1611–1624, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Danziger:2006:FCM

[DSZ+06] Samuel A. Danziger, S. Joshua Swamidass, Jue Zeng, Lawrence R. Dearth, Qiang Lu, Jonathan H. Chen, Jianlin Cheng, Vinh P. Hoang, Hiroto Saigo, Ray Luo, Pierre Baldi, Rainer K. Brachmann, and Richard H. Lathrop. Functional census of mutation sequence spaces: The example of p53 cancer rescue mutants. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):114–125, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dubrova:2011:SBA

[DT11] Elena Dubrova and Maxim Teslenko. A SAT-based algorithm for finding attractors in synchronous Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1393–1399, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Das:2023:BBR

[DTA+23] Pranab Das, Yogita Thakran, S. R. Ngamwal Anal, Vipin Pal, and Anju Yadav. BRMCF: Binary relevance and MLSMOTE based computational framework to predict drug functions from chemical and biological properties of drugs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1761–1773, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215645`.

Dost:2011:TFM

[DWSB11] Banu Dost, Chunlei Wu, Andrew Su, and Vineet Bafna. TCLUST: a fast method for clustering genome-scale expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):808–818, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ding:2015:SHO

[DWZ+15] Xiaojun Ding, Jianxin Wang,

Alex Zelikovsky, Xuan Guo, Minzhu Xie, and Yi Pan. Searching high-order SNP combinations for complex diseases based on energy distribution difference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):695–704, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dehghannasiri:2015:OED

[DYD15] Roozbeh Dehghannasiri, Byung-Jun Yoon, and Edward R. Dougherty. Optimal experimental design for gene regulatory networks in the presence of uncertainty. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):938–950, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Du:2023:IBQ

[DYL+23] Yongping Du, Jingya Yan, Yuxuan Lu, Yiliang Zhao, and Xingnan Jin. Improving biomedical question answering by data augmentation and model weighting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (2):1114–1124, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3171388`.

Ding:2022:NRG

[DYZC22] Xiaojian Ding, Fan Yang, Yaoyi Zhong, and Jie Cao. A novel recursive gene selection method based on least square kernel extreme learning machine. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2026–2038, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3068846`.

Dong:2011:NNK

[DZ11] Qiwen Dong and Shuigeng Zhou. Novel nonlinear knowledge-based mean force potentials based on machine learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):476–486, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Daras:2006:TDS

[DZA+06] Petros Daras, Dimitrios Zarpalas, Apostolos Axenopoulos, Dimitrios Tzovaras, and Michael Gerassimos Strintzis. Three-dimensional shape-structure comparison method for protein classification. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 3(3):193–207, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dharejo:2023:MBM

[DZD+23] Fayaz Ali Dharejo, Muhammad Zawish, Farah Deeba, Yuanchun Zhou, Kapal Dev, Sunder Ali Khowaja, and Nawab Muhammad Faseeh Qureshi. Multimodalboost: Multimodal medical image super-resolution using multi-attention network with wavelet transform. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (4):2420–2433, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3191387`.

Deng:2016:PHG

[DZH16] Su-Ping Deng, Lin Zhu, and De-Shuang Huang. Predicting hub genes associated with cervical cancer through gene co-expression networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):27–35, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Dhar:2022:PTT

[DZMB22] Saurav Dhar, Chengchen Zhang, Ion I. Mandoiu, and Mukul S. Bansal. TNet: Transmission network inference using within-host strain diversity and its application to geographical tracking of COVID-19 spread. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):230–242, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3096455`.

ElBakry:2012:IDE

[EAS12] Ola ElBakry, M. Omair Ahmad, and M. N. S. Swamy. Identification of differentially expressed genes for time-course microarray data based on modified RM ANOVA. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):451–466, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

ElBakry:2013:IGR

[EAS13] Ola ElBakry, M. Omair Ahmad, and M. N. S. Swamy. Inference of gene regulatory networks with variable time delay from time-series microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):671–687, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Elmsallati:2016:GAP

[ECK16] Ahed Elmsallati, Connor Clark, and Jugal Kalita. Global alignment of protein-protein interaction networks: a survey. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):689–705, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Esfahani:2014:IBP

[ED14] Mohammad Shahrokh Esfahani and Edward R. Dougherty. Incorporation of biological pathway knowledge in the construction of priors for optimal Bayesian classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1):202–218, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Esfahani:2015:OBF

[ED15] Mohammad Shahrokh Esfahani and Edward R. Dougherty. An optimization-based framework for the transformation of incomplete biological knowledge into a probabilistic structure and its application to the utilization of gene/protein signaling pathways in discrete phenotype classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1304–1321, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Eshra:2014:OPC

[EES14] Abeer Eshra and Ayman El-Sayed. An odd parity checker prototype using DNAzyme finite state machine. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (2):316–324, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Elo:2008:ROT

[EFLA08] Laura L. Elo, Sanna Filen, Riitta Lahesmaa, and Tero Aittokallio. Reproducibility-optimized test statistic for ranking genes in microarray studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):423–431, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Elias:2006:AAS

[EH06] Isaac Elias and Tzvika Hartman. A 1.375-approximation algorithm for sorting by transpositions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(4):369–379, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

ElZein:2024:PCP

[ELH24] Yamane El Zein, Mathieu Lemay, and Kévin Huguenin. PrivaTree: Collaborative privacy-preserving training of decision trees on biomedical data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):1–13, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3286274`.

El-Manzalawy:2011:PMI

[EMDH11] Yasser El-Manzalawy, Drena Dobbs, and Vasant Honavar. Predicting MHC-II binding affinity using multiple instance regression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):1067–1079, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Elmsallati:2018:IBN

[EMK18] Ahed Elmsallati, Abdulghani Msalati, and Jugal Kalita. Index-based network aligner of protein–protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):330–336, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Eisenhaber:2014:GEI

[ESW14] Frank Eisenhaber, Wing-Kin Sung, and Limsoon Wong. Guest editorial for the international conference on genome informatics (GIW 2013). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):5–6, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Evans:2004:UDT

[EW04] Steven N. Evans and Tandy Warnow. Unidentifiable divergence times in rates-across-sites models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(3):130–134, July 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ezzat:2017:DTI

[EZW+17] Ali Ezzat, Peilin Zhao, Min Wu, Xiao-Li Li, and Chee-Keong Kwoh. Drug-target interaction prediction with graph regularized matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):646–656, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Frasca:2019:MPF

[FB19] Marco Frasca and Nicolo Cesa Bianchi. Multitask

protein function prediction through task dissimilarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1550–1560, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fabris:2016:EEC

[FFT16] Fabio Fabris, Alex A. Freitas, and Jennifer M. A. Tullet. An extensive empirical comparison of probabilistic hierarchical classifiers in datasets of ageing-related genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1045–1058, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fober:2011:SAL

[FGKH11] Thomas Fober, Gerghei Glinca, Gerhard Klebe, and Eyke Hullermeier. Superposition and alignment of labeled point clouds. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1653–1666, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fang:2022:DES

[FHDU22] Min Fang, Yufeng He, Zhihua Du, and Vladimir N. Uversky. DeepCLD: an efficient sequence-based predictor of intrinsically disordered proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3154–3159, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3124273`.

Fellows:2011:HIC

[FHH+11] Michael R. Fellows, Tzvika Hartman, Danny Hermelin, Gad M. Landau, Frances Rosamond, and Liat Rozenberg. Haplotype inference constrained by plausible haplotype data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1692–1699, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fakhraei:2014:NBD

[FHRG14] Shobeir Fakhraei, Bert Huang, Louiqa Raschid, and Lise Getoor. Network-based drug-target interaction prediction with probabilistic soft logic. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):775–787, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feng:2011:MFB

[FJJ11] Jianxing Feng, Rui Jiang, and Tao Jiang. A max-flow-based approach to the identification of protein complexes using protein interaction and microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 621–634, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fan:2018:GES

[FJJ18] Xiaodan Fan, Xinglai Ji, and Rui Jiang. Guest editorial for special section on the Sixth National Conference on Bioinformatics and System Biology of China. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1092, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feret:2019:E

[FK19] Jerome Feret and Heinz Koeppl. Editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1561, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Foo:2019:MCG

[FKB19] Mathias Foo, Jongrae Kim, and Declan G. Bates. Modelling and control of gene regulatory networks for perturbation mitigation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):583–595, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2771775`.

Fujarewicz:2007:ASM

[FKLS07] Krzysztof Fujarewicz, Marek Kimmel, Tomasz Lipniacki, and Andrzej Swierniak. Adjoint systems for models of cell signaling pathways and their application to parameter fitting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):322–335, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feret:2018:LTA

[FL18] Jerome Feret and Kim Quyen Ly. Local traces: an over-approximation of the behavior of the proteins in rule-based models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1124–1137, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Frost:2015:IFG

[FLAM15] H. Robert Frost, Zhigang

Li, Folkert W. Asselbergs, and Jason H. Moore. An independent filter for gene set testing based on spectral enrichment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1076–1086, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fodeh:2020:CPC

[FLJS20] Samah J. Fodeh, Taihua Li, Haya Jarad, and Basmah Safdar. Classification of patients with coronary microvascular dysfunction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):704–711, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2019.2914442`.

Fernandez:2016:OBS

[FLM+16] Javier D. Fernandez, Maurizio Lenzerini, Marco Masseroli, Francesco Venco, and Stefano Ceri. Ontology-based search of genomic metadata. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):233–247, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fagundes-Lima:2012:CSS

[FLW12] Denise Fagundes-Lima and Gerald Weber. Comment on "SCS: Signal, Context, and Structure Features for Genome-Wide Human Promoter Recognition". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):940–941, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fan:2014:QSM

[FLW+14] Ying Fan, Ruoshui Lu, Lusheng Wang, Massimo Andreatta, and Shuai Cheng Li. Quantifying significance of MHC II residues. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):17–25, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feijao:2011:SBL

[FM11] Pedro Feijao and Joao Meidanis. SCJ: a breakpoint-like distance that simplifies several rearrangement problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1318–1329, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Felicioli:2012:BEA

[FM12] Claudio Felicioli and Roberto Marangoni. BpMatch: An efficient algorithm for a segmental analysis of genomic sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1120–1127, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feijao:2013:EAF

[FM13] Pedro Feijao and Joao Meidanis. Extending the algebraic formalism for genome rearrangements to include linear chromosomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):819–831, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fergus:2020:UDL

[FMA+20] Paul Fergus, Casimiro Curbelo Montañez, Basma Abdulaimma, Paulo Lisboa, Carl Chalmers, and Beth Pineles. Utilizing deep learning and genome wide association studies for epistatic-driven preterm birth classification in African–American women. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):668–678, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2868667`.

Fotoohifiroozabadi:2018:NFN

[FMD18] Samira Fotoohifiroozabadi, Mohd Saberi Mohamad, and Safaai Deris. NAHALFlex: a numerical and alphabetical hinge detection algorithm for flexible protein structure alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):934–943, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fages:2018:INC

[FMRS18] François Fages, Thierry Martinez, David A. Rosenblueth, and Sylvain Soliman. Influence networks compared with reaction networks: Semantics, expressivity and attractors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1138–1151, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fa:2014:NRG

[FN14] Rui Fa and Asoke K. Nandi. Noise resistant generalized parametric validity index of clustering for gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinfor-*

matics, 11(4):741–752, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fu:2020:PDM

[FPC20] Laiyi Fu, Qinke Peng, and Ling Chai. Predicting DNA methylation states with hybrid information based deep-learning model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1721–1728, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2909237`.

Ferraro:2011:ACQ

[FPPR11] Nicola Ferraro, Luigi Palopoli, Simona Panni, and Simona E. Rombo. Asymmetric comparison and querying of biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):876–889, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fages:2012:GEI

[FS12] François Fages and Sylvain Soliman. Guest Editors' introduction to the special section on computational methods in systems biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1314–1315, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fages:2013:GEI

[FS13a] François Fages and Sylvain Soliman. Guest Editors' introduction to the special section on computational methods in systems biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):308–309, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Florea:2013:GGT

[FS13b] Liliana D. Florea and Steven L. Salzberg. Genome-guided transcriptome assembly in the age of next-generation sequencing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1234–1240, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Frith:2018:SDC

[FS18] Martin C. Frith and Anish M. S. Shrestha. A simplified description of child tables for sequence similarity search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):2067–2073, November 2018.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Flores:2011:FFM

[FSB+11] Samuel Coulbourn Flores, Michael Sherman, Christopher M. Bruns, Peter Eastman, and Russ B. Altman. Fast flexible modeling of RNA structure using internal coordinates. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1247–1257, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fujita:2011:ICR

[FSD+11] Andre Fujita, Joao Ricardo Sato, Marcos Almeida Demasi, Rui Yamaguchi, Teppei Shimamura, Carlos Eduardo Ferreira, Mari Cleide Sogayar, and Satoru Miyano. Inferring contagion in regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):570–576, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fang:2016:IGS

[FSDR16] Yi Fang, Mengtian Sun, Guoxian Dai, and Karthik Ramain. The intrinsic geometric structure of protein-protein interaction networks for protein interaction prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):76–85, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feng:2015:RES

[FSL+15] Weixing Feng, Peichao Sang, Deyuan Lian, Yansheng Dong, Fengfei Song, Meng Li, Bo He, Fenglin Cao, and Yunlong Liu. ResSeq: enhancing short-read sequencing alignment by rescuing error-containing reads. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):795–798, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Furlanello:2005:SLM

[FSMJ05] Cesare Furlanello, Maria Serafini, Stefano Merler, and Giuseppe Jurman. Semisupervised learning for molecular profiling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):110–118, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fang:2021:EBB

[FSNF21] Qiong Fang, Dewei Su, Wilfred Ng, and Jianlin Feng. An effective

biclustering-based framework for identifying cell subpopulations from scRNA-seq data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (6):2249–2260, November/ December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2979717`.

Fan:2023:ECL

[FSP23] Yongxian Fan, Guicong Sun, and Xiaoyong Pan. ELMo4m6A: a contextual language embedding-based predictor for detecting RNA N6-methyladenosine sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):944–954, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3173323`.

Fang:2019:PPB

[FSX19] Chao Fang, Yi Shang, and Dong Xu. Prediction of protein backbone torsion angles using deep residual inception neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (3):1020–1028, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Fernandez:2015:FFB

[FVLN15] Edward B. Fernandez, Jason Villarreal, Stefano Lonardi, and Walid A. Najjar. FHAST: FPGA-based acceleration of bowtie in hardware. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5): 973–981, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Filipovic:2020:CNM

[FVP+20] Jirí Filipovic, Ondrej Vávra, Jan Plhák, David Bednár, Sérgio M. Marques, Jan Brezovský, Ludek Matyska, and Jirí Damborský. CaverDock: a novel method for the fast analysis of ligand transport. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5): 1625–1638, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2907492`.

Feng:2020:EEL

[FW20] Zhan-Ying Feng and Yong Wang. ELF: Extract landmark features by optimizing topology maintenance, redundancy, and specificity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):411–421, March 2020. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2846225.

Freitas:2010:ICC

[FWA10] Alex A. Freitas, Daniela C. Wieser, and Rolf Apweiler. On the importance of comprehensible classification models for protein function prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):172–182, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feng:2022:CMI

[FWW+22] Changli Feng, Jin Wu, Haiyan Wei, Lei Xu, and Quan Zou. CRCF: a method of identifying secretory proteins of malaria parasites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2149–2157, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3085589.

Fan:2019:ILS

[FWXZ19] Anjing Fan, Haitao Wang, Hua Xiang, and Xiufen Zou. Inferring large-scale gene regulatory networks using a randomized algorithm based on singular value decomposition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1997–2008, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2825446.

Fan:2015:AMD

[FWY+15] Yetian Fan, Wei Wu, Jie Yang, Wenyu Yang, and Rongrong Liu. An algorithm for motif discovery with iteration on lengths of motifs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):136–141, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feng:2019:PAP

[FWY19] Pengmian Feng, Zhenyi Wang, and Xiaoyu Yu. Predicting antimicrobial peptides by using increment of diversity with quadratic discriminant analysis method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1309–1312, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feng:2022:III

[FXZS22] Shi-Hao Feng, Chun-Qiu Xia, Pei-Dong Zhang, and Hong-Bin Shen. *Ab-Initio*

membrane protein amphipathic helix structure prediction using deep neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):795–805, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3029274`.

Feng:2012:LSL

[FYSM12] Zeny Z. Feng, Xiaojian Yang, Sanjeena Subedi, and Paul D. McNicholas. The LASSO and sparse least squares regression methods for SNP selection in predicting quantitative traits. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):629–636, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feng:2019:DLA

[FYZ+19] Yujie Feng, Fan Yang, Xichuan Zhou, Yanli Guo, Fang Tang, Fengbo Ren, Jishun Guo, and Shuiwang Ji. A deep learning approach for targeted contrast-enhanced ultrasound based prostate cancer detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1794–1801, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2835444`.

Faisal:2015:GNA

[FZM15] Fazle Elahi Faisal, Han Zhao, and Tijana Milenković. Global network alignment in the context of aging. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):40–52, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Feng:2020:DMP

[FZM20] Yangqin Feng, Lei Zhang, and Juan Mo. Deep manifold preserving autoencoder for classifying breast cancer histopathological images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):91–101, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2858763`.

Fu:2023:DRD

[FZNZ23] Haitao Fu, Cecheng Zhao, Xiaohui Niu, and Wen Zhang. DRLM: a robust drug representation learning method and its applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3451–3460, 2023.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3213979`.

Fan:2017:FTS

[FZWS17] Xiaofei Fan, Xian Zhang, Ligang Wu, and Michael Shi. Finite-time stability analysis of reaction-diffusion genetic regulatory networks with time-varying delays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):868–879, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gormez:2023:IMD

[GA23] Yasin Görmez and Zafer Aydin. IGPRED-MultiTask: a deep learning model to predict protein secondary structure, torsion angles and solvent accessibility. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1104–1113, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3191395`.

Giard:2011:FSB

[GAGM11] Joachim Giard, Patrice Rondao Alface, Jean-Luc Gala, and Benoit Macq. Fast surface-based travel depth estimation algorithm for macromolecule surface shape description. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):59–68, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gondeau:2021:OWN

[GAH+21] Alexandre Gondeau, Zahia Aouabed, Mohamed Hijri, Pedro R. Peres-Neto, and Vladimir Makarenkov. Object weighting: a new clustering approach to deal with outliers and cluster overlap in computational biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):633–643, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2921577`.

Giang:2022:FBA

[GAH22] Trinh Van Giang, Tatsuya Akutsu, and Kunihiko Hiraishi. An FVS-based approach to attractor detection in asynchronous random Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):806–818, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3028862`.

Ghaffari:2018:ENT

[GAJ+18] Noushin Ghaffari, Osama A. Arshad, Hyundoo Jeong, John Thiltges, Michael F. Criscitiello, Byung-Jun Yoon, Aniruddha Datta, and Charles D. Johnson. Examining De Novo transcriptome assemblies via a quality assessment pipeline. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):494–505, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gonzalez:2009:MLT

[GAR+09] Ana M. Gonzalez, Francisco J. Azuaje, Jose L. Ramirez, Jose F. da Silveira, and Jose R. Dorronsoro. Machine learning techniques for the automated classification of adhesin-like proteins in the human protozoan parasite *Trypanosoma cruzi*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (4):695–702, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gonzalez-Alvarez:2015:FPP

[GÁVRRL15] David L. González-Álvarez, Miguel A. Vega-Rodríguez, and Álvaro Rubio-Largo. Finding patterns in protein sequences by using a hybrid multiobjective teaching learning based optimization algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):656–666, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guan:2023:RRN

[GAX+23] Yuxia Guan, Ying An, Jingrui Xu, Ning Liu, and Jianxin Wang. HA-ResNet: Residual neural network with hidden attention for ECG arrhythmia detection using two-dimensional signal. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3389–3398, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3198998`.

Guillemot:2010:FPT

[GB10] Sylvain Guillemot and Vincent Berry. Fixed-parameter tractability of the maximum agreement supertree problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):342–353, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guziolowski:2011:DLR

[GBB+11] Carito Guziolowski, Sylvain Blachon, Tatiana Bau-

muratova, Gautier Stoll, Ovidiu Radulescu, and Anne Siegel. Designing logical rules to model the response of biomolecular networks with complex interactions: An application to cancer modeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1223–1234, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Galvao:2017:SCP

[GBD17] Gustavo Rodrigues Galvao, Christian Baudet, and Zanoni Dias. Sorting circular permutations by super short reversals. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):620–633, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gupta:2008:EDS

[GBJ08] Anupam Gupta and Ziv Bar-Joseph. Extracting dynamics from static cancer expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):172–182, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ghoraie:2014:RSS

[GBLZ14] Laleh Soltan Ghoraie, Forbes Burkowski, Shuai Cheng Li, and Mu Zhu. Residue-specific side-chain polymorphisms via particle belief propagation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):33–41, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gong:2011:ITM

[GBS11] Liuling Gong, Nidhal Bouaynaya, and Dan Schonfeld. Information-theoretic model of evolution over protein communication channel. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (1):143–151, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ghasemnejad:2021:DNM

[GBSB21] Atefeh Ghasemnejad, Samira Bazmara, Mahsa Shadmani, and Kamran Pooshang Bagheri. Designing a new multi-epitope pertussis vaccine with highly population coverage based on a novel sequence and structural filtration algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1885–1892, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2019.2958803.

Guan:2014:BDC

[GBTL14] Benjamin X. Guan, Bir Bhanu, Prue Talbot, and Sabrina Lin. Bio-driven cell region detection in human embryonic stem cell assay. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):604–611, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guan:2016:EBH

[GBTW16] Benjamin X. Guan, Bir Bhanu, Prue Talbot, and Nikki Jo-Hao Weng. Extraction of blebs in human embryonic stem cell videos. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):678–688, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ghosh:2022:ERF

[GC22] Debopriya Ghosh and Javier Cabrera. Enriched random forest for high dimensional genomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5): 2817–2828, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3089417.

Gossmann:2018:SRM

[GCB+18] Alexej Gossmann, Shaolong Cao, Damian Brzyski, Lan-Juan Zhao, Hong-Wen Deng, and Yu-Ping Wang. A sparse regression method for group-wise feature selection with false discovery rate control. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1066–1078, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2014:HTZ

[GCC+14] Yuan Gao, Rosa H. M. Chan, Tommy W. S. Chow, Liyun Zhang, Sylvia Bonilla, Chi-Pui Pang, Mingzhi Zhang, and Yuk Fai Leung. A high-throughput zebrafish screening method for visual mutants by light-induced locomotor response. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):693–701, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guo:2022:CMC

[GCC+22] Xiaojuan Guo, Kewei Chen, Yinghua Chen, Chengjie Xiong, Yi Su, Li Yao, and Eric M. Reiman. A computational Monte Carlo simulation strategy to deter-

mine the temporal ordering of abnormal age onset among biomarkers of Alzheimer#x0027;s disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5): 2613–2622, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3106939`.

Gonzalez-Crespo:2023:BMT

[GCGCP+23] Isabel González-Crespo, Antonio Gómez-Caamaño, Óscar López Pouso, John D. Fenwick, and Juan Pardo-Montero. A biomathematical model of tumor response to radioimmunotherapy with αPDL1 and αCTLA4. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):808–821, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3174454`.

Gu:2021:EBB

[GCJ+21] Xiaotong Gu, Zehong Cao, Alireza Jolfaei, Peng Xu, Dongrui Wu, Tzyy-Ping Jung, and Chin-Teng Lin. EEG-based brain-computer interfaces (BCIs): a survey of recent studies on signal sensing technologies and computational intelligence approaches and their applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1645–1666, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3052811`.

Guo:2018:RDM

[GCL+18] Yi-Nan Guo, Jian Cheng, Sha Luo, Dunwei Gong, and Yu Xue. Robust dynamic multi-objective vehicle routing optimization method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 1891–1903, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Cao:2010:IAM

[gCLL+10] Yong gang Cao, Zuofeng Li, Feifan Liu, Shashank Agarwal, Qing Zhang, and Hong Yu. An IR-aided machine learning framework for the BioCreative II.5 challenge. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):454–461, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guo:2021:SNG

[GCY+21] Guimu Guo, Hongzhi Chen, Da Yan, James Cheng,

Jake Y. Chen, and Zechen Chong. Scalable De Novo genome assembly using a pregel-like graph-parallel system. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):731–744, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2920912`.

Gao:2018:MMA

[GCZ18] Xin Gao, Jake Y. Chen, and Mohammed J. Zaki. Multiscale and multimodal analysis for computational biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1951–1952, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ghosh:2022:BSS

[GD22] Debraj Ghosh and Rajat K. De. Block search stochastic simulation algorithm (*BlSSSA*): a fast stochastic simulation algorithm for modeling large biochemical networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2111–2123, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3070123`.

Grassi:2012:KSP

[GDM12] Elena Grassi, Federico Di Gregorio, and Ivan Molineris. KungFQ: a simple and powerful approach to compress `fastq` files. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1837–1842, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gonzalez-Dominguez:2018:MPC

[GDM18] Jorge Gonzalez-Dominguez and Maria J. Martin. MPI-GeneNet: Parallel calculation of gene co-expression networks on multicore clusters. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1732–1737, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Grueter:2021:RRS

[GDRLH21] Melissa Grueter, Kalani Duran, Ramya Ramalingam, and Ran Libeskind-Hadas. Reconciliation reconsidered: In search of a most representative reconciliation in the duplication-transfer-loss model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2136–2143, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964

(electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2942015`.

Gonzalez-Dominguez:2015:PED

[GDWK+15] Jorge Gonzalez-Dominguez, Lars Wienbrandt, Jan Christian Kassens, David Ellinghaus, Manfred Schimmler, and Bertil Schmidt. Parallelizing epistasis detection in GWAS on FPGA and GPU-accelerated computing systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):982–994, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gorecki:2014:MDC

[GE14] Pawel Górecki and Oliver Eulenstein. Maximizing deep coalescence cost. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):231–242, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gorecki:2015:GTD

[GE15] Pawe Górecki and Oliver Eulenstein. Gene tree diameter for deep coalescence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):155–165, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gorecki:2018:BDG

[GE18] Pawel Gorecki and Oliver Eulenstein. Bijective diameters of gene tree parsimony costs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1723–1727, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Goodacre:2017:PND

[GED+17] Norman Goodacre, Nathan Edwards, Mark Danielsen, Peter Uetz, and Cathy Wu. Predicting nsSNPs that disrupt protein-protein interactions using docking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1082–1093, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gorecki:2013:UTR

[GET13] Pawel Gorecki, Oliver Eulenstein, and Jerzy Tiuryn. Unrooted tree reconciliation: a unified approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):522–536, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gorecki:2021:UDD

[GET21] Paweł Górecki, Oliver Eulenstein, and Jerzy Tiuryn. The unconstrained diameters of the duplication-loss cost and the loss cost. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2125–2135, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2919617`.

Godin:2010:QDS

[GF10] Christophe Godin and Pascal Ferraro. Quantifying the degree of self-nestedness of trees: Application to the structural analysis of plants. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):688–703, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gong:2016:PDA

[GFG16] Yanmin Gong, Yuguang Fang, and Yuanxiong Guo. Private data analytics on biomedical sensing data via distributed computation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):431–444, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guo:2021:DMS

[GFG+21] Hongzhe Guo, Yilei Fu, Yan Gao, Junyi Li, Yadong Wang, and Bo Liu. deGSM: Memory scalable construction of large scale de Bruijn graph. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2157–2166, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2913932`.

Gordon:2013:HWP

[GFS13] Kevaughn Gordon, Eric Ford, and Katherine St. John. Hamiltonian walks of phylogenetic treespaces. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1076–1079, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gysel:2011:EIC

[GG11] Rob Gysel and Daniel Gusfield. Extensions and improvements to the chordal graph approach to the multistate perfect phylogeny problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):912–917, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2013:MMA

[GGH+13] Qian Gao, David Gilbert, Monika Heiner, Fei Liu, Daniele Maccagnola, and David Tree. Multiscale modeling and analysis of planar cell polarity in the *Drosophila* wing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):337–351, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ganapathy:2006:PIB

[GGJ+06] Ganeshkumar Ganapathy, Barbara Goodson, Robert Jansen, Hai son Le, Vijaya Ramachandran, and Tandy Warnow. Pattern identification in biogeography. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3 (4):334–346, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gonzalez:2021:BIL

[GGM21] Miguel González, Cristina Gutiérrez, and Rodrigo Martínez. Bayesian inference in Y-linked two-sex branching processes with mutations: ABC approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):525–538, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2921308`.

Genovese:2008:SAH

[GGP08] Loredana M. Genovese, Filippo Geraci, and Marco Pellegrini. SpeedHap: An accurate heuristic for the single individual SNP haplotyping problem with many gaps, high reading error rate and low coverage. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):492–502, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gan:2014:ICR

[GGZZ14] Yanglan Gan, Jihong Guan, Shuigeng Zhou, and Weixiong Zhang. Identifying cis-regulatory elements and modules using conditional random fields. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):73–82, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gambette:2008:ILP

[GH08a] Philippe Gambette and Daniel H. Huson. Improved layout of phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):472–479, July 2008.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Giancarlo:2008:GEI

[GH08b] Raffaele Giancarlo and Sridhar Hannenhalli. Guest Editors' introduction to the special section on algorithms in bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):482–483, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Golshan:2015:OLB

[GH15] Hosein M. Golshan and Reza P. R. Hasanzadeh. An optimized LMMSE based method for 3D MRI denoising. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):861–870, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gustafsson:2005:CAL

[GHL05] Mika Gustafsson, Michael Hornquist, and Anna Lombardi. Constructing and analyzing a large-scale gene-to-gene regulatory network-lasso-constrained inference and biological validation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):254–261, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2022:MSC

[GHZ+22] Shan Gao, Renmin Han, Xiangrui Zeng, Zhiyong Liu, Min Xu, and Fa Zhang. Macromolecules structural classification with a 3D dilated dense network in cryo-electron tomography. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):209–219, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3065986`.

Guo:2019:GES

[GJH19] Feng-Biao Guo, Xinglai Ji, and Jian Huang. Guest editorial for special section on the 7th National Conference on Bioinformatics and Systems Biology of China. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1262–1263, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gopinath:2015:DKD

[GJK15] Krishnasamy Gopinath, Ramaraj Jayakumararaj, and Muthusamy Karthikeyan. DAPD: a knowledgebase for diabetes associated proteins. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 12(3):604–610, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Garcia-Jimenez:2014:PPR

[GJPSV14] Beatriz García-Jiménez, Tirso Pons, Araceli Sanchis, and Alfonso Valencia. Predicting protein relationships to human pathways through a relational learning approach based on simple sequence features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):753–765, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guillemot:2011:CSM

[GJS11] Sylvain Guillemot, Jesper Jansson, and Wing-Kin Sung. Computing a smallest multilabeled phylogenetic tree from rooted triplets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):1141–1147, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gong:2023:SNS

[GJSB23] Tiansu Gong, Fusong Ju, Shiwei Sun, and Dongbo Bu. SASA-Net: a spatial-aware self-attention mechanism for building protein 3D structure directly from inter- residue distances. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3482–3488, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3240456`.

Guo:2014:RFE

[GJY+14] Jing Guo, Ritika Jain, Peng Yang, Rui Fan, Chee Keong Kwoh, and Jie Zheng. Reliable and fast estimation of recombination rates by convergence diagnosis and parallel Markov Chain Monte Carlo. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):63–72, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gu:2017:RGS

[GJZH17] Deqing Gu, Xingxing Jian, Cheng Zhang, and Qiang Hua. Reframed genome-scale metabolic model to facilitate genetic design and integration with expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1410–1418, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gondro:2008:OCM

[GK08] Cedric Gondro and Brian P.

Kinghorn. Optimization of cDNA microarray experimental designs using an evolutionary algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):630–638, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ghosh:2019:FFS

[GK19] Priyanka Ghosh and Ananth Kalyanaraman. FastEtch: a fast sketch-based assembler for genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1091–1106, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gasbarra:2011:EHF

[GKPS11] Dario Gasbarra, Sangita Kulathinal, Matti Pirinen, and Mikko J. Sillanpaa. Estimating haplotype frequencies by combining data from large DNA pools with database information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):36–44, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guo:2022:SNU

[GKS+22] Yue Guo, Oleh Krupa, Jason Stein, Guorong Wu, and Ashok Krishnamurthy. SAU-Net: a unified network for cell counting in 2D and 3D microscopy images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):1920–1932, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3089608`.

Gong:2023:CLE

[GLF+23] Yinyin Gong, Rui Li, Bin Fu, Yan Liu, Jilong Wang, Renfa Li, and Danny Z. Chen. A CNN-LSTM ensemble model for predicting protein-protein interaction binding sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3588–3599, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3306948`.

Gupta:2010:AHD

[GLG10] Gunjan Gupta, Alexander Liu, and Joydeep Ghosh. Automated hierarchical density shaving: a robust automated clustering and visualization framework for large biological data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):223–237, April 2010. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic).

Gao:2018:NCD

[GLL+18] Chao Gao, Mingxin Liang, Xianghua Li, Zili Zhang, Zhen Wang, and Zhili Zhou. Network community detection based on the Physarum-inspired computational framework. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 1916–1928, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ganesan:2016:PSC

[GLS+16] Narayan Ganesan, Jie Li, Vishakha Sharma, Hanyu Jiang, and Adriana Compagnoni. Process simulation of complex biological pathways in physical reactive space and reformulated for massively parallel computing platforms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):365–379, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gonzalez:2012:PLB

[GLW12] Alvaro J. Gonzalez, Li Liao, and Cathy H. Wu. Predicting ligand binding residues and functional sites using multipositional correlations with graph theoretic clustering and kernel CCA. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):992–1001, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2022:PSC

[GLX+22] Jianliang Gao, Tengfei Lyu, Fan Xiong, Jianxin Wang, Weimao Ke, and Zhao Li. Predicting the survival of cancer patients with multimodal graph neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):699–709, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3083566`.

Guan:2021:MGS

[GLYZ21] Jiaqi Guan, Runzhe Li, Sheng Yu, and Xuegong Zhang. A method for generating synthetic electronic medical record text. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):173–182, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2948985`.

Grunewald:2009:MPT

[GM09] Stefan Grünewald and Vincent Moulton. Maximum parsimony for tree mixtures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (1):97–102, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Goncalves:2014:LEH

[GM14] Joana P. Gonçalves and Sara C. Madeira. LateBiclustering: efficient heuristic algorithm for time-lagged bicluster identification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):801–813, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guzzi:2016:GES

[GM16] Pietro H. Guzzi and Marco Mina. Guest editorial for special section on semantic-based approaches for analysis of biological data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2): 196, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gull:2022:PAS

[GM22] Sadaf Gull and Fayyaz Minhas. AMP_0: Species-specific prediction of antimicrobial peptides using zero and few shot learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):275–283, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2999399`.

Gudur:2022:FBE

[GMAS22] Venkateshwarlu Yellaswamy Gudur, Sidharth Maheshwari, Amit Acharyya, and Rishad Shafik. An FPGA based energy-efficient read mapper with parallel filtering and in-situ verification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2697–2711, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3106311`.

Gregory:2014:LFD

[GMCB14] Karl B. Gregory, Amin A. Momin, Kevin R. Coombes, and Veerabhadran Baladandayuthapani. Latent feature decompositions for integrative analysis of multi-platform genomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6): 984–994, November 2014. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Gusev:2008:HSG

[GMP08] Alexander Gusev, Ion I. Mãndoiu, and Bogdan Paşaniuc. Highly scalable genotype phasing by entropy minimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):252–261, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ghorai:2011:CCG

[GMSD11] Santanu Ghorai, Anirban Mukherjee, Sanghamitra Sengupta, and Pranab K. Dutta. Cancer classification from gene expression data by NPPC ensemble. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 659–671, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Goni:2013:NAI

[Gon13] Osman Goni. A new approach to implement absorbing boundary condition in biomolecular electrostatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):799–804, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gossler:2011:CBM

[Gos11] Gregor Gossler. Component-based modeling and reachability analysis of genetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):672–682, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Goutsias:2006:HMM

[Gou06] John Goutsias. A hidden Markov model for transcriptional regulation in single cells. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):57–71, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guo:2020:NEE

[GPC+20] Qian Guo, Tianhong Pan, Shan Chen, Xiaobo Zou, and Dorothy Yu Huang. A novel edge effect detection method for real-time cellular analyzer using functional principal component analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5): 1563–1572, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2903094`.

Gorecki:2017:UDD

[GPE17] Pawel Pawel Gorecki, Jaroslaw Paszek, and Oliver Eulenstein. Unconstrained diameters for deep coalescence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1002–1012, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gibbs:2020:AVS

[GPF+20] Jonathon A. Gibbs, Michael P. Pound, Andrew P. French, Darren M. Wells, Erik H. Murchie, and Tony P. Pridmore. Active vision and surface reconstruction for 3D plant shoot modelling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 1907–1917, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2896908`.

Gong:2016:GBN

[GPMH16] Maoguo Gong, Zhenglin Peng, Lijia Ma, and Jiaxiang Huang. Global biological network alignment by using efficient memetic algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6): 1117–1129, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gomez-Pulido:2015:ABA

[GPScF15] Juan A. Gomez-Pulido, Bertil Schmidt, and Wu chun Feng. Accelerating bioinformatics applications via emerging parallel computing systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):971–972, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ganor:2020:NGT

[GPZ20] Dor Ganor, Ron Y. Pinter, and Meirav Zehavi. A note on GRegNetSim: a tool for the discrete simulation and analysis of genetic regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):316–320, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2878749`.

Gramm:2004:PTA

[Gra04] Jens Gramm. A polynomial-time algorithm for the matching of crossing contact-map patterns. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(4):171–180, Octo-

ber 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ge:2021:CMB

[GRD+21] Yan Ge, Philipp Rosendahl, Claudio Durán, Nicole Töpfner, Sara Ciucci, Jochen Guck, and Carlo Vittorio Cannistraci. Cell mechanics based computational classification of red blood cells via machine intelligence applied to morpho-rheological markers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1405–1415, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2945762`.

GaneshKumar:2014:HAB

[GRDV14] Pugalendhi GaneshKumar, Chellasamy Rani, Durairaj Devaraj, and T. Aruldoss Albert Victoire. Hybrid ant bee algorithm for fuzzy expert system based sample classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):347–360, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Goeffon:2008:PTN

[GRH08] Adrien Goeffon, Jean-Michel Richer, and Jin-Kao Hao. Progressive tree neighborhood applied to the maximum parsimony problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):136–145, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ghasemi:2023:CDG

[GRK23] Mahdieh Ghasemi, Maseud Rahgozar, and Kaveh Kavousi. Complex disease genes identification using a heterogeneous network embedding approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):875–882, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3175598`.

Garcia:2013:GDA

[GRS+13] Sara P. Garcia, Joao M. O. S. Rodrigues, Sergio Santos, Diogo Pratas, Vera Afreixo, Carlos Bastos, Paulo J. S. G. Ferreira, and Armando J. Pinho. A genomic distance for assembly comparison based on compressed maximal exact matches. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):793–798, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Grusea:2011:DNC

[Gru11] Simona Grusea. On the distribution of the number of cycles in the breakpoint graph of a random signed permutation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1411–1416, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Grunewald:2013:SCS

[GSB+13] Stefan Grunewald, Andreas Spillner, Sarah Bastkowski, Anja Bogershausen, and Vincent Moulton. SuperQ: Computing supernetworks from quartets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):151–160, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Grewal:2017:EAO

[GSC17] Nivit Grewal, Shailendra Singh, and Trilok Chand. Effect of aggregation operators on network-based disease gene prioritization: a case study on blood disorders. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6): 1276–1287, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2018:ISE

[GSC+18] Shangce Gao, Shuangbao Song, Jiujun Cheng, Yuki Todo, and MengChu Zhou. Incorporation of solvent effect into multi-objective evolutionary algorithm for improved protein structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1365–1378, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gremme:2013:GCS

[GSK13] Gordon Gremme, Sascha Steinbiss, and Stefan Kurtz. GenomeTools: a comprehensive software library for efficient processing of structured genome annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):645–656, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guo:2018:GPS

[GSX+18] Weian Guo, Chengyong Si, Yu Xue, Yanfen Mao, Lei Wang, and Qidi Wu. A grouping particle swarm optimizer with personal-best-position guidance for large scale optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 1904–1915, November 2018.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ganaie:2024:EDR

[GT24] M. A. Ganaie and M. Tanveer. Ensemble deep random vector functional link network using privileged information for Alzheimer's disease diagnosis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):534–545, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3170351`.

Gabr:2015:RAP

[GTDK15] Haitham Gabr, Andrei Todor, Alin Dobra, and Tamer Kahveci. Reachability analysis in probabilistic biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):53–66, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2021:PAM

[GTL+21] Jianliang Gao, Ling Tian, Tengfei Lv, Jianxin Wang, Bo Song, and Xiaohua Hu. Protein2Vec: Aligning multiple PPI networks with representation learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):240–249, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2937771`.

Guo:2024:GBF

[GTL+24] Rui Guo, Xu Tian, Hanhe Lin, Stephen McKenna, Hong-Dong Li, Fei Guo, and Jin Liu. Graph-based fusion of imaging, genetic and clinical data for degenerative disease diagnosis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):57–68, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3335369`.

Goldweber:2017:PGB

[GTTR+17] Scott Goldweber, Jamal Theodore, John Torcivia-Rodriguez, Vahan Simonyan, and Raja Mazumder. Pubcast and Genecast: Browsing and exploring publications and associated curated content in biology through mobile devices. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):498–500, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2023:CCN

[GTX+23] Zhen Gao, Jin Tang, Junfeng Xia, Chun-Hou Zheng, and Pi-Jing Wei. CNNGRN: a convolutional neural network-based method for gene regulatory network inference from bulk time-series expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5): 2853–2861, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3282212`.

Gu:2016:MSO

[Gu16] Xu Gu. A multi-state optimization framework for parameter estimation in biological systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):472–482, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2004:INA

[Gus04a] Dan Gusfield. Introduction of new Associate Editors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1 (3):97, July 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2004:IIA

[Gus04b] Dan Gusfield. Introduction to the IEEE/ACM Transactions on Computational Biology and Bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):2–3, January 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2005:EST

[Gus05] Dan Gusfield. Editorial-state of the transaction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1): 39, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2006:INA

[Gus06a] Dan Gusfield. Introduction of new Associate Editors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):97, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2006:SJ

[Gus06b] Dan Gusfield. State of the journal. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):1, January 2006. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Gusfield:2007:AEAa

[Gus07a] Dan Gusfield. Associate Editor appreciation and welcome. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):2, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2007:AEAb

[Gus07b] Dan Gusfield. Associate Editor appreciation and welcome. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):321, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2007:SJ

[Gus07c] Dan Gusfield. State of the Journal. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):1, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2008:EE

[Gus08] Dan Gusfield. EIC editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):481, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2009:FFY

[Gus09a] Dan Gusfield. Final, five-year end, editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):1–2, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gusfield:2009:OEE

[Gus09b] Dan Gusfield. Outgoing EIC editorial for this special section of TCBB with the theme of phylogenetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):96, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2022:NMB

[GWW+22] Zhen Gao, Yu-Tian Wang, Qing-Wen Wu, Lei Li, Jian-Cheng Ni, and Chun-Hou Zheng. A new method based on matrix completion and non-negative matrix factorization for predicting disease-associated miRNAs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):763–772, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2020.3027444.

Ge:2017:CSD

[GXSZ17] Shu-Guang Ge, Junfeng Xia, Wen Sha, and Chun-Hou Zheng. Cancer subtype discovery based on integrative model of multigenomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1115–1121, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guan:2024:BDA

[GYW+24] Peiyuan Guan, Keping Yu, Wei Wei, YanLin Tan, and Jia Wu. Big data analytics on lung cancer diagnosis framework with deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):757–768, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3281638.

Guzzi:2022:EDL

[GZ22] Pietro Hiram Guzzi and Marinka Zitnik. Editorial deep learning and graph embeddings for network biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):653–654, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3110279.

Gao:2023:GES

[GZB23] Honghao Gao, Zijian Zhang, and Ramón J. Durán Barroso. Guest editorial special issue on multi-modal biomedical computing-deep transfer learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2363–2366, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3284603.

Guo:2017:SGW

[GZC+17] Xuan Guo, Jing Zhang, Zhipeng Cai, Ding-Zhu Du, and Yi Pan. Searching genome-wide multi-locus associations for multiple diseases based on Bayesian inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):600–610, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gao:2015:CCE

[GZFT15] Nan Gao, Yan Zhang, Bing Feng, and Jijun Tang. A cooperative co-evolutionary genetic algorithm for tree scoring and ancestral genome inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

12(6):1248–1254, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gangeh:2017:FSF

[GZG17] Mehrdad J. Gangeh, Hadi Zarkoob, and Ali Ghodsi. Fast and scalable feature selection for gene expression data using Hilbert–Schmidt independence criterion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (1):167–181, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gan:2014:NWB

[GZGX14] Yanglan Gan, Guobing Zou, Jihong Guan, and Guangwei Xu. A novel wavelet-based approach for predicting nucleosome positions using DNA structural information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):638–647, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gu:2021:HDS

[GZN21] Xiaoqing Gu, Cong Zhang, and TongGuang Ni. A hierarchical discriminative sparse representation classifier for EEG signal detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1679–1687, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3006699`.

Ghoshal:2018:DCM

[GZR+18] Asish Ghoshal, Jinyi Zhang, Michael A. Roth, Kevin Muyuan Xia, Ananth Y. Grama, and Somali Chaterji. A distributed classifier for MicroRNA target prediction with validation through TCGA expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1037–1051, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Giegerich:2011:SAS

[GzS11] Robert Giegerich and Christian Hoener zu Siederdissen. Semantics and ambiguity of stochastic RNA family models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (2):499–516, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Gyorffy:2012:PMR

[GZS12] Daniel Gyorffy, Peter Zavodszky, and Andras Szilagyi. "pull moves" for rectangu-

lar lattice polymer models are not fully reversible. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1847–1849, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Guan:2023:PDB

[GZWD23] Shixuan Guan, Quan Zou, Hongjie Wu, and Yijie Ding. Protein-DNA binding residues prediction using a deep learning model with hierarchical feature extraction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2619–2628, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3190933`.

Gu:2021:IMT

[GZXH21] Wanrong Gu, Ziye Zhang, Xianfen Xie, and Yichen He. An improved mutitask learning algorithm for analyzing cancer survival data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):500–511, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2920770`.

Guan:2022:DDA

[GZYL22] Boxin Guan, Yuhai Zhao, Ying Yin, and Yuan Li. Detecting disease-associated SNP–SNP interactions using progressive screening memetic algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):878–887, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3019256`.

Higa:2013:GSG

[HAH13] Carlos H. A. Higa, Tales P. Andrade, and Ronaldo Fumio Hashimoto. Growing seed genes from time series data and thresholded Boolean networks with perturbation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):37–49, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hashemikhabir:2012:LSS

[HAK+12] Seyedsasan Hashemikhabir, Eyup Serdar Ayaz, Yusuf Kavurucu, Tolga Can, and Tamer Kahveci. Large-scale signaling network reconstruction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1696–1708, November 2012. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Han:2010:NPC

[Han10] Xiaoxu Han. Nonnegative principal component analysis for cancer molecular pattern discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):537–549, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hawkins:2005:ARN

[HB05] John Hawkins and Mikael Boden. The applicability of recurrent neural networks for biological sequence analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):243–253, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hudek:2011:FSL

[HB11] Alexander K. Hudek and Daniel G. Brown. FEAST: Sensitive local alignment with multiple rates of evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):698–709, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hickey:2011:AAN

[HBC+11] Glenn Hickey, Mathieu Blanchette, Paz Carmi, Anil Maheshwari, and Norbert Zeh. An approximation algorithm for the Noah's Ark Problem with random feature loss. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):551–556, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2016:GES

[HBG16] De-Shuang Huang, Vitoantonio Bevilacqua, and M. Michael Gromiha. Guest editorial for special section on the 10th International Conference on Intelligent Computing (ICIC). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):1–3, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2017:GES

[HBG17] De-Shuang Huang, Vitoantonio Bevilacqua, and M. Michael Gromiha. Guest editorial for special section on the 11th International Conference on Intelligent Computing ICIC. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1104–1105, September 2017.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2018:GES

[HBG18] De-Shuang Huang, Vitoantonio Bevilacqua, and M. Michael Gromiha. Guest editorial for special section on the 12th International Conference on Intelligent Computing ICIC. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1433–1435, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2019:GES

[HBG19] De-Shuang Huang, Vitoantonio Bevilacqua, and M. Michael Gromiha. Guest editorial for special section on the 13th International Conference on Intelligent Computing ICIC. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):749–750, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2020:GES

[HBG20] De-Shuang Huang, Vitoantonio Bevilacqua, and Michael Gromiha. Guest editorial for special section on the 14th International Conference on Intelligent Computing (ICIC). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1474–1475, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2989800`.

Huang:2021:GES

[HBG21] De-Shuang Huang, Vitoantonio Bevilacqua, and M. Michael Gromiha. Guest editorial for special section on the 15th International Conference on Intelligent Computing (ICIC). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1730–1732, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3065722`.

Hanczar:2012:NMC

[HBH12] Blaise Hanczar and Avner Bar-Hen. A new measure of classifier performance for gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1379–1386, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hartmann:2019:EAS

[HBM19] Tom Hartmann, Matthias Bernt, and Martin Middendorf. An exact algorithm for sorting by weighted preserving genome rearrangements. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):52–62, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hartmann:2021:SSP

[HBM21] Tom Hartmann, Max Bannach, and Martin Middendorf. Sorting signed permutations by inverse tandem duplication random losses. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (6):2177–2188, November/ December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2917198`.

Haack:2013:SRL

[HBRU13] Fiete Haack, Kevin Burrage, Ronald Redmer, and Adelinde M. Uhrmacher. Studying the role of lipid rafts on protein receptor bindings with cellular automata. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):760–770, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2007:EGS

[HC07] D. Huang and Tommy Chow. Effective gene selection method with small sample sets using gradient-based and point injection techniques. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):467–475, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2013:UBT

[HC13] Allen L. Hu and Keith C. C. Chan. Utilizing both topological and attribute information for protein complex identification in PPI networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):780–792, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Healy:2014:AKM

[HC14a] John Healy and Desmond Chambers. Approximate k-mer matching using fuzzy hash maps. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):258–264, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Horta:2014:SMC

[HC14b] Danilo Horta and Ricardo J. G. B. Campello. Similarity measures for comparing biclusterings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):942–954, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2015:GEA

[HC15] Hsien-Da Huang and Yi-Ping Phoebe Chen. Guest editorial for the 13th Asia Pacific Bioinformatics Conference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1217–1218, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hsieh:2016:FCM

[HC16] Sun-Yuan Hsieh and Yu-Chun Chou. A faster cDNA microarray gene expression data classifier for diagnosing diseases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):43–54, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2017:ECF

[HC17] Lun Hu and Keith C. C. Chan. Extracting coevolutionary features from protein sequences for predicting protein–protein interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (1):155–166, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2018:EGC

[HC18] Tiantian He and Keith C. C. Chan. Evolutionary graph clustering for protein complex identification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):892–904, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2019:MBP

[HC19] Tiantian He and Keith C. C. Chan. Measuring boundedness for protein complex identification in PPI networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):967–979, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2024:QEQ

[HC24] Zaobo He and Zhipeng Cai. Quantifying the effect of quarantine control and optimizing its cost in COVID-19 pandemic.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 21(4):803–813, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215559`.

Han:2010:MPC

[HCA+10] Ju Han, Hang Chang, Kumari Andarawewa, Paul Yaswen, Mary Helen Barcellos-Hoff, and Bahram Parvin. Multidimensional profiling of cell surface proteins and nuclear markers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):80–90, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hoque:2011:TRG

[HCLS11] Md Tamjidul Hoque, Madhu Chetty, Andrew Lewis, and Abdul Sattar. Twin removal in genetic algorithms for protein structure prediction using low-resolution model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):234–245, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hartmann:2018:CTD

[HCMB18] Tom Hartmann, An-Chiang Chu, Martin Middendorf, and Matthias Bernt. Combinatorics of tandem duplication random loss mutations on circular genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):83–95, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Halder:2019:LII

[HCN+19] Anup Kumar Halder, Piyali Chatterjee, Mita Nasipuri, Dariusz Plewczynski, and Subhadip Basu. 3gClust: Human protein cluster analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1773–1784, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2840996`.

Huang:2014:SAI

[HCQ14] Yufei Huang, Yidong Chen, and Xiaoning Qian. Selected articles from the 2012 IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS 2012). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):981–983, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huson:2004:PSN

[HDKS04] Daniel H. Huson, Tobias Dezulian, Tobias Klopper, and Mike A. Steel. Phylogenetic super-networks from partial trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(4):151–158, October 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2018:FSO

[HDS+18] Bin Hu, Yongqiang Dai, Yun Su, Philip Moore, Xiaowei Zhang, Chengsheng Mao, Jing Chen, and Lixin Xu. Feature selection for optimized high-dimensional biomedical data using an improved shuffled frog leaping algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1765–1773, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hashem:2018:CML

[HEE+18] Somaya Hashem, Gamal Esmat, Wafaa Elakel, Shahira Habashy, Safaa Abdel Raouf, Mohamed Elhefnawi, Mohamed Eladawy, and Mahmoud ElHefnawi. Comparison of machine learning approaches for prediction of advanced liver fibrosis in chronic hepatitis C patients. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):861–868, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hayamizu:2017:CMS

[HEF17] Momoko Hayamizu, Hiroshi Endo, and Kenji Fukumizu. A characterization of minimum spanning tree-like metric spaces. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):468–471, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hamad:2018:DWU

[HEK18] Safwat Hamad, Ahmed Elhadad, and Amal Khalifa. DNA watermarking using codon postfix technique. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1605–1610, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hecht:2007:HTL

[HF07] David Hecht and Gary Fogel. High-throughput ligand screening via preclustering and evolved neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):476–484, July 2007.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2012:GCU

[HF12] Hong Huang and Hailiang Feng. Gene classification using parameter-free semi-supervised manifold learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):818–827, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2016:RTN

[HG16] Yuanqi Hu and Pantelis Georgiou. A real-time de novo DNA sequencing assembly platform based on an FPGA implementation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):291–300, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2020:DRL

[HGC+20] Haigen Hu, Qiu Guan, Shengyong Chen, Zhiwei Ji, and Yao Lin. Detection and recognition for life state of cell cancer using two-stage cascade CNNs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):887–898, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2017.2780842`.

Huang:2018:GNA

[HGM18] Jiaxiang Huang, Maoguo Gong, and Lijia Ma. A global network alignment method using discrete particle swarm optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):705–718, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2022:GES

[HHA22] De-Shuang Huang, Kyungsook Han, and Tatsuya Akutsu. Guest editorial for special section on the 16th International Conference on Intelligent Computing (ICIC). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3124–3125, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3150232`.

Hu:2024:NNO

[HHC+24] Zhao-Qi Hu, Yuan-Mao Hung, Li-Han Chen, Liang-Chuan Lai, Min-Hsiung Pan, Eric Y. Chuang, and Mong-Hsun Tsai. NURECON: a novel online system for determining nu-

trition requirements based on microbial composition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):254–264, March 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3349572`.

Hu:2020:LMN

[HHCY20] Pengwei Hu, Yu-An Huang, Keith C. C. Chan, and Zhu-Hong You. Learning multimodal networks from heterogeneous data for prediction of lncRNA–miRNA interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1516–1524, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2957094`.

Hu:2020:ICI

[HHL+20] Lun Hu, Pengwei Hu, Xin Luo, Xiaohui Yuan, and Zhu-Hong You. Incorporating the coevolving information of substrates in predicting HIV-1 protease cleavage sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2017–2028, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2914208`.

Haque:2013:GQB

[HHSC13] Md. Muksitul Haque, Lawrence B. Holder, Michael K. Skinner, and Diane J. Cook. Generalized query-based active learning to identify differentially methylated regions in DNA. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):632–644, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ho:2007:ITS

[HHYH07] Shinn-Ying Ho, Chih-Hung Hsieh, Fu-Chieh Yu, and Hui-Ling Huang. An intelligent two-stage evolutionary algorithm for dynamic pathway identification from gene expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):648–704, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hodgkinson:2012:ADM

[HK12] Luqman Hodgkinson and Richard M. Karp. Algorithms to detect multiprotein modularity conserved during evolution. *IEEE/ACM Transactions on Computational Biology and*

Bioinformatics, 9(4):1046–1058, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hsu:2015:CNE

[HK15] Yi-Yu Hsu and Hung-Yu Kao. Curatable named-entity recognition using semantic relations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):785–792, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Habibi:2020:DPC

[HK20] Mahnaz Habibi and Pegah Khosravi. Disruption of protein complexes from weighted complex networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (1):102–109, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2859952`.

Handl:2007:MOB

[HKK07] Julia Handl, Douglas B. Kell, and Joshua Knowles. Multiobjective optimization in bioinformatics and computational biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):279–292, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huffner:2014:PBN

[HKLN14] Falk Hüffner, Christian Komusiewicz, Adrian Liebtrau, and Rolf Niedermeier. Partitioning biological networks into highly connected clusters with maximum edge coverage. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):455–467, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hujdurovic:2018:CAF

[HKM+18] Ademir Hujdurovic, Ursa Kacar, Martin Milanic, Bernard Ries, and Alexandru I. Tomescu. Complexity and algorithms for finding a perfect phylogeny from mixed tumor samples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):96–108, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hafemeister:2011:SOP

[HKS11] Christoph Hafemeister, Roland Krause, and Alexander Schliep. Selecting oligonucleotide probes for whole-genome tiling arrays with a cross-hybridization potential. *IEEE/ACM Transac-*

tions on Computational Biology and Bioinformatics, 8(6):1642–1652, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hirose:2018:SCT

[HKT+18] Osamu Hirose, Shotaro Kawaguchi, Terumasa Tokunaga, Yu Toyoshima, Takayuki Teramoto, Sayuri Kuge, Takeshi Ishihara, Yuichi Iino, and Ryo Yoshida. SPF-CellTracker: Tracking multiple cells with strongly-correlated moves using a spatial particle filter. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 1822–1831, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Han:2016:GII

[HL16] Kyungsook Han and Jeonghoon Lee. GeneNetFinder2: Improved inference of dynamic gene regulatory relations with multiple regulators. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):4–11, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2021:NCP

[HL21] Hai-Hui Huang and Yong Liang. A novel Cox proportional hazards model for high-dimensional genomic data in cancer prognosis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1821–1830, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2961667`.

Hu:2017:GRS

[HLDZ17] Hailong Hu, Zhong Li, Hongwei Dong, and Tianhe Zhou. Graphical representation and similarity analysis of protein sequences based on fractal interpolation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (1):182–192, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2010:HRR

[HLG10] Liang-Tsung Huang, Lien-Fu Lai, and M. Michael Gromiha. Human-readable rule generator for integrating amino acid sequence information and stability of mutant proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):681–687, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2021:DDS

[HLGS21] Yue Hu, Jin-Xing Liu, Ying-Lian Gao, and Junliang Shang. DSTPCA: Double-sparse constrained tensor principal component analysis method for feature selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1481–1491, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2943459`.

Huang:2011:IHA

[HLH11] Chao-Wen Huang, Wun-Shiun Lee, and Sun-Yuan Hsieh. An improved heuristic algorithm for finding motif signals in DNA sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):959–975, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hind:2020:NAD

[HLHAJ20] Jade Hind, Paulo Lisboa, Abir J. Hussain, and Dhiya Al-Jumeily. A novel approach to detecting epistasis using random sampling regularisation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1535–1545, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2948330`.

He:2018:TSB

[HLL+18a] Xinyu He, Lishuang Li, Yang Liu, Xiaoming Yu, and Jun Meng. A two-stage biomedical event trigger detection method integrating feature selection and word embeddings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1325–1332, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2018:CBG

[HLL18b] Meng Hu, Wu Li, and Hualou Liang. A copula-based Granger causality measure for the analysis of neural spike train data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):562–569, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2022:NMC

[HLL+22] Xin Huang, Zhenqian Liao, Bing Liu, Fengmei Tao, Benzhe Su, and Xiaohui Lin. A novel method for constructing classification models by combining different biomarker patterns.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 19(2):786–794, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3022076`.

Harmer:2019:BCC

[HLLO19] Russ Harmer, Yves-Stan Le Cornec, Sebastien Legare, and Eugenia Oshurko. Biocuration for cellular signalling: The KAMI Project. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1562–1573, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Halasz:2013:ASS

[HLM+13] Adam M. Halasz, Hong-Jian Lai, Meghan M. McCabe, Krishnan Radhakrishnan, and Jeremy S. Edwards. Analytical solution of steady-state equations for chemical reaction networks with bilinear rate laws. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):957–969, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2011:DMF

[hLMBJ11] Tien ho Lin, Robert F. Murphy, and Ziv Bar-Joseph. Discriminative motif finding for predicting protein subcellular localization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):441–451, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2020:DSJ

[HLN20] Yicheng He, Junfeng Liu, and Xia Ning. Drug selection via joint push and learning to rank. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):110–123, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2848908`.

Hu:2018:ARE

[HLSR18] Bin Hu, Xiaowei Li, Shuting Sun, and Martyn Ratcliffe. Attention recognition in EEG-based affective learning research using CFS + KNN algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):38–45, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hakenberg:2010:EEP

[HLV+10] Jörg Hakenberg, Robert

Leaman, Nguyen Ha Vo, Siddhartha Jonnalagadda, Ryan Sullivan, Christopher Miller, Luis Tari, Chitta Baral, and Graciela Gonzalez. Efficient extraction of protein-protein interactions from full-text articles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):481–494, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2015:EMS

[HLW15] Lei Huang, Li Liao, and Cathy H. Wu. Evolutionary model selection and parameter estimation for protein–protein interaction network based on differential evolution algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):622–631, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2021:DSN

[HLX+21] Chenxi Huang, Yisha Lan, Gaowei Xu, Xiaojun Zhai, Jipeng Wu, Fan Lin, Nianyin Zeng, Qingqi Hong, E. Y. K. Ng, Yonghong Peng, Fei Chen, and Guokai Zhang. A deep segmentation network of multi-scale feature fusion based on attention mechanism for IVOCT lumen contour. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):62–69, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2973971`.

Hsiao:2016:PGI

[HLY+16] Yu-Ting Hsiao, Wei-Po Lee, Wei Yang, Stefan Muller, Christoph Flamm, Ivo Hofacker, and Philipp Kugler. Practical guidelines for incorporating knowledge-based and data-driven strategies into the inference of gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):64–75, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2022:CDV

[HLY+22] Runhua Huang, Chengchuang Lin, Aihua Yin, Hanbiao Chen, Li Guo, Gansen Zhao, Xiaomao Fan, Shuangyin Li, and Jinji Yang. A clinical dataset and various baselines for chromosome instance segmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):31–39, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2021.3089507.

Hu:2017:PPD

[HLZ+17] Jun Hu, Yang Li, Ming Zhang, Xibei Yang, Hong-Bin Shen, and Dong-Jun Yu. Predicting protein-DNA binding residues by weightedly combining sequence-based features and boosting multiple SVMs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1389–1398, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Henzinger:2013:PAC

[HM13] Thomas A. Henzinger and Maria Mateescu. The propagation approach for computing biochemical reaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (2):310–322, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Henriques:2015:BFP

[HM15] Rui Henriques and Sara C. Madeira. Biclustering with flexible plaid models to unravel interactions between biological processes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):738–752, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2007:PPP

[HMK+07] Chengbang Huang, Faruck Morcos, Simon P. Kanaan, Stefan Wuchty, Danny Z. Chen, and Jesus A. Izaguirre. Predicting protein-protein interactions from protein domains using a set cover approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):78–87, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huson:2009:SSP

[HMS09] Daniel H. Huson, Vincent Moulton, and Mike Steel. Special section: Phylogenetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):4–6, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hopfensitz:2012:MBG

[HMW+12] Martin Hopfensitz, Christoph Mussel, Christian Wawra, Markus Maucher, Michael Kuhl, Heiko Neumann, and Hans A. Kestler. Multiscale binarization of gene expression data for reconstructing Boolean networks. *IEEE/ACM Transactions on Computational Biology and*

Bioinformatics, 9(2):487–498, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Harrison:2017:GEI

[HMZ17] Robert W. Harrison, Ion I. Mandoiu, and Alexander Zelikovsky. Guest editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):576–577, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Handoko:2012:EQA

[HOS+12a] Stephanus Daniel Handoko, Xuchang Ouyang, Chinh Tran To Su, Chee Keong Kwoh, and Yew Soon Ong. Erratum to "QuickVina: Accelerating AutoDock Vina Using Gradient-Based Heuristics for Global Optimization". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1853, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Handoko:2012:QAA

[HOS+12b] Stephanus Daniel Handoko, Xuchang Ouyang, Chinh Tran To Su, Chee Keong Kwoh, and Yew Soon Ong. QuickVina: Accelerating AutoDock Vina using gradient-based heuristics for global optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1266–1272, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Howison:2013:HTC

[How13] Mark Howison. High-throughput compression of FASTQ data with SeqDB. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):213–218, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hsu:2015:SBF

[HPH+15] Chih-Yuan Hsu, Zhen-Ming Pan, Rei-Hsing Hu, Chih-Chun Chang, Hsiao-Chun Cheng, Che Lin, and Bor-Sen Chen. Systematic biological filter design with a desired I/O filtering response based on promoter-RBS libraries. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):712–725, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hossain:2013:IMS

[HPL+13] K. S. M. Tozammel Hos-

sain, Debprakash Patnaik, Srivatsan Laxman, Prateek Jain, Chris Bailey-Kellogg, and Naren Ramakrishnan. Improved multiple sequence alignments using coupled pattern mining. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1098–1112, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Herrera-Romero:2023:GIT

[HRAGS+23] Bryan Herrera-Romero, Diego Almeida-Galárraga, Graciela M. Salum, Fernando Villalba-Meneses, and Marco Esteban Gudiño-Gomezjurado. GUSignal: an informatics tool to analyze glucuronidase gene expression in *Arabidopsis thaliana* roots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (2):1073–1080, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3190427`.

Hulsman:2009:EOK

[HRdR09] Marc Hulsman, Marcel J. T. Reinders, and Dick de Ridder. Evolutionary optimization of kernel weights improves protein complex comembership prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):427–437, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2016:MMI

[HRHP16] Dan He, Irina Rish, David Haws, and Laxmi Parida. MINT: mutual information based transductive feature selection for genetic trait prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):578–583, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hendy:2008:HCK

[HS08] Michael D. Hendy and Sagi Snir. Hadamard conjugation for the Kimura 3ST model: Combinatorial proof using path sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):461–471, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Heath:2009:MNS

[HS09a] Lenwood S. Heath and Allan A. Sioson. Multimodal networks: Structure and operations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):321–332, April 2009. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Heath:2009:SMN

[HS09b] Lenwood S. Heath and Allan A. Sioson. Semantics of multimodal network models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):271–280, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hoksza:2015:MRS

[HS15] David Hoksza and Daniel Svozil. Multiple 3D RNA structure superposition using neighbor joining. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):520–530, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hua:2023:CER

[HSF+23] Yang Hua, Xiaoning Song, Zhenhua Feng, Xiao-Jun Wu, Josef Kittler, and Dong-Jun Yu. CPInformer for efficient and robust compound-protein interaction prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):285–296, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3144008`.

Huber:2011:MMT

[HSlSM11] Katharina T. Huber, Andreas Spillner, Rados law Suchecki, and Vincent Moulton. Metrics on multilabeled trees: Interrelationships and diameter bounds. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):1029–1040, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Handl:2018:AAD

[HSS18] J. Handl, A. Shehu, and Jose Santos Reyes. Advances in the application and development of non-linear global optimization techniques in computational structural biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):688–689, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hershkovitz:2006:SAR

[HSTW06] Eli Hershkovitz, Guillermo Sapiro, Allen Tannenbaum, and Loren Dean Williams. Statistical analysis of RNA backbone. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):33–46, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2023:DNC

[HSZ+23] Xin Huang, Benzhe Su, Chenbo Zhu, Xinyu He, and Xiaohui Lin. Dynamic network construction for identifying early warning signals based on a data-driven approach: Early diagnosis biomarker discovery for gastric cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):923–931, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3176319`.

Hong:2009:HRD

[HT09] Changjin Hong and Ahmed H. Tewfik. Heuristic reusable dynamic programming: Efficient updates of local sequence alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):570–582, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2012:PEL

[HTLL12] Qinghua Huang, Dacheng Tao, Xuelong Li, and Alan Liew. Parallelized evolutionary learning for detection of biclusters in gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (2):560–570, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2023:RFM

[HTZ+23] Weixian Huang, Kaiwen Tan, Ziye Zhang, Jinlong Hu, and Shoubin Dong. A review of fusion methods for omics and imaging data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (1):74–93, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3143900`.

Huson:2009:DRP

[Hus09] Daniel H. Huson. Drawing rooted phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (1):103–109, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Halioui:2018:BWE

[HVD18] Ahmed Halioui, Petko Valtchev, and Abdoulaye Banire Diallo. Bioinformatic workflow extraction from scientific texts based on word sense disambiguation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1979–1990, November 2018. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hochsmann:2004:PMR

[HVG04] Matthias Höchsmann, Björn Voss, and Robert Giegerich. Pure multiple RNA secondary structure alignments: a progressive profile approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):53–62, January 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huber:2011:PAR

[HvIKS11] Katharina T. Huber, Leo van Iersel, Steven Kelk, and Radosław Suchecki. A practical algorithm for reconstructing level-1 phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):635–649, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2007:DMP

[HW07] Xiaohua Hu and Daniel D. Wu. Data mining and predictive modeling of biomolecular network from biomedical literature databases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):251–263, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Humphries:2013:NT

[HW13] Peter J. Humphries and Taoyang Wu. On the neighborhoods of trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):721–728, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hsiao:2014:GND

[HWK14] Jui-Chen Hsiao, Chih-Hsuan Wei, and Hung-Yu Kao. Gene name disambiguation using multi-scope species detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):55–62, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2022:CCA

[HWM22] Zhihao Huang, Yan Wang, and Xiaoke Ma. Clustering of cancer attributed networks by dynamically and jointly factorizing multilayer graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2737–2748, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3090586`.

He:2017:IIP

[HWPE17] Dan He, Zhanyong Wang, Laxmi Parida, and Eleazar Eskin. IPED2: Inheritance path based pedigree reconstruction algorithm for complicated pedigrees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1094–1103, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hartmann:2018:GRI

[HWS+18] Tom Hartmann, Nicolas Wieseke, Roded Sharan, Martin Middendorf, and Matthias Bernt. Genome rearrangement with ILP. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1585–1593, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2023:DGE

[HWY+23] Zimo Huang, Jun Wang, Zhongmin Yan, Lin Wan, and Maozu Guo. Differential gene expression prediction by ensemble deep networks on histone modification data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):340–351, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3139634`.

Huang:2023:TDU

[HWZ+23] Chengxi Huang, Wei Wang, Xin Zhang, Shui-Hua Wang, and Yu-Dong Zhang. Tuberculosis diagnosis using deep transferred EfficientNet. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2639–2646, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3199572`.

Hu:2021:CNN

[HXS+21] ShanShan Hu, DeNan Xia, Benyue Su, Peng Chen, Bing Wang, and Jinyan Li. A convolutional neural network system to discriminate drug-target interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1315–1324, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2940187`.

Huang:2021:PHI

[HXX21] Chenxi Huang, Yutian Xiao, and Gaowei Xu. Predicting human intention-behavior through EEG signal analysis using multi-

scale CNN. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1722–1729, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3039834`.

Hashemikhabir:2018:FIG

[HXXJ18] Seyedsasan Hashemikhabir, Ran Xia, Yang Xiang, and Sarath Chandra Janga. A framework for identifying genotypic information from clinical records: Exploiting integrated ontology structures to transfer annotations between ICD codes and gene ontologies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1259–1269, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hennings-Yeomans:2012:IPC

[HYC12] Pablo H. Hennings-Yeomans and Gregory F. Cooper. Improving the prediction of clinical outcomes from genomic data using multiresolution analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1442–1450, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2019:EDP

[HYL+19] Lun Hu, Xiaohui Yuan, Xing Liu, Shengwu Xiong, and Xin Luo. Efficiently detecting protein complexes from protein interaction networks via alternating direction method of multipliers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1922–1935, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2844256`.

He:2020:IAC

[HYL+20] Zaobo He, Jiguo Yu, Ji Li, Qilong Han, Guangchun Luo, and Yingshu Li. Inference attacks and controls on genotypes and phenotypes for individual genomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):930–937, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2810180`.

Hao:2019:ICG

[HYR+19] Xiaoke Hao, Xiaohui Yao, Shannon L. Risacher, Andrew J. Saykin, Jintai Yu, Huifu Wang, Lan Tan, Li Shen, and Daoqiang Zhang. Identifying candidate genetic associa-

tions with MRI-derived AD-related ROI via tree-guided sparse learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1986–1996, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2833487`.

Hsieh:2008:OAI

[HYW08] Yong-Hsiang Hsieh, Chih-Chiang Yu, and Biing-Feng Wang. Optimal algorithms for the interval location problem with range constraints on length and average. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):281–290, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Han:2017:GSM

[HYW+17] Fei Han, Chun Yang, Ya-Qi Wu, Jian-Sheng Zhu, Qing-Hua Ling, Yu-Qing Song, and De-Shuang Huang. A gene selection method for microarray data based on binary PSO encoding gene-to-class sensitivity information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):85–96, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2011:PSC

[HYY11] Zengyou He, Can Yang, and Weichuan Yu. A partial set covering model for protein mixture identification using mass spectrometry data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):368–380, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hua:2016:GSM

[HYZ16] Keru Hua, Qin Yu, and Ruiming Zhang. A guaranteed similarity metric learning framework for biological sequence comparison. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):868–877, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2022:E

[HZG22] Xiuzhen Huang, Yu Zhang, and Xuan Guo. Editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1334–1335, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3131688`.

Hao:2019:ASS

[HZL19] FanChang Hao, Melvin Zhang, and Hon Wai Leong. A 2-approximation scheme for sorting signed permutations by reversals, transpositions, transreversals, and block-interchanges. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1702–1711, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2020:PCI

[HZL+20] Zengyou He, Can Zhao, Hao Liang, Bo Xu, and Quan Zou. Protein complexes identification with family-wise error rate control. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 2062–2073, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2912602`.

Haack:2019:CDS

[HZR+19] Jordan Haack, Eli Zupke, Andrew Ramirez, Yi-Chieh Wu, and Ran Libeskind-Hadas. Computing the diameter of the space of maximum parsimony reconciliations in the duplication–transfer–loss model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):14–22, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hawkins:2012:RFP

[HZTP12] John C. Hawkins, Hongbo Zhu, Joan Teyra, and M. Teresa Pisabarro. Reduced false positives in PDZ binding prediction using sequence and structural descriptors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1492–1503, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

He:2017:PNA

[HZW+17] Feng He, Guanghui Zhu, Yin-Ying Wang, Xing-Ming Zhao, and De-Shuang Huang. PCID: a novel approach for predicting disease comorbidity by integrating multi-scale data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):678–686, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hu:2014:PRA

[HZZT14] Fei Hu, Jun Zhou, Lingxi Zhou, and Jijun Tang. Probabilistic reconstruction of ancestral gene orders with insertions and deletions.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 11(4):667–672, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Hao:2016:NMU

[HZZY16] Xiao-Hu Hao, Gui-Jun Zhang, Xiao-Gen Zhou, and Xu-Feng Yu. A novel method using abstract convex underestimation in ab-initio protein structure prediction for guiding search in conformational feature space. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 887–900, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Azuma:2016:PAC

[iAOSS16] Shun ichi Azuma, Katsuya Owaki, Nobuhiro Shinohara, and Toshiharu Sugie. Performance analysis of chemotaxis controllers: Which has better chemotaxis controller, *Escherichia coli* or *Paramecium caudatum*? *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4): 730–741, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Imani:2019:CGR

[IBN19] Mahdi Imani and Ulisses M. Braga-Neto. Control of gene regulatory networks using Bayesian inverse reinforcement learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1250–1261, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Iravani:2023:IDL

[IC23] Sahar Iravani and Tim O. F. Conrad. An interpretable deep learning approach for biomarker detection in LC-MS proteomics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):151–161, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3141656`.

Irurozki:2011:PPH

[ICL11] Ekhine Irurozki, Borja Calvo, and Jose A. Lozano. A preprocessing procedure for haplotype inference by pure parsimony. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1183–1195, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ivanov:2013:QPP

[IDD13] Stefan Ivanov, Ivan Dimitrov, and Irina Doytchinova. Quantitative prediction of peptide binding to HLA-DP1 protein. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):811–815, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Staff:2005:RL

[IEE05] IEEE and ACM Transactions on Computational Biology and Bioinformatics staff. 2004 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):77, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Staff:2007:RL

[IEE07] IEEE and ACM Transactions on Computational Biology and Bioinformatics staff. 2006 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (1):158–160, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Iglesias:2018:IAF

[IGA18] Andres Iglesias, Akemi Galvez, and Andreina Avila. Immunological approach for full NURBS reconstruction of outline curves from noisy data points in medical imaging. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1929–1942, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Igel:2007:GBO

[IGM+07] Christian Igel, Tobias Glasmachers, Britta Mersch, Nico Pfeifer, and Peter Meinicke. Gradient-based optimization of kernel-target alignment for sequence kernels applied to bacterial gene start detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):216–226, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ironi:2018:MBT

[IL18] Liliana Ironi and Ettore Lanzarone. A model-based tool for the analysis and design of gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1301–1314, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ichikawa:2014:SPH

[IM14] Kazuki Ichikawa and Shinichi

Morishita. A simple but powerful heuristic method for accelerating k-means clustering of large-scale data in life science. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):681–692, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Irigoien:2013:DPI

[IMA13] Itziar Irigoien, Francesc Mestres, and Concepcion Arenas. The depth problem: Identifying the most representative units in a data group. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (1):161–172, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ibrahim:2011:UQP

[INT11] Zina Ibrahim, Alioune Ngom, and Ahmed Y. Tawfik. Using qualitative probability in reverse-engineering gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):326–334, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ikram:2018:ICB

[IQA18] Najmul Ikram, Muhammad Abdul Qadir, and Muhammad Tanvir Afzal. Investigating correlation between protein sequence similarity and semantic similarity using gene ontology annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):905–912, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ismail:2018:RNR

[ISK18] Hamid D. Ismail, Hiroto Saigo, and Dukka B. KC. RF-NR: Random forest based approach for improved classification of nuclear receptors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1844–1852, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Irigoien:2011:MTC

[IVA11] Itziar Irigoien, Sergi Vives, and Concepcion Arenas. Microarray time course experiments: Finding profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):464–475, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Irsoy:2012:DAC

[IYA12] Ozan Irsoy, Olcay Taner Yildiz, and Ethem Alpaydin.

Design and analysis of classifier learning experiments in bioinformatics: Survey and case studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1663–1675, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jamil:2013:DIC

[Jam13] Hasan M. Jamil. Designing integrated computational biology pipelines visually. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):605–618, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jamil:2015:IIE

[Jam15] Hasan M. Jamil. Improving integration effectiveness of ID mapping based biological record linkage. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):473–486, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jamil:2017:VIQ

[Jam17] Hasan M. Jamil. A visual interface for querying heterogeneous phylogenetic databases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):131–144, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jamil:2018:OPQ

[Jam18] Hasan M. Jamil. Optimizing phylogenetic queries for performance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1692–1705, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jhee:2019:CSC

[JBgLS19] Jong Ho Jhee, Sunjoo Bang, Dong gi Lee, and Hyunjung Shin. Comorbidity scoring with causal disease networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1627–1634, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jeong:2008:ISP

[JBP08] Jieun Jeong, Piotr Berman, and Teresa M. Przytycka. Improving strand pairing prediction through exploring folding cooperativity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5 (4):484–491, October 2008. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Jeong:2015:NSF

[JC15] Jong Cheol Jeong and Xuewen Chen. A new semantic functional similarity over gene ontology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):322–334, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jaskowiak:2013:PMC

[JCF13] Pablo A. Jaskowiak, Ricardo J. G. B. Campello, and Ivan G. Costa Filho. Proximity measures for clustering gene expression microarray data: a validation methodology and a comparative analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):845–857, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2022:GPC

[JCG+22] Tengsheng Jiang, Yuhui Chen, Shixuan Guan, Zhongtian Hu, Weizhong Lu, Qiming Fu, Yijie Ding, Haiou Li, and Hongjie Wu. G protein-coupled receptor interaction prediction based on deep transfer learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3126–3134, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3128172`.

Jacklin:2012:NCO

[JDCC12] Neil Jacklin, Zhi Ding, Wei Chen, and Chunqi Chang. Noniterative convex optimization methods for network component analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1472–1481, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jing:2020:AAE

[JDHL20] Xiaoyang Jing, Qiwen Dong, Daocheng Hong, and Ruqian Lu. Amino acid encoding methods for protein sequences: a comprehensive review and assessment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1918–1931, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2911677`.

John:2011:CCP

[JFN11] David J. John, Jacquelyn S. Fetrow, and James L. Norris. Continuous cotemporal probabilistic model-

ing of systems biology networks from sparse data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1208–1222, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jahanshad:2019:MSM

[JFR+19] Neda Jahanshad, Joshua Faskowitz, Gennady Roshchupkin, Derrek P. Hibar, Boris A. Gutman, Nicholas J. Tustison, Hieab H. H. Adams, Wiro J. Niessen, Meike W. Vernooij, M. Arfan Ikram, Marcel P. Zwiers, Alejandro Arias Vasquez, Barbara Franke, Jennifer L. Kroll, Benson Mwangi, Jair C. Soares, Alex Ing, Sylvane Desrivieres, Gunter Schumann, Narelle K. Hansell, Greig I. de Zubicaray, Katie L. McMahon, Nicholas G. Martin, Margaret J. Wright, and Paul M. Thompson. Multi-site meta-analysis of morphometry. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1508–1514, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jeannin-Girardon:2015:LST

[JGBR15] Anne Jeannin-Girardon, Pascal Ballet, and Vincent Rodin. Large scale tissue morphogenesis simulation on heterogeneous systems based on a flexible biomechanical cell model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1021–1033, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jokinen:2021:DBS

[JGKP21] Elmeri M. Jokinen, Krishnasamy Gopinath, Sami T. Kurkinen, and Olli T. Pentikäinen. Detection of binding sites on SARS-CoV-2 spike protein receptor-binding domain by molecular dynamics simulations in mixed solvents. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1281–1289, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3076259`.

Jiang:2021:NNT

[JGW+21] Yizhang Jiang, Xiaoqing Gu, Dongrui Wu, Wenlong Hang, Jing Xue, Shi Qiu, and Chin-Teng Lin. A novel negative-transfer-resistant fuzzy clustering model with a shared cross-domain transfer latent space and its application to brain CT image segmentation. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 18(1):40–52, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2963873`.

Jiang:2019:SSL

[JHW+19] Yichen Jiang, Jenny Hamer, Chenghong Wang, Xiaoqian Jiang, Miran Kim, Yongsoo Song, Yuhou Xia, Noman Mohammed, Md Nazmus Sadat, and Shuang Wang. SecureLR: Secure logistic regression model via a hybrid cryptographic protocol. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (1):113–123, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2017:MDR

[JHX17] Xingpeng Jiang, Xiaohua Hu, and Weiwei Xu. Microbiome data representation by joint nonnegative matrix factorization with Laplacian regularization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):353–359, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2015:PMI

[JHXP15] Xingpeng Jiang, Xiaohua Hu, Weiwei Xu, and E. K. Park. Predicting microbial interactions using vector autoregressive model with graph regularization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):254–261, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ju:2019:EDA

[JHZL19] Ronghui Ju, Chenhui Hu, Pan Zhou, and Quanzheng Li. Early diagnosis of Alzheimer's disease based on resting-state brain networks and deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):244–257, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2010:AAP

[Jia10] Minghui Jiang. Approximation algorithms for predicting RNA secondary structures with arbitrary pseudoknots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):323–332, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jang:2012:CMP

[JJH12] Woo-Hyuk Jang, Suk-Hoon Jung, and Dong-Soo Han.

A computational model for predicting protein interactions based on multidomain collaboration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1081–1090, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jin:2022:KEM

[JJZ+22] Yuanyuan Jin, Wendi Ji, Wei Zhang, Xiangnan He, Xinyu Wang, and Xiaoling Wang. A KG-enhanced multi-graph neural network for attentive herb recommendation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2560–2571, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3115489`.

Jee:2023:DNM

[JKC23] Dong Jun Jee, Yixin Kong, and Hyonho Chun. Deep nonnegative matrix factorization using a variational autoencoder with application to single-cell RNA sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):883–893, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3172723`.

Joseph:2012:CPT

[JKN+12] Shaini Joseph, Shreyas Karnik, Pravin Nilawe, V. K. Jayaraman, and Susan Idicula-Thomas. ClassAMP: a prediction tool for classification of antimicrobial peptides. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1535–1538, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Javadi:2021:FSM

[JKNE21] Afsaneh Javadi, Faezeh Keighobadi, Vahab Nekoukar, and Marzieh Ebrahimi. Finite-set model predictive control of melanoma cancer treatment using signaling pathway inhibitor of cancer stem cell. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1504–1511, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2940658`.

Jackups:2010:CAS

[JL10] Ronald Jackups, Jr. and Jie Liang. Combinatorial analysis for sequence and spatial motif discovery in short sequence frag-

ments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):524–536, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2016:UGB

[JLH16] Zhenchao Jiang, Lishuang Li, and Degen Huang. An unsupervised graph based continuous word representation method for biomedical text mining. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):634–642, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jia:2024:AAD

[JLJC24] Yuhang Jia, Siyu Li, Rui Jiang, and Shengquan Chen. Accurate annotation for differentiating and imbalanced cell types in single-cell chromatin accessibility data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):461–471, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3372970`.

Jiang:2021:MBR

[JLK+21] Xiran Jiang, Jiaxin Li, Yangyang Kan, Tao Yu, Shijie Chang, Xianzheng Sha, Hairong Zheng, Yahong Luo, and Shanshan Wang. MRI based radiomics approach with deep learning for prediction of vessel invasion in early-stage cervical cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 995–1002, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2963867`.

Ji:2017:CIF

[JLW17] Hao Ji, Yaohang Li, and Seth H. Weinberg. Calcium ion fluctuations alter channel gating in a stochastic luminal calcium release site model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):611–619, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jeong:2011:PSS

[JLwC11] Jong Cheol Jeong, Xiaotong Lin, and Xue wen Chen. On position-specific scoring matrix for protein function prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):308–315, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ji:2016:DFM

[JLYZ16] Junzhong Ji, Jiawei Luo, Cuicui Yang, and Aidong Zhang. Detecting functional modules based on a multiple-grain model in large-scale protein-protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):610–622, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2012:PPF

[JM12] Jonathan Q. Jiang and Lisa J. McQuay. Predicting protein function by multi-label correlated semi-supervised learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1059–1069, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jha:2017:GLB

[JMA17] Manjari Jha, Raunaq Malhotra, and Raj Acharya. A generalized lattice based probabilistic approach for metagenomic clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):749–761, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jia:2023:PMP

[JMCY23] Baoli Jia, Qingfang Meng, Yuehui Chen, and Hongri Yang. Prediction of membrane protein amphiphilic helix based on horizontal visibility graph and graph convolution network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3567–3574, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3305493`.

Jin:2009:PSP

[JNST09] Guohua Jin, Luay Nakhleh, Sagi Snir, and Tamir Tuller. Parsimony score of phylogenetic networks: Hardness results and a linear-time heuristic. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):495–505, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jin:2021:LTD

[JQGY21] Yong Jin, Zhenjiang Qian, Shengrong Gong, and Weiyong Yang. Learning transferable driven and drone assisted sustainable and robust regional disease surveillance for smart healthcare. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):114–

125, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3017041`.

Jiang:2020:DSE

[JQH+20] Hao Jiang, Yushan Qiu, Wenpin Hou, Xiaoqing Cheng, Man Yi Yim, and Wai-Ki Ching. Drug side-effect profiles prediction: From empirical to structural risk minimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):402–410, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2850884`.

Jauhari:2014:MGE

[JR14] Shaurya Jauhari and S. A. M. Rizvi. Mining gene expression data focusing cancer therapeutics: a digest. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):533–547, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2018:BET

[JRN+18] Nan Jiang, Wenge Rong, Yifan Nie, Yikang Shen, and Zhang Xiong. Biological event trigger identification with noise contrastive estimation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1549–1559, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jansson:2018:AMR

[JRSS18] Jesper Jansson, Ramesh Rajaby, Chuanqi Shen, and Wing-Kin Sung. Algorithms for the majority rule + consensus tree and the frequency difference consensus tree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):15–26, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jarvis:2012:MIP

[JS12] Peter Jarvis and Jeremy Sumner. Markov invariants for phylogenetic rate matrices derived from embedded submodels. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):828–836, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jha:2023:AEM

[JS23a] Kanchan Jha and Sriparna Saha. Analyzing effect of multi-modality in predicting protein-protein interactions. *IEEE/ACM Trans-*

actions on Computational Biology and Bioinformatics, 20(1):162–173, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3157531`.

Joseph:2023:ACM

[JS23b] Steffy Maria Joseph and P. S. Sathidevi. An automated cDNA microarray image analysis for the determination of gene expression ratios. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):136–150, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3135650`.

Jackson:2008:CGM

[JSA08] Benjamin N. Jackson, Patrick S. Schnable, and Srinivas Aluru. Consensus genetic maps as median orders from inconsistent sources. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):161–171, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jia:2022:MCA

[JSM+22] Xibin Jia, Zheng Sun, Qing Mi, Zhenghan Yang, and Dawei Yang. A multimodality-contribution-aware TripNet for histologic grading of hepatocellular carcinoma. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2003–2016, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3079216`.

Jiao:2018:FDA

[JSS+18] Hongmei Jiao, Michael Shi, Qikun Shen, Junwu Zhu, and Peng Shi. Filter design with adaptation to time-delay parameters for genetic regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):323–329, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jetten:2018:NTB

[JvI18] Laura Jetten and Leo van Iersel. Nonbinary tree-based phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):205–217, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ji:2022:SSL

[JWG+22] Cunmei Ji, Yutian Wang, Zhen Gao, Lei Li, Jiancheng

Ni, and Chunhou Zheng. A semi-supervised learning method for MiRNA-Disease association prediction based on variational autoencoder. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2049–2059, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3067338`.

Jiang:2024:SSL

[JWW+24] Zijing Jiang, Linyan Wang, Yaqi Wang, Gangyong Jia, Guodong Zeng, Jun Wang, Yunxiang Li, Dechao Chen, Guiping Qian, and Qun Jin. A self-supervised learning based framework for eyelid malignant melanoma diagnosis in whole slide images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):701–714, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3207352`.

Jia:2020:PIM

[JWZ+20] Huiqiang Jia, Haichao Wei, Daming Zhu, Jingjing Ma, Hai Yang, Ruizhi Wang, and Xianzhong Feng. PASA: Identifying more credible structural variants of Hedou12. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1493–1503, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2934463`.

Jian:2016:MKF

[JXN+16] Ling Jian, Zhonghang Xia, Xinnan Niu, Xijun Liang, Parimal Samir, and Andrew J. Link. ℓ_2 multiple kernel fuzzy SVM-based data fusion for improving peptide identification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):804–809, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ji:2021:CNN

[JY21] Junzhong Ji and Yao Yao. Convolutional neural network with graphical lasso to extract sparse topological features for brain disease classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2327–2338, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2989315`.

Janga:2015:KDU

[JZCZ15] Sarath Chandra Janga, Dongxiao Zhu, Jake Y.

Chen, and Mohammed J. Zaki. Knowledge discovery using big data in biomedical systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):726–728, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jia:2021:FPL

[JZF+21] Cangzhi Jia, Meng Zhang, Cunshuo Fan, Fuyi Li, and Jiangning Song. Formator: Predicting Lysine formylation sites based on the most distant undersampling and safe-level synthetic minority oversampling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1937–1945, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2957758`.

Ji:2013:PLS

[JZL13] Shuiwang Ji, Wenlu Zhang, and Rongjian Li. A probabilistic latent semantic analysis model for coclustering the mouse brain atlas. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1460–1468, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiao:2018:RGC

[JZS+18] Hongmei Jiao, Liping Zhang, Qikun Shen, Junwu Zhu, and Peng Shi. Robust gene circuit control design for time-delayed genetic regulatory networks without SUM regulatory logic. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 2086–2093, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2012:SFU

[JZSZ12] Haitao Jiang, Chunfang Zheng, David Sankoff, and Binhai Zhu. Scaffold filling under the breakpoint and related distances. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1220–1229, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ju:2017:EAC

[JZW17] Chelsea J. T. Ju, Zhuangtian Zhao, and Wei Wang. Efficient approach to correct read alignment for pseudogene abundance estimates. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):522–533, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Jiang:2022:RAB

[JZW+22] Hao Jiang, Fei Zhan, Congtao Wang, Jianfeng Qiu, Yansen Su, Chunhou Zheng, Xingyi Zhang, and Xiangxiang Zeng. A robust algorithm based on link label propagation for identifying functional modules from protein–protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1435–1448, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3038815`.

Jin:2024:SSS

[JZYL24] Sichen Jin, Yijia Zhang, Huimin Yu, and Mingyu Lu. SADR: Self-supervised graph learning with adaptive denoising for drug repositioning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):265–277, March 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3351079`.

Jiang:2021:BKG

[JZZ+21] Tianwen Jiang, Qingkai Zeng, Tong Zhao, Bing Qin, Ting Liu, Nitesh V. Chawla, and Meng Jiang. Biomedical knowledge graphs construction from conditional statements. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):823–835, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2979959`.

Jiang:2019:FNN

[JZZQ19] Xue Jiang, Han Zhang, Zhao Zhang, and Xiongwen Quan. Flexible non-negative matrix factorization to unravel disease-related genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1948–1957, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2823746`.

Kolchinsky:2010:CPP

[KAHK+10] Artemy Kolchinsky, Alaa Abi-Haidar, Jasleen Kaur, Ahmed Abdeen Hamed, and Luis M. Rocha. Classification of protein-protein interaction full-text documents using text and citation network features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):400–411, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Keller:2017:ISL

[KAL+17] Anne Florence Keller, Nicolas Ambert, Arnaud Legendre, Mathieu Bedez, Jean-Marie Bouteiller, Serge Bischoff, Michel Baudry, and Saliha Moussaoui. Impact of synaptic localization and subunit composition of ionotropic glutamate receptors on synaptic function: Modeling and simulation studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):892–904, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kountouris:2012:CSF

[KAP+12] Petros Kountouris, Michalis Agathocleous, Vasilis J. Promponas, Georgia Christodoulou, Simos Hadjicostas, Vassilis Vassiliades, and Chris Christodoulou. A comparative study on filtering protein secondary structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):731–739, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Karacali:2012:HMV

[Kar12a] Bilge Karacali. Hierarchical motif vectors for prediction of functional sites in amino acid sequences using quasi-supervised learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1432–1441, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Karafyllidis:2012:QGC

[Kar12b] Ioannis G. Karafyllidis. Quantum gate circuit model of signal integration in bacterial quorum sensing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):571–579, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kumari:2021:EMD

[KAS21] Chetna Kumari, Muhammad Abulaish, and Naidu Subbarao. Exploring molecular descriptors and fingerprints to predict mTOR kinase inhibitors using machine learning techniques. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1902–1913, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2964203`.

Kordi:2017:CDT

[KB17] Misagh Kordi and Mukul S. Bansal. On the complexity of

duplication-transfer-loss reconciliation with non-binary gene trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):587–599, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kordi:2019:EAD

[KB19] Misagh Kordi and Mukul S. Bansal. Exact algorithms for duplication-transfer-loss reconciliation with non-binary gene trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1077–1090, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Karimnezhad:2020:IPK

[KB20] Ali Karimnezhad and David R. Bickel. Incorporating prior knowledge about genetic variants into the analysis of genetic association data: an empirical Bayes approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):635–646, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2865420`.

Kifer:2017:OAD

[KBBD+17] Ilona Kifer, Rui M. Branca, Amir Ben-Dor, Linhui Zhai, Ping Xu, Janne Lehtio, and Zohar Yakhini. Optimizing analytical depth and cost efficiency of IEF-LC/MS proteomics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):272–281, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kimmel:2021:DCR

[KBM21] Jacob C. Kimmel, Andrew S. Brack, and Wallace F. Marshall. Deep convolutional and recurrent neural networks for cell motility discrimination and prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):562–574, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2919307`.

Karbalayghareh:2019:CSC

[KBND19] Alireza Karbalayghareh, Ulisses Braga-Neto, and Edward R. Dougherty. Classification of single-cell gene expression trajectories from incomplete and noisy data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):193–207, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Karbalayghareh:2018:CST

[KBNHD18] Alireza Karbalayghareh, Ulisses Braga-Neto, Jianping Hua, and Edward Russell Dougherty. Classification of state trajectories in gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):68–82, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kuruppu:2012:IDC

[KBSCZ12] Shanika Kuruppu, Bryan Beresford-Smith, Thomas Conway, and Justin Zobel. Iterative dictionary construction for compression of large DNA data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):137–149, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2011:PMS

[KC11] Jong Kyoung Kim and Seungjin Choi. Probabilistic models for semisupervised discriminative motif discovery in DNA sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1309–1317, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2015:IGN

[KCCC15] Jeong-Rae Kim, Sang-Mok Choo, Hyung-Seok Choi, and Kwang-Hyun Cho. Identification of gene networks with time delayed regulation based on temporal expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1161–1168, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kamath:2012:EAA

[KCD+12] Uday Kamath, Jack Compton, Rezarta Islamaj Dogan, Kenneth De Jong, and Amarda Shehu. An evolutionary algorithm approach for feature generation from sequence data and its application to DNA splice site prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1387–1398, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2018:GNA

[KCP18] Hyunjin Kim, Sang-Min Choi, and Sanghyun Park. GSEH: a novel approach to select prostate cancer-associated genes using gene expression heterogeneity. *IEEE/ACM Transactions on Computational Biology and*

Bioinformatics, 15(1):129–146, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

K:2019:PDL

[KCP19] MD Aksam V. K., V. M. Chandrasekaran, and Sundaramurthy Pandurangan. Protein domain level cancer drug targets in the network of MAPK pathways. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 2057–2065, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2829507`.

Ke:2024:DFL

[KCY+24] Hengjin Ke, Dan Chen, Quanming Yao, Yunbo Tang, Jia Wu, Jessica Monaghan, Paul Sowman, and David McAlpine. Deep factor learning for accurate brain neuroimaging data analysis on discrimination for structural MRI and functional MRI. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):582–595, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3252577`.

Kang:2015:ISO

[KCZ+15] Hao Kang, Kwang-Hyun Cho, Xiaohua Douglas Zhang, Tao Zeng, and Luonan Chen. Inferring sequential order of somatic mutations during tumorgenesis based on Markov chain model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1094–1103, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Koneru:2015:DCA

[KD15] Suvarna Vani Koneru and Bhavani S. Durga. Divide and conquer approach to contact map overlap problem using 2D-pattern mining of protein contact networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):729–737, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Knox:2016:MFG

[KD16] David A. Knox and Robin D. Dowell. A modeling framework for generation of positional and temporal simulations of transcriptional regulation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):459–471, May 2016. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Kapoor:2020:GMM

[KDS+20] Rajan Kapoor, Aniruddha Datta, Chao Sima, Jianping Hua, Rosana Lopes, and Michael L. Bittner. A Gaussian mixture-model exploiting pathway knowledge for dissecting cancer heterogeneity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):459–468, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2869813`.

Krotzky:2014:EGB

[KFHK14] Timo Krotzky, Thomas Fober, Eyke Hüllermeier, and Gerhard Klebe. Extended graph-based models for enhanced similarity search in Cavbase. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):878–890, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2012:SGE

[KG12] Haseong Kim and Erol Gelenbe. Stochastic gene expression modeling with Hill function for switch-like gene responses. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):973–979, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Konur:2015:PDM

[KG15] Savas Konur and Marian Gheorghe. A property-driven methodology for formal analysis of synthetic biology systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):360–371, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kazemi:2020:MSA

[KG20] Ehsan Kazemi and Matthias Grossglauser. MPGM: Scalable and accurate multiple network alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2040–2052, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2914050`.

Kong:2014:BSD

[KGF+14] Ao Kong, Chinmaya Gupta, Mauro Ferrari, Marco Agostini, Chiara Bedin, Ali Bouamrani, Ennio Tasciotti, and Robert Azencott. Biomarker signature discovery from mass spectrometry

data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):766–772, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kasarapu:2014:RPF

[KGK14] Parthan Kasarapu, Maria Garcia De La Banda, and Arun S. Konagurthu. On representing protein folding patterns using non-linear parametric curves. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6): 1218–1228, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kobayashi:2014:ISB

[KH14] Koichi Kobayashi and Kunihiko Hiraishi. ILP/SMT-based method for design of Boolean networks based on singleton attractors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1253–1259, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kitrungrotsakul:2021:CCB

[KHI+21] Titinunt Kitrungrotsakul, Xian-Hau Han, Yutaro Iwamoto, Satoko Takemoto, Hideo Yokota, Sari Ipponjima, Tomomi Nemoto, Wei Xiong, and Yen-Wei Chen. A cascade of 2.5D CNN and bidirectional CLSTM network for mitotic cell detection in 4D microscopy image. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):396–404, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2919015`.

Karim:2020:BNB

[KHO+20] Mohammad Bozlul Karim, Ming Huang, Naoaki Ono, Shigehiko Kanaya, and Md. Altaf-Ul-Amin. BiClusO: a novel biclustering approach and its application to species-VOC relational data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 1955–1965, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2914901`.

Kazmi:2012:HCA

[KHP12] N. Kazmi, M. A. Hossain, and R. M. Phillips. A hybrid cellular automaton model of solid tumor growth and bioreductive drug transport. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1595–1606, November 2012. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Kim:2018:ESP

[Kim18] Sun Kim. Editorial for selected papers of a Joint Conferences, Genome Informatics Workshop/International Conference on Bioinformatics GIW/InCoB 2015. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1821, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2004:GEW

[KJ04] Junhyong Kim and Inge Jonassen. Guest editorial: WABI special section part 1. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1 (4):137–138, October 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2005:GEW

[KJ05] Junhyong Kim and Inge Jonassen. Guest editorial: WABI special section. Part II. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):1–2, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2008:LSS

[KK08] Eagu Kim and John Kececioglu. Learning scoring schemes for sequence alignment from partial examples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5 (4):546–556, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Krejnik:2012:EEA

[KK12] Milos Krejnik and Jiri Klema. Empirical evidence of the applicability of functional clustering through gene expression classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):788–798, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kimura:2019:PCB

[KK19] Kouichi Kimura and Asako Koike. Parallel computation of the Burrows–Wheeler transform of short reads using prefix parallelism. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):3–13, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2014:MLS

[KKC+14] Chang-Kug Kim, Jin-A Kim, Ji-Weon Choi, In-Seon Jeong, Yi-Seul Moon, Dong-Suk Park, Young-Joo Seol, Yong-Kab Kim, Yong-Hwan Kim, and Yeon-Ki Kim. A multi-layered screening method to identify plant regulatory genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):293–303, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kwon:2016:DRA

[KKC16] Yung-Keun Kwon, Junil Kim, and Kwang-Hyun Cho. Dynamical robustness against multiple mutations in signaling networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):996–1002, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kawano:2020:SFB

[KKI20] Keisuke Kawano, Satoshi Koide, and Chie Imamura. Seq2seq fingerprint with byte-pair encoding for predicting changes in protein stability upon single point mutation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1762–1772, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2908641`.

Kim:2019:SDG

[KKK19] Man-Sun Kim, Dongsan Kim, and Jeong-Rae Kim. Stage-dependent gene expression profiling in colorectal cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1685–1692, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kumar:2021:AAP

[KKP+21] Gautam Kumar, Rajnish Kumar, Manoj Kumar Pal, Nilotpal Pramanik, Tapobrata Lahiri, Ankita Gupta, and Saket Pandey. APT: an automated probe tracker from gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1864–1874, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2958345`.

Kim:2022:HSC

[KKP22] Sun Ah Kim, Nayeon Kang, and Taesung Park. Hierarchical structured compo-

nent analysis for microbiome data using taxonomy assignments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1302–1312, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3039326`.

Ko:2022:IFM

[KKPP22] Young-Joon Ko, Sangsoo Kim, Cheol-Ho Pan, and Keunwan Park. Identification of functional microbial modules through network-based analysis of meta-microbial features using matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2851–2862, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3100893`.

Kc:2011:TIP

[KL11a] Dukka B. Kc and Dennis R. Livesay. Topology improves phylogenetic motif functional site predictions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (1):226–233, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Krishnamurthy:2011:TRL

[KL11b] Vikram Krishnamurthy and Kai-Yiu Luk. 2010 TCBB reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):282–284, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Krishnamurthy:2011:SMM

[KL11c] Vikram Krishnamurthy and Kai-Yiu Luk. Semi-Markov models for Brownian dynamics permeation in biological ion channels. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):273–281, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kaiser:2019:UDG

[KL19] Florian Kaiser and Dirk Labudde. Unsupervised discovery of geometrically common structural motifs and long-range contacts in protein 3D structures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):671–680, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2786250`.

KC:2022:PBI

[KLCH22] Kishan KC, Rui Li, Feng Cui, and Anne R. Haake. Predicting biomedical interactions with higher-order graph convolutional networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):676–687, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3059415`.

Kocak:2020:ABP

[KM20] Mehmet Kocak and Khyobeni Mozhui. An application of the Bayesian periodicity test to identify diurnal rhythm genes in the brain. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):47–55, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2859971`.

Kundaje:2005:CST

[KMG+05] Anshul Kundaje, Manuel Middendorf, Feng Gao, Chris Wiggins, and Christina Leslie. Combining sequence and time series expression data to learn transcriptional modules. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):194–202, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kaushik:2021:CAC

[KMS+21] Aman Chandra Kaushik, Aamir Mehmood, Gurudeeban Selvaraj, Xiaofeng Dai, Yi Pan, and Dong-Qing Wei. CoronaPep: an anticoronavirus peptide generation tool. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1299–1304, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3064630`.

Kang:2020:CGW

[KMSY20] Qiwen Kang, Neil Moore, Christopher L. Schardl, and Ruriko Yoshida. CURatio: Genome-wide phylogenomic analysis method using ratios of total branch lengths. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):981–989, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2878564`.

Keedwell:2005:DGN

[KN05] Edward Keedwell and Ajit Narayanan. Discovering gene networks with a neural-genetic hybrid. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 2(3):231–242, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kucherov:2005:MLF

[KNR05] Gregory Kucherov, Laurent Noe, and Mikhail Roytberg. Multiseed lossless filtration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):51–61, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kaski:2005:ACE

[KNS+05] Samuel Kaski, Janne Nikkila, Janne Sinkkonen, Leo Lahti, Juha E. A. Knuuttila, and Christophe Roos. Associative clustering for exploring dependencies between functional genomics data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):203–216, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Khan:2018:RPR

[KNTB18] Shujaat Khan, Imran Naseem, Roberto Togneri, and Mohammed Bennamoun. RAFP-Pred: Robust prediction of antifreeze proteins using localized analysis of n-peptide compositions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):244–250, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Keijsper:2015:TCB

[KO15] Judith Keijsper and Tim Oosterwijk. Tractable cases of $(*, 2)$-bounded parsimony haplotyping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):234–247, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kentzoglanakis:2012:SIF

[KP12] Kyriakos Kentzoglanakis and Matthew Poole. A swarm intelligence framework for reconstructing gene networks: Searching for biologically plausible architectures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):358–371, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kalathiya:2014:MME

[KPB14] Umesh Kalathiya, Monikaben Padariya, and Maciej Baginski. Molecular modeling and evaluation of novel dibenzopyrrole derivatives as telomerase inhibitors and

potential drug for cancer therapy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1196–1207, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kang:2017:MBB

[KPK+17] Mingon Kang, Juyoung Park, Dong-Chul Kim, Ashis K. Biswas, Chunyu Liu, and Jean Gao. Multi-block bipartite graph for integrative genomic analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6): 1350–1358, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kaloudas:2019:EEB

[KPP19] Dimitrios Kaloudas, Nikolet Pavlova, and Robert Penchovsky. EBWS: Essential bioinformatics Web services for sequence analyses. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):942–953, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kaddi:2013:MHS

[KPW13] Chanchala D. Kaddi, R. Mitchell Parry, and May D. Wang. Multivariate hypergeometric similarity measure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1505–1516, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Karbalayghareh:2021:OBT

[KQD21] Alireza Karbalayghareh, Xiaoning Qian, and Edward R. Dougherty. Optimal Bayesian transfer learning for count data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):644–655, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2920981`.

Kahveci:2013:GEA

[KS13] Tamer Kahveci and Mona Singh. Guest editorial for ACM BCB. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1089–1090, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kirkpatrick:2014:PPP

[KS14] Bonnie Kirkpatrick and Kristian Stevens. Perfect phylogeny problems with missing values. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):928–941,

September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Khalid:2018:PHD

[KS18] Zoya Khalid and Osman Ugur Sezerman. Prediction of HIV drug resistance by combining sequence and structural properties. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):966–973, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kocabas:2016:ESM

[KSA16] Ovunc Kocabas, Tolga Soyata, and Mehmet K. Aktas. Emerging security mechanisms for medical cyber physical systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):401–416, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Klarner:2012:TSD

[KSB12] Hannes Klarner, Heike Siebert, and Alexander Bockmayr. Time series dependent analysis of unparametrized Thomas networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1338–1351, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kulandaisamy:2018:IAK

[KSK+18] A. Kulandaisamy, Ambuj Srivastava, Pradeep Kumar, R. Nagarajan, S. Binny Priya, and M. Michael Gromiha. Identification and analysis of key residues in protein-RNA complexes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1436–1444, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Klosa:2023:FSG

[KSLW23] Jan Klosa, Noah Simon, Volkmar Liebscher, and Dörte Wittenburg. A fitted sparse-group lasso for genome-based evaluations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1): 30–38, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3156805`.

Kayano:2014:DDC

[KSM14] Mitsunori Kayano, Motoki Shiga, and Hiroshi Mamitsuka. Detecting differentially coexpressed genes from labeled expression data: a brief review. *IEEE/ACM Transactions on Computa-*

tional Biology and Bioinformatics, 11(1):154–167, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kapilevich:2019:CRC

[KSMT19] Viacheslav Kapilevich, Shigeto Seno, Hideo Matsuda, and Yoichi Takenaka. Chromatin 3D reconstruction from chromosomal contacts using a genetic algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1620–1626, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kawano:2012:IGP

[KSN+12] Shuichi Kawano, Teppei Shimamura, Atsushi Niida, Seiya Imoto, Rui Yamaguchi, Masao Nagasaki, Ryo Yoshida, Cristin Print, and Satoru Miyano. Identifying gene pathways associated with cancer characteristics via sparse statistical methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):966–972, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Khan:2022:CEE

[KSP22] Abhinandan Khan, Goutam Saha, and Rajat Kumar Pal. Controlling the effects of external perturbations on a gene regulatory network using proportional-integral-derivative controller. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1531–1544, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3039038`.

Kumozaki:2015:MLB

[KSS15] Shotaro Kumozaki, Kengo Sato, and Yasubumi Sakakibara. A machine learning based approach to de novo sequencing of glycans from tandem mass spectrometry spectrum. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1267–1274, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kelk:2012:EC

[KSvI12] Steven Kelk, Celine Scornavacca, and Leo van Iersel. On the elusiveness of clusters. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (2):517–534, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Korodi:2007:CAN

[KT07] Gergely Korodi and Ioan Tabus. Compression of annotated nucleotide sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):447–457, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kleftogiannis:2015:YNE

[KTLM15] Dimitrios Kleftogiannis, Konstantinos Theofilatos, Spiros Likothanassis, and Seferina Mavroudi. YamiPred: a novel evolutionary method for predicting Pre-miRNAs and selecting relevant features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1183–1192, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kuksa:2013:BSC

[Kuk13] Pavel P. Kuksa. Biological sequence classification with multivariate string kernels. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5): 1201–1210, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kuroshu:2013:NCP

[Kur13] Reginaldo M. Kuroshu. Nonoverlapping clone pooling for high-throughput sequencing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1091–1097, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kulekci:2012:EMR

[KVX12] M. Oguzhan Kulekci, Jeffrey Scott Vitter, and Bojian Xu. Efficient maximal repeat finding using the Burrows-Wheeler transform and wavelet tree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):421–429, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2007:AAD

[KWL07] Jong Hyun Kim, Michael S. Waterman, and Lei M. Li. Accuracy assessment of diploid consensus sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):88–97, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kang:2023:HTS

[KWP+23] Yan Kang, Haining Wang, Bin Pu, Liu Tao, Jianguo Chen, and Philip S. Yu. A hybrid two-stage

teaching-learning-based optimization algorithm for feature selection in bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1746–1760, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215129`.

Kwon:2019:EER

[KY19] Sunyoung Kwon and Sungroh Yoon. End-to-end representation learning for chemical-chemical interaction prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1436–1447, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2022:DTC

[KY22] Seonho Kim and Juntae Yoon. Dual triggered correspondence topic (DTCT) model for MeSH annotation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):899–911, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3016355`.

Kustra:2010:DFC

[KZ10] Rafal Kustra and Adam Zagdanski. Data-fusion in clustering microarray data: Balancing discovery and interpretability. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):50–63, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Kim:2018:CPP

[KZW+18] Mansuck Kim, Huan Zhang, Charles Woloshuk, Won-Bo Shim, and Byung-Jun Yoon. Computational prediction of pathogenic network modules in fusarium verticillioides. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):506–515, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Labarre:2006:NBT

[Lab06] Anthony Labarre. New bounds and tractable instances for the transposition distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(4):380–394, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Limpiti:2014:IIN

[LAI+14] Tulaya Limpiti, Chainarong Amornbunchornvej, Apichart Intarapanich, Anunchai Assawamakin, and Sissades

Tongsima. iNJclust: iterative neighbor-joining tree clustering framework for inferring population structure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5): 903–914, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:IRF

[LB19] Lei Li and Mukul S. Bansal. An integrated reconciliation framework for domain, gene, and species level evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):63–76, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lushbough:2010:BSI

[LBL+10] Carol Lushbough, Michael K. Bergman, Carolyn J. Lawrence, Doug Jennewein, and Volker Brendel. BioExtract Server — an integrated workflow-enabling system to access and analyze heterogeneous, distributed biomolecular data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):12–24, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2012:CPS

[LBL12a] Shuai Cheng Li, Dongbo Bu, and Ming Li. Clustering 100,000 protein structure decoys in minutes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):765–773, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2012:RSH

[LBL12b] Shuai Cheng Li, Dongbo Bu, and Ming Li. Residues with similar hexagon neighborhoods share similar side-chain conformations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):240–248, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Leale:2018:IUB

[LBM+18] Guillermo Leale, Ariel Emilio Baya, Diego H. Milone, Pablo M. Granitto, and Georgina Stegmayer. Inferring unknown biological function by integration of GO annotations and gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):168–180, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lorenz:2013:MQR

[LBQ+13] Ronny Lorenz, Stephan H. Bernhart, Jing Qin, Christian Honer zu Siederdissen, Andrea Tanzer, Fabian Amman, Ivo L. Hofacker, and Peter F. Stadler. 2D meets 4G: *G*-quadruplexes in RNA secondary structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):832–844, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lonardi:2010:DMB

[LC10] Stefano Lonardi and Jake Chen. Data mining in bioinformatics: Selected papers from BIOKDD. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):195–196, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:DTP

[LC19] Limin Li and Menglan Cai. Drug target prediction by multi-view low rank embedding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1712–1721, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lovato:2017:SNR

[LCB17] Pietro Lovato, Marco Cristani, and Manuele Bicego. Soft Ngram representation and modeling for protein remote homology detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6): 1482–1488, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Luo:2011:LTA

[LCC+11] Cheng-Wei Luo, Ming-Chiang Chen, Yi-Ching Chen, Roger W. L. Yang, Hsiao-Fei Liu, and Kun-Mao Chao. Linear-time algorithms for the multiple gene duplication problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (1):260–265, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lafond:2018:GTC

[LCEMO18] Manuel Lafond, Cedric Chauve, Nadia El-Mabrouk, and Aida Ouangraoua. Gene tree construction and correction using SuperTree and reconciliation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1560–1570, September 2018. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic).

Liu:2019:PRH

[LCGW19] Bin Liu, Junjie Chen, Mingyue Guo, and Xiaolong Wang. Protein remote homology detection and fold recognition based on sequence-order frequency matrix. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):292–300, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lopez-Caamal:2019:SAI

[LCH19] Fernando López-Caamal and Heinrich J. Huber. Stable IL-1β1β-activation in an inflammasome signalling model depends on positive and negative feedbacks and tight regulation of protein production. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):627–637, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2794971`.

Lu:2023:MMA

[LCL+23] Xinguo Lu, Guanyuan Chen, Jinxin Li, Xiangjin Hu, and Fengxu Sun. MAGCN: a multiple attention graph convolution networks for predicting synthetic lethality. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2681–2689, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3221736`.

Li:2010:CRA

[LCLL10] Gang Li, Tak-Ming Chan, Kwong-Sak Leung, and Kin-Hong Lee. A cluster refinement algorithm for motif discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):654–668, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lopez-Caamal:2014:SQC

[LCOMG14] Fernando López-Caamal, Diego A. Oyarzún, Richard H. Middleton, and Míriam R. García. Spatial quantification of cytosolic Ca2+ accumulation in nonexcitable cells: an analytical study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):592–603, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Luhmann:2018:SAC

[LCSW18] Nina Luhmann, Cedric Chauve, Jens Stoye, and

Roland Wittler. Scaffolding of ancient contigs and ancestral reconstruction in a phylogenetic framework. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 2094–2100, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lacroix:2008:IMN

[LCTS08] Vincent Lacroix, Ludovic Cottret, Patricia Thébault, and Marie-France Sagot. An introduction to metabolic networks and their structural analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):594–617, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lu:2024:MML

[LCTW24] Liangfu Lu, Xudong Cui, Zhiyuan Tan, and Yulei Wu. MedOptNet: Meta-learning framework for few-shot medical image classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):725–736, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3284846`.

Liu:2018:LRS

[LCW+18] Jian Liu, Yuhu Cheng, Xuesong Wang, Xiaoluo Cui, Yi Kong, and Junping Du. Low rank subspace clustering via discrete constraint and hypergraph regularization for tumor molecular pattern discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1500–1512, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2013:MLI

[LCWZ13] Si Li, Kwok Pui Choi, Taoyang Wu, and Louxin Zhang. Maximum likelihood inference of the evolutionary history of a PPI network from the duplication history of its proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1412–1421, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2016:MMH

[LCZN16] Yifeng Li, Haifen Chen, Jie Zheng, and Alioune Ngom. The max-min high-order dynamic Bayesian network for learning gene regulatory networks with time-delayed regulations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):792–803, 2016. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Lin:2021:MSA

[LDGY21] Bo Lin, Shuiguang Deng, Honghao Gao, and Jianwei Yin. A multi-scale activity transition network for data translation in EEG signals decoding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1699–1709, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3024228`.

Luo:2017:CPD

[LDL+17] Jiawei Luo, Pingjian Ding, Cheng Liang, Buwen Cao, and Xiangtao Chen. Collective prediction of disease-associated miRNAs based on transduction learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1468–1475, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2018:GGS

[LDM18] Juntao Li, Wenpeng Dong, and Deyuan Meng. Grouped gene selection of cancer via adaptive sparse group lasso based on conditional mutual information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):2028–2038, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lasker:2007:EDH

[LDS+07] Keren Lasker, Oranit Dror, Maxim Shatsky, Ruth Nussinov, and Haim J. Wolfson. EMatch: Discovery of high resolution structural homologues of protein domains in intermediate resolution cryo-EM maps. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):28–39, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2022:ECD

[LDYZ22] Chuang Liu, Yao Dai, Keping Yu, and Zi-Ke Zhang. Enhancing cancer driver gene prediction by protein–protein interaction network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2231–2240, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3063532`.

Li:2023:GSI

[LDZL23] Hong-Dong Li, Chao Deng, Xiao-Qi Zhang, and Cui-

Xiang Lin. A gene set-integrated approach for predicting disease-associated genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3440–3450, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3214517`.

Lahti:2011:PAP

[LEAK11] Leo Lahti, Laura L. Elo, Tero Aittokallio, and Samuel Kaski. Probabilistic analysis of probe reliability in differential gene expression studies with short oligonucleotide arrays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):217–225, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Leinweber:2018:GBP

[LFF18] Matthias Leinweber, Thomas Fober, and Bernd Freisleben. GPU-Based point cloud superpositioning for structural comparisons of protein binding sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):740–752, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Land:2016:MCS

[LFK16] Tyler A. Land, Perry Fizzano, and Robin B. Kodner. Measuring cluster stability in a large scale phylogenetic analysis of functional genes in metagenomes using `pplacer`. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):341–349, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lacroix:2006:MSG

[LFS06] Vincent Lacroix, Cristina G. Fernandes, and Marie-France Sagot. Motif search in graphs: Application to metabolic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3 (4):360–368, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:AIC

[LFZ+19] Min Li, Zhihui Fei, Min Zeng, Fang-Xiang Wu, Yaohang Li, Yi Pan, and Jianxin Wang. Automated ICD-9 coding via a deep learning approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1193–1202, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lovato:2015:MAP

[LGB15] Pietro Lovato, Alejandro Giorgetti, and Manuele Bicego. A multimodal approach for protein remote homology detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5): 1193–1198, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lv:2024:DLE

[LGL24] Zhihan Lv, Jinkang Guo, and Haibin Lv. Deep learning-empowered clinical big data analytics in healthcare digital twins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):660–669, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3252668`.

Luck:2019:HMM

[LGN+19] Alexander Luck, Pascal Giehr, Karl Nordstrom, Jorn Walter, and Verena Wolf. Hidden Markov modelling reveals neighborhood dependence of Dnmt3a and 3b activity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1598–1609, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2020:DDM

[LGW20] Feng Li, Lin Gao, and Bingbo Wang. Detection of driver modules with rarely mutated genes in cancers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):390–401, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2846262`.

Lu:2010:RNM

[LGX10] Xin Lu, Anthony Gamst, and Ronghui Xu. RD-Curve: a nonparametric method to evaluate the stability of ranking procedures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (4):719–726, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lu:2021:HEA

[LGYW21] Huijuan Lu, Huiyun Gao, Minchao Ye, and Xiuhui Wang. A hybrid ensemble algorithm combining AdaBoost and genetic algorithm for cancer classification with gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioin-*

formatics, 18(3):863–870, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2952102`.

Liu:2017:SNH

[LGZ+17] Yuxin Liu, Chao Gao, Zili Zhang, Yuxiao Lu, Shi Chen, Mingxin Liang, and Li Tao. Solving NP-hard problems with *Physarum*-based ant colony system. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):108–120, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Leung:2010:MFM

[LH10] Yukyee Leung and Yeungsam Hung. A multiple-filter-multiple-wrapper approach to gene selection and microarray data classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (1):108–117, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lee:2020:CPP

[LH20] Wook Lee and Kyungsook Han. Constructive prediction of potential RNA aptamers for a protein target. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5): 1476–1482, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2951114`.

Luo:2018:NAI

[LHC18] Jiawei Luo, Wei Huang, and Buwen Cao. A novel approach to identify the miRNA–mRNA causal regulatory modules in cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):309–315, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2020:DNN

[LHCL20] Yujie Li, Heng Huang, Hanbo Chen, and Tianming Liu. Deep neural networks for *In Situ* hybridization grid completion and clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):536–546, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2864262`.

Liu:2018:PWT

[LHDS18] Ke Liu, Sha Hou, Junbiao Dai, and Zhirong Sun. PyMut: a Web tool for

overlapping gene loss-of-function mutation design. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1107–1110, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ling:2016:MTH

[LHG+16] Cheng Ling, Tsuyoshi Hamada, Jingyang Gao, Guoguang Zhao, Donghong Sun, and Weifeng Shi. MrBayes tgMC 3++: a high performance and resource-efficient GPU-oriented phylogenetic analysis method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):845–854, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Le:2013:CRT

[LHH13] Ngoc Tu Le, Tu Bao Ho, and Bich Hai Ho. Computational reconstruction of transcriptional relationships from ChIP-chip data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):300–307, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2019:TBP

[LHH19] Hongyu Liu, Qinmin Vivian Hu, and Liang He. Term-based personalization for feature selection in clinical handover form autofilling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1219–1230, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:IFI

[LHHL19] Ying Li, Ye He, Siyu Han, and Yanchun Liang. Identification and functional inference for tumor-associated long non-coding RNA. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1288–1301, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2017:UBM

[LHKL17] Yun Liu, Tao Hou, Bing Kang, and Fu Liu. Unsupervised binning of metagenomic assembled contigs using improved fuzzy C-means method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1459–1467, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Le:2019:FPA

[LHL+19a] Thuc Duy Le, Tao Hoang, Jiuyong Li, Lin Liu, Huawen

Liu, and Shu Hu. A fast PC algorithm for high dimensional causal discovery with multi-core PCs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1483–1495, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2019:CPS

[LHL+19b] Bingqiang Liu, Ling Han, Xiangrong Liu, Jichang Wu, and Qin Ma. Computational prediction of sigma-54 promoters in bacterial genomes by integrating motif finding and machine learning strategies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1211–1218, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2011:FSF

[LHLY11] Yanpeng Li, Xiaohua Hu, Hongfei Lin, and Zhiahi Yang. A framework for semisupervised feature generation and its applications in biomedical literature mining. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (2):294–307, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2014:RSA

[LHN+14] Jing Li, Jun Hu, Matthew Newman, Kejun Liu, and Huanying Ge. RNA-seq analysis pipeline based on Oshell environment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5): 973–978, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2018:CPT

[LHQ+18] Min Liu, Yue He, Weili Qian, Yangliu Wei, and Xiaoyan Liu. Cell population tracking in a honeycomb structure using an IMM filter based 3D local graph matching model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1706–1717, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2016:PSE

[LHS16] Yongchao Liu, Thomas Hankeln, and Bertil Schmidt. Parallel and space-efficient construction of Burrows–Wheeler transform and suffix array for big genome data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):592–598, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

LeFaucheur:2011:NCS

[LHTT11] Xavier Le Faucheur, Eli Hershkovits, Rina Tannenbaum, and Allen Tannenbaum. Nonparametric clustering for studying RNA conformations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1604–1619, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2015:BLC

[LHWL15] Zhenhua Li, Ying He, Limsoon Wong, and Jinyan Li. Burial level change defines a high energetic relevance for protein binding interfaces. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (2):410–421, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Luo:2011:ICE

[LHY+11] Lin-Kai Luo, Deng-Feng Huang, Ling-Jun Ye, Qi-Feng Zhou, Gui-Fang Shao, and Hong Peng. Improving the computational efficiency of recursive cluster elimination for gene selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (1):122–129, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2019:RCM

[LHZ+19] Xiaohui Lin, Xin Huang, Lina Zhou, Weijie Ren, Jun Zeng, Weihong Yao, and Xingyuan Wang. The robust classification model based on combinatorial features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):650–657, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2779512`.

Li:2020:ILM

[LJ20] Lishuang Li and Yuxin Jiang. Integrating language model and reading control gate in BLSTM-CRF for biomedical named entity recognition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):841–846, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2868346`.

Liu:2022:DIR

[LJC+22] Zhonghao Liu, Jing Jin, Yuxin Cui, Zheng Xiong, Alireza Nasiri, Yong Zhao, and Jianjun Hu. DeepSeqPanII: an interpretable recurrent neural network

model with attention mechanism for peptide-HLA Class II binding prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):2188–2196, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3074927`.

Li:2012:DGE

[LJK+12] Ying-Xin Li, Shuiwang Ji, Sudhir Kumar, Jieping Ye, and Zhi-Hua Zhou. *Drosophila* gene expression pattern annotation through multi-instance multi-label learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):98–112, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liao:2014:GSU

[LJL+14] Bo Liao, Yan Jiang, Wei Liang, Wen Zhu, Lijun Cai, and Zhi Cao. Gene selection using locality sensitive Laplacian score. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1146–1156, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liao:2015:EFR

[LJL+15] Bo Liao, Yan Jiang, Wei Liang, Lihong Peng, Li Peng, Damien Hanyurwimfura, Zejun Li, and Min Chen. On efficient feature ranking methods for high-throughput data analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1374–1384, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2023:CNN

[LJN+23] Zhi-Hao Liu, Cun-Mei Ji, Jian-Cheng Ni, Yu-Tian Wang, Li-Juan Qiao, and Chun-Hou Zheng. Convolution neural networks using deep matrix factorization for predicting circrna-disease association. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):277–284, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3138339`.

Li:2024:FBI

[LJZ+24] Tiantian Li, Haitao Jiang, Binhai Zhu, Lusheng Wang, and Daming Zhu. Flanked block-interchange distance on strings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):301–311, March 2024. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3351440`.

Liu:2024:NMS

[LJZY24] Yuerui Liu, Yongquan Jiang, Fan Zhang, and Yan Yang. A novel multi-scale graph neural network for metabolic pathway prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):178–187, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3345647`.

Liu:2013:IAA

[LJZZ13] Nan Liu, Haitao Jiang, Daming Zhu, and Binhai Zhu. An improved approximation algorithm for scaffold filling to maximize the common adjacencies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):905–913, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2011:CED

[LK11] Qi Li and Chandra Kambhamettu. Contour extraction of *Drosophila* embryos. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1509–1521, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2023:GMD

[LKD23] Jiwen Liu, Zhufang Kuang, and Lei Deng. GCN-PCA: miRNA-Disease associations prediction algorithm based on graph convolutional neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1041–1052, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3203564`.

Lee:2023:EVI

[LKK+23] Hunmin Lee, Mingon Kang, Donghyun Kim, Daehee Seo, and Yingshu Li. Epidemic vulnerability index for effective vaccine distribution against pandemic. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3332–3342, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3198365`.

Lin:2023:ASD

[LKL+23] Xiangbin Lin, Weizhuang Kong, Jianxiu Li, Xuexiao Shao, Changting Jiang, Ruilan Yu, Xiaowei Li, and Bin Hu. Aberrant static and

dynamic functional brain network in depression based on EEG source localization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1876–1889, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3222592`.

Lo:2014:SCR

[LKLB14] Christine Lo, Boyko Kakaradov, Daniel Lokshtanov, and Christina Boucher. SeeSite: characterizing relationships between splice junctions and splicing enhancers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):648–656, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:CIC

[LKW+19] Donghe Li, Wonji Kim, Longfei Wang, Kyong-Ah Yoon, Boyoung Park, Charny Park, Sun-Young Kong, Yongdeuk Hwang, Daehyun Baek, Eun Sook Lee, and Sungho Won. Comparison of INDEL calling tools with simulation data and real short-read data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1635–1644, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2011:HHT

[LKY+11] Helong Li, Sam Kwong, Lihua Yang, Daren Huang, and Dongping Xiao. Hilbert–Huang Transform for analysis of heart rate variability in cardiac health. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1557–1567, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2011:DAN

[LL11] Ping Li and James Lam. Disturbance analysis of nonlinear differential equation models of genetic SUM regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):253–259, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2019:PCP

[LL19] Bin Liu and Shumin Li. ProtDet-CCH: Protein remote homology detection by combining long short-term memory and ranking methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1203–1210, July 2019. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Li:2022:DDC

[LL22] Yanbo Li and Yu Lin. DCHap: a divide-and-conquer haplotype phasing algorithm for third-generation sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1277–1284, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3005673`.

Lopez-Lopera:2019:SLF

[LLA19] Andres F. Lopez-Lopera and Mauricio A. Alvarez. Switched latent force models for reverse-engineering transcriptional regulation in gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):322–335, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2020:BLE

[LLBL20] Yuansheng Liu, Chaowang Lan, Michael Blumenstein, and Jinyan Li. Bi-level error correction for PacBio long reads. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):899–905, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2017.2780832`.

Li:2013:ISS

[LLC+13] Xiong Li, Bo Liao, Lijun Cai, Zhi Cao, and Wen Zhu. Informative SNPs selection based on two-locus and multilocus linkage disequilibrium: Criteria of max-correlation and min-redundancy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):688–695, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liao:2015:HCM

[LLC+15] Bo Liao, Xiong Li, Lijun Cai, Zhi Cao, and Haowen Chen. A hierarchical clustering method of selecting kernel SNP to unify informative SNP and tag SNP. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):113–122, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liang:2021:STA

[LLCC21] Shaoheng Liang, Qingnan Liang, Rui Chen, and Ken Chen. Stratified test accurately identifies differentially expressed genes under batch effects in single-

cell data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2072–2079, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3094650`.

Liang:2015:IDA

[LLCZ15] Muxuan Liang, Zhizhong Li, Ting Chen, and Jianyang Zeng. Integrative data analysis of multi-platform cancer data with a multimodal deep learning approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):928–937, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lopez-Lopera:2021:PIG

[LLDÁ21] Andrés F. López-Lopera, Nicolas Durrande, and Mauricio A. Álvarez. Physically-inspired Gaussian process models for post-transcriptional regulation in *Drosophila*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):656–666, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2918774`.

Lin:2018:MGD

[LLES18] Congping Lin, Laurent Lemarchand, Reinhardt Euler, and Imogen Sparkes. Modeling the geometry and dynamics of the endoplasmic reticulum network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):377–386, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2007:DSD

[LLH+07] Wenyuan Li, Ying Liu, Hung-Chung Huang, Yanxiong Peng, Yongjing Lin, Wee-Keong Ng, and Kok-Leong Ong. Dynamical systems for discovering protein complexes and functional modules from biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):233–250, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lu:2014:LPC

[LLH+14] Meng Lu, Hye-Seung Lee, David Hadley, Jianhua Z. Huang, and Xiaoning Qian. Logistic principal component analysis for rare variants in gene-environment interaction analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1020–1028,

November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2017:IIS

[LLH+17] Min Li, Zhongxiang Liao, Yiming He, Jianxin Wang, Junwei Luo, and Yi Pan. ISEA: Iterative seed-extension algorithm for De Novo assembly using paired-end information and insert size distribution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):916–925, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2018:PTB

[LLH18] Chengyu Liu, Rainer Lehtonen, and Sampsa Hautaniemi. PerPAS: Topology-based single sample pathway analysis method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):1022–1027, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lee:2023:CCP

[LLH23] Wook Lee, Seokwoo Lee, and Kyungsook Han. Constructing a cancer patient-specific network based on second-order partial correlations of gene expression and DNA methylation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):266–276, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3145796`.

Li:2015:RBC

[LLHF15] Han Li, Chun Li, Jie Hu, and Xiaodan Fan. A resampling based clustering algorithm for replicated gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1295–1303, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

LeMay:2022:PTA

[LLHW22] Matthew LeMay, Ran Libeskind-Hadas, and Yi-Chieh Wu. A polynomial-time algorithm for minimizing the deep coalescence cost for level-1 species networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5): 2642–2653, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3105922`.

Lv:2023:AMC

[LLJ+23] Ji Lv, Guixia Liu, Yuan Ju, Houhou Huang, and Ying Sun. AADB: a manually collected database for combina-

tions of antibiotics with adjuvants. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2827–2836, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3283221`.

Liu:2021:FFB

[LLK+21] Enze Liu, Jin Li, Garrett H. Kinnebrew, Pengyue Zhang, Yan Zhang, Lijun Cheng, and Lang Li. A fast and furious Bayesian network and its application of identifying colon cancer to liver metastasis gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1325–1335, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2944826`.

Li:2022:NED

[LLK+22] Hansheng Li, JianPing Li, Yuxin Kang, Chunbao Wang, Feihong Liu, Wenli Hui, Qirong Bo, Lei Cui, Jun Feng, and Lin Yang. A novel encoding and decoding calibration guiding pathway for pathological image analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):267–274, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3023467`.

Lo:2015:ITD

[LLL15] Leung-Yau Lo, Kwong-Sak Leung, and Kin-Hong Lee. Inferring time-delayed causal gene network using time-series expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5): 1169–1182, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liang:2016:NMD

[LLL16a] Cheng Liang, Yue Li, and Jiawei Luo. A novel method to detect functional microRNA regulatory modules by bicliques merging. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):549–556, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2016:DDS

[LLL16b] Yang Liu, Bowen Li, and Jungang Lou. Disturbance decoupling of singular Boolean control networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6): 1194–1200, November 2016.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liao:2020:ILI

[LLL+20] Xingyu Liao, Min Li, Junwei Luo, You Zou, Fang-Xiang Wu, Yi Pan, Feng Luo, and Jianxin Wang. Improving *de novo* assembly based on read classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (1):177–188, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2861380`.

Lian:2021:GLE

[LLL+21a] Sheng Lian, Lei Li, Guiren Lian, Xiao Xiao, Zhiming Luo, and Shaozi Li. A global and local enhanced residual U-Net for accurate retinal vessel segmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 852–862, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2917188`.

Liao:2021:ESF

[LLL+21b] Xingyu Liao, Min Li, Junwei Luo, You Zou, Fang-Xiang Wu, Yi-Pan, Feng Luo, and Jianxin Wang. EPGA-SC: a framework for *de novo* assembly of single-cell sequencing reads. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1492–1503, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2945761`.

Liu:2023:CTA

[LLL+23] Kun Liu, Hong-Dong Li, Yaohang Li, Jun Wang, and Jianxin Wang. A comparison of topologically associating domain callers based on Hi-C data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):15–29, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3147805`.

Li:2023:HDT

[LLMZ23] Jianyuan Li, Xiong Luo, Huimin Ma, and Wenbing Zhao. A hybrid deep transfer learning model with kernel metric for COVID-19 pneumonia classification using chest CT images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (4):2506–2517, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2022.3216661.

Li:2017:UCC

[LLNW17] Min Li, Yu Lu, Zhibei Niu, and Fang-Xiang Wu. United complex centrality for identification of essential proteins from PPI networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (2):370–380, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2016:EBE

[LLQ+16] Lishuang Li, Shanshan Liu, Meiyue Qin, Yiwen Wang, and Degen Huang. Extracting biomedical event with dual decomposition integrating word embeddings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4): 669–677, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2020:EBE

[LLQ20] Lishuang Li, Yang Liu, and Meiyue Qin. Extracting biomedical events with parallel multi-pooling convolutional neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):599–607, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2868078.

Liu:2021:DLG

[LLQW21] Min Liu, Yalan Liu, Weili Qian, and Yaonan Wang. DeepSeed local graph matching for densely packed cells tracking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):1060–1069, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2936851.

Lee:2023:CIC

[LLR+23] Seokwoo Lee, Wook Lee, Shulei Ren, Byungkyu Park, and Kyungsook Han. Constructing integrative ceRNA networks and finding prognostic biomarkers in renal cell carcinoma. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2671–2680, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3214190.

Li:2015:PIR

[LLRZ15] Hui Li, Xiaoyi Li, Murali Ramanathan, and Aidong Zhang. Prediction and informative risk factor selection of bone diseases.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 12(1):79–91, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2010:SSV

[LLT10] Zhenqiu Liu, Shili Lin, and Ming Tan. Sparse support vector machines with L_p penalty for biomarker identification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):100–107, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Luhmann:2019:SSP

[LLT+19] Nina Luhmann, Manuel Lafond, Annelyse Thevenin, Aida Ouangraoua, Roland Wittler, and Cedric Chauve. The SCJ small parsimony problem for weighted gene adjacencies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1364–1373, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2019:ISP

[LLTC19] Hao Lin, Zhi-Yong Liang, Hua Tang, and Wei Chen. Identifying sigma70 promoters with novel pseudo nucleotide composition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1316–1321, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2010:MPI

[LLW10] Xiaowen Liu, Jinyan Li, and Lusheng Wang. Modeling protein interacting groups by quasi-bicliques: Complexity, algorithm, and application. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):354–364, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Leung:2011:DMD

[LLW+11] KwongSak Leung, KinHong Lee, JinFeng Wang, Eddie YT Ng, Henry LY Chan, Stephen KW Tsui, Tony SK Mok, Pete Chi-Hang Tse, and Joseph JY Sung. Data mining on DNA sequences of Hepatitis B virus. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):428–440, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2015:TPB

[LLW+15] Min Li, Yu Lu, Jianxin Wang, Fang-Xiang Wu, and Yi Pan. A topology potential-based method for identifying essential pro-

teins from PPI networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):372–383, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lu:2022:LSS

[LLW+22] Shuai Lu, Yuguang Li, Fei Wang, Xiaofei Nan, and Shoutao Zhang. Leveraging sequential and spatial neighbors information by using CNNs linked with GCNs for paratope prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):68–74, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3083001`.

Li:2011:RUP

[LLX+11] Hong-Dong Li, Yi-Zeng Liang, Qing-Song Xu, Dong-Sheng Cao, Bin-Bin Tan, Bai-Chuan Deng, and Chen-Chen Lin. Recipe for uncovering predictive genes using support vector machines based on model population analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1633–1641, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2016:PSS

[LLX+16] Liqi Li, Jinhui Li, Weidong Xiao, Yongsheng Li, Yufang Qin, Shiwen Zhou, and Hua Yang. Prediction the substrate specificities of membrane transport proteins based on support vector machine and hybrid features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 947–953, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2023:CMU

[LLX+23] Xiong Li, Yangkai Lin, Chengwang Xie, Zejun Li, Min Chen, Peng Wang, and Juan Zhou. A clustering method unifying cell-type recognition and subtype identification for tumor heterogeneity analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):822–832, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3203185`.

Lv:2023:TTB

[LLY+23] Zhilong Lv, Yuexiao Lin, Rui Yan, Ying Wang, and Fa Zhang. TransSurv: Transformer-based survival analysis model integrating histopathological images and

genomic data for colorectal cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3411–3420, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3199244`.

Long:2021:FDE

[LLYS21] Wei Long, Tiange Li, Yang Yang, and Hong-Bin Shen. FlyIT: *Drosophila* embryogenesis image annotation based on image tiling and convolutional neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (1):194–204, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2935723`.

Liu:2013:RSN

[LLZ+13] Wei Liu, Dong Li, Yunping Zhu, Hongwei Xie, and Fuchu He. Reconstruction of signaling network from protein interactions based on function annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):514–521, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liao:2020:ETA

[LLZ+20a] Xingyu Liao, Min Li, You Zou, Fang-Xiang Wu, Yi Pan, and Jianxin Wang. An efficient trimming algorithm based on multi-feature fusion scoring model for NGS data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):728–738, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2897558`.

Liu:2020:EMX

[LLZ+20b] Jian Liu, Qiuru Liu, Lei Zhang, Shuhui Su, and Yongzhuang Liu. Enabling massive XML-based biological data management in HBase. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1994–2004, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2915811`.

Lu:2022:PMD

[LLZ+22] Xinguo Lu, Jinxin Li, Zhenghao Zhu, Yue Yuan, Guanyuan Chen, and Keren He. Predicting miRNA–disease associations via combining probability matrix feature decomposition with neighbor learn-

ing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3160–3170, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3097037`.

Liu:2023:HPL

[LLZ+23] Dayun Liu, Xianghui Li, Liangliang Zhang, Xiaowen Hu, Jiaxuan Zhang, Zhirong Liu, and Lei Deng. HGNNLDA: Predicting lncRNA–Drug sensitivity associations via a dual channel hypergraph neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3547–3555, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3302468`.

Liao:2012:NMS

[LLZC12] Bo Liao, Xiong Li, Wen Zhu, and Zhi Cao. A novel method to select informative SNPs and their application in genetic association studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1529–1534, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Leitner:2010:OBI

[LMK+10] Florian Leitner, Scott A. Mardis, Martin Krallinger, Gianni Cesareni, Lynette A. Hirschman, and Alfonso Valencia. An overview of BioCreative II.5. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):385–399, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Leoncini:2015:CCT

[LMPT15] Mauro Leoncini, Manuela Montangero, Marco Pellegrini, and Karina Panucia Tillan. CMStalker: a combinatorial tool for composite motif discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1123–1136, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2024:VHI

[LMW+24] Weiling Li, Raunaq Malhotra, Steven Wu, Manjari Jha, Allen Rodrigo, Mary Poss, and Raj Acharya. ViPRA-Haplo: *De Novo* reconstruction of viral populations using paired end sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):492–500, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964

(electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2024.3374595.

Li:2014:OSM

[LMZ14] Weiming Li, Bin Ma, and Kaizhong Zhang. Optimizing spaced k-mer neighbors for efficient filtration in protein similarity search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):398–406, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2020:IPC

[LMZ+20] Min Li, Xiangmao Meng, Ruiqing Zheng, Fang-Xiang Wu, Yaohang Li, Yi Pan, and Jianxin Wang. Identification of protein complexes by using a spatial and temporal active protein interaction network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):817–827, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2017.2749571.

Liu:2017:API

[LMZL17] Yi Liu, Bin Ma, Kaizhong Zhang, and Gilles Lajoie. An approach for peptide identification by De Novo sequencing of mixture spectra. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):326–336, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2013:NLS

[LN13] Yifeng Li and Alioune Ngom. Nonnegative least-squares methods for the classification of high-dimensional biological data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):447–456, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

L:2017:BDW

[LN17] Biji C. L. and Achuthsankar S. Nair. Benchmark dataset for whole genome sequence compression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1228–1236, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Le:2021:PFB

[LN21] Nguyen Quoc Khanh Le and Binh P. Nguyen. Prediction of FMN binding sites in electron transport chains based on 2-D CNN and PSSM profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2189–2197,

November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2932416`.

Liu:2005:TMB

[LNC+05] Ying Liu, Shamkant B. Navathe, Jorge Civera, Venu Dasigi, Ashwin Ram, Brian J. Ciliax, and Ray Dingledine. Text mining biomedical literature for discovering gene-to-gene relationships: a comparative study of algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):62–76, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:CRP

[LNC+19] Min Li, Peng Ni, Xiaopei Chen, Jianxin Wang, Fang-Xiang Wu, and Yi Pan. Construction of refined protein interaction network for predicting essential proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1386–1397, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2009:BWT

[LNR+09] Kevin Liu, Serita Nelesen, Sindhu Raghavan, C. Randal Linder, and Tandy Warnow. Barking up the wrong tree-length: The impact of gap penalty on alignment and tree accuracy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):7–21, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2020:MDN

[LNW20] Ye Liu, Michael K. Ng, and Stephen Wu. Multi-domain networks association for biological data using block signed graph clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):435–448, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2848904`.

Ling:2005:GEIb

[LNY05a] C. X. Ling, W. S. Noble, and Q. Yang. Guest Editor's introduction to the Special Issue: Machine Learning for Bioinformatics—Part 2. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):177–178, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ling:2005:GEIa

[LNY05b] Charles X. Ling, William Stafford Noble, and Qiang Yang. Guest Editors' introduction to the Special Issue: Machine Learning for Bioinformatics—Part 1. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):81–82, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2015:IDN

[LP15] Xueming Liu and Linqiang Pan. Identifying driver nodes in the human signaling network using structural controllability analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (2):467–472, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lyne:2021:CPA

[LP21] Anne-Marie Lyne and Leïla Perié. Comparing phylogenetic approaches to reconstructing cell lineage from microsatellites with missing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (6):2291–2301, November/ December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2992813`.

Liu:2013:CFS

[LPH+13] Hsi-Che Liu, Pei-Chen Peng, Tzung-Chien Hsieh, Ting-Chi Yeh, Chih-Jen Lin, Chien-Yu Chen, Jen-Yin Hou, Lee-Yung Shih, and Der-Cherng Liang. Comparison of feature selection methods for cross-laboratory microarray analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):593–604, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lee:2018:SBP

[LPH18] Wook Lee, Byungkyu Park, and Kyungsook Han. Sequence-based prediction of putative transcription factor binding sites in DNA sequences of any length. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1461–1469, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2021:AMI

[LPH+21] Dong Li, Zhisong Pan, Guyu Hu, Graham Anderson, and Shan He. Active module identification from multilayer weighted gene co-expression networks: a con-

tinuous optimization approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2239–2248, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2970400`.

Lozano:2008:STA

[LPR+08] Antoni Lozano, Ron Y. Pinter, Oleg Rokhlenko, Gabriel Valiente, and Michal Ziv-Ukelson. Seeded tree alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5 (4):503–513, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2023:CSS

[LQJ+23] Kailong Li, Lijun Quan, Yelu Jiang, Yan Li, Yiting Zhou, Tingfang Wu, and Qiang Lyu. ctP^{2}ISP: Protein–protein interaction sites prediction using convolution and transformer with data augmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):297–306, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3154413`.

Lamiable:2013:AGT

[LQV+13] Alexis Lamiable, Franck Quessette, Sandrine Vial, Dominique Barth, and Alain Denise. An algorithmic game-theory approach for coarse-grain prediction of RNA 3D structure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (1):193–199, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2023:EIC

[LQW+23] Xuan Lin, Zhe Quan, Zhi-Jie Wang, Yan Guo, Xiangxiang Zeng, and Philip S. Yu. Effectively identifying compound-protein interaction using graph neural representation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):932–943, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3198003`.

Lv:2021:AML

[LQWP21] Zhihan Lv, Liang Qiao, Qingjun Wang, and Francesco Piccialli. Advanced machine-learning methods for brain-computer interfacing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1688–1698,

September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3010014`.

Liu:2020:JIV

[LQY+20] Jian Liu, Zhi Qu, Mo Yang, Jialiang Sun, Shuhui Su, and Lei Zhang. Jointly integrating VCF-based variants and OWL-based biomedical ontologies in MongoDB. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5): 1504–1515, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2951137`.

Lecca:2020:RBM

[LR20] Paola Lecca and Angela Re. A reaction-based model of the state space of chemical reaction systems enables efficient simulations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):469–482, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2019.2894699`.

Lazarsfeld:2022:MVC

[LRE+22] John Lazarsfeld, Jonathan Rodríguez, Mert Erden, Yuelin Liu, and Lenore J. Cowen. Majority vote cascading: a semi-supervised framework for improving protein function prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):1933–1945, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3059812`.

Lee:2008:IEN

[LRM08] George Lee, Carlos Rodriguez, and Anant Madabhushi. Investigating the efficacy of nonlinear dimensionality reduction schemes in classifying gene and protein expression studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):368–384, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2012:MPT

[LRM12] Yu Lin, Vaibhav Rajan, and Bernard M. E. Moret. A metric for phylogenetic trees based on matching. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1014–1022, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lancia:2008:HDA

[LRR08] Giuseppe Lancia, R. Ravi, and Romeo Rizzi. Haplotyping for disease association: a combinatorial approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):245–251, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Linz:2009:HNT

[LS09] Simone Linz and Charles Semple. Hybridization in nonbinary trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):30–45, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lan:2010:EIF

[LS10] Man Lan and Jian Su. Empirical investigations into full-text protein interaction article categorization task (ACT) in the BioCreative II.5 challenge. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):421–427, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Loriot:2011:CSD

[LSB+11] Sebastien Loriot, Sushant Sachdeva, Karine Bastard, Chantal Prevost, and Frederic Cazals. On the characterization and selection of diverse conformational ensembles with applications to flexible docking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (2):487–498, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2022:ESI

[LSL+22a] Chao Li, Jun Sun, Li-Wei Li, Xiaojun Wu, and Vasile Palade. An effective swarm intelligence optimization algorithm for flexible ligand docking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2672–2684, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3103777`.

Liu:2022:EIB

[LSL22b] Jian Liu, Jialiang Sun, and Yongzhuang Liu. Effective identification of bacterial genomes from short and long read sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2806–2816, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2021.3095164.

Le:2021:UCS

[LSM+21] Thien Le, Aaron Sy, Erin K. Molloy, Qiuyi Zhang, Satish Rao, and Tandy Warnow. Using constrained-INC for large-scale gene tree and species tree estimation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):2–15, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2020.2990867.

Lamers:2008:PRX

[LSMF08] Susanna L. Lamers, Marco Salemi, Michael S. McGrath, and Gary B. Fogel. Prediction of R5, X4, and R5X4 HIV-1 coreceptor usage with evolved neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):291–300, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2011:CBA

[LSMW11] Weiguo Liu, Bertil Schmidt, and Wolfgang Muller-Wittig. CUDA-BLASTP: Accelerating BLASTP on CUDA-enabled graphics hardware. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1678–1684, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lee:2017:DPD

[LSTW+17] En-Shiun Annie Lee, Ho-Yin Antonio Sze-To, Man-Hon Wong, Kwong-Sak Leung, Terrence Chi-Kong Lau, and Andrew K. C. Wong. Discovering protein-DNA binding cores by aligned pattern clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):254–263, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2023:DCU

[LSW+23] Qiang Li, Hong Song, Zenghui Wei, Fengbo Yang, Jingfan Fan, Danni Ai, Yucong Lin, Xiaoling Yu, and Jian Yang. Densely connected U-Net with criss-cross attention for automatic liver tumor segmentation in CT images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6): 3399–3410, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3198425.

Li:2020:UWE

[LSY+20] Jianqiang Li, Xiaofeng Shi, Zhu-Hong You, Hai-Cheng Yi, Zhuangzhuang Chen, Qiuzhen Lin, and Min Fang. Using weighted extreme learning machine combined with scale-invariant feature transform to predict protein-protein interactions from protein evolutionary information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1546–1554, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2965919`.

Li:2023:DLF

[LSZ+23] Min Li, Wenbo Shi, Fuhao Zhang, Min Zeng, and Yaohang Li. A deep learning framework for predicting protein functions with co-occurrence of GO terms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):833–842, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3170719`.

Lones:2007:RMD

[LT07] Michael Lones and Andy Tyrrell. Regulatory motif discovery using a population clustering evolutionary algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):403–414, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2017:RRB

[LT17] Fangfei Li and Yang Tang. Robust reachability of Boolean control networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):740–745, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lei:2013:CRC

[LTaS13] Jikai Lei, Prapaporn Techaangkoon, and Yanni Sun. Chain-RNA: a comparative ncRNA search tool based on the two-dimensional chain algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):274–285, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lu:2007:ISL

[LTL+07] Yijuan Lu, Qi Tian, Feng Liu, Maribel Sanchez, and Yufeng Wang. Interactive semisupervised learning for microarray analysis. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 4(2):190–203, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:NSA

[LTL+19] Min Li, Li Tang, Zhongxiang Liao, Junwei Luo, Fang-Xiang Wu, Yi Pan, and Jianxin Wang. A novel scaffolding algorithm based on contig error correction and path extension. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):764–773, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2023:ENN

[LTLL23] Jinghang Lin, Xiaoran Tong, Chenxi Li, and Qing Lu. Expectile neural networks for genetic data analysis of complex diseases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):352–359, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3146795`.

Landry:2023:DPN

[LTLTS23] Kaari Landry, Aivee Teodocio, Manuel Lafond, and Olivier Tremblay-Savard. Defining phylogenetic network distances using cherry operations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1654–1666, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3162991`.

Lazar:2012:SFT

[LTM+12] Cosmin Lazar, Jonatan Taminau, Stijn Meganck, David Steenhoff, Alain Coletta, Colin Molter, Virginie de Schaetzen, Robin Duque, Hugues Bersini, and Ann Nowe. A survey on filter techniques for feature selection in gene expression microarray analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1106–1119, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lazar:2013:GNA

[LTM+13] Cosmin Lazar, Jonatan Taminau, Stijn Meganck, David Steenhoff, Alain Coletta, David Y. Weiss Solis, Colin Molter, Robin Duque, Hugues Bersini, and Ann Nowe. GENESHIFT: a nonparametric approach for integrating microarray gene expression data based on the inner product as a distance measure between the distributions of genes. *IEEE/ACM Transactions on Computational Biology and*

Bioinformatics, 10(2):383–392, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lei:2022:IMD

[LTP22] Xiujuan Lei, Jiaojiao Tie, and Yi Pan. Inferring metabolite-disease association using graph convolutional networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):688–698, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3065562`.

Luo:2019:DGP

[LTRW19] Ping Luo, Li-Ping Tian, Jishou Ruan, and Fang-Xiang Wu. Disease gene prediction by integrating PPI networks, clinical RNA-seq data and OMIM data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):222–232, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2022:PCL

[LTT+22] Bo Li, Yihui Tian, Yang Tian, Shihua Zhang, and Xiaolong Zhang. Predicting cancer lymph-node metastasis from LncRNA expression profiles using local linear reconstruction guided distance metric learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3179–3189, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3149791`.

Liu:2022:EHF

[LTW+22] Liangliang Liu, Shaojie Tang, Fang-Xiang Wu, Yu-Ping Wang, and Jianxin Wang. An ensemble hybrid feature selection method for neuropsychiatric disorder classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1459–1471, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3053181`.

Lieberman:2011:VEA

[LTwG+11] Michael D. Lieberman, Sima Taheri, whatever Guo, Fatemeh Mirrashed, Inbal Yahav, Aleks Aris, and Ben Shneiderman. Visual exploration across biomedical databases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):536–550, March 2011. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic).

Lv:2021:DPR

[LTX21] Jinxiong Lv, Shikui Tu, and Lei Xu. Detection of phenotype-related mutations of COVID-19 via the whole genomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1242–1249, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3049836`.

Langdon:2010:SSD

[LUdSCH10] W. B. Langdon, G. J. G. Upton, R. da Silva Camargo, and A. P. Harrison. A survey of spatial defects in Homo Sapiens Affymetrix GeneChips. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):647–653, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Labarre:2014:MPL

[LV14] Anthony Labarre and Sicco Verwer. Merging partially labelled trees: hardness and a declarative programming solution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (2):389–397, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Leuchtenberger:2024:LAN

[LvH24] Alina F. Leuchtenberger and Arndt von Haeseler. Learning from an artificial neural network in phylogenetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):278–288, March 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3352268`.

Liu:2013:NBC

[LW13a] Kuan-Liang Liu and Tzu-Tsung Wong. Naïve Bayesian classifiers with multinomial models for rRNA taxonomic assignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Luo:2013:ARA

[LW13b] Chao Luo and Xingyuan Wang. Algebraic representation of asynchronous multiple-valued networks and its dynamics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):927–938, July 2013. CODEN ITCBCY.

ISSN 1545-5963 (print), 1557-9964 (electronic).

Luo:2015:GES

[LW15] Feng Luo and Xintao Wu. Guest editorial for special section on BIBM 2013. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):252–253, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2017:TUG

[LW17] Jianqiang Li and Fei Wang. Towards unsupervised gene selection: a matrix factorization framework. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):514–521, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2018:CSI

[LW18] Xiangtao Li and Ka-Chun Wong. A comparative study for identifying the chromosome-wide spatial clusters from high-throughput chromatin conformation capture data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):774–787, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:EGW

[LW19a] Xiangtao Li and Ka-Chun Wong. Elucidating genome-wide protein-RNA interactions using differential evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (1):272–282, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2019:SPL

[LW19b] Cheng Liu and Hau San Wong. Structured penalized logistic regression for gene selection in gene expression data analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):312–321, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lu:2021:FFR

[LWD+21] Xinguo Lu, Xinyu Wang, Li Ding, Jinxin Li, Yan Gao, and Keren He. frDriver: a functional region driver identification for protein sequence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1773–1783, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3020096`.

Liu:2014:MCP

[LWG+14] Xiaoqing Liu, Jun Wu, Haipeng Gong, Shengchun Deng, and Zengyou He. Mining conditional phosphorylation motifs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):915–927, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2018:RNN

[LWG+18] Jin-Xing Liu, Dong Wang, Ying-Lian Gao, Chun-Hou Zheng, Yong Xu, and Jiguo Yu. Regularized nonnegative matrix factorization for identifying differentially expressed genes and clustering samples: a survey. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):974–987, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lan:2018:PMD

[LWL+18] Wei Lan, Jianxin Wang, Min Li, Jin Liu, Fang-Xiang Wu, and Yi Pan. Predicting MicroRNA-disease associations based on improved MicroRNA and disease similarities. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1774–1782, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Luo:2019:CDR

[LWL+19] Huimin Luo, Jianxin Wang, Min Li, Junwei Luo, Peng Ni, Kaijie Zhao, Fang-Xiang Wu, and Yi Pan. Computational drug repositioning with random walk on a heterogeneous network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 1890–1900, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2832078`.

Liu:2020:SSS

[LWL+20] Yong Liu, Min Wu, Chenghao Liu, Xiao-Li Li, and Jie Zheng. SL^{2}MF: Predicting synthetic lethality in human cancers via logistic matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):748–757, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2909908`.

Li:2021:DLB

[LWL+21] Menglu Li, Yanan Wang, Fuyi Li, Yun Zhao, Mengya Liu, Sijia Zhang, Yannan

Bin, A. Ian Smith, Geoffrey I. Webb, Jian Li, Jiangning Song, and Junfeng Xia. A deep learning-based method for identification of bacteriophage-host interaction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1801–1810, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3017386`.

Li:2022:IIM

[LWL+22] Jin Li, Jingru Wang, Hao Lv, Zhuoxuan Zhang, and Zaixia Wang. IMCHGAN: Inductive matrix completion with heterogeneous graph attention networks for drug-target interactions prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):655–665, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3088614`.

Loohuis:2014:IDD

[LWM14] Loes Olde Loohuis, Andreas Witzel, and Bud Mishra. Improving detection of driver genes: power-law null model of copy number variation in cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1260–1263, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Luo:2020:GGF

[LWS+20] Junwei Luo, Jianxin Wang, Juan Shang, Huimin Luo, Min Li, Fang-Xiang Wu, and Yi Pan. GapReduce: a gap filling algorithm based on partitioned read sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):877–886, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2789909`.

Liu:2018:IAD

[LWT+18] Jin Liu, Jianxin Wang, Zhenjun Tang, Bin Hu, Fang-Xiang Wu, and Yi Pan. Improving Alzheimer's disease classification by combining multiple measures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1649–1659, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2021:CDD

[LWW+21] Bing Nan Li, Xinle Wang, Rong Wang, Teng Zhou, Rongke Gao, Edward J. Ciaccio, and Peter H. Green.

Celiac disease detection from videocapsule endoscopy images using strip principal component analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1396–1404, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2953701`.

Li:2022:ILM

[LWXX22] Wen Li, Shulin Wang, Junlin Xu, and Ju Xiang. Inferring latent MicroRNA–disease associations on a gene-mediated tripartite heterogeneous multiplexing network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3190–3201, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3143770`.

Luo:2021:NDR

[LWY+21] Huimin Luo, Jianxin Wang, Cheng Yan, Min Li, Fang-Xiang Wu, and Yi Pan. A novel drug repositioning approach based on collaborative metric learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):463–471, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2926453`.

Li:2023:PMD

[LWY+23] Zheng-Wei Li, Qian-Kun Wang, Chang-An Yuan, Peng-Yong Han, Zhu-Hong You, and Lei Wang. Predicting MiRNA-Disease associations by graph representation learning based on jumping knowledge networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2629–2638, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3196394`.

Liu:2012:IBS

[LWZ12] Li-Zhi Liu, Fang-Xiang Wu, and W. J. Zhang. Inference of biological S-system using the separable estimation method and the genetic algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):955–965, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2021:DDL

[LWZ+21a] Min Li, Yake Wang, Ruiqing Zheng, Xinghua Shi, Yaohang Li, Fang-Xiang Wu, and Jianxin Wang. DeepDSC: a deep learning method

to predict drug sensitivity of cancer cell lines. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):575–582, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2919581`.

Liu:2021:SIE

[LWZ+21b] Shuaiqi Liu, Xu Wang, Ling Zhao, Jie Zhao, Qi Xin, and Shui-Hua Wang. Subject-independent emotion recognition of EEG signals based on dynamic empirical convolutional neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1710–1721, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3018137`.

Liu:2021:DPM

[LWZ+21c] Yue Liu, Shu-Lin Wang, Jun-Feng Zhang, Wei Zhang, Su Zhou, and Wen Li. DMFMDA: Prediction of microbe-disease associations based on deep matrix factorization using Bayesian personalized ranking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1763–1772, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3018138`.

Lim:2021:NWI

[LX21] Hansaim Lim and Lei Xie. A new weighted imputed neighborhood-regularized tri-factorization one-class collaborative filtering algorithm: Application to target gene prediction of transcription factors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):126–137, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2968442`.

Li:2024:ICF

[LXC+24] Zheng Li, Xiaolong Xu, Xuefei Cao, Wentao Liu, Yiwen Zhang, Dehua Chen, and Haipeng Dai. Integrated CNN and federated learning for COVID-19 detection on chest X-ray images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):835–845, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3184319`.

Liu:2016:CIB

[LXG+16] Jin-Xing Liu, Yong Xu, Ying-Lian Gao, Chun-Hou Zheng, Dong Wang, and Qi Zhu. A class-information-based sparse component analysis method to identify differentially expressed genes on RNA-Seq data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):392–398, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2021:MVM

[LXL+21] Cheng Li, Jingxu Xu, Qiegen Liu, Yongjin Zhou, Lisha Mou, Zuhui Pu, Yong Xia, Hairong Zheng, and Shanshan Wang. Multi-view mammographic density classification by dilated and attention-guided residual learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):1003–1013, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2970713`.

Li:2024:PDD

[LXS+24] Dandan Li, Zhen Xiao, Han Sun, Xingpeng Jiang, Weizhong Zhao, and Xianjun Shen. Prediction of drug–disease associations based on multi-kernel deep learning method in heterogeneous graph embedding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):120–128, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3339189`.

Li:2022:DRA

[LXWL22] Xingyi Li, Ju Xiang, Fang-Xiang Wu, and Min Li. A dual ranking algorithm based on the multiplex network for heterogeneous complex disease analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):1993–2002, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3059046`.

Liu:2015:RBT

[LXZ+15] Jin-Xing Liu, Yong Xu, Chun-Hou Zheng, Heng Kong, and Zhi-Hui Lai. RPCA-based tumor classification using gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):964–970, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liang:2023:TTE

[LXZ+23] Tingting Liang, Congying Xia, Ziqiang Zhao, Yixuan Jiang, Yuyu Yin, and Philip S. Yu. Transferring from textual entailment to biomedical named entity recognition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2577–2586, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3236477`.

Li:2016:EDP

[LYH+16] Cong Li, Can Yang, Greg Hather, Ray Liu, and Hongyu Zhao. Efficient drug-pathway association analysis via integrative penalized matrix decomposition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):531–540, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lerner:2007:CSI

[LYK07] Boaz Lerner, Josepha Yeshaya, and Lev Koushnir. On the classification of a small imbalanced cytogenetic image database. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):204–215, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2017:PSP

[LYL+17] Jian-Qiang Li, Zhu-Hong You, Xiao Li, Zhong Ming, and Xing Chen. PSPEL: In silico prediction of self-interacting proteins from amino acids sequences using ensemble learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1165–1172, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lei:2020:AFS

[LYW20] Xiujuan Lei, Xiaoqin Yang, and Fang-Xiang Wu. Artificial fish swarm optimization based method to identify essential proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):495–505, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2865567`.

Liu:2019:UMJ

[LYY+19] Kefei Liu, Jieping Ye, Yang Yang, Li Shen, and Hui Jiang. A unified model for joint normalization and differential gene expression detection in RNA-seq data. *IEEE/ACM Transactions on*

Computational Biology and Bioinformatics, 16(2):442–454, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2790918`.

Li:2018:FWI

[LZ18a] Youyuan Li and Yingping Zhuang. fmpRPMF: a Web implementation for protein identification by robust peptide mass fingerprinting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1728–1731, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2018:PHR

[LZ18b] Xiaoli Lin and Xiaolong Zhang. Prediction of hot regions in PPIs based on improved local community structure detecting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1470–1479, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2023:EDD

[LZC+23] Shichao Liu, Yang Zhang, Yuxin Cui, Yang Qiu, Yifan Deng, Zhongfei Zhang, and Wen Zhang. Enhancing drug-drug interaction prediction using deep attention neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):976–985, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3172421`.

Liao:2014:NUB

[LZGZ14] Ruiqi Liao, Ruichang Zhang, Jihong Guan, and Shuigeng Zhou. A new unsupervised binning approach for metagenomic sequences based on N-grams and automatic feature weighting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):42–54, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liang:2018:OGS

[LZH18] Xianpeng Liang, Lin Zhu, and De-Shuang Huang. Optimization of gene set annotations using robust trace-norm multitask learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):1016–1021, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Liu:2017:IMD

[LZHZ17] Yuansheng Liu, Xiangxiang

Zeng, Zengyou He, and Quan Zou. Inferring MicroRNA-disease associations by random walk on a heterogeneous network with multiple data sources. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):905–915, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Li:2019:MSM

[LZL+19] Min Li, Ruiqing Zheng, Yaohang Li, Fang-Xiang Wu, and Jianxin Wang. MGT–SM: a method for constructing cellular signal transduction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):417–424, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2705143`.

Li:2020:MMT

[LZL+20] Tao Li, Xiankai Zhang, Feng Luo, Fang-Xiang Wu, and Jianxin Wang. MultiMotifMaker: a multi-thread tool for identifying DNA methylation motifs from Pacbio reads. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):220–225, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2861399`.

Li:2022:APD

[LZL+22] Lechuan Li, Chonghao Zhang, Shiyu Liu, Hannah Guan, and Yu Zhang. Age prediction by DNA methylation in neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (3):1393–1402, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3084596`.

Li:2024:TTS

[LZL+24] Minglie Li, Shusen Zhou, Tong Liu, Chanjuan Liu, Mujun Zang, and Qingjun Wang. TSVM: Transfer support vector machine for predicting MPRA validated regulatory variants. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):472–479, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3374413`.

Li:2022:DMD

[LZM22] Dongyuan Li, Shuyao Zhang, and Xiaoke Ma. Dynamic module detection in temporal attributed networks of

cancers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2219–2230, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3069441`.

Liu:2020:BBP

[LZQ+20] Guang-Hui Liu, Bei-Wei Zhang, Gang Qian, Bin Wang, Bo Mao, and Isabelle Bichindaritz. Bioimage-based prediction of protein subcellular location in human tissue with ensemble features and deep networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1966–1980, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2917429`.

Liu:2023:GID

[LZS23] Shuhui Liu, Yupei Zhang, and Xuequn Shang. GLassonet: Identifying discriminative gene sets among molecular subtypes of breast cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1905–1916, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3220623`.

Li:2020:NIM

[LZW20] Xiangtao Li, Shixiong Zhang, and Ka-Chun Wong. Nature-inspired multiobjective epistasis elucidation from genome-wide association studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):226–237, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2849759`.

Liu:2021:GET

[LZW21] Liu Liu, Reza Zare, and Shuihua Wang. Guest editorial: Transfer learning methods used in medical imaging and health informatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):38–39, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3020460`.

Li:2022:APH

[LZW+22] Yiming Li, Min Zeng, Yifan Wu, Yaohang Li, and Min Li. Accurate prediction of human essential proteins using ensemble deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3263–3271, 2022. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3122294.

Liu:2023:CPC

[LZW+23a] Niannian Liu, Zequn Zhang, Yanan Wu, Yinglong Wang, and Ying Liang. CRBSP:Prediction of CircRNA–RBP binding sites based on multimodal intermediate fusion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2898–2906, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3272400.

Liu:2023:CEM

[LZW23b] Qiaoming Liu, Xudong Zhao, and Guohua Wang. A clustering ensemble method for cell type detection by multiobjective particle optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):1–14, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3132400.

Lin:2019:IBE

[LZX+19] Yan Lin, Fa-Zhan Zhang, Kai Xue, Yi-Zhou Gao, and Feng-Biao Guo. Identifying bacterial essential genes based on a feature-integrated method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1274–1279, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lin:2020:ECH

[LZX20] Xiaoli Lin, Xiaolong Zhang, and Xin Xu. Efficient classification of hot spots and hub protein interfaces by recursive feature elimination and gradient boosting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1525–1534, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2931717.

Li:2021:NAP

[LZX+21] Jiechen Li, Haochen Zhao, Zhanwei Xuan, Jingwen Yu, Xiang Feng, Bo Liao, and Lei Wang. A novel approach for potential human LncRNA-disease association prediction based on local random walk. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):1049–1059, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2934958.

Lin:2022:CNA

[LZY+22] Chengchuang Lin, Gansen Zhao, Zhirong Yang, Aihua Yin, Xinming Wang, Li Guo, Hanbiao Chen, Zhaohui Ma, Lei Zhao, Haoyu Luo, Tianxing Wang, Bichao Ding, Xiongwen Pang, and Qiren Chen. CIR-Net: Automatic classification of human chromosome based on Inception-ResNet architecture. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (3):1285–1293, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3003445`.

Liu:2016:NMP

[LZZ+16] Yuanning Liu, Qi Zhao, Hao Zhang, Rui Xu, Yang Li, and Liyan Wei. A new method to predict RNA secondary structure based on RNA folding simulation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 990–995, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Lu:2024:CCM

[LZZ+24] Fangfang Lu, Zhihao Zhang, Shuai Zhao, Xiantian Lin, Zhengyu Zhang, Bei Jin, Weiyan Gu, Jingjing Chen, and Xiaoxin Wu. CMM: a CNN-MLP model for COVID-19 lesion segmentation and severity grading. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):789–802, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3253901`.

Mimaroglu:2012:DDC

[MA12] Selim Mimaroglu and Emin Aksehirli. DICLENS: Divisive clustering ensemble with automatic cluster number. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (2):408–420, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2022:GES

[Ma22] Jian Ma. Guest editorial for selected papers from ACM-BCB 2019. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4): 1919, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3140625`.

Mahata:2010:ECH

[Mah10] Pritha Mahata. Exploratory consensus of hierarchical clusterings for

melanoma and breast cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (1):138–152, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maitra:2009:IPO

[Mai09] Ranjan Maitra. Initializing partition-optimization algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):144–157, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mamitsuka:2005:ELK

[Mam05] Hiroshi Mamitsuka. Essential latent knowledge for protein-protein interactions: Analysis by an unsupervised learning approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):119–130, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Matsen:2007:OCT

[Mat07] Frederick Matsen. Optimization over a class of tree shape statistics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):506–512, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Matsen:2009:FTI

[Mat09] Frederick A. Matsen. Fourier transform inequalities for phylogenetic trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):89–95, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Matthews:2015:HCL

[Mat15] Suzanne J. Matthews. Heterogeneous compression of large collections of evolutionary trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):807–814, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mazza:2012:HPC

[Maz12] Tommaso Mazza. High performance computational systems biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):641–642, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mazrouee:2022:AAR

[Maz22] Sepideh Mazrouee. ARHap: Association rule haplotype phasing. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 19(6):3281–3294, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3119955`.

Moore:2016:EMF

[MB16] Erin Jessica Moore and Thirmachos Bourlai. Expectation maximization of frequent patterns, a specific, local, pattern-based biclustering algorithm for biological datasets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):812–824, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mallik:2020:WWC

[MB20] Saurav Mallik and Sanghamitra Bandyopadhyay. WeCoMXP: Weighted connectivity measure integrating co-methylation, co-expression and protein-protein interactions for gene-module detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):690–703, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2868348`.

Mondal:2023:GDG

[MB23] Abhijit Mondal and Mukul S. Bansal. Generalizing the domain-gene-species reconciliation framework to microbial genes and domains. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3511–3522, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3294480`.

Murugesan:2017:BMI

[MBB+17] Sugeerth Murugesan, Kristopher Bouchard, Jesse A. Brown, Bernd Hamann, William W. Seeley, Andrew Trujillo, and Gunther H. Weber. Brain modulyzer: Interactive visual analysis of functional brain connectivity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):805–818, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Muselli:2011:MMV

[MBF+11] Marco Muselli, Alberto Bertoni, Marco Frasca, Alessandro Beghini, Francesca Ruffino, and Giorgio Valentini. A mathematical model for the validation of gene selection methods. *IEEE/ACM Transactions on Computational Biology*

and Bioinformatics, 8(5): 1385–1392, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Murthy:2013:CAC

[MBF+13] Abhishek Murthy, Ezio Bartocci, Flavio H. Fenton, James Glimm, Richard A. Gray, Elizabeth M. Cherry, Scott A. Smolka, and Radu Grosu. Curvature analysis of cardiac excitation wavefronts. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (2):323–336, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mazza:2012:RTP

[MBGP12] Tommaso Mazza, Paolo Ballarini, Rosita Guido, and Davide Prandi. The relevance of topology in parallel simulation of biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):911–923, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Michels:2019:RBM

[MBJ19] Tim Michels, Dimitri Berh, and Xiaoyi Jiang. An RJMCMC-based method for tracking and resolving collisions of *Drosophila* larvae. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):465–474, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2779141`.

Matsen:2018:TRT

[MBKK18] Frederick A. Matsen, Sara C. Billey, Arnold Kas, and Matjaz Konvalinka. Tanglegrams: a reduction tool for mathematical phylogenetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):343–349, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Martins:2018:CMT

[MBP+18] Daniel P. Martins, Michael Taynnan Barros, Massimiliano Pierobon, Meenakshisundaram Kandhavelu, Pietro Lio', and Sasitharan Balasubramaniam. Computational models for trapping Ebola virus using engineered bacteria. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):2017–2027, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Moon:2019:SIC

[MBP+19] SeongRyeol Moon, Curt

Balch, Sungjin Park, Jinhyuk Lee, Jiyong Sung, and Seungyoon Nam. Systematic inspection of the clinical relevance of TP53 missense mutations in gastric cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1693–1701, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mehmood:2015:PLS

[MBS15] Tahir Mehmood, Jon Bohlin, and Lars Snipen. A partial least squares based procedure for upstream sequence classification in prokaryotes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):560–567, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

McIntosh:2007:HCR

[MC07] Tara McIntosh and Sanjay Chawla. High confidence rule mining for microarray analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):611–623, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Masseroli:2016:IQG

[MCC16] Marco Masseroli, Arif Canakoglu, and Stefano Ceri. Integration and querying of genomic and proteomic semantic annotations for biomedical knowledge extraction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):209–219, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mena-Chalco:2008:IPC

[MCCZC08] Jesus Mena-Chalco, Helaine Carrer, Yossi Zana, and Roberto M. Cesar Jr. Identification of protein coding regions using the modified Gabor-wavelet transform. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):198–207, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Merelli:2011:IBS

[MCD+11] Ivan Merelli, Paolo Cozzi, Daniele D'Agostino, Andrea Clematis, and Luciano Milanesi. Image-based surface matching algorithm oriented to structural biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (4):1004–1016, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mirceva:2012:EAR

[MCDD12] Georgina Mirceva, Ivana Cingovska, Zoran Dimov, and Danco Davcev. Efficient approaches for retrieving protein tertiary structures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (4):1166–1179, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mei:2015:ESN

[MCH+15] Yongguo Mei, Adria Carbo, Stefan Hoops, Raquel Hontecillas, and Josep Bassaganya-Riera. ENISI SDE: a new web-based tool for modeling stochastic processes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):289–297, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Moskovitch:2017:PCO

[MCHT17] Robert Moskovitch, Hyunmi Choi, George Hripcsak, and Nicholas Tatonetti. Prognosis of clinical outcomes with temporal patterns and experiences with one class feature selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):555–563, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mongia:2022:CPD

[MCM22] Aanchal Mongia, Emilie Chouzenoux, and Angshul Majumdar. Computational prediction of drug-disease association based on graph-regularized one bit matrix completion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3332–3339, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3189879`.

Mkrtchyan:2017:OLS

[MCRC17] Katya Mkrtchyan, Anirban Chakraborty, and Amit K. Roy-Chowdhury. Optimal landmark selection for registration of 4D confocal image stacks in *Arabidopsis*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):457–467, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mohsenizadeh:2018:OOB

[MDD18] Daniel N. Mohsenizadeh, Roozbeh Dehghannasiri, and Edward R. Dougherty. Optimal objective-based experimental design for uncertain dynamical gene networks with experimental error. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15

(1):218–230, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mitra:2011:GNS

[MDH11] Sushmita Mitra, Ranajit Das, and Yoichi Hayashi. Genetic networks and soft computing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):94–107, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mourad:2013:DPS

[MDM13] Ramy Mourad, Zaher Dawy, and Faruck Morcos. Designing pooling systems for noisy high-throughput protein-protein interaction experiments using Boolean compressed sensing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1478–1490, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mukherjee:2022:FOR

[MDMR+22] Kingshuk Mukherjee, Daniel Dole-Muinos, Massimiliano Rossi, Ayomide Ajayi, Mattia Prosperi, and Christina Boucher. Finding overlapping Rmaps via clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3114–3123, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3132534`.

Mu:2018:OOC

[MDPR18] Chunyan Mu, Peter Dittrich, David Parker, and Jonathan E. Rowe. Organisation-oriented coarse graining and refinement of stochastic reaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1152–1166, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Markin:2019:CMP

[ME19a] Alexey Markin and Oliver Eulenstein. Computing Manhattan path-difference median trees: a practical local search approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1063–1076, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Markin:2019:CMT

[ME19b] Alexey Markin and Oliver Eulenstein. Cophenetic median trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1459–1470, September 2019. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Markin:2019:ELS

[ME19c] Alexey Markin and Oliver Eulenstein. Efficient local search for Euclidean path-difference median trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1374–1385, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Messaoudi:2014:BSS

[MEOL14] Imen Messaoudi, Afef Elloumi-Oueslati, and Zied Lachiri. Building specific signals from frequency chaos game and revealing periodicities using a smoothed Fourier analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5): 863–877, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Monteiro:2018:UML

[MFF+18] Miguel Monteiro, Ana Catarina Fonseca, Ana Teresa Freitas, Teresa Pinho e Melo, Alexandre P. Francisco, Jose M. Ferro, and Arlindo L. Oliveira. Using machine learning to improve the prediction of functional outcome in ischemic stroke patients. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1953–1959, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mazza:2015:FIA

[MFS+15] Tommaso Mazza, Caterina Fusilli, Chiara Saracino, Gianluigi Mazzoccoli, Francesca Tavano, Manlio Vinciguerra, and Valerio Pazienza. Functional impact of autophagy-related genes on the homeostasis and dynamics of pancreatic cancer cell lines. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):667–678, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mina:2014:IRL

[MG14] Marco Mina and Pietro Hiram Guzzi. Improving the robustness of local network alignment: design and extensive assessment of a Markov clustering-based approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):561–572, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mykowiecka:2019:CEE

[MG19] Agnieszka Mykowiecka and

Pawel Gorecki. Credibility of evolutionary events in gene trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):713–726, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Milano:2019:GNA

[MGC19] Marianna Milano, Pietro Hiram Guzzi, and Mario Cannataro. GLAlign: a novel algorithm for local network alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1958–1969, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2830323`.

Mak:2008:PPS

[MGK08] Man-Wai Mak, Jian Guo, and Sun-Yuan Kung. PairProSVM: Protein subcellular localization based on local pairwise profile alignment and SVM. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):416–422, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mohammadi:2017:TAT

[MGKG17] Shahin Mohammadi, David F. Gleich, Tamara G. Kolda, and Ananth Grama. Triangular alignment TAME: a tensor-based approach for higher-order network alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1446–1458, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2012:SBP

[MGL+12] Xin Ma, Jing Guo, Hong-De Liu, Jian-Ming Xie, and Xiao Sun. Sequence-based prediction of DNA-binding residues in proteins with conservation and correlation information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1766–1775, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Martins:2022:LPM

[MGP+22] Andreia S. Martins, Marta Gromicho, Susana Pinto, Mamede de Carvalho, and Sara C. Madeira. Learning prognostic models using disease progression patterns: Predicting the need for non-invasive ventilation in amyotrophic lateral sclerosis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2572–2583, 2022. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3078362`.

Manipur:2023:CDP

[MGP+23] Ichcha Manipur, Maurizio Giordano, Marina Piccirillo, Seetharaman Parashuraman, and Lucia Maddalena. Community detection in protein–protein interaction networks and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):217–237, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3138142`.

Mottelet:2017:MFA

[MGS17] Stephane Mottelet, Gil Gaullier, and Georges Sadaka. Metabolic flux analysis in isotope labeling experiments using the adjoint approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):491–497, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maheshwari:2021:CVA

[MGS+21] Sidharth Maheshwari, Venkateshwarlu Y. Gudur, Rishad Shafik, Ian Wilson, Alex Yakovlev, and Amit Acharyya. CORAL: Verification-aware OpenCL based read mapper for heterogeneous systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1426–1438, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2943856`.

Mahapatra:2022:DNN

[MGSP22] Satyajit Mahapatra, Vivek Raj Gupta, Sitanshu Sekhar Sahu, and Ganapati Panda. Deep neural network and extreme gradient boosting based hybrid classifier for improved prediction of protein-protein interaction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):155–165, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3061300`.

Ma:2015:PPR

[MGXS15] Xin Ma, Jing Guo, Ke Xiao, and Xiao Sun. PRBP: Prediction of RNA-binding proteins using a random forest algorithm combined with an RNA-binding residue predictor. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1385–1393, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Huang:2013:EEO

[mHB13] Yao ming Huang and Chris Bystroff. Expanded explorations into the optimization of an energy function for protein design. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1176–1187, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2020:CIH

[MHHJ20] Yuanyuan Ma, Xiaohua Hu, Tingting He, and Xingpeng Jiang. Clustering and integrating of heterogeneous microbiome data by joint symmetric nonnegative matrix factorization with Laplacian regularization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):788–795, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2017.2756628`.

Marschall:2012:PAA

[MHKR12] Tobias Marschall, Inke Herms, Hans-Michael Kaltenbach, and Sven Rahmann. Probabilistic arithmetic automata and their applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1737–1750, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2022:SBS

[MHTJ22] Yingjun Ma, Tingting He, Yuting Tan, and Xingpeng Jiang. Seq-BEL: Sequence-based ensemble learning for predicting virus-human protein–protein interaction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1322–1333, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3008157`.

Michal:2007:FCM

[MIC+07] Shahar Michal, Tor Ivry, Omer Cohen, Moshe Sipper, and Danny Barash. Finding a common motif of RNA sequences using genetic programming: The GeRNAMo system. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):596–610, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mirzal:2014:NTR

[Mir14] Andri Mirzal. Nonparametric Tikhonov regularized NMF and its application in cancer clustering. *IEEE/ACM Transactions on Computational Biology*

and Bioinformatics, 11(6): 1208–1217, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Milenkovic:2018:GLB

[MJ18] Tijana Milenkovic and Sarath Chandra Janga. Great Lakes Bioinformatics Conference GLBIO 2015 special section editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1229–1230, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mou:2023:STD

[MJ23] Chenqi Mou and Wenwen Ju. Sparse triangular decomposition for computing equilibria of biological dynamic systems based on chordal graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1667–1678, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3156759`.

Marczyk:2020:GXA

[MJPP20] Michal Marczyk, Roman Jaksik, Andrzej Polanski, and Joanna Polanska. GaMRed-adaptive filtering of high-throughput biological data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):149–157, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2858825`.

Ma:2022:AHS

[MJZY22] Jingjing Ma, Haitao Jiang, Daming Zhu, and Runmin Yang. Algorithms and hardness for scaffold filling to maximize increased duo-preservations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2071–2079, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3083896`.

Marhon:2016:PPC

[MK16] Sajid A. Marhon and Stefan C. Kremer. Prediction of protein coding regions using a wide-range wavelet window method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):742–753, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mozaffari-Kermani:2016:ISS

[MKARB16] Mehran Mozaffari-Kermani, Reza Azarderakhsh, Kui Ren, and Jean-Luc Beuchat. Introduction to the special

section on emerging security trends for biomedical computations, devices, and infrastructures: guest editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):399–400, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maji:2020:SEA

[MKG20] Ranjan Kumar Maji, Sunirmal Khatua, and Zhumur Ghosh. A supervised ensemble approach for sensitive microRNA target prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):37–46, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2858252`.

Mernberger:2011:SSG

[MKH11] Marco Mernberger, Gerhard Klebe, and Eyke Hullermeier. SEGA: Semiglobal graph alignment for structure-based protein comparison. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1330–1343, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Miyawaki-Kuwakado:2020:PMC

[MKKS20] Atsuko Miyawaki-Kuwakado, Soichiro Komori, and Fumihide Shiraishi. A promising method for calculating true steady-state metabolite concentrations in large-scale metabolic reaction network models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):27–36, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2853724`.

Matsieva:2017:RSF

[MKS+17] Julia Matsieva, Steven Kelk, Celine Scornavacca, Chris Whidden, and Dan Gusfield. A resolution of the static formulation question for the problem of computing the history bound. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):404–417, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Meyer:2018:MMP

[ML18] Karlene Nicole Meyer and Michelle R. Lacey. Modeling methylation patterns with long read sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1379–1389, July 2018.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Manduchi:2022:GAC

[MLFM22] Elisabetta Manduchi, Trang T. Le, Weixuan Fu, and Jason H. Moore. Genetic analysis of coronary artery disease using tree-based automated machine learning informed by biology-based feature selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1379–1386, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3099068`.

Mo:2017:NMB

[MLZ17] Hongwei Mo, Lili Liu, and Jiao Zhao. A new magnetotactic bacteria optimization algorithm based on moment migration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):15–26, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Min:2018:NRS

[MLZ18] Wenwen Min, Juan Liu, and Shihua Zhang. Network-regularized sparse logistic regression models for clinical risk prediction and biomarker discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):944–953, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2024:PPP

[MLZ+24] Ke Ma, Jiawei Li, Mengyuan Zhao, Ibrahim Zamit, Bin Lin, Fei Guo, and Jijun Tang. PPRTGI: a personalized PageRank graph neural network for TF-target gene interaction detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):480–491, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3374430`.

Moskon:2014:SAC

[MM14a] Miha Moskon and Miha Mraz. Systematic approach to computational design of gene regulatory networks with information processing capabilities. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):431–440, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mukhopadhyay:2014:INR

[MM14b] Anirban Mukhopadhyay and Monalisa Mandal. Identifying non-redundant gene

markers from microarray data: a multiobjective variable length PSO-based approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1170–1183, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Muki-Marttunen:2017:AMB

[MM17] Tuomo Muki-Marttunen. An algorithm for motif-based network design. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1181–1186, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maulik:2013:MQB

[MMB+13] Ujjwal Maulik, Anirban Mukhopadhyay, Malay Bhattacharyya, Lars Kaderali, Benedikt Brors, Sanghamitra Bandyopadhyay, and Roland Eils. Mining quasi-bicliques from HIV-1-human protein interaction network: a multiobjective biclustering approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):423–435, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mallick:2022:NGT

[MMBC22] Koushik Mallick, Saurav Mallik, Sanghamitra Bandyopadhyay, and Sikim Chakraborty. A novel graph topology-based GO-similarity measure for signature detection from multi-omics data and its application to other problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):773–785, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3020537`.

Madadi:2023:AIM

[MMC+23] Yeganeh Madadi, Aboozar Monavarfeshani, Hao Chen, W. Daniel Stamer, Robert W. Williams, and Siamak Yousefi. Artificial intelligence models for cell type and subtype identification based on single-cell RNA sequencing data in vision science. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2837–2852, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3284795`.

Meira:2014:AMA

[MMFD14] Luis A. A. Meira, Vinícius R. Máximo, Álvaro L. Fazenda, and Arlindo F. Da Con-

ceição. Acc-Motif: accelerated network motif detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):853–862, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Manipur:2022:NGE

[MMG+22] Ichcha Manipur, Mario Manzo, Ilaria Granata, Maurizio Giordano, Lucia Maddalena, and Mario R. Guarracino. Netpro2vec: a graph embedding framework for biomedical applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):729–740, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3078089`.

Meng:2015:ICG

[MMH15] Nan Meng, Raghu Machiraju, and Kun Huang. Identify critical genes in development with consistent H3K4me2 patterns across multiple tissues. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1104–1111, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Miklos:2010:MPI

[MMS10] Istvan Miklos, Bence Melykuti, and Krister Swenson. The Metropolized partial importance sampling MCMC mixes slowly on minimum reversal rearrangement paths. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):763–767, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Metsis:2014:DCN

[MMSH14] Vangelis Metsis, Fillia Makedon, Dinggang Shen, and Heng Huang. DNA copy number selection using robust structured sparsity-inducing norms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):138–181, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Marchiori:2014:GEP

[MNA14] Elena Marchiori, Alioune Ngom, and Raj Acharya. Guest editorial: pattern recognition in bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):498–499, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mneimneh:2009:AOS

[Mne09] Saad Mneimneh. On the approximation of optimal structures for RNA–RNA interaction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):682–688, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mendonca-Neto:2022:GSM

[MNLF+22] Rayol Mendonca-Neto, Zhi Li, David Fenyö, Claudio T. Silva, Fabíola G. Nakamura, and Eduardo F. Nakamura. A gene selection method based on outliers for breast cancer subtype classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2547–2559, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3132339`.

Meskin:2013:PEB

[MNND13] N. Meskin, H. Nounou, M. Nounou, and A. Datta. Parameter estimation of biological phenomena: an unscented Kalman filter approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):537–543, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mandou:2010:GEI

[MNPZ10] Ion Mandou, Giri Narasimhan, Yi Pan, and Yanqing Zhang. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):577–578, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2009:GCU

[MNR09] Jianmin Ma, Minh N. Nguyen, and Jagath C. Rajapakse. Gene classification using codon usage and support vector machines. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):134–143, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Moret:2004:PNM

[MNW+04] Bernard M. E. Moret, Luay Nakhleh, Tandy Warnow, C. Randal Linder, Anna Tholse, Anneke Padolina, Jerry Sun, and Ruth Timme. Phylogenetic networks: Modeling, reconstructibility, and accuracy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):13–23, January 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Madeira:2004:BAB

[MO04] Sara C. Madeira and Arlindo L. Oliveira. Biclustering algorithms for biological data analysis: a survey. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):24–45, January 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mossel:2007:DMT

[Mos07] Elchanan Mossel. Distorted metrics on trees and phylogenetic forests. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):108–116, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maji:2013:RFC

[MP13] Pradipta Maji and Sushmita Paul. Rough-fuzzy clustering for grouping functionally similar genes from microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):286–299, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Malik:2019:RCS

[MP19] Laraib Malik and Rob Patro. Rich chromatin structure prediction from Hi-C data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1448–1458, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Madhumita:2022:FWA

[MP22] Madhumita and Sushmita Paul. A feature weighting-assisted approach for cancer subtypes identification from paired expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (3):1403–1414, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3041723`.

Misra:2015:PMI

[MPA15] Sanchit Misra, Kiran Pamnany, and Srinivas Aluru. Parallel mutual information based construction of genome-scale networks on the Intel Xeon Phi coprocessor. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1008–1020, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mahoney:2012:MOB

[MPF12] Arthur W. Mahoney, Gregory J. Podgorski, and Nicholas S. Flann. Multiob-

jective optimization based-approach for discovering novel cancer therapies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):169–184, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Minh:2009:BPD

[MPKvH09] Bui Quang Minh, Fabio Pardi, Steffen Klaere, and Arndt von Haeseler. Budgeted phylogenetic diversity on circular split systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):22–29, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mitrofanova:2011:PPF

[MPM11] Antonina Mitrofanova, Vladimir Pavlovic, and Bud Mishra. Prediction of protein functions with gene ontology and interspecies protein homology data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):775–784, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Manica:2020:FAA

[MPP+20] Matteo Manica, Raphael Polig, Mitra Purandare, Roland Mathis, Christoph Hagleitner, and María Rodríguez Martínez. FPGA accelerated analysis of Boolean gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 2141–2147, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2936836`.

Mizera:2019:TAA

[MPQY19] Andrzej Mizera, Jun Pang, Hongyang Qu, and Qixia Yuan. Taming asynchrony for attractor detection in large Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):31–42, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maximova:2018:SGP

[MPS18] Tatiana Maximova, Erion Plaku, and Amarda Shehu. Structure-guided protein transition modeling with a probabilistic roadmap algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1783–1796, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mizera:2018:APT

[MPSY18] Andrzej Mizera, Jun Pang, Cui Su, and Qixia Yuan. ASSA-PBN: a toolbox for probabilistic Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1203–1216, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mandoiu:2009:GEI

[MPSZ09] Ion Mandoiu, Yi Pan, Raj Sunderraman, and Alexander Zelikovsky. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):178–179, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mizera:2018:RTS

[MPY18] Andrzej Mizera, Jun Pang, and Qixia Yuan. Reviving the two-state Markov chain approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1525–1537, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mandoiu:2007:GEI

[MPZ07] Ion I. Mãndoiu, Yi Pan, and Alexander Zelikovsky. Guest Editors' introduction to the Special Section on Bioinformatics Research and Applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):513–514, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mandoiu:2008:GEI

[MPZ08] Ion I. Mandoiu, Yi Pan, and Alexander Zelikovsky. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):321–322, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maharaj:2021:CNE

[MQOH21] Sridevi Maharaj, Taotao Qian, Zarin Ohiba, and Wayne Hayes. Common neighbors extension of the sticky model for PPI networks evaluated by global and local graphlet similarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):16–26, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964

(electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3017374`.

Mossel:2010:ILS

[MR10] Elchanan Mossel and Sebastien Roch. Incomplete lineage sorting: Consistent phylogeny estimation from multiple loci. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):166–171, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2012:RNH

[MRB12] Lingyu Ma, Marco Reisert, and Hans Burkhardt. RENNSH: a novel α-helix identification approach for intermediate resolution electron density maps. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):228–239, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Morris:2024:EDA

[MRB+24] Jordan Morris, Ashur Rafiev, Graeme M. Bragg, Mark L. Vousden, David B. Thomas, Alex Yakovlev, and Andrew D. Brown. An event-driven approach to genotype imputation on a custom RISC-V cluster. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):26–35, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3328714`.

Ma:2018:MLR

[MRK18] Eddie Y. T. Ma, Sujeevan Ratnasingham, and Stefan C. Kremer. Machine learned replacement of *N*-labels for basecalled sequences in DNA barcoding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):191–204, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mossel:2009:SEA

[MRS09] Elchanan Mossel, Sebastien Roch, and Mike Steel. Shrinkage effect in ancestral maximum likelihood. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):126–133, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Munoz:2010:RPG

[MS10] Adriana Munoz and David Sankoff. Rearrangement phylogeny of genomes in contig form. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

7(4):579–587, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mauch:2011:EFE

[MS11] Sean Mauch and Mark Stalzer. Efficient formulations for exact stochastic simulation of chemical systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):27–35, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Maji:2017:SFS

[MS17] Pradipta Maji and Ekta Shah. Significance and functional similarity for identification of disease genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6): 1419–1433, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Medhat:2021:FRA

[MS21] Belal Medhat and Ahmed Shawish. FLR: a revolutionary alignment-free similarity analysis methodology for DNA-sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1924–1936, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2967385`.

Mandal:2019:BIC

[MSB19] Koyel Mandal, Rosy Sarmah, and Dhruba Kumar Bhattacharyya. Biomarker identification for cancer disease using biclustering approach: an empirical study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):490–509, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2820695`.

Mykowiecka:2018:IGS

[MSG18] Agnieszka Mykowiecka, Pawel Szczesny, and Pawel Gorecki. Inferring gene-species assignments in the presence of horizontal gene transfer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1571–1578, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Magni:2011:SPI

[MSH+11] Paolo Magni, Angela Simeone, Sandra Healy, Antonella Isacchi, and Roberta Bosotti. Summarizing probe intensities of Affymetrix GeneChip 3' expression

arrays taking into account day-to-day variability. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1425–1430, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Malhotra:2019:PTE

[MSJP19] Anvita Gupta Malhotra, Sudha Singh, Mohit Jha, and Khushhali M. Pandey. A parametric targetability evaluation approach for vitiligo proteome extracted through integration of gene ontologies and protein interaction topologies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 1830–1842, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2835459`.

Mirzaei:2019:PSP

[MSKC19] Shokoufeh Mirzaei, Tomer Sidi, Chen Keasar, and Silvia Crivelli. Purely structural protein scoring functions using support vector machine and ensemble learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1515–1523, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mandon:2019:ASR

[MSP+19] Hugues Mandon, Cui Su, Jun Pang, Soumya Paul, Stefan Haar, and Loic Pauleve. Algorithms for the sequential reprogramming of Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1610–1619, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2018:ICS

[MSQ18] Xiaoke Ma, Penggang Sun, and Guimin Qin. Identifying condition-specific modules by clustering multiple networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1636–1648, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Meng:2013:WAC

[MSS+13a] Tao Meng, Ahmed T. Soliman, Mei-Ling Shyu, Yimin Yang, Shu-Ching Chen, S. S. Iyengar, John Yordy, and Puneeth Iyengar. Wavelet analysis in current cancer genome research: a survey. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):

1442–14359, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Molloy:2013:PSE

[MSS13b] Kevin Molloy, Sameh Saleh, and Amarda Shehu. Probabilistic search and energy guidance for biased decoy sampling in ab initio protein structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5): 1162–1175, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Majumder:2019:CMD

[MSS19a] Aurpan Majumder, Mrityunjay Sarkar, and Prolay Sharma. A composite mode differential gene regulatory architecture based on temporal expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 1785–1793, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2828418`.

Meysman:2019:MES

[MSS+19b] Pieter Meysman, Yvan Saeys, Ehsan Sabaghian, Wout Bittremieux, Yves Van de Peer, Bart Goethals, and Kris Laukens. Mining the enriched subgraphs for specific vertices in a biological graph. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1496–1507, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2019:IFP

[MSZ19a] Xiaoke Ma, Penggang Sun, and Zhong-Yuan Zhang. An integrative framework for protein interaction network and methylation data to discover epigenetic modules. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 1855–1866, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2831666`.

Mandoiu:2019:GEI

[MSZ19b] Ion I. Mandoiu, Pavel Skums, and Alexander Zelikovsky. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1362–1363, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mao:2011:RMS

[MT11] Kezhi Z. Mao and Wenyin Tang. Recursive Mahalanobis separability measure for gene subset selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (1):266–272, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Margaliot:2012:SSD

[MT12a] Michael Margaliot and Tamir Tuller. On the steady-state distribution in the homogeneous ribosome flow model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1724–1736, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Margaliot:2012:SAR

[MT12b] Michael Margaliot and Tamir Tuller. Stability analysis of the ribosome flow model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1545–1552, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Malik:2024:GEE

[MT24] Ashwani Kumar Malik and M. Tanveer. Graph embedded ensemble deep randomized network for diagnosis of Alzheimer's disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):546–558, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3202707`.

Matroud:2022:AAA

[MTH22] Atheer Matroud, Christopher Tuffley, and Michael Hendy. An asymmetric alignment algorithm for estimating ancestor-descendant edit distance for tandem repeats. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2080–2091, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3059239`.

Martinez:2015:CAS

[MTM+15] Hector Martinez, Joaquin Tarraga, Ignacio Medina, Sergio Barrachina, Maribel Castillo, Joaquin Dopazo, and Enrique S. Quintana-Orti. Concurrent and accurate short read mapping on multicore processors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5): 995–1007, September 2015. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Mahjani:2017:FCF

[MTNH17] Behrang Mahjani, Salman Toor, Carl Nettelblad, and Sverker Holmgren. A flexible computational framework using R and map-reduce for permutation tests of massive genetic analysis of complex traits. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):381–392, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mondol:2022:AAA

[MTR+22] Raktim Kumar Mondol, Nhan Duy Truong, Mohammad Reza, Samuel Ippolito, Esmaeil Ebrahimie, and Omid Kavehei. AFExNet: an adversarial autoencoder for differentiating breast cancer sub-types and extracting biologically relevant genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2060–2070, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3066086`.

Madeira:2010:IRM

[MTSCO10] Sara C. Madeira, Miguel C. Teixeira, Isabel Sa-Correia, and Arlindo L. Oliveira. Identification of regulatory modules in time series gene expression data using a linear time biclustering algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (1):153–165, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Murali:2018:GE

[Mur18] T. M. Murali. Guest editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1036, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Milotti:2013:CAB

[MVS+13] Edoardo Milotti, Vladislav Vyshemirsky, Michela Sega, Sabrina Stella, Federico Dogo, and Roberto Chignola. Computer-aided biophysical modeling: a quantitative approach to complex biological systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):805–810, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Martin-Vide:2019:ACB

[MVVR19] Carlos Martin-Vide and Miguel A. Vega-Rodriguez. Algorithms for computa-

tional biology: Third edition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):701–702, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Martin-Vide:2020:ACB

[MVVR20] Carlos Martín-Vide and Miguel A. Vega-Rodríguez. Algorithms for computational biology: Fifth edition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):1, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2019.2949851`.

Martin-Vide:2021:ACBb

[MVVR21a] Carlos Martín-Vide and Miguel A. Vega-Rodríguez. Algorithms for Computational Biology: Seventh edition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2059–2060, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3099915`.

Martin-Vide:2021:ACBa

[MVVR21b] Carlos Martín-Vide and Miguel A. Vega-Rodríguez. Algorithms for Computational Biology: Sixth edition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):1, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3023866`.

Martin-Vide:2023:ACB

[MVVR23] Carlos Martín-Vide and Miguel A. Vega-Rodríguez. Algorithms for computational biology: Eighth edition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1626–1627, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3218808`.

Muraro:2013:IGN

[MVW+13] Daniele Muraro, Ute Vob, Michael Wilson, Malcolm Bennett, Helen Byrne, Ive De Smet, Charlie Hodgman, and John King. Inference of the genetic network regulating lateral root initiation in *Arabidopsis thaliana*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):50–60, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mirzaei:2016:FCN

[MW16] Sajad Mirzaei and Yufeng Wu. Fast construction of near parsimonious hybridization networks for multiple phylogenetic trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):565–570, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mazrouee:2020:PMF

[MW20] Sepideh Mazrouee and Wei Wang. PolyCluster: Minimum fragment disagreement clustering for polyploid phasing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):264–277, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2858803`.

Mu:2021:CML

[MW21] Quanhua Mu and Jiguang Wang. CNAPE: a machine learning method for copy number alteration prediction from gene expression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (1):306–311, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2944827`.

Murphy:2011:TAP

[MWD11] James T. Murphy, Ray Walshe, and Marc Devocelle. A theoretical analysis of the Prodrug delivery system for treating antibiotic-resistant bacteria. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):650–658, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2023:PDA

[MWH+23] Yuxin Ma, Shuo Wang, Yang Hua, Ruhui Ma, Tao Song, Zhengui Xue, Heng Cao, and Haibing Guan. Perceptual data augmentation for biomedical coronary vessel segmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2494–2505, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3188148`.

Ma:2012:EAA

[MWL+12] Christopher Ma, Thomas K. F. Wong, T. W. Lam, W. K. Hon, K. Sadakane, and S. M. Yiu. An efficient alignment algorithm for searching simple pseudoknots over long genomic sequence. *IEEE/ACM Trans-*

actions on Computational Biology and Bioinformatics, 9(6):1629–1638, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mukund:2018:CEN

[MWLS18] Kavitha Mukund, Samuel R. Ward, Richard L. Lieber, and Shankar Subramaniam. Co-expression network approach to studying the effects of Botulinum Neurotoxin-A. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):2009–2016, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mooney:2012:GGU

[MWSM12] Michael Mooney, Beth Wilmot, The Bipolar Genome Study, and Shannon McWeeney. The GA and the GWAS: Using genetic algorithms to search for multilocus associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):899–910, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mandoiu:2013:GEI

[MWZ13] Ion I. Mandoiu, Jianxin Wang, and Alexander Zelikovsky. Guest Editors' introduction to the special section on bioinformatics research and applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1345–1346, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

McDermott:2020:DLB

[MWZ+20] Matthew B. A. McDermott, Jennifer Wang, Wen-Ning Zhao, Steven D. Sheridan, Peter Szolovits, Isaac Kohane, Stephen J. Haggarty, and Roy H. Perlis. Deep learning benchmarks on l1000 gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 1846–1857, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2910061`.

Ma:2017:EBS

[MWZY17] Lichun Ma, Debby D. Wang, Bin Zou, and Hong Yan. An eigen-binding site based method for the analysis of anti-EGFR drug resistance in lung cancer treatment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1187–1194, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2012:MRD

[MYCW12] Wenji Ma, Yong Yang, Zhi-Zhong Chen, and Lusheng Wang. Mutation region detection for closely related individuals without a known pedigree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):499–510, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Manu:2024:GFG

[MYLS24] Daniel Manu, Jingjing Yao, Wuji Liu, and Xiang Sun. GraphGANFed: a federated generative framework for graph-structured molecules towards efficient drug discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):240–253, March 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3349990`.

Ma:2017:OIS

[MZ17] Tianle Ma and Aidong Zhang. Omics informatics: From scattered individual software tools to integrated workflow management systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):926–946, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Meng:2015:GSI

[MZL15] Jun Meng, Jing Zhang, and Yushi Luan. Gene selection integrated with biological knowledge for plant stress response using neighborhood system and rough set theory. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):433–444, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ma:2022:BBR

[MZLL22] Jiani Ma, Lin Zhang, Shaojie Li, and Hui Liu. BRPCA: Bounded robust principal component analysis to incorporate similarity network for N7-methylguanosine(mo^7G) site-disease association prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3295–3306, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3109055`.

Macwan:2016:RSC

[MZS+16] Isaac G. Macwan, Zihe Zhao, Omar T. Sobh, Ishita Mukerji, Bhushan Dharmadhikari, and Prabir K. Patra. Residue specific and chirality dependent interactions between carbon nanotubes and

flagellin. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):541–548, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Mao:2019:MEP

[MZSL19] Chengsheng Mao, Yuan Zhao, Mengxin Sun, and Yuan Luo. Are my EHRs private enough? Event-level privacy protection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):103–112, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nebel:2011:AFE

[NA11] Markus E. Nebel and Scheid Anika. Analysis of the free energy in a stochastic RNA secondary structure model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1468–1482, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Noriega-Atala:2020:EIS

[NAHT+20] Enrique Noriega-Atala, Paul D. Hein, Shraddha S. Thumsi, Zechy Wong, Xia Wang, Sean M. Hendryx, and Clayton T. Morrison. Extracting inter-sentence relations for associating biological context with events in biomedical texts. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1895–1906, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2904231`.

Nakhleh:2010:MSR

[Nak10] Luay Nakhleh. A metric on the space of reduced phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):218–222, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nanni:2019:BCH

[NBGL19] Loris Nanni, Sheryl Brahnam, Stefano Ghidoni, and Alessandra Lumini. Bioimage classification with handcrafted and learned features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):874–885, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Newman:2024:DDI

[NCJ24] Tara Newman, Hiu Fung Kevin Chang, and Hosna Jabbari. DinoKnot: Duplex interaction of nucleic

acids with PseudoKnots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):348–359, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3362308`.

Ni:2023:MMS

[NCL+23] Zhichen Ni, Honglong Chen, Zhe Li, Xiaomeng Wang, Na Yan, Weifeng Liu, and Feng Xia. MSCET: a multi-scenario offloading schedule for biomedical data processing and analysis in cloud-edge-terminal collaborative vehicular networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2376–2386, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3131177`.

Nepomuceno-Chamorro:2015:BTA

[NCMCAR15] Isabel A. Nepomuceno-Chamorro, Alfonso Marquez-Chamorro, and Jesus S. Aguilar-Ruiz. Building transcriptional association networks in cytoscape with RegNetC. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):823–824, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Norkus:2012:AAL

[NFM+12] Mindaugas Norkus, Damien Fay, Mary J. Murphy, Frank Barry, Gearoid OLaighin, and Liam Kilmartin. On the application of active learning and Gaussian processes in postcryopreservation cell membrane integrity experiments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):846–856, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ni:2016:PME

[NGY+16] Xumin Ni, Wei Guo, Kai Yuan, Xiong Yang, Zhiming Ma, Shuhua Xu, and Shihua Zhang. A probabilistic method for estimating the sharing of identity by descent for populations with migration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):281–290, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ni:2022:AES

[NGZ+22] Xinzhe Ni, Bohao Geng, Haoyu Zheng, Jiawei Shi, Gang Hu, and Jianzhao Gao. Accurate estimation of single-cell differ-

entiation potency based on network topology and gene ontology information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6): 3255–3262, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3112951`.

Nguyen:2017:NSC

[NHH+17] Van-Nui Nguyen, Kai-Yao Huang, Chien-Hsun Huang, K. Robert Lai, and Tzong-Yi Lee. A new scheme to characterize and identify protein ubiquitination sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (2):393–403, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Niu:2017:SBA

[NHTD17] Ben Niu, Huali Huang, Lijing Tan, and Qiqi Duan. Symbiosis-based alternative learning multi-swarm particle swarm optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):4–14, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Noman:2007:IGR

[NI07] Nasimul Noman and Hitoshi Iba. Inferring gene regulatory networks using differential evolution with local search heuristics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):634–647, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Najafi:2019:SAM

[NJMF19] Amir Najafi, Sepehr Janghorbani, Seyed Abolfazl Motahari, and Emad Fatemizadeh. Statistical association mapping of population-structured genetic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):638–649, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2786239`.

Nanni:2012:IBV

[NLGG12] Loris Nanni, Alessandra Lumini, Dinesh Gupta, and Aarti Garg. Identifying bacterial virulent proteins by fusing a set of classifiers based on variants of Chou's pseudo amino acid composition and on evolutionary information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):467–475, March 2012. CODEN ITCBCY.

ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2017:BAR

[NLHL17] Thao Thi Phuong Nguyen, Vinh Sy Le, Hai Bich Ho, and Quang Si Le. Building ancestral recombination graphs for whole genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):478–483, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Niu:2018:CSR

[NLW+18] Ben Niu, Jing Liu, Teresa Wu, Xianghua Chu, Zhengxu Wang, and Yanmin Liu. Coevolutionary structure-redesigned-based bacterial foraging optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1865–1876, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nan:2024:MCA

[NLW+24] Fengtao Nan, Shunbao Li, Jiayu Wang, Yahui Tang, Jun Qi, Menghui Zhou, Zhong Zhao, Yun Yang, and Po Yang. A multi-classification accessment framework for reproducible evaluation of multimodal learning in Alzheimer's disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):559–572, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3204619`.

Nguyen:2019:NDL

[NLXS19] Son P. Nguyen, Zhaoyu Li, Dong Xu, and Yi Shang. New deep learning methods for protein loop modeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):596–606, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2784434`.

Newaz:2022:IDA

[NM22] Khalique Newaz and Tijana Milenković. Inference of a dynamic aging-related biological subnetwork via network propagation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):974–988, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3022767`.

Nguyen:2022:GEF

[NNLT22] Tri Minh Nguyen, Thin Nguyen, Thao Minh Le, and Truyen Tran. GEFA:

Early fusion approach in drug-target affinity prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):718–728, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3094217`.

Nounou:2012:FIB

[NNM+12a] Hazem N. Nounou, Mohamed N. Nounou, Nader Meskin, Aniruddha Datta, and Edward R. Dougherty. Fuzzy intervention in biological phenomena. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1819–1825, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nounou:2012:MDB

[NNM+12b] M. N. Nounou, H. N. Nounou, N. Meskin, A. Datta, and E. R. Dougherty. Multiscale denoising of biological data: a comparative analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1539–1545, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2022:GCN

[NNNL22] Tuan Nguyen, Giang T. T. Nguyen, Thin Nguyen, and Duc-Hau Le. Graph convolutional networks for drug response prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):146–154, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3060430`.

Nguyen:2007:RRN

[NNSZ07] C. Thach Nguyen, Nguyen Bao Nguyen, Wing-Kin Sung, and Louxin Zhang. Reconstructing recombination network from sequence data: The small parsimony problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):394–402, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nagda:2024:PHP

[NNW24] Bindi M. Nagda, Van Minh Nguyen, and Ryan T. White. promSEMBLE: Hard pattern mining and ensemble learning for detecting DNA promoter sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1): 208–214, 2024. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3339597`.

Niijima:2009:LLD

[NO09] Satoshi Niijima and Yasushi Okuno. Laplacian linear discriminant analysis approach to unsupervised feature selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):605–614, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2013:KBM

[NP13] Ken D. Nguyen and Yi Pan. A knowledge-based multiple-sequence alignment algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):884–896, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2016:LDA

[NPBD16] An Nguyen, Adam Prugel-Bennett, and Srinandan Dasmahapatra. A low dimensional approximation for competence in *Bacillus Subtilis*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):272–280, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ni:2017:NCH

[NPD+17] Qingjian Ni, Qianqian Pan, Huimin Du, Cen Cao, and Yuqing Zhai. A novel cluster head selection algorithm based on fuzzy clustering and particle swarm optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):76–84, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ng:2007:NGW

[NPK+07] Lydia Ng, Sayan Pathak, Chihchau Kuan, Chris Lau, Hong wei Dong, Andrew Sodt, Chinh Dang, Brian Avants, Paul Yushkevich, James Gee, David Haynor, Ed Lein, Allan Jones, and Mike Hawrylycz. Neuroinformatics for genome-wide 3-D gene expression mapping in the mouse brain. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):382–393, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2023:EBB

[NQNT23] Tri Minh Nguyen, Thomas P. Quinn, Thin Nguyen, and Truyen Tran. Explaining black box drug target prediction through model agnostic counterfactual samples. *IEEE/ACM Transac-*

tions on Computational Biology and Bioinformatics, 20 (2):1020–1029, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3190266`.

Narasimhan:2009:SPG

[NRV09] Sridharakumar Narasimhan, Raghunathan Rengaswamy, and Rajanikanth Vadigepalli. Structural properties of gene regulatory networks: Definitions and connections. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):158–170, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Naik:2022:IER

[NRV22] Musab Naik, Luis Rueda, and Akram Vasighizaker. Identification of enriched regions in ChIP-Seq data via a linear-time multilevel thresholding algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5): 2842–2850, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3104734`.

Nalbantoglu:2019:MAM

[NS19] O. Ufuk Nalbantoglu and Khalid Sayood. MIMOSA: Algorithms for microbial profiling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):2023–2034, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2830324`.

Nishida:2019:EEP

[NSAH19] Shimpei Nishida, Shun Sakuraba, Kiyoshi Asai, and Michiaki Hamada. Estimating energy parameters for RNA secondary structure predictions using both experimental and computational data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1645–1655, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nawab:2017:IBA

[NSC17] Rao Muhammad Adeel Nawab, Mark Stevenson, and Paul Clough. An IR-based approach utilizing query expansion for plagiarism detection in MEDLINE. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):796–804, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nizami:2019:EAS

[NSMH19] Bilal Nizami, Elham Mousavinezhad Sarasia, Mehbub I. K. Momin, and Bahareh Honarparvar. Estrogenic active stilbene derivatives as anticancer agents: a DFT and QSAR study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):560–568, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2779505`.

Nishiyama:2019:RCN

[NSNA19] Yuhei Nishiyama, Aleksandar Shurbevski, Hiroshi Nagamochi, and Tatsuya Akutsu. Resource cut, a new bounding procedure to algorithms for enumerating tree-like chemical graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):77–90, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Noor:2012:IGR

[NSNN12] Amina Noor, Erchin Serpedin, Mohamed Nounou, and Hazem Nounou. Inferring gene regulatory networks via nonlinear state-space models and exploiting sparsity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1203–1211, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2015:EAO

[NSZK15] Thuy-Diem Nguyen, Bertil Schmidt, Zejun Zheng, and Chee-Keong Kwoh. Efficient and accurate OTU clustering with GPU-based sequence alignment and dynamic dendrogram cutting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1060–1073, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Noland:2024:ESP

[NT24] Jonas Kristiansen Nøland and Steinar Thorvaldsen. The exact stochastic process of the haploid multiallelic Wright–Fisher mutation model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):69–83, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3336850`.

Neri:2007:AMA

[NTCO07] Ferrante Neri, Jari Toivanen, Giuseppe Leonardo Cascella, and Yew-Soon Ong. An adaptive multi-

meme algorithm for designing HIV multidrug therapies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):264–278, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2022:EED

[NTL+22] Trinh-Trung-Duong Nguyen, The-Anh Tran, Nguyen-Quoc-Khanh Le, Dinh-Minh Pham, and Yu-Yen Ou. An extensive examination of discovering 5-methylcytosine sites in genome-wide DNA promoters using machine learning based approaches. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):87–94, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3082184`.

Nogueira:2016:BBW

[NTR16] David Nogueira, Pedro Tomas, and Nuno Roma. BowMapCL: Burrows–Wheeler mapping on multiple heterogeneous accelerators. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5):926–938, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nagarajan:2006:CSC

[NU06] Radhakrishnan Nagarajan and Meenakshi Upreti. Correlation statistics for cDNA microarray image analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):232–238, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Nguyen:2022:IMG

[NVL22] Giang T. T. Nguyen, Hoa D. Vu, and Duc-Hau Le. Integrating molecular graph data of drugs and multiple -omic data of cell lines for drug response prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):710–717, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3096960`.

Nguyen:2018:HTN

[NVSH18] Nha Nguyen, An Vo, Haibin Sun, and Heng Huang. Heavy-tailed noise suppression and derivative wavelet scalogram for detecting DNA copy number aberrations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1625–1635, September 2018. CODEN ITCBCY.

ISSN 1545-5963 (print), 1557-9964 (electronic).

Niu:2019:PPI

[NWW19] Yun Niu, Hongmei Wu, and Yuwei Wang. Protein-protein interaction identification using a similarity-constrained graph model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):607–616, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2777448`.

Ni:2020:CDS

[NWZ+20] Peng Ni, Jianxin Wang, Ping Zhong, Yaohang Li, Fang-Xiang Wu, and Yi Pan. Constructing disease similarity networks based on disease module theory. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):906–915, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2817624`.

Nye:2014:ACP

[Nye14] Tom M. W. Nye. An algorithm for constructing principal geodesics in phylogenetic treespace. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):304–315, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ng:2015:FAL

[NYOL15] Yen Kaow Ng, Linzhi Yin, Hirotaka Ono, and Shuai Cheng Li. Finding all longest common segments in protein structures efficiently. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):644–655, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ning:2022:NMI

[NZM22] Qiao Ning, Xiaowei Zhao, and Zhiqiang Ma. A novel method for identification of glutarylation sites combining borderline-SMOTE with Tomek links technique in imbalanced data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2632–2641, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3095482`.

Nguyen:2011:TBU

[NZR11] Minh N. Nguyen, Jacek M. Zurada, and Jagath C. Rajapakse. Toward better understanding of protein secondary structure: Extracting prediction rules.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 8(3): 858–864, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ozgul:2021:CDC

[ÖBT21] Ozan Firat Özgül, Batuhan Bardak, and Mehmet Tan. A convolutional deep clustering framework for gene expression time series. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2198–2207, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2988985`.

Ozsoy:2013:DCA

[OC13] Oyku Eren Ozsoy and Tolga Can. A divide and conquer approach for construction of large-scale signaling networks from PPI and RNAi data using linear programming. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):869–883, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ochs:2014:OAT

[OFC+14] Michael F. Ochs, Jason E. Farrar, Michael Considine, Yingying Wei, Soheil Meshinchi, and Robert J. Arceci. Outlier analysis and top scoring pair for integrated data analysis and biomarker discovery. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):520–532, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Oh:2011:FKD

[OG11] Jung Hun Oh and Jean Gao. Fast kernel discriminant analysis for classification of liver cancer mass spectra. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1522–1534, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Occhipinti:2021:DEM

[OHK+21] Annalisa Occhipinti, Youssef Hamadi, Hillel Kugler, Christoph M. Wintersteiger, Boyan Yordanov, and Claudio Angione. Discovering essential multiple gene effects through large scale optimization: an application to human cancer metabolism. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2339–2352, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2020.2973386.

Oliveira:2021:SPI

[OJF+21] Andre Rodrigues Oliveira, Géraldine Jean, Guillaume Fertin, Klairton Lima Brito, Ulisses Dias, and Zanoni Dias. Sorting permutations by intergenic operations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (6):2080–2093, November/ December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3077418.

Ovaska:2013:GRO

[OLS+13] Kristian Ovaska, Lauri Lyly, Biswajyoti Sahu, Olli A. Janne, and Sampsa Hautaniemi. Genomic region operation kit for flexible processing of deep sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (1):200–206, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Oh:2011:ELA

[OLZ11] Sangyoon Oh, Min Su Lee, and Byoung-Tak Zhang. Ensemble learning with active example selection for imbalanced biomedical data classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):316–325, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ogul:2007:SLP

[OM07] Hasan Ogul and Erkan U. Mumcuoğlu. Subcellular localization prediction with new protein encoding schemes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):227–232, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Omony:2012:EDS

[OMAdG+12] Jimmy Omony, Astrid R. Mach-Aigner, Leo H. de Graaff, Gerrit van Straten, and Anton J. B. van Boxtel. Evaluation of design strategies for time course experiments in genetic networks: Case study of the XlnR regulon in *Aspergillus niger*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1316–1325, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Olman:2009:PCA

[OMWX09] Victor Olman, Fenglou Mao, Hongwei Wu, and Ying Xu. Parallel clustering algorithm for large data sets with applications in bioinformat-

ics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):344–352, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Owen:2011:FAC

[OP11] Megan Owen and J. Scott Provan. A fast algorithm for computing geodesic distances in tree space. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):2–13, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Oakley:2013:PSO

[ORCJ13] Mark T. Oakley, Elizabeth Grace Richardson, Harriet Carr, and Roy L. Johnston. Protein structure optimization with a "Lamarckian" ant colony algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1548–1552, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ozden:2021:DDR

[OSA+21] Furkan Ozden, Metin Can Siper, Necmi Acarsoy, Tugrulcan Elmas, Bryan Marty, Xinjian Qi, and A. Ercument Cicek. DORMAN: Database of Reconstructed MetAbolic Networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1474–1480, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2944905`.

Ogunleye:2020:XMC

[OW20] Adeola Ogunleye and Qing-Guo Wang. XGBoost model for chronic kidney disease diagnosis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2131–2140, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2911071`.

Ou-Yang:2015:DPC

[OYDZ15] Le Ou-Yang, Dao-Qing Dai, and Xiao-Fei Zhang. Detecting protein complexes from signed protein-protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1333–1344, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ogundijo:2021:CIT

[OZWA21] Oyetunji E. Ogundijo, Kaiyi Zhu, Xiaodong Wang, and

Dimitris Anastassiou. Characterizing intra-tumor heterogeneity from somatic mutations without copy-neutral assumption. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2271–2280, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2973635`.

Ozyurt:2012:AIC

[Ozy12] I. Burak Ozyurt. Automatic identification and classification of noun argument structures in biomedical literature. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1639–1648, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paul:2022:NFS

[PA22] Madhusudan Paul and Ashish Anand. A new family of similarity measures for scoring confidence of protein interactions using gene ontology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):19–30, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3083150`.

Ponzoni:2007:IAR

[PAAG07] Ignacio Ponzoni, Francisco Azuaje, Juan Augusto, and David Glass. Inferring adaptive regulation thresholds and association rules from gene expression data through combinatorial optimization learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):624–634, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Palaniappan:2012:HFF

[PAL+12] Sucheendra K. Palaniappan, S. Akshay, Bing Liu, Blaise Genest, and P. S. Thiagarajan. A hybrid factored frontier algorithm for dynamic Bayesian networks with a biopathways application. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1352–1365, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pattengale:2011:UHP

[PAS+11] Nicholas Pattengale, Andre Aberer, Krister Swenson, Alexandros Stamatakis, and Bernard Moret. Uncovering hidden phylogenetic consensus in large data sets. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 8(4):902–911, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pauleve:2018:RQM

[Pau18] Loic Pauleve. Reduction of qualitative models of biological networks for transient dynamics analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1167–1179, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pal:2012:TDR

[PB12a] Ranadip Pal and Sonal Bhattacharya. Transient dynamics of reduced-order models of genetic regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1230–1244, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Phipps:2012:OPN

[PB12b] Paul Phipps and Sergey Bereg. Optimizing phylogenetic networks for circular split systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):535–547, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paul:2019:IAI

[PB19] Sushmita Paul and Dhanajit Brahma. An integrated approach for identification of functionally similar MicroRNAs in colorectal cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (1):183–192, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Parvini:2022:CPD

[PBFB22] Ghazaleh Parvini, Katherine Braught, and David Fernández-Baca. Checking phylogenetics decisiveness in theory and in practice. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3307–3316, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3128381`.

Peters:2011:TSC

[PBhL+11] Tim Peters, David W. Bulger, To ha Loi, Jean Yee Hwa Yang, and David Ma. Two-step cross-entropy feature selection for microarrays — power through complementarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (4):1148–1151, July 2011. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Pirola:2012:EAH

[PBJ12] Yuri Pirola, Paola Bonizzoni, and Tao Jiang. An efficient algorithm for haplotype inference on pedigrees with recombinations and mutations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):12–25, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Petti:2020:CSD

[PBV+20] Manuela Petti, Daniele Bizzarri, Antonella Verrienti, Rosa Falcone, and Lorenzo Farina. Connectivity significance for disease gene prioritization in an expanding universe. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2155–2161, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2938512`.

Pinoli:2022:PDS

[PCCM22] Pietro Pinoli, Gaia Ceddia, Stefano Ceri, and Marco Masseroli. Predicting drug synergism by means of non-negative matrix trifactorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):1956–1967, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3091814`.

Peng:2023:PMD

[PCD+23] Wei Peng, Zicheng Che, Wei Dai, Shoulin Wei, and Wei Lan. Predicting miRNA-disease associations from miRNA-gene-disease heterogeneous network with multi-relational graph convolutional network model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3363–3375, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3187739`.

Pirayre:2018:BCC

[PCDP18] Aurelie Pirayre, Camille Couprie, Laurent Duval, and Jean-Christophe Pesquet. BRANE Clust: Cluster-assisted gene regulatory network inference refinement. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):850–860, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pisanti:2005:BMG

[PCGS05] Nadia Pisanti, Maxime

Crochemore, Roberto Grossi, and Marie-France Sagot. Bases of motifs for generating repeated patterns with wild cards. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(1):40–50, January 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pesantez-Cabrera:2019:EDC

[PCK19] Paola Pesantez-Cabrera and Ananth Kalyanaraman. Efficient detection of communities in biological bipartite networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):258–271, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pan:2022:IPS

[PCL+22] Xiaoyong Pan, Lei Chen, Min Liu, Zhibin Niu, Tao Huang, and Yu-Dong Cai. Identifying protein subcellular locations with embeddings-based node2loc. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):666–675, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3080386.

Peng:2019:CMC

[PCY+19] Shaoliang Peng, Yingbo Cui, Shunyun Yang, Wenhe Su, Xiaoyu Zhang, Tenglilang Zhang, Weiguo Liu, and Xing-Ming Zhao. A CPU–MIC collaborated parallel framework for GROMACS on Tianhe-2 supercomputer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):425–433, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2713362.

pour:2020:OBF

[pD20] Ali Foroughi pour and Lori A. Dalton. Optimal Bayesian filtering for biomarker discovery: Performance and robustness. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):250–263, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2858814.

Ponte-Fernandez:2022:EEM

[PFGDCRM22] Christian Ponte-Fernández, Jorge González-Domínguez, Antonio Carvajal-Rodríguez, and María J. Martín. Evaluation of existing methods for high-order epistasis detection. *IEEE/ACM Trans-*

actions on Computational Biology and Bioinformatics, 19(2):912–926, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3030312`.

Pan:2019:KFP

[PFJ+19] Tony Pan, Patrick Flick, Chirag Jain, Yongchao Liu, and Srinivas Aluru. Kmerind: a flexible parallel library for K-mer indexing of biological sequences on distributed memory systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1117–1131, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pirinen:2006:FCG

[PG06] Matti Pirinen and Dario Gasbarra. Finding consistent gene transmission patterns on large and complex pedigrees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):252–262, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Papadakis:2012:SSD

[PG12] George Papadakis and Electra Gizeli. In silico search of DNA drugs targeting oncogenes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1826–1830, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paszek:2018:EAG

[PG18] Jaroslaw Paszek and Pawel Gorecki. Efficient algorithms for genomic duplication models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1515–1524, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Poirier:2018:DAB

[PGF18] Carl Poirier, Benoit Gosselin, and Paul Fortier. DNA assembly with de Bruijn graphs using an FPGA platform. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (3):1003–1009, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pang:2012:GSU

[PGHT12] Herbert Pang, Stephen L. George, Ken Hui, and Tiejun Tong. Gene selection using iterative feature elimination random forests for survival outcomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1422–1431, September 2012. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pelikan:2010:EPL

[PH10a] Richard Pelikan and Milos Hauskrecht. Efficient peak-labeling algorithms for whole-sample mass spectrometry proteomics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):126–137, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Perkins:2010:TBS

[PH10b] Theodore J. Perkins and Michael T. Hallett. A trade-off between sample complexity and computational complexity in learning Boolean networks from time-series data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (1):118–125, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pham:2023:CBE

[Pha23] Tuan D. Pham. Classification of *Caenorhabditis elegans* locomotion behaviors with eigenfeature-enhanced long short-term memory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):206–216, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3153668`.

Parker:2008:SPT

[PHX+08] Douglass Stott Parker, Ruey-Lung Hsiao, Yi Xing, Alissa M. Resch, and Christopher J. Lee. Solving the problem of trans-genomic query with alignment tables. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):432–447, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paul:2009:PCC

[PI09] Topon Kumar Paul and Hitoshi Iba. Prediction of cancer class with majority voting genetic programming classifier using gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):353–367, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Patra:2018:RAP

[PIPC18] Pranjal Patra, Tatsuo Izawa, and Lourdes Pena-Castillo. REPA: Applying pathway analysis to genome-wide transcription factor binding data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15

(4):1270–1283, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Patton:2014:HPI

[PJN+14] Kristopher L. Patton, David J. John, James L. Norris, Daniel R. Lewis, and Gloria K. Muday. Hierarchical probabilistic interaction modeling for multiple gene expression replicates. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):336–346, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Piovesan:2013:SFP

[PK13] Teresa Piovesan and Steven Kelk. A simple fixed parameter tractable algorithm for computing the hybridization number of two (not necessarily binary) trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):18–25, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pyne:2020:RRT

[PKA20] Saptarshi Pyne, Alok Ranjan Kumar, and Ashish Anand. Rapid reconstruction of time-varying gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):278–291, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2861698`.

Popescu:2006:FMG

[PKM06] Mihail Popescu, James M. Keller, and Joyce A. Mitchell. Fuzzy measures on the gene ontology for gene product similarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):263–274, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paltun:2022:DBD

[PKM22] Betül Güvenç Paltun, Samuel Kaski, and Hiroshi Mamitsuka. DIVERSE: Bayesian Data IntegratiVE learning for precise drug ResponSE prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2197–2207, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3065535`.

Paoletti:2012:INC

[PKRD12] David R. Paoletti, Dan E. Krane, Michael L. Raymer, and Travis E. Doom. Inferring the number of con-

tributors to mixed DNA profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):113–122, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Peng:2017:HNB

[PL17] Chen Peng and Ao Li. A heterogeneous network based method for identifying GBM-related genes by integrating multi-dimensional data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):713–720, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paoletti:2020:DDR

[PLC+20] Nicola Paoletti, Kin Sum Liu, Hongkai Chen, Scott A. Smolka, and Shan Lin. Data-driven robust control for a closed-loop artificial pancreas. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1981–1993, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2912609`.

Peng:2017:PPF

[PLCW17] Wei Peng, Min Li, Lu Chen, and Lusheng Wang. Predicting protein functions by using unbalanced random walk algorithm on three biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):360–369, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Peng:2023:MVF

[PLD+23] Wei Peng, Ming Liu, Wei Dai, Tielin Chen, Yu Fu, and Yi Pan. Multi-view feature aggregation for predicting microbe-disease association. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2748–2758, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3132611`.

Passerini:2012:PMB

[PLF12] Andrea Passerini, Marco Lippi, and Paolo Frasconi. Predicting metal-binding sites from protein sequence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):203–213, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Park:2022:NAD

[PLH22] Byungkyu Park, Wook Lee, and Kyungsook Han. A

new approach to deriving prognostic gene pairs from cancer patient-specific gene correlation networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1267–1276, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3017209`.

Paoletti:2012:MCM

[PLMV12] Nicola Paoletti, Pietro Lio, Emanuela Merelli, and Marco Viceconti. Multilevel computational modeling and quantitative analysis of bone remodeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1366–1378, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pu:2022:DDT

[PLTG22] Yuqian Pu, Jiawei Li, Jijun Tang, and Fei Guo. DeepFusionDTA: Drug-target binding affinity prediction with information fusion and hybrid deep-learning ensemble model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2760–2769, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3103966`.

Paul:2020:IRS

[PM20] Sushmita Paul and Madhumita. RFCM^3: Computational method for identification of miRNA–mRNA regulatory modules in cervical cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1729–1740, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2910851`.

Pouyan:2017:ICP

[PN17] Maziyar Baran Pouyan and Mehrdad Nourani. Identifying cell populations in flow cytometry data using phenotypic signatures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):880–891, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pan:2020:FBG

[PNA20] Tony Pan, Rahul Nihalani, and Srinivas Aluru. Fast de Bruijn graph compaction in distributed memory environments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):136–148, January 2020. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2858797`.

Pesonen:2018:CPN

[PNP+18] Maiju Pesonen, Jaakko Nevalainen, Steven Potter, Somnath Datta, and Susmita Datta. A combined PLS and negative binomial regression model for inferring association networks from next-generation sequencing count data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):760–773, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pouryahya:2022:ANI

[POJ+22] Maryam Pouryahya, Jung Hun Oh, Pedram Javanmard, James C. Mathews, Zehor Belkhatir, Joseph O. Deasy, and Allen R. Tannenbaum. aWCluster: a novel integrative network-based clustering of multiomics for subtype analysis of cancer data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (3):1472–1483, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3039511`.

Poleksic:2011:OWU

[Pol11] Aleksandar Poleksic. Optimizing a widely used protein structure alignment measure in expected polynomial time. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1716–1720, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Poleksic:2012:CPS

[Pol12] Aleksandar Poleksic. On complexity of protein structure alignment problem under distance constraint. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):511–516, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Poleksic:2013:IAM

[Pol13] Aleksandar Poleksic. Improved algorithms for matching r-separated sets with applications to protein structure alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):226–229, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pizzi:2018:EAS

[POS+18] Cinzia Pizzi, Mattia Ornamenti, Simone Spangaro,

Simona E. Rombo, and Laxmi Parida. Efficient algorithms for sequence analysis with entropic profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):117–128, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pichene:2020:MVP

[PPFG20] Matthieu Pichené, Sucheendra K. Palaniappan, Eric Fabre, and Blaise Genest. Modeling variability in populations of cells using approximated multivariate distributions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1691–1702, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2904276`.

Panja:2013:CLC

[PPM+13] Surajit Panja, Sourav Patra, Anirban Mukherjee, Madhumita Basu, Sanghamitra Sengupta, and Pranab K. Dutta. A closed-loop control scheme for steering steady states of glycolysis and glycogenolysis pathway. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):858–868, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Piraveenan:2012:AMD

[PPZ12] Mahendra Piraveenan, Mikhail Prokopenko, and Albert Zomaya. Assortative mixing in directed biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):66–78, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pizzuti:2012:CAM

[PR12] Clara Pizzuti and Simona E. Rombo. A coclustering approach for mining large protein-protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):717–730, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pandey:2014:GES

[PR14] Gaurav Pandey and Huzefa Rangwala. Guest editorial for special section on BIOKDD2013. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):773–774, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pease:2018:EDU

[PR18] James B. Pease and Benjamin K. Rosenzweig. Encoding data using biological principles: The multisample variant format for phylogenomics and population genomics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1231–1238, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Preparata:2004:SHR

[Pre04] Franco P. Preparata. Sequencing-by-hybridization revisited: The analog-spectrum proposal. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):46–52, January 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pal:2021:IDR

[PRP21] Jayanta Kumar Pal, Shubhra Sankar Ray, and Sankar K. Pal. Identifying drug resistant miRNAs using entropy based ranking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):973–984, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2933205`.

Pizzi:2011:FSM

[PRU11] Cinzia Pizzi, Pasi Rastas, and Esko Ukkonen. Finding significant matches of position weight matrices in linear time. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):69–79, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Prabhakaran:2014:HHI

[PRZ+14] Sandhya Prabhakaran, Mélanie Rey, Osvaldo Zagordi, Niko Beerenwinkel, and Volker Roth. HIV haplotype inference using a propagating Dirichlet process mixture model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):182–191, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Peng:2011:MSA

[PS11] Qian Peng and Andrew D. Smith. Multiple sequence assembly from reads alignable to a common reference genome. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1283–1295, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Priyadarshana:2015:MBP

[PS15] W. J. R. M. Priyadarshana and Georgy Sofronov. Multiple break-points detection in array CGH data via the cross-entropy method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):487–498, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paul:2019:IDE

[PS19] Amit Paul and Jaya Sil. Identification of differentially expressed genes to establish new biomarker for cancer prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1970–1985, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2837095`.

Pathak:2021:DBC

[PSA21] Yadunath Pathak, Piyush Kumar Shukla, and K. V. Arya. Deep bidirectional classification model for COVID-19 disease infected patients. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1234–1241, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3009859`.

Pons:2020:GLL

[PSC20] Joan Carles Pons, Celine Scornavacca, and Gabriel Cardona. Generation of level-k k LGT networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):158–164, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2019.2895344`.

Park:2017:NAP

[PSIM17] Heewon Park, Yuichi Shiraishi, Seiya Imoto, and Satoru Miyano. A novel adaptive penalized logistic regression for uncovering biomarker associated with anti-cancer drug sensitivity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):771–782, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pang:2015:IAS

[PSK+15] Bin Pang, David Schlessman, Xingyan Kuang, Nan Zhao, Daniel Shyu, Dmitry Korkin, and Chi-Ren Shyu. An integrated approach to sequence-independent local alignment of protein binding sites. *IEEE/ACM Transactions on Computational Bi-*

ology and Bioinformatics, 12 (2):298–308, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pavelka:2016:CAA

[PSK+16] Antonin Pavelka, Eva Sebestova, Barbora Kozlikova, Jan Brezovsky, Jiri Sochor, and Jiri Damborsky. CAVER: algorithms for analyzing dynamics of tunnels in macromolecules. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):505–517, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pradeep:2015:NSB

[PSN+15] Prachi Pradeep, Craig Struble, Terrence Neumann, Daniel S. Sem, and Stephen J. Merrill. A novel scoring based distributed protein docking application to improve enrichment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1464–1469, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Paul:2020:EAT

[PSPM20] Soumya Paul, Cui Su, Jun Pang, and Andrzej Mizera. An efficient approach towards the source-target control of Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 1932–1945, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2915081`.

Park:2009:NBI

[PSS09] Yongjin Park, Stanley Shackney, and Russell Schwartz. Network-based inference of cancer progression from microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):200–212, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Prakash:2009:ADM

[PT09] Amol Prakash and Martin Tompa. Assessing the discordance of multiple sequence alignments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):542–551, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Peng:2018:JTL

[PTH+18] Xin Peng, Yang Tang, Wangli He, Wenli Du, and Feng Qian. A just-in-time learning based monitoring and classification method for hyper/hypocalcemia diagnosis. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 15(3):788–801, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Patoary:2019:PSD

[PTM+19] Mohammad Nazrul Ishlam Patoary, Carl Tropper, Robert A. McDougal, Zhongwei Lin, and William W. Lytton. Parallel stochastic discrete event simulation of calcium dynamics in neuron. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):1007–1019, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Puljiz:2016:DGV

[PV16] Zrinka Puljiz and Haris Vikalo. Decoding genetic variations: communications-inspired haplotype assembly. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):518–530, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pirola:2012:FPA

[PVB+12] Yuri Pirola, Gianluca Della Vedova, Stefano Biffani, Alessandra Stella, and Paola Bonizzoni. A fast and practical approach to genotype phasing and imputation on a pedigree with erroneous and incomplete information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1582–1594, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pathak:2020:PSR

[PvRV+20] Shreyasi Pathak, Jorit van Rossen, Onno Vijlbrief, Jeroen Geerdink, Christin Seifert, and Maurice van Keulen. Post-structuring radiology reports of breast cancer patients for clinical quality assurance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1883–1894, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2914678`.

Pattabiraman:2021:PHM

[PW21] Srilakshmi Pattabiraman and Tandy Warnow. Profile hidden Markov models are not identifiable. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):162–172, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2933821`.

Peng:2015:UAI

[PWC+15] Wei Peng, Jianxin Wang, Yingjiao Cheng, Yu Lu, Fangxiang Wu, and Yi Pan. UDoNC: an algorithm for identifying essential proteins based on protein domains and protein–protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):276–288, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Pehkonen:2010:HBS

[PWT10] Petri Pehkonen, Garry Wong, and Petri Toronen. Heuristic Bayesian segmentation for discovery of coexpressed genes within genomic regions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):37–49, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Peng:2021:PMM

[PWY+21] Cheng Peng, Xinyu Wu, Wen Yuan, Xinran Zhang, Yu Zhang, and Ying Li. MGRFE: Multilayer recursive feature elimination based on an embedded genetic algorithm for cancer classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):621–632, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2921961`.

Peng:2015:IPC

[PWZW15] Wei Peng, Jianxin Wang, Bihai Zhao, and Lusheng Wang. Identification of protein complexes using weighted PageRank–Nibble algorithm and core-attachment structure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):179–192, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Peng:2021:DPS

[PYL+21] Shaoliang Peng, Yaning Yang, Wei Liu, Fei Li, and Xiangke Liao. Discriminant projection shared dictionary learning for classification of tumors using gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1464–1473, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2950209`.

Peng:2023:AMC

[PZC+23] Xiaoqing Peng, Wenjin Zhang, Wanxin Cui, Bin-

rong Ding, Qingtong Lyu, and Jianxin Wang. ADmeth: a manually curated database for the differential methylation in Alzheimer's disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):843–851, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3178087`.

Peng:2020:CNB

[PZH20] Chen Peng, Yang Zheng, and De-Shuang Huang. Capsule network based modeling of multi-omics data for discovery of breast cancer-related genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1605–1612, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2909905`.

Peng:2020:HSC

[PZS+20] Shaoliang Peng, Xiaoyu Zhang, Wenhe Su, Dong Dong, Yutong Lu, Xiangke Liao, Kai Lu, Canqun Yang, Jie Liu, Weiliang Zhu, and Dongqing Wei. High-scalable collaborated parallel framework for large-scale molecular dynamic simulation on Tianhe-2 supercomputer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):804–816, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2805709`.

Peng:2020:MRA

[PZWC20] Jiajie Peng, Linjiao Zhu, Yadong Wang, and Jin Chen. Mining relationships among multiple entities in biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):769–776, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2904965`.

Quevedo:2012:DLP

[QBPEL12] Jose R. Quevedo, Antonio Bahamonde, Miguel Perez-Enciso, and Oscar Luaces. Disease liability prediction from large scale genotyping data using classifiers with a reject option. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):88–97, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qian:2012:IGR

[QD12] Xiaoning Qian and Edward R. Dougherty. Intervention in gene regulatory

networks via phenotypically constrained control policies based on long-run behavior. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):123–136, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qin:2021:OIR

[QDZ+21] Ruiqi Qin, Lei Duan, Huiru Zheng, Jesse Li-Ling, Kaiwen Song, and Yidan Zhang. An ontology-independent representation learning for similar disease detection based on multi-layer similarity network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):183–193, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2941475`.

Qiu:2014:UHD

[Qiu14] Peng Qiu. Unfold high-dimensional clouds for exhaustive gating of flow cytometry data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1045–1051, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qiao:2018:QDA

[QKÖ18] Shi Qiao, Mehmet Koyutürk, and Meral Z. Özsoyoğlu. Querying of disparate association and interaction data in biomedical applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1052–1065, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qiu:2009:FMK

[QL09] Shibin Qiu and Terran Lane. A framework for multiple kernel support vector regression and its applications to siRNA efficacy prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):190–199, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qi:2016:PEP

[QL16] Yi Qi and Jiawei Luo. Prediction of essential proteins based on local interaction density. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1170–1182, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qi:2010:SGR

[QLLX10] Xingqin Qi, Guojun Li, Shuguang Li, and Ying Xu. Sorting genomes by reciprocal translocations, insertions, and deletions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):365–374, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qin:2016:IDA

[QLZ16] Gui-Min Qin, Rui-Yi Li, and Xing-Ming Zhao. Identifying disease associated miRNAs based on protein domains. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1027–1035, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qian:2022:PSC

[QLZZ22] Ying Qian, Xuelian Li, Qian Zhang, and Jiongmin Zhang. SPP-CPI: Predicting compound–protein interactions based on neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):40–47, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3084397`.

Qiu:2021:PAR

[QQD+21] Jingxuan Qiu, Tianyi Qiu, Qingli Dong, Dongpo Xu, Xiang Wang, Qi Zhang, Jing Pan, and Qing Liu. Predicting the antigenic relationship of foot-and-mouth disease virus for vaccine selection through a computational model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):677–685, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2923396`.

Qayyum:2023:HDE

[QRT+23] Abdul Qayyum, Imran Razzak, M. Tanveer, Moona Mazher, and Bandar Alhaqbani. High-density electroencephalography and speech signal based deep framework for clinical depression diagnosis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2587–2597, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3257175`.

Qingge:2020:AOS

[QSJ+20] Letu Qingge, Killian Smith, Sean Jungst, Baihui Wang, Qing Yang, and Binhai Zhu. Approaching the one-sided exemplar adjacency num-

ber problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1946–1954, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2913834`.

Qiu:2015:IMA

[QTZ15] Yu-Qing Qiu, Xue Tian, and Shihua Zhang. Infer metagenomic abundance and reveal homologous genomes based on the structure of taxonomy tree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1112–1122, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qi:2017:SCM

[QV17] Zhen Qi and Eberhard O. Voit. Strategies for comparing metabolic profiles: Implications for the inference of biochemical mechanisms from metabolomics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6): 1434–1445, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qu:2016:PSL

[QWC+16] Xumi Qu, Dong Wang, Yuehui Chen, Shanping Qiao, and Qing Zhao. Predicting the subcellular localization of proteins with multiple sites based on multiple features fusion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):36–42, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Qureshi:2023:CMA

[QZA+23] Rizwan Qureshi, Bin Zou, Tanvir Alam, Jia Wu, Victor H. F. Lee, and Hong Yan. Computational methods for the analysis and prediction of EGFR-mutated lung cancer drug resistance: Recent advances in drug design, challenges and future prospects. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):238–255, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3141697`.

Qiu:2022:CRC

[QZD+22] Yang Qiu, Yang Zhang, Yifan Deng, Shichao Liu, and Wen Zhang. A comprehensive review of computational methods for drug-drug interaction detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):1968–1985, July 2022. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3081268.

Qian:2023:PCM

[QZJ+23] Yurong Qian, Jingjing Zheng, Ying Jiang, Shaoqiu Li, and Lei Deng. Prediction of circRNA-MiRNA association using singular value decomposition and graph neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6): 3461–3468, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3222777.

Qin:2022:ADP

[QZL+22] Xinyi Qin, Lu Zhang, Min Liu, Ziwei Xu, and Guangzhong Liu. ASFold-DNN: Protein fold recognition based on evolutionary features with variable parameters using full connected neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5): 2712–2722, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3089168.

Qian:2021:TUM

[QZZ+21a] Pengjiang Qian, Jiamin Zheng, Qiankun Zheng, Yuan Liu, Tingyu Wang, Rose Al Helo, Atallah Baydoun, Norbert Avril, Rodney J. Ellis, Harry Friel, Melanie S. Traughber, Ajit Devaraj, Bryan Traughber, and Raymond F. Muzic. Transforming UTE-mDixon MR abdomen–pelvis images into CT by jointly leveraging prior knowledge and partial supervision. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):70–82, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2020.2979841.

Qian:2021:AFS

[QZZ21b] Ying Qian, Yu Zhang, and Jiongmin Zhang. Alignment-free sequence comparison with multiple k values. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1841–1849, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2955081.

Roy:2016:DMB

[RA16] Indranil Roy and Srinivas Aluru. Discovering motifs in biological sequences using the Micron automata proces-

sor. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13 (1):99–111, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rajasekaran:2010:IAP

[RAA10] Sanguthevar Rajasekaran, Sahar Al Seesi, and Reda A. Ammar. Improved algorithms for parsing ESLT-AGs: a grammatical model suitable for RNA pseudoknots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (4):619–627, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Raza:2020:SPF

[RAA20] Saad Raza, Ghulam Abbas, and Syed Sikander Azam. Screening pipeline for flavivirus based inhibitors for Zika virus NS1. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1751–1761, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2911081`.

Ritz:2017:PAS

[RAM17] Anna Ritz, Brendan Avent, and T. M. Murali. Pathway analysis with signaling hypergraphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1042–1055, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rizvi:2014:DRO

[RB14] Ahsan Z. Rizvi and C. Bhattacharya. Detection of replication origin sites in herpesvirus genomes by clustering and scoring of palindromes with quadratic entropy measures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1108–1118, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ray:2016:DCS

[RB16] Sumanta Ray and Sanghamitra Bandyopadhyay. Discovering condition specific topological pattern changes in coexpression network: an application to HIV-1 progression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1086–1099, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rampogu:2019:INS

[RBB+19] Shailima Rampogu, Ay-

oung Baek, Rohit Bavi, Minky Son, Guang Ping Cao, Raj Kumar, Chanin Park, Amir Zeb, Rabia Mukthar Rana, Seok Ju Park, and Keun Woo Lee. Identification of novel scaffolds with dual role as antiepileptic and anti-breast cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1663–1674, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ropers:2011:MRU

[RBdJ11] Delphine Ropers, Valentina Baldazzi, and Hidde de Jong. Model reduction using piecewise-linear approximations preserves dynamic properties of the carbon starvation response in *Escherichia coli*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):166–181, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rivera-Borroto:2016:RAM

[RBdlVMPG16] Oscar Miguel Rivera-Borroto, Jose Manuel Garcia de la Vega, Yovani Marrero-Ponce, and Ricardo Grau. Relational agreement measures for similarity searching of cheminformatic data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13 (1):158–167, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ram:2011:MBB

[RC11] Ramesh Ram and Madhu Chetty. A Markov-Blanket-based model for gene regulatory network inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):353–367, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rasheed:2019:SFU

[RCBB19] Muhibur Rasheed, Nathan Clement, Abhishek Bhowmick, and Chandrajit L. Bajaj. Statistical framework for uncertainty quantification in computational molecular modeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1154–1167, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rizzi:2019:HCA

[RCM+19] Romeo Rizzi, Massimo Cairo, Veli Makinen, Alexandru I. Tomescu, and Daniel Valenzuela. Hardness of covering alignment: Phase transition in post-sequence genomics. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 16(1):23–30, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Raisaro:2018:PPS

[RCP+18] Jean Louis Raisaro, Gwangbae Choi, Sylvain Pradervand, Raphael Colsenet, Nathalie Jacquemont, Nicolas Rosat, Vincent Mooser, and Jean-Pierre Hubaux. Protecting privacy and security of genomic data in i2b2 with homomorphic encryption and differential privacy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1413–1426, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rasmussen:2009:MVU

[RdlCGW09] Carl Rasmussen, Bernard de la Cruz, Zoubin Ghahramani, and David Wild. Modeling and visualizing uncertainty in gene expression clusters using Dirichlet process mixtures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):615–628, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Requeno:2013:TLP

[RdMCBC13] Jose Ignacio Requeno, Gregorio de Miguel Casado, Roberto Blanco, and Jose Manuel Colom. Temporal logics for phylogenetic analysis via model checking. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1058–1070, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Riesen:2020:AGE

[RFB20] Kaspar Riesen, Miquel Ferrer, and Horst Bunke. Approximate graph edit distance in quadratic time. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):483–494, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2015.2478463`.

Ranjan:2022:ETI

[RFBTD22] Ashish Ranjan, David Fernández-Baca, Sudhakar Tripathi, and Akshay Deepak. An ensemble Tf-Idf based approach to protein function prediction via sequence segmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2685–2696, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3093060`.

Ranjan:2020:DRF

[RFFB+20] Ashish Ranjan, Md Shah Fahad, David Fernández-Baca, Akshay Deepak, and Sudhakar Tripathi. Deep robust framework for protein function prediction using variable-length protein sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1648–1659, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2911609`.

Raposo:2016:CAM

[RG16] Adriano N. Raposo and Abel J. P. Gomes. Computational 3D assembling methods for DNA: a survey. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1068–1085, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Raghu:2021:PIT

[RGB+21] Vineet K. Raghu, Xiaoyu Ge, Arun Balajiee, Daniel J. Shirer, Isha Das, Panayiotis V. Benos, and Panos K. Chrysanthis. A pipeline for integrated theory and data-driven modeling of biomedical data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):811–822, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3019237`.

Rogers:2005:LPD

[RGCB05] Simon Rogers, Mark Girolami, Colin Campbell, and Rainer Breitling. The latent process decomposition of cDNA microarray data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):143–156, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rajabli:2013:ADS

[RGI13] Farid Rajabli, Unal Goktas, and Gul Inan. Application of Dempster–Schafer method in family-based association studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1071–1075, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Roytberg:2009:SSP

[RGN+09] Mikhail Roytberg, Anna Gambin, Laurent Noe, Slawomir Lasota, Eugenia Furletova, Ewa Szczurek, and Gregory Kucherov. On subset seeds for protein alignment. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 6(3):483–494, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rossi:2024:IMC

[RGVP24] Nicolò Rossi, Nicola Gigante, Nicola Vitacolonna, and Carla Piazza. Inferring Markov chains to describe convergent tumor evolution with CIMICE. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):106–119, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3337258`.

Ren:2023:MIS

[RGZ+23] Sheng Ren, Kehua Guo, Xiaokang Zhou, Bin Hu, Feihong Zhu, and Entao Luo. Medical image super-resolution based on semantic perception transfer learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (4):2598–2609, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3212343`.

Rajapakse:2005:MED

[RH05] Jagath C. Rajapakse and Loi Sy Ho. Markov encoding for detecting signals in genomic sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):131–142, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rathore:2013:RSC

[RHAK13] Saima Rathore, Mutawarra Hussain, Ahmad Ali, and Asifullah Khan. A recent survey on colon cancer detection techniques. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):545–563, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ren:2016:FRA

[RHH16] Hai-Peng Ren, Xiao-Na Huang, and Jia-Xuan Hao. Finding robust adaptation gene regulatory networks using multi-objective genetic algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):571–577, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rathore:2014:GGE

[RHK14] Saima Rathore, Mutawarra Hussain, and Asifullah Khan. GECC: gene expression based ensemble classification of colon samples. *IEEE/ACM Transactions*

on Computational Biology and Bioinformatics, 11(6): 1131–1145, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rhodes:2020:TMT

[Rho20] John A. Rhodes. Topological metrizations of trees, and new quartet methods of tree inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2107–2118, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2917204`.

Rehman:2024:DLT

[RHZ+24] Amjad Rehman, Majid Harouni, Farzaneh Zogh, Tanzila Saba, Mohsen Karimi, Faten S. Alamri, and Gwanggil Jeon. Detection of lungs tumors in CT scan images using convolutional neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):769–777, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3315303`.

Rydzewski:2018:CSB

[RJNN18] Jakub Rydzewski, Rafal Jakubowski, Giuseppe Nicosia, and Wieslaw Nowak. Conformational sampling of a biomolecular rugged energy landscape. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):732–739, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Raiford:2010:AIT

[RKDR10] Douglas W. Raiford, Dan E. Krane, Travis E. Doom, and Michael L. Raymer. Automated isolation of translational efficiency bias that resists the confounding effect of GC(AT)-content. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):238–250, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Raiford:2011:GOA

[RKDR11] Douglas W. Raiford, Dan E. Krane, Travis E. Doom, and Michael L. Raymer. A genetic optimization approach for isolating translational efficiency bias. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):342–352, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ray:2016:IAC

[RKZ16] Meredith Ray, Jian Kang,

and Hongmei Zhang. Identifying activation centers with spatial Cox point processes using fMRI data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6): 1130–1141, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rahman:2020:PPM

[RLR20] Mohammad Arifur Rahman, Nathan LaPierre, and Huzefa Rangwala. Phenotype prediction from metagenomic data using clustering and assembly with multiple instance learning (CAMIL). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):828–840, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2017.2758782`.

Ramalho:2018:PEF

[RLRH18] Rodrigo F. Ramalho, Sujun Li, Predrag Radivojac, and Matthew W. Hahn. Proteomic evidence for in-frame and out-of-frame alternatively spliced isoforms in human and mouse. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1284–1289, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Romashchenko:2023:CPM

[RLRP23] Nikolai Romashchenko, Benjamin Linard, Eric Rivals, and Fabio Pardi. Computing phylo-k-mers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5): 2889–2897, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3278049`.

Raphael:2004:UPM

[RLV04] Benjamin Raphael, Lung-Tien Liu, and George Varghese. A uniform projection method for motif discovery in DNA sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(2):91–94, April 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rajapakse:2013:MGS

[RM13] Jagath C. Rajapakse and Piyushkumar A. Mundra. Multiclass gene selection using Pareto-fronts. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):87–97, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ray:2018:DPM

[RM18] Sumanta Ray and Ujjwal Maulik. Discovering perturbation of modular structure in HIV progression by integrating multiple data sources through non-negative matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):869–877, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rubiolo:2015:MGR

[RMS15] Mariano Rubiolo, Diego H. Milone, and Georgina Stegmayer. Mining gene regulatory networks by neural modeling of expression time-series. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1365–1373, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Re:2012:FRA

[RMV12] Matteo Re, Marco Mesiti, and Giorgio Valentini. A fast ranking algorithm for predicting gene functions in biomolecular networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1812–1818, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Razzak:2024:CME

[RNAR+24] Imran Razzak, Saeeda Naz, Hamid Alinejad-Rokny, Tu N. Nguyen, and Fahmi Khalifa. A cascaded multiresolution ensemble deep learning framework for large scale Alzheimer's disease detection using brain MRIs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):573–581, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3219032`.

Roch:2006:SPP

[Roc06] Sebastien Roch. A short proof that phylogenetic tree reconstruction by maximum likelihood is hard. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):92–94, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rocha:2011:GCL

[Roc11] J. Rocha. Graph comparison by log-odds score matrices with application to protein topology analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (2):564–569, March 2011. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Rosenberg:2013:CHC

[Ros13] Noah A. Rosenberg. Coalescent histories for caterpillar-like families. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1253–1262, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ray:2013:RSS

[RP13] Shubhra Sankar Ray and Sankar K. Pal. RNA secondary structure prediction using soft computing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):2–17, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rahman:2013:REM

[RPB+13] Ahsanur Rahman, Christopher L. Poirel, David J. Badger, Craig Estep, and T. M. Murali. Reverse engineering molecular hypergraphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5): 1113–1124, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Russo:2018:CPN

[RPBP18] Giulia Russo, Marzio Pennisi, Roberta Boscarino, and Francesco Pappalardo. Continuous Petri nets and microRNA analysis in melanoma. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1492–1499, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ragi:2023:AID

[RRD+23] Shankarachary Ragi, Md Hafizur Rahman, Jamison Duckworth, Kalimuthu Jawaharraj, Parvathi Chundi, and Venkataramana Gadhamshetty. Artificial intelligence-driven image analysis of bacterial cells and biofilms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1): 174–184, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3138304`.

Rottger:2012:HLD

[RRTB12] Richard Rottger, Ulrich Ruckert, Jan Taubert, and Jan Baumbach. How little do we actually know? On the size of gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1293–1300,

September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ren:2018:IAS

[RSCX18] Shuai Ren, Yan Shi, Maolin Cai, and Weiqing Xu. Influence of airway secretion on airflow dynamics of mechanical ventilated respiratory system. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1660–1668, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Roth:2018:TES

[RSG18] Adam Roth, Sandeep Subramanian, and Madhavi K. Ganapathiraju. Towards extracting supporting information about predicted protein-protein interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1239–1246, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rud:2013:RFL

[RSJK13] Ali Gholami Rud, Saeed Shahrivari, Saeed Jalili, and Zahra Razaghi Moghadam Kashani. RANGI: a fast list-colored graph motif finding algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):504–513, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rinaldi:2010:OBI

[RSK+10] Fabio Rinaldi, Gerold Schneider, Kaarel Kaljurand, Simon Clematide, Thérèse Vachon, and Martin Romacker. OntoGene in BioCreative II.5. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):472–480, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rashid:2023:ESP

[RSK23] Shamima Rashid, Suresh Sundaram, and Chee Keong Kwoh. Empirical study of protein feature representation on deep belief networks trained with small data for secondary structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):955–966, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3168676`.

Rother:2008:SCP

[RSP08] Diego Rother, Guillermo Sapiro, and Vijay Pande. Statistical characterization

of protein ensembles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):42–55, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Randhawa:2010:MCM

[RST10] Ranjit Randhawa, Cliff Shaffer, and John Tyson. Model composition for macromolecular regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):278–287, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ren:2022:PDM

[RSV+22] Yuanfang Ren, Aisharjya Sarkar, Pierangelo Veltri, Ahmet Ay, Alin Dobra, and Tamer Kahveci. Pattern discovery in multilayer networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):741–752, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3105001`.

Ranganarayanan:2016:IGB

[RTA+16] Preethi Ranganarayanan, Narmadha Thanigesan, Vivek Ananth, Valadi K. Jayaraman, and Vigneshwar Ramakrishnan. Identification of glucose-binding pockets in human serum albumin using support vector machine and molecular dynamics simulations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13 (1):148–157, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rehman:2023:DMI

[RTC23] Mobeen Ur Rehman, Hilal Tayara, and Kil To Chong. DL-m6A: Identification of N6-Methyladenosine sites in mammals using deep learning based on different encoding schemes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):904–911, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3192572`.

Ranjan:2023:SSB

[RTD23] Ashish Ranjan, Archana Tiwari, and Akshay Deepak. A sub-sequence based approach to protein function prediction via multi-attention based multi-aspect network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):94–105, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (elec-

tronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3130923`.

Raisaro:2019:MES

[RTPM+19] Jean Louis Raisaro, Juan Ramon Troncoso-Pastoriza, Mickael Misbach, Joao Sa Sousa, Sylvain Pradervand, Edoardo Missiaglia, Olivier Michielin, Bryan Ford, and Jean-Pierre Hubaux. MedCo: Enabling secure and privacy-preserving exploration of distributed clinical and genomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1328–1341, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ranjbar:2015:BNM

[RTWR15] Mohammad R. Nezami Ranjbar, Mahlet G. Tadesse, Yue Wang, and Habtom W. Ressom. Bayesian normalization model for label-free quantitative analysis by LC–MS. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):914–927, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rueda:2006:HCA

[RV06] Luis Rueda and Vidya Vidyadharan. A hill-climbing approach for automatic gridding of cDNA microarray images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):72–83, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Re:2013:NBD

[RV13] Matteo Re and Giorgio Valentini. Network-based drug ranking and repositioning with respect to DrugBank therapeutic categories. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1359–1371, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Reinert:2007:LLE

[RW07] Gesine Reinert and Michael S. Waterman. On the length of the longest exact position match in a random sequence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):153–156, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rubel:2010:IDC

[RWH+10] Oliver Rubel, Gunther H. Weber, Min-Yu Huang, E. Wes Bethel, Mark D. Biggin, Charless C. Fowlkes, Cris L. Luengo Hendriks, Soile V. E. Keranen, Michael B.

Eisen, David W. Knowles, Jitendra Malik, Hans Hagen, and Bernd Hamann. Integrating data clustering and visualization for the analysis of 3D gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):64–79, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ravikumar:2023:EIS

[RXAH+23] Visweswaran Ravikumar, Tong Xu, Wajd N. Al-Holou, Salar Fattahi, and Arvind Rao. Efficient inference of spatially-varying Gaussian Markov random fields with applications in gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5): 2920–2932, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3282028`.

Rhee:2019:ILC

[RYK+19] Je-Keun Rhee, Jinseon Yoo, Kyu Ryung Kim, Jeeyoon Kim, Yong-Jae Lee, Byoung Chul Cho, and Tae-Min Kim. Identification of local clusters of mutation hotspots in cancer-related genes and their biological relevance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1656–1662, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rajapakse:2007:GEI

[RZF07] Jagath C. Rajapakse, Yan-Qing Zhang, and Gary B. Fogel. Guest Editors' introduction to the Special Section: Computational Intelligence Approaches in Computational Biology and Bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):161–162, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Rajaraman:2017:ACR

[RZMC17] Ashok Rajaraman, Joao Paulo Pereira Zanetti, Jan Manuch, and Cedric Chauve. Algorithms and complexity results for genome mapping problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):418–430, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Raveh:2015:RFM

[RZMT15] Alon Raveh, Yoram Zarai, Michael Margaliot, and Tamir Tuller. Ribosome flow model on a ring. *IEEE/ACM Transactions on Computa-*

tional Biology and Bioinformatics, 12(6):1429–1439, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Setubal:2015:TSS

[SA15] João C. Setubal and Nalvo Almeida. TCBB special section on the Brazilian Symposium on Bioinformatics 2013. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):499, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sarkar:2020:EAI

[SAE+20] Aisharjya Sarkar, Yilmaz Atay, Alana Lorraine Erickson, Ivan Arisi, Cesare Saltini, and Tamer Kahveci. An efficient algorithm for identifying mutated subnetworks associated with survival in cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1582–1594, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2911069`.

Sagot:2009:EE

[Sag09a] Marie-France Sagot. EIC editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):177, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sagot:2009:EEI

[Sag09b] Marie-France Sagot. EIC editorial: Introducing new Associate Editors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):369, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sagot:2009:NEE

[Sag09c] Marie-France Sagot. New EIC editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):3, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sagot:2010:EE

[Sag10] Marie-France Sagot. EIC editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):193–194, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sagot:2011:EEa

[Sag11a] Marie-France Sagot. EIC editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):1, January 2011.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sagot:2011:EEb

[Sag11b] Marie-France Sagot. EIC editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):289–291, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sagot:2012:EE

[Sag12] Marie-France Sagot. EIC editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1553–1557, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Singh:2021:IBC

[SAK+21] Rishav Singh, Tanveer Ahmed, Abhinav Kumar, Amit Kumar Singh, Anil Kumar Pandey, and Sanjay Kumar Singh. Imbalanced breast cancer classification using transfer learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):83–93, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2980831`.

Sadat:2019:SSG

[SAM+19] Md Nazmus Sadat, Md Momin Al Aziz, Noman Mohammed, Feng Chen, Xiaoqian Jiang, and Shuang Wang. SAFETY: Secure gwAs in Federated Environment through a hYbrid Solution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):93–102, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Siniosoglou:2023:PPF

[SAS+23] Ilias Siniosoglou, Vasileios Argyriou, Panagiotis Sarigiannidis, Thomas Lagkas, Antonios Sarigiannidis, Sotirios K. Goudos, and Shaohua Wan. Post-processing fairness evaluation of federated models: an unsupervised approach in healthcare. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2518–2529, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3269767`.

Sun:2009:DPP

[SB09] Yanni Sun and Jeremy Buhler. Designing patterns and profiles for faster HMM search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):232–243, April 2009.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sengupta:2012:NDP

[SB12] Soumi Sengupta and Sanghamitra Bandyopadhyay. De novo design of potential RecA inhibitors using MultiObjective optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1139–1154, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Stamoulis:2016:OSD

[SB16] Catherine Stamoulis and Rebecca A. Betensky. Optimization of signal decomposition matched filtering (SDMF) for improved detection of copy-number variations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):584–591, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Siqueira:2021:HGR

[SBDD21] Gabriel Siqueira, Klairton Lima Brito, Ulisses Dias, and Zanoni Dias. Heuristics for genome rearrangement distance with replicated genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2094–2108, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3095021`.

Sriwastava:2015:PPP

[SBM15] Brijesh K. Sriwastava, Subhadip Basu, and Ujjwal Maulik. Predicting protein-protein interaction sites with a novel membership based fuzzy SVM classifier. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1394–1404, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Saheed:2023:MGE

[SBOA23] Yakub K. Saheed, Bukola F. Balogun, Braimah Joseph Odunayo, and Mustapha Abdulsalam. Microarray gene expression data classification via Wilcoxon sign rank sum and novel grey wolf optimized ensemble learning models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3575–3587, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3305429`.

Song:2011:MSS

[SBRK11] Bin Song, İ Esra Büyüktahtakin, Sanjay Ranka, and Tamer

Kahveci. Manipulating the steady state of metabolic pathways. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):732–747, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sengupta:2015:CAU

[SBW15] T. Sengupta, M. Bhushan, and P. P. Wangikar. A computational approach using ratio statistics for identifying housekeeping genes from cDNA microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1457–1463, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2012:DFF

[SBY12] Yanni Sun, Jeremy Buhler, and Cheng Yuan. Designing filters for fast-known NcRNA identification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):774–787, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shah:2011:GFA

[SC11] Mohak Shah and Jacques Corbeil. A general framework for analyzing data from two short time-series microarray experiments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):14–26, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Storato:2022:PKD

[SC22a] Davide Storato and Matteo Comin. K2Mem: Discovering discriminative K-mers from sequencing data for metagenomic reads classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):220–229, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3117406`.

Sun:2022:E

[SC22b] Sunny Sun and Yi-Ping Phoebe Chen. Editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):1–2, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3089195`.

Song:2015:PBM

[SCC+15] Dandan Song, Jiaxing Chen, Guang Chen, Ning Li, Jin Li, Jun Fan, Dongbo Bu,

and Shuai Cheng Li. Parameterized BLOSUM matrices for protein alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):686–694, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sotiropoulos:2009:MRM

[SCCDK09] Vassilios Sotiropoulos, Marrie-Nathalie Contou-Carrere, Prodromos Daoutidis, and Yiannis N. Kaznessis. Model reduction of multiscale chemical Langevin equations: a numerical case study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):470–482, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Stella:2019:DDB

[SCM19] Sabrina Stella, Roberto Chignola, and Edoardo Milotti. Dynamical detection of boundaries and cavities in biophysical cell-based simulations of growing tumor tissues. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1901–1911, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2827374`.

Swenson:2012:KMA

[SCPS12] Krister M. Swenson, Eric Chen, Nicholas D. Pattengale, and David Sankoff. The kernel of maximum agreement subtrees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1023–1031, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Schliep:2005:AGE

[SCSS05] Alexander Schliep, Ivan G. Costa, Christine Steinhoff, and Alexander Schonhuth. Analyzing gene expression time-courses. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):179–193, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Solanki:2024:ESV

[SCU+24] Arnav Solanki, James Cornette, Julia Udell, George Vasmatzis, and Marc Riedel. Evasive spike variants elucidate the preservation of T cell immune response to the SARS-CoV-2 omicron variant. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):450–460, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964

(electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3372100`.

Sebastian:2006:STA

[SDA+06] Rafael Sebastian, Maria-Elena Diaz, Guillermo Ayala, Kresimir Letinic, Jose Moncho-Bogani, and Derek Toomre. Spatio-temporal analysis of constitutive exocytosis in epithelial cells. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):17–32, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Seetan:2014:RRH

[SDAA+14] Raed I. Seetan, Anne M. Denton, Omar Al-Azzam, Ajay Kumar, M. Javed Iqbal, and Shahryar F. Kianian. Reliable radiation hybrid maps: an efficient scalable clustering-based approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):788–800, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sridhar:2007:AEN

[SDB+07] Srinath Sridhar, Kedar Dhamdhere, Guy Blelloch, Eran Halperin, R. Ravi, and Russell Schwartz. Algorithms for efficient near-perfect phylogenetic tree reconstruction in theory and practice. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):561–571, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sheng:2011:IAG

[SDCW11] Jinhua Sheng, Hong-Wen Deng, Vince Calhoun, and Yu-Ping Wang. Integrated analysis of gene expression and copy number data on gene shaving using independent component analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1568–1579, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shen:2020:CNP

[SDH20a] Zhen Shen, Su-Ping Deng, and De-Shuang Huang. Capsule network for predicting RNA–protein binding preferences using hybrid feature. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5): 1483–1492, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2943465`.

Shen:2020:RPB

[SDH20b] Zhen Shen, Su-Ping Deng, and De-Shuang Huang.

RNA-Protein binding sites prediction via multi scale convolutional gated recurrent unit networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1741–1750, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2910513`.

Sehgal:2011:IRD

[SDN+11] Aditya Kumar Sehgal, Sanmay Das, Keith Noto, Milton H. Saier, Jr., and Charles Elkan. Identifying relevant data for a biological database: Handcrafted rules versus machine learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 851–857, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sambo:2012:MMO

[SdOD+12] Francesco Sambo, Marco A. Montes de Oca, Barbara Di Camillo, Gianna Toffolo, and Thomas Stutzle. MORE: Mixed optimization for reverse engineering — an application to modeling biological networks response via sparse systems of nonlinear differential equations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1459–1471, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Selvaraj:2021:HTS

[SDP+21] Chandrabose Selvaraj, Dhurvas Chandrasekaran Dinesh, Umesh Panwar, Evzen Boura, and Sanjeev Kumar Singh. High-throughput screening and quantum mechanics for identifying potent inhibitors against Mac1 domain of SARS-CoV-2 Nsp3. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1262–1270, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3037136`.

Sapin:2018:OME

[SDS18] Emmanuel Sapin, Kenneth A. De Jong, and Amarda Shehu. From optimization to mapping: an evolutionary algorithm for protein energy landscapes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):719–731, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2019:EMM

[SDTK19] Mengmeng Sun, Tao Ding, Xu-Qing Tang, and Yu Kem-

ing. An efficient mixed-model for screening differentially expressed genes of breast cancer based on LR–RF. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (1):124–130, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Spencer:2015:DLN

[SEC15] Matt Spencer, Jesse Eickholt, and Jianlin Cheng. A deep learning network approach to ab initio protein secondary structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):103–112, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sefer:2022:BSI

[Sef22] Emre Sefer. BioCode: a data-driven procedure to learn the growth of biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3103–3113, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3165092`.

Senf:2019:EES

[Sen19] Alexander Senf. End-to-end security for local and remote human genetic data applications at the EGA. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1324–1327, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sadot:2008:TVB

[SFB+08] Avital Sadot, Jasmin Fisher, Dan Barak, Yishai Admanit, Michael J. Stern, E. Jane Albert Hubbard, and David Harel. Toward verified biological models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):223–234, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Stock:2014:IFR

[SFH+14] Michiel Stock, Thomas Fober, Eyke Hüllermeier, Serghei Glinca, Gerhard Klebe, Tapio Pahikkala, Antti Airola, Bernard De Baets, and Willem Waegeman. Identification of functionally related enzymes by learning-to-rank methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6): 1157–1169, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sedaghat:2018:CSU

[SFMS18] Nafiseh Sedaghat, Mahmood Fathy, Mohammad Hossein Modarressi, and Ali Shojaie. Combining supervised and unsupervised learning for improved miRNA target prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1594–1604, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Schneider:2007:SDM

[SGC07] Adrian Schneider, Gaston Gonnet, and Gina Cannarozzi. SynPAM—A distance measure based on synonymous codon substitutions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):553–560, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2012:PEU

[SGH12] Jianyong Sun, Jonathan M. Garibaldi, and Charlie Hodgman. Parameter estimation using metaheuristics in systems biology: a comprehensive review. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):185–202, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Schaller:2023:BMG

[SGHS23] David Schaller, Manuela Geiß, Marc Hellmuth, and Peter F. Stadler. Best match graphs with binary trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1679–1690, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3143870`.

Sun:2012:RBC

[SGK12] Jianyong Sun, Jonathan M. Garibaldi, and Kim Kenobi. Robust Bayesian clustering for replicated gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1504–1514, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sokolovsky:2020:DLA

[SGP+20] Michael Sokolovsky, Francisco Guerrero, Sarun Paisarnsrisomsuk, Carolina Ruiz, and Sergio A. Alvarez. Deep learning for automated feature discovery and classification of sleep stages. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):

1835–1845, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2912955`.

Stojanovic:2017:MHQ

[SGR+17] Jelena Stojanovic, Djordje Gligorijevic, Vladan Radosavljevic, Nemanja Djuric, Mihajlo Grbovic, and Zoran Obradovic. Modeling healthcare quality via compact representations of electronic health records. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):545–554, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sabnis:2011:CTD

[SH11a] Amit Sabnis and Robert W. Harrison. A continuous-time, discrete-state method for simulating the dynamics of biochemical systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):335–341, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shibberu:2011:SAP

[SH11b] Yosi Shibberu and Allen Holder. A spectral approach to protein structure alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):867–875, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sheng:2023:SCM

[SHG+23] Nan Sheng, Lan Huang, Ling Gao, Yangkun Cao, Xuping Xie, and Yan Wang. A survey of computational methods and databases for lncRNA-MiRNA interaction prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2810–2826, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3264254`.

Sharan:2006:ITP

[SHI06] Roded Sharan, Bjarni V. Halldorsson, and Sorin Istrail. Islands of tractability for parsimony haplotyping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):303–311, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shibuya:2010:FHD

[Shi10] Tetsuo Shibuya. Fast hinge detection algorithms for flexible protein structures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

7(2):333–341, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Smalter:2010:GGP

[SHJL10] Aaron Smalter, Jun Huan, Yi Jia, and Gerald Lushington. GPD: a graph pattern diffusion kernel for accurate graph classification with applications in cheminformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):197–207, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Saeed:2014:CRC

[SHK14] Fahad Saeed, Jason D. Hoffert, and Mark A. Knepper. CAMS–RS: clustering algorithm for large-scale mass spectrometry data using restricted search space and intelligent random sampling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1):128–141, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Siederdissen:2015:PGA

[SHS15] Christian Höner Zu Siederdissen, Ivo L. Hofacker, and Peter F. Stadler. Product grammars for alignment and folding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):507–519, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Siragusa:2019:LTA

[SHUP19] Enrico Siragusa, Niina Haiminen, Filippo Utro, and Laxmi Parida. Linear time algorithms to construct populations fitting multiple constraint distributions at genomic scales. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1132–1142, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Som-In:2020:EPS

[SIK20] Sarawoot Som-In and Warangkhana Kimpan. Enhancing of particle swarm optimization based method for multiple motifs detection in DNA sequences collections. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):990–998, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2872978`.

Sharma:2012:TRF

[SIM12] Alok Sharma, Seiya Imoto, and Satoru Miyano. A top-r feature selection algorithm for microarray gene

expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):754–764, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sudo:2019:SWM

[SJNS19] Hiroki Sudo, Masanobu Jimbo, Koji Nuida, and Kana Shimizu. Secure wavelet matrix: Alphabet-friendly privacy-preserving string search for bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1675–1684, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sharifi:2019:ARC

[SJS19] Maryam Sharifi, Arta A. Jamshidi, and Nazanin Namazi Sarvestani. An adaptive robust control strategy in a cancer tumor-immune system under uncertainties. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):865–873, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2023:HPS

[SJWW23] Junwei Sun, Haoping Ji, Yingcong Wang, and Yanfeng Wang. Hybrid projective synchronization via PI controller based on DNA Strand displacement. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1081–1091, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3190397`.

Shen:2019:MSS

[SJZ19] Bairong Shen, Xiaoqian Jiang, and Xingming Zhao. Modeling and simulation studies of complex biological systems for precision medicine and healthcare. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):91–92, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Schliep:2008:EAC

[SK08] Alexander Schliep and Roland Krause. Efficient algorithms for the computational design of optimal tiling arrays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5 (4):557–567, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Steinbiss:2012:NED

[SK12] Sascha Steinbiss and Stefan Kurtz. A new efficient data

structure for storage and retrieval of multiple biosequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):345–357, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shao:2019:THM

[SK19] Mingfu Shao and Carl Kingsford. Theory and a heuristic for the minimum path flow decomposition problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):658–670, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2779509`.

Sadeghi:2021:ARC

[SK21] Seyedeh Shaghayegh Sadeghi and Mohammad Reza Keyvanpour. An analytical review of computational drug repurposing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):472–488, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2933825`.

Sjahputera:2007:RAC

[SKD+07] Ozy Sjahputera, James M. Keller, J. Wade Davis, Kristen H. Taylor, Farahnaz Rahmatpanah, Huidong Shi, Derek T. Anderson, Samuel N. Blisard, Robert H. Luke, Mihail Popescu, Gerald C. Arthur, and Charles W. Caldwell. Relational analysis of CpG islands methylation and gene expression in human lymphomas using possibilistic C-means clustering and modified cluster fuzzy density. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):176–189, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Saha:2019:DFM

[SKDA19] Tanay Kumar Saha, Ataur Katebi, Wajdi Dhifli, and Mohammad Al Hasan. Discovery of functional motifs from the interface region of oligomeric proteins using frequent subgraph mining. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1537–1549, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Suvorova:2014:SPC

[SKK14] Yulia M. Suvorova, Maria A. Korotkova, and Eugene V. Korotkov. Study of the paired change points in bacterial genes. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 11(5):955–964, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sergeev:2019:GWA

[SKS+19] Roman Sergeevich Sergeev, Ivan S. Kavaliou, Uladzislau V. Sataneuski, Andrei Gabrielian, Alex Rosenthal, Michael Tartakovsky, and Alexander V. Tuzikov. Genome-wide analysis of MDR and XDR tuberculosis from Belarus: Machine-learning approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1398–1408, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sanyal:2022:CTC

[SKS22] Ritabrata Sanyal, Devroop Kar, and Ram Sarkar. Carcinoma type classification from high-resolution breast microscopy images using a hybrid ensemble of deep convolutional features and gradient boosting trees classifiers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):2124–2136, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3071022`.

Sridhar:2008:MIL

[SLB+08] Srinath Sridhar, Fumei Lam, Guy E. Blelloch, R. Ravi, and Russell Schwartz. Mixed integer linear programming for maximum-parsimony phylogeny inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):323–331, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Su:2022:DRL

[SLCL22] Yu-Ting Su, Yao Lu, Mei Chen, and An-An Liu. Deep reinforcement learning-based progressive sequence saliency discovery network for mitosis detection in time-lapse phase-contrast microscopy images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):854–865, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3019042`.

Sang:2022:SEB

[SLCZ22] Shengtian Sang, Xiaoxia Liu, Xiaoyu Chen, and Di Zhao. A scalable embedding based neural network method for discovering knowledge from biomedical literature. *IEEE/ACM Transactions on*

Computational Biology and Bioinformatics, 19(3):1294–1301, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3003947`.

Savel:2017:PEL

[SLGK17] Daniel Savel, Thomas LaFramboise, Ananth Grama, and Mehmet Koyuturk. Pluribus — exploring the limits of error correction using a suffix tree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1378–1388, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2006:EPA

[SLH+06a] Yinglei Song, Chunmei Liu, Xiuzhen Huang, Russell L. Malmberg, Ying Xu, and Liming Cai. Efficient parameterized algorithms for biopolymer structure-sequence alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3 (4):423–432, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2006:CAP

[SLH06b] Yun S. Song, Rune Lyngso, and Jotun Hein. Counting all possible ancestral configurations of sample sequences in population genetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):239–251, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2019:IAL

[SLL+19] Weiping Sun, Yi Liu, Gills A. Lajoie, Bin Ma, and Kaizhong Zhang. An improved approach for *N*-linked glycan structure identification from HCD MS/MS spectra. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):388–395, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2701819`.

Singh:2019:TSK

[SLRQ19] Ritambhara Singh, Jack Lanchantin, Gabriel Robins, and Yanjun Qi. Transfer string kernel for cross-context DNA–protein binding prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1524–1536, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2014:MSS

[SLS+14] Xuebo Song, Lin Li, Pradip K. Srimani, Philip S. Yu, and James Z. Wang. Measure the semantic similarity of GO terms using aggregate information content. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):468–476, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2015:MLA

[SLW15] Yinglei Song, Chunmei Liu, and Zhi Wang. A machine learning approach for accurate annotation of noncoding RNAs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):551–559, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shao:2018:OCG

[SLX+18] Wei Shao, Mingxia Liu, Ying-Ying Xu, Hong-Bin Shen, and Daoqiang Zhang. An organelle correlation-guided feature selection approach for classifying multi-label subcellular bio-images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):828–838, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Satya:2008:UIP

[SM08] Ravi Vijaya Satya and Amar Mukherjee. The undirected incomplete perfect phylogeny problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):618–629, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sengupta:2012:WMC

[SMB12] Debarka Sengupta, Ujjwal Maulik, and Sanghamitra Bandyopadhyay. Weighted Markov chain based aggregation of biomolecule orderings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):924–933, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Smith:2009:RSD

[Smi09] Jennifer A. Smith. RNA search with decision trees and partial covariance models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):517–527, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Stegmayer:2012:BIV

[SMK+12] Georgina Stegmayer, Diego H. Milone, Laura Kamenetzky, Mariana G. Lopez,

and Fernando Carrari. A biologically inspired validity measure for comparison of clustering methods over metabolic data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):706–716, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sarkar:2022:DPR

[SMK22] Aisharjya Sarkar, Prabhat Mishra, and Tamer Kahveci. Data perturbation and recovery of time series gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):830–842, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3058342`.

Shahdoust:2020:NBC

[SMPS20] Maryam Shahdoust, Hossein Mahjub, Hamid Pezeshk, and Mehdi Sadeghi. A network-based comparison between molecular apocrine breast cancer tumor and basal and luminal tumors by joint graphical lasso. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1555–1562, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2911074`.

Sehhati:2015:SGS

[SMRP15] Mohammadreza Sehhati, Alireza Mehridehnavi, Hossein Rabbani, and Meraj Pourhossein. Stable gene signature selection for prediction of breast cancer recurrence using joint mutual information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1440–1448, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Stalidzans:2017:SMS

[SMSZ17] Egils Stalidzans, Ivars Mozga, Jurijs Sulins, and Peteris Zikmanis. Search for a minimal set of parameters by assessing the total optimization potential for a dynamic model of a biochemical network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):978–985, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Serang:2012:FMS

[SN12] Oliver Serang and William Stratford Noble. Faster mass spectrometry-based protein inference: Junction trees are more efficient than sampling and marginalization by

enumeration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):809–817, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

S:2024:GNC

[SN24] Sheena K. S. and Madhu S. Nair. GenCoder: a novel convolutional neural network based autoencoder for genomic sequence data compression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):405–415, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3366240`.

Shi:2016:OEM

[SNC+16] Yan Shi, Jinglong Niu, Zhixin Cao, Maolin Cai, Jian Zhu, and Weiqing Xu. Online estimation method for respiratory parameters based on a pneumatic model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 939–946, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shetta:2022:CMV

[SND22] Omar Shetta, Mahesan Niranjan, and Srinandan Dasmahapatra. Convex multi-view clustering via robust low rank approximation with application to multi-omic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3340–3352, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3122961`.

Seabolt:2022:FGP

[SNK+22] Edward E. Seabolt, Gowri Nayar, Harsha Krishnareddy, Akshay Agarwal, Kristen L. Beck, Ignacio Terrizzano, Eser Kandogan, Mark Kunitomi, Mary Roth, Vandana Mukherjee, and James H. Kaufman. Functional genomics platform, a cloud-based platform for studying microbial life at scale. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):940–952, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3021231`.

Spillner:2008:CPD

[SNM08] Andreas Spillner, Binh T. Nguyen, and Vincent Moulton. Computing phylogenetic diversity for split systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):235–244, April 2008. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Spillner:2012:CDR

[SNM12] Andreas Spillner, Binh Nguyen, and Vincent Moulton. Constructing and drawing regular planar split networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):395–407, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2006:CNS

[Son06] Yun S. Song. A concise necessary and sufficient condition for the existence of a galled-tree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):186–191, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sahu:2011:ELH

[SP11] Sitanshu Sekhar Sahu and Ganapati Panda. Efficient localization of hot spots in proteins using a novel S-transform based filtering approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1235–1246, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sirin:2017:BMT

[SPA17] Utku Sirin, Faruk Polat, and Reda Alhajj. Batch mode TDλ for controlling partially observable gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1214–1227, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sinha:2024:ESA

[SPD24] Rituparna Sinha, Rajat Kumar Pal, and Rajat K. De. ENLIGHTENMENT: a scalable annotated database of genomics and NGS-based nucleotide level profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):155–168, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3340067`.

Shehu:2019:GEA

[SPK19] Amarda Shehu, Giuseppe Pozzi, and Tamer Kahveci. Guest editorial for the ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1409, September 2019. CODEN ITCBCY.

ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2023:CMD

[SPL+23] Jing Sun, Li Pan, Bin Li, Haoyue Wang, Bo Yang, and Wenbin Li. A construction method of dynamic protein interaction networks by using relevant features of gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2790–2801, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3264241`.

Sengupta:2013:RKO

[SPMB13] Debarka Sengupta, Aroonalok Pyne, Ujjwal Maulik, and Sanghamitra Bandyopadhyay. Reformulated Kemeny optimal aggregation with application in consensus ranking of microRNA targets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):742–751, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Su:2021:TOD

[SPP21] Cui Su, Jun Pang, and Soumya Paul. Towards optimal decomposition of Boolean networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2167–2176, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2914051`.

Song:2020:EBM

[SPW20] Junrong Song, Wei Peng, and Feng Wang. An entropy-based method for identifying mutual exclusive driver genes in cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):758–768, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2897931`.

Song:2022:ICP

[SPW22] Junrong Song, Wei Peng, and Feng Wang. Identifying cancer patient subgroups by finding co-modules from the driver mutation profiles and downstream gene expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2863–2872, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3106344`.

Sun:2014:MSA

[SPWF14] Jun Sun, Vasile Palade, Xi-

aojun Wu, and Wei Fang. Multiple sequence alignment with hidden Markov models learned by random drift particle swarm optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1):243–257, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sajjadi:2014:NBM

[SQZA14] Seyed Javad Sajjadi, Xiaoning Qian, Bo Zeng, and Amin Ahmadi Adl. Network-based methods to identify highly discriminating subsets of biomarkers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6): 1029–1037, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Snir:2006:UMC

[SR06] Sagi Snir and Satish Rao. Using max cut to enhance rooted trees consistency. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3 (4):323–333, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Snir:2010:QMD

[SR10] Sagi Snir and Satish Rao. Quartets MaxCut: a divide and conquer quartets algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (4):704–718, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sarkar:2019:NAC

[SREK19] Aisharjya Sarkar, Yuanfang Ren, Rasha Elhesha, and Tamer Kahveci. A new algorithm for counting independent motifs in probabilistic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1049–1062, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Srihari:2014:ECC

[SRLR14] Sriganesh Srihari, Venkatesh Raman, Hon Wai Leong, and Mark A. Ragan. Evolution and controllability of cancer networks: a Boolean perspective. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):83–94, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shekhar:2018:STE

[SRM18] Shubhanshu Shekhar, Sebastien Roch, and Siavash Mirarab. Species tree estimation using ASTRAL: How

many genes are enough? *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1738–1747, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sarkar:2024:HSB

[SRM+24] Joy Lal Sarkar, Ramasamy V, Abhishek Majumder, Bibudhendu Pati, Chhabi Rani Panigrahi, Weizheng Wang, Nawab Muhammad Faseeh Qureshi, Chunhua Su, and Kapal Dev. I-Health: SDN-based fog architecture for IIoT applications in healthcare. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):644–651, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3193918`.

Scheid:2004:SDS

[SS04] Stefanie Scheid and Rainer Spang. A stochastic downhill search algorithm for estimating the local false discovery rate. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(3):98–108, July 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sammeth:2006:CTR

[SS06a] Michael Sammeth and Jens Stoye. Comparing tandem repeats with duplications and excisions of variable degree. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3 (4):395–407, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Semple:2006:UNC

[SS06b] Charles Semple and Mike Steel. Unicyclic networks: Compatibility and enumeration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(1):84–91, January 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sigdel:2016:FFS

[SSD+16] Madhu S. Sigdel, Madhav Sigdel, Semih Dinc, Imren Dinc, Marc L. Pusey, and Ramazan S. Aygun. FocusALL: Focal stacking of microscopic images using modified Harris corner response measure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):326–340, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Samaddar:2019:MDP

[SSD19] Sandip Samaddar, Rituparna Sinha, and Rajat K.

De. A model for distributed processing and analyses of NGS data under map-reduce paradigm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):827–840, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sargsyan:2012:MSR

[SSDN12] Khachik Sargsyan, Cosmin Safta, Bert Debusschere, and Habib Najm. Multiparameter spectral representation of noise-induced competence in *Bacillus Subtilis*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1709–1723, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Suryanto:2018:SCC

[SSF18] Chendra Hadi Suryanto, Hiroto Saigo, and Kazuhiro Fukui. Structural class classification of 3D protein structure based on multiview 2D images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):286–299, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2012:SSM

[SSFW12] Hong Sun, Ahmet Sacan, Hakan Ferhatosmanoglu, and Yusu Wang. Smolign: a spatial motifs-based protein multiple structural alignment method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):249–261, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Saribudak:2020:GEH

[SSK+20] Aydin Saribudak, Adarsha A. Subick, Na Hyun Kim, Joshua A. Rutta, and M. Ümit Uyar. Gene expressions, hippocampal volume loss, and MMSE scores in computation of progression and pharmacologic therapy effects for Alzheimer's disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):608–622, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2870363`.

Seok:2015:ESA

[SSKH15] Ho-Sik Seok, Taemin Song, Sek Won Kong, and Kyu-Baek Hwang. An efficient search algorithm for finding genomic-range overlaps based on the maximum range length. *IEEE/ACM Transactions on Computational Biology and Bioinfor-*

matics, 12(4):778–784, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Segar:2015:MTD

[SSML15] Matthew W. Segar, Cynthia J. Sakofsky, Anna Malkova, and Yunlong Liu. MMBIRFinder: a tool to detect microhomology-mediated break-induced replication. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):799–806, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sevilla:2005:CBG

[SSP+05] Jose L. Sevilla, Victor Segura, Adam Podhorski, Elizabeth Guruceaga, Jose M. Mato, Luis A. Martinez-Cruz, Fernando J. Corrales, and Angel Rubio. Correlation between gene expression and GO semantic similarity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2 (4):330–338, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sinha:2017:PDV

[SSP+17] Arvind Kumar Sinha, Pradeep Singh, Anand Prakash, Dharm Pal, Anuradha Dube, and Awanish Kumar. Putative drug and vaccine target identification in *Leishmania donovani* membrane proteins using naïve Bayes probabilistic classifier. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):204–211, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Saraswathi:2011:IPE

[SSS+11] Saras Saraswathi, Suresh Sundaram, Narasimhan Sundararajan, Michael Zimmermann, and Marit Nilsen-Hamilton. ICGA-PSO-ELM approach for accurate multiclass cancer classification resulting in reduced gene sets in which genes encoding secreted proteins are highly represented. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):452–463, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shakya:2013:AWL

[SSS13a] Devendra K. Shakya, Rajiv Saxena, and Sanjeev N. Sharma. An adaptive window length strategy for eukaryotic CDS prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5): 1241–1252, September 2013. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Subramanian:2013:NMS

[SSS13b] Ayshwarya Subramanian, Stanley Shackney, and Russell Schwartz. Novel multi-sample scheme for inferring phylogenetic markers from whole genome tumor profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1422–1431, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sung:2015:MLM

[SSS+15] Wing-Kin Sung, Kunihiko Sadakane, Tetsuo Shibuya, Abha Belorkar, and Iana Pyrogova. An $O(m \log m)$-time algorithm for detecting superbubbles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):770–777, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sharma:2020:ESL

[SSS20a] Nirmala Sharma, Harish Sharma, and Ajay Sharma. An effective solution for large scale single machine total weighted tardiness problem using lunar cycle inspired artificial bee colony algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1573–1581, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2897302`.

Sharma:2020:ISE

[SSS20b] Sunildatt Sharma, Sanjeev Narayan Sharma, and Rajiv Saxena. Identification of short exons disunited by a short intron in eukaryotic DNA regions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1660–1670, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2900040`.

Sevakula:2019:TLM

[SSV+19] Rahul K. Sevakula, Vikas Singh, Nishchal K. Verma, Chandan Kumar, and Yan Cui. Transfer learning for molecular cancer classification using deep neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):2089–2100, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2822803`.

Si:2023:BAM

[SSZ+23] Jiasheng Si, Liu Sun, Deyu Zhou, Jie Ren, and Lin Li. Biomedical argument mining based on sequential multi-task learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):864–874, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3173447`.

Shen:2005:DRB

[ST05] Li Shen and Eng Chong Tan. Dimension reduction-based penalized logistic regression for cancer classification using microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):166–175, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Salmela:2019:SFG

[ST19] Leena Salmela and Alexandru I. Tomescu. Safely filling gaps with partial solutions common to all solutions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):617–626, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2785831`.

Sutanto:2023:AGL

[ST23] Kevin Sutanto and Marcel Turcotte. Assessing global-local secondary structure fingerprints to classify RNA sequences with deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2736–2747, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3118358`.

Singh:2019:EPG

[STB+19] Kumar Saurabh Singh, Bartlomiej J. Troczka, Katherine Beadle, Linda M. Field, T. G. Emyr Davies, Martin S. Williamson, Ralf Nauen, and Chris Bass. Extension of partial gene transcripts by iterative mapping of RNA-Seq raw reads. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):1036–1041, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shrestha:2020:SMD

[STB+20] Midusha Shrestha, Truong X. Tran, Bidhan Bhattarai, Marc L. Pusey, and Ramazan S. Aygun. Schema matching and data integra-

tion with consistent naming on protein crystallization screens. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2074–2085, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2913368`.

Sen:2020:AAS

[STD20] Rishika Sen, Somnath Tagore, and Rajat K. De. ASAPP: Architectural similarity-based automated pathway prediction system and its application in host-pathogen interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):506–515, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2872527`.

Shibuya:2015:GEI

[STHA15] Tetsuo Shibuya, Chuan Yi Tang, Paul Horton, and Kiyoshi Asai. Guest editorial for the 25th International Conference on Genome Informatics (GIW/ISCB-Asia 2014). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):761–762, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sevon:2006:TTP

[STO06] Petteri Sevon, Hannu Toivonen, and Vesa Ollikainen. TreeDT: Tree pattern mining for gene mapping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):174–185, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Strutz:2011:SRL

[Str11] Tilo Strutz. 3D shape reconstruction of loop objects in X-ray protein crystallography. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):797–807, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sreedharan:2021:RPE

[STS21] Jithin K. Sreedharan, Krzysztof Turowski, and Wojciech Szpankowski. Revisiting parameter estimation in biological networks: Influence of symmetries. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):836–849, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2980260`.

Shen:2014:LKS

[STT+14] Qingliang Shen, Hong Tian, Daoqi Tang, Wenbing Yao, and Xiangdong Gao. Ligand-K* sequence elimination: a novel algorithm for ensemble-based redesign of receptor-ligand binding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):573–578, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2023:IPL

[STY+23] Jinmiao Song, Shengwei Tian, Long Yu, Qimeng Yang, Yuanxu Wang, Qiguo Dai, and Xiaodong Duan. ISLMI: Predicting lncRNA–miRNA interactions based on information injection and second-order graph convolution network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1737–1745, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215151`.

Singh:2016:BAI

[SV16] Nitin Singh and Mathukumalli Vidyasagar. bLARS: an algorithm to infer gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):301–314, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sato:2018:CNM

[SVdSS+18] Joao Ricardo Sato, Maciel Calebe Vidal, Suzana de Siqueira Santos, Katlin Brauer Massirer, and Andre Fujita. Complex network measures in autism spectrum disorders. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):581–587, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Souza:2021:DCI

[SVE21] Mauricio Guevara Souza, Edgar E. Vallejo, and Karol Estrada. Detecting clustered independent rare variant associations using genetic algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):932–939, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2930505`.

Shanthappa:2024:CPP

[SVG+24] Pallavi M. Shanthappa, Neeraj Verma, Anu George, Pawan K. Dhar, and Prashanth Athri. Computational prediction of potential vaccine candidates from tRNA en-

coded peptides (tREP) using a bioinformatic workflow and molecular dynamics validations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):439–449, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3371984`.

Siren:2014:IGP

[SVM14] Jouni Sirén, Niko Välimäki, and Veli Mäkinen. Indexing graphs for path queries with applications in genome research. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):375–388, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Salicru:2009:ICA

[SVZ09] Miquel Salicru, Sergi Vives, and Tian Zheng. Inferential clustering approach for microarray experiments with replicated measurements. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):594–604, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Stoye:2009:UAR

[SW09] Jens Stoye and Roland Wittler. A unified approach for reconstructing ancient gene clusters. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):387–400, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shabash:2017:RVR

[SW17] Boris Shabash and Kay C. Wiese. RNA visualization: Relevance and the current state-of-the-art focusing on pseudoknots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):696–712, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Su:2012:INP

[SWH+12] Chien-Hao Su, Tse-Yi Wang, Ming-Tsung Hsu, Francis Cheng-Hsuan Weng, Cheng-Yan Kao, Daryi Wang, and Huai-Kuang Tsai. The impact of normalization and phylogenetic information on estimating the distance for metagenomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):619–628, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sun:2019:MDN

[SWL19] Dongdong Sun, Minghui Wang, and Ao Li. A multimodal deep neural network

for human breast cancer prognosis prediction by integrating multi-dimensional data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):841–850, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2021:SDS

[SWSA21] Xiaona Song, Mi Wang, Shuai Song, and Choon Ki Ahn. Sampled-data state estimation of reaction diffusion genetic regulatory networks via space-dividing approaches. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):718–730, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2919532`.

Su:2019:DMD

[SWX+19] Ran Su, Huichen Wu, Bo Xu, Xiaofeng Liu, and Leyi Wei. Developing a multi-dose computational model for drug-induced hepatotoxicity prediction based on toxicogenomics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1231–1239, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Su:2014:AMD

[SXL+14] Hai Su, Fuyong Xing, Jonah D. Lee, Charlotte A. Peterson, and Lin Yang. Automatic myonuclear detection in isolated single muscle fibers using robust ellipse fitting and sparse representation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):714–726, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sheng:2024:SDL

[SXW+24] Nan Sheng, Xuping Xie, Yan Wang, Lan Huang, Shuangquan Zhang, Ling Gao, and Hao Wang. A survey of deep learning for detecting miRNA-disease associations: Databases, computational methods, challenges, and future directions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):328–347, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3351752`.

Shaik:2009:FAS

[SY09] Jahangheer Shaik and Mohammed Yeasin. Fuzzy-adaptive-subspace-iteration-based two-way clustering of microarray data. *IEEE/ACM Transactions on Com-*

putational Biology and Bioinformatics, 6(2):244–259, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Stegmayer:2017:HCI

[SYKM17] Georgina Stegmayer, Cristian Yones, Laura Kamenetzky, and Diego H. Milone. High class-imbalance in pre-miRNA prediction: a novel approach based on deepSOM. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1316–1326, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Seniya:2015:SSS

[SYKS15] Chandrabhan Seniya, Ajay Yadav, G. J. Khan, and Nand K. Sah. In-silico studies show potent inhibition of HIV-1 reverse transcriptase activity by a herbal drug. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1355–1364, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Song:2019:PGA

[SYL19] You Song, Siyu Yang, and Jinzhi Lei. ParaCells: a GPU architecture for cell-centered models in computational biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):994–1006, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Saetre:2010:EPI

[SYM+10] Rune Sætre, Kazuhiro Yoshida, Makoto Miwa, Takuya Matsuzaki, Yoshinobu Kano, and Jun'ichi Tsujii. Extracting protein interactions from text with the unified AkaneRE event extraction system. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):442–453, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shiraishi:2014:EVA

[SYV14] Fumihide Shiraishi, Erika Yoshida, and Eberhard O. Voit. An efficient and very accurate method for calculating steady-state sensitivities in metabolic reaction systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1077–1086, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shao:2013:UMB

[SYZ+13] Gui-Fang Shao, Fan Yang, Qian Zhang, Qi-Feng Zhou, and Lin-Kai Luo. Using

the maximum between-class variance for automatic gridding of cDNA microarray images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):181–192, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sadjad:2011:TRS

[SZ11] Bashir Sadjad and Zsolt Zsoldos. Toward a robust search method for the protein–drug docking problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (4):1120–1133, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shi:2019:CED

[SZCX19] Yan Shi, Bolun Zhang, Maolin Cai, and Weiqing Xu. Coupling effect of double lungs on a VCV ventilator with automatic secretion clearance function. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1280–1287, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Shen:2023:EED

[SZD+23] Yang Shen, Jinlin Zhu, Zhaohong Deng, Wenwei Lu, and Hongchao Wang. EnsDeepDP: an ensemble deep learning approach for disease prediction through metagenomics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):986–998, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3201295`.

Steinauer:2021:CMG

[SZGZ21] Nickolas Steinauer, Kevin Zhang, Chun Guo, and Jinsong Zhang. Computational modeling of gene-specific transcriptional repression, activation and chromatin interactions in leukemogenesis by LASSO-regularized logistic regression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2109–2122, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3078128`.

Shen:2022:DLM

[SZHH22] Zhen Shen, Qinhu Zhang, Kyungsook Han, and De-Shuang Huang. A deep learning model for RNA-protein binding preference prediction based on hierarchical LSTM and attention network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

19(2):753–762, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3007544`.

Shi:2020:QDD

[SZL+20] Jifan Shi, Juan Zhao, Xiaoping Liu, Luonan Chen, and Tiejun Li. Quantifying direct dependencies in biological networks by multiscale association analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):449–458, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2846648`.

Sun:2011:CFS

[SZLL11] Bing-Yu Sun, Zhi-Hua Zhu, Jiuyong Li, and Bin Linghu. Combined feature selection and cancer prognosis using support vector machine regression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1671–1677, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Sankoff:2019:MSD

[SZZ+19] David Sankoff, Chunfang Zheng, Yue Zhang, Joao Meidanis, Eric Lyons, and Haibao Tang. Models for similarity distributions of syntenic homologs and applications to phylogenomics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):727–737, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tan:2011:IPK

[TAAP11] Mehmet Tan, Mohammed Alshalalfa, Reda Alhajj, and Faruk Polat. Influence of prior knowledge in constraint-based learning of gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (1):130–142, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Taha:2014:DSR

[Tah14] Kamal Taha. Determining semantically related significant genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1119–1130, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Taha:2018:IFP

[Tah18] Kamal Taha. Inferring the functions of proteins from the interrelationships be-

tween functional categories. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):157–167, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tsompanas:2019:MMF

[TAI+19] Michail-Antisthenis Tsompanas, Andrew Adamatzky, Ioannis Ieropoulos, Neil William Phillips, Georgios Ch. Sirakoulis, and John Greenman. Modelling microbial fuel cells using lattice Boltzmann methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):2035–2045, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2831223`.

Torii:2015:RPG

[TAL+15] Manabu Torii, Cecilia N. Arighi, Gang Li, Qinghua Wang, Cathy H. Wu, and K. Vijay-Shanker. RLIMS-P 2.0: a generalizable rule-based information extraction system for literature mining of protein phosphorylation information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):17–29, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tanaka:2014:IEE

[Tan14] Shunji Tanaka. Improved exact enumerative algorithms for the planted (l, d)-motif search problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):361–374, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tripathi:2023:AGC

[TB23] Prasun Chandra Tripathi and Soumen Bag. An attention-guided CNN framework for segmentation and grading of glioma using 3D MRI scans. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1890–1904, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3220902`.

Tininini:2010:CHA

[TBGL10] Leonardo Tininini, Paola Bertolazzi, Alessandra Godi, and Giuseppe Lancia. CollHaps: a heuristic approach to haplotype inference by parsimony. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):511–523, July 2010. CODEN ITCBCY.

ISSN 1545-5963 (print), 1557-9964 (electronic).

Turner:2005:BMS

[TBKH05] Heather L. Turner, Trevor C. Bailey, Wojtek J. Krzanowski, and Cheryl A. Hemingway. Biclustering models for structured microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2 (4):316–329, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tsai:2011:CTA

[TBRS11] Ming-Chi Tsai, Guy E. Blelloch, R. Ravi, and Russell Schwartz. A consensus tree approach for reconstructing human evolutionary history and detecting population substructure. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):918–928, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tsai:2013:CBM

[TBRS13] Ming-Chi Tsai, Guy E. Blelloch, R. Ravi, and Russell Schwartz. Coalescent-based method for learning parameters of admixture events from large-scale genetic variation data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1137–1149, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tu:2013:INR

[TC13] Chien-Ta Tu and Bor-Sen Chen. On the increase in network robustness and decrease in network response ability during the aging process: a systems biology approach via microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):468–480, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tran:2016:AOP

[TC16] Ngoc Hieu Tran and Xin Chen. AMAS: Optimizing the partition and filtration of adaptive seeds to speed up read mapping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):623–633, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Treangen:2009:NHL

[TDA+09] Todd J. Treangen, Aaron E. Darling, Guillaume Achaz, Mark A. Ragan, Xavier Messeguer, and Eduardo P. C. Rocha. A novel heuristic for local multiple alignment of interspersed DNA

repeats. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):180–189, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Thomas:2014:MLE

[TDD14] Minta Thomas, Anneleen Daemen, and Bart De Moor. Maximum likelihood estimation of GEVD: applications in bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):673–680, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Todor:2013:CTP

[TDK13a] Andrei Todor, Alin Dobra, and Tamer Kahveci. Characterizing the topology of probabilistic biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):970–983, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Todor:2013:PBN

[TDK13b] Andrei Todor, Alin Dobra, and Tamer Kahveci. Probabilistic biological network alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):109–121, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tang:2018:SRS

[TDY+18] Qirong Tang, Lu Ding, Fangchao Yu, Yuan Zhang, Yinghao Li, and Haibo Tu. Swarm robots search for multiple targets based on an improved grouping strategy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 1943–1950, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tian:2019:REA

[TDZ+19] Bo Tian, Qiong Duan, Can Zhao, Ben Teng, and Zengyou He. Reinforce: an ensemble approach for inferring PPI network from AP–MS data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):365–376, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2705060`.

Tang:2024:MNM

[TDZ+24] Wenliang Tang, Zhaohong Deng, Hanwen Zhou, Wei Zhang, Fuping Hu, Kup-Sze Choi, and Shitong Wang. MVDINET: a novel

multi-level enzyme function predictor with multi-view deep interactive learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21 (1):84–94, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3337158`.

Tu:2024:DMD

[TDZZ24] Chao Tu, Denghui Du, Tieyong Zeng, and Yu Zhang. Deep multi-dictionary learning for survival prediction with multi-zoom histopathological whole slide images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1): 14–25, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3321593`.

Torres:2012:UGE

[TED+12] Jose Salavert Torres, Ignacio Blanquer Espert, Andres Tomas Dominguez, Vicente Hernendez, Ignacio Medina, Joaquin Terraga, and Joaquin Dopazo. Using GPUs for the exact alignment of short-read genetic sequences by means of the Burrows–Wheeler transform. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (4):1245–1256, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tian:2023:GGC

[TFTY23] Zhen Tian, Haichuan Fang, Zhixia Teng, and Yangdong Ye. GOGCN: Graph convolutional network on gene ontology for functional similarity analysis of genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1053–1064, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3181300`.

Tang:2016:RMC

[TGD+16] Yang Tang, Huijun Gao, Wei Du, Jianquan Lu, Athanasios V. Vasilakos, and Jürgen Kurths. Robust multi-objective controllability of complex neuronal networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4): 778–791, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tenenhaus:2010:GAN

[TGGF10] Arthur Tenenhaus, Vincent Guillemot, Xavier Gidrol, and Vincent Frouin. Gene association networks from microarray data using a regularized estimation of partial

correlation based on PLS regression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):251–262, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tang:2013:MIC

[TGK13] Yang Tang, Huijun Gao, and Jurgen Kurths. Multiobjective identification of controlling areas in neuronal networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):708–720, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Taliun:2016:FSB

[TGLP16] Daniel Taliun, Johann Gamper, Ulf Leser, and Cristian Pattaro. Fast sampling-based whole-genome haplotype block recognition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):315–325, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tabaszewski:2021:CAS

[TGM+21] P. Tabaszewski, P. Górecki, A. Markin, T. Anderson, and O. Eulenstein. Consensus of all solutions for intractable phylogenetic tree inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):149–161, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2947051`.

Tomescu:2015:EWD

[TGP+15] Alexandru I. Tomescu, Travis Gagie, Alexandru Popa, Romeo Rizzi, Anna Kuosmanen, and Veli Makinen. Explaining a weighted DAG with few paths for solving genome-guided multi-assembly. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1345–1354, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tian:2018:GES

[TH18] Tianhai Tian and Jingshan Huang. Guest editorial for special section on BIBM 2015. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1752–1753, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Thiele:2019:DOE

[THH+19] Sven Thiele, Sandra Heise, Wiebke Hessenkemper, Hannes Bongartz, Melissa Fensky,

Fred Schaper, and Steffen Klamt. Designing optimal experiments to discriminate interaction graph models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):925–935, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tofigh:2011:SID

[THL11] Ali Tofigh, Michael Hallett, and Jens Lagergren. Simultaneous identification of duplications and lateral gene transfers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):517–535, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Thorvaldsen:2016:MMF

[Tho16] Steinar Thorvaldsen. A mutation model from first principles of the genetic code. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 878–886, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tamada:2011:EGW

[TIA+11] Yoshinori Tamada, Seiya Imoto, Hiromitsu Araki, Masao Nagasaki, Cristin Print, D. Stephen Charnock-Jones, and Satoru Miyano. Estimating genome-wide gene networks using nonparametric Bayesian network models on massively parallel computers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):683–697, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Title:2013:AI

[Tit13] Title. 2012 annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (1):244–270, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Title:2016:IIA

[Tit16] Title. 2015 index IEEE/ ACM Transactions on Computational Biology and Bioinformatics vol. 12. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):172–195, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tseng:2005:EMG

[TK05] Vincent S. Tseng and Ching-Pin Kao. Efficiently mining gene expression data via a novel parameterless clustering method. *IEEE/ACM Transactions on Computa-*

tional Biology and Bioinformatics, 2(4):355–365, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tamura:2018:CMR

[TLSA18] Takeyuki Tamura, Wei Lu, Jiangning Song, and Tatsuya Akutsu. Computing minimum reaction modifications in a Boolean metabolic network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1853–1862, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tuller:2011:CEI

[TM11] Tamir Tuller and Elchanan Mossel. Co-evolution is incompatible with the Markov assumption in phylogenetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1667–1670, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Timonen:2019:PFM

[TMLI19] Juho Timonen, Henrik Mannerström, Harri Lähdesmäki, and Jukka Intosalmi. A probabilistic framework for molecular network structure inference by means of mechanistic modeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1843–1854, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2825327`.

Tan:2008:NBP

[TNQ08] Tuan Zea Tan, Geok See Ng, and Chai Quek. A novel biologically and psychologically inspired fuzzy decision support system: Hierarchical complementary learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):67–79, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tu:2019:IGN

[TOYHZ19] Jia-Juan Tu, Le Ou-Yang, Xiaohua Hu, and Xiao-Fei Zhang. Inferring gene network rewiring by combining gene expression and gene mutation data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):1042–1048, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Torshizi:2018:SPI

[TP18] Abolfazl Doostparast Torshizi and Linda Petzold. Sparse pathway-induced dynamic network biomarker

discovery for early warning signal detection in complex diseases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):1028–1034, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Thireou:2007:BLS

[TR07] Trias Thireou and Martin Reczko. Bidirectional long short-term memory networks for predicting the subcellular localization of eukaryotic proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):441–446, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Than:2013:MPD

[TR13] Cuong V. Than and Noah A. Rosenberg. Mathematical properties of the deep coalescence cost. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):61–72, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Thomas:2008:GMR

[TRBK08] John Thomas, Naren Ramakrishnan, and Chris Bailey-Kellogg. Graphical models of residue coupling in protein families. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):183–197, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Thomas:2009:PDS

[TRBK09] John Thomas, Naren Ramakrishnan, and Chris Bailey-Kellogg. Protein design by sampling an undirected graphical model of residue constraints. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):506–516, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tataw:2013:QAL

[TRKRC13] Oben M. Tataw, Gonehal Venugopala Reddy, Eamonn J. Keogh, and Amit K. Roy-Chowdhury. Quantitative analysis of live-cell growth at the shoot apex of *Arabidopsis thaliana*: Algorithms for feature measurement and temporal alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1150–1161, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tan:2017:ESS

[TS17] Ying Tan and Yuhui Shi. Editorial: Special section on bio-inspired swarm com-

puting and engineering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):1–3, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tan:2018:SSS

[TS18] Ying Tan and Yuhui Shi. Special section on swarm-based algorithms and applications in computational biology and bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 1863–1864, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tsai:2012:IPP

[Tsa12] Richard Tzong-Han Tsai. Improving protein-protein interaction pair ranking with an integrated global association score. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1690–1695, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tulpan:2014:TPP

[TSM14] Dan Tulpan, Derek H. Smith, and Roberto Montemanni. Thermodynamic post-processing versus GC-content pre-processing for DNA codes satisfying the Hamming distance and reverse-complement constraints. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):441–452, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Torres-Sanchez:2013:GFG

[TSMMG+13] Sergio Torres-Sanchez, Nuria Medina-Medina, Chris Gignoux, Maria del Mar Abad-Grau, and Esteban Gonzalez-Burchard. GeneOnEarth: Fitting genetic PC plots on the globe. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1009–1016, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tsui:2022:E

[Tsu22] Stephen Kwok-Wing Tsui. Editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1255–1256, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3155845`.

Tsai:2013:PBL

[TTWR13] Tsung-Heng Tsai, Mahlet G. Tadesse, Yue Wang, and Habtom W. Ressom. Profile-based LC-MS data align-

ment — a Bayesian approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):494–503, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tenazinha:2011:SMM

[TV11] Nuno Tenazinha and Susana Vinga. A survey on methods for modeling and analyzing integrated biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):943–958, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tsang:2010:SPA

[TW10] Herbert H. Tsang and Kay C. Wiese. SARNA-Predict: Accuracy improvement of RNA secondary structure prediction using permutation-based simulated annealing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):727–740, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tang:2012:CEC

[TWG+12] Yang Tang, Zidong Wang, Huijun Gao, Stephen Swift, and Jurgen Kurths. A constrained evolutionary computation method for detecting controlling regions of cortical networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1569–1581, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tan:2020:EEH

[TWW+20] Renjie Tan, Jixuan Wang, Xiaoliang Wu, Liran Juan, Tianjiao Zhang, Rui Ma, Qing Zhan, Tao Wang, Shuilin Jin, Qinghua Jiang, and Yadong Wang. ERDS-Exome: a hybrid approach for copy number variant detection from whole-exome sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):796–803, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2017.2758779`.

Tian:2014:INB

[TWZ+14] Ye Tian, Sean S. Wang, Zhen Zhang, Olga C. Rodriguez, Emanuel Petricoin, Ie-Ming Shih, Daniel Chan, Maria Avantaggiati, Guoqiang Yu, Shaozhen Ye, Robert Clarke, Chao Wang, Bai Zhang, Yue Wang, and Chris Albanese. Integration of network biology and imaging to study cancer phenotypes and responses. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 11(6):1009–1019, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tang:2014:PEP

[TWZP14] Xiwei Tang, Jianxin Wang, Jiancheng Zhong, and Yi Pan. Predicting essential proteins based on weighted degree centrality. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(2):407–418, March 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tu:2016:UFC

[TWZW16] Xudong Tu, Yuanliang Wang, Maolan Zhang, and Jinchuan Wu. Using formal concept analysis to identify negative correlations in gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):380–391, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Taha:2015:ISI

[TYA15] Kamal Taha, Paul D. Yoo, and Mohammed Alzaabi. iPFPi: a system for improving protein function prediction through cumulative iterations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):825–836, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tchendji:2023:PTS

[TYDZ23] Vianney Kengne Tchendji, Franklin Ingrid Kamga Youmbi, Clémentin Tayou Djamegni, and Jerry Lacmou Zeutouo. A parallel tiled and sparsified four-Russians algorithm for Nussinov's RNA folding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1795–1806, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3216826`.

Teng:2016:EGP

[TYL+16] Ben Teng, Can Yang, Jiming Liu, Zhipeng Cai, and Xiang Wan. Exploring the genetic patterns of complex diseases via the integrative genome-wide approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):557–564, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tang:2016:NAF

[TZ16] Jian Tang and Shuigeng

Zhou. A new approach for feature selection from microarray data based on mutual information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1004–1015, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tang:2007:DTS

[TZH07] Yuchun Tang, Yan-Qing Zhang, and Zhen Huang. Development of two-stage SVM-RFE gene selection strategy for microarray expression data analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):365–381, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Thanh:2017:ECT

[TZP17] Vo Hong Thanh, Roberto Zunino, and Corrado Priami. Efficient constant-time complexity algorithm for stochastic simulation of large reaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):657–667, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Tang:2023:FMP

[TZWZ23] Chunyan Tang, Cheng Zhong, Mian Wang, and Fengfeng Zhou. FMGNN: a method to predict compound-protein interaction with pharmacophore features and physicochemical properties of amino acids. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1030–1040, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3172340`.

Tino:2011:SCG

[TZY11] Peter Tiňo, Hongya Zhao, and Hong Yan. Searching for coexpressed genes in three-color cDNA microarray data using a probabilistic model-based Hough Transform. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (4):1093–1107, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ullah:2016:GAC

[UAH16] Ehsan Ullah, Shuchin Aeron, and Soha Hassoun. gEFM: an algorithm for computing elementary flux modes using graph traversal. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):122–134,

January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Urban:2019:DLD

[UBP+19] Gregor Urban, Kevin Bache, Duc T. T. Phan, Agua Sobrino, Alexander K. Shmakov, Stephanie J. Hachey, Christopher C. W. Hughes, and Pierre Baldi. Deep learning for drug discovery and cancer research: Automated analysis of vascularization images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):1029–1035, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Unger:2010:LSG

[UC10] Giora Unger and Benny Chor. Linear separability of gene expression data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):375–381, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Uehara:2009:PDC

[UJ09] Hiroaki Uehara and Masakazu Jimbo. A positive detecting code and its decoding algorithm for DNA library screening. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):652–666, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Uner:2023:DDL

[UKC+23] Onur Can Uner, Halil Ibrahim Kuru, R. Gokberk Cinbis, Oznur Tastan, and A. Ercument Cicek. DeepSide: a deep learning approach for drug side effect prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):330–339, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3141103`.

Ushakov:2018:BLB

[UKV18] Anton V. Ushakov, Xenia Klimentova, and Igor Vasilyev. Bi-level and bi-objective p-median type problems for integrative clustering: Application to analysis of cancer gene-expression and drug-response data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):46–59, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Urbini:2019:ERP

[USMS19] Laura Urbini, Blerina Sinaimeri, Catherine Matias, and Marie-France Sagot. Exploring the

robustness of the parsimonious reconciliation method in host-symbiont cophylogeny. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):738–748, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ullah:2015:PUA

[UWLH15] Ehsan Ullah, Mark Walker, Kyongbum Lee, and Soha Hassoun. PreProPath: an uncertainty-aware algorithm for identifying predictable profitable pathways in biochemical networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1405–1415, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Valentini:2011:TPR

[Val11] Giorgio Valentini. True path rule hierarchical ensembles for genome-wide gene function prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 832–847, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Venkatachalam:2010:UTC

[VASG10] Balaji Venkatachalam, Jim Apple, Katherine St. John, and Daniel Gusfield. Untangling tanglegrams: Comparing trees by their drawings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (4):588–597, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Villaverde:2018:PTI

[VBB18] Alejandro F. Villaverde, Kolja Becker, and Julio R. Banga. PREMER: a tool to infer biological networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1193–1202, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

vanBerlo:2011:PMF

[vBdRD+11] Rogier J. P. van Berlo, Dick de Ridder, Jean-Marc Daran, Pascale A. S. Daran-Lapujade, Bas Teusink, and Marcel J. T. Reinders. Predicting metabolic fluxes using gene expression differences as constraints. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):206–216, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vyas:2018:AGP

[VBG+18] Renu Vyas, Sanket Ba-

pat, Purva Goel, Muthukumarasamy Karthikeyan, Sanjeev S. Tambe, and Bhaskar D. Kulkarni. Application of genetic programming GP formalism for building disease predictive models from protein–protein interactions PPI data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):27–37, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vundavilli:2020:SDE

[VDS+20] Haswanth Vundavilli, Aniruddha Datta, Chao Sima, Jianping Hua, Rosana Lopes, and Michael Bittner. In silico design and experimental validation of combination therapy for pancreatic cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (3):1010–1018, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2872573`.

VanDyck:2019:RSP

[VdTVV19] Michiel Van Dyck, Xavier Wootde Trixhe, An Vermeulen, and Wim Vanroose. A robust simulator for physiologically structured population models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):851–864, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vignes:2009:GCI

[VF09] Matthieu Vignes and Florence Forbes. Gene clustering via integrated Markov models combining individual and pairwise features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):260–270, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Verma:2019:POC

[VGBK19] Deeptak Verma, Gevorg Grigoryan, and Chris Bailey-Kellogg. Pareto optimization of combinatorial mutagenesis libraries. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1143–1153, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

vanIersel:2020:PTA

[vIJJ+20] Leo van Iersel, Remie Janssen, Mark Jones, Yukihiro Murakami, and Norbert Zeh. Polynomial-time algorithms for phylogenetic inference problems involving duplication and reticulation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

17(1):14–26, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2019.2934957`.

vanIersel:2009:CLP

[vIKK+09] Leo van Iersel, Judith Keijsper, Steven Kelk, Leen Stougie, Ferry Hagen, and Teun Boekhout. Constructing level-2 phylogenetic networks from triplets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(4):667–681, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

vanIersel:2008:SIT

[vIKKS08] Leo van Iersel, Judith Keijsper, Steven Kelk, and Leen Stougie. Shorelines of islands of tractability: Algorithms for parsimony and minimum perfect phylogeny haplotyping problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):301–312, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Viswanath:2018:CET

[Vis18] Narayanan C. Viswanath. Calculating the expected time to eradicate HIV-1 using a Markov chain. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):60–67, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Valdes-Jimenez:2024:PAD

[VJRPNVJG24] Alejandro Valdés-Jiménez, Miguel Reyes-Parada, Gabriel Núñez-Vivanco, and Daniel Jiménez-González. Parallel algorithm for discovering and comparing three-dimensional proteins patterns. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):508–515, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3367789`.

Vashist:2007:OCM

[VKM07] Akshay Vashist, Casimir A. Kulikowski, and Ilya Muchnik. Ortholog clustering on a multipartite graph. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):17–27, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Veltri:2017:IRA

[VKS17] Daniel Veltri, Uday Kamath, and Amarda Shehu. Improving recognition of an-

timicrobial peptides and target selectivity through machine learning and genetic programming. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):300–313, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vijayan:2018:MNA

[VM18] Vipin Vijayan and Tijana Milenkovic. Multiple network alignment via MultiMAGNA++. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1669–1682, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Viaud:2022:RLC

[VMC22] Gautier Viaud, Prasanna Mayilvahanan, and Paul-Henry Cournède. Representation learning for the clustering of multi-omics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):135–145, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3060340`.

Vassura:2008:RSP

[VMD+08] Marco Vassura, Luciano Margara, Pietro Di Lena, Filippo Medri, Piero Fariselli, and Rita Casadio. Reconstruction of 3D structures from protein contact maps. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):357–367, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vasylchenkova:2017:CMA

[VMZM17] Anastasiia Vasylchenkova, Miha Mraz, Nikolaj Zimic, and Miha Moskon. Classical mechanics approach applied to analysis of genetic oscillators. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):721–727, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vogt:2015:USD

[Vog15] Julia E. Vogt. Unsupervised structure detection in biomedical data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):753–760, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Varghese:2015:RLW

[VPB15] Blesson Varghese, Ishan Patel, and Adam Barker. RBioCloud: a light-weight framework for bioconductor and

R-based jobs on the cloud. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):871–878, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Villaverde:2023:APU

[VRHB23] Alejandro F. Villaverde, Elba Raimúndez, Jan Hasenauer, and Julio R. Banga. Assessment of prediction uncertainty quantification methods in systems biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1725–1736, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3213914`.

Verspoor:2010:ESB

[VRJ+10] Karin Verspoor, Christophe Roeder, Helen L. Johnson, Kevin Bretonnel Cohen, William A. Baumgartner, Jr., and Lawrence E. Hunter. Exploring species-based strategies for gene normalization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):462–471, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vasic:2012:ITA

[VRK12] Bane Vasic, Vida Ravanmehr, and Anantha Raman Krishnan. An information theoretic approach to constructing robust Boolean gene regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):52–65, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Venkateswaran:2011:TTF

[VSKJ11] Jayendra Gnanaskandan Venkateswaran, Bin Song, Tamer Kahveci, and Christopher Jermaine. TRIAL: a tool for finding distant structural similarities. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 819–831, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vass:2006:JMB

[VSR+06] Marc T. Vass, Clifford A. Shaffer, Naren Ramakrishnan, Layne T. Watson, and John J. Tyson. The JigCell model builder: a spreadsheet interface for creating biochemical reaction network models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(2):155–164, April 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Vilor-Tejedor:2016:EPM

[VTGC16] Natalia Vilor-Tejedor, Juan R. Gonzalez, and M. Luz Calle. Efficient and powerful method for combining P-values in genome-wide association studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1100–1106, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

V:2022:HIN

[VTMG22] Sunil Kumar P. V., Adheeba Thahsin, Manju M., and Gopakumar G. A heterogeneous information network model for long noncoding RNA function prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):255–266, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3000518`.

Weidman:2019:SIP

[WAG19] Jake Weidman, William Aurite, and Jens Grossklags. On sharing intentions, and personal and interdependent privacy considerations for genetic data: a vignette study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1349–1361, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wohlers:2013:DOD

[WAK13] Inken Wohlers, Rumen Andonov, and Gunnar W. Klau. DALIX: Optimal DALI protein structure alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):26–36, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2012:OSA

[Wan12] Biing-Feng Wang. Output-sensitive algorithms for finding the nested common intervals of two general sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):548–559, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2016:NEA

[Wan16] Biing-Feng Wang. A new efficient algorithm for the all sorting reversals problem with no bad components. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):599–609, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wong:2011:UKA

[WB11] William W. L. Wong and Forbes J. Burkowski. Using kernel alignment to select features of molecular descriptors in a QSAR study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5): 1373–1384, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2017:BCO

[WB17] Xin Wang and Jinbo Bi. Bi-convex optimization to learn classifiers from multiple biomedical annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):564–575, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wehe:2013:EAK

[WBE13] Andre Wehe, J. Gordon Burleigh, and Oliver Eulenstein. Efficient algorithms for knowledge-enhanced supertree and supermatrix phylogenetic problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1432–1441, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2012:EMM

[WBP+12] Chong Wang, Peter Beyerlein, Heike Pospisil, Antje Krause, Chris Nugent, and Werner Dubitzky. An efficient method for modeling kinetic behavior of channel proteins in cardiomyocytes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):40–51, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2019:MMV

[WCA+19] Aiguo Wang, Ye Chen, Ning An, Jing Yang, Lian Li, and Lili Jiang. Microarray missing value imputation: a regularized local learning method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):980–993, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2018:PHR

[WCC+18] Haishuai Wang, Zhicheng Cui, Yixin Chen, Michael Avidan, Arbi Ben Abdallah, and Alexander Kronzer. Predicting hospital readmission via cost-sensitive deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1968–1978, November 2018. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2023:CAB

[WCDM23] Qingbin Wang, Kaiyi Chen, Wanrong Dou, and Yutao Ma. Cross-attention based multi-resolution feature fusion model for self-supervised cervical OCT image classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2541–2554, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3246979`.

Wu:2011:ACC

[WCL11] Yonghui Wu, Timothy J. Close, and Stefano Lonardi. Accurate construction of consensus genetic maps via integer linear programming. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):381–394, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wong:2012:MEA

[WCLY12] Thomas K. F. Wong, Y. S. Chiu, T. W. Lam, and S. M. Yiu. Memory efficient algorithms for structural alignment of RNAs with pseudoknots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):161–168, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2020:GDI

[WCLY20] Shunfang Wang, Zicheng Cao, Mingyuan Li, and Yaoting Yue. G-DipC: an improved feature representation method for short sequences to predict the type of cargo in cell-penetrating peptides. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):739–747, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2930993`.

Wingfield:2019:RMM

[WCMB19] Benjamin Wingfield, Sonya Coleman, TM McGinnity, and AJ Bjourson. Robust microbial markers for non-invasive inflammatory bowel disease identification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 2078–2088, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2831212`.

Wang:2015:BMM

[WCMZ15] Beichen Wang, Xiaodong Chen, Hiroshi Mamitsuka,

and Shanfeng Zhu. BMExpert: Mining MEDLINE for finding experts in biomedical domains based on language model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1286–1294, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2019:DDR

[WCQ+19] Yin-Ying Wang, Chunfeng Cui, Liqun Qi, Hong Yan, and Xing-Ming Zhao. DrPOCS: Drug repositioning based on projection onto convex sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):154–162, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2007:ACC

[WCX07] Lipo Wang, Feng Chu, and Wei Xie. Accurate cancer classification using expressions of very few genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):40–53, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2022:ETM

[WCX+22] Qing-Wen Wu, Rui-Fen Cao, Jun-Feng Xia, Jian-Cheng Ni, Chun-Hou Zheng, and Yan-Sen Su. Extra trees method for predicting LncRNA–disease association based on multi-layer graph embedding aggregation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3171–3178, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3113122`.

Wu:2018:UDL

[WCXL18] Hongjie Wu, Chengyuan Cao, Xiaoyan Xia, and Qiang Lu. Unified deep learning architecture for modeling biology sequence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1445–1452, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wei:2023:CMB

[WCZ+23] Ze-Gang Wei, Xu Chen, Xiao-Dan Zhang, Hao Zhang, Xing-Guo Fan, Hong-Yan Gao, Fei Liu, and Yu Qian. Comparison of methods for biological sequence clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2874–2888, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964

(electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3253138`.

Wiese:2008:REA

[WDH08] Kay C. Wiese, Alain A. Deschenes, and Andrew G. Hendriks. RnaPredict—An evolutionary algorithm for RNA secondary structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):25–41, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2017:SAL

[WDL+17] Chao Wang, Dong Dai, Xi Li, Aili Wang, and Xuehai Zhou. SuperMIC: Analyzing large biological datasets in bioinformatics with maximal information coefficient. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):783–795, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2022:IGS

[WDL+22] Fei Wang, Yulian Ding, Xiujuan Lei, Bo Liao, and Fang-Xiang Wu. Identifying gene signatures for cancer drug repositioning based on sample clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):953–965, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3019781`.

Wu:2012:BIC

[WDS+12] Meng-Yun Wu, Dao-Qing Dai, Yu Shi, Hong Yan, and Xiao-Fei Zhang. Biomarker identification and cancer classification based on microarray data using Laplace naive Bayes model with mean shrinkage. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1649–1662, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2015:PDC

[WDX+15] Kun Wang, Avinash Das, Zheng-Mei Xiong, Kan Cao, and Sridhar Hannenhalli. Phenotype-dependent coexpression gene clusters: application to normal and premature ageing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):30–39, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wernicke:2006:EDN

[Wer06] Sebastian Wernicke. Efficient detection of network motifs. *IEEE/ACM Trans-*

actions on Computational Biology and Bioinformatics, 3(4):347–359, October 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wan:2015:PPL

[WFD15] Cen Wan, Alex A. Freitas, and João Pedro De Magalhães. Predicting the prolongevity or anti-longevity effect of model organism genes with new hierarchical feature selection methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (2):262–275, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2019:NCA

[WFY+19] Yishu Wang, Huaying Fang, Dejie Yang, Hongyu Zhao, and Minghua Deng. Network clustering analysis using mixture exponential-family random graph models and its application in genetic interaction data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1743–1752, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2021:HGR

[WFY21] Xiuhui Wang, Shiling Feng, and Wei Qi Yan. Human gait recognition based on self-adaptive hidden Markov model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):963–972, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2951146`.

Wu:2016:NBM

[WGK16] Hao Wu, Lin Gao, and Nikola K. Kasabov. Network-based method for inferring cancer progression at the pathway level from cross-sectional mutation data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6): 1036–1044, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2021:GSH

[WGL+21] Chao Wang, Lei Gong, Shiming Lei, Haijie Fang, Xi Li, Aili Wang, and Xuehai Zhou. GenSeq+: a scalable high-performance accelerator for genome sequencing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1512–1523, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2947059`.

Wang:2011:IMG

[WGP11] Wenxue Wang, Bijoy K. Ghosh, and Himadri Pakrasi. Identification and modeling of genes with diurnal oscillations from microarray time series data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):108–121, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2017:HBH

[WGX+17] Pu Wang, Ruiquan Ge, Xuan Xiao, Manli Zhou, and Fengfeng Zhou. hMuLab: a biomedical hybrid MUlti-LABel classifier based on multiple linear regression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1173–1180, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2011:GES

[WH11] Fang-Xiang Wu and Jun Huan. Guest editorial: Special focus on bioinformatics and systems biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (2):292–293, March 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wieseke:2015:CRI

[WHBM15] Nicolas Wieseke, Tom Hartmann, Matthias Bernt, and Martin Middendorf. Cophylogenetic reconciliation with ILP. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1227–1235, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2020:IIE

[WHF+20] Min Wang, Ting-Zhu Huang, Jian Fang, Vince D. Calhoun, and Yu-Ping Wang. Integration of imaging (epi)genomics data for the study of schizophrenia using group sparse joint nonnegative matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1671–1681, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2899568`.

Weskamp:2007:MGA

[WHKK07] Nils Weskamp, Eyke Hullermeier, Daniel Kuhn, and Gerhard Klebe. Multiple graph alignment for the structural analysis of protein active sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):310–320, April

2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2024:LGN

[WHL+24] Wenjing Wang, Pengyong Han, Zhengwei Li, Ru Nie, Kangwei Wang, Lei Wang, and Hongmei Liao. LMGATCDA: Graph neural network with labeling trick for predicting circRNA-disease associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):289–300, March 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3355093`.

Witwer:2004:PCR

[WHS04] Christina Witwer, Ivo L. Hofacker, and Peter F. Stadler. Prediction of consensus RNA secondary structures including pseudoknots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(2):66–77, April 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2021:MCI

[WHW21] Zilu Wang, Qinghui Hong, and Xiaoping Wang. A memristive circuit implementation of eyes state detection in fatigue driving based on biological long short-term memory rule. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2218–2229, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2974944`.

Wang:2012:SCM

[WHWP12] Jianxin Wang, Yuannan Huang, Fang-Xiang Wu, and Yi Pan. Symmetry compression method for discovering network motifs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6):1776–1789, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2017:SLF

[WHXS17] Zhiyong Wang, Benika Hall, Jinbo Xu, and Xinghua Shi. A sparse learning framework for joint effect analysis of copy number variants. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5): 1013–1027, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2014:GWP

[WHZ14] Jian-Sheng Wu, Sheng-Jun Huang, and Zhi-Hua

Zhou. Genome-wide protein function prediction through multi-instance multi-label learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):891–902, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wigren:2015:MOI

[Wig15] Torbjorn Wigren. Model order and identifiability of non-linear biological systems in stable oscillation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1479–1484, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Williams:2004:INA

[Wil04a] Michael R. Williams. Introduction of new Associate Editors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):4–12, January 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Williams:2004:WM

[Wil04b] Michael R. Williams. Welcome message. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):1, January 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Willson:2009:RTS

[Wil09] Stephen J. Willson. Robustness of topological supertree methods for reconciling dense incompatible data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(1):62–75, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Willson:2011:RNC

[Wil11] Stephen J. Willson. Regular networks can be uniquely constructed from their trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 785–796, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Willson:2012:CHB

[Wil12] Stephen Willson. CSD homomorphisms between phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1128–1138, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wiedenhoeft:2011:PMI

[WKE11] John Wiedenhoeft, Roland Krause, and Oliver Eulenstein. The plexus model

for the inference of ancestral multidomain proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):890–901, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2012:NEA

[WKLL12] Biing-Feng Wang, Chung-Chin Kuo, Shang-Ju Liu, and Chien-Hsin Lin. A new efficient algorithm for the gene-team problem on general sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):330–344, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wei:2021:ECG

[WKSP21] Dong-Qing Wei, Aman Chandra Kaushik, Gurudeeban Selvaraj, and Yi Pan. Editorial: Computational genomics and molecular medicine for emerging COVID-19. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1227–1229, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3088319`.

Wu:2024:CCC

[WKZ+24] Yirui Wu, Qiran Kong, Lilai Zhang, Aniello Castiglione, Michele Nappi, and Shaohua Wan. CDT-CAD: Context-aware deformable transformers for end-to-end chest abnormality detection on X-ray images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):823–834, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3258455`.

Wan:2007:CCN

[WL07] Xiang Wan and Guohui Lin. CISA: Combined NMR resonance connectivity information determination and sequential assignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):336–348, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2011:IAF

[WL11] Biing-Feng Wang and Chien-Hsin Lin. Improved algorithms for finding gene teams and constructing gene team trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1258–1272, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wandelt:2013:FRC

[WL13a] Sebastian Wandelt and Ulf Leser. FRESCO: Referential compression of highly similar sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1275–1288, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2013:MLR

[WL13b] Xiao Wang and Guo-Zheng Li. Multilabel learning via random label selection for protein subcellular multilocations prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):436–446, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wong:2014:ACP

[WL14] Andrew K. C. Wong and En-Shiun Annie Lee. Aligning and clustering patterns to reveal the protein functionality of sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):548–560, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2019:FAC

[WL19] Biing-Feng Wang and Chih-Yu Li. Fast algorithms for computing path-difference distances. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):569–582, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2790957`.

Wickramarachchi:2022:PGR

[WL22] Anuradha Wickramarachchi and Yu Lin. GraphPlas: Refined classification of plasmid sequences using assembly graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):57–67, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3082915`.

Wu:2013:ROC

[WLA+13] Xia Wu, Juan Li, Napatkamon Ayutyanont, Hillary Protas, William Jagust, Adam Fleisher, Eric Reiman, Li Yao, and Kewei Chen. The receiver operational characteristic for binary classification with multiple indices and its application to the neuroimaging study of Alzheimer's disease. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):173–180, January 2013.

CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wong:2011:EAE

[WLC11] Samuel S. Y. Wong, Weimin Luo, and Keith C. C. Chan. EvoMD: An algorithm for evolutionary molecular design. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):987–1003, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2015:HCF

[WLC+15] Chao Wang, Xi Li, Peng Chen, Aili Wang, Xuehai Zhou, and Hong Yu. Heterogeneous cloud framework for big data genome sequencing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):166–178, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2018:GEA

[WLC18] Lusheng Wang, Shuai Cheng Li, and Yi-Ping Phoebe Chen. Guest editorial for the 15th Asia Pacific Bioinformatics Conference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1513–1514, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2011:FHC

[WLCP11] Jianxin Wang, Min Li, Jianer Chen, and Yi Pan. A fast hierarchical clustering algorithm for functional modules discovery in protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 607–620, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2018:AMR

[WLCX18] Annie Wang, Hansaim Lim, Shu-Yuan Cheng, and Lei Xie. ANTENNA, a multi-rank, multi-layered recommender system for inferring reliable drug-gene-disease associations: Repurposing diazoxide as a targeted anti-cancer therapy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1960–1967, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wei:2014:IPI

[WLG+14] Leyi Wei, Minghong Liao, Yue Gao, Rongrong Ji, Zengyou He, and Quan Zou. Improved and promising identification of human MicroRNAs by incorporat-

ing a high-quality negative set. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1):192–201, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2016:CGS

[WLG+16] Dong Wang, Jin-Xing Liu, Ying-Lian Gao, Chun-Hou Zheng, and Yong Xu. Characteristic gene selection based on robust graph regularized non-negative matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1059–1067, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2021:EPE

[WLG+21] Hongjie Wu, Huajing Ling, Lei Gao, Qiming Fu, Weizhong Lu, Yijie Ding, Min Jiang, and Haiou Li. Empirical potential energy function toward ab initio folding G protein-coupled receptors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1752–1762, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3008014`.

Wang:2019:LSF

[WLHY19] Yanbo Wang, Quan Liu, Shan Huang, and Bo Yuan. Learning a structural and functional representation for gene expressions: To systematically dissect complex cancer phenotypes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1729–1742, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2009:EKF

[WLL+09] Zidong Wang, Xiaohui Liu, Yurong Liu, Jinling Liang, and Veronica Vinciotti. An extended Kalman filtering approach to modeling nonlinear dynamic gene regulatory networks via short gene expression time series. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3):410–419, July 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wong:2013:PPL

[WLL13] Ginny Y. Wong, Frank H. F. Leung, and Sai-Ho Ling. Predicting protein-ligand binding site using support vector machine with protein properties. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1517–1529,

November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2020:MME

[WLL+20] Binbin Wu, Min Li, Xingyu Liao, Junwei Luo, Fang-Xiang Wu, Yi Pan, and Jianxin Wang. MEC: Misassembly error correction in contigs based on distribution of paired-end reads and statistics of GC-contents. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):847–857, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2876855`.

Wang:2024:MTI

[WLL+24] Wenyan Wang, Yongtao Li, Kun Lu, Jun Zhang, Peng Chen, Ke Yan, and Bing Wang. Medical tumor image classification based on few-shot learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):715–724, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3282226`.

Wang:2011:IMP

[WLMW+11] Li-San Wang, Jim Leebens-Mack, P. Kerr Wall, Kevin Beckmann, Claude W. dePamphilis, and Tandy Warnow. The impact of multiple protein sequence alignment on phylogenetic estimation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):1108–1119, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2022:CRR

[WLMZ22] Conghua Wang, Haihong Liu, Zhonghua Miao, and Jin Zhou. Circadian rhythm regulated by tumor suppressor p53 and time delay in unstressed cells. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1523–1530, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3040368`.

Wang:2023:MDA

[WLP23] Yueyue Wang, Xiujuan Lei, and Yi Pan. Microbe-disease association prediction using RGCN through microbe-drug-disease network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3353–3362, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2023.3247035.

Wong:2016:CSD

[WLPW16] Ka-Chun Wong, Yue Li, Chengbin Peng, and Hau-San Wong. A comparison study for DNA motif modeling on protein binding microarray. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):261–271, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2023:MPM

[WLW+23a] Huan Wang, Ruigang Liu, Baijing Wang, Yifan Hong, Ziwen Cui, and Qiufen Ni. Multitype perception method for drug-target interaction prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3489–3498, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3285042.

Wang:2023:MPI

[WLW23b] Xin Wang, Jie Li, and Guohua Wang. MicroRNA promoter identification in human with a three-level prediction method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3600–3608, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3305992.

Wang:2022:NBG

[WLWJ22] Shiming Wang, Jie Li, Yadong Wang, and Liran Juan. A neighborhood-based global network model to predict drug-target interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):2017–2025, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3064614.

Wang:2017:GES

[WLWN17] Fei Wang, Xiao-Li Li, Jason T. L. Wang, and See-Kiong Ng. Guest editorial: Special section on biological data mining and its applications in healthcare. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):501–502, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2012:IEP

[WLWP12] Jianxin Wang, Min Li, Huan Wang, and Yi Pan. Identification of essential proteins based on edge clustering coefficient. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

9(4):1070–1080, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2014:CGT

[WLY14] Biing-Feng Wang, Chien-Hsin Lin, and I-Tse Yang. Constructing a gene team tree in almost $O(n \lg n)$ time. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 (1):142–153, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2015:CNI

[WLY15] Pei Wang, Jinhu Lü, and Xinghuo Yu. Colored noise induced bistable switch in the genetic toggle switch systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):579–589, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2009:EPS

[WLYZ+09] Yong Wang, Wu Ling-Yun, Ji-Hong Zhang, Zhong-Wei Zhan, Zhang Xiang-Sun, and Chen Luonan. Evaluating protein similarity from coarse structures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (4):583–593, October 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2019:MNL

[WLZ+19] Juan Wang, Jin-Xing Liu, Chun-Hou Zheng, Ya-Xuan Wang, Xiang-Zhen Kong, and Chang-Gang Wen. A mixed-norm Laplacian regularized low-rank representation method for tumor samples clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):172–182, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2019:AIR

[WM19a] Tiancong Wang and Bin Ma. Adjacent Y-ion ratio distributions and its application in peptide sequencing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):43–51, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Whidden:2019:CUS

[WM19b] Chris Whidden and Frederick A. Matsen. Calculating the unrooted subtree prune-and-regraft distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):898–911, May 2019. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Wan:2016:MMP

[WMK16] Shibiao Wan, Man-Wai Mak, and Sun-Yuan Kung. MemmEN: Predicting multi-functional types of membrane proteins by interpretable elastic nets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):706–718, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wan:2017:TLM

[WMK17] Shibiao Wan, Man-Wai Mak, and Sun-Yuan Kung. Transductive learning for multi-label protein subchloroplast localization prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (1):212–224, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2009:RPT

[WMS09] Taoyang Wu, Vincent Moulton, and Mike Steel. Refining phylogenetic trees given additional data: An algorithm based on parsimony. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6 (1):118–125, January 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2021:IDP

[WMW+21] Bing Wang, Changqing Mei, Yuanyuan Wang, Yuming Zhou, Mu-Tian Cheng, Chun-Hou Zheng, Lei Wang, Jun Zhang, Peng Chen, and Yan Xiong. Imbalance data processing strategy for protein interaction sites prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):985–994, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2953908`.

Wang:2012:EGS

[WMWA12] Daifeng Wang, Mia K. Markey, Claus O. Wilke, and Ari Arapostathis. Eigengenomic system dynamic-pattern analysis (ESDA): Modeling mRNA degradation and self-regulation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):430–437, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Walker:2017:ATS

[WNT+17] Peter B. Walker, Jacob N. Norris, Anna E. Tschiffely, Melissa L. Mehalick,

Craig A. Cunningham, and Ian N. Davidson. Applications of transductive spectral clustering methods in a military medical concussion database. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):534–544, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2017:PCD

[WOYL17] Min Wu, Le Ou-Yang, and Xiao-Li Li. Protein complex detection via effective integration of base clustering solutions and co-complex affinity scores. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):733–739, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wei:2008:IGF

[WP08] Peng Wei and Wei Pan. Incorporating gene functions into regression analysis of DNA-protein binding data and gene expression data to construct transcriptional networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):401–415, July 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wong:2015:PIM

[WPL15] Ka-Chun Wong, Chengbin Peng, and Yue Li. Probabilistic inference on multiple normalized signal profiles from next generation sequencing: Transcription factor binding sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1416–1428, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wei:2016:MDD

[WQL+16] Guanyun Wei, Sheng Qin, Wenjuan Li, Liming Chen, and Fei Ma. MDTE DB: a database for MicroRNAs derived from transposable element. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1155–1160, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2023:DTL

[WQLL23] Jinxia Wang, Liang Qiao, Haibin Lv, and Zhihan Lv. Deep transfer learning-based multi-modal digital twins for enhancement and diagnostic analysis of brain MRI image. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (4):2407–2419, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964

(electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3168189`.

Wang:2018:GMS

[WQY18] Yanbo Wang, Weikang Qian, and Bo Yuan. A graphical model of smoking-induced global instability in lung cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(1):1–14, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Weber:2009:VET

[WRH+09] Gunther H. Weber, Oliver Rubel, Min-Yu Huang, Angela H. DePace, Charless C. Fowlkes, Soile V. E. Keranen, Cris L. Luengo Hendriks, Hans Hagen, David W. Knowles, Jitendra Malik, Mark D. Biggin, and Bernd Hamann. Visual exploration of three-dimensional gene expression using physical views and linked abstract views. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):296–309, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2008:DCO

[WS08] Xueyi Wang and Jack Snoeyink. Defining and computing optimum RMSD for gapped and weighted multiple-structure alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5 (4):525–533, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wan:2012:CAD

[WS12] Lin Wan and Fengzhu Sun. CEDER: Accurate detection of differentially expressed genes by combining significance of exons using RNA-Seq. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5):1281–1292, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2021:FAC

[WS21] Biing-Feng Wang and Krister M. Swenson. A faster algorithm for computing the kernel of maximum agreement subtrees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):416–430, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2922955`.

Willing:2021:CII

[WSB21] Eyla Willing, Jens Stoye, and Marília D. V. Braga.

Computing the inversion-indel distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2314–2326, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2988950`.

Wang:2021:EDP

[WSJ21] Yaqi Wang, Lingling Sun, and Qun Jin. Enhanced diagnosis of pneumothorax with an improved real-time augmentation for imbalanced chest X-rays data based on DCNN. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 951–962, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2911947`.

Wang:2024:MPH

[WSL+24] Wei Wang, Zhenxi Sun, Dong Liu, Hongjun Zhang, Juntao Li, Xianfang Wang, and Yun Zhou. MAHyNet: Parallel hybrid network for RNA-Protein binding sites prediction based on multi-head attention and expectation pooling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):416–427, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3366545`.

Wong:2015:DBC

[WSTL+15] Man-Hon Wong, Ho-Yin Sze-To, Leung-Yau Lo, Tak-Ming Chan, and Kwong-Sak Leung. Discovering binding cores in Protein–DNA binding using association rule mining with statistical measures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):142–154, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2011:ICA

[WSX11] Qingguo Wang, Yi Shang, and Dong Xu. Improving a consensus approach for protein structure selection by removing redundancy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1708–1715, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

weiTan:2020:DLP

[wTCAK+20] Jing wei Tan, Siow-Wee Chang, Sameem Abdul-Kareem, Hwa Jen Yap, and Kien-Thai Yong. Deep learning for plant species classification using leaf vein morphometric. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 17(1):82–90, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2848653`.

Williams:2023:FDS

[WTM23] Lucia Williams, Alexandru I. Tomescu, and Brendan Mumey. Flow decomposition with subpath constraints. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):360–370, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3147697`.

Wu:2010:ECC

[Wu10] Yufeng Wu. Exact computation of coalescent likelihood for panmictic and subdivided populations under the infinite sites model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):611–618, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2011:NMI

[Wu11] Yufeng Wu. New methods for inference of local tree topologies with recombinant SNP sequences in populations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (1):182–193, January 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2019:CDM

[WW19] Peng Wu and Dong Wang. Classification of a DNA microarray for diagnosing cancer using a complex network based method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):801–808, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2022:GDC

[WW22] Pei Wang and Daojie Wang. Gene differential co-expression networks based on RNA-Seq: Construction and its applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2829–2841, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3103280`.

Wassan:2019:CSP

[WWBZ19] Jyotsna Talreja Wassan, Haiying Wang, Fiona Browne, and Huiru Zheng. A comprehensive study on predicting functional role of

metagenomes using machine learning methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):751–763, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2018:NCG

[WWC18] Ho-Chun Wu, Xi-Guang Wei, and Shing-Chow Chan. Novel consensus gene selection criteria for distributed GPU partial least squares-based gene microarray analysis in diffused Large B Cell Lymphoma DLBCL and related findings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):2039–2052, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2021:AMA

[WWF+21] Liguang Wang, Yujia Wang, Yi Fu, Yunge Gao, Jiawei Du, Chen Yang, and Jianxiao Liu. AFSBN: a method of artificial fish swarm optimizing Bayesian network for epistasis detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1369–1383, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2949780`.

Wu:2017:DCR

[WWL+17] Hongjie Wu, Kun Wang, Liyao Lu, Yu Xue, Qiang Lyu, and Min Jiang. Deep conditional random field approach to transmembrane topology prediction and application to GPCR three-dimensional structure modeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1106–1114, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2019:CAG

[WWL19] Pei Wang, Daojie Wang, and Jinhu Lu. Controllability analysis of a gene network for *Arabidopsis thaliana* reveals characteristics of functional gene families. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):912–924, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2023:PPB

[WWL+23a] Shanshan Wang, Ruoyou Wu, Cheng Li, Juan Zou, Ziyao Zhang, Qiegen Liu, Yan Xi, and Hairong Zheng. PARCEL: Physics-based unsupervised contrastive representation learning for

multi-coil MR imaging. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5): 2659–2670, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3213669`.

Wu:2023:PCS

[WWL+23b] Kaitao Wu, Lexiang Wang, Bo Liu, Yang Liu, Yadong Wang, and Junyi Li. PSPGO: Cross-species heterogeneous network propagation for protein function prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1713–1724, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215257`.

Wang:2016:KBP

[WWLL16] Hong Wang, Xicheng Wang, Zheng Li, and Keqiu Li. Kriging-based parameter estimation algorithm for metabolic networks combined with single-dimensional optimization and dynamic coordinate perturbation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6): 1142–1154, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2020:PNC

[WWT+20] Sijia Wu, Xiaoming Wu, Jie Tian, Xiaobo Zhou, and Liyu Huang. PredictFP2: a new computational model to predict fusion peptide domain in all retroviruses. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5): 1714–1720, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2898943`.

Wang:2024:CMS

[WWY+24] Juan Wang, Zhenchang Wang, Shasha Yuan, Chunhou Zheng, Jinxing Liu, and Junliang Shang. A clustering method for single-cell RNA-Seq data based on automatic weighting penalty and low-rank representation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):360–371, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3362472`.

Wei:2019:FPP

[WXS+19] Leyi Wei, Pengwei Xing, Gaotao Shi, Zhiliang Ji, and Quan Zou. Fast prediction of protein methylation sites using a sequence-based feature selection tech-

nique. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1264–1273, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2020:DLS

[WXWL20] Hang Wang, Jianing Xi, Minghui Wang, and Ao Li. Dual-layer strengthened collaborative topic regression modeling for predicting drug sensitivity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):587–598, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2864739`.

Wang:2023:CNN

[WXY+23] Mei-Neng Wang, Xue-Jun Xie, Zhu-Hong You, Leon Wong, Li-Ping Li, and Zhan-Heng Chen. Combining K nearest neighbor with nonnegative matrix factorization for predicting CircRNA-disease associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2610–2618, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3180903`.

Wang:2023:CML

[WYF+23] Wei Wang, Xinhua Yu, Bo Fang, Yue Zhao, Yongyong Chen, Wei Wei, and Junxin Chen. Cross-modality LGE-CMR segmentation using image-to-image translation based data augmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2367–2375, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3140306`.

Weyenberg:2017:NKB

[WYH17] Grady Weyenberg, Ruriko Yoshida, and Daniel Howe. Normalizing kernels in the Billera–Holmes–Vogtmann treespace. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1359–1365, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2017:PSP

[WYHD17] Hua Wang, Lin Yan, Heng Huang, and Chris Ding. From protein sequence to protein function via multi-label linear discriminant analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):503–513, May 2017. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Wang:2020:CHS

[WYHZ20] Lei Wang, Zhu-Hong You, De-Shuang Huang, and Fengfeng Zhou. Combining high speed ELM learning with a deep convolutional neural network feature encoding for predicting Protein-RNA interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):972–980, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2874267`.

Wu:2007:QBP

[WYL07] Gang Wu, Jia-Huai You, and Guohui Lin. Quartet-based phylogeny reconstruction with answer set programming. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (1):139–152, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2024:SMS

[WYS+24] Wei Wang, Mengxue Yu, Bin Sun, Juntao Li, Dong Liu, Hongjun Zhang, Xianfang Wang, and Yun Zhou. SMGCN: Multiple similarity and multiple kernel fusion based graph convolutional neural network for drug-target interactions prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):143–154, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3339645`.

Wang:2016:GES

[WYWX16] Chao Wang, Hong Yu, Aili Wang, and Kai Xia. Guest editorial for special section on big data computing and processing in computational biology and bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 810–811, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wan:2013:HFA

[WYY+13] Xiang Wan, Can Yang, Qiang Yang, Hongyu Zhao, and Weichuan Yu. HapBoost: a fast approach to boosting haplotype association analyses in genome-wide association studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):207–212, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wu:2013:SBP

[WZ13a] Jian-Sheng Wu and Zhi-

Hua Zhou. Sequence-based prediction of microRNA-binding residues in proteins using cost-sensitive Laplacian support vector machines. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):752–759, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wylie:2013:PCP

[WZ13b] Tim Wylie and Binhai Zhu. Protein chain pair simplification under the discrete Fréchet distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1372–1383, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2014:OMI

[WZ14] Haiying Wang and Huiru Zheng. Organized modularity in the interactome: evidence from the analysis of dynamic organization in the cell cycle. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1264–1270, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2007:PBS

[WZA07] Haiying Wang, Huiru Zheng, and Francisco Azuaje. Poisson-based self-organizing feature maps and hierarchical clustering for serial analysis of gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(2):163–175, April 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2015:CCA

[WZC+15] Jianxin Wang, Jiancheng Zhong, Gang Chen, Min Li, Fang xiang Wu, and Yi Pan. ClusterViz: a cytoscape APP for cluster analysis of biological network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):815–822, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2021:PPG

[WZC+21] Wenyan Wang, Yuming Zhou, Mu-Tian Cheng, Yan Wang, Chun-Hou Zheng, Yan Xiong, Peng Chen, Zhiwei Ji, and Bing Wang. Potential pathogenic genes prioritization based on protein domain interaction network analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):1026–1034, May/June 2021. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2020.2983894.

Wu:2023:MVC

[WZHM23] Wenming Wu, Wensheng Zhang, Weimin Hou, and Xiaoke Ma. Multi-view clustering with graph learning for scRNA-Seq data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6): 3535–3546, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3298334.

Wang:2012:RCM

[WZJH12] Shu-Lin Wang, Yi-Hai Zhu, Wei Jia, and De-Shuang Huang. Robust classification method of tumor subtype by using correlation filters. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (2):580–591, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2023:EFI

[WZJS23] Chao Wang, Quan Zou, Ying Ju, and Hua Shi. EnhancerFRL: Improved and robust identification of enhancers and their activities using feature representation learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):967–975, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3204365.

Wang:2022:PED

[WZR+22] Jun Wang, Huiling Zhang, Wei Ren, Maozu Guo, and Guoxian Yu. EpiMC: Detecting epistatic interactions using multiple clusterings. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (1):243–254, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3080462.

Wang:2022:FSD

[WZS+22] Yan Wang, Lei Zhang, Xin Shu, Yangqin Feng, Zhang Yi, and Qing Lv. Feature-sensitive deep convolutional neural network for multi-instance breast cancer detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):2241–2251, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3060183.

Wang:2018:CDB

[WZZ+18] Bin Wang, Xuedong Zheng, Shihua Zhou, Changjun

Zhou, Xiaopeng Wei, Qiang Zhang, and Ziqi Wei. Constructing DNA barcode sets based on particle swarm optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):999–1002, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Wang:2022:DPI

[WZZ+22] Jun Wang, Long Zhang, An Zeng, Dawen Xia, Jiantao Yu, and Guoxian Yu. DeepIII: Predicting isoform-isoform interactions by deep neural networks and data fusion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):2177–2187, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3068875`.

Xu:2007:MCC

[XAW07] Rui Xu, Georgios C. Anagnostopoulos, and Donald C. Wunsch. Multiclass cancer classification using semisupervised ellipsoid ARTMAP and particle swarm optimization with gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):65–77, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xiao:2021:EIA

[XCR21] Peng Xiao, Xingyu Cai, and Sanguthevar Rajasekaran. EMS3: an improved algorithm for finding edit-distance based motifs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):27–37, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3024222`.

Xu:2023:IDI

[XDZ+23] Wuli Xu, Lei Duan, Huiru Zheng, Jesse Li-Ling, Weipeng Jiang, Yidan Zhang, Tingting Wang, and Ruiqi Qin. An integrative disease information network approach to similar disease detection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2724–2735, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3110127`.

Xu:2014:FIN

[XG14] Bin Xu and Jihong Guan. From function to interaction: a new paradigm for accurately predicting protein complexes based on protein-to-protein interaction networks. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 11(4):616–627, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2019:EPD

[XGWW19] Bin Xu, Jihong Guan, Yang Wang, and Zewei Wang. Essential protein detection by random walk on weighted protein–protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):377–387, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2701824`.

Xia:2018:STS

[XHQ+18] Chun-Qiu Xia, Ke Han, Yong Qi, Yang Zhang, and Dong-Jun Yu. A self-training subspace clustering algorithm under low-rank representation for cancer classification on gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1315–1324, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2015:GEI

[XHS15] Dong Xu, Kun Huang, and Jeanette Schmidt. Guest editors introduction to the special section on software and databases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):793–794, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xiong:2022:MFI

[XHW+22] Zhankun Xiong, Feng Huang, Ziyan Wang, Shichao Liu, and Wen Zhang. A multimodal framework for improving *in Silico* drug repositioning with the prior knowledge from knowledge graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2623–2631, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3103595`.

Xie:2018:AGS

[XHY+18] Qian Xie, Xiaoyan He, Fangji Yang, Xuling Liu, Ying Li, Yujing Liu, Zheng-Meng Yang, Jianhai Yu, Bao Zhang, and Wei Zhao. Analysis of the genome sequence and prediction of B-cell epitopes of the envelope protein of Middle East respiratory syndrome-coronavirus. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1344–1350, July 2018. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic).

Xia:2021:GEA

[XJZS21] Kaijian Xia, Yizhang Jiang, Yudong Zhang, and Wen Si. Guest editorial: Advanced machine-learning methods for brain-machine interfacing or brain-computer interfacing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1643–1644, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3078145`.

Xi:2016:DRC

[XL16] Jianing Xi and Ao Li. Discovering recurrent copy number aberrations in complex patterns via non-negative sparse singular value decomposition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):656–668, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xiang:2015:RAA

[XLC+15] Yan-Ping Xiang, Ke Liu, Xian-Ying Cheng, Cheng Cheng, Fang Gong, Jian-Bo Pan, and Zhi-Liang Ji. Rapid assessment of adverse drug reactions by statistical solution of gene association network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):844–850, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2018:IBI

[XLL+18] Bo Xu, Hongfei Lin, Yuan Lin, Yunlong Ma, Liang Yang, Jian Wang, and Zhihao Yang. Improve biomedical information retrieval using modified learning to rank methods. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1797–1809, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2019:LRE

[XLL19] Bo Xu, Hongfei Lin, and Yuan Lin. Learning to refine expansion terms for biomedical information retrieval using semantic resources. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):954–966, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xiao:2020:ILM

[XLL+20] Qiu Xiao, Jiawei Luo, Cheng Liang, Guanghui Li, Jie Cai, Pingjian Ding, and Ying Liu. Identifying lncRNA and

mRNA co-expression modules from matched expression data in ovarian cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):623–634, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2864129`.

Xu:2021:GRB

[XLP+21] Yunpei Xu, Hong-Dong Li, Yi Pan, Feng Luo, Fang-Xiang Wu, and Jianxin Wang. A gene rank based approach for single cell similarity assessment and clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):431–442, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2931582`.

Xi:2020:HNM

[XLW20] Jianing Xi, Ao Li, and Minghui Wang. HetRCNA: a novel method to identify recurrent copy number alternations from heterogeneous tumor samples based on matrix decomposition framework. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):422–434, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2846599`.

Xia:2015:IGA

[XLWL15] Hong Xia, Yuanning Liu, Minghui Wang, and Ao Li. Identification of genomic aberrations in cancer subclones from heterogeneous tumor samples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):679–685, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xiao:2021:DWS

[XLX+21] Ming Xiao, Guangdi Liu, Jianghang Xie, Zichun Dai, Zihao Wei, Ziyao Ren, Jun Yu, and Le Zhang. 2019nCoVAS: Developing the web service for epidemic transmission prediction, genome analysis, and psychological stress assessment for 2019-nCoV. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1250–1261, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3049617`.

Xin:2015:ASI

[XLZ+15] Yao Xin, Will X. Y. Li, Zhaorui Zhang, Ray C. C. Cheung, Dong Song, and

Theodore W. Berger. An application specific instruction set processor (ASIP) for adaptive filters in neural prosthetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1034–1047, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xie:2022:DLP

[XLZW22] Yulian Xie, Min Liu, Shirui Zhou, and Yaonan Wang. A deep local patch matching network for cell tracking in microscopy image sequences without registration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3202–3212, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3113129`.

Xia:2021:CDC

[XNYC21] Kaijian Xia, TongGuang Ni, Hongsheng Yin, and Bo Chen. Cross-domain classification model with knowledge utilization maximization for recognition of epileptic EEG signals. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):53–61, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2973978`.

Xu:2018:IGN

[XOYHZ18] Ting Xu, Le Ou-Yang, Xiaohua Hu, and Xiao-Fei Zhang. Identifying gene network rewiring by integrating gene expression and gene network data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):2079–2085, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xiang:2012:TDT

[XPH12] Yang Xiang, Philip R. O. Payne, and Kun Huang. Transactional database transformation and its application in prioritizing human disease genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):294–304, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2020:CCP

[XPH20] Hongming Xu, Sunho Park, and Tae Hyun Hwang. Computerized classification of prostate cancer Gleason scores from whole slide images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):1871–1882,

November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2941195`.

Xu:2011:MLP

[XPXY11] Qian Xu, Sinno Jialin Pan, Hannah Hong Xue, and Qiang Yang. Multitask learning for protein subcellular location prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3): 748–759, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2021:ACT

[XSL+21] Benlian Xu, Jian Shi, Mingli Lu, Jinliang Cong, Ling Wang, and Brett Nener. An automated cell tracking approach with multi-Bernoulli filtering and ant colony labor division. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1850–1863, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2954502`.

Xie:2017:DFO

[XSS17] Lu Xie, Gregory R. Smith, and Russell Schwartz. Derivative-free optimization of rate parameters of capsid assembly models from bulk in vitro data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):844–855, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2012:AI

[XTL12a] Yun Xu, Da Teng, and Yiming Lei. 2011 annual index. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1):??, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2012:RL

[XTL12b] Yun Xu, Da Teng, and Yiming Lei. 2011 reviewers list. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):316–318, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2012:MLM

[XTL12c] Yun Xu, Da Teng, and Yiming Lei. MinePhos: a literature mining system for protein phoshphorylation information extraction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):311–315, January 2012. CODEN ITCBCY. ISSN

1545-5963 (print), 1557-9964 (electronic).

Xie:2024:RCA

[XTO+24] Xia Xie, Yuanyishu Tian, Kaoru Ota, Mianxiong Dong, Zhelong Liu, Hai Jin, and Dezhong Yao. Reinforced computer-aided framework for diagnosing thyroid cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):737–747, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3251323`.

Xu:2005:FRP

[Xu05] Jinbo Xu. Fold recognition by predicted alignment accuracy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(2):157–165, April 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2013:ENE

[Xu13] Ying Xu. Editorial from the new Editor-in–Chief. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1): 1, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2014:EEC

[Xu14a] Ying Xu. Editorial from the Editor-in-Chief. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):1, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2014:RAE

[Xu14b] Ying Xu. Reviewer appreciation editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):613, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2015:EEC

[Xu15] Ying Xu. Editorial from the Editor-in-Chief. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):1, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2016:IDA

[XW16] Xiaoyi Xu and Minghui Wang. Inferring disease associated phosphorylation sites via random walk on multilayer heterogeneous network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 836–844, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xie:2015:LFA

[XWC15] Minzhu Xie, Jianxin Wang, and Xin Chen. LGH: a fast and accurate algorithm for single individual haplotyping based on a two-locus linkage graph. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6):1255–1266, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2007:IGR

[XWF07] Rui Xu, Donald Wunsch II, and Ronald Frank. Inference of genetic regulatory networks with recurrent neural network models using particle swarm optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):681–692, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2024:SNS

[XWP+24] Guoxia Xu, Hao Wang, Marius Pedersen, Meng Zhao, and Hu Zhu. SSP-Net: a Siamese-based structure-preserving generative adversarial network for unpaired medical image enhancement. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):681–691, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3256709`.

Xin:2024:BLH

[XWQ+24] Junchang Xin, Mingcan Wang, Luxuan Qu, Qi Chen, Weiyiqi Wang, and Zhiqiong Wang. BIC-LP: a hybrid higher-order dynamic Bayesian network score function for gene regulatory network reconstruction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):188–199, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3345317`.

Xie:2016:AHA

[XXM+16] Jiang Xie, Chaojuan Xiang, Jin Ma, Jun Tan, Tieqiao Wen, Jinzhi Lei, and Qing Nie. An adaptive hybrid algorithm for global network alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(3):483–493, May 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2023:HMD

[XXW+23] Xiaolong Xu, Haoyan Xu, Liying Wang, Yuanyuan Zhang, and Fu Xaio. Hygeia:

a multilabel deep learning-based classification method for imbalanced electrocardiogram data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2480–2493, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3176905`.

Xu:2023:IGR

[XYLL23] Jie Xu, Guanxue Yang, Guohai Liu, and Hui Liu. Inferring gene regulatory networks via ensemble path consistency algorithm based on conditional mutual information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1807–1816, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3220581`.

Xiao:2020:CDW

[XYYZ20] Ming Xiao, Xiangyu Yang, Jun Yu, and Le Zhang. CGIDLA: Developing the Web server for CpG Island related density and LAUPs (lineage-associated underrepresented permutations) study. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2148–2154, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2935971`.

Xie:2019:EEM

[XYZ19] Wen-Bin Xie, Hong Yan, and Xing-Ming Zhao. EmDL: Extracting miRNA–drug interactions from literature. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1722–1728, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xiong:2007:DDK

[XZC07] Huilin Xiong, Ya Zhang, and Xue-Wen Chen. Data-dependent kernel machines for microarray data classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):583–595, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xie:2015:CTC

[XZG15] Xiaojing Xie, Shuigeng Zhou, and Jihong Guan. CoGI: Towards compressing genomes as an image. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1275–1285, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xu:2018:ESB

[XZG+18] Biao Xu, Yong Zhang, Dunwei Gong, Yinan Guo, and Miao Rong. Environment sensitivity-based cooperative co-evolutionary algorithms for dynamic multi-objective optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1877–1890, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Xi:2023:LPL

[XZG+23] Wen-Yu Xi, Feng Zhou, Ying-Lian Gao, Jin-Xing Liu, and Chun-Hou Zheng. LDCMFC: Predicting long non-coding RNA and disease association using collaborative matrix factorization based on correntropy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (3):1774–1782, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3215194`.

Xie:2021:PEG

[XZS+21] Jiang Xie, Chang Zhao, Jiamin Sun, Jiaxin Li, Fuzhang Yang, Jiao Wang, and Qing Nie. Prediction of essential genes in comparison states using machine learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1784–1792, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3027392`.

Xu:2014:BSB

[XZY+14] Yanxun Xu, Xiaofeng Zheng, Yuan Yuan, Marcos R. Estecio, Jean-Pierre Issa, Peng Qiu, Yuan Ji, and Shoudan Liang. BM-SNP: a Bayesian model for SNP calling using high throughput sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1038–1044, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2013:PEL

[YAB13] Ye Yang, Farnoosh A. Aghababazadeh, and David R. Bickel. Parametric estimation of the local false discovery rate for identifying genetic associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):98–108, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2022:AMI

[Yan22] Tzu-Hsien Yang. An ag-

gregation method to identify the RNA meta-stable secondary structure and its functionally interpretable structure ensemble. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):75–86, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3082396`.

Yu:2008:CAA

[YB08] Zeyun Yu and Chandrajit Bajaj. Computational approaches for automatic structural analysis of large biomolecular complexes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):568–582, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

You:2010:UGP

[YBGB10] Liwen You, Vladimir Brusic, Marcus Gallagher, and Mikael Boden. Using Gaussian process with test rejection to detect T-cell epitopes in pathogen genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(4):741–751, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yin:2008:NAC

[YC08] Zong-Xian Yin and Jung-Hsien Chiang. Novel algorithm for coexpression detection in time-varying microarray data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(1):120–135, January 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yuan:2012:SRN

[YCCM12] Yinyin Yuan, Christina Curtis, Carlos Caldas, and Florian Markowetz. A sparse regulatory network of copy-number driven gene expression reveals putative breast cancer oncogenes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):947–954, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yazdani:2020:BFP

[YCCY20] Hossein Yazdani, Leo L. Cheng, David C. Christiani, and Azam Yazdani. Bounded fuzzy possibilistic method reveals information about lung cancer through analysis of metabolomics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):526–535, March 2020. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2869757`.

Yan:2021:MIP

[YCX+21] Xiaodan Yan, Baojiang Cui, Yang Xu, Peilin Shi, and Ziqi Wang. A method of information protection for collaborative deep learning under GAN model attack. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 871–881, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2940583`.

Yu:2013:HFC

[YCY+13] Zhiwen Yu, Hantao Chen, Jane You, Guoqiang Han, and Le Li. Hybrid fuzzy cluster ensemble framework for tumor clustering from biomolecular data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):657–670, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2014:DSB

[YCY+14] Zhiwen Yu, Hongsheng Chen, Jane You, Hau-San Wong, Jiming Liu, Le Li, and Guoqiang Han. Double selection based semi-supervised clustering ensemble for tumor clustering from gene expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):727–740, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2015:AFC

[YCY+15] Zhiwen Yu, Hantao Chen, Jane You, Jiming Liu, Hau-San Wong, Guoqiang Han, and Le Li. Adaptive fuzzy consensus clustering framework for clustering analysis of cancer data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):887–901, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2012:MPD

[YCYC12] Cheng-Hong Yang, Yu-Huei Cheng, Cheng-Huei Yang, and Li-Yeh Chuang. Mutagenic primer design for mismatch PCR-RFLP SNP genotyping using a genetic algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):837–845, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yuan:2018:GIH

[YCZ+18] Lin Yuan, Fanglin Chen,

Ling-Li Zeng, Lubin Wang, and Dewen Hu. Gender identification of human brain image with a novel 3D descriptor. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (2):551–561, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yan:2024:PPM

[YD24] Cheng Yan and Guihua Duan. PMDAGS: Predicting miRNA-Disease associations with graph nonlinear diffusion convolution network and similarities. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):394–404, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3366175`.

Yao:2008:EAE

[YDM+08] Peggy Yao, Ankur Dhanik, Nathan Marz, Ryan Propper, Charles Kou, Guanfeng Liu, Henry van den Bedem, Jean-Claude Latombe, Inbal Halperin-Landsberg, and Russ B. Altman. Efficient algorithms to explore conformation spaces of flexible protein loops. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(4):534–545, October 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yan:2020:BPM

[YDW+20] Cheng Yan, Guihua Duan, Fang-Xiang Wu, Yi Pan, and Jianxin Wang. BRWMDA:Predicting microbe-disease associations based on similarities and bi-random walk on disease and microbe networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1595–1604, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2907626`.

Yan:2021:PMP

[YDW+21] Cheng Yan, Guihua Duan, Fang-Xiang Wu, Yi Pan, and Jianxin Wang. MCHMDA: Predicting microbe-disease associations based on similarities and low-rank matrix completion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):611–620, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2926716`.

Yan:2022:PDD

[YDZ+22] Cheng Yan, Guihua Duan, Yayan Zhang, Fang-Xiang Wu, Yi Pan, and Jianxin

Wang. Predicting drug-drug interactions based on integrated similarity and semi-supervised learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):168–179, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2988018`.

Yao:2023:IDV

[YF23] Yin Yao and Martin C. Frith. Improved DNA-versus-protein homology search for protein fossils. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1691–1699, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3177855`.

Yoo:2017:IIK

[YFCM17] Boyoung Yoo, Fazle Elahi Faisal, Huili Chen, and Tijana Milenkovic. Improving identification of key players in aging via network denoising and core inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1056–1069, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2016:PPF

[YFWZ16] Guoxian Yu, Guangyuan Fu, Jun Wang, and Hailong Zhu. Predicting protein function via semantic integration of multiple networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(2):220–232, March 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2018:NPN

[YFWZ18] Guoxian Yu, Guangyuan Fu, Jun Wang, and Yingwen Zhao. NewGOA: Predicting new GO annotations of proteins by bi-random walks on a hybrid graph. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1390–1402, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2022:EEP

[YFY+22] Ken Hung-On Yu, Xiunan Fang, Haobin Yao, Bond Ng, Tak Kwan Leung, Ling-Ling Wang, Chi Ho Lin, Agnes Sze Wah Chan, Wai Keung Leung, Suet Yi Leung, and Joshua Wing Kei Ho. Evaluation of experimental protocols for shotgun whole-genome metagenomic discovery of antibiotic resistance genes. *IEEE/ACM Transactions on Computational Bi-*

ology and Bioinformatics, 19 (3):1313–1321, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3004063`.

Yang:2023:LRD

[YFYW23] Chengzhuan Yang, Lincong Fang, Qian Yu, and Hui Wei. A learning robust and discriminative shape descriptor for plant species identification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):39–51, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3148463`.

Yu:2019:HPB

[YG19] Liang Yu and Lin Gao. Human pathway-based disease network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(4):1240–1249, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yan:2020:GES

[YGFC20] Da Yan, Xin Gao, Samah J. Fodeh, and Jake Y. Chen. Guest editorial for selected papers from BIOKDD 2018 and DMBIH 2018. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 1832–1834, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3020443`.

Yan:2023:DTL

[YGJZ23] Ke Yan, Xinlu Guo, Zhiwei Ji, and Xiaokang Zhou. Deep transfer learning for cross-species plant disease diagnosis adapting mixed subdomains. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2555–2564, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3135882`.

Yuan:2019:IMO

[YGY+19] Lin Yuan, Le-Hang Guo, Chang-An Yuan, Youhua Zhang, Kyungsook Han, Asoke K. Nandi, Barry Honig, and De-Shuang Huang. Integration of multi-omics data for gene regulatory network inference and application to breast cancer. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):782–791, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2013:NFV

[YH13] Hong-Jie Yu and De-Shuang Huang. Normalized feature

vectors: a novel alignment-free sequence comparison method based on the numbers of adjacent amino acids. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):457–467, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2012:SGS

[YHB12] Lei Yu, Yue Han, and Michael E. Berens. Stable gene selection from microarray data via sample weighting. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (1):262–272, January 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2019:RHD

[YHCS19] Xi Yang, Guoqiang Han, Hongmin Cai, and Yan Song. Recovering hidden diagonal structures via nonnegative matrix factorization with multiple constraints. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1760–1772, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2015:EEA

[YHV+15] Qiang Yu, Hongwei Huo, Jeffrey Scott Vitter, Jun Huan, and Yakov Nekrich. An efficient exact algorithm for the motif stem search problem over large alphabets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (2):384–397, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yan:2021:DED

[YHW+21] Lu Yan, Weihong Huang, Liming Wang, Song Feng, Yonghong Peng, and Jie Peng. Data-enabled digestive medicine: a new big data analytics platform. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 922–931, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2951555`.

Yang:2013:CPP

[YHY13] Chao Yang, Zengyou He, and Weichuan Yu. A combinatorial perspective of the protein inference problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6): 1542–1547, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2012:PRP

[YHYY12] Chao Yang, Zengyou He,

Can Yang, and Weichuan Yu. Peptide reranking with protein-peptide correspondence and precursor peak intensity information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (4):1212–1219, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

You:2019:EEL

[YHZ+19] Zhu-Hong You, Wen-Zhun Huang, Shanwen Zhang, Yu-An Huang, Chang-Qing Yu, and Li-Ping Li. An efficient ensemble learning approach for predicting protein-protein interactions by integrating protein primary sequence and evolutionary information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):809–817, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yella:2022:MDD

[YJ22] Jaswanth K. Yella and Anil G. Jegga. MGATRx: Discovering drug repositioning candidates using multi-view graph attention. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2596–2604, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3082466`.

Yan:2021:GEM

[YJJW21] Ke Yan, Zhiwei Ji, Qun Jin, and Qing-Guo Wang. Guest editorial: Machine learning for AI-enhanced healthcare and medical services: New development and promising solution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):850–851, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3050935`.

Yoo:2024:IPS

[YJS+24] Sunyong Yoo, Myeonghyeon Jeong, Subhin Seomun, Kiseong Kim, and Youngmahn Han. Interpretable prediction of SARS-CoV-2 epitope-specific TCR recognition using a pre-trained protein language model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):428–438, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3368046`.

Yu:2021:RSB

[YKG+21] Xiang Yu, Cheng Kang,

David S. Guttery, Seifedine Kadry, Yang Chen, and Yu-Dong Zhang. ResNet–SCDA–50 for breast abnormality classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):94–102, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2986544`.

Yan:2017:NNP

[YKW17] Yan, Anthony J. Kusalik, and Fang-Xiang Wu. NovoExD: De novo peptide sequencing for ETD/ECD spectra. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):337–344, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yerneni:2018:IIS

[YKWK18] Satwica Yerneni, Ishita K. Khan, Qing Wei, and Daisuke Kihara. IAS: Interaction specific GO term associations for predicting protein-protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1247–1258, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yoon:2012:SLP

[YL12] Yongwook Yoon and Gary Geunbae Lee. Subcellular localization prediction through boosting association rules. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(2):609–618, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yuan:2021:LOF

[YLBX21] Xiguo Yuan, Junping Li, Jun Bai, and Jianing Xi. A local outlier factor-based detection of copy number variations from NGS data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1811–1820, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2961886`.

Yang:2020:CBM

[YLC20] Cheng-Hong Yang, Yu-Da Lin, and Li-Yeh Chuang. Class balanced multifactor dimensionality reduction to detect gene–gene interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(1):71–81, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https:/`

/dl.acm.org/doi/abs/10.1109/TCBB.2018.2858776.

Yang:2023:GCG

[YLC+23] Jing Yang, Zhengshu Lu, Xu Chen, Deling Xu, Dewu Ding, and Yanrui Ding. GCNA-Cluster: a gene co-expression network alignment to cluster cancer patients algorithm for identifying subtypes of pancreatic ductal adenocarcinoma. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3556–3566, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3300102.

Yang:2013:EBC

[YLCC13] Cheng-Hong Yang, Yu-Da Lin, Li-Yeh Chaung, and Hsueh-Wei Chang. Evaluation of breast cancer susceptibility using improved genetic algorithms to generate genotype SNP barcodes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (2):361–371, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ye:2015:GAM

[YlCW+15] Yongtao Ye, David Wai lok Cheung, Yadong Wang, Siu-Ming Yiu, Qing Zhang, Tak-Wah Lam, and Hing-Fung Ting. GLProbs: aligning multiple sequences adaptively. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):67–78, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2015:DCP

[YLH+15] Dong-Jun Yu, Yang Li, Jun Hu, Xibei Yang, Jing-Yu Yang, and Hong-Bin Shen. Disulfide connectivity prediction based on modelled protein 3D structural information and random forest regression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(3):611–621, May 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2021:KEM

[YLJY21] Zhimiao Yu, Jiarui Lu, Yuan Jin, and Yang Yang. KenDTI: an ensemble model for predicting drug-target interaction by integrating multi-source information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1305–1314, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3074401.

Yu:2006:MPA

[YLL+06] Weichuan Yu, Xiaoye Li, Junfeng Liu, Baolin Wu, Kenneth R. Williams, and Hongyu Zhao. Multiple peak alignment in sequential data analysis: a scale-space-based approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):208–219, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2023:DDG

[YLS23] Hui Yu, KangKang Li, and JianYu Shi. DGANDDI: Double generative adversarial networks for drug-drug interaction prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1854–1863, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3219883`.

Yu:2024:CGE

[YLW+24] Xiao Yu, Weimin Li, Jianjia Wang, Xing Wu, and Bin Sheng. Construction of gene expression patterns to identify critical genes under SARS-CoV-2 infection conditions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):607–618, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3283534`.

Yuan:2021:CMC

[YLWS21] Shaoxun Yuan, Haitao Li, Jiansheng Wu, and Xiao Sun. Classification of mild cognitive impairment with multimodal data using both labeled and unlabeled samples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (6):2281–2290, November/ December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3053061`.

Ye:2004:UUD

[YLXJ04] Jieping Ye, Tao Li, Tao Xiong, and Ravi Janardan. Using uncorrelated discriminant analysis for tissue classification with gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(4):181–190, October 2004. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yan:2017:TNW

[YLXS17] Zhangming Yan, Ke Liu, Shunian Xiang, and Zhirong Sun. txCoords: a novel Web application for transcriptomic peak re-mapping. *IEEE/ACM Transactions on*

Computational Biology and Bioinformatics, 14(3):746–748, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2012:STS

[YLY+12] Zhiwen Yu, Le Li, Jane You, Hau-San Wong, and Guoqiang Han. SC^3: Triple spectral clustering-based consensus Clustering framework for class discovery from cancer gene expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(6): 1751–1765, November 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2021:DBF

[YLZW21] Tingting Yu, Jianxing Liu, Qingshuang Zeng, and Ligang Wu. Dissipativity-based filtering for switched genetic regulatory networks with stochastic disturbances and time-varying delays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 1082–1092, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2936351`.

Yang:2011:RFS

[YM11] Feng Yang and K. Z. Mao. Robust feature selection for microarray data based on multicriterion fusion. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (4):1080–1092, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yeganeh:2020:CDA

[YM20] Pourya Naderi Yeganeh and M. Taghi Mostafavi. Causal disturbance analysis: a novel graph centrality based method for pathway enrichment analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1613–1624, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2907246`.

Yoo:2014:ICM

[YMT+14] Paul D. Yoo, Sami Muhaidat, Kamal Taha, Jamal Bentahar, and Abdallah Shami. Intelligent consensus modeling for proline cis-trans isomerization prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):26–32, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2012:IXT

[YMW+12] Pengyi Yang, Jie Ma, Penghao Wang, Yunping Zhu, Bing B. Zhou, and Yee Hwa Yang. Improving X!Tandem on peptide identification from mass spectrometry by self-boosted percolator. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(5): 1273–1280, September 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2014:IEL

[YN14] Hualong Yu and Jun Ni. An improved ensemble learning method for classifying high-dimensional and imbalanced biomedicine data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):657–666, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yoon:2005:DCB

[YNBM05] Sungroh Yoon, Christine Nardini, Luca Benini, and Giovanni De Micheli. Discovering coherent biclusters from gene expression data using zero-suppressed binary decision diagrams. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(4):339–354, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yue:2018:SGS

[YNN+18] Zongliang Yue, Michael T. Neylon, Thanh Nguyen, Timothy Ratliff, and Jake Y. Chen. "Super Gene Set" causal relationship discovery from functional genomics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1991–1998, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yip:2007:SIS

[YNWC07] Andy M. Yip, Michael K. Ng, Edmond H. Wu, and Tony F. Chan. Strategies for identifying statistically significant dense regions in microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):415–429, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yoruk:2011:CSM

[YOGY11] Erdem Yoruk, Michael F. Ochs, Donald Geman, and Laurent Younes. A comprehensive statistical model for cell signaling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):592–606, May/June 2011. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yukinawa:2009:OAB

[YOKI09] Naoto Yukinawa, Shigeyuki Oba, Kikuya Kato, and Shin Ishii. Optimal aggregation of binary classifiers for multiclass cancer diagnosis using gene expression profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):333–343, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2013:HCH

[YP13] Tianwei Yu and Hesen Peng. Hierarchical clustering of high-throughput expression data based on general dependences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1080–1085, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2023:DPD

[YPL+23] Zhong-Ze Yu, Chun-Xiang Peng, Jun Liu, Biao Zhang, Xiao-Gen Zhou, and Gui-Jun Zhang. DomBpred: Protein domain boundary prediction based on domain-residue clustering using inter-residue distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):912–922, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3175905`.

Yu:2011:INR

[YPS11] Tianwei Yu, Hesen Peng, and Wei Sun. Incorporating nonlinear relationships in microarray missing value imputation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):723–731, May/June 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yan:2022:GESb

[YQBC22] Da Yan, Zhaohui S. Qin, Debswapna Bhattacharya, and Jake Y. Chen. Guest editorial for selected papers from BIOKDD 2021. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3068–3069, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3208759`.

Yan:2022:GESa

[YQWC22] Da Yan, Hong Qin, Hsiang-Yun Wu, and Jake Y. Chen. Guest editorial for selected papers from BIOKDD

2020. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2545–2546, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3176912`.

Yu:2013:PFP

[YRD+13] Guoxian Yu, Huzefa Rangwala, Carlotta Domeniconi, Guoji Zhang, and Zhiwen Yu. Protein function prediction using multilabel ensemble classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10 (4):1, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2014:EPF

[YRD+14a] Guoxian Yu, Huzefa Rangwala, Carlotta Domeniconi, Guoji Zhang, and Zhiwen Yu. Erratum to "Protein function prediction using multilabel ensemble classification". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):265, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2014:PFP

[YRD+14b] Guoxian Yu, Huzefa Rangwala, Carlotta Domeniconi, Guoji Zhang, and Zhiwen Yu. Protein function prediction with incomplete annotations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):579–591, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2015:PPF

[YRD+15] Guoxian Yu, Huzefa Rangwala, Carlotta Domeniconi, Guoji Zhang, and Zili Zhang. Predicting protein function using multiple kernels. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12 (1):219–233, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2020:LBE

[YRL+20] Xinyi Yu, Wenge Rong, Jingshuang Liu, Deyu Zhou, Yuanxin Ouyang, and Zhang Xiong. LSTM-based end-to-end framework for biomedical event extraction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2029–2039, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2916346`.

Yoo:2017:GES

[YS17] Illhoi Yoo and Amarda Shehu. Guest editorial for special section on BIBM 2014. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):252–253, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Ye:2022:KGE

[YSBB22] Cheng Ye, Rowan Swiers, Stephen Bonner, and Ian Barrett. A knowledge graph-enhanced tensor factorisation model for discovering drug targets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3070–3080, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3197320`.

Yan:2013:CNE

[YSC13] Su Yan, W. Scott Spangler, and Ying Chen. Chemical name extraction based on automatic training data generation and rich feature set. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5): 1218–1233, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yamanishi:2019:GEA

[YSC19] Yoshihiro Yamanishi, Yasubumi Sakakibara, and Yi-Ping Phoebe Chen. Guest editorial for the 16th Asia Pacific Bioinformatics Conference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):1–2, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yao:2020:ADP

[YSGZ20] Heng Yao, Yunjia Shi, Jihong Guan, and Shuigeng Zhou. Accurately detecting protein complexes by graph embedding and combining functions with interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):777–787, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2897769`.

Yu:2017:PND

[YSW+17] Liang Yu, Ruidan Su, Bingbo Wang, Long Zhang, Yapeng Zou, Jing Zhang, and Lin Gao. Prediction of novel drugs for hepatocellular carcinoma based on multi-source random walk. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):966–977, July 2017. CODEN

ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yan:2021:GES

[YTC21] Da Yan, Sharma Thankachan, and Jake Y. Chen. Guest editorial for selected papers from BIOKDD 2019. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 809–810, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3067071`.

Yang:2015:FDW

[YTLL15] Lina Yang, Yuan Yan Tang, Yang Lu, and Huiwu Luo. A fractal dimension and wavelet transform based method for protein sequence similarity analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):348–369, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2022:DDL

[YWCC22] Cheng-Hong Yang, Kuo-Chuan Wu, Li-Yeh Chuang, and Hsueh-Wei Chang. DeepBarcoding: Deep learning for species classification using DNA barcoding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):2158–2165, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3056570`.

Yu:2020:NGF

[YWF+20] Guoxian Yu, Keyao Wang, Guangyuan Fu, Maozu Guo, and Jun Wang. NMFGO: Gene function prediction via nonnegative matrix factorization with gene ontology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (1):238–249, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2861379`.

Yang:2007:MFE

[YWK+07] Jing Yang, Sarawan Wongsa, Visakan Kadirkamanathan, Stephen A. Billings, and Phillip C. Wright. Metabolic flux estimation — a self-adaptive evolutionary algorithm with singular value decomposition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):126–138, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2024:MRG

[YWL+24] Shengpeng Yu, Hong Wang, Jing Li, Jun Zhao, Cheng

Liang, and Yanshen Sun. A multi-relational graph encoder network for fine-grained prediction of MiRNA-disease associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):45–56, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3335007`.

Yan:2019:DMP

[YWN+19] Cheng Yan, Jianxin Wang, Peng Ni, Wei Lan, Fang-Xiang Wu, and Yi Pan. DNRLMF–MDA: Predicting microRNA-Disease associations based on similarities of microRNAs and diseases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (1):233–243, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yu:2018:NFN

[YWW+18] Chunjiang Yu, Wentao Wu, Jing Wang, Yuxin Lin, Yang, Jiajia Chen, Fei Zhu, and Bairong Shen. NGS-FC: a next-generation sequencing data format converter. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5): 1683–1691, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2020:DDF

[YWW20] Shengping Yang, Mitchell S. Wachtel, and Jiangrong Wu. DFseq: Distribution-free method to detect differential gene expression for RNA-sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):558–565, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2866994`.

Yang:2024:SNR

[YWW+24] Xiao-Hui Yang, Ye-Tong Wang, Ming-Hui Wu, Fan Li, Cheng-Long Zhou, Li-Jun Yang, Chen Zheng, Yong Li, Zhi Li, Si-Yi Guo, and Chun-Peng Song. SLPA-Net: a real-time recognition network for intelligent stomata localization and phenotypic analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):372–382, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3364208`.

Yang:2023:DTL

[YXL+23] Xiao-Hui Yang, Zi-Jun Xi, Jie-Ping Li, Xin-Lei Feng, Xiao-Hong Zhu, Si-Yi Guo, and Chun-Peng Song. Deep transfer learning-based

multi-object detection for plant stomata phenotypic traits intelligent recognition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):321–329, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3137810`.

Yin:2016:EPT

[YXS16] Xi Yin, Ying-Ying Xu, and Hong-Bin Shen. Enhancing the prediction of transmembrane β-barrel segments with chain learning and feature sparse representation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6): 1016–1026, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2013:FNF

[YXYC13] Jiaoyun Yang, Yun Xu, Xiaohui Yao, and Guoliang Chen. FNphasing: a novel fast heuristic algorithm for haplotype phasing based on flow network model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(2):372–382, March 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yuan:2021:ENS

[YXZD21] Xiguo Yuan, Xiangyan Xu, Haiyong Zhao, and Junbo Duan. ERINS: Novel sequence insertion detection by constructing an extended reference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1893–1901, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2954315`.

Yang:2021:CCD

[YYG+21] Ziying Yang, Guoxian Yu, Maozu Guo, Jiantao Yu, Xiangliang Zhang, and Jun Wang. CDPath: Cooperative driver pathways discovery using integer linear programming and Markov clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1384–1395, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2945029`.

Yang:2022:AED

[YYLL22] Xuan Yang, Chen Yang, Jimeng Lei, and Jianxiao Liu. An approach of epistasis detection using integer linear programming optimizing Bayesian net-

work. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2654–2671, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3092719`.

Yuan:2021:PCI

[YYX+21] Xiguo Yuan, Jiaao Yu, Jianing Xi, Liying Yang, Junliang Shang, Zhe Li, and Junbo Duan. CNV_IFTV: an isolation forest and total variation-based detection of CNVs from short-read sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):539–549, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2920889`.

Yu:2022:DPI

[YYY+22] Guoxian Yu, Yeqian Yang, Yangyang Yan, Maozu Guo, Xiangliang Zhang, and Jun Wang. DeepIDA: Predicting isoform-disease associations by data fusion and deep neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):2166–2176, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3058801`.

Yang:2023:CPD

[YZC+23] Jingbo Yang, Denan Zhang, Yiyang Cai, Kexin Yu, Mingming Li, Lei Liu, and Xiujie Chen. Computational prediction of drug phenotypic effects based on substructure-phenotype associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):256–265, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3155453`.

Yuan:2017:NPB

[YZG+17] Lin Yuan, Lin Zhu, Wei-Li Guo, Xiaobo Zhou, Youhua Zhang, Zhenhua Huang, and De-Shuang Huang. Nonconvex penalty based low-rank representation and sparse regression for eQTL mapping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1154–1164, September 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Yang:2019:PFI

[YZG+19] Runtao Yang, Chengjin Zhang, Rui Gao, Lina Zhang, and Qing Song. Predicting FAD interacting residues with feature

selection and comprehensive sequence descriptors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6): 2046–2056, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2824332.

Yu:2023:MPD

[YZH+23] Qiang Yu, Xiao Zhang, Yana Hu, Shengpin Chen, and Liying Yang. A method for predicting DNA motif length based on deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20 (1):61–73, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3158471.

Yang:2022:RGI

[YZL+22] Yueran Yang, Yu Zhang, Shuai Li, Xubin Zheng, Man-Hon Wong, Kwong-Sak Leung, and Lixin Cheng. A robust and generalizable immune-related signature for sepsis diagnostics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3246–3254, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3107874.

Ye:2023:DTI

[YZL23] Qing Ye, Xiaolong Zhang, and Xiaoli Lin. Drug-target interaction prediction via graph auto-encoder and multi-subspace deep neural networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2647–2658, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2022.3206907.

Yang:2021:IMO

[YZP+21] Bo Yang, Yupei Zhang, Shanmin Pang, Xuequn Shang, Xueqing Zhao, and Minghui Han. Integrating multi-omic data with deep subspace fusion clustering for cancer subtype prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (1):216–226, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2951413.

Yu:2024:MNM

[YZZ+24] Changyong Yu, Yuhai Zhao, Chu Zhao, Jianyu Jin, Keming Mao, and Guoren Wang. MiniDBG: a novel and minimal de Bruijn graph for read mapping. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 21(1):129–142, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3340251`.

Zhu:2009:GGA

[ZACS09] Qian Zhu, Zaky Adam, Vicky Choi, and David Sankoff. Generalized gene adjacencies, graph bandwidth, and clusters in yeast evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(2):213–220, April 2009. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zare:2020:PSC

[ZANN20] Fatima Zare, Sardar Ansari, Kayvan Najarian, and Sheida Nabavi. Preprocessing sequence coverage data for more precise detection of copy number variations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):868–876, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2869738`.

Zhu:2011:GMA

[ZAZ11] Dongxiao Zhu, Lipi Acharya, and Hui Zhang. A generalized multivariate approach to pattern discovery from replicated and incomplete genome-wide measurements. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1153–1169, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhu:2022:NMI

[ZAZ+22] Jianshen Zhu, Naveed Ahmed Azam, Fan Zhang, Aleksandar Shurbevski, Kazuya Haraguchi, Liang Zhao, Hiroshi Nagamochi, and Tatsuya Akutsu. A novel method for inferring chemical compounds with prescribed topological substructures based on integer programming. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3233–3245, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3112598`.

Zimek:2010:SHF

[ZBFK10] Arthur Zimek, Fabian Buchwald, Eibe Frank, and Stefan Kramer. A study of hierarchical and flat classification of proteins. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):563–571, July 2010. CODEN ITCBCY.

ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2023:EBR

[ZBL+23] Bo Zhao, Jun Bai, Chen Li, Jianfei Zhang, Wenge Rong, Yuanxin Ouyang, and Zhang Xiong. Enhancing biomedical ReQA with adversarial hard in-batch negative samples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2933–2944, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3261315`.

Zhang:2021:USC

[ZBY+21] Qingchen Zhang, Changchuan Bai, Laurence T. Yang, Zhikui Chen, Peng Li, and Hang Yu. A unified smart Chinese medicine framework for healthcare and medical services. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3):882–890, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2914447`.

Zhao:2011:MKI

[ZC11] Xin Zhao and Leo Wang-Kit Cheung. Multiclass kernel-imbedded Gaussian processes for microarray data analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(4):1041–1053, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhou:2014:GEA

[ZC14] Shuigeng Zhou and Yi-Ping Phoebe Chen. Guest editorial for the 12th Asia Pacific Bioinformatics Conference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(4):614–615, July 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2015:GES

[ZC15] Shihua Zhang and Luonan Chen. Guest editorial for special section on ISB/TBC 2014. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1074–1075, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2018:HSB

[ZCG+18] Jian Zhang, Haiting Chai, Bo Gao, Guifu Yang, and Zhiqiang Ma. HEMEsPred: Structure-based ligand-specific heme binding residues prediction by using fast-adaptive ensemble learning scheme. *IEEE/*

ACM Transactions on Computational Biology and Bioinformatics, 15(1):147–156, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:DNG

[ZCL21] Jun Zhang, Qingcai Chen, and Bin Liu. DeepDRBP-2L: a new genome annotation predictor for identifying DNA-binding proteins and RNA-binding proteins using convolutional neural network and long short-term memory. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1451–1463, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2952338`.

Zhang:2022:CSD

[ZCL22] Yiding Zhang, Lyujie Chen, and Shao Li. CIPHER-SC: Disease-gene association inference using graph convolution on a context-aware network with single-cell data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2):819–829, March 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3017547`.

Zhou:2019:E

[ZCM19] Shuigeng Zhou, Yi-Ping Phoebe Chen, and Hiroshi Mamitsuka. Editorial. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):350–351, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2827138`.

Zhang:2017:TPI

[ZCR+17] Fa Zhang, Yu Chen, Fei Ren, Xuan Wang, Zhiyong Liu, and Xiaohua Wan. A two-phase improved correlation method for automatic particle selection in Cryo-EM. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):316–325, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2022:BIS

[ZCT22] Hu Zhang, Jingsong Chen, and Tianhai Tian. Bayesian inference of stochastic dynamic models using early-rejection methods based on sequential stochastic simulations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1484–1494, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2020.3039490.

Zhu:2019:ARC

[ZCWW19] Wenliang Zhu, Xiaohe Chen, Yan Wang, and Lirong Wang. Arrhythmia recognition and classification using ECG morphology and segment feature analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):131–138, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2012:FIF

[ZD12] Xiao-Fei Zhang and Dao-Qing Dai. A framework for incorporating functional interrelationships into protein function prediction algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):740–753, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2017:TDP

[ZD17] Bo Zhang and Haibin Duan. Three-dimensional path planning for uninhabited combat aerial vehicle based on predator-prey pigeon-inspired optimization in dynamic environment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (1):97–107, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:PRB

[ZD21] Chen Zhang and Yanrui Ding. Probing the relation between community evolution in dynamic residue interaction networks and xylanase thermostability. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):686–696, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2922906.

Zhang:2012:PCD

[ZDL12] Xiao-Fei Zhang, Dao-Qing Dai, and Xiao-Xin Li. Protein complexes discovery based on protein-protein interaction data via a regularized sparse generative network model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):857–870, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zeng:2019:NLP

[ZDL+19] Zexian Zeng, Yu Deng, Xiaoyu Li, Tristan Naumann, and Yuan Luo. Natural language processing for EHR-based computational pheno-

typing. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1):139–153, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2023:RDR

[ZDN+23] Haochen Zhao, Guihua Duan, Peng Ni, Cheng Yan, Yaohang Li, and Jianxin Wang. RNPredATC: a deep residual learning-based model with applications to the prediction of Drug-ATC code association. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2712–2723, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3088256`.

Zhao:2023:ADT

[ZDY+23] Qichang Zhao, Guihua Duan, Mengyun Yang, Zhongjian Cheng, Yaohang Li, and Jianxin Wang. AttentionDTA: Drug-target binding affinity prediction by sequence-based deep learning with attention mechanism. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):852–863, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3170365`.

Zhu:2017:ISI

[ZDYH17] Lin Zhu, Su-Ping Deng, Zhu-Hong You, and De-Shuang Huang. Identifying spurious interactions in the protein-protein interaction networks using local similarity preserving embedding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (2):345–352, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2023:GPD

[ZDZ+23] Qichang Zhao, Guihua Duan, Haochen Zhao, Kai Zheng, Yaohang Li, and Jianxin Wang. GIFDTI: Prediction of drug-target interactions based on global molecular and intermolecular interaction representation learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1943–1952, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3225423`.

Zhang:2021:LGC

[ZFH+21] Aiying Zhang, Jian Fang, Wenxing Hu, Vince D. Calhoun, and Yu-Ping Wang. A latent Gaussian copula

model for mixed data analysis in brain imaging genetics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1350–1360, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2950904`.

Zhao:2020:INF

[ZFZ+20] Jin Zhao, Haodi Feng, Daming Zhu, Chi Zhang, and Ying Xu. IsoTree: a new framework for de novo transcriptome assembly from RNA-seq reads. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):938–948, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2808350`.

Zhao:2022:PMA

[ZFZL22] Jin Zhao, Haodi Feng, Daming Zhu, and Yu Lin. MultiTrans: an algorithm for path extraction through mixed integer linear programming for transcriptome assembly. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):48–56, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3083277`.

Zhao:2019:PPI

[ZG19] Zhenni Zhao and Xinqi Gong. Protein–protein interaction interface residue pair prediction based on deep learning architecture. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5):1753–1759, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zoppis:2012:MIO

[ZGB+12] Italo Zoppis, Erica Gianazza, Massimiliano Borsani, Clizia Chinello, Veronica Mainini, Carmen Galbusera, Carlo Ferrarese, Gloria Galimberti, Sandro Sorbi, Barbara Borroni, Fulvio Magni, Marco Antoniotti, and Giancarlo Mauri. Mutual information optimization for mass spectra data alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):934–939, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2005:PMF

[ZGC+05] Jingfen Zhang, Wen Gao, Jinjin Cai, Simin He, Rong Zeng, and Runsheng Chen. Predicting molecular formulas of fragment ions with

isotope patterns in tandem mass spectra. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(3):217–230, July 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhu:2016:CPE

[ZGDH16] Lin Zhu, Wei-Li Guo, Su-Ping Deng, and De-Shuang Huang. ChIP–PIT: Enhancing the analysis of ChIP-Seq data using convex-relaxed pair-wise interaction tensor decomposition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):55–63, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2024:SHO

[ZGW+24] Yongting Zhang, Yonggang Gao, Huanhuan Wang, Huaming Wu, Youbing Xia, and Xiang Wu. A secure high-order gene interaction detection algorithm based on deep neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):619–630, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3214863`.

Zhang:2020:EMM

[ZGZ+20] Jingsong Zhang, Jianmei Guo, Ming Zhang, Xiangtian Yu, Xiaoqing Yu, Weifeng Guo, Tao Zeng, and Luonan Chen. Efficient mining multi-mers in a variety of biological sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):949–958, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2828313`.

Zhang:2007:SSS

[Zha07] Louxin Zhang. Superiority of spaced seeds for homology search. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):496–505, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2011:GTS

[Zha11] Louxin Zhang. From gene trees to species trees II: Species tree inference by minimizing deep coalescence events. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1685–1691, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2016:DMS

[Zha16] Xing-Ming Zhao. Data mining in systems biology. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(6):1003, November 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2017:ENE

[Zha17] Aidong Zhang. Editorial from the new Editor-in-Chief. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):251, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2018:AIP

[Zha18] Xizhe Zhang. Altering indispensable proteins in controlling directed human protein interaction network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6): 2074–2078, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhou:2021:DUD

[ZHD+21] Yongjin Zhou, Weijian Huang, Pei Dong, Yong Xia, and Shanshan Wang. D-UNet: a dimension-fusion U shape network for chronic stroke lesion segmentation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 940–950, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2939522`.

Zhu:2019:TSS

[ZHE19] Lu Zhu, Ralf Hofestadt, and Martin Ester. Tissue-specific subcellular localization prediction using multi-label Markov random fields. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(5): 1471–1482, September 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2005:SGN

[ZHEB05] Shaojie Zhang, Brian Haas, Eleazar Eskin, and Vineet Bafna. Searching genomes for noncoding RNA using FastR. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2(4):366–379, October 2005. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2020:DDA

[ZHG20] Jingyi Zheng, Fushing Hsieh, and Linqiang Ge. A data-driven approach to predict and classify epileptic seizures from brain-wide calcium imaging video data.

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 17(6): 1858–1870, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2895077`.

Zhang:2017:MVC

[ZHJ17] Yong Zhang, Xiaohua Hu, and Xingpeng Jiang. Multi-view clustering of microbiome samples by robust similarity network fusion and spectral clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):264–271, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2014:CGE

[ZHL+14] Liang Zhao, Steven C. H. Hoi, Zhenhua Li, Limsoon Wong, Hung Nguyen, and Jinyan Li. Coupling graphs, efficient algorithms and B-cell epitope prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(1):7–16, January 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zeng:2024:PFF

[ZHL+24] Lirong Zeng, Mengxing Huang, Yuchun Li, Qiong Chen, and Hong-Ning Dai. Progressive feature fusion attention dense network for speckle noise removal in OCT images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):748–756, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3205217`.

Zhang:2007:MCU

[ZHSS07] Runxuan Zhang, Guang-Bin Huang, N. Sundararajan, and P. Saratchandran. Multicategory classification using an extreme learning machine for microarray gene expression cancer diagnosis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(3):485–495, July 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhou:2024:SDR

[ZHX+24] Yichao Zhou, Zhisen Hu, Zuxing Xuan, Yangang Wang, and Xiyuan Hu. Synchronizing detection and removal of smoke in endoscopic images with cyclic consistency adversarial nets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):670–680, July 2024. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3204673`.

Zhang:2020:ISO

[ZHZ+20] Rongrong Zhang, Ming Hu, Yu Zhu, Zhaohui Qin, Ke Deng, and Jun S. Liu. Inferring spatial organization of individual topologically associated domains via piecewise helical model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):647–656, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2865349`.

Zhanpeng:2022:MCM

[ZJ22] Huang Zhanpeng and Wu Jiekang. A multiview clustering method with low-rank and sparsity constraints for cancer subtyping. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6):3213–3223, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3122917`.

Zhang:2023:PRD

[ZJ23] Shengli Zhang and Yuanyuan Jing. PreVFs-RG: a deep hybrid model for identifying virulence factors based on residual block and gated recurrent unit. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1926–1934, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3223038`.

Zhou:2022:SDC

[ZJW+22] Jieli Zhou, Baoyu Jing, Zeya Wang, Hongyi Xin, and Hanghang Tong. SODA: Detecting COVID-19 in chest X-rays with semi-supervised open set domain adaptation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2605–2612, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3066331`.

Zhang:2024:GIK

[ZJZ+24] Hao Zhang, Jiao Jiao, Tianheng Zhao, Enshuang Zhao, Lanhui Li, Guihua Li, Borui Zhang, and Qing-Ming Qin. GERWR: Identifying the key pathogenicity-associated sRNAs of *Magnaporthe oryzae* infection in rice based on graph embedding and random walk with restart. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(2):227–239, March 2024. CODEN ITCBCY. ISSN 1545-5963

(print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2023.3348080.

Zhao:2016:PBN

[ZK16] Yun-Bo Zhao and J. Krishnan. Probabilistic Boolean network modelling and analysis framework for mRNA translation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):754–766, 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2018:BMV

[ZKL18] Yize Zhao, Jian Kang, and Qi Long. Bayesian multiresolution variable selection for ultra-high dimensional neuroimaging data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):537–550, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhi:2007:CBA

[ZKP+07] Degui Zhi, Uri Keich, Pavel Pevzner, Steffen Heber, and Haixu Tang. Correcting base-assignment errors in repeat regions of shotgun assembly. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(1):54–64, January 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:TGP

[ZKW19] Jiao Zhang, Sam Kwong, and Ka-Chun Wong. To-Bio: Global pathway similarity search based on topological and biological features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (1):336–349, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zrimec:2015:FPD

[ZL15] Jan Zrimec and Ales Lapanje. Fast prediction of DNA melting bubbles using DNA thermodynamic stability. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1137–1145, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zou:2019:AML

[ZL19] Quan Zou and Qi Liu. Advanced machine learning techniques for bioinformatics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1182–1183, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zeng:2024:SIT

[ZL24] Pengcheng Zeng and Zhixiang Lin. scICML: Information-theoretic co-clustering-based multi-view learning for the integrative analysis of single-cell multi-omics data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(1):200–207, 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3305989`.

Zhou:2024:AUD

[ZLB24] Hanchong Zhou, Henry Leung, and Bhashyam Balaji. AR-UNet: a deformable image registration network with cyclic training. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):692–700, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3284215`.

Zhang:2021:CES

[ZLC+21] Wenju Zhang, Zhewei Liang, Xin Chen, Lei Xin, Baozhen Shan, Zhigang Luo, and Ming Li. ChimST: an efficient spectral library search tool for peptide identification from chimeric spectra in data-dependent acquisition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1416–1425, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2945954`.

Zeng:2021:DLF

[ZLF+21a] Min Zeng, Min Li, Zhihui Fei, Fang-Xiang Wu, Yaohang Li, Yi Pan, and Jianxin Wang. A deep learning framework for identifying essential proteins by integrating multiple types of biological information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(1):296–305, January 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2897679`.

Zeng:2021:DDL

[ZLF+21b] Min Zeng, Chengqian Lu, Zhihui Fei, Fang-Xiang Wu, Yaohang Li, Jianxin Wang, and Min Li. DMFLDA: a deep learning framework for predicting lncRNA–disease associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2353–2363, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2983958`.

Zhang:2021:FLN

[ZLG+21] Wen Zhang, Zhishuai Li, Wenzheng Guo, Weitai Yang, and Feng Huang. A fast linear neighborhood similarity-based network link inference method to predict MicroRNA–disease associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):405–415, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2931546`.

Zhang:2012:QDS

[ZLH12] Yong Zhang, Peng Li, and Garng Huang. Quantifying dynamic stability of genetic memory circuits. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(3):871–884, May 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2017:CPP

[ZLH+17] Lin Zhang, Hui Liu, Yufei Huang, Xuesong Wang, Yidong Chen, and Jia Meng. Cancer progression prediction using gene interaction regularized elastic net. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):145–154, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zeng:2020:DCF

[ZLH+20] Xiangxiang Zeng, Yinglai Lin, Yuying He, Linyuan Lü, Xiaoping Min, and Alfonso Rodríguez-Patón. Deep collaborative filtering for prediction of disease genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1639–1647, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2907536`.

Zheng:2017:CFF

[ZLJT17] Shaoqiu Zheng, Junzhi Li, Andreas Janecek, and Ying Tan. A cooperative framework for fireworks algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):27–41, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2020:ODP

[ZLL+20] Yuan Zhang, Haihong Liu, Zhouhong Li, Zhonghua Miao, and Jin Zhou. Oscillatory dynamics of p53-Mdm2 circuit in response to DNA damage caused by ionizing radiation. *IEEE/ACM Transactions on Computational Biology and Bioin-*

formatics, 17(5):1703–1713, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2899574`.

Zhou:2021:CRB

[ZLL21] Xiaokang Zhou, Yue Li, and Wei Liang. CNN-RNN based intelligent recommendation for online medical pre-diagnosis support. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 912–921, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2994780`.

Zheng:2017:MMA

[ZLLS17] Weihua Zheng, Kenli Li, Keqin Li, and Hing Cheung So. A modified multiple alignment Fast Fourier Transform with higher efficiency. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):634–645, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zeng:2017:PVD

[ZLLZ17] Xiangxiang Zeng, Yuanlu Liao, Yuansheng Liu, and Quan Zou. Prediction and validation of disease genes using HeteSim scores. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3):687–695, May 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2016:IGM

[ZLPW16] Ya Zhang, Ao Li, Chen Peng, and Minghui Wang. Improve glioblastoma multiforme prognosis prediction by using feature selection and multiple kernel learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 825–835, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhu:2015:PIM

[ZLS+15] Xiangyuan Zhu, Kenli Li, Ahmad Salah, Lin Shi, and Keqin Li. Parallel implementation of MAFFT on CUDA-enabled graphics hardware. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1):205–218, January 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:CMV

[ZLS+19] Jun-Ping Zhang, Yi Liu, Wei Sun, Xiao-Yang Zhao, La Ta, and Wei-Sheng Guo. Characteristics of myosin V processivity. *IEEE/ACM*

Transactions on Computational Biology and Bioinformatics, 16(4):1302–1308, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:DDM

[ZLS+21] Zhen Zhang, Junwei Luo, Juan Shang, Min Li, Fang-Xiang Wu, Yi Pan, and Jianxin Wang. Deletion detection method using the distribution of insert size and a precise alignment strategy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3): 1070–1081, May/June 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2934407`.

Zhang:2011:PTN

[ZLW+11] Peng Zhang, Houqiang Li, Honghui Wang, Wong Stephen, and Xiaobo Zhou. Peak tree: a new tool for multiscale hierarchical representation and peak detection of mass spectrometry data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (4):1054–1066, July 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhou:2024:EDL

[ZLWF24] Xiaokang Zhou, Carson K. Leung, Kevin I-Kai Wang, and Giancarlo Fortino. Editorial deep learning-empowered big data analytics in biomedical applications and digital healthcare. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):516–520, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3371808`.

Zhou:2020:EPD

[ZLX+20] Jiyun Zhou, Qin Lu, Ruifeng Xu, Lin Gui, and Hongpeng Wang. EL_LSTM: Prediction of DNA-binding residue from protein sequence by combining long short-term memory and ensemble learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (1):124–135, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2858806`.

Zhang:2019:DPC

[ZLXL19] Yi-Yan Zhang, Qin Li, Yi Xin, and Wei-Qi Lv. Differentiating prostate cancer from benign prostatic hyperplasia using PSAD based on machine learning: Single-center retrospective study in China. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*,

16(3):936–941, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2012:HSP

[ZLY+12] Yijia Zhang, Hongfei Lin, Zhihao Yang, Jian Wang, and Yanpeng Li. Hash subgraph pairwise kernel for protein-protein interaction extraction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1190–1202, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2013:PCP

[ZLY+13] Yijia Zhang, Hongfei Lin, Zhihao Yang, Jian Wang, Yanpeng Li, and Bo Xu. Protein complex prediction in large ontology attributed protein-protein interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):729–741, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2006:SGR

[ZLZ06] Chaolin Zhang, Xuesong Lu, and Xuegong Zhang. Significance of gene ranking for classification of microarray samples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(3):312–320, July 2006. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:EPH

[ZLZ+19] Xiaolong Zhang, Xiaoli Lin, Jiafu Zhao, Qianqian Huang, and Xin Xu. Efficiently predicting hot spots in PPIs by combining random forest and synthetic minority over-sampling technique. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):774–781, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2020:GEI

[ZLZ20] Jie Zheng, Jinyan Li, and Yun Zheng. Guest editorial for the 29th International Conference on Genome Informatics (GIW 2018). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):726–727, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2978606`.

Zhuang:2022:DEP

[ZLZW22] Yuanying Zhuang, Xiangrong Liu, Yue Zhong, and Longxin Wu. A deep ensemble predictor for identifying anti-hypertensive peptides using pretrained protein em-

bedding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(4):1986–1992, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3068381`.

Zhao:2023:KGF

[ZLZZ23] Qing Zhao, Jianqiang Li, Linna Zhao, and Zhichao Zhu. Knowledge guided feature aggregation for the prediction of chronic obstructive pulmonary disease with Chinese EMRs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6): 3343–3352, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3198798`.

Zhang:2012:RRN

[ZM12] Xiuwei Zhang and Bernard M. E. Moret. Refining regulatory networks through phylogenetic transfer of information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1032–1045, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zuanetti:2022:BME

[ZM22] Daiane Aparecida Zuanetti and Luis Aparecido Milan. Bayesian modeling for epistasis analysis using data-driven reversible jump. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (3):1495–1506, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3043857`.

Zhou:2014:DSC

[ZMC+14] Cheng Zhou, Pieter Meysman, Boris Cule, Kris Laukens, and Bart Goethals. Discovery of spatially cohesive itemsets in three-dimensional protein structures. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):814–825, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2017:DCN

[ZmCXS17] Yue Zhang, Yiu ming Cheung, Bo Xu, and Weifeng Su. Detection copy number variants from NGS with sparse and smooth constraints. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):856–867, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2022:ILE

[ZMKL22] Siyuan Zhao, Jun Meng,

Qiang Kang, and Yushi Luan. Identifying LncRNA-Encoded short peptides using optimized hybrid features and ensemble learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2873–2881, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3104288`.

Zeller:2014:GAP

[ZMP+14] Michael Zeller, Christophe N. Magnan, Vishal R. Patel, Paul Rigor, Leonard Sender, and Pierre Baldi. A genomic analysis pipeline and its application to pediatric cancers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):826–839, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zarai:2018:CAC

[ZMST18] Yoram Zarai, Michael Margaliot, Eduardo D. Sontag, and Tamir Tuller. Controllability analysis and control synthesis for the ribosome flow model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1351–1364, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zarai:2013:EES

[ZMT13] Yoram Zarai, Michael Margaliot, and Tamir Tuller. Explicit expression for the steady-state translation rate in the infinite-dimensional homogeneous ribosome flow model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1322–1328, September 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zarai:2014:MPT

[ZMT14] Yoram Zarai, Michael Margaliot, and Tamir Tuller. Maximizing protein translation rate in the ribosome flow model: the homogeneous case. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1184–1195, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zanetti:2024:CSS

[ZOMC24] João Paulo Pereira Zanetti, Lucas Peres Oliveira, João Meidanis, and Leonid Chindelevitch. Counting sorting scenarios and intermediate genomes for the rank distance. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):316–327, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964

(electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3277733`.

Zou:2013:BNM

[Zou13] Yi Ming Zou. Boolean networks with multiexpressions and parameters. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):584–592, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhu:2010:IFP

[ZOZ10] Zexuan Zhu, Yew-Soon Ong, and Jacek M. Zurada. Identification of full and partial class relevant genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2):263–277, April 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:GEA

[ZPC+21] Louxin Zhang, Shaoliang Peng, Yi-Ping Phoebe Chen, David Sankoff, Guoliang Li, and Hong-Yu Zhang. Guest editorial for the 17th Asia Pacific Bioinformatics Conference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2123–2124, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3099948`.

Zhang:2019:BNC

[ZPW+19] Lu Zhang, Qiuping Pan, Yue Wang, Xintao Wu, and Xinghua Shi. Bayesian network construction and genotype-phenotype inference using GWAS statistics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):475–489, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2779498`.

Zhou:2021:LDS

[ZPW+21] Deshan Zhou, Shaoliang Peng, Dong-Qing Wei, Wu Zhong, Yutao Dou, and Xiaolan Xie. LUNAR: Drug screening for novel coronavirus based on representation learning graph convolutional network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1290–1298, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3085972`.

Zhang:2019:DPD

[ZRK19] Huanan Zhang, David Roe, and Rui Kuang. Detecting population-differentiation copy

number variants in human population tree by sparse group selection. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):538–549, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2779481`.

Zhou:2018:BNR

[ZS18] Jie Zhou and Yuan-Yuan Shi. A bipartite network and resource transfer-based approach to infer lncRNA-environmental factor associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):753–759, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhong:2019:FEF

[ZS19] Hua Zhong and Mingzhou Song. A fast exact functional test for directional association and cancer biology applications. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(3):818–826, May 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhou:2010:FNN

[ZSC+10] Jianjun Zhou, Jorg Sander, Zhipeng Cai, Lusheng Wang, and Guohui Lin. Finding the nearest neighbors in biological databases using less distance computations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7 (4):669–680, October 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2008:ICG

[ZSD08] Wentao Zhao, Erchin Serpedin, and Edward R. Dougherty. Inferring connectivity of genetic regulatory networks using information-theoretic criteria. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(2):262–274, April 2008. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:PVT

[ZSH21] Qinhu Zhang, Zhen Shen, and De-Shuang Huang. Predicting *in-vitro* transcription factor binding sites using DNA sequence + shape. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):667–676, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2947461`.

Zaharias:2023:LSM

[ZSW23] Paul Zaharias, Vladimir Smirnov, and Tandy Warnow. Large-scale multiple sequence alignment and the maximum weight trace alignment merging problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1700–1712, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3191848`.

Zhan:2014:PEM

[ZSY+14] Choujun Zhan, Wuchao Situ, Lam Fat Yeung, Peter Wai-Ming Tsang, and Genke Yang. A parameter estimation method for biological systems modelled by ODE/DDE models using spline approximation and differential evolution algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(6):1066–1076, November 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:DLF

[ZSZ+21] Fuhao Zhang, Hong Song, Min Zeng, Fang-Xiang Wu, Yaohang Li, Yi Pan, and Min Li. A deep learning framework for gene ontology annotations with sequence- and network-based information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(6):2208–2217, November/December 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2968882`.

Zhao:2022:CAD

[ZSZ+22] Fengpan Zhao, Pavel Skums, Alex Zelikovsky, Eric L. Sevigny, Monica Haavisto Swahn, Sheryl M. Strasser, Yan Huang, and Yubao Wu. Computational approaches to detect illicit drug ads and find vendor communities within social media platforms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(1):180–191, January 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2978476`.

Zheng:2023:ITU

[ZSZ23] Vicky Zheng, Ahmet Erdem Sariyuce, and Jaroslaw Zola. Identifying taxonomic units in metagenomic DNA streams on mobile devices. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2):1092–1103, March 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2022.3172661.

Zhou:2022:NEM

[ZTY22] Lewei Zhou, Yucong Tang, and Guiying Yan. A new estimation method for the biological interaction predicting problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1415–1423, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3049642.

Zhu:2013:EAZ

[ZW13] Daming Zhu and Lusheng Wang. An exact algorithm for the zero exemplar breakpoint distance problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1469–1477, November 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:IFI

[ZW19] Wei Zhang and Shu-Lin Wang. An integrated framework for identifying mutated driver pathway and cancer progression. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):455–464, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2788016.

Zhang:2015:III

[ZWC15] Xian Zhang, Ligang Wu, and Shaochun Cui. An improved integral inequality to stability analysis of genetic regulatory networks with interval time-varying delays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(2):398–409, March 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2017:CFG

[ZWcF17] Jing Zhang, Hao Wang, and Wu chun Feng. cuBLASTP: Fine-grained parallelization of protein sequence search on CPU + GPU. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):830–843, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhong:2017:PII

[ZWD+17] Jiancheng Zhong, Jianxing Wang, Xiaojun Ding, Zhen Zhang, Min Li, Fang-Xiang Wu, and Yi Pan. Protein inference from the integration of tandem MS data and interactome networks. *IEEE/ACM Transactions on Computational Biology*

and Bioinformatics, 14(6): 1399–1409, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2020:IIC

[ZWDR20] Huiru Zheng, Haiying Wang, Richard J. Dewhurst, and Rainer Roehe. Improving the inference of co-occurrence networks in the bovine rumen microbiome. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(3):858–867, May 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2018.2879342`.

Zhao:2021:CSP

[ZWG+21] Yingwen Zhao, Jun Wang, Maozu Guo, Xiangliang Zhang, and Guoxian Yu. Cross-species protein function prediction with asynchronous-random walk. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(4):1439–1450, July/August 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2943342`.

Zhang:2017:MOP

[ZwGC17] Yong Zhang, Dun wei Gong, and Jian Cheng. Multi-objective particle swarm optimization approach for cost-based feature selection in classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):64–75, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:MLP

[ZWHC19] Li Zhang, Ho-Chun Wu, Cheuk-Hei Ho, and Shing-Chow Chan. A multi-Laplacian prior and augmented Lagrangian approach to the exploratory analysis of time-varying gene and transcriptional regulatory networks for gene microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1816–1829, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2828810`.

Zhang:2021:PTD

[ZWHH21] Qinhu Zhang, Dailun Wang, Kyungsook Han, and De-Shuang Huang. Predicting TF-DNA binding motifs from ChIP-seq datasets using the bag-based classifier combined with a multi-fold learning scheme. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1743–1751, September/

October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3025007`.

Zhao:2011:ASB

[ZWL11] Liang Zhao, Limsoon Wong, and Jinyan Li. Antibody-specified B-cell epitope prediction in line with the principle of context-awareness. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1483–1494, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zeng:2012:HES

[ZWL+12] Nianyin Zeng, Zidong Wang, Yurong Li, Min Du, and Xiaohui Liu. A hybrid EKF and switching PSO algorithm for joint state and parameter estimation of lateral flow immunoassay models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (2):321–329, March 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2014:SBN

[ZWL14a] Hao Zhang, Xingyuan Wang, and Xiaohui Lin. Synchronization of Boolean networks with different update schemes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(5):965–972, September 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2014:DPC

[ZWL+14b] Bihai Zhao, Jianxin Wang, Min Li, Fang-Xiang Wu, and Yi Pan. Detecting protein complexes based on uncertain graph model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):486–497, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2015:SAS

[ZWL15] Hao Zhang, Xingyuan Wang, and Xiaohui Lin. Synchronization of asynchronous switched Boolean network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(6): 1449–1456, November 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2023:PPG

[ZWL+23] Xiaoshuai Zhang, Lixin Wang, Hucheng Liu, Xiaofeng Zhang, Bo Liu, Yadong Wang, and Junyi Li. Prot2GO: Predicting GO annotations from protein sequences and interactions. *IEEE/ACM Transactions on Computational*

Biology and Bioinformatics, 20(5):2772–2780, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3139841`.

Zhang:2021:IRP

[ZWLZ21] Jingrong Zhang, Zihao Wang, Zhiyong Liu, and Fa Zhang. Improve the resolution and parallel performance of the three-dimensional refine algorithm in RELION using CUDA and MPI. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):583–595, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2929171`.

Zhang:2020:TSD

[ZWM+20] Gui-Jun Zhang, Xiao-Qi Wang, Lai-Fa Ma, Liu-Jing Wang, Jun Hu, and Xiao-Gen Zhou. Two-stage distance feature-based optimization algorithm for *De novo* protein structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6):2119–2130, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2917452`.

Zhang:2018:CTC

[ZWS+18] Lijun Zhang, Ming Wang, Nicholas W. Sterling, Eun-Young Lee, Paul J. Eslinger, Daymond Wagner, Guangwei Du, Mechelle M. Lewis, Young Truong, F. DuBois Bowman, and Xuemei Huang. Cortical thinning and cognitive impairment in Parkinson's disease without dementia. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(2):570–580, March 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2012:NUF

[ZWSX12] Shaohong Zhang, Hau-San Wong, Ying Shen, and Dongqing Xie. A new unsupervised feature ranking method for gene expression data based on consensus affinity. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(4):1257–1263, July 2012. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2017:AOI

[ZWW17] Huiru Zheng, Chaoyang Wang, and Haiying Wang. Analysis of organization of the interactome using dominating sets: a case study

on cell cycle interaction networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(2):282–289, March 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2020:LPL

[ZWXL20] Tianyi Zhang, Minghui Wang, Jianing Xi, and Ao Li. LPGNMF: Predicting long non-coding RNA and protein interaction using graph regularized nonnegative matrix factorization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17 (1):189–197, January 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2861009`.

Zhu:2010:FSG

[ZWY+10] Shenghuo Zhu, Dingding Wang, Kai Yu, Tao Li, and Yihong Gong. Feature selection for gene expression using model-based entropy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(1):25–36, January 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2016:GAS

[ZWZ16] Xian Zhang, Ligang Wu, and Jiahua Zou. Globally asymptotic stability analysis for genetic regulatory networks with mixed delays: an M-matrix-based approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(1):135–147, January 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2016:MCS

[ZWZS16] Jingsong Zhang, Yinglin Wang, Chao Zhang, and Yongyong Shi. Mining contiguous sequential generators in biological sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(5): 855–867, September 2016. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zou:2022:NAL

[ZWZZ22] Chengye Zou, Xiaopeng Wei, Qiang Zhang, and Changjun Zhou. A novel adaptive linear neuron based on DNA strand displacement reaction network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1424–1434, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3045567`.

Zhao:2011:ASM

[ZXB11] Wenqi Zhao, Guoliang Xu, and Chandrajit L. Bajaj. An algebraic spline model of molecular surfaces for energetic computations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6): 1458–1467, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2023:MMF

[ZXJ+23] Yuanpeng Zhang, Kaijian Xia, Yizhang Jiang, Pengjiang Qian, Weiwei Cai, Chengyu Qiu, Khin Wee Lai, and Dongrui Wu. Multimodality fusion & inductive knowledge transfer underlying non-sparse multikernel learning and distribution adaption. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(4):2387–2397, July 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3142748`.

Zhang:2018:CDE

[ZXLZ18a] Wei Zhang, Jia Xu, Yuanyuan Li, and Xiufen Zou. Correction to "Detecting Essential Proteins Based on Network Topology, Gene Expression Data, and Gene Ontology Information". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):1035, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). See [ZXLZ18b].

Zhang:2018:DEP

[ZXLZ18b] Wei Zhang, Jia Xu, Yuanyuan Li, and Xiufen Zou. Detecting essential proteins based on network topology, gene expression data, and gene ontology information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (1):109–116, January 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). See correction [ZXLZ18a].

Zhang:2023:UFC

[ZXW+23] Qinhu Zhang, Youhong Xu, Siguo Wang, Yong Wu, Yuannong Ye, Chang-An Yuan, Valeriya Gribova, Vladimir Fedorovich Filaretov, and De-Shuang Huang. Using fully convolutional network to locate transcription factor binding sites based on DNA sequence and conservation information. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5):2690–2699, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://`

dl.acm.org/doi/10.1109/TCBB.2022.3219831.

Zhang:2020:PEP

[ZXZ20] Wei Zhang, Jia Xu, and Xiufen Zou. Predicting essential proteins by integrating network topology, subcellular localization information, gene expression profile and GO annotation data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(6): 2053–2061, November 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2916038.

Zhang:2021:PSP

[ZXZ+21] Gui-Jun Zhang, Teng-Yu Xie, Xiao-Gen Zhou, Liu-Jing Wang, and Jun Hu. Protein structure prediction using population-based algorithm guided by information entropy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(2):697–707, March 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2921958.

Zhao:2020:MNM

[ZY20] Lan Zhao and Hong Yan. MCNF: a novel method for cancer subtyping by integrating multi-omics and clinical data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(5):1682–1690, September 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2019.2910515.

Zhao:2022:BDD

[ZYC+22] Qichang Zhao, Mengyun Yang, Zhongjian Cheng, Yaohang Li, and Jianxin Wang. Biomedical data and deep learning computational models for predicting compound-protein relations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (4):2092–2110, July 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL https://dl.acm.org/doi/10.1109/TCBB.2021.3069040.

Zhou:2018:STM

[ZYF+18] Xichuan Zhou, Fan Yang, Yujie Feng, Qin Li, Fang Tang, Shengdong Hu, Zhi Lin, and Lei Zhang. A spatial-temporal method to detect global influenza epidemics using heterogeneous data collected from the Internet. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):802–812, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:MSC

[ZYH+21] Qinhu Zhang, Wenbo Yu, Kyungsook Han, Asoke K. Nandi, and De-Shuang Huang. Multi-scale capsule network for predicting DNA-Protein binding sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1793–1800, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3025579`.

Zhao:2023:EFP

[ZYJ+23] Weizhong Zhao, Wenjie Yao, Xingpeng Jiang, Tingting He, Chuan Shi, and Xiaohua Hu. An explainable framework for predicting drug-side effect associations via meta-path-based feature learning in heterogeneous information network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6):3635–3647, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3308094`.

Zhou:2019:CCK

[ZYN+19] Huiwei Zhou, Yunlong Yang, Shixian Ning, Zhuang Liu, Chengkun Lang, Yingyu Lin, and Degen Huang. Combining context and knowledge representations for chemical-disease relation extraction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(6):1879–1889, November 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2838661`.

Zhou:2013:MAD

[ZYW+13] Xiaowei Zhou, Can Yang, Xiang Wan, Hongyu Zhao, and Weichuan Yu. Multisample aCGH data analysis via total variation and spectral regularization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):230–235, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2017:PCI

[ZYW17] Jianhua Zhang, Zhong Yin, and Rubin Wang. Pattern classification of instantaneous cognitive task-load through GMM clustering, Laplacian eigenmap, and ensemble SVMs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(4):947–965, July 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2021:MIL

[ZYW+21] Kai Zheng, Zhu-Hong You, Lei Wang, Yi-Ran Li, Ji-Ren Zhou, and Hai-Tao Zeng. MISSIM: an incremental learning-based model with applications to the prediction of miRNA-disease association. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1733–1742, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3013837`.

Zhang:2023:CGI

[ZYX+23] Hao Zhang, Chuanxu Yan, Yewei Xia, Jihong Guan, and Shuigeng Zhou. Causal gene identification using nonlinear regression-based independence tests. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):185–195, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3149864`.

Zhao:2023:CPC

[ZYYX23] Minghua Zhao, Min Yuan, Yaning Yang, and Steven X. Xu. CPGL: Prediction of compound-protein interaction by integrating graph attention network with long short-term memory neural network. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(3):1935–1942, May 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2022.3225296`.

Zhou:2023:MBD

[ZYZ+23] Feng Zhou, Meng-Meng Yin, Jing-Xiu Zhao, Junliang Shang, and Jin-Xing Liu. A method based on dual-network information fusion to predict MiRNA–disease associations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(1):52–60, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3133006`.

Zhang:2013:SAM

[ZZ13] Wei Zhang and Xiufen Zou. Systematic analysis of the mechanisms of virus-triggered Type I IFN signaling pathways through mathematical modeling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(3):771–779, May 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2014:EIL

[ZZ14] Yu Zheng and Louxin

Zhang. Effect of incomplete lineage sorting on tree-reconciliation-based inference of gene duplication. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11(3):477–485, May 2014. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2015:NMD

[ZZ15] Wei Zhang and Xiufen Zou. A new method for detecting protein complexes based on the three node cliques. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(4):879–886, July 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2018:DMD

[ZZ18] Junhua Zhang and Shihua Zhang. The discovery of mutated driver pathways in cancer: Models and algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):988–998, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2020:CCM

[ZZ20] Lihua Zhang and Shihua Zhang. Comparison of computational methods for imputing single-cell RNA-sequencing data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):376–389, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2848633`.

Zhang:2020:WSC

[ZZBH20] Qinhu Zhang, Lin Zhu, Wenzheng Bao, and De-Shuang Huang. Weakly-supervised convolutional neural network architecture for predicting protein–DNA binding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 17(2):679–689, March 2020. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2018.2864203`.

Zhang:2019:IMH

[ZZCD19] Jingpu Zhang, Zuping Zhang, Zhigang Chen, and Lei Deng. Integrating multiple heterogeneous networks for novel LncRNA-disease association inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):396–406, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2701379`.

Zeng:2010:SSC

[ZZCY10] Jia Zeng, Xiao-Yu Zhao, Xiao-Qin Cao, and Hong Yan. SCS: Signal, context, and structure features for genome-wide human promoter recognition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(3):550–562, July 2010. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhu:2013:ISI

[ZZDW13] Yuan Zhu, Xiao-Fei Zhang, Dao-Qing Dai, and Meng-Yun Wu. Identifying spurious interactions and predicting missing interactions in the protein-protein interaction networks via a generative network model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(1):219–225, January 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhu:2013:IDB

[ZZDY13] Yuan Zhu, Weiqiang Zhou, Dao-Qing Dai, and Hong Yan. Identification of DNA-binding and protein-binding proteins using enhanced graph wavelet features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(4):1017–1031, July 2013. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:KLS

[ZZF+19] Zuping Zhang, Jingpu Zhang, Chao Fan, Yongjun Tang, and Lei Deng. KATZLGO: Large-scale prediction of LncRNA functions by using the KATZ measure based on multiple networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):407–416, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2704587`.

Zhang:2024:FNN

[ZZGL24] Shan Zhang, Yuan Zhou, Pei Geng, and Qing Lu. Functional neural networks for high-dimensional genetic data analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(3):383–393, May 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2024.3364614`.

Zhang:2018:DED

[ZZH18a] Hongbo Zhang, Lin Zhu, and De-Shuang Huang. DiscMLA: an efficient discriminative Motif learning algorithm over high-throughput

datasets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6):1810–1820, November 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhu:2018:LLM

[ZZH18b] Lin Zhu, Hong-Bo Zhang, and De-Shuang Huang. LMMO: a large margin approach for refining regulatory motifs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):913–925, May 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:HOC

[ZZH19] Qinhu Zhang, Lin Zhu, and De-Shuang Huang. High-order convolutional neural network architecture for predicting DNA-protein binding sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (4):1184–1192, July 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhou:2024:HHN

[ZZH+24] Qingguo Zhou, Rui Zhao, Yilin Hu, Jinqiang Wang, and Rui Zhou. Hierarchical hybrid networks for automatic pulmonary blood vessel segmentation in computed tomography images. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 21(4):778–788, July 2024. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3281828`.

Zhang:2021:BSM

[ZZI+21] Yue Zhang, Chunfang Zheng, Sindeed Islam, Yong-Min Kim, and David Sankoff. Branching out to speciation in a model of fractionation: The Malvaceae. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(5):1875–1884, September/October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2019.2955649`.

Zamanighomi:2018:GRN

[ZZKW18] Mahdi Zamanighomi, Mostafa Zamanian, Michael Kimber, and Zhengdao Wang. Gene regulatory network inference from perturbed time-series expression data via ordered dynamical expansion of non-steady state actors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15 (4):1093–1106, July 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2023:NBD

[ZZLH23] Han Zhang, Zexuan Zhu, Hui Li, and Shan He. Network biomarker detection from gene co-expression network using Gaussian mixture model clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(6): 3523–3534, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3297388`.

Zhang:2017:AIB

[ZZM17] Kuize Zhang, Lijun Zhang, and Shaoshuai Mou. An application of invertibility of Boolean control networks to the control of the mammalian cell cycle. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14 (1):225–229, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2011:MBS

[ZZN+11a] Chun-Hou Zheng, Lei Zhang, To-Yee Ng, Chi Keung Shiu, and De-Shuang Huang. Metasample-based sparse representation for tumor classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(5):1273–1282, September 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2011:MPD

[ZZN+11b] Chun-Hou Zheng, Lei Zhang, Vincent To-Yee Ng, Chi Keung Shiu, and D.-S. Huang. Molecular pattern discovery based on penalized matrix decomposition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(6):1592–1603, November 2011. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2015:FMA

[ZZN15] Shuqin Zhang, Hongyu Zhao, and Michael K. Ng. Functional module analysis for gene coexpression networks with network integration. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(5):1146–1160, September 2015. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2021:AEP

[ZZP+21a] Jinhao Zhang, Zehua Zhang, Lianrong Pu, Jijun Tang, and Fei Guo. AIEpred: an ensemble predictive model of classifier chain to identify anti-inflammatory peptides. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18

(5):1831–1840, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.2968419`.

Zhang:2021:ESR

[ZZP+21b] Yuanpeng Zhang, Ziyuan Zhou, Wenjie Pan, Heming Bai, Wei Liu, Li Wang, and Chuang Lin. Epilepsy signal recognition using online transfer TSK fuzzy classifier underlying classification error and joint distribution consensus regularization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18 (5):1667–1678, September/ October 2021. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3002562`.

Zhang:2022:PPP

[ZZQ22] Jiongmin Zhang, Man Zhu, and Ying Qian. protein2vec: Predicting protein–protein interactions based on LSTM. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(3):1257–1266, May 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2020.3003941`.

Zhang:2019:MPM

[ZZRPZ19] Xuan Zhang, Quan Zou, Alfonso Rodriguez-Paton, and Xiangxiang Zeng. Metapath methods for prioritizing candidate disease miRNAs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16 (1):283–291, January 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zheng:2007:RNA

[ZZS07] Chunfang Zheng, Qian Zhu, and David Sankoff. Removing noise and ambiguities from comparative maps in rearrangement analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4 (4):515–522, October 2007. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2018:EMS

[ZZS18] Yue Zhang, Chunfang Zheng, and David Sankoff. Evolutionary model for the statistical divergence of paralogous and orthologous gene pairs generated by whole genome duplication and speciation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1579–1584, September 2018. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2022:PVD

[ZZW+22] Qinhu Zhang, Yindong Zhang, Siguo Wang, Zhan-Heng Chen, Valeriya Gribova, Vladimir Fedorovich Filaretov, and De-Shuang Huang. Predicting in-vitro DNA–protein binding with a spatially aligned fusion of sequence and shape. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(6): 3144–3153, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3133869`.

Zhang:2017:EPC

[ZZY+17] Gui-Jun Zhang, Xiao-Gen Zhou, Xu-Feng Yu, Xiao-Hu Hao, and Li Yu. Enhancing protein conformational space sampling using distance profile-guided differential evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(6):1288–1301, November 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhao:2022:DLC

[ZZY+22] Weizhong Zhao, Jinyong Zhang, Jincai Yang, Xingpeng Jiang, and Tingting He. Document-level chemical-induced disease relation extraction via hierarchical representation learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(5):2782–2793, 2022. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2021.3086090`.

Zhang:2023:DPP

[ZZZ+23] Fan Zhang, Yawei Zhang, Xiaoke Zhu, Xiaopan Chen, Fuhao Lu, and Xinhong Zhang. DeepSG2PPI: a protein-protein interaction prediction method based on deep learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(5): 2907–2919, 2023. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/10.1109/TCBB.2023.3268661`.

Zhang:2017:FAE

[ZZZC17] Bei Zhang, Yu-Jun Zheng, Min-Xia Zhang, and Sheng-Yong Chen. Fireworks algorithm with enhanced fireworks interaction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(1):42–55, January 2017. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic).

Zhang:2019:FSS

[ZZZW19] Jie Zhang, Zhigen Zhao, Kai Zhang, and Zhi Wei. A feature sampling strategy for analysis of high dimensional genomic data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(2):434–441, March 2019. CODEN ITCBCY. ISSN 1545-5963 (print), 1557-9964 (electronic). URL `https://dl.acm.org/doi/abs/10.1109/TCBB.2017.2779492`.