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This index covers all technical items—papers, correspondence, reviews, etc.—that appeared in this periodical during 2020, and items from previous years that were commented upon or corrected in 2020. Departments and other items may also be covered if they have been judged to have archival value.

The Author Index contains the primary entry for each item, listed under the first author's name. The primary entry includes the coauthors' names, the title of the paper or other item, and its location, specified by the publication abbreviation, year, month, and inclusive pagination. The Subject Index contains entries describing the item under all appropriate subject headings, plus the first author's name, the publication abbreviation, month, and year, and inclusive pages. Note that the item title is found only under the primary entry in the Author Index.

AUTHOR INDEX

A

- Abbas, G.,** see Raza, S., *TCBB Sept.-Oct. 2020* 1751-1761
Abdul-Kareem, S., see Tan, J.W., *TCBB Jan.-Feb. 2020* 82-90
Abdulaimma, B., see Fergus, P., *TCBB March-April 2020* 668-678
Acar, A.C., see Tercan, B., *TCBB Sept.-Oct. 2020* 1810-1821
Acharya, S., Saha, S., and Pradhan, P., Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering; *TCBB Jan.-Feb. 2020* 207-219
Acharyya, A., see Gudur, V.Y., *TCBB July-Aug. 2020* 1198-1210
Ahmed, S.S., Roy, S., and Kalita, J., Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks; *TCBB Jan.-Feb. 2020* 56-70
Al Kawam, A., see Alshawaqfeh, M., *TCBB May-June 2020* 1056-1067
Al-Jumeily, D., see Hind, J., *TCBB Sept.-Oct. 2020* 1535-1545
Al-Matouq, A.A., Laleg-Kirati, T., Novara, C., Rabbone, I., and Vincent, T., Sparse Reconstruction of Glucose Fluxes Using Continuous Glucose Monitors; *TCBB Sept.-Oct. 2020* 1797-1809
Alastruey-Benede, J., see Herruzo, J.M., *TCBB July-Aug. 2020* 1093-1104
Alden, K., Cosgrove, J., Coles, M., and Timmis, J., Using Emulation to Engineer and Understand Simulations of Biological Systems; *TCBB Jan.-Feb. 2020* 302-315
Alshawaqfeh, M., Al Kawam, A., Serpedin, E., and Datta, A., Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability; *TCBB May-June 2020* 1056-1067
Altuntas, V., Gok, M., and Kahveci, T., Stability Analysis of Biological Networks' Diffusion State; *TCBB July-Aug. 2020* 1406-1418
Aluru, S., see Pan, T., *TCBB Jan.-Feb. 2020* 136-148
Alvarez, S.A., see Sokolovsky, M., *TCBB Nov.-Dec. 2020* 1835-1845
Alvarez, W.A., see Pinzon-Reyes, E., *TCBB Jan.-Feb. 2020* 354-357
Amin, M.A., see Karim, M.B., *TCBB Nov.-Dec. 2020* 1955-1965
Amirkhani, A., Kolahdozi, M., Wang, C., and Kurgan, L.A., Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps; *TCBB July-Aug. 2020* 1372-1382
Anand, A., see Pyne, S., *TCBB Jan.-Feb. 2020* 278-291
Ansari, S., see Zare, F., *TCBB May-June 2020* 868-876
Arabameri, A., Asemani, D., and Teymourpour, P., Detection of Colorectal Carcinoma Based on Microbiota Analysis Using Generalized Regression Neural Networks and Nonlinear Feature Selection; *TCBB March-April 2020* 547-557
Arisi, I., see Sarkar, A., *TCBB Sept.-Oct. 2020* 1582-1594
Asemani, D., see Arabameri, A., *TCBB March-April 2020* 547-557
Atay, Y., see Sarkar, A., *TCBB Sept.-Oct. 2020* 1582-1594
Aygun, R.S., see Shrestha, M., *TCBB Nov.-Dec. 2020* 2074-2085
Azam, S.S., see Raza, S., *TCBB Sept.-Oct. 2020* 1751-1761

B

- Azuma, S.,** Kure, T., and Sugie, T., Structural Bistability Analysis of Flower-Shaped and Chain-Shaped Boolean Networks; *TCBB Nov.-Dec. 2020* 2098-2106
Baek, A., see Rampogu, S., *TCBB Jan.-Feb. 2020* 365
Bahadorinejad, A., Imani, M., and Braga-Neto, U.M., Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems; *TCBB July-Aug. 2020* 1105-1114
Bai, J., see Yuan, X., *TCBB May-June 2020* 1082-1091
Bai, J., see Yuan, X., *TCBB July-Aug. 2020* 1141-1153
Bai, X., see Chen, Z., *TCBB March-April 2020* 366-375
Bakhteh, S., Ghaffari-Hadigheh, A., and Chaparzadeh, N., Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks; *TCBB May-June 2020* 999-1009
Bandyopadhyay, S., see Mallik, S., *TCBB March-April 2020* 690-703
Bang, S., see Jhee, J.H., *TCBB Nov.-Dec. 2020* 2196
Bao, W., see Zhang, Q., *TCBB March-April 2020* 679-689
Barron, J.L., see Chaudhury, A., *TCBB May-June 2020* 1042-1055
Barros, M.T., and Dey, S., Feed-Forward and Feedback Control in Astrocytes for Ca^{2+} -Based Molecular Communications Nanonetworks; *TCBB July-Aug. 2020* 1174-1186
Bavi, R., see Rampogu, S., *TCBB Jan.-Feb. 2020* 365
Bayat, A., Deshpande, N.P., Wilkins, M.R., and Parameswaran, S., Fast Short Read De-Novo Assembly Using Overlap-Layout-Consensus Approach; *TCBB Jan.-Feb. 2020* 334-338
Bayat, A., see Gamaarachchi, H., *TCBB July-Aug. 2020* 1125-1133
Bednar, D., see Filipovic, J., *TCBB Sept.-Oct. 2020* 1625-1638
Bevilacqua, V., see Huang, D., *TCBB Sept.-Oct. 2020* 1474-1475
Bhattacharyya, D.K., see Chowdhury, H.A., *TCBB March-April 2020* 566-586
Bhattacharyya, D.K., see Chowdhury, H.A., *TCBB July-Aug. 2020* 1154-1173
Bhattarai, B., see Shrestha, M., *TCBB Nov.-Dec. 2020* 2074-2085
Bichindaritz, I., see Liu, G., *TCBB Nov.-Dec. 2020* 1966-1980
Bickel, D.R., see Karimnezhad, A., *TCBB March-April 2020* 635-646
Bittner, M., see Vundavilli, H., *TCBB May-June 2020* 1010-1018
Bittner, M.L., see Kapoor, R., *TCBB March-April 2020* 459-468
Bizzarri, D., see Petti, M., *TCBB Nov.-Dec. 2020* 2155-2161
Blumenstein, M., see Liu, Y., *TCBB May-June 2020* 899-905
Boukari, F., and Makrogiannis, S., Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling; *TCBB May-June 2020* 959-971
Braga-Neto, U.M., see Bahadorinejad, A., *TCBB July-Aug. 2020* 1105-1114
Brezovsky, J., see Filipovic, J., *TCBB Sept.-Oct. 2020* 1625-1638
Brito, K.L., Oliveira, A.R., Dias, U., and Dias, Z., Heuristics for the Reversal and Transposition Distance Problem; *TCBB Jan.-Feb. 2020* 2-13
Bunke, H., see Riesen, K., *TCBB March-April 2020* 483-494

C

- Cai, H.,** see Cai, J., *TCBB Jan.-Feb. 2020* 165-176
Cai, J., Cai, H., Chen, J., and Yang, X., Identifying "Many-to-Many" Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching; *TCBB Jan.-Feb. 2020* 165-176
Cai, J., see Xiao, Q., *TCBB March-April 2020* 623-634
Calhoun, V.D., see Wang, M., *TCBB Sept.-Oct. 2020* 1671-1681
Cao, G.P., see Rampogu, S., *TCBB Jan.-Feb. 2020* 365
Cao, Z., see Wang, S., *TCBB May-June 2020* 739-747

- Cao, Z.**, and Zhang, S., Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks; *TCBB March-April 2020* 657-667
- Cardona, G.**, *see* Pons, J.C., *TCBB Jan.-Feb. 2020* 158-164
- Carroll, T.C.**, Ojiaku, J., and Wong, P.W., Semiglobal Sequence Alignment with Gaps Using GPU; *TCBB Nov.-Dec. 2020* 2086-2097
- Carvajal-Lopez, P.**, Von Borstel, F.D., Torres, A., Rustici, G., Gutierrez, J., and Romero-Vivas, E., Microarray-Based Quality Assessment as a Supporting Criterion for *de novo* Transcriptome Assembly Selection; *TCBB Jan.-Feb. 2020* 198-206
- Cavill, R.**, *see* Ismailoglu, F., *TCBB Jan.-Feb. 2020* 347-353
- Celik, E.**, *see* Damgacioglu, H., *TCBB July-Aug. 2020* 1241-1252
- Celik, N.**, *see* Damgacioglu, H., *TCBB July-Aug. 2020* 1241-1252
- Chai, L.**, *see* Fu, L., *TCBB Sept.-Oct. 2020* 1721-1728
- Chakraborty, R.**, and Hasija, Y., Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture; *TCBB Nov.-Dec. 2020* 2183-2188
- Chalmers, C.**, *see* Fergus, P., *TCBB March-April 2020* 668-678
- Chan, K.C.**, *see* Hu, P., *TCBB Sept.-Oct. 2020* 1516-1524
- Chandrasekaran, S.N.**, *see* Lan, C., *TCBB July-Aug. 2020* 1352-1363
- Chang, S.**, *see* Tan, J.W., *TCBB Jan.-Feb. 2020* 82-90
- Chaparzadeh, N.**, *see* Bakhteh, S., *TCBB May-June 2020* 999-1009
- Chaudhury, A.**, and Barron, J.L., Plant Species Identification from Occluded Leaf Images; *TCBB May-June 2020* 1042-1055
- Chen, H.**, *see* Li, Y., *TCBB March-April 2020* 536-546
- Chen, H.**, Maduranga, D.A.K., Mundra, P.A., and Zheng, J., Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network; *TCBB March-April 2020* 516-525
- Chen, H.**, *see* Paoletti, N., *TCBB Nov.-Dec. 2020* 1981-1993
- Chen, J.**, *see* Peng, J., *TCBB May-June 2020* 769-776
- Chen, J.**, *see* Cai, J., *TCBB Jan.-Feb. 2020* 165-176
- Chen, J.Y.**, *see* Yan, D., *TCBB Nov.-Dec. 2020* 1832-1834
- Chen, L.**, *see* Zhang, J., *TCBB May-June 2020* 949-958
- Chen, L.**, *see* Chen, Z., *TCBB March-April 2020* 366-375
- Chen, L.**, *see* Shi, J., *TCBB March-April 2020* 449-458
- Chen, S.**, *see* Hu, H., *TCBB May-June 2020* 887-898
- Chen, S.**, *see* Guo, Q., *TCBB Sept.-Oct. 2020* 1563-1572
- Chen, Y.**, *see* Yang, X., *TCBB July-Aug. 2020* 1262-1275
- Chen, Z.**, Harada, Y., Nakamura, Y., and Wang, L., Faster Exact Computation of rSPR Distance via Better Approximation; *TCBB May-June 2020* 916-929
- Chen, Z.**, *see* Delgado, R.A., *TCBB Jan.-Feb. 2020* 292-301
- Chen, Z.**, Bai, X., Ma, L., Wang, X., Liu, X., Liu, Y., Chen, L., and Wan, L., A Branch Point on Differentiation Trajectory is the Bifurcating Event Revealed by Dynamical Network Biomarker Analysis of Single-Cell Data; *TCBB March-April 2020* 366-375
- Chen, Z.**, *see* Li, J., *TCBB Sept.-Oct. 2020* 1546-1554
- Cheng, L.L.**, *see* Yazdani, H., *TCBB March-April 2020* 526-535
- Cheng, X.**, *see* Jiang, H., *TCBB March-April 2020* 402-410
- Chi, Q.**, *see* Hu, F., *TCBB July-Aug. 2020* 1187-1197
- Ching, W.**, *see* Jiang, H., *TCBB March-April 2020* 402-410
- Choi, D.**, and Lee, S., SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling; *TCBB Sept.-Oct. 2020* 1785-1796
- Chopra, S.**, *see* Dutta, P., *TCBB Nov.-Dec. 2020* 2005-2016
- Chowdhury, H.A.**, Bhattacharyya, D.K., and Kalita, J.K., Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools; *TCBB March-April 2020* 566-586
- Chowdhury, H.A.**, Bhattacharyya, D.K., and Kalita, J.K., (Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices; *TCBB July-Aug. 2020* 1154-1173
- Chowriappa, P.**, *see* Mapes, N., *TCBB July-Aug. 2020* 1276-1289
- Christiani, D.C.**, *see* Yazdani, H., *TCBB March-April 2020* 526-535
- Chuang, L.**, *see* Yang, C., *TCBB Jan.-Feb. 2020* 71-81
- Cicek, A.E.**, *see* Karakaslar, E.O., *TCBB March-April 2020* 719-725
- Coles, M.**, *see* Alden, K., *TCBB Jan.-Feb. 2020* 302-315
- Collins, P.**, *see* Ismailoglu, F., *TCBB Jan.-Feb. 2020* 347-353
- Cosgrove, J.**, *see* Alden, K., *TCBB Jan.-Feb. 2020* 302-315
- Coskun, B.**, *see* Karakaslar, E.O., *TCBB March-April 2020* 719-725

D

- Dalton, L.A.**, *see* Foroughi pour, A., *TCBB Jan.-Feb. 2020* 250-263
- Damborsky, J.**, *see* Filipovic, J., *TCBB Sept.-Oct. 2020* 1625-1638
- Damgacioglu, H.**, Celik, E., and Celik, N., Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterative-Medoids Clustering Algorithm (T-CLUST); *TCBB July-Aug. 2020* 1241-1252
- Datta, A.**, *see* Alshawafreh, M., *TCBB May-June 2020* 1056-1067
- Datta, A.**, *see* Vundavilli, H., *TCBB May-June 2020* 1010-1018
- Datta, A.**, *see* Kapoor, R., *TCBB March-April 2020* 459-468
- De, R.K.**, *see* Sen, R., *TCBB March-April 2020* 506-515
- de Melo-Minardi, R.C.**, *see* Fassio, A.V., *TCBB July-Aug. 2020* 1317-1328
- Deepak, A.**, *see* Ranjan, A., *TCBB Sept.-Oct. 2020* 1648-1659
- Delgado, R.A.**, Chen, Z., and Middleton, R.H., Stepwise Tikhonov Regularization: Application to the Prediction of HIV-1 Drug Resistance; *TCBB Jan.-Feb. 2020* 292-301
- Deng, K.**, *see* Zhang, R., *TCBB March-April 2020* 647-656
- Deng, S.**, *see* Shen, Z., *TCBB Sept.-Oct. 2020* 1741-1750
- Deng, S.**, *see* Shen, Z., *TCBB Sept.-Oct. 2020* 1483-1492
- Deng, Z.**, Zhang, X., and Tian, T., Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions; *TCBB July-Aug. 2020* 1231-1240
- Deshpande, N.P.**, *see* Bayat, A., *TCBB Jan.-Feb. 2020* 334-338
- Dewhurst, R.J.**, *see* Zheng, H., *TCBB May-June 2020* 858-867
- Dey, S.**, *see* Barros, M.T., *TCBB July-Aug. 2020* 1174-1186
- Dey, S.K.**, *see* Majumder, P., *TCBB July-Aug. 2020* 1364-1371
- Dias, U.**, *see* Brito, K.L., *TCBB Jan.-Feb. 2020* 2-13
- Dias, Z.**, *see* Brito, K.L., *TCBB Jan.-Feb. 2020* 2-13
- Ding, P.**, *see* Xiao, Q., *TCBB March-April 2020* 623-634
- Dong, D.**, *see* Peng, S., *TCBB May-June 2020* 804-816
- Dong, Q.**, *see* Jing, X., *TCBB Nov.-Dec. 2020* 1918-1931
- Dong, Y.**, Sun, Y., Qin, C., and Zhu, W., EPMDA: Edge Perturbation Based Method for miRNA-Disease Association Prediction; *TCBB Nov.-Dec. 2020* 2170-2175
- Dua, S.**, *see* Mapes, N., *TCBB July-Aug. 2020* 1276-1289
- Duan, G.**, *see* Yan, C., *TCBB Sept.-Oct. 2020* 1595-1604
- Duan, J.**, *see* Yuan, X., *TCBB May-June 2020* 1082-1091
- Duan, J.**, *see* Yuan, X., *TCBB July-Aug. 2020* 1141-1153
- Dutta, P.**, Saha, S., Chopra, S., and Miglani, V., Ensembling of Gene Clusters Utilizing Deep Learning and Protein-Protein Interaction Information; *TCBB Nov.-Dec. 2020* 2005-2016

E

- Erickson, A.L.**, *see* Sarkar, A., *TCBB Sept.-Oct. 2020* 1582-1594

F

- Fabre, E.**, *see* Pichene, M., *TCBB Sept.-Oct. 2020* 1691-1702
- Fahad, M.S.**, *see* Ranjan, A., *TCBB Sept.-Oct. 2020* 1648-1659
- Falcone, R.**, *see* Petti, M., *TCBB Nov.-Dec. 2020* 2155-2161
- Fang, J.**, *see* Wang, M., *TCBB Sept.-Oct. 2020* 1671-1681
- Fang, M.**, *see* Li, J., *TCBB Sept.-Oct. 2020* 1546-1554
- Farina, L.**, *see* Petti, M., *TCBB Nov.-Dec. 2020* 2155-2161
- Fassio, A.V.**, Santos, L.H., Silveira, S.A., Ferreira, R.S., de Melo-Minardi, R.C., nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale; *TCBB July-Aug. 2020* 1317-1328
- Feng, H.**, *see* Zhao, J., *TCBB May-June 2020* 938-948
- Feng, H.**, *see* Zhao, J., *TCBB Nov.-Dec. 2020* 2197
- Feng, X.**, *see* Jia, H., *TCBB Sept.-Oct. 2020* 1493-1503
- Feng, Y.**, Zhang, L., and Mo, J., Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images; *TCBB Jan.-Feb. 2020* 91-101
- Feng, Z.**, and Wang, Y., ELF: Extract Landmark Features By Optimizing Topology Maintenance, Redundancy, and Specificity; *TCBB March-April 2020* 411-421

- Fergus, P.**, Montanez, C.C., Abdulaimma, B., Lisboa, P., Chalmers, C., and Pineles, B., Utilizing Deep Learning and Genome Wide Association Studies for Epistatic-Driven Preterm Birth Classification in African-American Women; *TCBB March-April 2020* 668-678
- Fernandez-Baca, D.**, *see* Ranjan, A., *TCBB Sept.-Oct. 2020* 1648-1659
- Ferreira, R.S.**, *see* Fassio, A.V., *TCBB July-Aug. 2020* 1317-1328
- Ferrer, M.**, *see* Riesen, K., *TCBB March-April 2020* 483-494
- Filipovic, J.**, Vavra, O., Plhak, J., Bednar, D., Marques, S.M., Brezovsky, J., Matyska, L., and Damborsky, J., CaverDock: A Novel Method for the Fast Analysis of Ligand Transport; *TCBB Sept.-Oct. 2020* 1625-1638
- Filipovic, V.**, *see* Grbic, M., *TCBB Sept.-Oct. 2020* 1822-1831
- Fodeh, S.J.**, Li, T., Jarad, H., and Safdar, B., Classification of Patients with Coronary Microvascular Dysfunction; *TCBB March-April 2020* 704-711
- Fodeh, S.J.**, *see* Yan, D., *TCBB Nov.-Dec. 2020* 1832-1834
- Foughi pour, A.**, and Dalton, L.A., Optimal Bayesian Filtering for Biomarker Discovery: Performance and Robustness; *TCBB Jan.-Feb. 2020* 250-263
- Forslund, S.K.**, *see* Sokolovska, N., *TCBB Jan.-Feb. 2020* 358-364
- French, A.P.**, *see* Gibbs, J.A., *TCBB Nov.-Dec. 2020* 1907-1917
- Fu, G.**, *see* Yu, G., *TCBB Jan.-Feb. 2020* 238-249
- Fu, L.**, Peng, Q., and Chai, L., Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model; *TCBB Sept.-Oct. 2020* 1721-1728
- Fugenschuh, A.**, *see* Moreno, L.A., *TCBB July-Aug. 2020* 1440-1450
- Fukumizu, K.**, *see* Yasui, N., *TCBB July-Aug. 2020* 1222-1230

G

- Gaeta, B.**, *see* Gamaarachchi, H., *TCBB July-Aug. 2020* 1125-1133
- Gamaarachchi, H.**, Bayat, A., Gaeta, B., and Parameswaran, S., Cache Friendly Optimisation of de Bruijn Graph Based Local Re-Assembly in Variant Calling; *TCBB July-Aug. 2020* 1125-1133
- Ganor, D.**, Pinter, R.Y., and Zehavi, M., A Note on GRegNetSim: A Tool for the Discrete Simulation and Analysis of Genetic Regulatory Networks; *TCBB Jan.-Feb. 2020* 316-320
- Gao, L.**, *see* Li, F., *TCBB March-April 2020* 390-401
- Gao, L.**, *see* Zhao, G., *TCBB July-Aug. 2020* 1211-1221
- Gao, M.**, *see* Yuan, X., *TCBB May-June 2020* 1082-1091
- Gao, M.**, *see* Yuan, X., *TCBB July-Aug. 2020* 1141-1153
- Gao, X.**, *see* Yan, D., *TCBB Nov.-Dec. 2020* 1832-1834
- Ge, L.**, *see* Zheng, J., *TCBB Nov.-Dec. 2020* 1858-1870
- Geerdink, J.**, *see* Pathak, S., *TCBB Nov.-Dec. 2020* 1883-1894
- Genest, B.**, *see* Pichene, M., *TCBB Sept.-Oct. 2020* 1691-1702
- Ghaffari-Hadigheh, A.**, *see* Bakhteh, S., *TCBB May-June 2020* 999-1009
- Ghosh, S.**, *see* Majumder, P., *TCBB July-Aug. 2020* 1364-1371
- Ghosh, Z.**, *see* Maji, R.K., *TCBB Jan.-Feb. 2020* 37-46
- Gibbs, J.A.**, Pound, M.P., French, A.P., Wells, D.M., Murchie, E.H., and Pridmore, T.P., Active Vision and Surface Reconstruction for 3D Plant Shoot Modelling; *TCBB Nov.-Dec. 2020* 1907-1917
- Gok, M.**, *see* Altuntas, V., *TCBB July-Aug. 2020* 1406-1418
- Gonzalez-Navarro, S.**, *see* Herruzo, J.M., *TCBB July-Aug. 2020* 1093-1104
- Grbic, M.**, Kartelj, A., Jankovic, S., Matic, D., and Filipovic, V., Variable Neighborhood Search for Partitioning Sparse Biological Networks into the Maximum Edge-Weightedk-Plexes; *TCBB Sept.-Oct. 2020* 1822-1831
- Groher, F.**, *see* Schmidt, M., *TCBB Nov.-Dec. 2020* 2189-2195
- Gromiha, M.**, *see* Huang, D., *TCBB Sept.-Oct. 2020* 1474-1475
- Grossglauser, M.**, *see* Kazemi, E., *TCBB Nov.-Dec. 2020* 2040-2052
- Guan, J.**, *see* Yao, H., *TCBB May-June 2020* 777-787
- Guan, Q.**, *see* Hu, H., *TCBB May-June 2020* 887-898
- Guan, Y.L.**, *see* Wang, Y., *TCBB Nov.-Dec. 2020* 2176-2182
- Gudur, V.Y.**, and Acharyya, A., Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications; *TCBB July-Aug. 2020* 1198-1210
- Guerrero, F.**, *see* Sokolovsky, M., *TCBB Nov.-Dec. 2020* 1835-1845
- Gui, L.**, *see* Zhou, J., *TCBB Jan.-Feb. 2020* 124-135
- Gui, L.**, *see* Zhou, J., *TCBB July-Aug. 2020* 1383-1393
- Gunawan, E.**, *see* Wang, Y., *TCBB Nov.-Dec. 2020* 2176-2182
- Guo, J.**, *see* Zhang, J., *TCBB May-June 2020* 949-958
- Guo, L.**, *see* Zhao, G., *TCBB July-Aug. 2020* 1211-1221

- Guo, M.**, *see* Yu, G., *TCBB Jan.-Feb. 2020* 238-249
- Guo, Q.**, Pan, T., Chen, S., Zou, X., and Huang, D.Y., A Novel Edge Effect Detection Method for Real-Time Cellular Analyzer Using Functional Principal Component Analysis; *TCBB Sept.-Oct. 2020* 1563-1572
- Guo, W.**, *see* Zhang, J., *TCBB May-June 2020* 949-958
- Gutierrez, J.**, *see* Carvajal-Lopez, P., *TCBB Jan.-Feb. 2020* 198-206

H

- Habibi, M.**, and Khosravi, P., Disruption of Protein Complexes from Weighted Complex Networks; *TCBB Jan.-Feb. 2020* 102-109
- Haggarty, S.J.**, *see* McDermott, M.B., *TCBB Nov.-Dec. 2020* 1846-1857
- Hagleitner, C.**, *see* Manica, M., *TCBB Nov.-Dec. 2020* 2141-2147
- Hamacher, K.**, *see* Schmidt, M., *TCBB Nov.-Dec. 2020* 2189-2195
- Han, K.**, *see* Lee, W., *TCBB Sept.-Oct. 2020* 1476-1482
- Han, Q.**, *see* He, Z., *TCBB May-June 2020* 930-937
- Hao, S.**, *see* Liu, J., *TCBB Jan.-Feb. 2020* 339-346
- Harada, Y.**, *see* Chen, Z., *TCBB May-June 2020* 916-929
- Hasija, Y.**, *see* Chakraborty, R., *TCBB Nov.-Dec. 2020* 2183-2188
- He, T.**, *see* Ma, Y., *TCBB May-June 2020* 788-795
- He, Y.**, Liu, J., and Ning, X., Drug Selection via Joint Push and Learning to Rank; *TCBB Jan.-Feb. 2020* 110-123
- He, Y.**, *see* Zeng, X., *TCBB Sept.-Oct. 2020* 1639-1647
- He, Z.**, Yu, J., Li, J., Han, Q., Luo, G., and Li, Y., Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data; *TCBB May-June 2020* 930-937
- He, Z.**, Zhao, C., Liang, H., Xu, B., and Zou, Q., Protein Complexes Identification with Family-Wise Error Rate Control; *TCBB Nov.-Dec. 2020* 2062-2073
- Hein, P.D.**, *see* Noriega-Atala, E., *TCBB Nov.-Dec. 2020* 1895-1906
- Heinitz, F.**, *see* Klarner, H., *TCBB July-Aug. 2020* 1115-1124
- Helmholtz, H.**, *see* Moreno, L.A., *TCBB July-Aug. 2020* 1440-1450
- Hendryx, S.M.**, *see* Noriega-Atala, E., *TCBB Nov.-Dec. 2020* 1895-1906
- Hernandez, H.G.**, *see* Pinzon-Reyes, E., *TCBB Jan.-Feb. 2020* 354-357
- Herruzo, J.M.**, Gonzalez-Navarro, S., Ibanez-Marin, P., Vinals-Yufera, V., Alastuey-Benede, J., and Plata, O., Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor; *TCBB July-Aug. 2020* 1093-1104
- Hind, J.**, Lisboa, P., Hussain, A.J., and Al-Jumeily, D., A Novel Approach to Detecting Epistasis using Random Sampling Regularisation; *TCBB Sept.-Oct. 2020* 1535-1545
- Hong, D.**, *see* Jing, X., *TCBB Nov.-Dec. 2020* 1918-1931
- Hou, W.**, *see* Jiang, H., *TCBB March-April 2020* 402-410
- Hsieh, F.**, *see* Zheng, J., *TCBB Nov.-Dec. 2020* 1858-1870
- Hu, F.**, Zhou, Y., Wang, Q., Yang, Z., Shi, Y., and Chi, Q., Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes; *TCBB July-Aug. 2020* 1187-1197
- Hu, H.**, Guan, Q., Chen, S., Ji, Z., and Lin, Y., Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs; *TCBB May-June 2020* 887-898
- Hu, J.**, Zhou, X., Zhu, Y., Yu, D., and Zhang, G., TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning; *TCBB July-Aug. 2020* 1419-1429
- Hu, J.**, *see* Zhang, G., *TCBB Nov.-Dec. 2020* 2119-2130
- Hu, L.**, Hu, P., Luo, X., Yuan, X., and You, Z., Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites; *TCBB Nov.-Dec. 2020* 2017-2028
- Hu, M.**, *see* Zhang, R., *TCBB March-April 2020* 647-656
- Hu, P.**, Huang, Y., Chan, K.C., and You, Z., Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA-miRNA Interactions; *TCBB Sept.-Oct. 2020* 1516-1524
- Hu, P.**, *see* Hu, L., *TCBB Nov.-Dec. 2020* 2017-2028
- Hu, X.**, *see* Ma, Y., *TCBB May-June 2020* 788-795
- Hu, X.**, *see* Yuan, R., *TCBB March-April 2020* 712-718
- Hu, X.**, *see* Ou-Yang, L., *TCBB Nov.-Dec. 2020* 2162-2169
- Hua, J.**, *see* Vundavilli, H., *TCBB May-June 2020* 1010-1018
- Hua, J.**, *see* Kapoor, R., *TCBB March-April 2020* 459-468
- Huan, J.**, *see* Lan, C., *TCBB July-Aug. 2020* 1352-1363
- Huang, D.**, *see* Wang, L., *TCBB May-June 2020* 972-980

- Huang, D., *see* Zhang, Q., *TCBB* March-April 2020 679-689
 Huang, D., *see* Peng, C., *TCBB* Sept.-Oct. 2020 1605-1612
 Huang, D., *see* Shen, Z., *TCBB* Sept.-Oct. 2020 1741-1750
 Huang, D., Bevilacqua, V., and Gromiha, M., Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC); *TCBB* Sept.-Oct. 2020 1474-1475
 Huang, D., *see* Shen, Z., *TCBB* Sept.-Oct. 2020 1483-1492
 Huang, D.Y., *see* Guo, Q., *TCBB* Sept.-Oct. 2020 1563-1572
 Huang, H., *see* Li, Y., *TCBB* March-April 2020 536-546
 Huang, L., *see* Wu, S., *TCBB* Sept.-Oct. 2020 1714-1720
 Huang, M., *see* Karim, M.B., *TCBB* Nov.-Dec. 2020 1955-1965
 Huang, S., *see* Shao, W., *TCBB* July-Aug. 2020 1394-1405
 Huang, T., *see* Wang, M., *TCBB* Sept.-Oct. 2020 1671-1681
 Huang, Y., *see* Hu, P., *TCBB* Sept.-Oct. 2020 1516-1524
 Hussain, A.J., *see* Hind, J., *TCBB* Sept.-Oct. 2020 1535-1545
 Hwang, T.H., *see* Xu, H., *TCBB* Nov.-Dec. 2020 1871-1882

I

- Ibanez-Marin, P., *see* Herruzo, J.M., *TCBB* July-Aug. 2020 1093-1104
 Imamura, C., *see* Kawano, K., *TCBB* Sept.-Oct. 2020 1762-1772
 Imani, M., *see* Bahadorinejad, A., *TCBB* July-Aug. 2020 1105-1114
 Ismailoglu, F., Cavill, R., Smirnov, E., Zhou, S., Collins, P., and Peeters, R., Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes; *TCBB* Jan.-Feb. 2020 347-353

J

- Jager, S., *see* Schmidt, M., *TCBB* Nov.-Dec. 2020 2189-2195
 Jaksik, R., *see* Marczyk, M., *TCBB* Jan.-Feb. 2020 149-157
 Jamil, H.M., *see* Mou, X., *TCBB* July-Aug. 2020 1459-1473
 Jankovic, S., *see* Grbic, M., *TCBB* Sept.-Oct. 2020 1822-1831
 Janssen, R., *see* van Iersel, L., *TCBB* Jan.-Feb. 2020 14-26
 Jarad, H., *see* Fodeh, S.J., *TCBB* March-April 2020 704-711
 Jhee, J.H., Bang, S., Lee, D., and Shin, H., Corrections to “Comorbidity Scoring With Causal Disease Networks” *TCBB* Nov.-Dec. 2020 2196
 Ji, Z., *see* Hu, H., *TCBB* May-June 2020 887-898
 Jia, H., Wei, H., Zhu, D., Ma, J., Yang, H., Wang, R., and Feng, X., PASA: Identifying More Credible Structural Variants of Hedou12; *TCBB* Sept.-Oct. 2020 1493-1503
 Jiang, H., Wang, J., Li, M., Lan, W., Wu, F., and Pan, Y., miRTS: A Recommendation Algorithm for Predicting miRNA Targets; *TCBB* May-June 2020 1032-1041
 Jiang, H., Qiu, Y., Hou, W., Cheng, X., Yim, M.Y., and Ching, W., Drug Side-Effect Profiles Prediction: From Empirical to Structural Risk Minimization; *TCBB* March-April 2020 402-410
 Jiang, Q., *see* Tan, R., *TCBB* May-June 2020 796-803
 Jiang, X., *see* Ma, Y., *TCBB* May-June 2020 788-795
 Jiang, Y., *see* Li, L., *TCBB* May-June 2020 841-846
 Jin, S., *see* Tan, R., *TCBB* May-June 2020 796-803
 Jing, X., Dong, Q., Hong, D., and Lu, R., Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment; *TCBB* Nov.-Dec. 2020 1918-1931
 Jones, M., *see* van Iersel, L., *TCBB* Jan.-Feb. 2020 14-26
 Juan, L., *see* Tan, R., *TCBB* May-June 2020 796-803
 Jungst, S., *see* Qingge, L., *TCBB* Nov.-Dec. 2020 1946-1954

K

- Kahveci, T., *see* Altuntas, V., *TCBB* July-Aug. 2020 1406-1418
 Kahveci, T., *see* Sarkar, A., *TCBB* Sept.-Oct. 2020 1582-1594
 Kalita, J., *see* Ahmed, S.S., *TCBB* Jan.-Feb. 2020 56-70
 Kalita, J.K., *see* Chowdhury, H.A., *TCBB* March-April 2020 566-586
 Kalita, J.K., *see* Chowdhury, H.A., *TCBB* July-Aug. 2020 1154-1173
 Kanaya, S., *see* Karim, M.B., *TCBB* Nov.-Dec. 2020 1955-1965

+ Check author entry for coauthors

- Kang, Q., Moore, N., Schardl, C.L., and Yoshida, R., CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths; *TCBB* May-June 2020 981-989

- Kapoor, R., Datta, A., Sima, C., Hua, J., Lopes, R., and Bittner, M.L., A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity; *TCBB* March-April 2020 459-468

- Karakaslar, E.O., Coskun, B., Outilaft, H., Namer, I.J., and Cicak, A.E., Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery; *TCBB* March-April 2020 719-725

- Karim, M.B., Huang, M., Ono, N., Kanaya, S., and Amin, M.A., BiClusO: A Novel Biclustering Approach and Its Application to Species-VOC Relational Data; *TCBB* Nov.-Dec. 2020 1955-1965

- Karimnezhad, A., and Bickel, D.R., Incorporating Prior Knowledge about Genetic Variants into the Analysis of Genetic Association Data: An Empirical Bayes Approach; *TCBB* March-April 2020 635-646

- Kartelj, A., *see* Grbic, M., *TCBB* Sept.-Oct. 2020 1822-1831

- Kawano, K., Koide, S., and Imamura, C., Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation; *TCBB* Sept.-Oct. 2020 1762-1772

- Kazemi, E., and Grossglauser, M., MPGM: Scalable and Accurate Multiple Network Alignment; *TCBB* Nov.-Dec. 2020 2040-2052

- Khan, A., Saha, G., and Pal, R.K., Modified Half-System Based Method for Reverse Engineering of Gene Regulatory Networks; *TCBB* July-Aug. 2020 1303-1316

- Khan, A., and Maji, P., Low-Rank Joint Subspace Construction for Cancer Sub-type Discovery; *TCBB* July-Aug. 2020 1290-1302

- Khatua, S., *see* Maji, R.K., *TCBB* Jan.-Feb. 2020 37-46

- Khosravi, P., *see* Habibi, M., *TCBB* Jan.-Feb. 2020 102-109

- Kim, N.H., *see* Saribudak, A., *TCBB* March-April 2020 608-622

- Kimpan, W., *see* Som-In, S., *TCBB* May-June 2020 990-998

- Klarner, H., Heinitz, F., Nee, S., and Siebert, H., Basins of Attraction, Commitment Sets, and Phenotypes of Boolean Networks; *TCBB* July-Aug. 2020 1115-1124

- Kocak, M., and Mozhui, K., An Application of the Bayesian Periodicity Test to Identify Diurnal Rhythm Genes in the Brain; *TCBB* Jan.-Feb. 2020 47-55

- Kohane, I., *see* McDermott, M.B., *TCBB* Nov.-Dec. 2020 1846-1857

- Koide, S., *see* Kawano, K., *TCBB* Sept.-Oct. 2020 1762-1772

- Kolahdoobi, M., *see* Amirkhani, A., *TCBB* July-Aug. 2020 1372-1382

- Komori, S., *see* Miyawaki-Kuwakado, A., *TCBB* Jan.-Feb. 2020 27-36

- Kumar, A.R., *see* Pyne, S., *TCBB* Jan.-Feb. 2020 278-291

- Kumar, R., *see* Rampogu, S., *TCBB* Jan.-Feb. 2020 365

- Kure, T., *see* Azuma, S., *TCBB* Nov.-Dec. 2020 2098-2106

- Kurgan, L.A., *see* Amirkhani, A., *TCBB* July-Aug. 2020 1372-1382

L

- Laleg-Kirati, T., *see* Al-Matouq, A.A., *TCBB* Sept.-Oct. 2020 1797-1809

- Lan, C., *see* Liu, Y., *TCBB* May-June 2020 899-905

- Lan, C., Chandrasekaran, S.N., and Huan, J., On the Unreported-Profile-is-Negative Assumption for Predictive Cheminformatics; *TCBB* July-Aug. 2020 1352-1363

- Lan, W., *see* Jiang, H., *TCBB* May-June 2020 1032-1041

- LaPierre, N., *see* Rahman, M.A., *TCBB* May-June 2020 828-840

- Lecca, P., and Re, A., Correction to “A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations” *TCBB* May-June 2020 1092

- Lecca, P., and Re, A., A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations; *TCBB* March-April 2020 469-482

- Lee, D., *see* Jhee, J.H., *TCBB* Nov.-Dec. 2020 2196

- Lee, K.W., *see* Rampogu, S., *TCBB* Jan.-Feb. 2020 365

- Lee, S., *see* Choi, D., *TCBB* Sept.-Oct. 2020 1785-1796

- Lee, W., and Han, K., Constructive Prediction of Potential RNA Aptamers for a Protein Target; *TCBB* Sept.-Oct. 2020 1476-1482

- Lei, X., Yang, X., and Wu, F., Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins; *TCBB* March-April 2020 495-505

- Lei, X.,** see Sun, Y., *TCBB July-Aug. 2020* 1253-1261
- Li, A.,** see Zhang, T., *TCBB Jan.-Feb. 2020* 189-197
- Li, A.,** see Xi, J., *TCBB March-April 2020* 422-434
- Li, A.,** see Wang, H., *TCBB March-April 2020* 587-598
- Li, F.,** Gao, L., and Wang, B., Detection of Driver Modules with Rarely Mutated Genes in Cancers; *TCBB March-April 2020* 390-401
- Li, G.,** see Xiao, Q., *TCBB March-April 2020* 623-634
- Li, G.,** Li, M., Wang, J., Li, Y., and Pan, Y., United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins; *TCBB July-Aug. 2020* 1451-1458
- Li, J.,** see Liu, Y., *TCBB May-June 2020* 899-905
- Li, J.,** see He, Z., *TCBB May-June 2020* 930-937
- Li, J.,** see Zheng, J., *TCBB May-June 2020* 726-727
- Li, J.,** Shi, X., You, Z., Yi, H., Chen, Z., Lin, Q., and Fang, M., Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information; *TCBB Sept.-Oct. 2020* 1546-1554
- Li, L.,** and Jiang, Y., Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition; *TCBB May-June 2020* 841-846
- Li, L.,** Liu, Y., and Qin, M., Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks; *TCBB March-April 2020* 599-607
- Li, M.,** see Luo, J., *TCBB May-June 2020* 877-886
- Li, M.,** see Wu, B., *TCBB May-June 2020* 847-857
- Li, M.,** see Liao, X., *TCBB May-June 2020* 728-738
- Li, M.,** see Wang, S., *TCBB May-June 2020* 739-747
- Li, M.,** see Jiang, H., *TCBB May-June 2020* 1032-1041
- Li, M.,** Meng, X., Zheng, R., Wu, F., Li, Y., Pan, Y., and Wang, J., Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network; *TCBB May-June 2020* 817-827
- Li, M.,** see Liao, X., *TCBB Jan.-Feb. 2020* 177-188
- Li, M.,** see Li, G., *TCBB July-Aug. 2020* 1451-1458
- Li, T.,** Zhang, X., Luo, F., Wu, F., and Wang, J., MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads; *TCBB Jan.-Feb. 2020* 220-225
- Li, T.,** see Fodeh, S.J., *TCBB March-April 2020* 704-711
- Li, T.,** see Shi, J., *TCBB March-April 2020* 449-458
- Li, X.,** see Liu, Y., *TCBB May-June 2020* 748-757
- Li, X.,** see Wong, K., *TCBB Jan.-Feb. 2020* 327-333
- Li, X.,** Zhang, S., and Wong, K., Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies; *TCBB Jan.-Feb. 2020* 226-237
- Li, X.,** see Pan, C., *TCBB Jan.-Feb. 2020* 321-326
- Li, X.,** and Wong, K., Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering; *TCBB Sept.-Oct. 2020* 1773-1784
- Li, Y.,** see He, Z., *TCBB May-June 2020* 930-937
- Li, Y.,** see Ni, P., *TCBB May-June 2020* 906-915
- Li, Y.,** see Li, M., *TCBB May-June 2020* 817-827
- Li, Y.,** Huang, H., Chen, H., and Liu, T., Deep Neural Networks for *In Situ* Hybridization Grid Completion and Clustering; *TCBB March-April 2020* 536-546
- Li, Y.,** see Li, G., *TCBB July-Aug. 2020* 1451-1458
- Li, Y.,** see Yuan, X., *TCBB July-Aug. 2020* 1141-1153
- Li, Z.,** see Zhang, Y., *TCBB Sept.-Oct. 2020* 1703-1713
- Liang, C.,** see Xiao, Q., *TCBB March-April 2020* 623-634
- Liang, H.,** see He, Z., *TCBB Nov.-Dec. 2020* 2062-2073
- Liang, Y.,** see Liu, X., *TCBB July-Aug. 2020* 1329-1340
- Liao, X.,** see Peng, S., *TCBB May-June 2020* 804-816
- Liao, X.,** see Wu, B., *TCBB May-June 2020* 847-857
- Liao, X.,** Li, M., Zou, Y., Wu, F., Pan, Y., and Wang, J., An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data; *TCBB May-June 2020* 728-738
- Liao, X.,** Li, M., Luo, J., Zou, Y., Wu, F., Pan, Y., Luo, F., and Wang, J., Improving *de novo* Assembly Based on Read Classification; *TCBB Jan.-Feb. 2020* 177-188
- Lin, Q.,** see Wong, K., *TCBB Jan.-Feb. 2020* 327-333
- Lin, Q.,** see Li, J., *TCBB Sept.-Oct. 2020* 1546-1554
- Lin, S.,** see Paoletti, N., *TCBB Nov.-Dec. 2020* 1981-1993
- Lin, X.,** Zhang, X., and Xu, X., Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting; *TCBB Sept.-Oct. 2020* 1525-1534
- Lin, Y.,** see Hu, H., *TCBB May-June 2020* 887-898
- Lin, Y.,** see Yang, C., *TCBB Jan.-Feb. 2020* 71-81
- Lin, Y.,** see Zeng, X., *TCBB Sept.-Oct. 2020* 1639-1647
- Lisboa, P.,** see Fergus, P., *TCBB March-April 2020* 668-678
- Lisboa, P.,** see Hind, J., *TCBB Sept.-Oct. 2020* 1535-1545
- Liu, C.,** see Liu, Y., *TCBB May-June 2020* 748-757
- Liu, G.,** Zhang, B., Qian, G., Wang, B., Mao, B., and Bichindaritz, I., Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks; *TCBB Nov.-Dec. 2020* 1966-1980
- Liu, H.,** see Liu, J., *TCBB Jan.-Feb. 2020* 339-346
- Liu, H.,** see Zhang, Y., *TCBB Sept.-Oct. 2020* 1703-1713
- Liu, J.,** see Peng, S., *TCBB May-June 2020* 804-816
- Liu, J.,** see He, Y., *TCBB Jan.-Feb. 2020* 110-123
- Liu, J.,** Tian, Z., Xiao, Y., Liu, H., Hao, S., Zhang, X., Wang, C., Sun, J., Yu, H., and Yan, J., Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach; *TCBB Jan.-Feb. 2020* 339-346
- Liu, J.,** see Sun, Y., *TCBB July-Aug. 2020* 1253-1261
- Liu, J.,** Qu, Z., Yang, M., Sun, J., Su, S., and Zhang, L., Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB; *TCBB Sept.-Oct. 2020* 1504-1515
- Liu, J.,** Liu, Q., Zhang, L., Su, S., and Liu, Y., Enabling Massive XML-Based Biological Data Management in HBase; *TCBB Nov.-Dec. 2020* 1994-2004
- Liu, J.,** see Yu, X., *TCBB Nov.-Dec. 2020* 2029-2039
- Liu, J.S.,** see Zhang, R., *TCBB March-April 2020* 647-656
- Liu, K.S.,** see Paoletti, N., *TCBB Nov.-Dec. 2020* 1981-1993
- Liu, M.,** see Shao, W., *TCBB July-Aug. 2020* 1394-1405
- Liu, Q.,** see Liu, J., *TCBB Nov.-Dec. 2020* 1994-2004
- Liu, T.,** see Li, Y., *TCBB March-April 2020* 536-546
- Liu, X.,** see Chen, Z., *TCBB March-April 2020* 366-375
- Liu, X.,** see Shi, J., *TCBB March-April 2020* 449-458
- Liu, X.,** Wang, S., Zhang, H., Zhang, H., Yang, Z., and Liang, Y., Novel Regularization Method for Biomarker Selection and Cancer Classification; *TCBB July-Aug. 2020* 1329-1340
- Liu, Y.,** Lan, C., Blumenstein, M., and Li, J., Bi-Level Error Correction for PacBio Long Reads; *TCBB May-June 2020* 899-905
- Liu, Y.,** Wu, M., Liu, C., Li, X., and Zheng, J., SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization; *TCBB May-June 2020* 748-757
- Liu, Y.,** see Li, L., *TCBB March-April 2020* 599-607
- Liu, Y.,** see Chen, Z., *TCBB March-April 2020* 366-375
- Liu, Y.,** Ng, M.K., and Wu, S., Multi-Domain Networks Association for Biological Data Using Block Signed Graph Clustering; *TCBB March-April 2020* 435-448
- Liu, Y.,** see Xiao, Q., *TCBB March-April 2020* 623-634
- Liu, Y.,** see Liu, J., *TCBB Nov.-Dec. 2020* 1994-2004
- Long, Y.,** see Luo, J., *TCBB July-Aug. 2020* 1341-1351
- Lopes, R.,** see Vundavilli, H., *TCBB May-June 2020* 1010-1018
- Lopes, R.,** see Kapoor, R., *TCBB March-April 2020* 459-468
- Lotz, T.S.,** see Schmidt, M., *TCBB Nov.-Dec. 2020* 2189-2195
- Lu, K.,** see Peng, S., *TCBB May-June 2020* 804-816
- Lu, L.,** see Zeng, X., *TCBB Sept.-Oct. 2020* 1639-1647
- Lu, Q.,** see Zhou, J., *TCBB Jan.-Feb. 2020* 124-135
- Lu, Q.,** see Zhou, J., *TCBB July-Aug. 2020* 1383-1393
- Lu, R.,** see Jing, X., *TCBB Nov.-Dec. 2020* 1918-1931
- Lu, Y.,** see Peng, S., *TCBB May-June 2020* 804-816
- Luo, F.,** see Li, T., *TCBB Jan.-Feb. 2020* 220-225
- Luo, F.,** see Liao, X., *TCBB Jan.-Feb. 2020* 177-188
- Luo, G.,** see He, Z., *TCBB May-June 2020* 930-937
- Luo, H.,** see Luo, J., *TCBB May-June 2020* 877-886
- Luo, J.,** Wang, J., Shang, J., Luo, H., Li, M., Wu, F., and Pan, Y., GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets; *TCBB May-June 2020* 877-886

- Luo, J.**, *see* Wu, B., *TCBB* May-June 2020 847-857
Luo, J., *see* Liao, X., *TCBB* Jan.-Feb. 2020 177-188
Luo, J., *see* Pan, C., *TCBB* Jan.-Feb. 2020 321-326
Luo, J., *see* Xiao, Q., *TCBB* March-April 2020 623-634
Luo, J., and Long, Y., NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity; *TCBB* July-Aug. 2020 1341-1351
Luo, X., *see* Hu, L., *TCBB* Nov.-Dec. 2020 2017-2028
Luthringer, B., *see* Moreno, L.A., *TCBB* July-Aug. 2020 1440-1450

M

- Ma, J.**, *see* Jia, H., *TCBB* Sept.-Oct. 2020 1493-1503
Ma, L., *see* Zhang, G., *TCBB* May-June 2020 1068-1081
Ma, L., *see* Chen, Z., *TCBB* March-April 2020 366-375
Ma, L., *see* Zhao, G., *TCBB* July-Aug. 2020 1211-1221
Ma, L., *see* Zhang, G., *TCBB* Nov.-Dec. 2020 2119-2130
Ma, R., *see* Tan, R., *TCBB* May-June 2020 796-803
Ma, Y., Hu, X., He, T., and Jiang, X., Clustering and Integrating of Heterogeneous Microbiome Data by Joint Symmetric Nonnegative Matrix Factorization with Laplacian Regularization; *TCBB* May-June 2020 788-795
Madhumita, *see* Paul, S., *TCBB* Sept.-Oct. 2020 1729-1740
Maduranga, D.A.K., *see* Chen, H., *TCBB* March-April 2020 516-525
Mahjub, H., *see* Shahdoust, M., *TCBB* Sept.-Oct. 2020 1555-1562
Maji, P., *see* Khan, A., *TCBB* July-Aug. 2020 1290-1302
Maji, R.K., Khatua, S., and Ghosh, Z., A Supervised Ensemble Approach for Sensitive microRNA Target Prediction; *TCBB* Jan.-Feb. 2020 37-46
Majumder, P., Ray, P.P., Ghosh, S., and Dey, S.K., Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study; *TCBB* July-Aug. 2020 1364-1371
Makrogiannis, S., *see* Boukari, F., *TCBB* May-June 2020 959-971
Mallik, S., and Bandyopadhyay, S., WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection; *TCBB* March-April 2020 690-703
Manica, M., Polig, R., Purandare, M., Mathis, R., Hagleitner, C., and Martinez, M.R., FPGA Accelerated Analysis of Boolean Gene Regulatory Networks; *TCBB* Nov.-Dec. 2020 2141-2147
Mao, B., *see* Liu, G., *TCBB* Nov.-Dec. 2020 1966-1980
Mapes, N., Rodriguez, C., Chowriappa, P., and Dua, S., Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences; *TCBB* July-Aug. 2020 1276-1289
Marczyk, M., Jaksik, R., Polanski, A., and Polanska, J., GaMRed—Adaptive Filtering of High-Throughput Biological Data; *TCBB* Jan.-Feb. 2020 149-157
Marques, S.M., *see* Filipovic, J., *TCBB* Sept.-Oct. 2020 1625-1638
Martin-Vide, C., and Vega-Rodriguez, M.A., Algorithms for Computational Biology: Fifth Edition; *TCBB* Jan.-Feb. 2020 I
Martinez, M.R., *see* Manica, M., *TCBB* Nov.-Dec. 2020 2141-2147
Mathis, R., *see* Manica, M., *TCBB* Nov.-Dec. 2020 2141-2147
Matic, D., *see* Grbic, M., *TCBB* Sept.-Oct. 2020 1822-1831
Matyska, L., *see* Filipovic, J., *TCBB* Sept.-Oct. 2020 1625-1638
Mazrouee, S., and Wang, W., PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing; *TCBB* Jan.-Feb. 2020 264-277
McDermott, M.B., Wang, J., Zhao, W., Sheridan, S.D., Szolovits, P., Kohane, I., Haggarty, S.J., and Perlis, R.H., Deep Learning Benchmarks on L1000 Gene Expression Data; *TCBB* Nov.-Dec. 2020 1846-1857
Meng, X., *see* Li, M., *TCBB* May-June 2020 817-827
Miao, Z., *see* Zhang, Y., *TCBB* Sept.-Oct. 2020 1703-1713
Middleton, R.H., *see* Delgado, R.A., *TCBB* Jan.-Feb. 2020 292-301
Miglani, V., *see* Dutta, P., *TCBB* Nov.-Dec. 2020 2005-2016
Min, X., *see* Zeng, X., *TCBB* Sept.-Oct. 2020 1639-1647
Miyawaki-Kuwakado, A., Komori, S., and Shiraishi, F., A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models; *TCBB* Jan.-Feb. 2020 27-36
Mizera, A., *see* Paul, S., *TCBB* Nov.-Dec. 2020 1932-1945
Mo, J., *see* Feng, Y., *TCBB* Jan.-Feb. 2020 91-101

- Montanez, C.C.**, *see* Fergus, P., *TCBB* March-April 2020 668-678
Moore, N., *see* Kang, Q., *TCBB* May-June 2020 981-989
Moreno, L.A., Omidi, M., Wurlitzer, M., Luthringer, B., Helmholz, H., Schluter, H., Willumeit-Romer, R., and Fugenschuh, A., Understanding Protein Networks Using Vester's Sensitivity Model; *TCBB* July-Aug. 2020 1440-1450
Morrison, C.T., *see* Noriega-Atala, E., *TCBB* Nov.-Dec. 2020 1895-1906
Mostafavi, M.T., *see* Yeganeh, P.N., *TCBB* Sept.-Oct. 2020 1613-1624
Mou, X., and Jamil, H.M., Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources; *TCBB* July-Aug. 2020 1459-1473
Mozhui, K., *see* Kocak, M., *TCBB* Jan.-Feb. 2020 47-55
Mundra, P.A., *see* Chen, H., *TCBB* March-April 2020 516-525
Murakami, Y., *see* van Iersel, L., *TCBB* Jan.-Feb. 2020 14-26
Murchie, E.H., *see* Gibbs, J.A., *TCBB* Nov.-Dec. 2020 1907-1917

N

- Nabavi, S.**, *see* Zare, F., *TCBB* May-June 2020 868-876
Najarian, K., *see* Zare, F., *TCBB* May-June 2020 868-876
Nakamura, Y., *see* Chen, Z., *TCBB* May-June 2020 916-929
Namer, I.J., *see* Karakaslar, E.O., *TCBB* March-April 2020 719-725
Nee, S., *see* Klärner, H., *TCBB* July-Aug. 2020 1115-1124
Ng, M.K., *see* Liu, Y., *TCBB* March-April 2020 435-448
Ni, P., Wang, J., Zhong, P., Li, Y., Wu, F., and Pan, Y., Constructing Disease Similarity Networks Based on Disease Module Theory; *TCBB* May-June 2020 906-915
Nihalani, R., *see* Pan, T., *TCBB* Jan.-Feb. 2020 136-148
Ning, X., *see* He, Y., *TCBB* Jan.-Feb. 2020 110-123
Noor-A-Rahim, M., *see* Wang, Y., *TCBB* Nov.-Dec. 2020 2176-2182
Noriega-Atala, E., Hein, P.D., Thumsi, S.S., Wong, Z., Wang, X., Hendryx, S.M., and Morrison, C.T., Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts; *TCBB* Nov.-Dec. 2020 1895-1906
Novara, C., *see* Al-Matouq, A.A., *TCBB* Sept.-Oct. 2020 1797-1809

O

- Ogunleye, A.**, and Wang, Q., XGBoost Model for Chronic Kidney Disease Diagnosis; *TCBB* Nov.-Dec. 2020 2131-2140
Ojiaku, J., *see* Carroll, T.C., *TCBB* Nov.-Dec. 2020 2086-2097
Oliveira, A.R., *see* Brito, K.L., *TCBB* Jan.-Feb. 2020 2-13
Omidi, M., *see* Moreno, L.A., *TCBB* July-Aug. 2020 1440-1450
Ono, N., *see* Karim, M.B., *TCBB* Nov.-Dec. 2020 1955-1965
Ou-Yang, L., *see* Yuan, R., *TCBB* March-April 2020 712-718
Ou-Yang, L., Zhang, X., Hu, X., and Yan, H., Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model; *TCBB* Nov.-Dec. 2020 2162-2169
Outilaft, H., *see* Karakaslar, E.O., *TCBB* March-April 2020 719-725
Ouyang, Y., *see* Yu, X., *TCBB* Nov.-Dec. 2020 2029-2039

P

- Paisarnsrisomsuk, S.**, *see* Sokolovsky, M., *TCBB* Nov.-Dec. 2020 1835-1845
Pal, R.K., *see* Khan, A., *TCBB* July-Aug. 2020 1303-1316
Palaniappan, S.K., *see* Pichene, M., *TCBB* Sept.-Oct. 2020 1691-1702
Pan, C., Luo, J., Zhang, J., and Li, X., BiModule: Bi clique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules; *TCBB* Jan.-Feb. 2020 321-326
Pan, T., Nihalani, R., and Aluru, S., Fast de Bruijn Graph Compaction in Distributed Memory Environments; *TCBB* Jan.-Feb. 2020 136-148
Pan, T., *see* Guo, Q., *TCBB* Sept.-Oct. 2020 1563-1572
Pan, Y., *see* Luo, J., *TCBB* May-June 2020 877-886
Pan, Y., *see* Wu, B., *TCBB* May-June 2020 847-857
Pan, Y., *see* Liao, X., *TCBB* May-June 2020 728-738
Pan, Y., *see* Jiang, H., *TCBB* May-June 2020 1032-1041
Pan, Y., *see* Ni, P., *TCBB* May-June 2020 906-915
Pan, Y., *see* Li, M., *TCBB* May-June 2020 817-827
Pan, Y., *see* Liao, X., *TCBB* Jan.-Feb. 2020 177-188

- Pan, Y.,** see Li, G., *TCBB July-Aug. 2020* 1451-1458
Pan, Y., see Yan, C., *TCBB Sept.-Oct. 2020* 1595-1604
Pang, J., see Paul, S., *TCBB Nov.-Dec. 2020* 1932-1945
Paoletti, N., Liu, K.S., Chen, H., Smolka, S.A., and Lin, S., Data-Driven Robust Control for a Closed-Loop Artificial Pancreas; *TCBB Nov.-Dec. 2020* 1981-1993
Parameswaran, S., see Bayat, A., *TCBB Jan.-Feb. 2020* 334-338
Parameswaran, S., see Gamaarachchi, H., *TCBB July-Aug. 2020* 1125-1133
Park, C., see Rampogu, S., *TCBB Jan.-Feb. 2020* 365
Park, S., see Xu, H., *TCBB Nov.-Dec. 2020* 1871-1882
Park, S.J., see Rampogu, S., *TCBB Jan.-Feb. 2020* 365
Pathak, S., van Rossen, J., Vijlbrief, O., Geerdink, J., Seifert, C., and van Keulen, M., Post-Structuring Radiology Reports of Breast Cancer Patients for Clinical Quality Assurance; *TCBB Nov.-Dec. 2020* 1883-1894
Paul, S., and Madhumita, *RFCM³: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer;* *TCBB Sept.-Oct. 2020* 1729-1740
Paul, S., Su, C., Pang, J., and Mizera, A., An Efficient Approach Towards the Source-Target Control of Boolean Networks; *TCBB Nov.-Dec. 2020* 1932-1945
Peeters, R., see Ismailoglu, F., *TCBB Jan.-Feb. 2020* 347-353
Peng, C., see Wong, K., *TCBB Jan.-Feb. 2020* 327-333
Peng, C., Zheng, Y., and Huang, D., Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes; *TCBB Sept.-Oct. 2020* 1605-1612
Peng, J., Zhu, L., Wang, Y., and Chen, J., Mining Relationships among Multiple Entities in Biological Networks; *TCBB May-June 2020* 769-776
Peng, Q., see Fu, L., *TCBB Sept.-Oct. 2020* 1721-1728
Peng, S., Zhang, X., Su, W., Dong, D., Lu, Y., Liao, X., Lu, K., Yang, C., Liu, J., Zhu, W., and Wei, D., High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer; *TCBB May-June 2020* 804-816
Peng, W., see Song, J., *TCBB May-June 2020* 758-768
Perlis, R.H., see McDermott, M.B., *TCBB Nov.-Dec. 2020* 1846-1857
Permiakova, O., see Sokolovska, N., *TCBB Jan.-Feb. 2020* 358-364
Petti, M., Bizzarri, D., Verriente, A., Falcone, R., and Farina, L., Connectivity Significance for Disease Gene Prioritization in an Expanding Universe; *TCBB Nov.-Dec. 2020* 2155-2161
Pezeshk, H., see Shahdoust, M., *TCBB Sept.-Oct. 2020* 1555-1562
Pichene, M., Palaniappan, S.K., Fabre, E., and Genest, B., Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions; *TCBB Sept.-Oct. 2020* 1691-1702
Pineles, B., see Fergus, P., *TCBB March-April 2020* 668-678
Pinter, R.Y., see Ganor, D., *TCBB Jan.-Feb. 2020* 316-320
Pinzon-Reyes, E., Alvarez, W.A., Rondon-Villarreal, P., and Hernandez, H.G., Softeigen: Primers Design Web-Based Tool for MS-HRM Technique; *TCBB Jan.-Feb. 2020* 354-357
Plata, O., see Herruzzo, J.M., *TCBB July-Aug. 2020* 1093-1104
Pilhak, J., see Filipovic, J., *TCBB Sept.-Oct. 2020* 1625-1638
Poh, C.L., see Wang, Y., *TCBB Nov.-Dec. 2020* 2176-2182
Polanska, J., see Marczyk, M., *TCBB Jan.-Feb. 2020* 149-157
Polanski, A., see Marczyk, M., *TCBB Jan.-Feb. 2020* 149-157
Polig, R., see Manica, M., *TCBB Nov.-Dec. 2020* 2141-2147
Pons, J.C., Scornavacca, C., and Cardona, G., Generation of Level-k LGT Networks; *TCBB Jan.-Feb. 2020* 158-164
Pound, M.P., see Gibbs, J.A., *TCBB Nov.-Dec. 2020* 1907-1917
Pradhan, P., see Acharya, S., *TCBB Jan.-Feb. 2020* 207-219
Pridmore, T.P., see Gibbs, J.A., *TCBB Nov.-Dec. 2020* 1907-1917
Purandare, M., see Manica, M., *TCBB Nov.-Dec. 2020* 2141-2147
Pusey, M.L., see Shrestha, M., *TCBB Nov.-Dec. 2020* 2074-2085
Pyne, S., Kumar, A.R., and Anand, A., Rapid Reconstruction of Time-Varying Gene Regulatory Networks; *TCBB Jan.-Feb. 2020* 278-291

Q

- Qian, G.,** see Liu, G., *TCBB Nov.-Dec. 2020* 1966-1980
Qin, C., see Dong, Y., *TCBB Nov.-Dec. 2020* 2170-2175

- Qin, M.,** see Li, L., *TCBB March-April 2020* 599-607
Qin, Z., see Zhang, R., *TCBB March-April 2020* 647-656
Qingga, L., Smith, K., Jungst, S., Wang, B., Yang, Q., and Zhu, B., Approaching the One-Sided Exemplar Adjacency Number Problem; *TCBB Nov.-Dec. 2020* 1946-1954
Qiu, P., see Youmans, M., *TCBB July-Aug. 2020* 1134-1140
Qiu, Y., see Jiang, H., *TCBB March-April 2020* 402-410
Qu, Z., see Liu, J., *TCBB Sept.-Oct. 2020* 1504-1515

R

- Rabbone, I.,** see Al-Matouq, A.A., *TCBB Sept.-Oct. 2020* 1797-1809
Rahman, M.A., LaPierre, N., and Rangwala, H., Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL); *TCBB May-June 2020* 828-840
Rampogu, S., Baek, A., Bavi, R., Son, M., Cao, G.P., Kumar, R., Park, C., Zeb, A., Rana, R.M., Park, S.J., and Lee, K.W., Correction to “Identification of Novel Scaffolds with Dual Role as Antiepileptic and Anti-Breast Cancer” *TCBB Jan.-Feb. 2020* 365
Rana, R.M., see Rampogu, S., *TCBB Jan.-Feb. 2020* 365
Rangwala, H., see Rahman, M.A., *TCBB May-June 2020* 828-840
Ranjan, A., Fahad, M.S., Fernandez-Baca, D., Deepak, A., and Tripathi, S., Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences; *TCBB Sept.-Oct. 2020* 1648-1659
Ray, P.P., see Majumder, P., *TCBB July-Aug. 2020* 1364-1371
Raza, S., Abbas, G., and Azam, S.S., Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1; *TCBB Sept.-Oct. 2020* 1751-1761
Re, A., see Lecca, P., *TCBB May-June 2020* 1092
Re, A., see Lecca, P., *TCBB March-April 2020* 469-482
Reinhardt, F., see Schmidt, M., *TCBB Nov.-Dec. 2020* 2189-2195
Rhodes, J.A., Topological Metrizations of Trees, and New Quartet Methods of Tree Inference; *TCBB Nov.-Dec. 2020* 2107-2118
Riesen, K., Ferrer, M., and Bunke, H., Approximate Graph Edit Distance in Quadratic Time; *TCBB March-April 2020* 483-494
Rodriguez, C., see Mapes, N., *TCBB July-Aug. 2020* 1276-1289
Rodriguez-Paton, A., see Zeng, X., *TCBB Sept.-Oct. 2020* 1639-1647
Roehle, R., see Zheng, H., *TCBB May-June 2020* 858-867
Romero-Vivas, E., see Carvajal-Lopez, P., *TCBB Jan.-Feb. 2020* 198-206
Rondon-Villarreal, P., see Pinzon-Reyes, E., *TCBB Jan.-Feb. 2020* 354-357
Rong, W., see Yu, X., *TCBB Nov.-Dec. 2020* 2029-2039
Roy, S., see Ahmed, S.S., *TCBB Jan.-Feb. 2020* 56-70
Ruiz, C., see Sokolovsky, M., *TCBB Nov.-Dec. 2020* 1835-1845
Rustici, G., see Carvajal-Lopez, P., *TCBB Jan.-Feb. 2020* 198-206
Rutta, J.A., see Saribudak, A., *TCBB March-April 2020* 608-622

S

- Sadeghi, M.,** see Shahdoust, M., *TCBB Sept.-Oct. 2020* 1555-1562
Safdar, B., see Fodeh, S.J., *TCBB March-April 2020* 704-711
Saha, G., see Khan, A., *TCBB July-Aug. 2020* 1303-1316
Saha, S., see Acharya, S., *TCBB Jan.-Feb. 2020* 207-219
Saha, S., see Dutta, P., *TCBB Nov.-Dec. 2020* 2005-2016
Saltini, C., see Sarkar, A., *TCBB Sept.-Oct. 2020* 1582-1594
Santos, L.H., see Fassio, A.V., *TCBB July-Aug. 2020* 1317-1328
Saribudak, A., Subick, A.A., Kim, N.H., Rutta, J.A., and Uyar, M.U., Gene Expressions, Hippocampal Volume Loss, and MMSE Scores in Computation of Progression and Pharmacologic Therapy Effects for Alzheimer's Disease; *TCBB March-April 2020* 608-622
Sarkar, A., Atay, Y., Erickson, A.L., Arisi, I., Saltini, C., and Kahveci, T., An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer; *TCBB Sept.-Oct. 2020* 1582-1594
Saxena, R., see Sharma, S., *TCBB Sept.-Oct. 2020* 1660-1670
Schardl, C.L., see Kang, Q., *TCBB May-June 2020* 981-989
Schluter, H., see Moreno, L.A., *TCBB July-Aug. 2020* 1440-1450
Schmidt, M., Hamacher, K., Reinhardt, F., Lotz, T.S., Groher, F., Suess, B., and Jager, S., SICOR: Subgraph Isomorphism Comparison of RNA Secondary Structures; *TCBB Nov.-Dec. 2020* 2189-2195

- Scornavacca, C.**, *see* Pons, J.C., *TCBB Jan.-Feb. 2020* 158-164
- Seifert, C.**, *see* Pathak, S., *TCBB Nov.-Dec. 2020* 1883-1894
- Sen, R.**, Tagore, S., and De, R.K., ASAPP: Architectural Similarity-Based Automated Pathway Prediction System and Its Application in Host-Pathogen Interactions; *TCBB March-April 2020* 506-515
- Serpedin, E.**, *see* Alshawafeh, M., *TCBB May-June 2020* 1056-1067
- Shahdoust, M.**, Mahjub, H., Pezeshk, H., and Sadeghi, M., A Network-Based Comparison Between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso; *TCBB Sept.-Oct. 2020* 1555-1562
- Shang, J.**, *see* Luo, J., *TCBB May-June 2020* 877-886
- Shang, J.**, *see* Sun, Y., *TCBB July-Aug. 2020* 1253-1261
- Shang, Y.**, *see* Wang, W., *TCBB July-Aug. 2020* 1430-1439
- Shao, W.**, Huang, S., Liu, M., and Zhang, D., Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages; *TCBB July-Aug. 2020* 1394-1405
- Sharma, A.**, *see* Sharma, N., *TCBB Sept.-Oct. 2020* 1573-1581
- Sharma, H.**, *see* Sharma, N., *TCBB Sept.-Oct. 2020* 1573-1581
- Sharma, N.**, Sharma, H., and Sharma, A., An Effective Solution for Large Scale Single Machine Total Weighted Tardiness Problem using Lunar Cycle Inspired Artificial Bee Colony Algorithm; *TCBB Sept.-Oct. 2020* 1573-1581
- Sharma, S.**, Sharma, S.N., and Saxena, R., Identification of Short Exons Disunited by a Short Intron in Eukaryotic DNA Regions; *TCBB Sept.-Oct. 2020* 1660-1670
- Sharma, S.N.**, *see* Sharma, S., *TCBB Sept.-Oct. 2020* 1660-1670
- Shen, T.**, *see* Xuan, P., *TCBB May-June 2020* 1019-1031
- Shen, Z.**, Deng, S., and Huang, D., RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks; *TCBB Sept.-Oct. 2020* 1741-1750
- Shen, Z.**, Deng, S., and Huang, D., Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature; *TCBB Sept.-Oct. 2020* 1483-1492
- Sheridan, S.D.**, *see* McDermott, M.B., *TCBB Nov.-Dec. 2020* 1846-1857
- Shi, J.**, Zhao, J., Liu, X., Chen, L., and Li, T., Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis; *TCBB March-April 2020* 449-458
- Shi, X.**, *see* Li, J., *TCBB Sept.-Oct. 2020* 1546-1554
- Shi, Y.**, *see* Yao, H., *TCBB May-June 2020* 777-787
- Shi, Y.**, *see* Hu, F., *TCBB July-Aug. 2020* 1187-1197
- Shin, H.**, *see* Jhee, J.H., *TCBB Nov.-Dec. 2020* 2196
- Shiraishi, F.**, *see* Miyawaki-Kuwakado, A., *TCBB Jan.-Feb. 2020* 27-36
- Shrestha, M.**, Tran, T.X., Bhattacharai, B., Pusey, M.L., and Aygun, R.S., Schema Matching and Data Integration with Consistent Naming on Protein Crystallization Screens; *TCBB Nov.-Dec. 2020* 2074-2085
- Siebert, H.**, *see* Klarner, H., *TCBB July-Aug. 2020* 1115-1124
- Silveira, S.A.**, *see* Fassio, A.V., *TCBB July-Aug. 2020* 1317-1328
- Sima, C.**, *see* Vundavilli, H., *TCBB May-June 2020* 1010-1018
- Sima, C.**, *see* Kapoor, R., *TCBB March-April 2020* 459-468
- Smirnov, E.**, *see* Ismailoglu, F., *TCBB Jan.-Feb. 2020* 347-353
- Smith, K.**, *see* Qingge, L., *TCBB Nov.-Dec. 2020* 1946-1954
- Smolka, S.A.**, *see* Paoletti, N., *TCBB Nov.-Dec. 2020* 1981-1993
- Sokolovska, N.**, Permiakova, O., Forslund, S.K., and Zucker, J., Using Unlabeled Data to Discover Bivariate Causality with Deep Restricted Boltzmann Machines; *TCBB Jan.-Feb. 2020* 358-364
- Sokolovsky, M.**, Guerrero, F., Paisarnsrisomsuk, S., Ruiz, C., and Alvarez, S.A., Deep Learning for Automated Feature Discovery and Classification of Sleep Stages; *TCBB Nov.-Dec. 2020* 1835-1845
- Som-In, S.**, and Kimpan, W., Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections; *TCBB May-June 2020* 990-998
- Son, M.**, *see* Rampogu, S., *TCBB Jan.-Feb. 2020* 365
- Song, J.**, Peng, W., and Wang, F., An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer; *TCBB May-June 2020* 758-768
- Spainhour, J.C.G.**, *see* Youmans, M., *TCBB July-Aug. 2020* 1134-1140
- Su, C.**, *see* Paul, S., *TCBB Nov.-Dec. 2020* 1932-1945
- Su, S.**, *see* Liu, J., *TCBB Sept.-Oct. 2020* 1504-1515
- Su, S.**, *see* Liu, J., *TCBB Nov.-Dec. 2020* 1994-2004
- Su, W.**, *see* Peng, S., *TCBB May-June 2020* 804-816
- Subick, A.A.**, *see* Saribudak, A., *TCBB March-April 2020* 608-622
- Suess, B.**, *see* Schmidt, M., *TCBB Nov.-Dec. 2020* 2189-2195
- Sugie, T.**, *see* Azuma, S., *TCBB Nov.-Dec. 2020* 2098-2106
- Sun, J.**, *see* Liu, J., *TCBB Jan.-Feb. 2020* 339-346
- Sun, J.**, *see* Liu, J., *TCBB Sept.-Oct. 2020* 1504-1515
- Sun, Y.**, Wang, X., Shang, J., Liu, J., Zheng, C., and Lei, X., Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis; *TCBB July-Aug. 2020* 1253-1261
- Szolovits, P.**, *see* McDermott, M.B., *TCBB Nov.-Dec. 2020* 1846-1857

T

- Tagore, S.**, *see* Sen, R., *TCBB March-April 2020* 506-515
- Tan, J.W.**, Chang, S., Abdul-Kareem, S., Yap, H.J., and Yong, K., Deep Learning for Plant Species Classification Using Leaf Vein Morphometric; *TCBB Jan.-Feb. 2020* 82-90
- Tan, R.**, Wang, J., Wu, X., Juan, L., Zhang, T., Ma, R., Zhan, Q., Wang, T., Jin, S., Jiang, Q., and Wang, Y., ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data; *TCBB May-June 2020* 796-803
- Tercan, B.**, and Acar, A.C., The Use of Informed Priors in Biclustering of Gene Expression with the Hierarchical Dirichlet Process; *TCBB Sept.-Oct. 2020* 1810-1821
- Teymourpour, P.**, *see* Arabameri, A., *TCBB March-April 2020* 547-557
- Thumsi, S.S.**, *see* Noriega-Atala, E., *TCBB Nov.-Dec. 2020* 1895-1906
- Tian, J.**, *see* Wu, S., *TCBB Sept.-Oct. 2020* 1714-1720
- Tian, L.**, *see* Yang, X., *TCBB July-Aug. 2020* 1262-1275
- Tian, T.**, *see* Deng, Z., *TCBB July-Aug. 2020* 1231-1240
- Tian, Z.**, *see* Liu, J., *TCBB Jan.-Feb. 2020* 339-346
- Timmis, J.**, *see* Alden, K., *TCBB Jan.-Feb. 2020* 302-315
- Torres, A.**, *see* Carvajal-Lopez, P., *TCBB Jan.-Feb. 2020* 198-206
- Tran, T.X.**, *see* Shrestha, M., *TCBB Nov.-Dec. 2020* 2074-2085
- Tripathi, S.**, *see* Ranjan, A., *TCBB Sept.-Oct. 2020* 1648-1659

U

- Uyar, M.U.**, *see* Saribudak, A., *TCBB March-April 2020* 608-622

V

- van Iersel, L.**, Janssen, R., Jones, M., Murakami, Y., and Zeh, N., Polynomi-al-Time Algorithms for Phylogenetic Inference Problems Involving Duplication and Reticulation; *TCBB Jan.-Feb. 2020* 14-26
- van Keulen, M.**, *see* Pathak, S., *TCBB Nov.-Dec. 2020* 1883-1894
- van Rossen, J.**, *see* Pathak, S., *TCBB Nov.-Dec. 2020* 1883-1894
- Vavra, O.**, *see* Filipovic, J., *TCBB Sept.-Oct. 2020* 1625-1638
- Vega-Rodriguez, M.A.**, *see* Martin-Vide, C., *TCBB Jan.-Feb. 2020* 1
- Verriente, A.**, *see* Pettit, M., *TCBB Nov.-Dec. 2020* 2155-2161
- Vijlbrief, O.**, *see* Pathak, S., *TCBB Nov.-Dec. 2020* 1883-1894
- Vinals-Yufera, V.**, *see* Herruzo, J.M., *TCBB July-Aug. 2020* 1093-1104
- Vincent, T.**, *see* Al-Matouq, A.A., *TCBB Sept.-Oct. 2020* 1797-1809
- Vogiatzis, C.**, *see* Yasui, N., *TCBB July-Aug. 2020* 1222-1230
- Von Borstel, F.D.**, *see* Carvajal-Lopez, P., *TCBB Jan.-Feb. 2020* 198-206
- Vundavilli, H.**, Datta, A., Sima, C., Hua, J., Lopes, R., and Bittner, M., In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer; *TCBB May-June 2020* 1010-1018

W

- Wachtel, M.S.**, *see* Yang, S., *TCBB March-April 2020* 558-565
- Wan, L.**, *see* Chen, Z., *TCBB March-April 2020* 366-375
- Wang, B.**, *see* Li, F., *TCBB March-April 2020* 390-401
- Wang, B.**, *see* Qingge, L., *TCBB Nov.-Dec. 2020* 1946-1954
- Wang, B.**, *see* Liu, G., *TCBB Nov.-Dec. 2020* 1966-1980
- Wang, C.**, *see* Liu, J., *TCBB Jan.-Feb. 2020* 339-346

- Wang, C.**, *see* Amirkhani, A., *TCBB July-Aug. 2020* 1372-1382
- Wang, F.**, *see* Song, J., *TCBB May-June 2020* 758-768
- Wang, H.**, *see* Zheng, H., *TCBB May-June 2020* 858-867
- Wang, H.**, *see* Zhou, J., *TCBB Jan.-Feb. 2020* 124-135
- Wang, H.**, Xi, J., Wang, M., and Li, A., Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity; *TCBB March-April 2020* 587-598
- Wang, H.**, *see* Zhou, J., *TCBB July-Aug. 2020* 1383-1393
- Wang, J.**, *see* Luo, J., *TCBB May-June 2020* 877-886
- Wang, J.**, *see* Wu, B., *TCBB May-June 2020* 847-857
- Wang, J.**, *see* Liao, X., *TCBB May-June 2020* 728-738
- Wang, J.**, *see* Jiang, H., *TCBB May-June 2020* 1032-1041
- Wang, J.**, *see* Tan, R., *TCBB May-June 2020* 796-803
- Wang, J.**, *see* Ni, P., *TCBB May-June 2020* 906-915
- Wang, J.**, *see* Li, M., *TCBB May-June 2020* 817-827
- Wang, J.**, *see* Li, T., *TCBB Jan.-Feb. 2020* 220-225
- Wang, J.**, *see* Liao, X., *TCBB Jan.-Feb. 2020* 177-188
- Wang, J.**, *see* Yu, G., *TCBB Jan.-Feb. 2020* 238-249
- Wang, J.**, *see* Wang, W., *TCBB July-Aug. 2020* 1430-1439
- Wang, J.**, *see* Li, G., *TCBB July-Aug. 2020* 1451-1458
- Wang, J.**, *see* Yan, C., *TCBB Sept.-Oct. 2020* 1595-1604
- Wang, J.**, *see* McDermott, M.B., *TCBB Nov.-Dec. 2020* 1846-1857
- Wang, K.**, *see* Yu, G., *TCBB Jan.-Feb. 2020* 238-249
- Wang, L.**, *see* Chen, Z., *TCBB May-June 2020* 916-929
- Wang, L.**, You, Z., Huang, D., and Zhou, F., Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions; *TCBB May-June 2020* 972-980
- Wang, L.**, *see* Zhang, G., *TCBB Nov.-Dec. 2020* 2119-2130
- Wang, M.**, *see* Zhang, T., *TCBB Jan.-Feb. 2020* 189-197
- Wang, M.**, *see* Xi, J., *TCBB March-April 2020* 422-434
- Wang, M.**, *see* Wang, H., *TCBB March-April 2020* 587-598
- Wang, M.**, Huang, T., Fang, J., Calhoun, V.D., and Wang, Y., Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization; *TCBB Sept.-Oct. 2020* 1671-1681
- Wang, Q.**, *see* Hu, F., *TCBB July-Aug. 2020* 1187-1197
- Wang, Q.**, *see* Ogunleye, A., *TCBB Nov.-Dec. 2020* 2131-2140
- Wang, R.**, *see* Jia, H., *TCBB Sept.-Oct. 2020* 1493-1503
- Wang, S.**, Cao, Z., Li, M., and Yue, Y., G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides; *TCBB May-June 2020* 739-747
- Wang, S.**, *see* Liu, X., *TCBB July-Aug. 2020* 1329-1340
- Wang, T.**, *see* Tan, R., *TCBB May-June 2020* 796-803
- Wang, W.**, *see* Mazrouee, S., *TCBB Jan.-Feb. 2020* 264-277
- Wang, W.**, Wang, J., Xu, D., and Shang, Y., Two New Heuristic Methods for Protein Model Quality Assessment; *TCBB July-Aug. 2020* 1430-1439
- Wang, X.**, *see* Xuan, P., *TCBB May-June 2020* 1019-1031
- Wang, X.**, *see* Zhang, G., *TCBB May-June 2020* 1068-1081
- Wang, X.**, *see* Chen, Z., *TCBB March-April 2020* 366-375
- Wang, X.**, *see* Sun, Y., *TCBB July-Aug. 2020* 1253-1261
- Wang, X.**, *see* Noriega-Atala, E., *TCBB Nov.-Dec. 2020* 1895-1906
- Wang, X.**, *see* Zhang, G., *TCBB Nov.-Dec. 2020* 2119-2130
- Wang, Y.**, *see* Tan, R., *TCBB May-June 2020* 796-803
- Wang, Y.**, *see* Peng, J., *TCBB May-June 2020* 769-776
- Wang, Y.**, *see* Feng, Z., *TCBB March-April 2020* 411-421
- Wang, Y.**, *see* Wang, M., *TCBB Sept.-Oct. 2020* 1671-1681
- Wang, Y.**, Noor-A-Rahim, M., Zhang, J., Gunawan, E., Guan, Y.L., and Poh, C.L., Oligo Design with Single Primer Binding Site for High Capacity DNA-Based Data Storage; *TCBB Nov.-Dec. 2020* 2176-2182
- Wei, D.**, *see* Peng, S., *TCBB May-June 2020* 804-816
- Wei, H.**, *see* Jia, H., *TCBB Sept.-Oct. 2020* 1493-1503
- Wells, D.M.**, *see* Gibbs, J.A., *TCBB Nov.-Dec. 2020* 1907-1917
- Wilkins, M.R.**, *see* Bayat, A., *TCBB Jan.-Feb. 2020* 334-338
- Willumeit-Romer, R.**, *see* Moreno, L.A., *TCBB July-Aug. 2020* 1440-1450
- Wong, K.**, Yan, S., Lin, Q., Li, X., and Peng, C., Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors; *TCBB Jan.-Feb. 2020* 327-333
- Wong, K.**, *see* Li, X., *TCBB Jan.-Feb. 2020* 226-237
- Wong, K.**, *see* Li, X., *TCBB Sept.-Oct. 2020* 1773-1784
- Wong, P.W.**, *see* Carroll, T.C., *TCBB Nov.-Dec. 2020* 2086-2097
- Wong, Z.**, *see* Noriega-Atala, E., *TCBB Nov.-Dec. 2020* 1895-1906
- Wu, B.**, Li, M., Liao, X., Luo, J., Wu, F., Pan, Y., and Wang, J., MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents; *TCBB May-June 2020* 847-857
- Wu, F.**, *see* Luo, J., *TCBB May-June 2020* 877-886
- Wu, F.**, *see* Wu, B., *TCBB May-June 2020* 847-857
- Wu, F.**, *see* Liao, X., *TCBB May-June 2020* 728-738
- Wu, F.**, *see* Jiang, H., *TCBB May-June 2020* 1032-1041
- Wu, F.**, *see* Ni, P., *TCBB May-June 2020* 906-915
- Wu, F.**, *see* Li, M., *TCBB May-June 2020* 817-827
- Wu, F.**, *see* Li, T., *TCBB Jan.-Feb. 2020* 220-225
- Wu, F.**, *see* Liao, X., *TCBB Jan.-Feb. 2020* 177-188
- Wu, F.**, *see* Lei, X., *TCBB March-April 2020* 495-505
- Wu, F.**, *see* Yan, C., *TCBB Sept.-Oct. 2020* 1595-1604
- Wu, J.**, *see* Yang, S., *TCBB March-April 2020* 558-565
- Wu, M.**, *see* Liu, Y., *TCBB May-June 2020* 748-757
- Wu, S.**, *see* Liu, Y., *TCBB March-April 2020* 435-448
- Wu, S.**, Wu, X., Tian, J., Zhou, X., and Huang, L., PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses; *TCBB Sept.-Oct. 2020* 1714-1720
- Wu, W.**, *see* Yang, X., *TCBB July-Aug. 2020* 1262-1275
- Wu, X.**, *see* Tan, R., *TCBB May-June 2020* 796-803
- Wu, X.**, *see* Wu, S., *TCBB Sept.-Oct. 2020* 1714-1720
- Wurlitzer, M.**, *see* Moreno, L.A., *TCBB July-Aug. 2020* 1440-1450

X

- Xi, J.**, *see* Zhang, T., *TCBB Jan.-Feb. 2020* 189-197
- Xi, J.**, Li, A., and Wang, M., HetRCNA: A Novel Method to Identify Recurrent Copy Number Alterations from Heterogeneous Tumor Samples Based on Matrix Decomposition Framework; *TCBB March-April 2020* 422-434
- Xi, J.**, *see* Wang, H., *TCBB March-April 2020* 587-598
- Xiao, M.**, Yang, X., Yu, J., and Zhang, L., CGIDLA:Developing the Web Server for CpG Island Related Density and LAUPs (Lineage-Associated Underrepresented Permutations) Study; *TCBB Nov.-Dec. 2020* 2148-2154
- Xiao, Q.**, Luo, J., Liang, C., Li, G., Cai, J., Ding, P., and Liu, Y., Identifying lncRNA and mRNA Co-Expression Modules from Matched Expression Data in Ovarian Cancer; *TCBB March-April 2020* 623-634
- Xiao, Y.**, *see* Liu, J., *TCBB Jan.-Feb. 2020* 339-346
- Xiong, Z.**, *see* Yu, X., *TCBB Nov.-Dec. 2020* 2029-2039
- Xu, B.**, *see* He, Z., *TCBB Nov.-Dec. 2020* 2062-2073
- Xu, D.**, *see* Wang, W., *TCBB July-Aug. 2020* 1430-1439
- Xu, H.**, Park, S., and Hwang, T.H., Computerized Classification of Prostate Cancer Gleason Scores from Whole Slide Images; *TCBB Nov.-Dec. 2020* 1871-1882
- Xu, J.**, *see* Zhang, W., *TCBB Nov.-Dec. 2020* 2053-2061
- Xu, R.**, *see* Zhou, J., *TCBB Jan.-Feb. 2020* 124-135
- Xu, R.**, *see* Zhou, J., *TCBB July-Aug. 2020* 1383-1393
- Xu, S.**, *see* Yang, X., *TCBB July-Aug. 2020* 1262-1275
- Xu, X.**, *see* Lin, X., *TCBB Sept.-Oct. 2020* 1525-1534
- Xu, Y.**, *see* Zhao, J., *TCBB May-June 2020* 938-948
- Xu, Y.**, *see* Zhao, J., *TCBB Nov.-Dec. 2020* 2197
- Xuan, P.**, Shen, T., Wang, X., Zhang, T., and Zhang, W., Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes; *TCBB May-June 2020* 1019-1031

Y

- Yan, C.**, Duan, G., Wu, F., Pan, Y., and Wang, J., BRWMDA:Predicting Microbe-Disease Associations Based on Similarities and Bi-Random Walk on Disease and Microbe Networks; *TCBB Sept.-Oct. 2020* 1595-1604
- Yan, D.**, Gao, X., Fodeh, S.J., and Chen, J.Y., Guest Editorial for Selected Papers from BIOKDD 2018 and DMBIH 2018; *TCBB Nov.-Dec. 2020* 1832-1834
- Yan, H.**, *see* Zhao, L., *TCBB Sept.-Oct. 2020* 1682-1690

- Yan, H.,** see Ou-Yang, L., *TCBB Nov.-Dec. 2020* 2162-2169
- Yan, J.,** see Liu, J., *TCBB Jan.-Feb. 2020* 339-346
- Yan, S.,** see Wong, K., *TCBB Jan.-Feb. 2020* 327-333
- Yang, C.,** see Peng, S., *TCBB May-June 2020* 804-816
- Yang, C.,** Lin, Y., and Chuang, L., Class Balanced Multifactor Dimensionality Reduction to Detect Gene–Gene Interactions; *TCBB Jan.-Feb. 2020* 71-81
- Yang, H.,** see Jia, H., *TCBB Sept.-Oct. 2020* 1493-1503
- Yang, L.,** see Yang, X., *TCBB July-Aug. 2020* 1262-1275
- Yang, L.,** see Yuan, X., *TCBB July-Aug. 2020* 1141-1153
- Yang, M.,** see Liu, J., *TCBB Sept.-Oct. 2020* 1504-1515
- Yang, Q.,** see Qingge, L., *TCBB Nov.-Dec. 2020* 1946-1954
- Yang, S.,** Wachtel, M.S., and Wu, J., DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data; *TCBB March-April 2020* 558-565
- Yang, X.,** see Cai, J., *TCBB Jan.-Feb. 2020* 165-176
- Yang, X.,** see Lei, X., *TCBB March-April 2020* 495-505
- Yang, X.,** Tian, L., Chen, Y., Yang, L., Xu, S., and Wu, W., Inverse Projection Representation and Category Contribution Rate for Robust Tumor Recognition; *TCBB July-Aug. 2020* 1262-1275
- Yang, X.,** see Xiao, M., *TCBB Nov.-Dec. 2020* 2148-2154
- Yang, Z.,** see Liu, X., *TCBB July-Aug. 2020* 1329-1340
- Yang, Z.,** see Hu, F., *TCBB July-Aug. 2020* 1187-1197
- Yao, H.,** Shi, Y., Guan, J., and Zhou, S., Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions; *TCBB May-June 2020* 777-787
- Yap, H.J.,** see Tan, J.W., *TCBB Jan.-Feb. 2020* 82-90
- Yasui, N.,** Vogiatzis, C., Yoshida, R., and Fukumizu, K., imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming; *TCBB July-Aug. 2020* 1222-1230
- Yazdani, A.,** see Yazdani, H., *TCBB March-April 2020* 526-535
- Yazdani, H.,** Cheng, L.L., Christiani, D.C., and Yazdani, A., Bounded Fuzzy Possibilistic Method Reveals Information about Lung Cancer through Analysis of Metabolomics; *TCBB March-April 2020* 526-535
- Yeganeh, P.N.,** and Mostafavi, M.T., Causal Disturbance Analysis: A Novel Graph Centrality Based Method for Pathway Enrichment Analysis; *TCBB Sept.-Oct. 2020* 1613-1624
- Yi, H.,** see Li, J., *TCBB Sept.-Oct. 2020* 1546-1554
- Yim, M.Y.,** see Jiang, H., *TCBB March-April 2020* 402-410
- Yong, K.,** see Tan, J.W., *TCBB Jan.-Feb. 2020* 82-90
- Yoshida, R.,** see Kang, Q., *TCBB May-June 2020* 981-989
- Yoshida, R.,** see Yasui, N., *TCBB July-Aug. 2020* 1222-1230
- You, Z.,** see Wang, L., *TCBB May-June 2020* 972-980
- You, Z.,** see Hu, P., *TCBB Sept.-Oct. 2020* 1516-1524
- You, Z.,** see Li, J., *TCBB Sept.-Oct. 2020* 1546-1554
- You, Z.,** see Hu, L., *TCBB Nov.-Dec. 2020* 2017-2028
- Youmans, M.,** Spainhour, J.C.G., and Qiu, P., Classification of Antibacterial Peptides Using Long Short-Term Memory Recurrent Neural Networks; *TCBB July-Aug. 2020* 1134-1140
- Yu, D.,** see Hu, J., *TCBB July-Aug. 2020* 1419-1429
- Yu, G.,** Wang, K., Fu, G., Guo, M., and Wang, J., NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology; *TCBB Jan.-Feb. 2020* 238-249
- Yu, H.,** see Liu, J., *TCBB Jan.-Feb. 2020* 339-346
- Yu, J.,** see He, Z., *TCBB May-June 2020* 930-937
- Yu, J.,** see Xiao, M., *TCBB Nov.-Dec. 2020* 2148-2154
- Yu, X.,** see Zhang, J., *TCBB May-June 2020* 949-958
- Yu, X.,** see Zhang, J., *TCBB May-June 2020* 949-958
- Yu, X.,** Rong, W., Liu, J., Zhou, D., Ouyang, Y., and Xiong, Z., LSTM-Based End-to-End Framework for Biomedical Event Extraction; *TCBB Nov.-Dec. 2020* 2029-2039
- Yuan, R.,** Ou-Yang, L., Hu, X., and Zhang, X., Identifying Gene Network Rewiring Using Robust Differential Graphical Model with Multivariate-Distribution; *TCBB March-April 2020* 712-718
- Yuan, X.,** Gao, M., Bai, J., and Duan, J., SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms; *TCBB May-June 2020* 1082-1091
- Yuan, X.,** Bai, J., Zhang, J., Yang, L., Duan, J., Li, Y., and Gao, M., CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data; *TCBB July-Aug. 2020* 1141-1153
- Yuan, X.,** see Hu, L., *TCBB Nov.-Dec. 2020* 2017-2028
- Yue, Y.,** see Wang, S., *TCBB May-June 2020* 739-747

Z

- Zare, F.,** Ansari, S., Najarian, K., and Nabavi, S., Preprocessing Sequence Coverage Data for More Precise Detection of Copy Number Variations; *TCBB May-June 2020* 868-876
- Zeb, A.,** see Rampogu, S., *TCBB Jan.-Feb. 2020* 365
- Zeh, N.,** see van Iersel, L., *TCBB Jan.-Feb. 2020* 14-26
- Zehavi, M.,** see Ganor, D., *TCBB Jan.-Feb. 2020* 316-320
- Zeng, T.,** see Zhang, J., *TCBB May-June 2020* 949-958
- Zeng, X.,** Lin, Y., He, Y., Lu, L., Min, X., and Rodriguez-Paton, A., Deep Collaborative Filtering for Prediction of Disease Genes; *TCBB Sept.-Oct. 2020* 1639-1647
- Zhan, Q.,** see Tan, R., *TCBB May-June 2020* 796-803
- Zhang, B.,** see Liu, G., *TCBB Nov.-Dec. 2020* 1966-1980
- Zhang, C.,** see Zhao, J., *TCBB May-June 2020* 938-948
- Zhang, C.,** see Zhao, J., *TCBB Nov.-Dec. 2020* 2197
- Zhang, D.,** see Shao, W., *TCBB July-Aug. 2020* 1394-1405
- Zhang, G.,** Ma, L., Wang, X., and Zhou, X., Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction; *TCBB May-June 2020* 1068-1081
- Zhang, G.,** see Hu, J., *TCBB July-Aug. 2020* 1419-1429
- Zhang, G.,** Wang, X., Ma, L., Wang, L., Hu, J., and Zhou, X., Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction; *TCBB Nov.-Dec. 2020* 2119-2130
- Zhang, H.,** see Liu, X., *TCBB July-Aug. 2020* 1329-1340
- Zhang, H.,** see Liu, X., *TCBB July-Aug. 2020* 1329-1340
- Zhang, J.,** Guo, J., Zhang, M., Yu, X., Yu, X., Guo, W., Zeng, T., and Chen, L., Efficient Mining Multi-Mers in a Variety of Biological Sequences; *TCBB May-June 2020* 949-958
- Zhang, J.,** see Pan, C., *TCBB Jan.-Feb. 2020* 321-326
- Zhang, J.,** see Yuan, X., *TCBB July-Aug. 2020* 1141-1153
- Zhang, J.,** see Wang, Y., *TCBB Nov.-Dec. 2020* 2176-2182
- Zhang, L.,** see Feng, Y., *TCBB Jan.-Feb. 2020* 91-101
- Zhang, L.,** and Zhang, S., Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data; *TCBB March-April 2020* 376-389
- Zhang, L.,** see Liu, J., *TCBB Sept.-Oct. 2020* 1504-1515
- Zhang, L.,** see Liu, J., *TCBB Nov.-Dec. 2020* 1994-2004
- Zhang, L.,** see Xiao, M., *TCBB Nov.-Dec. 2020* 2148-2154
- Zhang, M.,** see Zhang, J., *TCBB May-June 2020* 949-958
- Zhang, Q.,** Zhu, L., Bao, W., and Huang, D., Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding; *TCBB March-April 2020* 679-689
- Zhang, R.,** Hu, M., Zhu, Y., Qin, Z., Deng, K., and Liu, J.S., Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model; *TCBB March-April 2020* 647-656
- Zhang, S.,** see Li, X., *TCBB Jan.-Feb. 2020* 226-237
- Zhang, S.,** see Cao, Z., *TCBB March-April 2020* 657-667
- Zhang, S.,** see Zhang, L., *TCBB March-April 2020* 376-389
- Zhang, T.,** see Xuan, P., *TCBB May-June 2020* 1019-1031
- Zhang, T.,** see Tan, R., *TCBB May-June 2020* 796-803
- Zhang, T.,** Wang, M., Xi, J., and Li, A., LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization; *TCBB Jan.-Feb. 2020* 189-197
- Zhang, W.,** see Xuan, P., *TCBB May-June 2020* 1019-1031
- Zhang, W.,** Xu, J., and Zou, X., Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data; *TCBB Nov.-Dec. 2020* 2053-2061
- Zhang, X.,** see Peng, S., *TCBB May-June 2020* 804-816
- Zhang, X.,** see Li, T., *TCBB Jan.-Feb. 2020* 220-225
- Zhang, X.,** see Liu, J., *TCBB Jan.-Feb. 2020* 339-346

- Zhang, X.,** see Yuan, R., *TCBB March-April 2020* 712-718
Zhang, X., see Deng, Z., *TCBB July-Aug. 2020* 1231-1240
Zhang, X., see Lin, X., *TCBB Sept.-Oct. 2020* 1525-1534
Zhang, X., see Ou-Yang, L., *TCBB Nov.-Dec. 2020* 2162-2169
Zhang, Y., see Zhao, G., *TCBB July-Aug. 2020* 1211-1221
Zhang, Y., Liu, H., Li, Z., Miao, Z., and Zhou, J., Oscillatory Dynamics of p53-Mdm2 Circuit in Response to DNA Damage Caused by Ionizing Radiation; *TCBB Sept.-Oct. 2020* 1703-1713
Zhao, C., see He, Z., *TCBB Nov.-Dec. 2020* 2062-2073
Zhao, G., Guo, L., Zhang, Y., Gao, L., and Ma, L., Identifying TF Binding Motifs from a Partial Set of Target Genes and its Application to Regulatory Network Inference; *TCBB July-Aug. 2020* 1211-1221
Zhao, J., Feng, H., Zhu, D., Zhang, C., and Xu, Y., IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads; *TCBB May-June 2020* 938-948
Zhao, J., see Shi, J., *TCBB March-April 2020* 449-458
Zhao, J., Feng, H., Zhu, D., Zhang, C., and Xu, Y., Corrections to “IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads” *TCBB Nov.-Dec. 2020* 2197
Zhao, L., and Yan, H., MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data; *TCBB Sept.-Oct. 2020* 1682-1690
Zhao, W., see McDermott, M.B., *TCBB Nov.-Dec. 2020* 1846-1857
Zheng, C., see Sun, Y., *TCBB July-Aug. 2020* 1253-1261
Zheng, H., Wang, H., Dewhurst, R.J., and Roehe, R., Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome; *TCBB May-June 2020* 858-867
Zheng, J., see Liu, Y., *TCBB May-June 2020* 748-757
Zheng, J., Li, J., and Zheng, Y., Guest Editorial for the 29th International Conference on Genome Informatics (GIW 2018); *TCBB May-June 2020* 726-727
Zheng, J., see Chen, H., *TCBB March-April 2020* 516-525
Zheng, J., Hsieh, F., and Ge, L., A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data; *TCBB Nov.-Dec. 2020* 1858-1870
Zheng, R., see Li, M., *TCBB May-June 2020* 817-827
Zheng, Y., see Zheng, J., *TCBB May-June 2020* 726-727
Zheng, Y., see Peng, C., *TCBB Sept.-Oct. 2020* 1605-1612
Zhong, P., see Ni, P., *TCBB May-June 2020* 906-915
Zhou, D., see Yu, X., *TCBB Nov.-Dec. 2020* 2029-2039
Zhou, F., see Wang, L., *TCBB May-June 2020* 972-980
Zhou, J., Lu, Q., Xu, R., Gui, L., and Wang, H., EL_LSTM: Prediction of DNA-Binding Residue from Protein Sequence by Combining Long Short-Term Memory and Ensemble Learning; *TCBB Jan.-Feb. 2020* 124-135
Zhou, J., Lu, Q., Xu, R., Gui, L., and Wang, H., Prediction of TF-Binding Site by Inclusion of Higher Order Position Dependencies; *TCBB July-Aug. 2020* 1383-1393
Zhou, J., see Zhang, Y., *TCBB Sept.-Oct. 2020* 1703-1713
Zhou, S., see Yao, H., *TCBB May-June 2020* 777-787
Zhou, S., see Ismailoglu, F., *TCBB Jan.-Feb. 2020* 347-353
Zhou, X., see Zhang, G., *TCBB May-June 2020* 1068-1081
Zhou, X., see Hu, J., *TCBB July-Aug. 2020* 1419-1429
Zhou, X., see Wu, S., *TCBB Sept.-Oct. 2020* 1714-1720
Zhou, X., see Zhang, G., *TCBB Nov.-Dec. 2020* 2119-2130
Zhou, Y., see Hu, F., *TCBB July-Aug. 2020* 1187-1197
Zhu, B., see Qingge, L., *TCBB Nov.-Dec. 2020* 1946-1954
Zhu, D., see Zhao, J., *TCBB May-June 2020* 938-948
Zhu, D., see Jia, H., *TCBB Sept.-Oct. 2020* 1493-1503
Zhu, D., see Zhao, J., *TCBB Nov.-Dec. 2020* 2197
Zhu, L., see Peng, J., *TCBB May-June 2020* 769-776
Zhu, L., see Zhang, Q., *TCBB March-April 2020* 679-689
Zhu, W., see Peng, S., *TCBB May-June 2020* 804-816
Zhu, W., see Dong, Y., *TCBB Nov.-Dec. 2020* 2170-2175
Zhu, Y., see Zhang, R., *TCBB March-April 2020* 647-656
Zhu, Y., see Hu, J., *TCBB July-Aug. 2020* 1419-1429
Zou, Q., see He, Z., *TCBB Nov.-Dec. 2020* 2062-2073
Zou, X., see Guo, Q., *TCBB Sept.-Oct. 2020* 1563-1572
Zou, X., see Zhang, W., *TCBB Nov.-Dec. 2020* 2053-2061

- Zou, Y.,** see Liao, X., *TCBB May-June 2020* 728-738
Zou, Y., see Liao, X., *TCBB Jan.-Feb. 2020* 177-188
Zucker, J., see Sokolovska, N., *TCBB Jan.-Feb. 2020* 358-364

SUBJECT INDEX

A

- Ab initio calculations**
Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. *Zhang, G., +, TCBB May-June 2020* 1068-1081
- Adaptive estimation**
Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020* 1105-1114
- Adaptive filters**
GaMRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020* 149-157
- Amino acids**
Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment. *Jing, X., +, TCBB Nov.-Dec. 2020* 1918-1931
Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. *Hu, L., +, TCBB Nov.-Dec. 2020* 2017-2028
- Analytical models**
FPGA Accelerated Analysis of Boolean Gene Regulatory Networks. *Manica, M., +, TCBB Nov.-Dec. 2020* 2141-2147
- Approximation algorithms**
Approaching the One-Sided Exemplar Adjacency Number Problem. *Qingge, L., +, TCBB Nov.-Dec. 2020* 1946-1954
Approximate Graph Edit Distance in Quadratic Time. *Riesen, K., +, TCBB March-April 2020* 483-494
MPGM: Scalable and Accurate Multiple Network Alignment. *Kazemi, E., +, TCBB Nov.-Dec. 2020* 2040-2052
- Approximation methods**
Approximate Graph Edit Distance in Quadratic Time. *Riesen, K., +, TCBB March-April 2020* 483-494
- Approximation theory**
Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions. *Pichene, M., +, TCBB Sept.-Oct. 2020* 1691-1702
NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. *Yu, G., +, TCBB Jan.-Feb. 2020* 238-249
- Artificial bee colony algorithm**
Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020* 226-237
- Artificial intelligence**
XGBoost Model for Chronic Kidney Disease Diagnosis. *Ogunleye, A., +, TCBB Nov.-Dec. 2020* 2131-2140
- Assembling**
Fast Short Read De-Novo Assembly Using Overlap-Layout-Consensus Approach. *Bayat, A., +, TCBB Jan.-Feb. 2020* 334-338
- Autoregressive processes**
Data-Driven Robust Control for a Closed-Loop Artificial Pancreas. *Paoletti, N., +, TCBB Nov.-Dec. 2020* 1981-1993
- B**
- Bayes methods**
An Application of the Bayesian Periodicity Test to Identify Diurnal Rhythm Genes in the Brain. *Kocak, M., +, TCBB Jan.-Feb. 2020* 47-55
Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network. *Chen, H., +, TCBB March-April 2020* 516-525
Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data. *Zhang, L., +, TCBB March-April 2020* 376-389
CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020* 1141-1153

- Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020* 339-346
- Incorporating Prior Knowledge about Genetic Variants into the Analysis of Genetic Association Data: An Empirical Bayes Approach. *Karimnezhad, A., +, TCBB March-April 2020* 635-646
- Optimal Bayesian Filtering for Biomarker Discovery: Performance and Robustness. *Foroughi pour, A., +, TCBB Jan.-Feb. 2020* 250-263
- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020* 264-277
- Rapid Reconstruction of Time-Varying Gene Regulatory Networks. *Pyne, S., +, TCBB Jan.-Feb. 2020* 278-291
- Using Emulation to Engineer and Understand Simulations of Biological Systems. *Alden, K., +, TCBB Jan.-Feb. 2020* 302-315
- Belief networks**
- Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020* 56-70
- Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020* 339-346
- Benchmark testing**
- Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks. *Liu, G., +, TCBB Nov.-Dec. 2020* 1966-1980
- Deep Learning Benchmarks on L1000 Gene Expression Data. *McDermott, M.B., +, TCBB Nov.-Dec. 2020* 1846-1857
- Detection of Driver Modules with Rarely Mutated Genes in Cancers. *Li, F., +, TCBB March-April 2020* 390-401
- Big Data**
- Novel Regularization Method for Biomarker Selection and Cancer Classification. *Liu, X., +, TCBB July-Aug. 2020* 1329-1340
- Biochemistry**
- A Novel Edge Effect Detection Method for Real-Time Cellular Analyzer Using Functional Principal Component Analysis. *Guo, Q., +, TCBB Sept.-Oct. 2020* 1563-1572
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020* 1187-1197
- High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020* 804-816
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020* 1276-1289
- nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale. *Fassio, A.V., +, TCBB July-Aug. 2020* 1317-1328
- Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020* 1364-1371
- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020* 1751-1761
- Sparse Reconstruction of Glucose Fluxes Using Continuous Glucose Monitors. *Al-Matouq, A.A., +, TCBB Sept.-Oct. 2020* 1797-1809
- Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020* 1440-1450
- Biodegradable materials**
- Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020* 1440-1450
- Bioinformatics**
- A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity. *Kapoor, R., +, TCBB March-April 2020* 459-468
- A Note on GRegNetSim: A Tool for the Discrete Simulation and Analysis of Genetic Regulatory Networks. *Ganor, D., +, TCBB Jan.-Feb. 2020* 316-320
- Algorithms for Computational Biology: Fifth Edition. *Martin-Vide, C., +, TCBB Jan.-Feb. 2020* 1
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- Approaching the One-Sided Exemplar Adjacency Number Problem. *Qingge, L., +, TCBB Nov.-Dec. 2020* 1946-1954
- Approximate Graph Edit Distance in Quadratic Time. *Riesen, K., +, TCBB March-April 2020* 483-494
- BiClusO: A Novel Bioclustering Approach and Its Application to Species-VOC Relational Data. *Karim, M.B., +, TCBB Nov.-Dec. 2020* 1955-1965
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- BRWMDA: Predicting Microbe-Disease Associations Based on Similarities and Bi-Random Walk on Disease and Microbe Networks. *Yan, C., +, TCBB Sept.-Oct. 2020* 1595-1604
- Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020* 1605-1612
- CGIDLA: Developing the Web Server for CpG Island Related Density and LAUPs (Lineage-Associated Underrepresented Permutations) Study. *Xiao, M., +, TCBB Nov.-Dec. 2020* 2148-2154
- Class Balanced Multifactor Dimensionality Reduction to Detect Gene–Gene Interactions. *Yang, C., +, TCBB Jan.-Feb. 2020* 71-81
- Clustering and Integrating of Heterogeneous Microbiome Data by Joint Symmetric Nonnegative Matrix Factorization with Laplacian Regularization. *Ma, Y., +, TCBB May-June 2020* 788-795
- Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data. *Zhang, L., +, TCBB March-April 2020* 376-389
- CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020* 1141-1153
- Connectivity Significance for Disease Gene Prioritization in an Expanding Universe. *Petti, M., +, TCBB Nov.-Dec. 2020* 2155-2161
- Constructing Disease Similarity Networks Based on Disease Module Theory. *Ni, P., +, TCBB May-June 2020* 906-915
- CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. *Kang, Q., +, TCBB May-June 2020* 981-989
- Deep Neural Networks for *In Situ* Hybridization Grid Completion and Clustering. *Li, Y., +, TCBB March-April 2020* 536-546
- Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020* 1648-1659
- Detection of Driver Modules with Rarely Mutated Genes in Cancers. *Li, F., +, TCBB March-April 2020* 390-401
- DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data. *Yang, S., +, TCBB March-April 2020* 558-565
- Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools. *Chowdhury, H.A., +, TCBB March-April 2020* 566-586
- Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. *Wang, H., +, TCBB March-April 2020* 587-598
- Efficient Mining Multi-Mers in a Variety of Biological Sequences. *Zhang, J., +, TCBB May-June 2020* 949-958
- Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections. *Som-In, S., +, TCBB May-June 2020* 990-998
- ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data. *Tan, R., +, TCBB May-June 2020* 796-803
- Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts. *Noriega-Atala, E., +, TCBB Nov.-Dec. 2020* 1895-1906
- Fast de Bruijn Graph Compaction in Distributed Memory Environments. *Pan, T., +, TCBB Jan.-Feb. 2020* 136-148
- GaMRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020* 149-157
- GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets. *Luo, J., +, TCBB May-June 2020* 877-886
- Guest Editorial for Selected Papers from BIOKDD 2018 and DMBIH 2018. *Yan, D., +, TCBB Nov.-Dec. 2020* 1832-1834

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- Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications. *Gudur, V.Y., +, TCBB July-Aug. 2020 1198-1210*
- HetRCNA: A Novel Method to Identify Recurrent Copy Number Alterations from Heterogeneous Tumor Samples Based on Matrix Decomposition Framework. *Xi, J., +, TCBB March-April 2020 422-434*
- Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. *Li, M., +, TCBB May-June 2020 817-827*
- Identification of Short Exons Disunited by a Short Intron in Eukaryotic DNA Regions. *Sharma, S., +, TCBB Sept.-Oct. 2020 1660-1670*
- Identifying “Many-to-Many” Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020 165-176*
- Identifying lncRNA and mRNA Co-Expression Modules from Matched Expression Data in Ovarian Cancer. *Xiao, Q., +, TCBB March-April 2020 623-634*
- Identifying TF Binding Motifs from a Partial Set of Target Genes and its Application to Regulatory Network Inference. *Zhao, G., +, TCBB July-Aug. 2020 1211-1221*
- imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020 1222-1230*
- Improving *de novo* Assembly Based on Read Classification. *Liao, X., +, TCBB Jan.-Feb. 2020 177-188*
- Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. *Xuan, P., +, TCBB May-June 2020 1019-1031*
- Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *Zhang, R., +, TCBB March-April 2020 647-656*
- Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020 1253-1261*
- Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA-miRNA Interactions. *Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524*
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*
- LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*
- MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data. *Zhao, L., +, TCBB Sept.-Oct. 2020 1682-1690*
- MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. *Wu, B., +, TCBB May-June 2020 847-857*
- miRTS: A Recommendation Algorithm for Predicting miRNA Targets. *Jiang, H., +, TCBB May-June 2020 1032-1041*
- Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. *Acharya, S., +, TCBB Jan.-Feb. 2020 207-219*
- nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale. *Fassio, A.V., +, TCBB July-Aug. 2020 1317-1328*
- NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. *Yu, G., +, TCBB Jan.-Feb. 2020 238-249*
- Novel Regularization Method for Biomarker Selection and Cancer Classification. *Liu, X., +, TCBB July-Aug. 2020 1329-1340*
- NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*
- PASA: Identifying More Credible Structural Variants of Hedou12. *Jia, H., +, TCBB Sept.-Oct. 2020 1493-1503*
- Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*
- Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. *Fu, L., +, TCBB Sept.-Oct. 2020 1721-1728*
- Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*
- Prediction of TF-Binding Site by Inclusion of Higher Order Position Dependencies. *Zhou, J., +, TCBB July-Aug. 2020 1383-1393*
- Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. *Cao, Z., +, TCBB March-April 2020 657-667*
- Protein Complexes Identification with Family-Wise Error Rate Control. *He, Z., +, TCBB Nov.-Dec. 2020 2062-2073*
- Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. *Zhang, G., +, TCBB May-June 2020 1068-1081*
- Semiglobal Sequence Alignment with Gaps Using GPU. *Carroll, T.C., +, TCBB Nov.-Dec. 2020 2086-2097*
- Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation. *Kawano, K., +, TCBB Sept.-Oct. 2020 1762-1772*
- SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*
- Stability Analysis of Biological Networks’ Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*
- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
- The Use of Informed Priors in Bioclustering of Gene Expression with the Hierarchical Dirichlet Process. *Tercan, B., +, TCBB Sept.-Oct. 2020 1810-1821*
- Two New Heuristic Methods for Protein Model Quality Assessment. *Wang, W., +, TCBB July-Aug. 2020 1430-1439*
- United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*
- Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information. *Li, J., +, TCBB Sept.-Oct. 2020 1546-1554*
- Utilizing Deep Learning and Genome Wide Association Studies for Epistatic-Driven Preterm Birth Classification in African-American Women. *Fergus, P., +, TCBB March-April 2020 668-678*
- Biological cells**
- Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *Zhang, R., +, TCBB March-April 2020 647-656*
- Biological effects of ionizing radiation**
- Oscillatory Dynamics of p53-Mdm2 Circuit in Response to DNA Damage Caused by Ionizing Radiation. *Zhang, Y., +, TCBB Sept.-Oct. 2020 1703-1713*
- Biological information theory**
- Enabling Massive XML-Based Biological Data Management in HBase. *Liu, J., +, TCBB Nov.-Dec. 2020 1994-2004*
- Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts. *Noriega-Atala, E., +, TCBB Nov.-Dec. 2020 1895-1906*
- Biological neural networks**
- Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks. *Li, L., +, TCBB March-April 2020 599-607*
- Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture. *Chakraborty, R., +, TCBB Nov.-Dec. 2020 2183-2188*
- Biological organs**
- Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020 1605-1612*
- In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020 1010-1018*
- NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*

Biological system modeling

A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations. *Lecca, P., +, TCBB March-April 2020 469-482*

An Efficient Approach Towards the Source-Target Control of Boolean Networks. *Paul, S., +, TCBB Nov.-Dec. 2020 1932-1945*

Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network. *Chen, H., +, TCBB March-April 2020 516-525*

Correction to “A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations”. *Lecca, P., +, TCBB May-June 2020 1092*

Deep Learning Benchmarks on L1000 Gene Expression Data. *McDermott, M.B., +, TCBB Nov.-Dec. 2020 1846-1857*

Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. *Ou-Yang, L., +, TCBB Nov.-Dec. 2020 2162-2169*

Enabling Massive XML-Based Biological Data Management in HBase. *Liu, J., +, TCBB Nov.-Dec. 2020 1994-2004*

EPMDA: Edge Perturbation Based Method for miRNA-Disease Association Prediction. *Dong, Y., +, TCBB Nov.-Dec. 2020 2170-2175*

Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks. *Li, L., +, TCBB March-April 2020 599-607*

FPGA Accelerated Analysis of Boolean Gene Regulatory Networks. *Manica, M., +, TCBB Nov.-Dec. 2020 2141-2147*

Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *Zhang, R., +, TCBB March-April 2020 647-656*

LSTM-Based End-to-End Framework for Biomedical Event Extraction. *Yu, X., +, TCBB Nov.-Dec. 2020 2029-2039*

MPGM: Scalable and Accurate Multiple Network Alignment. *Kazemi, E., +, TCBB Nov.-Dec. 2020 2040-2052*

Biological systems

An Efficient Approach Towards the Source-Target Control of Boolean Networks. *Paul, S., +, TCBB Nov.-Dec. 2020 1932-1945*

Structural Bistability Analysis of Flower-Shaped and Chain-Shaped Boolean Networks. *Azuma, S., +, TCBB Nov.-Dec. 2020 2098-2106*

Biological techniques

Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature. *Shen, Z., +, TCBB Sept.-Oct. 2020 1483-1492*

CaverDock: A Novel Method for the Fast Analysis of Ligand Transport. *Filipovic, J., +, TCBB Sept.-Oct. 2020 1625-1638*

Constructive Prediction of Potential RNA Aptamers for a Protein Target. *Lee, W., +, TCBB Sept.-Oct. 2020 1476-1482*

CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. *Kang, Q., +, TCBB May-June 2020 981-989*

Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. *Bakhteh, S., +, TCBB May-June 2020 999-1009*

MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. *Li, T., +, TCBB Jan.-Feb. 2020 220-225*

Biological tissues

Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*

Biology

Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. *Shi, J., +, TCBB March-April 2020 449-458*

Biology computing

(Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. *Chowdhury, H.A., +, TCBB July-Aug. 2020 1154-1173*

A Network-Based Comparison Between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso. *Shahdoust, M., +, TCBB Sept.-Oct. 2020 1555-1562*

A Supervised Ensemble Approach for Sensitive microRNA Target Prediction. *Maji, R.K., +, TCBB Jan.-Feb. 2020 37-46*

Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020 1093-1104*

Accurately Detecting Protein Complexes by Graph Embedding and Combinig Functions with Interactions. *Yao, H., +, TCBB May-June 2020 777-787*

An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. *Liao, X., +, TCBB May-June 2020 728-738*

Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020 56-70*

Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020 959-971*

Basins of Attraction, Commitment Sets, and Phenotypes of Boolean Networks. *Klarner, H., +, TCBB July-Aug. 2020 1115-1124*

Bi-Level Error Correction for PacBio Long Reads. *Liu, Y., +, TCBB May-June 2020 899-905*

Cache Friendly Optimisation of de Bruijn Graph Based Local Re-Assembly in Variant Calling. *Gamaarachchi, H., +, TCBB July-Aug. 2020 1125-1133*

Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature. *Shen, Z., +, TCBB Sept.-Oct. 2020 1483-1492*

Causal Disturbance Analysis: A Novel Graph Centrality Based Method for Pathway Enrichment Analysis. *Yeganeh, P.N., +, TCBB Sept.-Oct. 2020 1613-1624*

CaverDock: A Novel Method for the Fast Analysis of Ligand Transport. *Filipovic, J., +, TCBB Sept.-Oct. 2020 1625-1638*

Classification of Antibacterial Peptides Using Long Short-Term Memory Recurrent Neural Networks. *Youmans, M., +, TCBB July-Aug. 2020 1134-1140*

Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*

CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygoty from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020 1141-1153*

Constructive Prediction of Potential RNA Aptamers for a Protein Target. *Lee, W., +, TCBB Sept.-Oct. 2020 1476-1482*

Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*

Disruption of Protein Complexes from Weighted Complex Networks. *Hasibi, M., +, TCBB Jan.-Feb. 2020 102-109*

Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting. *Lin, X., +, TCBB Sept.-Oct. 2020 1525-1534*

EL_LSTM: Prediction of DNA-Binding Residue from Protein Sequence by Combining Long Short-Term Memory and Ensemble Learning. *Zhou, J., +, TCBB Jan.-Feb. 2020 124-135*

Fast Short Read De-Novo Assembly Using Overlap-Layout-Consensus Approach. *Bayat, A., +, TCBB Jan.-Feb. 2020 334-338*

Faster Exact Computation of rSPR Distance via Better Approximation. *Chen, Z., +, TCBB May-June 2020 916-929*

G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides. *Wang, S., +, TCBB May-June 2020 739-747*

GaPRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020 149-157*

Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*

Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*

Generation of Level-k LGT Networks. *Pons, J.C., +, TCBB Jan.-Feb. 2020 158-164*

Heuristics for the Reversal and Transposition Distance Problem. *Brito, K.L., +, TCBB Jan.-Feb. 2020 2-13*

High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*

Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. *Bakhteh, S., +, TCBB May-June 2020 999-1009*

Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020 858-867*

- Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020* 930-937
- Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020* 1253-1261
- Inverse Projection Representation and Category Contribution Rate for Robust Tumor Recognition. *Yang, X., +, TCBB July-Aug. 2020* 1262-1275
- IsoTree: A New Framework for *de novo* Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020* 938-948
- Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB. *Liu, J., +, TCBB Sept.-Oct. 2020* 1504-1515
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020* 1276-1289
- Microarray-Based Quality Assessment as a Supporting Criterion for *de novo* Transcriptome Assembly Selection. *Carvajal-Lopez, P., +, TCBB Jan.-Feb. 2020* 198-206
- Mining Relationships among Multiple Entities in Biological Networks. *Peng, J., +, TCBB May-June 2020* 769-776
- Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions. *Pichene, M., +, TCBB Sept.-Oct. 2020* 1691-1702
- Modified Half-System Based Method for Reverse Engineering of Gene Regulatory Networks. *Khan, A., +, TCBB July-Aug. 2020* 1303-1316
- MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. *Li, T., +, TCBB Jan.-Feb. 2020* 220-225
- nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale. *Fassio, A.V., +, TCBB July-Aug. 2020* 1317-1328
- Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020* 226-237
- Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020* 1042-1055
- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020* 264-277
- Polynomial-Time Algorithms for Phylogenetic Inference Problems Involving Duplication and Reticulation. *van Iersel, L., +, TCBB Jan.-Feb. 2020* 14-26
- Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020* 1372-1382
- Preprocessing Sequence Coverage Data for More Precise Detection of Copy Number Variations. *Zare, F., +, TCBB May-June 2020* 868-876
- RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020* 1741-1750
- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020* 1773-1784
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020* 748-757
- SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020* 1785-1796
- Softeigen: Primers Design Web-Based Tool for MS-HRM Technique. *Pinzon-Reyes, E., +, TCBB Jan.-Feb. 2020* 354-357
- Stability Analysis of Biological Networks' Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020* 1406-1418
- SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. *Yuan, X., +, TCBB May-June 2020* 1082-1091
- Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020* 1440-1450
- Using Emulation to Engineer and Understand Simulations of Biological Systems. *Alden, K., +, TCBB Jan.-Feb. 2020* 302-315
- Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020* 1459-1473
- Biomarkers**
- Gene Expressions, Hippocampal Volume Loss, and MMSE Scores in Computation of Progression and Pharmacologic Therapy Effects for Alzheimer's Disease. *Saribudak, A., +, TCBB March-April 2020* 608-622

Biomedical imaging

A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020* 1858-1870

Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks. *Liu, G., +, TCBB Nov.-Dec. 2020* 1966-1980

Biomedical materials

Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020* 1187-1197

Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020* 1364-1371

Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020* 1440-1450

Biomedical MRI

Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020* 1671-1681

Biomolecular effects of radiation

Oscillatory Dynamics of p53-Mdm2 Circuit in Response to DNA Damage Caused by Ionizing Radiation. *Zhang, Y., +, TCBB Sept.-Oct. 2020* 1703-1713

Bipartite graph

BiClusO: A Novel Biclustering Approach and Its Application to Species-VOC Relational Data. *Karim, M.B., +, TCBB Nov.-Dec. 2020* 1955-1965

Blood

Sparse Reconstruction of Glucose Fluxes Using Continuous Glucose Monitors. *Al-Matoug, A.A., +, TCBB Sept.-Oct. 2020* 1797-1809

Blood vessels

Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020* 1394-1405

Boltzmann machines

Using Unlabeled Data to Discover Bivariate Causality with Deep Restricted Boltzmann Machines. *Sokolovska, N., +, TCBB Jan.-Feb. 2020* 358-364

Bone

Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020* 1440-1450

Boolean algebra

Faster Exact Computation of rSPR Distance via Better Approximation. *Chen, Z., +, TCBB May-June 2020* 916-929

Boolean functions

Basins of Attraction, Commitment Sets, and Phenotypes of Boolean Networks. *Klarner, H., +, TCBB July-Aug. 2020* 1115-1124

In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020* 1010-1018

Structural Bistability Analysis of Flower-Shaped and Chain-Shaped Boolean Networks. *Azuma, S., +, TCBB Nov.-Dec. 2020* 2098-2106

Botany

Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020* 82-90

Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020* 1042-1055

Brain

An Application of the Bayesian Periodicity Test to Identify Diurnal Rhythm Genes in the Brain. *Kocak, M., +, TCBB Jan.-Feb. 2020* 47-55

Deep Neural Networks for *In Situ* Hybridization Grid Completion and Clustering. *Li, Y., +, TCBB March-April 2020* 536-546

Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020* 1671-1681

Breast cancer

Identifying Gene Network Rewiring Using Robust Differential Graphical Model with Multivariaten-Distribution. *Yuan, R., +, TCBB March-April 2020* 712-718

- Post-Structuring Radiology Reports of Breast Cancer Patients for Clinical Quality Assurance. *Pathak, S., +, TCBB Nov.-Dec. 2020 1883-1894*
- C**
- C++ language**
- Bi-Level Error Correction for PacBio Long Reads. *Liu, Y., +, TCBB May-June 2020 899-905*
- Cache storage**
- Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020 1093-1104*
- Cache Friendly Optimisation of de Bruijn Graph Based Local Re-Assembly in Variant Calling. *Gamaarachchi, H., +, TCBB July-Aug. 2020 1125-1133*
- Calcium**
- A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020 1858-1870*
- Feed-Forward and Feedback Control in Astrocytes for Ca^{2+} -Based Molecular Communications Nanonetworks. *Barros, M.T., +, TCBB July-Aug. 2020 1174-1186*
- Calibration**
- Active Vision and Surface Reconstruction for 3D Plant Shoot Modelling. *Gibbs, J.A., +, TCBB Nov.-Dec. 2020 1907-1917*
- Cancer**
- RFCM³*: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. *Paul, S., +, TCBB Sept.-Oct. 2020 1729-1740*
- A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity. *Kapoor, R., +, TCBB March-April 2020 459-468*
- A Network-Based Comparison Between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso. *Shahdoust, M., +, TCBB Sept.-Oct. 2020 1555-1562*
- A Novel Approach to Detecting Epistasis using Random Sampling Regularisation. *Hind, J., +, TCBB Sept.-Oct. 2020 1535-1545*
- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020 1582-1594*
- An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer. *Song, J., +, TCBB May-June 2020 758-768*
- Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020 56-70*
- BiModule: Bi clique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules. *Pan, C., +, TCBB Jan.-Feb. 2020 321-326*
- Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020 1605-1612*
- CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020 1141-1153*
- Correction to “Identification of Novel Scaffolds with Dual Role as Antiepileptic and Anti-Breast Cancer”. *Rampogu, S., +, TCBB Jan.-Feb. 2020 365*
- Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*
- Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs. *Hu, H., +, TCBB May-June 2020 887-898*
- Detection of Colorectal Carcinoma Based on Microbiota Analysis Using Generalized Regression Neural Networks and Nonlinear Feature Selection. *Arabameri, A., +, TCBB March-April 2020 547-557*
- Detection of Driver Modules with Rarely Mutated Genes in Cancers. *Li, F., +, TCBB March-April 2020 390-401*
- Drug Selection via Joint Push and Learning to Rank. *He, Y., +, TCBB Jan.-Feb. 2020 110-123*
- Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. *Wang, H., +, TCBB March-April 2020 587-598*
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*
- Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes. *Ismailoglu, F., +, TCBB Jan.-Feb. 2020 347-353*

- HetRCNA: A Novel Method to Identify Recurrent Copy Number Alterations from Heterogeneous Tumor Samples Based on Matrix Decomposition Framework. *Xi, J., +, TCBB March-April 2020 422-434*
- Identifying lncRNA and mRNA Co-Expression Modules from Matched Expression Data in Ovarian Cancer. *Xiao, Q., +, TCBB March-April 2020 623-634*
- In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020 1010-1018*
- Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*
- Low-Rank Joint Subspace Construction for Cancer Subtype Discovery. *Khan, A., +, TCBB July-Aug. 2020 1290-1302*
- MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data. *Zhao, L., +, TCBB Sept.-Oct. 2020 1682-1690*
- Novel Regularization Method for Biomarker Selection and Cancer Classification. *Liu, X., +, TCBB July-Aug. 2020 1329-1340*
- Optimal Bayesian Filtering for Biomarker Discovery: Performance and Robustness. *Foroughi pour, A., +, TCBB Jan.-Feb. 2020 250-263*
- Preprocessing Sequence Coverage Data for More Precise Detection of Copy Number Variations. *Zare, F., +, TCBB May-June 2020 868-876*
- Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. *Shi, J., +, TCBB March-April 2020 449-458*
- Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability. *Alshawafreh, M., +, TCBB May-June 2020 1056-1067*
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*
- SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*
- Causality**
- Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020 56-70*
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- Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020 56-70*
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- Cellular biophysics**
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- Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020 1605-1612*
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- In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020 1010-1018*

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- LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*
- Modified Half-System Based Method for Reverse Engineering of Gene Regulatory Networks. *Khan, A., +, TCBB July-Aug. 2020 1303-1316*
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- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*
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- Cellular effects of radiation**
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- Channel coding**
- Oligo Design with Single Primer Binding Site for High Capacity DNA-Based Data Storage. *Wang, Y., +, TCBB Nov.-Dec. 2020 2176-2182*
- Chemicals**
- A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations. *Lecca, P., +, TCBB March-April 2020 469-482*
- Correction to “A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations”. *Lecca, P., +, TCBB May-June 2020 1092*
- Drug Side-Effect Profiles Prediction: From Empirical to Structural Risk Minimization. *Jiang, H., +, TCBB March-April 2020 402-410*
- Schema Matching and Data Integration with Consistent Naming on Protein Crystallization Screens. *Shrestha, M., +, TCBB Nov.-Dec. 2020 2074-2085*
- Chemistry computing**
- A Novel Edge Effect Detection Method for Real-Time Cellular Analyzer Using Functional Principal Component Analysis. *Guo, Q., +, TCBB Sept.-Oct. 2020 1563-1572*
- High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*
- On the Unreported-Profile-is-Negative Assumption for Predictive Cheminformatics. *Lan, C., +, TCBB July-Aug. 2020 1352-1363*
- Circadian rhythms**
- An Application of the Bayesian Periodicity Test to Identify Diurnal Rhythm Genes in the Brain. *Kocak, M., +, TCBB Jan.-Feb. 2020 47-55*
- Clinical diagnosis**
- Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*
- Closed loop systems**
- Data-Driven Robust Control for a Closed-Loop Artificial Pancreas. *Paoletti, N., +, TCBB Nov.-Dec. 2020 1981-1993*
- Clustering algorithms**
- BiClusO: A Novel Biclustering Approach and Its Application to Species-VOC Relational Data. *Karim, M.B., +, TCBB Nov.-Dec. 2020 1955-1965*
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- Ensembling of Gene Clusters Utilizing Deep Learning and Protein-Protein Interaction Information. *Dutta, P., +, TCBB Nov.-Dec. 2020 2005-2016*
- Multi-Domain Networks Association for Biological Data Using Block Signed Graph Clustering. *Liu, Y., +, TCBB March-April 2020 435-448*
- Colonoscopy**
- Detection of Colorectal Carcinoma Based on Microbiota Analysis Using Generalized Regression Neural Networks and Nonlinear Feature Selection. *Arabameri, A., +, TCBB March-April 2020 547-557*
- Color**
- Approaching the One-Sided Exemplar Adjacency Number Problem. *Qingge, L., +, TCBB Nov.-Dec. 2020 1946-1954*
- Combinatorial mathematics**
- An Effective Solution for Large Scale Single Machine Total Weighted Tardiness Problem using Lunar Cycle Inspired Artificial Bee Colony Algorithm. *Sharma, N., +, TCBB Sept.-Oct. 2020 1573-1581*
- Complex networks**
- Disruption of Protein Complexes from Weighted Complex Networks. *Habibi, M., +, TCBB Jan.-Feb. 2020 102-109*
- Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. *Bakhteh, S., +, TCBB May-June 2020 999-1009*
- Compounds**
- Correction to “Identification of Novel Scaffolds with Dual Role as Antiepileptic and Anti-Breast Cancer”. *Rampogu, S., +, TCBB Jan.-Feb. 2020 365*
- Computability**
- Faster Exact Computation of rSPR Distance via Better Approximation. *Chen, Z., +, TCBB May-June 2020 916-929*
- Computational biology**
- Algorithms for Computational Biology: Fifth Edition. *Martin-Vide, C., +, TCBB Jan.-Feb. 2020 1*
- Approximate Graph Edit Distance in Quadratic Time. *Riesen, K., +, TCBB March-April 2020 483-494*
- BiClusO: A Novel Biclustering Approach and Its Application to Species-VOC Relational Data. *Karim, M.B., +, TCBB Nov.-Dec. 2020 1955-1965*
- Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data. *Zhang, L., +, TCBB March-April 2020 376-389*
- Guest Editorial for Selected Papers from BIOKDD 2018 and DMBIH 2018. *Yan, D., +, TCBB Nov.-Dec. 2020 1832-1834*
- Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC). *Huang, D., +, TCBB Sept.-Oct. 2020 1474-1475*
- Guest Editorial for the 29th International Conference on Genome Informatics (GIW 2018). *Zheng, J., +, TCBB May-June 2020 726-727*
- Computational complexity**
- A Novel Approach to Detecting Epistasis using Random Sampling Regularisation. *Hind, J., +, TCBB Sept.-Oct. 2020 1535-1545*
- Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*
- An Effective Solution for Large Scale Single Machine Total Weighted Tardiness Problem using Lunar Cycle Inspired Artificial Bee Colony Algorithm. *Sharma, N., +, TCBB Sept.-Oct. 2020 1573-1581*
- Faster Exact Computation of rSPR Distance via Better Approximation. *Chen, Z., +, TCBB May-June 2020 916-929*
- Generation of Level-k LGT Networks. *Pons, J.C., +, TCBB Jan.-Feb. 2020 158-164*
- Heuristics for the Reversal and Transposition Distance Problem. *Brito, K.L., +, TCBB Jan.-Feb. 2020 2-13*
- Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020 226-237*

- Plant Species Identification from Occluded Leaf Images.** *Chaudhury, A., +, TCBB May-June 2020 1042-1055*
- Polynomial-Time Algorithms for Phylogenetic Inference Problems Involving Duplication and Reticulation.** *van Iersel, L., +, TCBB Jan.-Feb. 2020 14-26*
- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering.** *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*
- Using Unlabeled Data to Discover Bivariate Causality with Deep Restricted Boltzmann Machines.** *Sokolovska, N., +, TCBB Jan.-Feb. 2020 358-364*
- Variable Neighborhood Search for Partitioning Sparse Biological Networks into the Maximum Edge-Weightedk-Plexes.** *Grbic, M., +, TCBB Sept.-Oct. 2020 1822-1831*
- Computational intelligence**
- Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC). *Huang, D., +, TCBB Sept.-Oct. 2020 1474-1475*
- Computational modeling**
- A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations. *Lecca, P., +, TCBB March-April 2020 469-482*
- Active Vision and Surface Reconstruction for 3D Plant Shoot Modelling. *Gibbs, J.A., +, TCBB Nov.-Dec. 2020 1907-1917*
- Classification of Patients with Coronary Microvascular Dysfunction. *Fodeh, S.J., +, TCBB March-April 2020 704-711*
- Correction to “A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations”. *Lecca, P., +, TCBB May-June 2020 1092*
- EPMDA: Edge Perturbation Based Method for miRNA-Disease Association Prediction. *Dong, Y., +, TCBB Nov.-Dec. 2020 2170-2175*
- FPGA Accelerated Analysis of Boolean Gene Regulatory Networks. *Manica, M., +, TCBB Nov.-Dec. 2020 2141-2147*
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- XGBoost Model for Chronic Kidney Disease Diagnosis. *Ogunleye, A., +, TCBB Nov.-Dec. 2020 2131-2140*
- Computer architecture**
- Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*
- Deep Neural Networks for *In Situ* Hybridization Grid Completion and Clustering. *Li, Y., +, TCBB March-April 2020 536-546*
- Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture. *Chakraborty, R., +, TCBB Nov.-Dec. 2020 2183-2188*
- Semiglobal Sequence Alignment with Gaps Using GPU. *Carroll, T.C., +, TCBB Nov.-Dec. 2020 2086-2097*
- WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. *Mallik, S., +, TCBB March-April 2020 690-703*
- Computer science**
- Correction to “A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations”. *Lecca, P., +, TCBB May-June 2020 1092*
- Computer vision**
- Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs. *Hu, H., +, TCBB May-June 2020 887-898*
- Context awareness**
- Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts. *Noriega-Atala, E., +, TCBB Nov.-Dec. 2020 1895-1906*
- Controllability**
- An Efficient Approach Towards the Source-Target Control of Boolean Networks. *Paul, S., +, TCBB Nov.-Dec. 2020 1932-1945*
- Convergence of numerical methods**
- A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models. *Miyawaki-Kuwakado, A., +, TCBB Jan.-Feb. 2020 27-36*
- Convex programming**
- Identifying “Many-to-Many” Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020 165-176*
- Convolution**
- Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks. *Li, L., +, TCBB March-April 2020 599-607*
- Convolutional neural nets**
- Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*
- Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*
- Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs. *Hu, H., +, TCBB May-June 2020 887-898*
- Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition. *Li, L., +, TCBB May-June 2020 841-846*
- RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020 1741-1750*
- Convolutional neural networks**
- Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*
- Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks. *Li, L., +, TCBB March-April 2020 599-607*
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- Correlation**
- A Branch Point on Differentiation Trajectory is the Bifurcating Event Revealed by Dynamical Network Biomarker Analysis of Single-Cell Data. *Chen, Z., +, TCBB March-April 2020 366-375*
- CGIDLA:Developing the Web Server for CpG Island Related Density and LAUPs (Lineage-Associated Underrepresented Permutations) Study. *Xiao, M., +, TCBB Nov.-Dec. 2020 2148-2154*
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- Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery. *Karakaslar, E.O., +, TCBB March-April 2020 719-725*
- Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. *Shi, J., +, TCBB March-April 2020 449-458*
- WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. *Mallik, S., +, TCBB March-April 2020 690-703*
- Couplings**
- Rapid Reconstruction of Time-Varying Gene Regulatory Networks. *Pyne, S., +, TCBB Jan.-Feb. 2020 278-291*
- Covariance matrices**
- Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. *Ou-Yang, L., +, TCBB Nov.-Dec. 2020 2162-2169*
- Identifying Gene Network Rewiring Using Robust Differential Graphical Model with Multivariatet-Distribution. *Yuan, R., +, TCBB March-April 2020 712-718*
- Crystallization**
- Schema Matching and Data Integration with Consistent Naming on Protein Crystallization Screens. *Shrestha, M., +, TCBB Nov.-Dec. 2020 2074-2085*

D

- Data analysis**
- (Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. *Chowdhury, H.A., +, TCBB July-Aug. 2020 1154-1173*
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- DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data. *Yang, S., +, TCBB March-April 2020 558-565*

- Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools. *Chowdhury, H.A., +, TCBB March-April 2020 566-586*
- GaMRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020 149-157*
- Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020 858-867*
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- SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*
- Using Unlabeled Data to Discover Bivariate Causality with Deep Restricted Boltzmann Machines. *Sokolovska, N., +, TCBB Jan.-Feb. 2020 358-364*
- Data compression**
- Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation. *Kawano, K., +, TCBB Sept.-Oct. 2020 1762-1772*
- Data handling**
- Disruption of Protein Complexes from Weighted Complex Networks. *Habibi, M., +, TCBB Jan.-Feb. 2020 102-109*
- Data integration**
- Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network. *Chen, H., +, TCBB March-April 2020 516-525*
- Clustering and Integrating of Heterogeneous Microbiome Data by Joint Symmetric Nonnegative Matrix Factorization with Laplacian Regularization. *Ma, Y., +, TCBB May-June 2020 788-795*
- Low-Rank Joint Subspace Construction for Cancer Subtype Discovery. *Khan, A., +, TCBB July-Aug. 2020 1290-1302*
- Multi-Domain Networks Association for Biological Data Using Block Signed Graph Clustering. *Liu, Y., +, TCBB March-April 2020 435-448*
- Schema Matching and Data Integration with Consistent Naming on Protein Crystallization Screens. *Shrestha, M., +, TCBB Nov.-Dec. 2020 2074-2085*
- Data mining**
- Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. *Yao, H., +, TCBB May-June 2020 777-787*
- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020 1582-1594*
- BiModule: Bi clique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules. *Pan, C., +, TCBB Jan.-Feb. 2020 321-326*
- Deep Collaborative Filtering for Prediction of Disease Genes. *Zeng, X., +, TCBB Sept.-Oct. 2020 1639-1647*
- Efficient Mining Multi-Mers in a Variety of Biological Sequences. *Zhang, J., +, TCBB May-June 2020 949-958*
- Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks. *Li, L., +, TCBB March-April 2020 599-607*
- Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts. *Noriega-Atala, E., +, TCBB Nov.-Dec. 2020 1895-1906*
- Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*
- Guest Editorial for Selected Papers from BIOKDD 2018 and DMBIH 2018. *Yan, D., +, TCBB Nov.-Dec. 2020 1832-1834*
- Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition. *Li, L., +, TCBB May-June 2020 841-846*
- Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*
- LSTM-Based End-to-End Framework for Biomedical Event Extraction. *Yu, X., +, TCBB Nov.-Dec. 2020 2029-2039*
- Mining Relationships among Multiple Entities in Biological Networks. *Peng, J., +, TCBB May-June 2020 769-776*
- Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. *Acharya, S., +, TCBB Jan.-Feb. 2020 207-219*
- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020 264-277*
- Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*
- Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. *Zhang, G., +, TCBB Nov.-Dec. 2020 2119-2130*
- Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020 1440-1450*
- Data models**
- Bounded Fuzzy Possibilistic Method Reveals Information about Lung Cancer through Analysis of Metabolomics. *Yazdani, H., +, TCBB March-April 2020 526-535*
- Classification of Patients with Coronary Microvascular Dysfunction. *Fodeh, S.J., +, TCBB March-April 2020 704-711*
- Deep Learning Benchmarks on L1000 Gene Expression Data. *McDermott, M.B., +, TCBB Nov.-Dec. 2020 1846-1857*
- Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. *Ou-Yang, L., +, TCBB Nov.-Dec. 2020 2162-2169*
- Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. *Wang, H., +, TCBB March-April 2020 587-598*
- Enabling Massive XML-Based Biological Data Management in HBase. *Liu, J., +, TCBB Nov.-Dec. 2020 1994-2004*
- Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *Zhang, R., +, TCBB March-April 2020 647-656*
- Data privacy**
- Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020 930-937*
- Data structures**
- Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020 1093-1104*
- Cache Friendly Optimisation of de Bruijn Graph Based Local Re-Assembly in Variant Calling. *Gamaarachchi, H., +, TCBB July-Aug. 2020 1125-1133*
- Fast de Bruijn Graph Compaction in Distributed Memory Environments. *Pan, T., +, TCBB Jan.-Feb. 2020 136-148*
- Data visualization**
- A Note on GRegNetSim: A Tool for the Discrete Simulation and Analysis of Genetic Regulatory Networks. *Ganor, D., +, TCBB Jan.-Feb. 2020 316-320*
- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020 264-277*
- Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020 1459-1473*
- Databases**
- BiClusO: A Novel Biclustering Approach and Its Application to Species-VOC Relational Data. *Karim, M.B., +, TCBB Nov.-Dec. 2020 1955-1965*
- Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. *Wong, K., +, TCBB Jan.-Feb. 2020 327-333*
- Drug Side-Effect Profiles Prediction: From Empirical to Structural Risk Minimization. *Jiang, H., +, TCBB March-April 2020 402-410*
- Enabling Massive XML-Based Biological Data Management in HBase. *Liu, J., +, TCBB Nov.-Dec. 2020 1994-2004*
- Decision making**
- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020 264-277*
- Decision support systems**
- XGBoost Model for Chronic Kidney Disease Diagnosis. *Ogunleye, A., +, TCBB Nov.-Dec. 2020 2131-2140*

Deep learning

Deep Learning Benchmarks on L1000 Gene Expression Data. *McDermott, M.B., +, TCBB Nov.-Dec. 2020 1846-1857*

Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*

Ensembling of Gene Clusters Utilizing Deep Learning and Protein-Protein Interaction Information. *Dutta, P., +, TCBB Nov.-Dec. 2020 2005-2016*

Delays

Oscillatory Dynamics of p53-Mdm2 Circuit in Response to DNA Damage Caused by Ionizing Radiation. *Zhang, Y., +, TCBB Sept.-Oct. 2020 1703-1713*

Dentistry

Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*

Diamond

Connectivity Significance for Disease Gene Prioritization in an Expanding Universe. *Petti, M., +, TCBB Nov.-Dec. 2020 2155-2161*

Differential equations

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Differentiation

A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models. *Miyawaki-Kuwakado, A., +, TCBB Jan.-Feb. 2020 27-36*

Diseases

(Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. *Chowdhury, H.A., +, TCBB July-Aug. 2020 1154-1173*

Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020 959-971*

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Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. *Ou-Yang, L., +, TCBB Nov.-Dec. 2020 2162-2169*

EPMDA: Edge Perturbation Based Method for miRNA-Disease Association Prediction. *Dong, Y., +, TCBB Nov.-Dec. 2020 2170-2175*

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Feed-Forward and Feedback Control in Astrocytes for Ca^{2+} -Based Molecular Communications Nanonetworks. *Barros, M.T., +, TCBB July-Aug. 2020 1174-1186*

Gene Expressions, Hippocampal Volume Loss, and MMSE Scores in Computation of Progression and Pharmacologic Therapy Effects for Alzheimer's Disease. *Saribudak, A., +, TCBB March-April 2020 608-622*

Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. *Li, M., +, TCBB May-June 2020 817-827*

Identifying “Many-to-Many” Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020 165-176*

Incorporating Prior Knowledge about Genetic Variants into the Analysis of Genetic Association Data: An Empirical Bayes Approach. *Karimnezhad, A., +, TCBB March-April 2020 635-646*

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Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*

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Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*

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Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. *Acharya, S., +, TCBB Jan.-Feb. 2020 207-219*

Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020 226-237*

NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*

Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*

Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*

Preprocessing Sequence Coverage Data for More Precise Detection of Copy Number Variations. *Zare, F., +, TCBB May-June 2020 868-876*

Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*

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Stepwise Tikhonov Regularisation: Application to the Prediction of HIV-1 Drug Resistance. *Delgado, R.A., +, TCBB Jan.-Feb. 2020 292-301*

SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. *Yuan, X., +, TCBB May-June 2020 1082-1091*

United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*

Utilizing Deep Learning and Genome Wide Association Studies for Epistatic-Driven Preterm Birth Classification in African-American Women. *Fergus, P., +, TCBB March-April 2020 668-678*

WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. *Mallik, S., +, TCBB March-April 2020 690-703*

XGBoost Model for Chronic Kidney Disease Diagnosis. *Ogunleye, A., +, TCBB Nov.-Dec. 2020 2131-2140*

Distributed memory systems

Fast de Bruijn Graph Compaction in Distributed Memory Environments. *Pan, T., +, TCBB Jan.-Feb. 2020 136-148*

DNA

Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network. *Chen, H., +, TCBB March-April 2020 516-525*

Bi-Level Error Correction for PacBio Long Reads. *Liu, Y., +, TCBB May-June 2020 899-905*

Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks. *Liu, G., +, TCBB Nov.-Dec. 2020 1966-1980*

- Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020 1605-1612*
- Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. *Wong, K., +, TCBB Jan.-Feb. 2020 327-333*
- Efficient Mining Multi-Mers in a Variety of Biological Sequences. *Zhang, J., +, TCBB May-June 2020 949-958*
- EL_LSTM: Prediction of DNA-Binding Residue from Protein Sequence by Combining Long Short-Term Memory and Ensemble Learning. *Zhou, J., +, TCBB Jan.-Feb. 2020 124-135*
- Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections. *Som-In, S., +, TCBB May-June 2020 990-998*
- Fast Short Read De-Novo Assembly Using Overlap-Layout-Consensus Approach. *Bayat, A., +, TCBB Jan.-Feb. 2020 334-338*
- Identification of Short Exons Disunited by a Short Intron in Eukaryotic DNA Regions. *Sharma, S., +, TCBB Sept.-Oct. 2020 1660-1670*
- Identifying TF Binding Motifs from a Partial Set of Target Genes and its Application to Regulatory Network Inference. *Zhao, G., +, TCBB July-Aug. 2020 1211-1221*
- Improving *de novo* Assembly Based on Read Classification. *Liao, X., +, TCBB Jan.-Feb. 2020 177-188*
- Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020 930-937*
- Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020 1671-1681*
- Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*
- Microarray-Based Quality Assessment as a Supporting Criterion for *de novo* Transcriptome Assembly Selection. *Carvajal-Lopez, P., +, TCBB Jan.-Feb. 2020 198-206*
- MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. *Li, T., +, TCBB Jan.-Feb. 2020 220-225*
- Oligo Design with Single Primer Binding Site for High Capacity DNA-Based Data Storage. *Wang, Y., +, TCBB Nov.-Dec. 2020 2176-2182*
- Oscillatory Dynamics of p53-Mdm2 Circuit in Response to DNA Damage Caused by Ionizing Radiation. *Zhang, Y., +, TCBB Sept.-Oct. 2020 1703-1713*
- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020 264-277*
- PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*
- Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. *Fu, L., +, TCBB Sept.-Oct. 2020 1721-1728*
- Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*
- Prediction of TF-Binding Site by Inclusion of Higher Order Position Dependencies. *Zhou, J., +, TCBB July-Aug. 2020 1383-1393*
- Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. *Cao, Z., +, TCBB March-April 2020 657-667*
- Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability. *Alshawafreh, M., +, TCBB May-June 2020 1056-1067*
- Softepigen: Primers Design Web-Based Tool for MS-HRM Technique. *Pinzon-Reyes, E., +, TCBB Jan.-Feb. 2020 354-357*
- SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. *Yuan, X., +, TCBB May-June 2020 1082-1091*
- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
- Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. *Zhang, Q., +, TCBB March-April 2020 679-689*
- WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. *Mallik, S., +, TCBB March-April 2020 690-703*
- Drug delivery systems**
- Drug Selection via Joint Push and Learning to Rank. *He, Y., +, TCBB Jan.-Feb. 2020 110-123*
- Stepwise Tikhonov Regularisation: Application to the Prediction of HIV-1 Drug Resistance. *Delgado, R.A., +, TCBB Jan.-Feb. 2020 292-301*
- Drugs**
- A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity. *Kapoor, R., +, TCBB March-April 2020 459-468*
- Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs. *Hu, H., +, TCBB May-June 2020 887-898*
- Drug Side-Effect Profiles Prediction: From Empirical to Structural Risk Minimization. *Jiang, H., +, TCBB March-April 2020 402-410*
- Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. *Wang, H., +, TCBB March-April 2020 587-598*
- G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides. *Wang, S., +, TCBB May-June 2020 739-747*
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*
- Gene Expressions, Hippocampal Volume Loss, and MMSE Scores in Computation of Progression and Pharmacologic Therapy Effects for Alzheimer's Disease. *Saribudak, A., +, TCBB March-April 2020 608-622*
- Identifying "Many-to-Many" Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020 165-176*
- In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020 1010-1018*
- nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale. *Fassio, A.V., +, TCBB July-Aug. 2020 1317-1328*
- NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*
- Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*
- PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*
- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*
- United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*
- E**
- Edge detection**
- Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*
- Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020 1042-1055*
- Eigenvalues and eigenfunctions**
- United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*
- Electric potential**
- Correction to "Identification of Novel Scaffolds with Dual Role as Antiepileptic and Anti-Breast Cancer". *Rampogu, S., +, TCBB Jan.-Feb. 2020 365*
- Electroencephalography**
- A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020 1858-1870*
- Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*

Electronic data interchange

Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB. *Liu, J., +, TCBB Sept.-Oct. 2020 1504-1515*

Electrooculography

Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*

Electrostatics

Correction to “Identification of Novel Scaffolds with Dual Role as Antiepileptic and Anti-Breast Cancer”. *Rampogi, S., +, TCBB Jan.-Feb. 2020 365*

Encoding

Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment. *Jing, X., +, TCBB Nov.-Dec. 2020 1918-1931*

Entropy

An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer. *Song, J., +, TCBB May-June 2020 758-768*

Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020 56-70*

Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*

Epigenetics

Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network. *Chen, H., +, TCBB March-April 2020 516-525*

Epilepsy

A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020 1858-1870*

Error analysis

Protein Complexes Identification with Family-Wise Error Rate Control. *He, Z., +, TCBB Nov.-Dec. 2020 2062-2073*

Error correction

Bi-Level Error Correction for PacBio Long Reads. *Liu, Y., +, TCBB May-June 2020 899-905*

MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. *Wu, B., +, TCBB May-June 2020 847-857*

Estimation

Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. *Ou-Yang, L., +, TCBB Nov.-Dec. 2020 2162-2169*

Incorporating Prior Knowledge about Genetic Variants into the Analysis of Genetic Association Data: An Empirical Bayes Approach. *Karimnezhad, A., +, TCBB March-April 2020 635-646*

Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions. *Deng, Z., +, TCBB July-Aug. 2020 1231-1240*

Evolution (biological)

CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. *Kang, Q., +, TCBB May-June 2020 981-989*

Faster Exact Computation of rSPR Distance via Better Approximation. *Chen, Z., +, TCBB May-June 2020 916-929*

Generation of Level- k LGT Networks. *Pons, J.C., +, TCBB Jan.-Feb. 2020 158-164*

imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020 1222-1230*

Polynomial-Time Algorithms for Phylogenetic Inference Problems Involving Duplication and Reticulation. *van Iersel, L., +, TCBB Jan.-Feb. 2020 14-26*

Evolutionary computation

An Effective Solution for Large Scale Single Machine Total Weighted Tardiness Problem using Lunar Cycle Inspired Artificial Bee Colony Algorithm. *Sharma, N., +, TCBB Sept.-Oct. 2020 1573-1581*

Generation of Level- k LGT Networks. *Pons, J.C., +, TCBB Jan.-Feb. 2020 158-164*

Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. *Zhang, G., +, TCBB May-June 2020 1068-1081*

Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*

Stability Analysis of Biological Networks’ Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*

TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. *Zhang, G., +, TCBB Nov.-Dec. 2020 2119-2130*

Expectation-maximization algorithms

Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*

F**Fault diagnosis**

Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*

Fault location

A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity. *Kapoor, R., +, TCBB March-April 2020 459-468*

Feature extraction

A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020 1858-1870*

Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment. *Jing, X., +, TCBB Nov.-Dec. 2020 1918-1931*

An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. *Liao, X., +, TCBB May-June 2020 728-738*

Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks. *Liu, G., +, TCBB Nov.-Dec. 2020 1966-1980*

Classification of Antibacterial Peptides Using Long Short-Term Memory Recurrent Neural Networks. *Youmans, M., +, TCBB July-Aug. 2020 1134-1140*

Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*

Computerized Classification of Prostate Cancer Gleason Scores from Whole Slide Images. *Xu, H., +, TCBB Nov.-Dec. 2020 1871-1882*

Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*

Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*

Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*

Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020 1648-1659*

Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs. *Hu, H., +, TCBB May-June 2020 887-898*

Detection of Colorectal Carcinoma Based on Microbiota Analysis Using Generalized Regression Neural Networks and Nonlinear Feature Selection. *Arabameri, A., +, TCBB March-April 2020 547-557*

Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting. *Lin, X., +, TCBB Sept.-Oct. 2020 1525-1534*

ELF: Extract Landmark Features By Optimizing Topology Maintenance, Redundancy, and Specificity. *Feng, Z., +, TCBB March-April 2020 411-421*

EPMDA: Edge Perturbation Based Method for miRNA-Disease Association Prediction. *Dong, Y., +, TCBB Nov.-Dec. 2020 2170-2175*

Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks. *Li, L., +, TCBB March-April 2020 599-607*

Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts. *Noriega-Atala, E., +, TCBB Nov.-Dec. 2020 1895-1906*

G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides. *Wang, S., +, TCBB May-June 2020 739-747*

- Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. *Hu, L., +, TCBB Nov.-Dec. 2020 2017-2028*
- Low-Rank Joint Subspace Construction for Cancer Subtype Discovery. *Khan, A., +, TCBB July-Aug. 2020 1290-1302*
- LSTM-Based End-to-End Framework for Biomedical Event Extraction. *Yu, X., +, TCBB Nov.-Dec. 2020 2029-2039*
- Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*
- Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020 1042-1055*
- Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture. *Chakraborty, R., +, TCBB Nov.-Dec. 2020 2183-2188*
- Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. *Cao, Z., +, TCBB March-April 2020 657-667*
- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*
- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
- Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. *Zhang, G., +, TCBB Nov.-Dec. 2020 2119-2130*
- Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information. *Li, J., +, TCBB Sept.-Oct. 2020 1546-1554*
- XGBoost Model for Chronic Kidney Disease Diagnosis. *Ogunleye, A., +, TCBB Nov.-Dec. 2020 2131-2140*
- Feature selection**
- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
- Feedback**
- Feed-Forward and Feedback Control in Astrocytes for Ca^{2+} -Based Molecular Communications Nanonetworks. *Barros, M.T., +, TCBB July-Aug. 2020 1174-1186*
- Feedforward neural networks**
- Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. *Fu, L., +, TCBB Sept.-Oct. 2020 1721-1728*
- Field programmable gate arrays**
- FPGA Accelerated Analysis of Boolean Gene Regulatory Networks. *Mancica, M., +, TCBB Nov.-Dec. 2020 2141-2147*
- Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications. *Gudur, V.Y., +, TCBB July-Aug. 2020 1198-1210*
- Filtering theory**
- GaMRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020 149-157*
- Low-Rank Joint Subspace Construction for Cancer Subtype Discovery. *Khan, A., +, TCBB July-Aug. 2020 1290-1302*
- Finite element analysis**
- Enabling Massive XML-Based Biological Data Management in HBase. *Liu, J., +, TCBB Nov.-Dec. 2020 1994-2004*
- Fish**
- Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. *Lei, X., +, TCBB March-April 2020 495-505*
- Forestry**
- Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. *Wong, K., +, TCBB Jan.-Feb. 2020 327-333*
- SICOR: Subgraph Isomorphism Comparison of RNA Secondary Structures. *Schmidt, M., +, TCBB Nov.-Dec. 2020 2189-2195*
- Formal specification**
- Basins of Attraction, Commitment Sets, and Phenotypes of Boolean Networks. *Klarner, H., +, TCBB July-Aug. 2020 1115-1124*
- Formal verification**
- Basins of Attraction, Commitment Sets, and Phenotypes of Boolean Networks. *Klarner, H., +, TCBB July-Aug. 2020 1115-1124*

Free energy

- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*

Functional analysis

- Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. *Shi, J., +, TCBB March-April 2020 449-458*

G**Gaussian distribution**

- A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity. *Kapoor, R., +, TCBB March-April 2020 459-468*
- Identifying Gene Network Rewiring Using Robust Differential Graphical Model with Multivariaten-Distribution. *Yuan, R., +, TCBB March-April 2020 712-718*

Gaussian mixture model

- A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity. *Kapoor, R., +, TCBB March-April 2020 459-468*

Gaussian noise

- Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability. *Alshawaqfeh, M., +, TCBB May-June 2020 1056-1067*

Gaussian processes

- A Network-Based Comparison Between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso. *Shahdoust, M., +, TCBB Sept.-Oct. 2020 1555-1562*
- Optimal Bayesian Filtering for Biomarker Discovery: Performance and Robustness. *Foroughi pour, A., +, TCBB Jan.-Feb. 2020 250-263*
- Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020 1394-1405*

Gene expression

- Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. *Lei, X., +, TCBB March-April 2020 495-505*

- Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network. *Chen, H., +, TCBB March-April 2020 516-525*

- Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data. *Zhang, L., +, TCBB March-April 2020 376-389*

- Deep Learning Benchmarks on L1000 Gene Expression Data. *McDermott, M.B., +, TCBB Nov.-Dec. 2020 1846-1857*

- Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools. *Chowdhury, H.A., +, TCBB March-April 2020 566-586*

- Ensembling of Gene Clusters Utilizing Deep Learning and Protein-Protein Interaction Information. *Dutta, P., +, TCBB Nov.-Dec. 2020 2005-2016*

- Gene Expressions, Hippocampal Volume Loss, and MMSE Scores in Computation of Progression and Pharmacologic Therapy Effects for Alzheimer's Disease. *Saribudak, A., +, TCBB March-April 2020 608-622*

- Identifying Gene Network Rewiring Using Robust Differential Graphical Model with Multivariaten-Distribution. *Yuan, R., +, TCBB March-April 2020 712-718*

- Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data. *Zhang, W., +, TCBB Nov.-Dec. 2020 2053-2061*

- Rapid Reconstruction of Time-Varying Gene Regulatory Networks. *Pyne, S., +, TCBB Jan.-Feb. 2020 278-291*

- WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. *Mallik, S., +, TCBB March-April 2020 690-703*

Genetic algorithms

- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020 1582-1594*

Genetics

- (Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. *Chowdhury, H.A., +, TCBB July-Aug. 2020 1154-1173*

- RFCM³: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. *Paul, S., +, TCBB Sept.-Oct. 2020 1729-1740*

- A Network-Based Comparison Between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso. *Shahdoust, M., +, TCBB Sept.-Oct. 2020 1555-1562*
- A Note on GRegNetSim: A Tool for the Discrete Simulation and Analysis of Genetic Regulatory Networks. *Ganor, D., +, TCBB Jan.-Feb. 2020 316-320*
- A Novel Approach to Detecting Epistasis using Random Sampling Regularisation. *Hind, J., +, TCBB Sept.-Oct. 2020 1535-1545*
- Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*
- An Application of the Bayesian Periodicity Test to Identify Diurnal Rhythm Genes in the Brain. *Kocak, M., +, TCBB Jan.-Feb. 2020 47-55*
- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020 1582-1594*
- An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer. *Song, J., +, TCBB May-June 2020 758-768*
- Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020 56-70*
- BiModule: Biclique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules. *Pan, C., +, TCBB Jan.-Feb. 2020 321-326*
- Causal Disturbance Analysis: A Novel Graph Centrality Based Method for Pathway Enrichment Analysis. *Yeganeh, P.N., +, TCBB Sept.-Oct. 2020 1613-1624*
- Class Balanced Multifactor Dimensionality Reduction to Detect Gene–Gene Interactions. *Yang, C., +, TCBB Jan.-Feb. 2020 71-81*
- CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020 1141-1153*
- CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. *Kang, Q., +, TCBB May-June 2020 981-989*
- Deep Collaborative Filtering for Prediction of Disease Genes. *Zeng, X., +, TCBB Sept.-Oct. 2020 1639-1647*
- DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data. *Yang, S., +, TCBB March-April 2020 558-565*
- Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections. *Som-In, S., +, TCBB May-June 2020 990-998*
- ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data. *Tan, R., +, TCBB May-June 2020 796-803*
- Fast Short Read De-Novo Assembly Using Overlap-Layout-Consensus Approach. *Bayat, A., +, TCBB Jan.-Feb. 2020 334-338*
- Faster Exact Computation of rSPR Distance via Better Approximation. *Chen, Z., +, TCBB May-June 2020 916-929*
- GaMRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020 149-157*
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*
- Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*
- Generation of Level- k LGT Networks. *Pons, J.C., +, TCBB Jan.-Feb. 2020 158-164*
- Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes. *Ismailoglu, F., +, TCBB Jan.-Feb. 2020 347-353*
- Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. *Bakhsh, S., +, TCBB May-June 2020 999-1009*
- Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. *Li, M., +, TCBB May-June 2020 817-827*
- Identification of Short Exons Disunited by a Short Intron in Eukaryotic DNA Regions. *Sharma, S., +, TCBB Sept.-Oct. 2020 1660-1670*
- Identifying “Many-to-Many” Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020 165-176*
- Identifying TF Binding Motifs from a Partial Set of Target Genes and its Application to Regulatory Network Inference. *Zhao, G., +, TCBB July-Aug. 2020 1211-1221*
- imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020 1222-1230*
- Improving *de novo* Assembly Based on Read Classification. *Liao, X., +, TCBB Jan.-Feb. 2020 177-188*
- Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020 858-867*
- Incorporating Prior Knowledge about Genetic Variants into the Analysis of Genetic Association Data: An Empirical Bayes Approach. *Karimnezhad, A., +, TCBB March-April 2020 635-646*
- Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020 930-937*
- Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions. *Deng, Z., +, TCBB July-Aug. 2020 1231-1240*
- Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. *Xuan, P., +, TCBB May-June 2020 1019-1031*
- Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020 1671-1681*
- Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*
- Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020 1253-1261*
- Inverse Projection Representation and Category Contribution Rate for Robust Tumor Recognition. *Yang, X., +, TCBB July-Aug. 2020 1262-1275*
- IsoTree: A New Framework for *de novo* Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020 938-948*
- Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB. *Liu, J., +, TCBB Sept.-Oct. 2020 1504-1515*
- Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA–miRNA Interactions. *Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524*
- LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*
- MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. *Wu, B., +, TCBB May-June 2020 847-857*
- miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. *Jiang, H., +, TCBB May-June 2020 1032-1041*
- Modified Half-System Based Method for Reverse Engineering of Gene Regulatory Networks. *Khan, A., +, TCBB July-Aug. 2020 1303-1316*
- Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. *Acharya, S., +, TCBB Jan.-Feb. 2020 207-219*
- MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. *Li, T., +, TCBB Jan.-Feb. 2020 220-225*
- Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020 226-237*
- NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. *Yu, G., +, TCBB Jan.-Feb. 2020 238-249*
- Novel Regularization Method for Biomarker Selection and Cancer Classification. *Liu, X., +, TCBB July-Aug. 2020 1329-1340*
- NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*
- Optimal Bayesian Filtering for Biomarker Discovery: Performance and Robustness. *Foroughi pour, A., +, TCBB Jan.-Feb. 2020 250-263*
- Oscillatory Dynamics of p53-Mdm2 Circuit in Response to DNA Damage Caused by Ionizing Radiation. *Zhang, Y., +, TCBB Sept.-Oct. 2020 1703-1713*
- Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*

- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020* 264-277
- Polynomial-Time Algorithms for Phylogenetic Inference Problems Involving Duplication and Reticulation. *van Iersel, L., +, TCBB Jan.-Feb. 2020* 14-26
- Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020* 1364-1371
- Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. *Fu, L., +, TCBB Sept.-Oct. 2020* 1721-1728
- Prediction of TF-Binding Site by Inclusion of Higher Order Position Dependencies. *Zhou, J., +, TCBB July-Aug. 2020* 1383-1393
- Preprocessing Sequence Coverage Data for More Precise Detection of Copy Number Variations. *Zare, F., +, TCBB May-June 2020* 868-876
- RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020* 1741-1750
- Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability. *Alshawafreh, M., +, TCBB May-June 2020* 1056-1067
- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020* 1773-1784
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020* 748-757
- SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020* 1785-1796
- Stability Analysis of Biological Networks' Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020* 1406-1418
- Structural Bistability Analysis of Flower-Shaped and Chain-Shaped Boolean Networks. *Azuma, S., +, TCBB Nov.-Dec. 2020* 2098-2106
- SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. *Yuan, X., +, TCBB May-June 2020* 1082-1091
- The Use of Informed Priors in Biclustering of Gene Expression with the Hierarchical Dirichlet Process. *Tercan, B., +, TCBB Sept.-Oct. 2020* 1810-1821
- United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020* 1451-1458
- Genomics**
- (Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. *Chowdhury, H.A., +, TCBB July-Aug. 2020* 1154-1173
- RFCM³: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. *Paul, S., +, TCBB Sept.-Oct. 2020* 1729-1740
- Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020* 1093-1104
- Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020* 1105-1114
- An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. *Liao, X., +, TCBB May-June 2020* 728-738
- An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer. *Song, J., +, TCBB May-June 2020* 758-768
- Approaching the One-Sided Exemplar Adjacency Number Problem. *Qingge, L., +, TCBB Nov.-Dec. 2020* 1946-1954
- BiModule: Bi clique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules. *Pan, C., +, TCBB Jan.-Feb. 2020* 321-326
- Cache Friendly Optimisation of de Bruijn Graph Based Local Re-Assembly in Variant Calling. *Gamaarachchi, H., +, TCBB July-Aug. 2020* 1125-1133
- Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020* 1605-1612
- CGIDLA:Developing the Web Server for CpG Island Related Density and LAUPs (Lineage-Associated Underrepresented Permutations) Study. *Xiao, M., +, TCBB Nov.-Dec. 2020* 2148-2154
- Class Balanced Multifactor Dimensionality Reduction to Detect Gene–Gene Interactions. *Yang, C., +, TCBB Jan.-Feb. 2020* 71-81
- CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygoty from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020* 1141-1153
- Connectivity Significance for Disease Gene Prioritization in an Expanding Universe. *Petti, M., +, TCBB Nov.-Dec. 2020* 2155-2161
- CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. *Kang, Q., +, TCBB May-June 2020* 981-989
- Detection of Driver Modules with Rarely Mutated Genes in Cancers. *Li, F., +, TCBB March-April 2020* 390-401
- Drug Selection via Joint Push and Learning to Rank. *He, Y., +, TCBB Jan.-Feb. 2020* 110-123
- Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. *Wang, H., +, TCBB March-April 2020* 587-598
- Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections. *Som-In, S., +, TCBB May-June 2020* 990-998
- ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data. *Tan, R., +, TCBB May-June 2020* 796-803
- Fast Short Read De-Novo Assembly Using Overlap-Layout-Consensus Approach. *Bayat, A., +, TCBB Jan.-Feb. 2020* 334-338
- Fast de Bruijn Graph Compaction in Distributed Memory Environments. *Pan, T., +, TCBB Jan.-Feb. 2020* 136-148
- GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets. *Luo, J., +, TCBB May-June 2020* 877-886
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020* 1187-1197
- Guest Editorial for the 29th International Conference on Genome Informatics (GIW 2018). *Zheng, J., +, TCBB May-June 2020* 726-727
- HetRCNA: A Novel Method to Identify Recurrent Copy Number Alterations from Heterogeneous Tumor Samples Based on Matrix Decomposition Framework. *Xi, J., +, TCBB March-April 2020* 422-434
- Heuristics for the Reversal and Transposition Distance Problem. *Brito, K.L., +, TCBB Jan.-Feb. 2020* 2-13
- Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. *Li, M., +, TCBB May-June 2020* 817-827
- Identification of Short Exons Disunited by a Short Intron in Eukaryotic DNA Regions. *Sharma, S., +, TCBB Sept.-Oct. 2020* 1660-1670
- Identifying “Many-to-Many” Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020* 165-176
- Identifying lncRNA and mRNA Co-Expression Modules from Matched Expression Data in Ovarian Cancer. *Xiao, Q., +, TCBB March-April 2020* 623-634
- Identifying TF Binding Motifs from a Partial Set of Target Genes and its Application to Regulatory Network Inference. *Zhao, G., +, TCBB July-Aug. 2020* 1211-1221
- imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020* 1222-1230
- Improving *de novo* Assembly Based on Read Classification. *Liao, X., +, TCBB Jan.-Feb. 2020* 177-188
- Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020* 858-867
- Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020* 930-937
- Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *Zhang, R., +, TCBB March-April 2020* 647-656
- Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020* 1671-1681
- Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020* 1253-1261
- IsoTree: A New Framework for *de novo* Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020* 938-948

- Glands**
- Computerized Classification of Prostate Cancer Gleason Scores from Whole Slide Images. Xu, H., +, TCBB Nov.-Dec. 2020 1871-1882
- Gradient methods**
- SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796
- Graph theory**
- Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB. Liu, J., +, TCBB Sept.-Oct. 2020 1504-1515
 - Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA-miRNA Interactions. Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524
 - MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data. Zhao, L., +, TCBB Sept.-Oct. 2020 1682-1690
 - MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. Wu, B., +, TCBB May-June 2020 847-857
 - miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. Jiang, H., +, TCBB May-June 2020 1032-1041
 - Modified Half-System Based Method for Reverse Engineering of Gene Regulatory Networks. Khan, A., +, TCBB July-Aug. 2020 1303-1316
 - Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. Acharya, S., +, TCBB Jan.-Feb. 2020 207-219
 - MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. Li, T., +, TCBB Jan.-Feb. 2020 220-225
 - Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. Li, X., +, TCBB Jan.-Feb. 2020 226-237
 - NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. Luo, J., +, TCBB July-Aug. 2020 1341-1351
 - PASA: Identifying More Credible Structural Variants of Hedou12. Jia, H., +, TCBB Sept.-Oct. 2020 1493-1503
 - Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). Rahman, M.A., +, TCBB May-June 2020 828-840
 - PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. Mazrouee, S., +, TCBB Jan.-Feb. 2020 264-277
 - Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. Fu, L., +, TCBB Sept.-Oct. 2020 1721-1728
 - Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382
 - Preprocessing Sequence Coverage Data for More Precise Detection of Copy Number Variations. Zare, F., +, TCBB May-June 2020 868-876
 - Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. Cao, Z., +, TCBB March-April 2020 657-667
 - Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability. Alshawafreh, M., +, TCBB May-June 2020 1056-1067
 - Semiglobal Sequence Alignment with Gaps Using GPU. Carroll, T.C., +, TCBB Nov.-Dec. 2020 2086-2097
 - SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796
 - Softepigen: Primers Design Web-Based Tool for MS-HRM Technique. Pinzon-Reyes, E., +, TCBB Jan.-Feb. 2020 354-357
 - SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. Yuan, X., +, TCBB May-June 2020 1082-1091
 - The Use of Informed Priors in Biclustering of Gene Expression with the Hierarchical Dirichlet Process. Tercan, B., +, TCBB Sept.-Oct. 2020 1810-1821
 - Utilizing Deep Learning and Genome Wide Association Studies for Epistatic-Driven Preterm Birth Classification in African-American Women. Ferguson, P., +, TCBB March-April 2020 668-678
- Graphical models**
- Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. Yao, H., +, TCBB May-June 2020 777-787
 - Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. Boukari, F., +, TCBB May-June 2020 959-971
 - Basins of Attraction, Commitment Sets, and Phenotypes of Boolean Networks. Klarner, H., +, TCBB July-Aug. 2020 1115-1124
 - Bi-Level Error Correction for PacBio Long Reads. Liu, Y., +, TCBB May-June 2020 899-905
 - BiModule: Biclique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules. Pan, C., +, TCBB Jan.-Feb. 2020 321-326
 - Cache Friendly Optimisation of de Bruijn Graph Based Local Re-Assembly in Variant Calling. Gamaarachchi, H., +, TCBB July-Aug. 2020 1125-1133
 - Causal Disturbance Analysis: A Novel Graph Centrality Based Method for Pathway Enrichment Analysis. Yeganeh, P.N., +, TCBB Sept.-Oct. 2020 1613-1624
 - Disruption of Protein Complexes from Weighted Complex Networks. Habibi, M., +, TCBB Jan.-Feb. 2020 102-109
 - Fast de Bruijn Graph Compaction in Distributed Memory Environments. Pan, T., +, TCBB Jan.-Feb. 2020 136-148
 - GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets. Luo, J., +, TCBB May-June 2020 877-886
 - Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. He, Z., +, TCBB May-June 2020 930-937
 - LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. Zhang, T., +, TCBB Jan.-Feb. 2020 189-197
 - Plant Species Identification from Occluded Leaf Images. Chaudhury, A., +, TCBB May-June 2020 1042-1055
 - The Use of Informed Priors in Biclustering of Gene Expression with the Hierarchical Dirichlet Process. Tercan, B., +, TCBB Sept.-Oct. 2020 1810-1821
 - Variable Neighborhood Search for Partitioning Sparse Biological Networks into the Maximum Edge-Weightedk-Plexes. Grbic, M., +, TCBB Sept.-Oct. 2020 1822-1831
- Graphical user interfaces**
- A Note on GRegNetSim: A Tool for the Discrete Simulation and Analysis of Genetic Regulatory Networks. Ganor, D., +, TCBB Jan.-Feb. 2020 316-320
- Graphics processing units**
- Semiglobal Sequence Alignment with Gaps Using GPU. Carroll, T.C., +, TCBB Nov.-Dec. 2020 2086-2097
- Greedy algorithms**
- Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. Yao, H., +, TCBB May-June 2020 777-787
- H**
- Hardware-software codesign**
- Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications. Gudur, V.Y., +, TCBB July-Aug. 2020 1198-1210
- Heuristic algorithms**
- A Branch Point on Differentiation Trajectory is the Bifurcating Event Revealed by Dynamical Network Biomarker Analysis of Single-Cell Data. Chen, Z., +, TCBB March-April 2020 366-375
 - A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations. Lecca, P., +, TCBB March-April 2020 469-482
 - An Efficient Approach Towards the Source-Target Control of Boolean Networks. Paul, S., +, TCBB Nov.-Dec. 2020 1932-1945

- MPGM: Scalable and Accurate Multiple Network Alignment.** *Kazemi, E., +, TCBB Nov.-Dec. 2020 2040-2052*
- Hidden Markov models**
- ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data. *Tan, R., +, TCBB May-June 2020 796-803*
- Hydrogen bonds**
- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*
- Hydrophobicity**
- PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*
- I**
- Image classification**
- Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*
- Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*
- Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020 1042-1055*
- Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020 1394-1405*
- Image matching**
- Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020 959-971*
- Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020 1042-1055*
- Image representation**
- Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*
- Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020 1042-1055*
- Image segmentation**
- Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020 959-971*
- Computerized Classification of Prostate Cancer Gleason Scores from Whole Slide Images. *Xu, H., +, TCBB Nov.-Dec. 2020 1871-1882*
- Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020 1394-1405*
- Image sequences**
- Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020 959-971*
- Immune system**
- Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. *Hu, L., +, TCBB Nov.-Dec. 2020 2017-2028*
- In vitro**
- Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. *Zhang, Q., +, TCBB March-April 2020 679-689*
- In vivo**
- Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. *Zhang, Q., +, TCBB March-April 2020 679-689*
- Indexes**
- Detection of Driver Modules with Rarely Mutated Genes in Cancers. *Li, F., +, TCBB March-April 2020 390-401*
- Efficient Mining Multi-Mers in a Variety of Biological Sequences. *Zhang, J., +, TCBB May-June 2020 949-958*
- Inference mechanisms**
- Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. *Ahmed, S.S., +, TCBB Jan.-Feb. 2020 56-70*
- Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020 858-867*
- Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions. *Pichene, M., +, TCBB Sept.-Oct. 2020 1691-1702*
- Modified Half-System Based Method for Reverse Engineering of Gene Regulatory Networks. *Khan, A., +, TCBB July-Aug. 2020 1303-1316*
- Preprocessing Sequence Coverage Data for More Precise Detection of Copy Number Variations. *Zare, F., +, TCBB May-June 2020 868-876*
- Using Unlabeled Data to Discover Bivariate Causality with Deep Restricted Boltzmann Machines. *Sokolovska, N., +, TCBB Jan.-Feb. 2020 358-364*
- Informatics**
- Approaching the One-Sided Exemplar Adjacency Number Problem. *Qingge, L., +, TCBB Nov.-Dec. 2020 1946-1954*
- Information entropy**
- Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. *Wong, K., +, TCBB Jan.-Feb. 2020 327-333*
- Information management**
- Rapid Reconstruction of Time-Varying Gene Regulatory Networks. *Pyne, S., +, TCBB Jan.-Feb. 2020 278-291*
- Inhibitors**
- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*
- Initial value problems**
- A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models. *Miyawaki-Kuwakado, A., +, TCBB Jan.-Feb. 2020 27-36*
- Instruction sets**
- Semiglobal Sequence Alignment with Gaps Using GPU. *Carroll, T.C., +, TCBB Nov.-Dec. 2020 2086-2097*
- Insulin**
- Data-Driven Robust Control for a Closed-Loop Artificial Pancreas. *Paoletti, N., +, TCBB Nov.-Dec. 2020 1981-1993*
- Integer linear programming**
- Approaching the One-Sided Exemplar Adjacency Number Problem. *Qingge, L., +, TCBB Nov.-Dec. 2020 1946-1954*
- Integer programming**
- imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020 1222-1230*
- IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020 938-948*
- Variable Neighborhood Search for Partitioning Sparse Biological Networks into the Maximum Edge-Weightedk-Plexes. *Grbic, M., +, TCBB Sept.-Oct. 2020 1822-1831*
- Integrated circuit modeling**
- FPGA Accelerated Analysis of Boolean Gene Regulatory Networks. *Manica, M., +, TCBB Nov.-Dec. 2020 2141-2147*
- Iterative methods**
- Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020 1394-1405*
- J**
- Java**
- Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020 1459-1473*
- K**
- Kalman filters**
- Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*
- Kidney**
- XGBoost Model for Chronic Kidney Disease Diagnosis. *Ogunleye, A., +, TCBB Nov.-Dec. 2020 2131-2140*
- Knowledge based systems**
- Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts. *Noriega-Atala, E., +, TCBB Nov.-Dec. 2020 1895-1906*
- Knowledge engineering**
- MPGM: Scalable and Accurate Multiple Network Alignment. *Kazemi, E., +, TCBB Nov.-Dec. 2020 2040-2052*

Knowledge representation languages

Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB. *Liu, J., +, TCBB Sept.-Oct. 2020 1504-1515*

L**Lab-on-a-chip**

Microarray-Based Quality Assessment as a Supporting Criterion for *de novo* Transcriptome Assembly Selection. *Carvajal-Lopez, P., +, TCBB Jan.-Feb. 2020 198-206*

Laplace equations

Multi-Domain Networks Association for Biological Data Using Block Signed Graph Clustering. *Liu, Y., +, TCBB March-April 2020 435-448*

Learning (artificial intelligence)

Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020 1605-1612*

Classification of Antibacterial Peptides Using Long Short-Term Memory Recurrent Neural Networks. *Youmans, M., +, TCBB July-Aug. 2020 1134-1140*

Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*

Deep Collaborative Filtering for Prediction of Disease Genes. *Zeng, X., +, TCBB Sept.-Oct. 2020 1639-1647*

Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*

Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020 1648-1659*

Drug Selection via Joint Push and Learning to Rank. *He, Y., +, TCBB Jan.-Feb. 2020 110-123*

Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting. *Lin, X., +, TCBB Sept.-Oct. 2020 1525-1534*

EL_LSTM: Prediction of DNA-Binding Residue from Protein Sequence by Combining Long Short-Term Memory and Ensemble Learning. *Zhou, J., +, TCBB Jan.-Feb. 2020 124-135*

Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*

Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes. *Ismailoglu, F., +, TCBB Jan.-Feb. 2020 347-353*

Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. *Bakhteh, S., +, TCBB May-June 2020 999-1009*

Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020 930-937*

Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition. *Li, L., +, TCBB May-June 2020 841-846*

Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA-miRNA Interactions. *Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524*

Novel Regularization Method for Biomarker Selection and Cancer Classification. *Liu, X., +, TCBB July-Aug. 2020 1329-1340*

On the Unreported-Profile-is-Negative Assumption for Predictive Cheminformatics. *Lan, C., +, TCBB July-Aug. 2020 1352-1363*

Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*

PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020 264-277*

Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. *Fu, L., +, TCBB Sept.-Oct. 2020 1721-1728*

Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*

Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020 1394-1405*

RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020 1741-1750*
Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation. *Kawano, K., +, TCBB Sept.-Oct. 2020 1762-1772*

Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*

SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*

Using Emulation to Engineer and Understand Simulations of Biological Systems. *Alden, K., +, TCBB Jan.-Feb. 2020 302-315*

Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information. *Li, J., +, TCBB Sept.-Oct. 2020 1546-1554*

Least squares approximations

Stepwise Tikhonov Regularisation: Application to the Prediction of HIV-1 Drug Resistance. *Delgado, R.A., +, TCBB Jan.-Feb. 2020 292-301*

Life sciences

Correction to “Identification of Novel Scaffolds with Dual Role as Antiepileptic and Anti-Breast Cancer”. *Rampogu, S., +, TCBB Jan.-Feb. 2020 365*

Linear programming

imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020 1222-1230*

IsoTree: A New Framework for *de novo* Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020 938-948*

PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrouee, S., +, TCBB Jan.-Feb. 2020 264-277*

Variable Neighborhood Search for Partitioning Sparse Biological Networks into the Maximum Edge-Weightedk-Plexes. *Grbic, M., +, TCBB Sept.-Oct. 2020 1822-1831*

Linguistics

Extracting Inter-Sentence Relations for Associating Biological Context with Events in Biomedical Texts. *Noriega-Atala, E., +, TCBB Nov.-Dec. 2020 1895-1906*

Schema Matching and Data Integration with Consistent Naming on Protein Crystallization Screens. *Shrestha, M., +, TCBB Nov.-Dec. 2020 2074-2085*

Liver

Sparse Reconstruction of Glucose Fluxes Using Continuous Glucose Monitors. *Al-Matouq, A.A., +, TCBB Sept.-Oct. 2020 1797-1809*

Logic gates

LSTM-Based End-to-End Framework for Biomedical Event Extraction. *Yu, X., +, TCBB Nov.-Dec. 2020 2029-2039*

Loss measurement

Gene Expressions, Hippocampal Volume Loss, and MMSE Scores in Computation of Progression and Pharmacologic Therapy Effects for Alzheimer's Disease. *Saribudak, A., +, TCBB March-April 2020 608-622*

Incorporating Prior Knowledge about Genetic Variants into the Analysis of Genetic Association Data: An Empirical Bayes Approach. *Karimnezhad, A., +, TCBB March-April 2020 635-646*

Lungs

An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer. *Song, J., +, TCBB May-June 2020 758-768*

Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*

Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. *Xuan, P., +, TCBB May-June 2020 1019-1031*

Lung cancer

Bounded Fuzzy Possibilistic Method Reveals Information about Lung Cancer through Analysis of Metabolomics. *Yazdani, H., +, TCBB March-April 2020 526-535*

M**Machine learning**

A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020 1858-1870*

- Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment. *Jing, X., +, TCBB Nov.-Dec. 2020 1918-1931*
 Classification of Patients with Coronary Microvascular Dysfunction. *Fodeh, S.J., +, TCBB March-April 2020 704-711*
 Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC). *Huang, D., +, TCBB Sept.-Oct. 2020 1474-1475*
 Post-Structuring Radiology Reports of Breast Cancer Patients for Clinical Quality Assurance. *Pathak, S., +, TCBB Nov.-Dec. 2020 1883-1894*
 Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. *Cao, Z., +, TCBB March-April 2020 657-667*
 Utilizing Deep Learning and Genome Wide Association Studies for Epistatic-Driven Preterm Birth Classification in African-American Women. *Fergus, P., +, TCBB March-April 2020 668-678*

Machine learning algorithms

- Ensembling of Gene Clusters Utilizing Deep Learning and Protein-Protein Interaction Information. *Dutta, P., +, TCBB Nov.-Dec. 2020 2005-2016*

Macromolecules

- miRTS: A Recommendation Algorithm for Predicting miRNA Targets. *Jiang, H., +, TCBB May-June 2020 1032-1041*

Mammography

- Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*

Markov processes

- Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020 959-971*

Mathematical model

- A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations. *Lecca, P., +, TCBB March-April 2020 469-482*

- Correction to “A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations”. *Lecca, P., +, TCBB May-June 2020 1092*

- Detection of Colorectal Carcinoma Based on Microbiota Analysis Using Generalized Regression Neural Networks and Nonlinear Feature Selection. *Arabameri, A., +, TCBB March-April 2020 547-557*

- FPGA Accelerated Analysis of Boolean Gene Regulatory Networks. *Manica, M., +, TCBB Nov.-Dec. 2020 2141-2147*

- Identifying Gene Network Rewiring Using Robust Differential Graphical Model with Multivariate-t-Distribution. *Yuan, R., +, TCBB March-April 2020 712-718*

- Structural Bistability Analysis of Flower-Shaped and Chain-Shaped Boolean Networks. *Azuma, S., +, TCBB Nov.-Dec. 2020 2098-2106*

Matrix algebra

- Accurately Detecting Protein Complexes by Graph Embedding and Combinig Functions with Interactions. *Yao, H., +, TCBB May-June 2020 777-787*

- On the Unreported-Profile-is-Negative Assumption for Predictive Cheminformatics. *Lan, C., +, TCBB July-Aug. 2020 1352-1363*

- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*

Matrix converters

- Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data. *Zhang, L., +, TCBB March-April 2020 376-389*

Matrix decomposition

- Clustering and Integrating of Heterogeneous Microbiome Data by Joint Symmetric Nonnegative Matrix Factorization with Laplacian Regularization. *Ma, Y., +, TCBB May-June 2020 788-795*

- HetRCNA: A Novel Method to Identify Recurrent Copy Number Alterations from Heterogeneous Tumor Samples Based on Matrix Decomposition Framework. *Xi, J., +, TCBB March-April 2020 422-434*

- Identifying lncRNA and mRNA Co-Expression Modules from Matched Expression Data in Ovarian Cancer. *Xiao, Q., +, TCBB March-April 2020 623-634*

- Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. *Xuan, P., +, TCBB May-June 2020 1019-1031*

- Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020 1671-1681*

- LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*

- NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. *Yu, G., +, TCBB Jan.-Feb. 2020 238-249*

- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*

- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*

- SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*

Measurement

- Deep Neural Networks for *In Situ* Hybridization Grid Completion and Clustering. *Li, Y., +, TCBB March-April 2020 536-546*

- SICOR: Subgraph Isomorphism Comparison of RNA Secondary Structures. *Schmidt, M., +, TCBB Nov.-Dec. 2020 2189-2195*

Media

- Oligo Design with Single Primer Binding Site for High Capacity DNA-Based Data Storage. *Wang, Y., +, TCBB Nov.-Dec. 2020 2176-2182*

Medical computing

- RFCM³: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. *Paul, S., +, TCBB Sept.-Oct. 2020 1729-1740*

- A Novel Approach to Detecting Epistasis using Random Sampling Regularisation. *Hind, J., +, TCBB Sept.-Oct. 2020 1535-1545*

- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020 1582-1594*

- An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer. *Song, J., +, TCBB May-June 2020 758-768*

- Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020 1605-1612*

- Deep Collaborative Filtering for Prediction of Disease Genes. *Zeng, X., +, TCBB Sept.-Oct. 2020 1639-1647*

- Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs. *Hu, H., +, TCBB May-June 2020 887-898*

- Drug Selection via Joint Push and Learning to Rank. *He, Y., +, TCBB Jan.-Feb. 2020 110-123*

- Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes. *Ismailoglu, F., +, TCBB Jan.-Feb. 2020 347-353*

- In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020 1010-1018*

- Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020 930-937*

- Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. *Xuan, P., +, TCBB May-June 2020 1019-1031*

- Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition. *Li, L., +, TCBB May-June 2020 841-846*

- Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020 1671-1681*

- MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data. *Zhao, L., +, TCBB Sept.-Oct. 2020 1682-1690*

- Optimal Bayesian Filtering for Biomarker Discovery: Performance and Robustness. *Foroughi pour, A., +, TCBB Jan.-Feb. 2020 250-263*

- PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*

- Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*

- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*

- Stepwise Tikhonov Regularisation: Application to the Prediction of HIV-1 Drug Resistance. *Delgado, R.A., +, TCBB Jan.-Feb. 2020* 292-301
- Using Unlabeled Data to Discover Bivariate Causality with Deep Restricted Boltzmann Machines. *Sokolovska, N., +, TCBB Jan.-Feb. 2020* 358-364
- Medical diagnosis**
- XGBoost Model for Chronic Kidney Disease Diagnosis. *Ogunleye, A., +, TCBB Nov.-Dec. 2020* 2131-2140
- Medical diagnostic computing**
- Constructing Disease Similarity Networks Based on Disease Module Theory. *Ni, P., +, TCBB May-June 2020* 906-915
- Medical image processing**
- Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020* 91-101
- Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020* 1394-1405
- Medical information systems**
- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020* 1582-1594
- Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition. *Li, L., +, TCBB May-June 2020* 841-846
- Medical signal detection**
- Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability. *Alshawafreh, M., +, TCBB May-June 2020* 1056-1067
- Medical signal processing**
- Low-Rank Joint Subspace Construction for Cancer Subtype Discovery. *Khan, A., +, TCBB July-Aug. 2020* 1290-1302
- Meetings**
- Algorithms for Computational Biology: Fifth Edition. *Martin-Vide, C., +, TCBB Jan.-Feb. 2020* 1
- Guest Editorial for Selected Papers from BIOKDD 2018 and DMBIH 2018. *Yan, D., +, TCBB Nov.-Dec. 2020* 1832-1834
- Guest Editorial for the 29th International Conference on Genome Informatics (GIW 2018). *Zheng, J., +, TCBB May-June 2020* 726-727
- Memory**
- Oligo Design with Single Primer Binding Site for High Capacity DNA-Based Data Storage. *Wang, Y., +, TCBB Nov.-Dec. 2020* 2176-2182
- Memory architecture**
- Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020* 1093-1104
- Message passing**
- High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020* 804-816
- Metabolomics**
- Bounded Fuzzy Possibilistic Method Reveals Information about Lung Cancer through Analysis of Metabolomics. *Yazdani, H., +, TCBB March-April 2020* 526-535
- Microorganisms**
- BRWMDA: Predicting Microbe-Disease Associations Based on Similarities and Bi-Random Walk on Disease and Microbe Networks. *Yan, C., +, TCBB Sept.-Oct. 2020* 1595-1604
- Detection of Colorectal Carcinoma Based on Microbiota Analysis Using Generalized Regression Neural Networks and Nonlinear Feature Selection. *Arabameri, A., +, TCBB March-April 2020* 547-557
- Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020* 858-867
- NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020* 1341-1351
- Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020* 828-840
- PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020* 1714-1720
- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020* 1751-1761
- Stepwise Tikhonov Regularisation: Application to the Prediction of HIV-1 Drug Resistance. *Delgado, R.A., +, TCBB Jan.-Feb. 2020* 292-301
- Microprocessor chips**
- Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020* 1093-1104
- Cache Friendly Optimisation of de Bruijn Graph Based Local Re-Assembly in Variant Calling. *Gamaarachchi, H., +, TCBB July-Aug. 2020* 1125-1133
- Microscopy**
- Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks. *Liu, G., +, TCBB Nov.-Dec. 2020* 1966-1980
- Minimization**
- Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020* 959-971
- Identifying “Many-to-Many” Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020* 165-176
- Modeling**
- A Gaussian Mixture-Model Exploiting Pathway Knowledge for Dissecting Cancer Heterogeneity. *Kapoor, R., +, TCBB March-April 2020* 459-468
- Molecular biophysics**
- (Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. *Chowdhury, H.A., +, TCBB July-Aug. 2020* 1154-1173
- RCFM³: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. *Paul, S., +, TCBB Sept.-Oct. 2020* 1729-1740
- A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models. *Miyawaki-Kuwakado, A., +, TCBB Jan.-Feb. 2020* 27-36
- A Supervised Ensemble Approach for Sensitive microRNA Target Prediction. *Maji, R.K., +, TCBB Jan.-Feb. 2020* 37-46
- Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. *Yao, H., +, TCBB May-June 2020* 777-787
- An Application of the Bayesian Periodicity Test to Identify Diurnal Rhythm Genes in the Brain. *Kocak, M., +, TCBB Jan.-Feb. 2020* 47-55
- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020* 1582-1594
- Bi-Level Error Correction for PacBio Long Reads. *Liu, Y., +, TCBB May-June 2020* 899-905
- BiModule: Biclique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules. *Pan, C., +, TCBB Jan.-Feb. 2020* 321-326
- BRWMDA: Predicting Microbe-Disease Associations Based on Similarities and Bi-Random Walk on Disease and Microbe Networks. *Yan, C., +, TCBB Sept.-Oct. 2020* 1595-1604
- Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature. *Shen, Z., +, TCBB Sept.-Oct. 2020* 1483-1492
- Causal Disturbance Analysis: A Novel Graph Centrality Based Method for Pathway Enrichment Analysis. *Yeganeh, P.N., +, TCBB Sept.-Oct. 2020* 1613-1624
- CaverDock: A Novel Method for the Fast Analysis of Ligand Transport. *Filipovic, J., +, TCBB Sept.-Oct. 2020* 1625-1638
- Classification of Antibacterial Peptides Using Long Short-Term Memory Recurrent Neural Networks. *Youmans, M., +, TCBB July-Aug. 2020* 1134-1140
- Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020* 972-980
- CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020* 1141-1153
- Constructive Prediction of Potential RNA Aptamers for a Protein Target. *Lee, W., +, TCBB Sept.-Oct. 2020* 1476-1482
- CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. *Kang, Q., +, TCBB May-June 2020* 981-989
- Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020* 1648-1659

- Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. *Ou-Yang, L., +, TCBB Nov.-Dec. 2020 2162-2169*
- Disruption of Protein Complexes from Weighted Complex Networks. *Habibi, M., +, TCBB Jan.-Feb. 2020 102-109*
- Efficient Mining Multi-Mers in a Variety of Biological Sequences. *Zhang, J., +, TCBB May-June 2020 949-958*
- EL_LSTM: Prediction of DNA-Binding Residue from Protein Sequence by Combining Long Short-Term Memory and Ensemble Learning. *Zhou, J., +, TCBB Jan.-Feb. 2020 124-135*
- Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections. *Som-In, S., +, TCBB May-June 2020 990-998*
- ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data. *Tan, R., +, TCBB May-June 2020 796-803*
- G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides. *Wang, S., +, TCBB May-June 2020 739-747*
- GaMRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020 149-157*
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*
- Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*
- Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes. *Ismailoglu, F., +, TCBB Jan.-Feb. 2020 347-353*
- Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. *Li, M., +, TCBB May-June 2020 817-827*
- Identification of Short Exons Disunited by a Short Intron in Eukaryotic DNA Regions. *Sharma, S., +, TCBB Sept.-Oct. 2020 1660-1670*
- imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020 1222-1230*
- Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020 858-867*
- In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020 1010-1018*
- Inference Attacks and Controls on Genotypes and Phenotypes for Individual Genomic Data. *He, Z., +, TCBB May-June 2020 930-937*
- Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. *Xuan, P., +, TCBB May-June 2020 1019-1031*
- Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020 1671-1681*
- Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*
- Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020 1253-1261*
- IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020 938-948*
- Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA–miRNA Interactions. *Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524*
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*
- LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*
- MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. *Wu, B., +, TCBB May-June 2020 847-857*
- Microarray-Based Quality Assessment as a Supporting Criterion for *de novo* Transcriptome Assembly Selection. *Carvajal-Lopez, P., +, TCBB Jan.-Feb. 2020 198-206*
- miRTS: A Recommendation Algorithm for Predicting miRNA Targets. *Jiang, H., +, TCBB May-June 2020 1032-1041*
- Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. *Acharya, S., +, TCBB Jan.-Feb. 2020 207-219*
- MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. *Li, T., +, TCBB Jan.-Feb. 2020 220-225*
- nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale. *Fassio, A.V., +, TCBB July-Aug. 2020 1317-1328*
- NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. *Yu, G., +, TCBB Jan.-Feb. 2020 238-249*
- NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*
- Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*
- PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*
- Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. *Fu, L., +, TCBB Sept.-Oct. 2020 1721-1728*
- Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*
- Prediction of TF-Binding Site by Inclusion of Higher Order Position Dependencies. *Zhou, J., +, TCBB July-Aug. 2020 1383-1393*
- RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020 1741-1750*
- Robust Recurrent CNV Detection in the Presence of Inter-Subject Variability. *Alshawafreh, M., +, TCBB May-June 2020 1056-1067*
- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*
- Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. *Zhang, G., +, TCBB May-June 2020 1068-1081*
- Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation. *Kawano, K., +, TCBB Sept.-Oct. 2020 1762-1772*
- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*
- SNECT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*
- Softeigen: Primers Design Web-Based Tool for MS-HRM Technique. *Pinzon-Reyes, E., +, TCBB Jan.-Feb. 2020 354-357*
- Stability Analysis of Biological Networks' Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*
- SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. *Yuan, X., +, TCBB May-June 2020 1082-1091*
- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
- Two New Heuristic Methods for Protein Model Quality Assessment. *Wang, W., +, TCBB July-Aug. 2020 1430-1439*
- Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020 1440-1450*
- United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*
- Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information. *Li, J., +, TCBB Sept.-Oct. 2020 1546-1554*
- Molecular configurations**
- Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature. *Shen, Z., +, TCBB Sept.-Oct. 2020 1483-1492*

Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020 1648-1659*

Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*

nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale. *Fassio, A.V., +, TCBB July-Aug. 2020 1317-1328*

PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*

RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020 1741-1750*

Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*

Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. *Zhang, G., +, TCBB May-June 2020 1068-1081*

TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*

Two New Heuristic Methods for Protein Model Quality Assessment. *Wang, W., +, TCBB July-Aug. 2020 1430-1439*

Molecular dynamics method

CaverDock: A Novel Method for the Fast Analysis of Ligand Transport. *Filipovic, J., +, TCBB Sept.-Oct. 2020 1625-1638*

High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*

Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*

Multi-agent systems

Using Emulation to Engineer and Understand Simulations of Biological Systems. *Alden, K., +, TCBB Jan.-Feb. 2020 302-315*

Multi-threading

An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. *Liao, X., +, TCBB May-June 2020 728-738*

MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. *Li, T., +, TCBB Jan.-Feb. 2020 220-225*

Multiprocessing systems

Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020 1093-1104*

High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*

Mutual information

Protein Complexes Identification with Family-Wise Error Rate Control. *He, Z., +, TCBB Nov.-Dec. 2020 2062-2073*

Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. *Shi, J., +, TCBB March-April 2020 449-458*

N

Naive Bayes methods

Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*

Nanomedicine

Feed-Forward and Feedback Control in Astrocytes for Ca²⁺-Based Molecular Communications Nanonetworks. *Barros, M.T., +, TCBB July-Aug. 2020 1174-1186*

Natural language processing

Classification of Patients with Coronary Microvascular Dysfunction. *Fodeh, S.J., +, TCBB March-April 2020 704-711*

Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition. *Li, L., +, TCBB May-June 2020 841-846*

Post-Structuring Radiology Reports of Breast Cancer Patients for Clinical Quality Assurance. *Pathak, S., +, TCBB Nov.-Dec. 2020 1883-1894*

Nearest neighbor methods

Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*

Network theory (graphs)

Disruption of Protein Complexes from Weighted Complex Networks. *Habibi, M., +, TCBB Jan.-Feb. 2020 102-109*

Stability Analysis of Biological Networks' Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*

United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*

Network topology

Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data. *Zhang, W., +, TCBB Nov.-Dec. 2020 2053-2061*

Neural networks

Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*

Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*

Deep Neural Networks for *In Situ* Hybridization Grid Completion and Clustering. *Li, Y., +, TCBB March-April 2020 536-546*

Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020 1648-1659*

Feed-Forward and Feedback Control in Astrocytes for Ca²⁺-Based Molecular Communications Nanonetworks. *Barros, M.T., +, TCBB July-Aug. 2020 1174-1186*

Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture. *Chakraborty, R., +, TCBB Nov.-Dec. 2020 2183-2188*

Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation. *Kawano, K., +, TCBB Sept.-Oct. 2020 1762-1772*

Neurons

A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020 1858-1870*

Multi-Domain Networks Association for Biological Data Using Block Signed Graph Clustering. *Liu, Y., +, TCBB March-April 2020 435-448*

Neurophysiology

An Application of the Bayesian Periodicity Test to Identify Diurnal Rhythm Genes in the Brain. *Kocak, M., +, TCBB Jan.-Feb. 2020 47-55*

Feed-Forward and Feedback Control in Astrocytes for Ca²⁺-Based Molecular Communications Nanonetworks. *Barros, M.T., +, TCBB July-Aug. 2020 1174-1186*

Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020 1671-1681*

Neuroscience

Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020 1835-1845*

Newton-Raphson method

A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models. *Miyawaki-Kuwakado, A., +, TCBB Jan.-Feb. 2020 27-36*

Next generation networking

Oligo Design with Single Primer Binding Site for High Capacity DNA-Based Data Storage. *Wang, Y., +, TCBB Nov.-Dec. 2020 2176-2182*

Nickel

Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. *Lei, X., +, TCBB March-April 2020 495-505*

Nonlinear differential equations

A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models. *Miyawaki-Kuwakado, A., +, TCBB Jan.-Feb. 2020 27-36*

Nuclear magnetic resonance

Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery. *Karakaslar, E.O., +, TCBB March-April 2020 719-725*

Numerical models

A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations. *Lecca, P., +, TCBB March-April 2020 469-482*

O**Object detection**

Detection and Recognition for Life State of Cell Cancer Using Two-Stage Cascade CNNs. *Hu, H., +, TCBB May-June 2020 887-898*

Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture. *Chakraborty, R., +, TCBB Nov.-Dec. 2020 2183-2188*

Occupational safety

Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*

Ontologies (artificial intelligence)

Constructing Disease Similarity Networks Based on Disease Module Theory. *Ni, P., +, TCBB May-June 2020 906-915*

GaMRed—Adaptive Filtering of High-Throughput Biological Data. *Marczyk, M., +, TCBB Jan.-Feb. 2020 149-157*

Identifying “Many-to-Many” Relationships between Gene-Expression Data and Drug-Response Data via Sparse Binary Matching. *Cai, J., +, TCBB Jan.-Feb. 2020 165-176*

Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB. *Liu, J., +, TCBB Sept.-Oct. 2020 1504-1515*

LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*

Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. *Acharya, S., +, TCBB Jan.-Feb. 2020 207-219*

NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. *Yu, G., +, TCBB Jan.-Feb. 2020 238-249*

SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*

Optimization

An Effective Solution for Large Scale Single Machine Total Weighted Tardiness Problem using Lunar Cycle Inspired Artificial Bee Colony Algorithm. *Sharma, N., +, TCBB Sept.-Oct. 2020 1573-1581*

Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. *Lei, X., +, TCBB March-April 2020 495-505*

ELF: Extract Landmark Features By Optimizing Topology Maintenance, Redundancy, and Specificity. *Feng, Z., +, TCBB March-April 2020 411-421*

Identifying lncRNA and mRNA Co-Expression Modules from Matched Expression Data in Ovarian Cancer. *Xiao, Q., +, TCBB March-April 2020 623-634*

Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020 1253-1261*

Stability Analysis of Biological Networks’ Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*

Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. *Zhang, G., +, TCBB Nov.-Dec. 2020 2119-2130*

Using Emulation to Engineer and Understand Simulations of Biological Systems. *Alden, K., +, TCBB Jan.-Feb. 2020 302-315*

Organizations

Deep Neural Networks for *In Situ* Hybridization Grid Completion and Clustering. *Li, Y., +, TCBB March-April 2020 536-546*

Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *Zhang, R., +, TCBB March-April 2020 647-656*

P**Pain**

Classification of Patients with Coronary Microvascular Dysfunction. *Fodeh, S.J., +, TCBB March-April 2020 704-711*

Pancreas

Data-Driven Robust Control for a Closed-Loop Artificial Pancreas. *Paoletti, N., +, TCBB Nov.-Dec. 2020 1981-1993*

Parallel algorithms

Fast de Bruijn Graph Compaction in Distributed Memory Environments. *Pan, T., +, TCBB Jan.-Feb. 2020 136-148*

High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*

Parallel machines

High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*

Parallel processing

Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020 1093-1104*

High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*

Parameter estimation

Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions. *Deng, Z., +, TCBB July-Aug. 2020 1231-1240*

Partial differential equations

Automated Cell Tracking Using Motion Prediction-Based Matching and Event Handling. *Boukari, F., +, TCBB May-June 2020 959-971*

Particle filtering (numerical methods)

Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*

Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions. *Deng, Z., +, TCBB July-Aug. 2020 1231-1240*

Particle swarm optimization

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Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. *Lei, X., +, TCBB March-April 2020 495-505*

Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections. *Som-In, S., +, TCBB May-June 2020 990-998*

Partitioning algorithms

Ensembling of Gene Clusters Utilizing Deep Learning and Protein-Protein Interaction Information. *Dutta, P., +, TCBB Nov.-Dec. 2020 2005-2016*

Pathogens

ASAPP: Architectural Similarity-Based Automated Pathway Prediction System and Its Application in Host-Pathogen Interactions. *Sen, R., +, TCBB March-April 2020 506-515*

Pathology

Bounded Fuzzy Possibilistic Method Reveals Information about Lung Cancer through Analysis of Metabolomics. *Yazdani, H., +, TCBB March-April 2020 526-535*

Computerized Classification of Prostate Cancer Gleason Scores from Whole Slide Images. *Xu, H., +, TCBB Nov.-Dec. 2020 1871-1882*

Patient diagnosis

NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*

Patient monitoring

Sparse Reconstruction of Glucose Fluxes Using Continuous Glucose Monitors. *Al-Matouq, A.A., +, TCBB Sept.-Oct. 2020 1797-1809*

Patient treatment

Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*

- In Silico Design and Experimental Validation of Combination Therapy for Pancreatic Cancer. *Vundavilli, H., +, TCBB May-June 2020 1010-1018*
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*
- NTSHMDA: Prediction of Human Microbe-Disease Association Based on Random Walk by Integrating Network Topological Similarity. *Luo, J., +, TCBB July-Aug. 2020 1341-1351*
- Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*
- Sparse Reconstruction of Glucose Fluxes Using Continuous Glucose Monitors. *Al-Matouq, A.A., +, TCBB Sept.-Oct. 2020 1797-1809*
- Pattern classification**
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- A Novel Approach to Detecting Epistasis using Random Sampling Regularisation. *Hind, J., +, TCBB Sept.-Oct. 2020 1535-1545*
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- Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*
- CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020 1141-1153*
- Constructing Disease Similarity Networks Based on Disease Module Theory. *Ni, P., +, TCBB May-June 2020 906-915*
- Deep Manifold Preserving Autoencoder for Classifying Breast Cancer Histopathological Images. *Feng, Y., +, TCBB Jan.-Feb. 2020 91-101*
- Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020 1648-1659*
- Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting. *Lin, X., +, TCBB Sept.-Oct. 2020 1525-1534*
- EL_LSTM: Prediction of DNA-Binding Residue from Protein Sequence by Combining Long Short-Term Memory and Ensemble Learning. *Zhou, J., +, TCBB Jan.-Feb. 2020 124-135*
- G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides. *Wang, S., +, TCBB May-June 2020 739-747*
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*
- Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes. *Ismailoglu, F., +, TCBB Jan.-Feb. 2020 347-353*
- Improving *de novo* Assembly Based on Read Classification. *Liao, X., +, TCBB Jan.-Feb. 2020 177-188*
- Inverse Projection Representation and Category Contribution Rate for Robust Tumor Recognition. *Yang, X., +, TCBB July-Aug. 2020 1262-1275*
- Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA-miRNA Interactions. *Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524*
- MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data. *Zhao, L., +, TCBB Sept.-Oct. 2020 1682-1690*
- Novel Regularization Method for Biomarker Selection and Cancer Classification. *Liu, X., +, TCBB July-Aug. 2020 1329-1340*
- Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*
- Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020 1394-1405*
- Pattern clustering**
- Clustering and Integrating of Heterogeneous Microbiome Data by Joint Symmetric Nonnegative Matrix Factorization with Laplacian Regularization. *Ma, Y., +, TCBB May-June 2020 788-795*
- DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data. *Yang, S., +, TCBB March-April 2020 558-565*
- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*
- Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. *Li, M., +, TCBB May-June 2020 817-827*
- Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*
- Low-Rank Joint Subspace Construction for Cancer Subtype Discovery. *Khan, A., +, TCBB July-Aug. 2020 1290-1302*
- Multi-Factored Gene-Gene Proximity Measures Exploiting Biological Knowledge Extracted from Gene Ontology: Application in Gene Clustering. *Acharya, S., +, TCBB Jan.-Feb. 2020 207-219*
- Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*
- PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. *Mazrrouee, S., +, TCBB Jan.-Feb. 2020 264-277*
- Querying Representative and Informative Super-Pixels for Filament Segmentation in Bioimages. *Shao, W., +, TCBB July-Aug. 2020 1394-1405*
- Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*
- SNect: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*
- The Use of Informed Priors in Bioclustering of Gene Expression with the Hierarchical Dirichlet Process. *Tercan, B., +, TCBB Sept.-Oct. 2020 1810-1821*
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- A Data-Driven Approach to Predict and Classify Epileptic Seizures from Brain-Wide Calcium Imaging Video Data. *Zheng, J., +, TCBB Nov.-Dec. 2020 1858-1870*
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- Perturbation methods**
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- ASAPP: Architectural Similarity-Based Automated Pathway Prediction System and Its Application in Host-Pathogen Interactions. *Sen, R., +, TCBB March-April 2020 506-515*
- EPMDA: Edge Perturbation Based Method for miRNA-Disease Association Prediction. *Dong, Y., +, TCBB Nov.-Dec. 2020 2170-2175*
- Phylogeny**
- Topological Metrizations of Trees, and New Quartet Methods of Tree Inference. *Rhodes, J.A., TCBB Nov-Dec. 2020 2107-2118*
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- Correction to “A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations”. *Lecca, P., +, TCBB May-June 2020 1092*
- Physics computing**
- High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020 804-816*
- Polymorphism**
- Class Balanced Multifactor Dimensionality Reduction to Detect Gene–Gene Interactions. *Yang, C., +, TCBB Jan.-Feb. 2020 71-81*
- Integration of Imaging (epi)Genomics Data for the Study of Schizophrenia Using Group Sparse Joint Nonnegative Matrix Factorization. *Wang, M., +, TCBB Sept.-Oct. 2020 1671-1681*
- Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020 1253-1261*
- Prediction algorithms**
- ASAPP: Architectural Similarity-Based Automated Pathway Prediction System and Its Application in Host-Pathogen Interactions. *Sen, R., +, TCBB March-April 2020 506-515*

- Rapid Reconstruction of Time-Varying Gene Regulatory Networks. *Pyne, S., +, TCBB Jan.-Feb. 2020 278-291*
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- Predictive models**
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- Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. *Wang, H., +, TCBB March-April 2020 587-598*
- EPMDA: Edge Perturbation Based Method for miRNA-Disease Association Prediction. *Dong, Y., +, TCBB Nov.-Dec. 2020 2170-2175*
- Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. *Hu, L., +, TCBB Nov.-Dec. 2020 2017-2028*
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- Pregnancy**
- Utilizing Deep Learning and Genome Wide Association Studies for Epistatic-Driven Preterm Birth Classification in African-American Women. *Fergus, P., +, TCBB March-April 2020 668-678*
- Principal component analysis**
- A Novel Edge Effect Detection Method for Real-Time Cellular Analyzer Using Functional Principal Component Analysis. *Guo, Q., +, TCBB Sept.-Oct. 2020 1563-1572*
- Identification of Short Exons Disunited by a Short Intron in Eukaryotic DNA Regions. *Sharma, S., +, TCBB Sept.-Oct. 2020 1660-1670*
- Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information. *Li, J., +, TCBB Sept.-Oct. 2020 1546-1554*
- Probabilistic logic**
- SICOR: Subgraph Isomorphism Comparison of RNA Secondary Structures. *Schmidt, M., +, TCBB Nov.-Dec. 2020 2189-2195*
- Probability**
- Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*
- Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions. *Pichene, M., +, TCBB Sept.-Oct. 2020 1691-1702*
- Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020 226-237*
- PASA: Identifying More Credible Structural Variants of Hedou12. *Jia, H., +, TCBB Sept.-Oct. 2020 1493-1503*
- Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. *Zhang, G., +, TCBB May-June 2020 1068-1081*
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*
- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
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- Probability density function**
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- Prostate cancer**
- Computerized Classification of Prostate Cancer Gleason Scores from Whole Slide Images. *Xu, H., +, TCBB Nov.-Dec. 2020 1871-1882*
- Protein sequence**
- Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment. *Jing, X., +, TCBB Nov.-Dec. 2020 1918-1931*
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- Proteins**
- Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. *Yao, H., +, TCBB May-June 2020 777-787*
- An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020 1582-1594*
- Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. *Lei, X., +, TCBB March-April 2020 495-505*
- ASAPP: Architectural Similarity-Based Automated Pathway Prediction System and Its Application in Host-Pathogen Interactions. *Sen, R., +, TCBB March-April 2020 506-515*
- Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks. *Liu, G., +, TCBB Nov.-Dec. 2020 1966-1980*
- Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature. *Shen, Z., +, TCBB Sept.-Oct. 2020 1483-1492*
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- CGIDLA: Developing the Web Server for CpG Island Related Density and LAUPs (Lineage-Associated Underrepresented Permutations) Study. *Xiao, M., +, TCBB Nov.-Dec. 2020 2148-2154*
- Classification of Antibacterial Peptides Using Long Short-Term Memory Recurrent Neural Networks. *Youmans, M., +, TCBB July-Aug. 2020 1134-1140*
- Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*
- Connectivity Significance for Disease Gene Prioritization in an Expanding Universe. *Petti, M., +, TCBB Nov.-Dec. 2020 2155-2161*
- Constructing Disease Similarity Networks Based on Disease Module Theory. *Ni, P., +, TCBB May-June 2020 906-915*
- Constructive Prediction of Potential RNA Aptamers for a Protein Target. *Lee, W., +, TCBB Sept.-Oct. 2020 1476-1482*
- Deep Robust Framework for Protein Function Prediction Using Variable-Length Protein Sequences. *Ranjan, A., +, TCBB Sept.-Oct. 2020 1648-1659*
- Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. *Wong, K., +, TCBB Jan.-Feb. 2020 327-333*
- Detection of Driver Modules with Rarely Mutated Genes in Cancers. *Li, F., +, TCBB March-April 2020 390-401*
- Disruption of Protein Complexes from Weighted Complex Networks. *Hadibi, M., +, TCBB Jan.-Feb. 2020 102-109*
- Drug Side-Effect Profiles Prediction: From Empirical to Structural Risk Minimization. *Jiang, H., +, TCBB March-April 2020 402-410*
- Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting. *Lin, X., +, TCBB Sept.-Oct. 2020 1525-1534*
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- EL_LSTM: Prediction of DNA-Binding Residue from Protein Sequence by Combining Long Short-Term Memory and Ensemble Learning. *Zhou, J., +, TCBB Jan.-Feb. 2020 124-135*
- Enhancing of Particle Swarm Optimization Based Method for Multiple Motifs Detection in DNA Sequences Collections. *Som-In, S., +, TCBB May-June 2020 990-998*
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- Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*
- Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications. *Gudur, V.Y., +, TCBB July-Aug. 2020 1198-1210*
- Heterogeneous Domain Adaptation for IHC Classification of Breast Cancer Subtypes. *Ismailoglu, F., +, TCBB Jan.-Feb. 2020 347-353*
- Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. *Li, M., +, TCBB May-June 2020 817-827*
- Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. *Hu, L., +, TCBB Nov.-Dec. 2020 2017-2028*
- Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA–miRNA Interactions. *Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524*
- Local Similarity Matrix for Cysteine Disulfide Connectivity Prediction from Protein Sequences. *Mapes, N., +, TCBB July-Aug. 2020 1276-1289*
- LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*
- LSTM-Based End-to-End Framework for Biomedical Event Extraction. *Yu, X., +, TCBB Nov.-Dec. 2020 2029-2039*
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- nAPOLI: A Graph-Based Strategy to Detect and Visualize Conserved Protein-Ligand Interactions in Large-Scale. *Fassio, A.V., +, TCBB July-Aug. 2020 1317-1328*
- NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. *Yu, G., +, TCBB Jan.-Feb. 2020 238-249*
- Oscillatory Dynamics of p53-Mdm2 Circuit in Response to DNA Damage Caused by Ionizing Radiation. *Zhang, Y., +, TCBB Sept.-Oct. 2020 1703-1713*
- Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*
- PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*
- Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data. *Zhang, W., +, TCBB Nov.-Dec. 2020 2053-2061*
- Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*
- Protein Complexes Identification with Family-Wise Error Rate Control. *He, Z., +, TCBB Nov.-Dec. 2020 2062-2073*
- RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020 1741-1750*
- Schema Matching and Data Integration with Consistent Naming on Protein Crystallization Screens. *Shrestha, M., +, TCBB Nov.-Dec. 2020 2074-2085*
- Screening Pipeline for Flavivirus Based Inhibitors for Zika Virus NS1. *Raza, S., +, TCBB Sept.-Oct. 2020 1751-1761*
- Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. *Zhang, G., +, TCBB May-June 2020 1068-1081*
- Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation. *Kawano, K., +, TCBB Sept.-Oct. 2020 1762-1772*
- SL²MF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. *Liu, Y., +, TCBB May-June 2020 748-757*
- Stability Analysis of Biological Networks' Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*
- TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*
- Two New Heuristic Methods for Protein Model Quality Assessment. *Wang, W., +, TCBB July-Aug. 2020 1430-1439*
- Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. *Zhang, G., +, TCBB Nov.-Dec. 2020 2119-2130*
- Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020 1440-1450*
- United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*
- Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information. *Li, J., +, TCBB Sept.-Oct. 2020 1546-1554*
- Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. *Zhang, Q., +, TCBB March-April 2020 679-689*
- WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. *Mallik, S., +, TCBB March-April 2020 690-703*
- Protocols**
- SICOR: Subgraph Isomorphism Comparison of RNA Secondary Structures. *Schmidt, M., +, TCBB Nov.-Dec. 2020 2189-2195*
- Public domain software**
- A Note on GRegNetSim: A Tool for the Discrete Simulation and Analysis of Genetic Regulatory Networks. *Ganor, D., +, TCBB Jan.-Feb. 2020 316-320*
- Q**
- Quality assurance**
- Post-Structuring Radiology Reports of Breast Cancer Patients for Clinical Quality Assurance. *Pathak, S., +, TCBB Nov.-Dec. 2020 1883-1894*
- Quality control**
- Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools. *Chowdhury, H.A., +, TCBB March-April 2020 566-586*
- Query processing**
- Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020 1459-1473*
- R**
- Radio frequency**
- Detection of Colorectal Carcinoma Based on Microbiota Analysis Using Generalized Regression Neural Networks and Nonlinear Feature Selection. *Arabameri, A., +, TCBB March-April 2020 547-557*
- Radiology**
- Post-Structuring Radiology Reports of Breast Cancer Patients for Clinical Quality Assurance. *Pathak, S., +, TCBB Nov.-Dec. 2020 1883-1894*
- Random forests**
- Constructive Prediction of Potential RNA Aptamers for a Protein Target. *Lee, W., +, TCBB Sept.-Oct. 2020 1476-1482*
- Random processes**
- A Novel Approach to Detecting Epistasis using Random Sampling Regularisation. *Hind, J., +, TCBB Sept.-Oct. 2020 1535-1545*
- Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions. *Pichene, M., +, TCBB Sept.-Oct. 2020 1691-1702*
- Random variables**
- Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. *Shi, J., +, TCBB March-April 2020 449-458*
- Reactive power**
- A Branch Point on Differentiation Trajectory is the Bifurcating Event Revealed by Dynamical Network Biomarker Analysis of Single-Cell Data. *Chen, Z., +, TCBB March-April 2020 366-375*
- Recommender systems**
- miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. *Jiang, H., +, TCBB May-June 2020 1032-1041*
- Reconfigurable architectures**
- Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications. *Gudur, V.Y., +, TCBB July-Aug. 2020 1198-1210*

Recurrent neural networks

Classification of Antibacterial Peptides Using Long Short-Term Memory Recurrent Neural Networks. *Youmans, M., +, TCBB July-Aug. 2020 1134-1140*

Redundancy

ELF: Extract Landmark Features By Optimizing Topology Maintenance, Redundancy, and Specificity. *Feng, Z., +, TCBB March-April 2020 411-421*

Protein Complexes Identification with Family-Wise Error Rate Control. *He, Z., +, TCBB Nov.-Dec. 2020 2062-2073*

Regression analysis

Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. *Bakhteh, S., +, TCBB May-June 2020 999-1009*

Regulators

Rapid Reconstruction of Time-Varying Gene Regulatory Networks. *Pyne, S., +, TCBB Jan.-Feb. 2020 278-291*

Reverse engineering

Modified Half-System Based Method for Reverse Engineering of Gene Regulatory Networks. *Khan, A., +, TCBB July-Aug. 2020 1303-1316*

RNA

(Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. *Chowdhury, H.A., +, TCBB July-Aug. 2020 1154-1173*

RFCM³: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. *Paul, S., +, TCBB Sept.-Oct. 2020 1729-1740*

A Supervised Ensemble Approach for Sensitive microRNA Target Prediction. *Maji, R.K., +, TCBB Jan.-Feb. 2020 37-46*

Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*

BiModule: Biclique Modularity Strategy for Identifying Transcription Factor and microRNA Co-Regulatory Modules. *Pan, C., +, TCBB Jan.-Feb. 2020 321-326*

BRWMDA: Predicting Microbe-Disease Associations Based on Similarities and Bi-Random Walk on Disease and Microbe Networks. *Yan, C., +, TCBB Sept.-Oct. 2020 1595-1604*

Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature. *Shen, Z., +, TCBB Sept.-Oct. 2020 1483-1492*

Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*

Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data. *Zhang, L., +, TCBB March-April 2020 376-389*

Constructive Prediction of Potential RNA Aptamers for a Protein Target. *Lee, W., +, TCBB Sept.-Oct. 2020 1476-1482*

DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data. *Yang, S., +, TCBB March-April 2020 558-565*

Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools. *Chowdhury, H.A., +, TCBB March-April 2020 566-586*

Efficient Mining Multi-Mers in a Variety of Biological Sequences. *Zhang, J., +, TCBB May-June 2020 949-958*

ELF: Extract Landmark Features By Optimizing Topology Maintenance, Redundancy, and Specificity. *Feng, Z., +, TCBB March-April 2020 411-421*

Gene Regulatory Relationship Mining Using Improved Three-Phase Dependency Analysis Approach. *Liu, J., +, TCBB Jan.-Feb. 2020 339-346*

Improving the Inference of Co-Occurrence Networks in the Bovine Rumen Microbiome. *Zheng, H., +, TCBB May-June 2020 858-867*

Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. *Xuan, P., +, TCBB May-June 2020 1019-1031*

IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020 938-948*

Learning Multimodal Networks From Heterogeneous Data for Prediction of lncRNA-miRNA Interactions. *Hu, P., +, TCBB Sept.-Oct. 2020 1516-1524*

LPGNMF: Predicting Long Non-Coding RNA and Protein Interaction Using Graph Regularized Nonnegative Matrix Factorization. *Zhang, T., +, TCBB Jan.-Feb. 2020 189-197*

Microarray-Based Quality Assessment as a Supporting Criterion for *de novo* Transcriptome Assembly Selection. *Carvajal-Lopez, P., +, TCBB Jan.-Feb. 2020 198-206*

miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. *Jiang, H., +, TCBB May-June 2020 1032-1041*

Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture. *Chakraborty, R., +, TCBB Nov.-Dec. 2020 2183-2188*

RNA-Protein Binding Sites Prediction via Multi Scale Convolutional Gated Recurrent Unit Networks. *Shen, Z., +, TCBB Sept.-Oct. 2020 1741-1750*

SICOR: Subgraph Isomorphism Comparison of RNA Secondary Structures. *Schmidt, M., +, TCBB Nov.-Dec. 2020 2189-2195*

Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *Li, X., +, TCBB Sept.-Oct. 2020 1773-1784*

SNeCT: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*

Robots

Active Vision and Surface Reconstruction for 3D Plant Shoot Modelling. *Gibbs, J.A., +, TCBB Nov.-Dec. 2020 1907-1917*

Robust control

Data-Driven Robust Control for a Closed-Loop Artificial Pancreas. *Paoletti, N., +, TCBB Nov.-Dec. 2020 1981-1993*

S**Sampling methods**

A Novel Approach to Detecting Epistasis using Random Sampling Regularisation. *Hind, J., +, TCBB Sept.-Oct. 2020 1535-1545*

Search problems

An Effective Solution for Large Scale Single Machine Total Weighted Tardiness Problem using Lunar Cycle Inspired Artificial Bee Colony Algorithm. *Sharma, N., +, TCBB Sept.-Oct. 2020 1573-1581*

Intra-Cluster Distance Minimization in DNA Methylation Analysis Using an Advanced Tabu-Based Iterativek-Medoids Clustering Algorithm (T-CLUST). *Damgacioglu, H., +, TCBB July-Aug. 2020 1241-1252*

Introducing Heuristic Information Into Ant Colony Optimization Algorithm for Identifying Epistasis. *Sun, Y., +, TCBB July-Aug. 2020 1253-1261*

Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020 226-237*

Stability Analysis of Biological Networks' Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*

Variable Neighborhood Search for Partitioning Sparse Biological Networks into the Maximum Edge-Weightedk-Plexes. *Grbic, M., +, TCBB Sept.-Oct. 2020 1822-1831*

Self-organizing feature maps

Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*

Semantics

Extracting Biomedical Events with Parallel Multi-Pooling Convolutional Neural Networks. *Li, L., +, TCBB March-April 2020 599-607*

LSTM-Based End-to-End Framework for Biomedical Event Extraction. *Yu, X., +, TCBB Nov.-Dec. 2020 2029-2039*

Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data. *Zhang, W., +, TCBB Nov.-Dec. 2020 2053-2061*

Sensitivity

Dual-Layer Strengthened Collaborative Topic Regression Modeling for Predicting Drug Sensitivity. *Wang, H., +, TCBB March-April 2020 587-598*

Sensitivity analysis

A Promising Method for Calculating True Steady-State Metabolite Concentrations in Large-Scale Metabolic Reaction Network Models. *Miyawaki-Kuwakado, A., +, TCBB Jan.-Feb. 2020 27-36*

Sequences

Improving *de novo* Assembly Based on Read Classification. *Liao, X., +, TCBB Jan.-Feb. 2020 177-188*

PASA: Identifying More Credible Structural Variants of Hedou12. *Jia, H., +, TCBB Sept.-Oct. 2020 1493-1503*

Sequential analysis

Comparison of Computational Methods for Imputing Single-Cell RNA-Sequencing Data. *Zhang, L., +, TCBB March-April 2020* 376-389

Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools. *Chowdhury, H.A., +, TCBB March-April 2020* 566-586

Oligo Design with Single Primer Binding Site for High Capacity DNA-Based Data Storage. *Wang, Y., +, TCBB Nov.-Dec. 2020* 2176-2182

Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. *Zhang, Q., +, TCBB March-April 2020* 679-689

Set theory

Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. *Bakhsh, S., +, TCBB May-June 2020* 999-1009

Identifying TF Binding Motifs from a Partial Set of Target Genes and its Application to Regulatory Network Inference. *Zhao, G., +, TCBB July-Aug. 2020* 1211-1221

Shape recognition

Identifying Gene Network Rewiring Using Robust Differential Graphical Model with Multivariate-t-Distribution. *Yuan, R., +, TCBB March-April 2020* 712-718

Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020* 1042-1055

Shared memory systems

Fast de Bruijn Graph Compaction in Distributed Memory Environments. *Pan, T., +, TCBB Jan.-Feb. 2020* 136-148

Simulation

Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data. *Zhang, W., +, TCBB Nov.-Dec. 2020* 2053-2061

Single machine scheduling

An Effective Solution for Large Scale Single Machine Total Weighted Tardiness Problem using Lunar Cycle Inspired Artificial Bee Colony Algorithm. *Sharma, N., +, TCBB Sept.-Oct. 2020* 1573-1581

Sleep apnea

Deep Learning for Automated Feature Discovery and Classification of Sleep Stages. *Sokolovsky, M., +, TCBB Nov.-Dec. 2020* 1835-1845

Software algorithms

Approaching the One-Sided Exemplar Adjacency Number Problem. *Qingge, L., +, TCBB Nov.-Dec. 2020* 1946-1954

Topological Metrizations of Trees, and New Quartet Methods of Tree Inference. *Rhodes, J.A., TCBB Nov.-Dec. 2020* 2107-2118

Software libraries

Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020* 1459-1473

Software packages

Fast Short Read De-Novo Assembly Using Overlap-Layout-Consensus Approach. *Bayat, A., +, TCBB Jan.-Feb. 2020* 334-338

High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. *Peng, S., +, TCBB May-June 2020* 804-816

Solid modeling

Active Vision and Surface Reconstruction for 3D Plant Shoot Modelling. *Gibbs, J.A., +, TCBB Nov.-Dec. 2020* 1907-1917

Classification of Patients with Coronary Microvascular Dysfunction. *Fodeh, S.J., +, TCBB March-April 2020* 704-711

Sorting

Heuristics for the Reversal and Transposition Distance Problem. *Brito, K.L., +, TCBB Jan.-Feb. 2020* 2-13

Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *Li, X., +, TCBB Jan.-Feb. 2020* 226-237

Source code (software)

Bi-Level Error Correction for PacBio Long Reads. *Liu, Y., +, TCBB May-June 2020* 899-905

Special issues and sections

Algorithms for Computational Biology: Fifth Edition. *Martin-Vide, C., +, TCBB Jan.-Feb. 2020* 1

Guest Editorial for Selected Papers from BIOKDD 2018 and DMBIH 2018. *Yan, D., +, TCBB Nov.-Dec. 2020* 1832-1834

Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC). *Huang, D., +, TCBB Sept.-Oct. 2020* 1474-1475

Guest Editorial for the 29th International Conference on Genome Informatics (GIW 2018). *Zheng, J., +, TCBB May-June 2020* 726-727

Spectroscopy

Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery. *Karakaslar, E.O., +, TCBB March-April 2020* 719-725

Splines (mathematics)

Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020* 1042-1055

SQL

Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020* 1459-1473

State estimation

Two-Stage Distance Feature-based Optimization Algorithm for *De novo* Protein Structure Prediction. *Zhang, G., +, TCBB Nov.-Dec. 2020* 2119-2130

Statistical analysis

An Efficient Algorithm for Identifying Mutated Subnetworks Associated with Survival in Cancer. *Sarkar, A., +, TCBB Sept.-Oct. 2020* 1582-1594

An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. *Liao, X., +, TCBB May-June 2020* 728-738

Causal Disturbance Analysis: A Novel Graph Centrality Based Method for Pathway Enrichment Analysis. *Yeganeh, P.N., +, TCBB Sept.-Oct. 2020* 1613-1624

Class Balanced Multifactor Dimensionality Reduction to Detect Gene-Gene Interactions. *Yang, C., +, TCBB Jan.-Feb. 2020* 71-81

MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. *Wu, B., +, TCBB May-June 2020* 847-857

Microarray-Based Quality Assessment as a Supporting Criterion for *de novo* Transcriptome Assembly Selection. *Carvajal-Lopez, P., +, TCBB Jan.-Feb. 2020* 198-206

PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020* 1714-1720

Statistical distributions

Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions. *Deng, Z., +, TCBB July-Aug. 2020* 1231-1240

Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions. *Pichene, M., +, TCBB Sept.-Oct. 2020* 1691-1702

Novel Regularization Method for Biomarker Selection and Cancer Classification. *Liu, X., +, TCBB July-Aug. 2020* 1329-1340

Using Emulation to Engineer and Understand Simulations of Biological Systems. *Alden, K., +, TCBB Jan.-Feb. 2020* 302-315

Statistical testing

Low-Rank Joint Subspace Construction for Cancer Subtype Discovery. *Khan, A., +, TCBB July-Aug. 2020* 1290-1302

Stochastic processes

A Reaction-Based Model of the State Space of Chemical Reaction Systems Enables Efficient Simulations. *Lecca, P., +, TCBB March-April 2020* 469-482

Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020* 1105-1114

Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions. *Deng, Z., +, TCBB July-Aug. 2020* 1231-1240

Storage management

Accelerating Sequence Alignments Based on FM-Index Using the Intel KNL Processor. *Herruzo, J.M., +, TCBB July-Aug. 2020* 1093-1104

String matching

Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications. *Gudur, V.Y., +, TCBB July-Aug. 2020* 1198-1210

Seq2seq Fingerprint with Byte-Pair Encoding for Predicting Changes in Protein Stability upon Single Point Mutation. *Kawano, K., +, TCBB Sept.-Oct. 2020* 1762-1772

Substrates

Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. *Hu, L., +, TCBB Nov.-Dec. 2020 2017-2028*

Sugar

Sparse Reconstruction of Glucose Fluxes Using Continuous Glucose Monitors. *Al-Matouq, A.A., +, TCBB Sept.-Oct. 2020 1797-1809*

Supervised learning

A Supervised Ensemble Approach for Sensitive microRNA Target Prediction. *Maji, R.K., +, TCBB Jan.-Feb. 2020 37-46*

Support vector machines

A Network-Based Comparison Between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso. *Shahdoust, M., +, TCBB Sept.-Oct. 2020 1555-1562*

Bioimage-Based Prediction of Protein Subcellular Location in Human Tissue with Ensemble Features and Deep Networks. *Liu, G., +, TCBB Nov.-Dec. 2020 1966-1980*

Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. *Wang, L., +, TCBB May-June 2020 972-980*

Deep Learning for Plant Species Classification Using Leaf Vein Morphometric. *Tan, J.W., +, TCBB Jan.-Feb. 2020 82-90*

Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. *Wong, K., +, TCBB Jan.-Feb. 2020 327-333*

Drug Side-Effect Profiles Prediction: From Empirical to Structural Risk Minimization. *Jiang, H., +, TCBB March-April 2020 402-410*

Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting. *Lin, X., +, TCBB Sept.-Oct. 2020 1525-1534*

Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). *Rahman, M.A., +, TCBB May-June 2020 828-840*

PredictFP2: A New Computational Model to Predict Fusion Peptide Domain in All Retroviruses. *Wu, S., +, TCBB Sept.-Oct. 2020 1714-1720*

Predicting DNA Methylation States with Hybrid Information Based Deep-Learning Model. *Fu, L., +, TCBB Sept.-Oct. 2020 1721-1728*

Prediction of DNA-Binding Residues in Local Segments of Protein Sequences with Fuzzy Cognitive Maps. *Amirkhani, A., +, TCBB July-Aug. 2020 1372-1382*

Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. *Cao, Z., +, TCBB March-April 2020 657-667*

TargetDBP: Accurate DNA-Binding Protein Prediction Via Sequence-Based Multi-View Feature Learning. *Hu, J., +, TCBB July-Aug. 2020 1419-1429*

Using Weighted Extreme Learning Machine Combined With Scale-Invariant Feature Transform to Predict Protein-Protein Interactions From Protein Evolutionary Information. *Li, J., +, TCBB Sept.-Oct. 2020 1546-1554*

Surface reconstruction

Active Vision and Surface Reconstruction for 3D Plant Shoot Modelling. *Gibbs, J.A., +, TCBB Nov.-Dec. 2020 1907-1917*

Surgery

Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery. *Karakaslar, E.O., +, TCBB March-April 2020 719-725*

Symmetric matrices

BiClusO: A Novel Biclustering Approach and Its Application to Species-VOC Relational Data. *Karim, M.B., +, TCBB Nov.-Dec. 2020 1955-1965*

System-on-chip

Hardware-Software Codesign Based Accelerated and Reconfigurable Methodology for String Matching in Computational Bioinformatics Applications. *Gudur, V.Y., +, TCBB July-Aug. 2020 1198-1210*

T**Temporal logic**

Basins of Attraction, Commitment Sets, and Phenotypes of Boolean Networks. *Klarner, H., +, TCBB July-Aug. 2020 1115-1124*

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Tensors

SNect: Scalable Network Constrained Tucker Decomposition for Multi-Platform Data Profiling. *Choi, D., +, TCBB Sept.-Oct. 2020 1785-1796*

Testing

Incorporating Prior Knowledge about Genetic Variants into the Analysis of Genetic Association Data: An Empirical Bayes Approach. *Karimnezhad, A., +, TCBB March-April 2020 635-646*

Text analysis

Integrating Language Model and Reading Control Gate in BLSTM-CRF for Biomedical Named Entity Recognition. *Li, L., +, TCBB May-June 2020 841-846*

Three-dimensional displays

Active Vision and Surface Reconstruction for 3D Plant Shoot Modelling. *Gibbs, J.A., +, TCBB Nov.-Dec. 2020 1907-1917*

Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *Zhang, R., +, TCBB March-April 2020 647-656*

Throughput

Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data. *Zhang, W., +, TCBB Nov.-Dec. 2020 2053-2061*

Time complexity

Approximate Graph Edit Distance in Quadratic Time. *Riesen, K., +, TCBB March-April 2020 483-494*

Time series

Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. *Bahadorinejad, A., +, TCBB July-Aug. 2020 1105-1114*

Time series analysis

Rapid Reconstruction of Time-Varying Gene Regulatory Networks. *Pyne, S., +, TCBB Jan.-Feb. 2020 278-291*

Tissue engineering

Understanding Protein Networks Using Vester's Sensitivity Model. *Moreno, L.A., +, TCBB July-Aug. 2020 1440-1450*

Tobacco products

Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*

Topology

ELF: Extract Landmark Features By Optimizing Topology Maintenance, Redundancy, and Specificity. *Feng, Z., +, TCBB March-April 2020 411-421*

Stability Analysis of Biological Networks' Diffusion State. *Altuntas, V., +, TCBB July-Aug. 2020 1406-1418*

United Neighborhood Closeness Centrality and Orthology for Predicting Essential Proteins. *Li, G., +, TCBB July-Aug. 2020 1451-1458*

Toxicology

A Novel Edge Effect Detection Method for Real-Time Cellular Analyzer Using Functional Principal Component Analysis. *Guo, Q., +, TCBB Sept.-Oct. 2020 1563-1572*

Potential Effect of Tobacco Consumption through Smoking and Chewing Tobacco on IL1beta Protein Expression in Chronic Periodontitis Patients: In Silico Molecular Docking Study. *Majumder, P., +, TCBB July-Aug. 2020 1364-1371*

Training data

Correction to "Identification of Novel Scaffolds with Dual Role as Antiepileptic and Anti-Breast Cancer". *Rampogu, S., +, TCBB Jan.-Feb. 2020 365 Deep Neural Networks for In Situ Hybridization Grid Completion and Clustering. Li, Y., +, TCBB March-April 2020 536-546*

Predicting MicroRNA Sequence Using CNN and LSTM Stacked in Seq2Seq Architecture. *Chakraborty, R., +, TCBB Nov.-Dec. 2020 2183-2188*

Trajectory

A Branch Point on Differentiation Trajectory is the Bifurcating Event Revealed by Dynamical Network Biomarker Analysis of Single-Cell Data. *Chen, Z., +, TCBB March-April 2020 366-375*

Transmission line matrix methods

SICOR: Subgraph Isomorphism Comparison of RNA Secondary Structures.
Schmidt, M., +, TCBB Nov.-Dec. 2020 2189-2195

Tree searching

Faster Exact Computation of rSPR Distance via Better Approximation.
Chen, Z., +, TCBB May-June 2020 916-929

Trees (mathematics)

CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. *Kang, Q., +, TCBB May-June 2020 981-989*

Faster Exact Computation of rSPR Distance via Better Approximation.
Chen, Z., +, TCBB May-June 2020 916-929

Generation of Level- k LGT Networks. *Pons, J.C., +, TCBB Jan.-Feb. 2020 158-164*

imPhy: Imputing Phylogenetic Trees with Missing Information Using Mathematical Programming. *Yasui, N., +, TCBB July-Aug. 2020 1222-1230*

IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. *Zhao, J., +, TCBB May-June 2020 938-948*

Mining Relationships among Multiple Entities in Biological Networks.
Peng, J., +, TCBB May-June 2020 769-776

Modeling Variability in Populations of Cells Using Approximated Multivariate Distributions. *Pichene, M., +, TCBB Sept.-Oct. 2020 1691-1702*

Polynomial-Time Algorithms for Phylogenetic Inference Problems Involving Duplication and Reticulation. *van Iersel, L., +, TCBB Jan.-Feb. 2020 14-26*

Tumors

RFCM³: Computational Method for Identification of miRNA-mRNA Regulatory Modules in Cervical Cancer. *Paul, S., +, TCBB Sept.-Oct. 2020 1729-1740*

A Network-Based Comparison Between Molecular Apocrine Breast Cancer Tumor and Basal and Luminal Tumors by Joint Graphical Lasso. *Shahdoust, M., +, TCBB Sept.-Oct. 2020 1555-1562*

Capsule Network Based Modeling of Multi-omics Data for Discovery of Breast Cancer-Related Genes. *Peng, C., +, TCBB Sept.-Oct. 2020 1605-1612*

Computerized Classification of Prostate Cancer Gleason Scores from Whole Slide Images. *Xu, H., +, TCBB Nov.-Dec. 2020 1871-1882*

CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples Using Sequence Data. *Yuan, X., +, TCBB July-Aug. 2020 1141-1153*

Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. *Hu, F., +, TCBB July-Aug. 2020 1187-1197*

HetRCNA: A Novel Method to Identify Recurrent Copy Number Alterations from Heterogeneous Tumor Samples Based on Matrix Decomposition Framework. *Xi, J., +, TCBB March-April 2020 422-434*

Inverse Projection Representation and Category Contribution Rate for Robust Tumor Recognition. *Yang, X., +, TCBB July-Aug. 2020 1262-1275*

Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery. *Karakaslar, E.O., +, TCBB March-April 2020 719-725*

SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. *Yuan, X., +, TCBB May-June 2020 1082-1091*

Two dimensional displays

Predicting Carbon Spectrum in Heteronuclear Single Quantum Coherence Spectroscopy for Online Feedback During Surgery. *Karakaslar, E.O., +, TCBB March-April 2020 719-725*

V**Vegetation**

Topological Metrizations of Trees, and New Quartet Methods of Tree Inference. *Rhodes, J.A., TCBB Nov.-Dec. 2020 2107-2118*

Visual databases

Plant Species Identification from Occluded Leaf Images. *Chaudhury, A., +, TCBB May-June 2020 1042-1055*

Visualization

Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. *Lei, X., +, TCBB March-April 2020 495-505*

Volatile organic compounds

BiClusO: A Novel Bioclustering Approach and Its Application to Species-VOC Relational Data. *Karim, M.B., +, TCBB Nov.-Dec. 2020 1955-1965*

Volume measurement

Gene Expressions, Hippocampal Volume Loss, and MMSE Scores in Computation of Progression and Pharmacologic Therapy Effects for Alzheimer's Disease. *Saribudak, A., +, TCBB March-April 2020 608-622*

W**Web servers**

CGIDLA:Developing the Web Server for CpG Island Related Density and LAUPs (Lineage-Associated Underrepresented Permutations) Study. *Xiao, M., +, TCBB Nov.-Dec. 2020 2148-2154*

Web services

Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020 1459-1473*

Weight measurement

WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. *Mallik, S., +, TCBB March-April 2020 690-703*

White noise

Inference of Model Parameters Using Particle Filter Algorithm and Copula Distributions. *Deng, Z., +, TCBB July-Aug. 2020 1231-1240*

Workflow management software

Visual Life Sciences Workflow Design Using Distributed and Heterogeneous Resources. *Mou, X., +, TCBB July-Aug. 2020 1459-1473*

X**XML**

Enabling Massive XML-Based Biological Data Management in HBase. *Liu, J., +, TCBB Nov.-Dec. 2020 1994-2004*