Tatsuya Akutsu

List of Publications by Year
in descending order

340 papers	8,744 citations	61984 43 h-index	69250 77 g-index

357 all docs	357 docs citations	357 times ranked	6458 citing authors

#	Article	IF	Citations
1	Control of Boolean networks: Hardness results and algorithms for tree structured networks. Journal of Theoretical Biology, 2007, 244, 670-679.	1.7	470
2	IDENTIFICATION OF GENETIC NETWORKS FROM A SMALL NUMBER OF GENE EXPRESSION PATTERNS UNDER THE BOOLEAN NETWORK MODEL. , 1998, , 17-28.		346
3	Protein homology detection using string alignment kernels. Bioinformatics, 2004, 20, 1682-1689.	4.1	310
4	iLearn: an integrated platform and meta-learner for feature engineering, machine-learning analysis and modeling of DNA, RNA and protein sequence data. Briefings in Bioinformatics, 2020, 21, 1047-1057.	6.5	294
5	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. PLoS ONE, 2012, 7, e50300.	2.5	265
6	IPknot: fast and accurate prediction of RNA secondary structures with pseudoknots using integer programming. Bioinformatics, 2011, 27, i85-i93.	4.1	253
7	Dynamic programming algorithms for RNA secondary structure prediction with pseudoknots. Discrete Applied Mathematics, 2000, 104, 45-62.	0.9	251
8	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. Briefings in Bioinformatics, 2019, 20, 638-658.	6.5	166
9	Graph Kernels for Molecular Structureâ^'Activity Relationship Analysis with Support Vector Machines. Journal of Chemical Information and Modeling, 2005, 45, 939-951.	5.4	163
10	Quokka: a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. Bioinformatics, 2018, 34, 4223-4231.	4.1	151
11	Cascleave: towards more accurate prediction of caspase substrate cleavage sites. Bioinformatics, 2010, 26, 752-760.	4.1	148
12	Algorithms for Identifying Boolean Networks and Related Biological Networks Based on Matrix Multiplication and Fingerprint Function. Journal of Computational Biology, 2000, 7, 331-343.	1.6	145
13	Dominating scale-free networks with variable scaling exponent: heterogeneous networks are not difficult to control. New Journal of Physics, 2012, 14, 073005.	2.9	137
14	A novel representation of protein sequences for prediction of subcellular location using support vector machines. Protein Science, 2005, 14, 2804-2813.	7.6	134
15	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	4.1	131
16	A comprehensive review and performance evaluation of bioinformatics tools for HLA class I peptide-binding prediction. Briefings in Bioinformatics, 2020, 21, 1119-1135.	6.5	127
17	PREvaIL, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. Journal of Theoretical Biology, 2018, 443, 125-137.	1.7	124
18	iLearnPlus:a comprehensive and automated machine-learning platform for nucleic acid and protein sequence analysis, prediction and visualization. Nucleic Acids Research, 2021, 49, e60-e60.	14.5	124

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19	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. Bioinformatics, 2018, 34, 2546-2555.	4.1	108
20	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	4.1	102
21	RactIP: fast and accurate prediction of RNA-RNA interaction using integer programming. Bioinformatics, 2010, 26, i460-i466.	4.1	99
22	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	6.5	99
23	Comprehensive review and assessment of computational methods for predicting RNA post-transcriptional modification sites from RNA sequences. Briefings in Bioinformatics, 2020, 21, 1676-1696.	6.5	98
24	Extensions of marginalized graph kernels. , 2004, , .		96
25	KCaM (KEGG Carbohydrate Matcher): a software tool for analyzing the structures of carbohydrate sugar chains. Nucleic Acids Research, 2004, 32, W267-W272.	14.5	95
26	Structural controllability of unidirectional bipartite networks. Scientific Reports, 2013, 3, 1647.	3.3	88
27	Computational analysis and prediction of lysine malonylation sites by exploiting informative features in an integrative machine-learning framework. Briefings in Bioinformatics, 2019, 20, 2185-2199.	6.5	82
28	An approximation method for solving the steady-state probability distribution of probabilistic Boolean networks. Bioinformatics, 2007, 23, 1511-1518.	4.1	75
29	PhosphoPredict: A bioinformatics tool for prediction of human kinase-specific phosphorylation substrates and sites by integrating heterogeneous feature selection. Scientific Reports, 2017, 7, 6862.	3.3	72
30	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	6.9	71
31	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. Briefings in Bioinformatics, 2019, 20, 2150-2166.	6.5	70
32	Bastion3: a two-layer ensemble predictor of type III secreted effectors. Bioinformatics, 2019, 35, 2017-2028.	4.1	69
33	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. Briefings in Bioinformatics, 2019, 20, 931-951.	6.5	65
34	Cascleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. Bioinformatics, 2014, 30, 71-80.	4.1	63
35	Identification of genetic networks by strategic gene disruptions and gene overexpressions under a boolean model. Theoretical Computer Science, 2003, 298, 235-251.	0.9	61
36	Prediction using step-wise L1, L2 regularization and feature selection for small data sets with large number of features. BMC Bioinformatics, 2011, 12, 412.	2.6	60

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37	Algorithms for Finding Small Attractors in Boolean Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2007, 2007, 1-13.	1.4	58
38	Minimum dominating set-based methods for analyzing biological networks. Methods, 2016, 102, 57-63.	3.8	57
39	HSEpred: predict half-sphere exposure from protein sequences. Bioinformatics, 2008, 24, 1489-1497.	4.1	53
40	On the approximation of largest common subtrees and largest common point sets. Theoretical Computer Science, 2000, 233, 33-50.	0.9	50
41	Analysis of critical and redundant nodes in controlling directed and undirected complex networks using dominating sets. Journal of Complex Networks, 2014, 2, 394-412.	1.8	50
42	ON CONSTRUCTION OF STOCHASTIC GENETIC NETWORKS BASED ON GENE EXPRESSION SEQUENCES. International Journal of Neural Systems, 2005, 15, 297-310.	5.2	49
43	Prediction of RNA secondary structure with pseudoknots using integer programming. BMC Bioinformatics, 2009, 10, S38.	2.6	49
44	Subcellular location prediction of proteins using support vector machines with alignment of block sequences utilizing amino acid composition. BMC Bioinformatics, 2007, 8, 466.	2.6	44
45	Finding Minimum Reaction Cuts of Metabolic Networks Under a Boolean Model Using Integer Programming and Feedback Vertex Sets. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 14-31.	0.8	44
46	Computational identification of eukaryotic promoters based on cascaded deep capsule neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	44
47	Simulation study in Probabilistic Boolean Network models for genetic regulatory networks. International Journal of Data Mining and Bioinformatics, 2007, 1, 217.	0.1	43
48	FunSAV: Predicting the Functional Effect of Single Amino Acid Variants Using a Two-Stage Random Forest Model. PLoS ONE, 2012, 7, e43847.	2.5	43
49	Distribution of Distances and Triangles in a Point Set and Algorithms for Computing the Largest Common Point Sets. Discrete and Computational Geometry, 1998, 20, 307-331.	0.6	42
50	On the approximation of protein threading. Theoretical Computer Science, 1999, 210, 261-275.	0.9	42
51	Enumerating Treelike Chemical Graphs with Given Path Frequency. Journal of Chemical Information and Modeling, 2008, 48, 1345-1357.	5.4	42
52	DAFS: simultaneous aligning and folding of RNA sequences via dual decomposition. Bioinformatics, 2012, 28, 3218-3224.	4.1	40
53	DeepVF: a deep learning-based hybrid framework for identifying virulence factors using the stacking strategy. Briefings in Bioinformatics, 2021, 22, .	6.5	40
54	Prodepth: Predict Residue Depth by Support Vector Regression Approach from Protein Sequences Only. PLoS ONE, 2009, 4, e7072.	2.5	40

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55	Causalcall: Nanopore Basecalling Using a Temporal Convolutional Network. Frontiers in Genetics, 2019, 10, 1332.	2.3	39
56	ALGORITHMS FOR INFERRING QUALITATIVE MODELS OF BIOLOGICAL NETWORKS. , 1999, , 293-304.		39
57	SecretEPDB: a comprehensive web-based resource for secreted effector proteins of the bacterial types III, IV and VI secretion systems. Scientific Reports, 2017, 7, 41031.	3.3	38
58	Recent Progress on the Analysis of Power-law Features in Complex Cellular Networks. Cell Biochemistry and Biophysics, 2007, 49, 37-47.	1.8	37
59	Finding a Periodic Attractor of a Boolean Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1410-1421.	3.0	37
60	Anthem: a user customised tool for fast and accurate prediction of binding between peptides and HLA class I molecules. Briefings in Bioinformatics, 2021, 22, .	6.5	37
61	TANGLE: Two-Level Support Vector Regression Approach for Protein Backbone Torsion Angle Prediction from Primary Sequences. PLoS ONE, 2012, 7, e30361.	2.5	36
62	PeNGaRoo, a combined gradient boosting and ensemble learning framework for predicting non-classical secreted proteins. Bioinformatics, 2020, 36, 704-712.	4.1	36
63	Correlation between structure and temperature in prokaryotic metabolic networks. BMC Bioinformatics, 2007, 8, 303.	2.6	35
64	A score matrix to reveal the hidden links in glycans. Bioinformatics, 2005, 21, 1457-1463.	4.1	34
65	Feature weight estimation for gene selection: a local hyperlinear learning approach. BMC Bioinformatics, 2014, 15, 70.	2.6	34
66	Optimizing amino acid substitution matrices with a local alignment kernel. BMC Bioinformatics, 2006, 7, 246.	2.6	33
67	Structurally robust control of complex networks. Physical Review E, 2015, 91, 012826.	2.1	33
68	Computational Methods for Modification of Metabolic Networks. Computational and Structural Biotechnology Journal, 2015, 13, 376-381.	4.1	33
69	BIOINFORMATIC APPROACHES FOR PREDICTING SUBSTRATES OF PROTEASES. Journal of Bioinformatics and Computational Biology, 2011, 09, 149-178.	0.8	31
70	Efficient Extraction of Mapping Rules of Atoms from Enzymatic Reaction Data. Journal of Computational Biology, 2004, 11, 449-462.	1.6	30
71	Network control principles for identifying personalized driver genes in cancer. Briefings in Bioinformatics, 2020, 21, 1641-1662.	6.5	29
72	Detecting a Singleton Attractor in a Boolean Network Utilizing SAT Algorithms. IEICE Transactions on Fundamentals of Electronics, Communications and Computer Sciences, 2009, E92-A, 493-501.	0.3	27

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73	On approximation algorithms for local multiple alignment. , 2000, , .		26
74	Point matching under non-uniform distortions. Discrete Applied Mathematics, 2003, 127, 5-21.	0.9	26
75	Sector dominance ratio analysis of financial markets. Physica A: Statistical Mechanics and Its Applications, 2015, 421, 488-509.	2.6	25
76	Determining a singleton attractor of an AND/OR Boolean network in time. Information Processing Letters, 2010, 110, 565-569.	0.6	24
77	Conditional random field approach to prediction of protein-protein interactions using domain information. BMC Systems Biology, 2011, 5, S8.	3.0	24
78	An Integrative Computational Framework Based on a Two-Step Random Forest Algorithm Improves Prediction of Zinc-Binding Sites in Proteins. PLoS ONE, 2012, 7, e49716.	2.5	24
79	Critical controllability in proteome-wide protein interaction network integrating transcriptome. Scientific Reports, 2016, 6, 23541.	3.3	24
80	A Control Model for Markovian Genetic Regulatory Networks. Lecture Notes in Computer Science, 2006, , 36-48.	1.3	24
81	Prediction of Heterodimeric Protein Complexes from Weighted Protein-Protein Interaction Networks Using Novel Features and Kernel Functions. PLoS ONE, 2013, 8, e65265.	2.5	24
82	iFeatureOmega:an integrative platform for engineering, visualization and analysis of features from molecular sequences, structural and ligand data sets. Nucleic Acids Research, 2022, 50, W434-W447.	14.5	24
83	Inferring strengths of protein-protein interactions from experimental data using linear programming. Bioinformatics, 2003, 19, ii58-ii65.	4.1	23
84	Identification of novel DNA repair proteins via primary sequence, secondary structure, and homology. BMC Bioinformatics, 2009, 10, 25.	2.6	23
85	A grammatical approach to RNAâ€“RNA interaction prediction. Pattern Recognition, 2009, 42, 531-538.	8.1	23
86	Determining Associations between Human Diseases and non-coding RNAs with Critical Roles in Network Control. Scientific Reports, 2015, 5, 14577.	3.3	23
87	A Mathematical Model for the Detection Mechanism of DNA Double-Strand Breaks Depending on Autophosphorylation of ATM. PLoS ONE, 2009, 4, e5131.	2.5	22
88	Approximation and parameterized algorithms for common subtrees and edit distance between unordered trees. Theoretical Computer Science, 2013, 470, 10-22.	0.9	22
89	On control of singleton attractors in multiple Boolean networks: integer programming-based method. BMC Systems Biology, 2014, 8, S7.	3.0	22
90	Critical evaluation ofin silicomethods for prediction of coiled-coil domains in proteins. Briefings in Bioinformatics, 2016, 17, 270-282.	6.5	22

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91	On determining the congruence of point sets in d dimensions. Computational Geometry: Theory and Applications, 1998, 9, 247-256.	0.5	21
92	Title is missing!. Journal of Combinatorial Optimization, 1999, 3, 321-336.	1.3	21
93	Two complementary representations of a scale-free network. Physica A: Statistical Mechanics and Its Applications, 2005, 349, 349-363.	2.6	21
94	A probabilistic model for mining labeled ordered trees: capturing patterns in carbohydrate sugar chains. IEEE Transactions on Knowledge and Data Engineering, 2005, 17, 1051-1064.	5.7	21
95	Convolutional neural network approach to lung cancer classification integrating protein interaction network and gene expression profiles. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940007.	0.8	21
96	Tree Edit Distance Problems: Algorithms and Applications to Bioinformatics. IEICE Transactions on Information and Systems, 2010, E93-D, 208-218.	0.7	20
97	Exact algorithms for computing the tree edit distance between unordered trees. Theoretical Computer Science, 2011, 412, 352-364.	0.9	20
98	Determining a Singleton Attractor of a Boolean Network with Nested Canalyzing Functions. Journal of Computational Biology, 2011, 18, 1275-1290.	1.6	20
99	Integer Programming-Based Approach to Attractor Detection and Control of Boolean Networks. IEICE Transactions on Information and Systems, 2012, E95.D, 2960-2970.	0.7	20
100	Circulating Exosomal miRNA Profiles Predict the Occurrence and Recurrence of Hepatocellular Carcinoma in Patients with Direct-Acting Antiviral-Induced Sustained Viral Response. Biomedicines, 2019, 7, 87.	3.2	20
101	Efficient tree-matching methods for accurate carbohydrate database queries. Genome Informatics, 2003, 14, 134-43.	0.4	20
102	Fast and accurate database homology search using upper bounds of local alignment scores. Bioinformatics, 2005, 21, 912-921.	4.1	19
103	Inferring a graph from path frequency. Discrete Applied Mathematics, 2012, 160, 1416-1428.	0.9	19
104	COMPARISON AND ENUMERATION OF CHEMICAL GRAPHS. Computational and Structural Biotechnology Journal, 2013, 5, e201302004.	4.1	19
105	Prediction of heterotrimeric protein complexes by two-phase learning using neighboring kernels. BMC Bioinformatics, 2014, 15, S6.	2.6	19
106	Network controllability analysis of intracellular signalling reveals viruses are actively controlling molecular systems. Scientific Reports, 2019, 9, 2066.	3.3	19
107	Stochastic simulation of Boolean rxncon models: towards quantitative analysis of large signaling networks. BMC Systems Biology, 2015, 9, 45.	3.0	18
108	Identifying a Probabilistic Boolean Threshold Network From Samples. IEEE Transactions on Neural Networks and Learning Systems, 2018, 29, 869-881.	11.3	18

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109	Approximate string matching with don't care characters. Information Processing Letters, 1995, 55, 235-239.	0.6	17
110	Structure of n-clique networks embedded in a complex network. Physica A: Statistical Mechanics and Its Applications, 2007, 380, 665-672.	2.6	17
111	COMPOUND ANALYSIS VIA GRAPH KERNELS INCORPORATING CHIRALITY. Journal of Bioinformatics and Computational Biology, 2010, 08, 63-81.	0.8	17
112	A clique-based method for the edit distance between unordered trees and its application to analysis of glycan structures. BMC Bioinformatics, 2011, 12, S13.	2.6	17
113	Rtips: fast and accurate tools for RNA 2D structure prediction using integer programming. Nucleic Acids Research, 2012, 40, W29-W34.	14.5	17
114	A Clique-Based Method Using Dynamic Programming for Computing Edit Distance Between Unordered Trees. Journal of Computational Biology, 2012, 19, 1089-1104.	1.6	17
115	Finding optimal degenerate patterns in DNA sequences. Bioinformatics, 2003, 19, ii206-ii214.	4.1	16
116	A relation between edit distance for ordered trees and edit distance for Euler strings. Information Processing Letters, 2006, 100, 105-109.	0.6	16
117	Prediction of Protein Folding Rates from Structural Topology and Complex Network Properties. IPSJ Transactions on Bioinformatics, 2010, 3, 40-53.	0.2	16
118	Comparing biological networks via graph compression. BMC Systems Biology, 2010, 4, S13.	3.0	16
119	Efficient Enumeration of Stereoisomers of Outerplanar Chemical Graphs Using Dynamic Programming. Journal of Chemical Information and Modeling, 2011, 51, 2788-2807.	5.4	16
120	Analysis on critical nodes in controlling complex networks using dominating sets. , 2013, , .		16
121	Complex network-based approaches to biomarker discovery. Biomarkers in Medicine, 2016, 10, 621-632.	1.4	16
122	Algorithms for Inference, Analysis and Control of Boolean Networks. Lecture Notes in Computer Science, 2008, , 1-15.	1.3	16
123	Inferring a Graph from Path Frequency. Lecture Notes in Computer Science, 2005, , 371-382.	1.3	15
124	Approximating Tree Edit Distance through String Edit Distance. Algorithmica, 2010, 57, 325-348.	1.3	15
125	Branch-and-Bound Algorithms for Enumerating Treelike Chemical Graphs with Given Path Frequency Using Detachment-Cut. Journal of Chemical Information and Modeling, 2010, 50, 934-946.	5.4	15
126	Probabilistic controllability approach to metabolic fluxes in normal and cancer tissues. Nature Communications, 2019, 10, 2725.	12.8	15

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127	Inhibitory neurons exhibit high controlling ability in the cortical microconnectome. PLoS Computational Biology, 2021, 17, e1008846.	3.2	15
128	Clustering under the line graph transformation: application to reaction network. BMC Bioinformatics, 2004, 5, 207.	2.6	14
129	PROTEIN SIDE-CHAIN PACKING PROBLEM: A MAXIMUM EDGE-WEIGHT CLIQUE ALGORITHMIC APPROACH. Journal of Bioinformatics and Computational Biology, 2005, 03, 103-126.	0.8	14
130	Efficient enumeration of monocyclic chemical graphs with given path frequencies. Journal of Cheminformatics, 2014, 6, 31.	6.1	14
131	Improving prediction of heterodimeric protein complexes using combination with pairwise kernel. BMC Bioinformatics, 2018, 19, 39.	2.6	14
132	ncRNA-disease association prediction based on sequence information and tripartite network. BMC Systems Biology, 2018, 12, 37.	3.0	14
133	Finding and analysing the minimum set of driver nodes required to control multilayer networks. Scientific Reports, 2019, 9, 576.	3.3	14
134	Protease target prediction via matrix factorization. Bioinformatics, 2019, 35, 923-929.	4.1	14
135	Approximating minimum keys and optimal substructure screens. Lecture Notes in Computer Science, 1996, , 290-299.	1.3	14
136	Completing Networks Using Observed Data. Lecture Notes in Computer Science, 2009, , 126-140.	1.3	14
137	Application of a new probabilistic model for recognizing complex patterns in glycans. Bioinformatics, 2004, 20, i6-i14.	4.1	13
138	Optimizing substitution matrices by separating score distributions. Bioinformatics, 2004, 20, 863-873.	4.1	13
139	Origin of structural difference in metabolic networks with respect to temperature. BMC Systems Biology, 2008, 2, 82.	3.0	13
140	LBSizeCleav: improved support vector machine (SVM)-based prediction of Dicer cleavage sites using loop/bulge length. BMC Bioinformatics, 2016, 17, 487.	2.6	13
141	Determining the minimum number of protein-protein interactions required to support known protein complexes. PLoS ONE, 2018, 13, e0195545.	2.5	13
142	Toward more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. Briefings in Bioinformatics, 2019, 20, 1669-1684.	6.5	13
143	A simple method for inferring strengths of protein-protein interactions. Genome Informatics, 2004, 15, 56-68.	0.4	13
144	A bisection algorithm for grammar-based compression of ordered trees. Information Processing Letters, 2010, 110, 815-820.	0.6	12

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145	Enumerating tree-like chemical graphs with given upper and lower bounds on path frequencies. BMC Bioinformatics, 2011, 12, S3.	2.6	12
146	A Polynomial-Time Algorithm for Computing the Maximum Common Connected Edge Subgraph of Outerplanar Graphs of Bounded Degree. Algorithms, 2013, 6, 119-135.	2.1	12
147	Deep learning with evolutionary and genomic profiles for identifying cancer subtypes. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940005.	0.8	12
148	Algorithms for identifying Boolean networks and related biological networks based on matrix multiplication and fingerprint function. , 2000, , .		11
149	Network Completion Using Dynamic Programming and Least-Squares Fitting. Scientific World Journal, The, 2012, 2012, 1-8.	2.1	11
150	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
151	A new method of computer representation of stereochemistry. Transforming a stereochemical structure into a graph. Journal of Chemical Information and Computer Sciences, 1991, 31, 414-417.	2.8	10
152	A simple greedy algorithm for finding functional relations: efficient implementation and average case analysis. Theoretical Computer Science, 2003, 292, 481-495.	0.9	10
153	Algorithms for Singleton Attractor Detection in Planar and Nonplanar AND/OR Boolean Networks. Mathematics in Computer Science, 2009, 2, 401-420.	0.4	10
154	Prediction of protein-RNA residue-base contacts using two-dimensional conditional random field with the lasso. BMC Systems Biology, 2013, 7, S15.	3.0	10
155	Prediction of Protein-Protein Interaction Strength Using Domain Features with Supervised Regression. Scientific World Journal, The, 2014, 2014, 1-7.	2.1	10
156	Analysis of the Effect of Degree Correlation on the Size of Minimum Dominating Sets in Complex Networks. PLoS ONE, 2016, 11, e0157868.	2.5	10
157	Enumerating Substituted Benzene Isomers of Tree-Like Chemical Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 633-646.	3.0	10
158	PROTEIN THREADING WITH PROFILES AND DISTANCE CONSTRAINTS USING CLIQUE BASED ALGORITHMS. Journal of Bioinformatics and Computational Biology, 2006, 04, 19-42.	0.8	9
159	Efficient enumeration of stereoisomers of tree structured molecules using dynamic programming. Journal of Mathematical Chemistry, 2011, 49, 910-970.	1.5	9
160	Proteome compression via protein domain compositions. Methods, 2014, 67, 380-385.	3.8	9
161	Exact Identification of the Structure of a Probabilistic Boolean Network from Samples. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 1107-1116.	3.0	9
162	Convolutional Neural Network Approach to Lung Cancer Classification Integrating Protein Interaction Network and Gene Expression Profiles. , 2018, , .		9

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163	DeepBL: a deep learning-based approach for in silico discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	6.5	9
164	A Novel Method for Inference of Chemical Compounds of Cycle Index Two with Desired Properties Based on Artificial Neural Networks and Integer Programming. Algorithms, 2020, 13, 124.	2.1	9
165	IMPROVED ALGORITHMS FOR ENUMERATING TREE-LIKE CHEMICAL GRAPHS WITH GIVEN PATH FREQUENCY. , 2008, , .		9
166	Distribution of distances and triangles in a point set and algorithms for computing the largest common point sets. , 1997, , .		8
167	Algorithms and Complexity Analyses for Control of Singleton Attractors in Boolean Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2008, 2008, 1-16.	1.4	8
168	Integer programming-based methods for attractor detection and control of boolean networks. , 2009, , .		8
169	Analysis on controlling complex networks based on dominating sets. Journal of Physics: Conference Series, 2013, 410, 012104.	0.4	8
170	Critical controllability analysis of directed biological networks using efficient graph reduction. Scientific Reports, 2017, 7, 14361.	3.3	8
171	Analysis of Critical and Redundant Vertices in Controlling Directed Complex Networks Using Feedback Vertex Sets. Journal of Computational Biology, 2018, 25, 1071-1090.	1.6	8
172	Identification of the Structure of a Probabilistic Boolean Network From Samples Including Frequencies of Outcomes. IEEE Transactions on Neural Networks and Learning Systems, 2019, 30, 2383-2396.	11.3	8
173	A Novel Method for the Inverse QSAR/QSPR based on Artificial Neural Networks and Mixed Integer Linear Programming with Guaranteed Admissibility. , 2020, , .		8
174	Improved algorithms for enumerating tree-like chemical graphs with given path frequency. Genome Informatics, 2008, 21, 53-64.	0.4	8
175	Performance analysis of a greedy algorithm for inferring Boolean functions. Information Processing Letters, 2005, 93, 7-12.	0.6	7
176	Recent Advances in RNA Secondary Structure Prediction with Pseudoknots. Current Bioinformatics, 2006, 1, 115-129.	1.5	7
177	Statistical Learning Algorithm for Tree Similarity. , 2007, , .		7
178	Improved approximation of the largest common subtree of two unordered trees of bounded height. Information Processing Letters, 2008, 109, 165-170.	0.6	7
179	Measuring Structural Robustness of Metabolic Networks under a Boolean Model Using Integer Programming and Feedback Vertex Sets. , 2009, , .		7
180	USING BINDING PROFILES TO PREDICT BINDING SITES OF TARGET RNAs. Journal of Bioinformatics and Computational Biology, 2011, 09, 697-713.	0.8	7

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181	Conservation Laws and Symmetries in Competitive Systems. Progress of Theoretical Physics Supplement, 2012, 194, 210-222.	0.1	7
182	An Improved Satisfiability Algorithm for Nested Canalyzing Functions and its Application to Determining a Singleton Attractor of a Boolean Network. Journal of Computational Biology, 2013, 20, 958-969.	1.6	7
183	Computing Smallest Intervention Strategies for Multiple Metabolic Networks in a Boolean Model. Journal of Computational Biology, 2015, 22, 85-110.	1.6	7
184	FINDING AND ANALYZING THE MINIMUM SET OF DRIVER NODES IN CONTROL OF BOOLEAN NETWORKS. International Journal of Modeling, Simulation, and Scientific Computing, 2016, 19, 1650006.	1.4	7
185	An accessibility-incorporated method for accurate prediction of RNAâ€“RNA interactions from sequence data. Bioinformatics, 2017, 33, 202-209.	4.1	7
186	A Mixed Integer Linear Programming Formulation to Artificial Neural Networks. , 2019, , .		7
187	On the approximation of largest common subtrees and largest common point sets. Lecture Notes in Computer Science, 1994, , 405-413.	1.3	7
188	An Improved Algorithm for Detecting a Singleton Attractor in a Boolean Network Consisting of AND/OR Nodes. Lecture Notes in Computer Science, 2008, , 216-229.	1.3	7
189	Integer Programming-Based Method for Designing Synthetic Metabolic Networks by Minimum Reaction Insertion in a Boolean Model. PLoS ONE, 2014, 9, e92637.	2.5	7
190	Recent Advances in Predicting Functional Impact of Single Amino Acid Polymorphisms: A Review of Useful Features, Computational Methods and Available Tools. Current Bioinformatics, 2013, 8, 161-176.	1.5	7
191	Enumerating Stereoisomers of Tree Structured Molecules Using Dynamic Programming. Lecture Notes in Computer Science, 2009, , 14-23.	1.3	7
192	Point matching under non-uniform distortions and protein side chain packing based on an efficient maximum clique algorithm. Genome Informatics, 2002, 13, 143-52.	0.4	7
193	Matching of Spots in 2D Electrophoresis Images. Point Matching Under Non-uniform Distortions. Lecture Notes in Computer Science, 1999, , 212-222.	1.3	6
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