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	On the Compressive Power of Boolean Threshold Autoencoders. IEEE Transactions on Neural Networks and Learning Systems, 2023, 34, 921-931.	11.3	0
2	On the Distribution of Successor States in Boolean Threshold Networks. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 4147-4159.	11.3	1
3	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
4	Identification of periodic attractors in Boolean networks using a priori information. PLoS Computational Biology, 2022, 18, e1009702.	3.2	1
5	A Method for Molecular Design Based on Linear Regression and Integer Programming. , 2022, , .		0
6	*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
7	Attractor detection and enumeration algorithms for Boolean networks. Computational and Structural Biotechnology Journal, 2022, 20, 2512-2520.	4.1	2
8	DeepBL: a deep learning-based approach for *in silico* discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	6.5	9
9	Computational identification of eukaryotic promoters based on cascaded deep capsule neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	44
10	DeepVF: a deep learning-based hybrid framework for identifying virulence factors using the stacking strategy. Briefings in Bioinformatics, 2021, 22, .	6.5	40
11	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
12	An Inverse QSAR Method Based on Decision Tree and Integer Programming. Lecture Notes in Computer Science, 2021, , 628-644.	1.3	1
13	An Improved Integer Programming Formulation for Inferring Chemical Compounds with Prescribed Topological Structures. Lecture Notes in Computer Science, 2021, , 197-209.	1.3	0
14	*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
15	ReCGBM: a gradient boosting-based method for predicting human dicer cleavage sites. BMC Bioinformatics, 2021, 22, 63.	2.6	2
16	Weighted minimum feedback vertex sets and implementation in human cancer genes detection. BMC Bioinformatics, 2021, 22, 143.	2.6	3
17	An Inverse QSAR Method Based on a Two-Layered Model and Integer Programming. International Journal of Molecular Sciences, 2021, 22, 2847.	4.1	5
18	Inhibitory neurons exhibit high controlling ability in the cortical microconnectome. PLoS Computational Biology, 2021, 17, e1008846.	3.2	15

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19	Uncovering and classifying the role of driven nodes in control of complex networks. Scientific Reports, 2021, 11, 9627.	3.3	1
20	Discrimination of attractors with noisy nodes in Boolean networks. Automatica, 2021, 130, 109630.	5.0	4
21	A novel method for inference of acyclic chemical compounds with bounded branch-height based on artificial neural networks and integer programming. Algorithms for Molecular Biology, 2021, 16, 18.	1.2	4
22	New and improved algorithms for unordered tree inclusion. Theoretical Computer Science, 2021, 883, 83-98.	0.9	3
23	Probabilistic Critical Controllability Analysis of Protein Interaction Networks Integrating Normal Brain Ageing Gene Expression Profiles. International Journal of Molecular Sciences, 2021, 22, 9891.	4.1	0
24	A Novel Method for the Inverse QSAR/QSPR to Monocyclic Chemical Compounds Based on Artificial Neural Networks and Integer Programming. Transactions on Computational Science and Computational Intelligence, 2021, , 641-655.	0.3	3
25	æ©Ÿæ¢°å¦ç¿'QSARã®æ•´æ•°è¯ç»»æ³•ã«åŸºã¥ã€†è§£æžæ³•. Journal of Computer Chemistry Japan, 2021, 20, 106-111.	6.1	0
26	Molecular Design Based on Artificial Neural Networks, Integer Programming and Grid Neighbor Search. , 2021, , .		1
27	PeNGaRoo, a combined gradient boosting and ensemble learning framework for predicting non-classical secreted proteins. Bioinformatics, 2020, 36, 704-712.	4.1	36
28	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
29	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
30	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	4.1	102
31	Network control principles for identifying personalized driver genes in cancer. Briefings in Bioinformatics, 2020, 21, 1641-1662.	6.5	29
32	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
33	An FVS-based Approach to Attractor Detection in Asynchronous Random Boolean Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	5
34	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	6.9	71
35	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
36	Improved Hardness of Maximum Common Subgraph Problems on Labeled Graphs of Bounded Treewidth and Bounded Degree. International Journal of Foundations of Computer Science, 2020, 31, 253-273.	1.1	1

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37	Comparison of Pseudoknotted RNA Secondary Structures by Topological Centroid Identification and Tree Edit Distance. Journal of Computational Biology, 2020, 27, 1443-1451.	1.6	6
38	A New Integer Linear Programming Formulation to the Inverse QSAR/QSPR for Acyclic Chemical Compounds Using Skeleton Trees. Lecture Notes in Computer Science, 2020, , 433-444.	1.3	6
39	Extracting boolean and probabilistic rules from trained neural networks. Neural Networks, 2020, 126, 300-311.	5.9	3
40	A Method for the Inverse QSAR/QSPR Based on Artificial Neural Networks and Mixed Integer Linear Programming. , 2020, , .		5
41	Breast Cancer Subtype by Imbalanced Omics Data through A Deep Learning Fusion Model. , 2020, , .		4
42	An Overview of Bioinformatics Methods for Analyzing Autism Spectrum Disorders. Current Pharmaceutical Design, 2020, 25, 4552-4559.	1.9	4
43	A Novel Method for the Inverse QSAR/QSPR based on Artificial Neural Networks and Mixed Integer Linear Programming with Guaranteed Admissibility. , 2020, , .		8
44	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
45	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
46	Optimal string clustering based on a Laplace-like mixture and EM algorithm on a set of strings. Journal of Computer and System Sciences, 2019, 106, 94-128.	1.2	2
47	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
48	A Mixed Integer Linear Programming Formulation to Artificial Neural Networks. , 2019, , .		7
49	Probabilistic controllability approach to metabolic fluxes in normal and cancer tissues. Nature Communications, 2019, 10, 2725.	12.8	15
50	Deep learning with evolutionary and genomic profiles for identifying cancer subtypes. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940005.	0.8	12
51	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
52	Finding and analysing the minimum set of driver nodes required to control multilayer networks. Scientific Reports, 2019, 9, 576.	3.3	14
53	Network controllability analysis of intracellular signalling reveals viruses are actively controlling molecular systems. Scientific Reports, 2019, 9, 2066.	3.3	19
54	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

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55	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
56	On the number of driver nodes for controlling a Boolean network when the targets are restricted to attractors. Journal of Theoretical Biology, 2019, 463, 1-11.	1.7	5
57	Resource Cut, a New Bounding Procedure to Algorithms for Enumerating Tree-Like Chemical Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 77-90.	3.0	1
58	Controllability Methods for Identifying Associations Between Critical Control ncRNAs and Human Diseases. Methods in Molecular Biology, 2019, 1912, 289-300.	0.9	5
59	Bastion3: a two-layer ensemble predictor of type III secreted effectors. Bioinformatics, 2019, 35, 2017-2028.	4.1	69
60	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	6.5	99
61	Protease target prediction via matrix factorization. Bioinformatics, 2019, 35, 923-929.	4.1	14
62	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
63	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. Briefings in Bioinformatics, 2019, 20, 931-951.	6.5	65
64	Causalcall: Nanopore Basecalling Using a Temporal Convolutional Network. Frontiers in Genetics, 2019, 10, 1332.	2.3	39
65	Domain-Based Approaches to Prediction and Analysis of Protein-Protein Interactions. , 2019, , 406-427.		0
66	Analysis of Boolean Networks and Boolean Models of Metabolic Networks. , 2019, , 141-158.		0
67	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
68	Improving prediction of heterodimeric protein complexes using combination with pairwise kernel. BMC Bioinformatics, 2018, 19, 39.	2.6	14
69	Computing Minimum Reaction Modifications in a Boolean Metabolic Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1853-1862.	3.0	2
70	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. Bioinformatics, 2018, 34, 2546-2555.	4.1	108
71	Enumerating Substituted Benzene Isomers of Tree-Like Chemical Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 633-646.	3.0	10
72	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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73	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	4.1	131
74	Deep Learning with Evolutionary and Genomic Profiles for Identifying Cancer Subtypes. , 2018, , .		1
75	Convolutional Neural Network Approach to Lung Cancer Classification Integrating Protein Interaction Network and Gene Expression Profiles. , 2018, , .		9
76	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
77	Euler String-Based Compression of Tree-Structured Data and its Application to Analysis of RNAs. Current Bioinformatics, 2018, 13, 25-33.	1.5	0
78	*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
79	Algorithms for Analysis and Control of Boolean Networks. Lecture Notes in Computer Science, 2018, , 3-7.	1.3	0
80	Enumerating Chemical Mono-Block 3-Augmented Trees with Two Junctions. , 2018, , .		0
81	Determining the minimum number of protein-protein interactions required to support known protein complexes. PLoS ONE, 2018, 13, e0195545.	2.5	13
82	ncRNA-disease association prediction based on sequence information and tripartite network. BMC Systems Biology, 2018, 12, 37.	3.0	14
83	Grammar-based Compression for Directed and Undirected Generalized Series-parallel Graphs using Integer Linear Programming. , 2018, , .		0
84	On the parameterized complexity of associative and commutative unification. Theoretical Computer Science, 2017, 660, 57-74.	0.9	0
85	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
86	Critical controllability analysis of directed biological networks using efficient graph reduction. Scientific Reports, 2017, 7, 14361.	3.3	8
87	Selected Papers from the 16th International Conference on Bioinformatics (InCoB 2017). Journal of Bioinformatics and Computational Biology, 2017, 15, 1702003.	0.8	0
88	Discrimination of singleton and periodic attractors in Boolean networks. Automatica, 2017, 84, 205-213.	5.0	5
89	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
90	An accessibility-incorporated method for accurate prediction of RNA–RNA interactions from sequence data. Bioinformatics, 2017, 33, 202-209.	4.1	7

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91	Intelligent Informatics in Translational Medicine 2016. BioMed Research International, 2017, 2017, 1-2.	1.9	1
92	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
93	LBSizeCleav: improved support vector machine (SVM)-based prediction of Dicer cleavage sites using loop/bulge length. BMC Bioinformatics, 2016, 17, 487.	2.6	13
94	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
95	Host-Pathogen Protein Interaction Prediction Based on Local Topology Structures of a Protein Interaction Network. , 2016, , .		2
96	Critical controllability in proteome-wide protein interaction network integrating transcriptome. Scientific Reports, 2016, 6, 23541.	3.3	24
97	Finding Influential Genes Using Gene Expression Data and Boolean Models of Metabolic Networks. , 2016, , .		2
98	Similar subtree search using extended tree inclusion. , 2016, , .		0
99	Enumeration Method for Structural Isomers Containing User-Defined Structures Based on Breadth-First Search Approach. Journal of Computational Biology, 2016, 23, 625-640.	1.6	1
100	Enumeration method for tree-like chemical compounds with benzene rings and naphthalene rings by breadth-first search order. BMC Bioinformatics, 2016, 17, 113.	2.6	3
101	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
102	Maximum margin classifier working in a set of strings. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2016, 472, 20150551.	2.1	2
103	Complex network-based approaches to biomarker discovery. Biomarkers in Medicine, 2016, 10, 621-632.	1.4	16
104	Minimum dominating set-based methods for analyzing biological networks. Methods, 2016, 102, 57-63.	3.8	57
105	A likelihood-free filtering method via approximate Bayesian computation in evaluating biological simulation models. Computational Statistics and Data Analysis, 2016, 94, 63-74.	1.2	2
106	Critical evaluation of *in silico* methods for prediction of coiled-coil domains in proteins. Briefings in Bioinformatics, 2016, 17, 270-282.	6.5	22
107	Enumerating Naphthalene Isomers of Tree-like Chemical Graphs. , 2016, , .		0
108	Determining Associations between Human Diseases and non-coding RNAs with Critical Roles in Network Control. Scientific Reports, 2015, 5, 14577.	3.3	23

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109	Matrix Network: A New Data Structure for Efficient Enumeration of Microstates of a Genetic Regulatory Network. Journal of Information Processing, 2015, 23, 804-813.	0.4	0
110	Parallelization of enumerating tree-like chemical compounds by breadth-first search order. BMC Medical Genomics, 2015, 8, S15.	1.5	1
111	Intelligent Informatics in Translational Medicine. BioMed Research International, 2015, 2015, 1-2.	1.9	1
112	Stochastic simulation of Boolean rxncon models: towards quantitative analysis of large signaling networks. BMC Systems Biology, 2015, 9, 45.	3.0	18
113	On observability of attractors in Boolean Networks. , 2015, , .		0
114	Structurally robust control of complex networks. Physical Review E, 2015, 91, 012826.	2.1	33
115	Computing Smallest Intervention Strategies for Multiple Metabolic Networks in a Boolean Model. Journal of Computational Biology, 2015, 22, 85-110.	1.6	7
116	On the complexity of finding a largest common subtree of bounded degree. Theoretical Computer Science, 2015, 590, 2-16.	0.9	6
117	Genomic data assimilation using a higher moment filtering technique for restoration of gene regulatory networks. BMC Systems Biology, 2015, 9, 14.	3.0	2
118	Grammar-based compression approach to extraction of common rules among multiple trees of glycans and RNAs. BMC Bioinformatics, 2015, 16, 128.	2.6	3
119	Similar Subtree Search Using Extended Tree Inclusion. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 3360-3373.	5.7	1
120	Computational Methods for Modification of Metabolic Networks. Computational and Structural Biotechnology Journal, 2015, 13, 376-381.	4.1	33
121	Sector dominance ratio analysis of financial markets. Physica A: Statistical Mechanics and Its Applications, 2015, 421, 488-509.	2.6	25
122	A Fixed-Parameter Algorithm for Detecting a Singleton Attractor in an AND/OR Boolean Network with Bounded Treewidth. IEICE Transactions on Fundamentals of Electronics, Communications and Computer Sciences, 2015, E98.A, 384-390.	0.3	1
123	Exact and Heuristic Methods for Network Completion for Time-Varying Genetic Networks. BioMed Research International, 2014, 2014, 1-13.	1.9	2
124	Prediction of Protein-Protein Interaction Strength Using Domain Features with Supervised Regression. Scientific World Journal, The, 2014, 2014, 1-7.	2.1	10
125	Network Completion for Static Gene Expression Data. Advances in Bioinformatics, 2014, 2014, 1-9.	5.7	2
126	Novel Bioinformatics Approaches for Analysis of High-Throughput Biological Data. BioMed Research International, 2014, 2014, 1-3.	1.9	5

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127	Domain-Based Approaches to Prediction and Analysis of Protein-Protein Interactions. International Journal of Knowledge Discovery in Bioinformatics, 2014, 4, 24-41.	0.8	2
128	Measuring the similarity of protein structures using image local feature descriptors SIFT and SURF. , 2014, , .		1
129	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
130	Cascleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. Bioinformatics, 2014, 30, 71-80.	4.1	63
131	Feature weight estimation for gene selection: a local hyperlinear learning approach. BMC Bioinformatics, 2014, 15, 70.	2.6	34
132	Prediction of heterotrimeric protein complexes by two-phase learning using neighboring kernels. BMC Bioinformatics, 2014, 15, S6.	2.6	19
133	On control of singleton attractors in multiple Boolean networks: integer programming-based method. BMC Systems Biology, 2014, 8, S7.	3.0	22
134	An Efficient Data Assimilation Schema for Restoration and Extension of Gene Regulatory Networks Using Time-Course Observation Data. Journal of Computational Biology, 2014, 21, 785-798.	1.6	3
135	Archaeal β diversity patterns under the seafloor along geochemical gradients. Journal of Geophysical Research G: Biogeosciences, 2014, 119, 1770-1788.	3.0	4
136	Efficient enumeration of monocyclic chemical graphs with given path frequencies. Journal of Cheminformatics, 2014, 6, 31.	6.1	14
137	Proteome compression via protein domain compositions. Methods, 2014, 67, 380-385.	3.8	9
138	Efficient exponential-time algorithms for edit distance between unordered trees. Journal of Discrete Algorithms, 2014, 25, 79-93.	0.7	3
139	Chapter 5: Theory and Method of Completion for a Boolean Regulatory Network Using Observed Data. Science, Engineering, and Biology Informatics, 2014, , 123-145.	0.1	1
140	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
141	Structural controllability of unidirectional bipartite networks. Scientific Reports, 2013, 3, 1647.	3.3	88
142	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
143	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
144	Network Completion for Time Varying Genetic Networks. , 2013, , .		1

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145	Approximation and parameterized algorithms for common subtrees and edit distance between unordered trees. Theoretical Computer Science, 2013, 470, 10-22.	0.9	22
146	Theoretical estimation of metabolic network robustness against multiple reaction knockouts using branching process approximation. Physica A: Statistical Mechanics and Its Applications, 2013, 392, 5525-5535.	2.6	4
147	COMPARISON AND ENUMERATION OF CHEMICAL GRAPHS. Computational and Structural Biotechnology Journal, 2013, 5, e201302004.	4.1	19
148	Analysis on critical nodes in controlling complex networks using dominating sets. , 2013, , .		16
149	Flux balance impact degree: a new definition of impact degree to properly treat reversible reactions in metabolic networks. Bioinformatics, 2013, 29, 2178-2185.	4.1	6
150	Stability and restoration phenomena in competitive systems. Progress of Theoretical and Experimental Physics, 2013, 2013, .	6.6	3
151	BREADTH-FIRST SEARCH APPROACH TO ENUMERATION OF TREE-LIKE CHEMICAL COMPOUNDS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1343007.	0.8	5
152	Finding optimal control policy in probabilistic Boolean Networks with hard constraints by using integer programming and dynamic programming. International Journal of Data Mining and Bioinformatics, 2013, 7, 321.	0.1	6
153	Analysis on controlling complex networks based on dominating sets. Journal of Physics: Conference Series, 2013, 410, 012104.	0.4	8
154	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
155	Survival Analysis by Penalized Regression and Matrix Factorization. Scientific World Journal, The, 2013, 2013, 1-11.	2.1	5
156	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
157	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
158	On the Complexity of Finding a Largest Common Subtree of Bounded Degree. Lecture Notes in Computer Science, 2013, , 4-15.	1.3	0
159	On the Complexity of Inference and Completion of Boolean Networks from Given Singleton Attractors. IEICE Transactions on Fundamentals of Electronics, Communications and Computer Sciences, 2013, E96.A, 2265-2274.	0.3	3
160	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
161	DAFS: simultaneous aligning and folding of RNA sequences via dual decomposition. Bioinformatics, 2012, 28, 3218-3224.	4.1	40
162	Rtips: fast and accurate tools for RNA 2D structure prediction using integer programming. Nucleic Acids Research, 2012, 40, W29-W34.	14.5	17

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163	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
164	Conservation Laws and Symmetries in Competitive Systems. Progress of Theoretical Physics Supplement, 2012, 194, 210-222.	0.1	7
165	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
166	Protein complex prediction via improved verification methods using constrained domain-domain matching. International Journal of Bioinformatics Research and Applications, 2012, 8, 210.	0.2	1
167	A quadsection algorithm for grammar-based image compression. Integrated Computer-Aided Engineering, 2012, 19, 23-38.	4.6	5
168	Finding a Periodic Attractor of a Boolean Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1410-1421.	3.0	37
169	Predicting protein-RNA residue-base contacts using two-dimensional conditional random field. , 2012, , .		1
170	Efficient Exponential Time Algorithms for Edit Distance between Unordered Trees. Lecture Notes in Computer Science, 2012, , 360-372.	1.3	4
171	TANGLE: Two-Level Support Vector Regression Approach for Protein Backbone Torsion Angle Prediction from Primary Sequences. PLoS ONE, 2012, 7, e30361.	2.5	36
172	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
173	Network Completion Using Dynamic Programming and Least-Squares Fitting. Scientific World Journal, The, 2012, 2012, 1-8.	2.1	11
174	Inferring a graph from path frequency. Discrete Applied Mathematics, 2012, 160, 1416-1428.	0.9	19
175	Singleton and 2-periodic attractors of sign-definite Boolean networks. Information Processing Letters, 2012, 112, 35-38.	0.6	5
176	Analysis of the impact degree distribution in metabolic networks using branching process approximation. Physica A: Statistical Mechanics and Its Applications, 2012, 391, 379-387.	2.6	3
177	A Polynomial-Time Algorithm for Computing the Maximum Common Subgraph of Outerplanar Graphs of Bounded Degree. Lecture Notes in Computer Science, 2012, , 76-87.	1.3	5
178	On the Complexity of the Maximum Common Subgraph Problem for Partial k-Trees of Bounded Degree. Lecture Notes in Computer Science, 2012, , 146-155.	1.3	4
179	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
180	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. PLoS ONE, 2012, 7, e50300.	2.5	265

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181	Finding Conserved Regions in Protein Structures Using Support Vector Machines and Structure Alignment. Lecture Notes in Computer Science, 2012, , 233-242.	1.3	0
182	Discriminative random field approach to prediction of protein residue contacts. , 2011, , .		5
183	An Improved Clique-Based Method for Computing Edit Distance between Unordered Trees and Its Application to Comparison of Glycan Structures. , 2011, , .		4
184	Predicting functional impact of single amino acid polymorphisms by integrating sequence and structural features. , 2011, , .		3
185	USING BINDING PROFILES TO PREDICT BINDING SITES OF TARGET RNAs. Journal of Bioinformatics and Computational Biology, 2011, 09, 697-713.	0.8	7
186	Efficient Enumeration of Stereoisomers of Outerplanar Chemical Graphs Using Dynamic Programming. Journal of Chemical Information and Modeling, 2011, 51, 2788-2807.	5.4	16
187	Measuring the Similarity of Protein Structures Using Image Compression Algorithms. IEICE Transactions on Information and Systems, 2011, E94-D, 2468-2478.	0.7	1
188	An Efficient Method of Computing Impact Degrees for Multiple Reactions in Metabolic Networks with Cycles. IEICE Transactions on Information and Systems, 2011, E94-D, 2393-2399.	0.7	3
189	Kernel Methods for Chemical Compounds: From Classification to Design. IEICE Transactions on Information and Systems, 2011, E94-D, 1846-1853.	0.7	2
190	Efficient enumeration of stereoisomers of tree structured molecules using dynamic programming. Journal of Mathematical Chemistry, 2011, 49, 910-970.	1.5	9
191	Conditional random field approach to prediction of protein-protein interactions using domain information. BMC Systems Biology, 2011, 5, S8.	3.0	24
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