Xiangxiang Zeng

List of Publications by Year
in descending order

152	7,900	48	84
papers	citations	h-index	g-index
		44069	54911

155	155	155	4288
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Multi-Population Multi-Objective Evolutionary Algorithm Based on the Contribution of Decision Variables to Objectives for Large-Scale Multi/Many-Objective Optimization. IEEE Transactions on Cybernetics, 2023, 53, 6998-7007.	9.5	9
2	Deep learning in retrosynthesis planning: datasets, models and tools. Briefings in Bioinformatics, 2022, 23, .	6.5	45
3	Monodirectional Evolutional Symport Tissue P Systems With Promoters and Cell Division. IEEE Transactions on Parallel and Distributed Systems, 2022, 33, 332-342.	5.6	20
4	Are dropout imputation methods for scRNA-seq effective for scATAC-seq data?. Briefings in Bioinformatics, 2022, 23, .	6.5	5
5	preMLI: a pre-trained method to uncover microRNAâ€“lncRNA potential interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	14
6	Toward better drug discovery with knowledge graph. Current Opinion in Structural Biology, 2022, 72, 114-126.	5.7	108
7	Learning spatial structures of proteins improves proteinâ€“protein interaction prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	51
8	Deep learning for drug repurposing: Methods, databases, and applications. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	14.6	48
9	Editorial: Artificial Intelligence in Bioinformatics and Drug Repurposing: Methods and Applications. Frontiers in Genetics, 2022, 13, 870795.	2.3	4
10	Rule synchronization for monodirectional tissue-like P systems with channel states. Information and Computation, 2022, 285, 104895.	0.7	4
11	Normal forms for spiking neural P systems and some of its variants. Information Sciences, 2022, 595, 344-363.	6.9	9
12	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. Nucleic Acids Research, 2022, 50, 4877-4899.	14.5	12
13	KG-MTL: Knowledge Graph Enhanced Multi-Task Learning for Molecular Interaction. IEEE Transactions on Knowledge and Data Engineering, 2022, , 1-12.	5.7	4
14	Predicting enhancer-promoter interactions by deep learning and matching heuristic. Briefings in Bioinformatics, 2021, 22, .	6.5	32
15	Minirmd: accurate and fast duplicate removal tool for short reads via multiple minimizers. Bioinformatics, 2021, 37, 1604-1606.	4.1	14
16	A Polar-Metric-Based Evolutionary Algorithm. IEEE Transactions on Cybernetics, 2021, 51, 3429-3440.	9.5	21
17	Application of deep learning methods in biological networks. Briefings in Bioinformatics, 2021, 22, 1902-1917.	6.5	111
18	Mobility Based Trust Evaluation for Heterogeneous Electric Vehicles Network in Smart Cities. IEEE Transactions on Intelligent Transportation Systems, 2021, 22, 1797-1806.	8.0	77

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19	Monodirectional Tissue <i>P</i> Systems With Promoters. IEEE Transactions on Cybernetics, 2021, 51, 438-450.	9.5	53
20	Monodirectional tissue P systems with channel states. Information Sciences, 2021, 546, 206-219.	6.9	31
21	iEnhancer-XG: interpretable sequence-based enhancers and their strength predictor. Bioinformatics, 2021, 37, 1060-1067.	4.1	61
22	Homogeneous spiking neural P systems with structural plasticity. Journal of Membrane Computing, 2021, 3, 10-21.	1.8	28
23	MUFFIN: multi-scale feature fusion for drugâ€“drug interaction prediction. Bioinformatics, 2021, 37, 2651-2658.	4.1	91
24	A drug information embedding method based on graph convolution neural network. , 2021, , .		0
25	CarSite-II: an integrated classification algorithm for identifying carbonylated sites based on K-means similarity-based undersampling and synthetic minority oversampling techniques. BMC Bioinformatics, 2021, 22, 216.	2.6	4
26	A spatial-temporal gated attention module for molecular property prediction based on molecular geometry. Briefings in Bioinformatics, 2021, 22, .	6.5	15
27	ADMETlab 2.0: an integrated online platform for accurate and comprehensive predictions of ADMET properties. Nucleic Acids Research, 2021, 49, W5-W14.	14.5	915
28	Neural-like P systems with plasmids. Information and Computation, 2021, 281, 104766.	0.7	12
29	The computational power of monodirectional tissue P systems with symport rules. Information and Computation, 2021, 281, 104751.	0.7	8
30	Artificialâ€Intelligenceâ€Enabled Reagentâ€Free Imaging Hematology Analyzer. Advanced Intelligent Systems, 2021, 3, 2000277.	6.1	11
31	Deep learning methods for biomedical named entity recognition: a survey and qualitative comparison. Briefings in Bioinformatics, 2021, 22, .	6.5	52
32	HeTDR: Drug repositioning based on heterogeneous networks and text mining. Patterns, 2021, 2, 100307.	5.9	12
33	Review of unsupervised pretraining strategies for molecules representation. Briefings in Functional Genomics, 2021, 20, 323-332.	2.7	20
34	Artificialâ€Intelligenceâ€Enabled Reagentâ€Free Imaging Hematology Analyzer. Advanced Intelligent Systems, 2021, 3, 2170060.	6.1	2
35	Active Semisupervised Model for Improving the Identification of Anticancer Peptides. ACS Omega, 2021, 6, 23998-24008.	3.5	4
36	<i>De novo</i> generation of dual-target ligands using adversarial training and reinforcement learning. Briefings in Bioinformatics, 2021, 22, .	6.5	7

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37	Solving a PSPACE-complete problem by symport/antiport P systems with promoters and membrane division. Journal of Membrane Computing, 2021, 3, 296-302.	1.8	6
38	Pm⁶ A: an Integrated Classification Algorithm for 2021 IEEE International Conference on Bioinformatics and Biomedicine (BIBM) Identifying m⁶ A Sites. , 2021, , .		0
39	LADstackING: Stacking Ensemble Learning-based Computational Model for Predicting Potential LncRNA-disease Associations. , 2021, , .		1
40	Identifying enhancerâ€“promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. Bioinformatics, 2020, 36, 1037-1043.	4.1	127
41	A Network Reduction-Based Multiobjective Evolutionary Algorithm for Community Detection in Large-Scale Complex Networks. IEEE Transactions on Cybernetics, 2020, 50, 703-716.	9.5	83
42	Computational methods for identifying the critical nodes in biological networks. Briefings in Bioinformatics, 2020, 21, 486-497.	6.5	69
43	On the Computational Power of Asynchronous Axon Membrane Systems. IEEE Transactions on Emerging Topics in Computational Intelligence, 2020, 4, 696-704.	4.9	7
44	A Consensus Community-Based Particle Swarm Optimization for Dynamic Community Detection. IEEE Transactions on Cybernetics, 2020, 50, 2502-2513.	9.5	115
45	Predicting disease-associated circular RNAs using deep forests combined with positive-unlabeled learning methods. Briefings in Bioinformatics, 2020, 21, 1425-1436.	6.5	96
46	Investigating Maize Yield-Related Genes in Multiple Omics Interaction Network Data. IEEE Transactions on Nanobioscience, 2020, 19, 142-151.	3.3	3
47	A novel molecular representation with BiGRU neural networks for learning atom. Briefings in Bioinformatics, 2020, 21, 2099-2111.	6.5	69
48	Repurpose Open Data to Discover Therapeutics for COVID-19 Using Deep Learning. Journal of Proteome Research, 2020, 19, 4624-4636.	3.7	183
49	The computational power of cell-like P systems with one protein on membrane. Journal of Membrane Computing, 2020, 2, 332-340.	1.8	14
50	StackCPPred: a stacking and pairwise energy content-based prediction of cell-penetrating peptides and their uptake efficiency. Bioinformatics, 2020, 36, 3028-3034.	4.1	111
51	Multiobjective Particle Swarm Optimization Based on Network Embedding for Complex Network Community Detection. IEEE Transactions on Computational Social Systems, 2020, 7, 437-449.	4.4	28
52	Target identification among known drugs by deep learning from heterogeneous networks. Chemical Science, 2020, 11, 1775-1797.	7.4	193
53	Network-based prediction of drugâ€“target interactions using an arbitrary-order proximity embedded deep forest. Bioinformatics, 2020, 36, 2805-2812.	4.1	101
54	A multi-task learning method for analyzing microbiota as cancer immunotherapy signal. , 2020, , .		0

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55	An Evolutionary Algorithm Based on Minkowski Distance for Many-Objective Optimization. IEEE Transactions on Cybernetics, 2019, 49, 3968-3979.	9.5	85
56	Meta-Path Methods for Prioritizing Candidate Disease miRNAs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 283-291.	3.0	126
57	Matrix representation and simulation algorithm of spiking neural P systems with structural plasticity. Journal of Membrane Computing, 2019, 1, 145-160.	1.8	21
58	On solutions and representations of spiking neural P systems with rules on synapses. Information Sciences, 2019, 501, 30-49.	6.9	31
59	Investigation and development of maize fused network analysis with multi-omics. Plant Physiology and Biochemistry, 2019, 141, 380-387.	5.8	14
60	deepDR: a network-based deep learning approach to<i>in silico</i>drug repositioning. Bioinformatics, 2019, 35, 5191-5198.	4.1	343
61	Prediction of Potential Disease-Associated MicroRNAs by Using Neural Networks. Molecular Therapy - Nucleic Acids, 2019, 16, 566-575.	5.1	70
62	Learning to Predict Drug Target Interaction From Missing Not at Random Labels. IEEE Transactions on Nanobioscience, 2019, 18, 353-359.	3.3	5
63	Details in the evaluation of circular RNA detection tools: Reply to Chen and Chuang. PLoS Computational Biology, 2019, 15, e1006916.	3.2	8
64	Deep collaborative filtering for prediction of disease genes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	25
65	A component overlapping attribute clustering (COAC) algorithm for single-cell RNA sequencing data analysis and potential pathobiological implications. PLoS Computational Biology, 2019, 15, e1006772.	3.2	14
66	GraphCPI: Graph Neural Representation Learning for Compound-Protein Interaction. , 2019, , .		20
67	A Deep Neural Network for Antimicrobial Peptide Recognition. , 2019, , .		1
68	A network-based approach to uncover microRNA-mediated disease comorbidities and potential pathobiological implications. Npj Systems Biology and Applications, 2019, 5, 41.	3.0	24
69	MOEA/HD: A Multiobjective Evolutionary Algorithm Based on Hierarchical Decomposition. IEEE Transactions on Cybernetics, 2019, 49, 517-526.	9.5	109
70	Integrative Approaches for Predicting microRNA Function and Prioritizing Disease-Related microRNA Using Biological Interaction Networks. , 2019, , 75-105.		3
71	Prediction of potential disease-associated microRNAs using structural perturbation method. Bioinformatics, 2018, 34, 2425-2432.	4.1	229
72	Spiking Neural P Systems With Colored Spikes. IEEE Transactions on Cognitive and Developmental Systems, 2018, 10, 1106-1115.	3.8	116

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73	Drug Target Interaction Prediction with Non-random Missing Labels. , 2018, , .		1
74	LncRNA-disease association prediction based on neighborhood information aggregation in neural network. , 2018, , .		3
75	Identification and Analysis of Rice Yield-Related Candidate Genes by Walking on the Functional Network. Frontiers in Plant Science, 2018, 9, 1685.	3.6	4
76	A Parallel Workflow Pattern Modeling Using Spiking Neural P Systems With Colored Spikes. IEEE Transactions on Nanobioscience, 2018, 17, 474-484.	3.3	54
77	On String Languages Generated by Spiking Neural P Systems With Structural Plasticity. IEEE Transactions on Nanobioscience, 2018, 17, 560-566.	3.3	22
78	Sc-ncDNAPred: A Sequence-Based Predictor for Identifying Non-coding DNA in Saccharomyces cerevisiae. Frontiers in Microbiology, 2018, 9, 2174.	3.5	19
79	Sequence clustering in bioinformatics: an empirical study. Briefings in Bioinformatics, 2018, , .	6.5	104
80	Prediction of Drugâ€"Gene Interaction by Using Metapath2vec. Frontiers in Genetics, 2018, 9, 248.	2.3	29
81	RicyerDB: A Database For Collecting Rice Yield-related Genes with Biological Analysis. International Journal of Biological Sciences, 2018, 14, 965-970.	6.4	20
82	Using MOEA with Redistribution and Consensus Branches to Infer Phylogenies. International Journal of Molecular Sciences, 2018, 19, 62.	4.1	5
83	Structural Hole Spanner in HumanNet Identifies Disease Gene and Drug targets. IEEE Access, 2018, 6, 35392-35401.	4.2	3
84	An Implementation of Elementary Arithmetic with Virus Machine. Lecture Notes in Computer Science, 2018, , 304-317.	1.3	0
85	Small Spiking Neural P Systems with Structural Plasticity. Lecture Notes in Computer Science, 2018, , 45-56.	1.3	0
86	Prediction and Validation of Disease Genes Using HeteSim Scores. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 687-695.	3.0	199
87	Inferring MicroRNA-Disease Associations by Random Walk on a Heterogeneous Network with Multiple Data Sources. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 905-915.	3.0	265
88	Reconstructing evolutionary trees in parallel for massive sequences. BMC Systems Biology, 2017, 11, 100.	3.0	15
89	Spiking Neural P Systems With Scheduled Synapses. IEEE Transactions on Nanobioscience, 2017, 16, 792-801.	3.3	82
90	Predict the Relationship between Gene and Large Yellow Croakerâ€™s Economic Traits. Molecules, 2017, 22, 1978.	3.8	5

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91	A comprehensive overview and evaluation of circular RNA detection tools. PLoS Computational Biology, 2017, 13, e1005420.	3.2	313
92	Probability-based collaborative filtering model for predicting geneâ€“disease associations. BMC Medical Genomics, 2017, 10, 76.	1.5	73
93	Iteratively collective prediction of disease-gene associations through the incomplete network. , 2017, , .		8
94	A decision support model for investment on P2P lending platform. PLoS ONE, 2017, 12, e0184242.	2.5	12
95	Similarity computation strategies in the microRNA-disease network: a survey. Briefings in Functional Genomics, 2016, 15, elv024.	2.7	172
96	Embedded Based Miniaturized Universal Electrochemical Sensing Platform. Journal of Sensors, 2016, 2016, 1-8.	1.1	2
97	Pretata: predicting TATA binding proteins with novel features and dimensionality reduction strategy. BMC Systems Biology, 2016, 10, 114.	3.0	143
98	HPTree: Reconstructing phylogenetic trees for ultra-large unaligned DNA sequences via NJ model and Hadoop. , 2016, , .		8
99	Latent factor model with heterogeneous similarity regularization for predicting gene-disease associations. , 2016, , .		3
100	Computing with viruses. Theoretical Computer Science, 2016, 623, 146-159.	0.9	28
101	Investment behavior prediction in heterogeneous information network. Neurocomputing, 2016, 217, 125-132.	5.9	11
102	Complex Network Clustering by a Multi-objective Evolutionary Algorithm Based on Decomposition and Membrane Structure. Scientific Reports, 2016, 6, 33870.	3.3	32
103	Integrative approaches for predicting microRNA function and prioritizing disease-related microRNA using biological interaction networks. Briefings in Bioinformatics, 2016, 17, 193-203.	6.5	307
104	Prediction and validation of association between microRNAs and diseases by multipath methods. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 2735-2739.	2.4	43
105	Prediction of MicroRNA-disease Associations by Matrix Completion. Current Proteomics, 2016, 13, 151-157.	0.3	12
106	A Classification Method for Microarrays Based on Diversity. Current Bioinformatics, 2016, 11, 590-597.	1.5	7
107	Molecular Logic Computation with Debugging Method. Journal of Nanomaterials, 2015, 2015, 1-11.	2.7	0
108	Implementation of Arithmetic Operations With Time-Free Spiking Neural P Systems. IEEE Transactions on Nanobioscience, 2015, 14, 617-624.	3.3	52

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109	A Stable Matching-Based Selection and Memory Enhanced MOEA/D for Evolutionary Dynamic Multiobjective Optimization. , 2015, , .		7
110	Improving tRNAscanâ€SE Annotation Results via Ensemble Classifiers. Molecular Informatics, 2015, 34, 761-770.	2.5	66
111	Simulating Spiking Neural P Systems with Circuits. Journal of Computational and Theoretical Nanoscience, 2015, 12, 2023-2026.	0.4	3
112	MOEA/D for Energy-Aware Scheduling on Heterogeneous Computing Systems. Communications in Computer and Information Science, 2015, , 94-106.	0.5	1
113	Asynchronous Spiking Neural P Systems with Anti-Spikes. Neural Processing Letters, 2015, 42, 633-647.	3.2	25
114	The power of time-free tissue P systems: Attacking NP-complete problems. Neurocomputing, 2015, 159, 151-156.	5.9	23
115	Identification of cytokine via an improved genetic algorithm. Frontiers of Computer Science, 2015, 9, 643-651.	2.4	26
116	A decision-making framework for precision marketing. Expert Systems With Applications, 2015, 42, 3357-3367.	7.6	76
117	Asynchronous spiking neural P systems with rules on synapses. Neurocomputing, 2015, 151, 1439-1445.	5.9	65
118	Spiking Neural P Systems with Thresholds. Neural Computation, 2014, 26, 1340-1361.	2.2	113
119	Solving Multidimensional 0-1 Knapsack Problem with Time-Free Tissue P Systems. Journal of Applied Mathematics, 2014, 2014, 1-6.	0.9	4
120	On Some Classes of Sequential Spiking Neural P Systems. Neural Computation, 2014, 26, 974-997.	2.2	57
121	Weighted Spiking Neural P Systems with Rules on Synapses. Fundamenta Informaticae, 2014, 134, 201-218.	0.4	16
122	Decision Tree Classification Model for Popularity Forecast of Chinese Colleges. Journal of Applied Mathematics, 2014, 2014, 1-7.	0.9	12
123	Approaches for Recognizing Disease Genes Based on Network. BioMed Research International, 2014, 2014, 1-10.	1.9	46
124	nDNA-prot: identification of DNA-binding proteins based on unbalanced classification. BMC Bioinformatics, 2014, 15, 298.	2.6	158
125	On languages generated by spiking neural P systems with weights. Information Sciences, 2014, 278, 423-433.	6.9	75
126	Small universal simple spiking neural P systems with weights. Science China Information Sciences, 2014, 57, 1-11.	4.3	30

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127	A hybrid heuristic algorithm for the 2D variable-sized bin packing problem. European Journal of Operational Research, 2014, 238, 95-103.	5.7	38
128	Time-Free Tissue P Systems for Solving the Hamilton Path Problem. Communications in Computer and Information Science, 2014, , 562-565.	0.5	1
129	Review of Protein Subcellular Localization Prediction. Current Bioinformatics, 2014, 9, 331-342.	1.5	32
130	A New Graphical Representation of Protein Sequences Based on Dual-Vector Model. Communications in Computer and Information Science, 2014, , 629-632.	0.5	0
131	Spiking neural P systems with anti-spikes and without annihilating priority working in a 'flip-flop' way. International Journal of Computing Science and Mathematics, 2013, 4, 152.	0.3	3
132	WormStep: An Improved Compact Graphical Representation of DNA Sequences Based on Worm Curve. Journal of Computational and Theoretical Nanoscience, 2013, 10, 189-193.	0.4	2
133	Small Universal Spiking Neural P Systems with Anti-Spikes. Journal of Computational and Theoretical Nanoscience, 2013, 10, 999-1006.	0.4	38
134	A Bayesian Investment Model for Online P2P Lending. Communications in Computer and Information Science, 2013, , 21-30.	0.5	4
135	Several Applications of Spiking Neural P Systems with Weights. Journal of Computational and Theoretical Nanoscience, 2012, 9, 769-777.	0.4	10
136	Performing Four Basic Arithmetic Operations With Spiking Neural P Systems. IEEE Transactions on Nanobioscience, 2012, 11, 366-374.	3.3	57
137	A uniform solution to the independent set problem through tissue P systems with cell separation. Frontiers of Computer Science, 2012, 6, 477.	2.4	1
138	Spiking Neural P Systems with Weighted Synapses. Neural Processing Letters, 2012, 35, 13-27.	3.2	68
139	P Systems with 2D Picture Grammars. , 2011, , .		0
140	A Modified Estimation of Distribution Algorithm for Numeric Optimization. , 2011, , .		0
141	Spiking Neural P Systems for Arithmetic Operations. , 2011, , .		3
142	Small Universal Spiking Neural P Systems Working in Exhaustive Mode. IEEE Transactions on Nanobioscience, 2011, 10, 99-105.	3.3	45
143	Time-Free Spiking Neural P Systems. Neural Computation, 2011, 23, 1320-1342.	2.2	69
144	Deterministic solutions to QSAT and Q3SAT by spiking neural P systems with pre-computed resources. Theoretical Computer Science, 2010, 411, 2345-2358.	0.9	111

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145	A weakly universal spiking neural P system. Mathematical and Computer Modelling, 2010, 52, 1940-1946.	2.0	5
146	Small universal asynchronous spiking neural P systems. , 2010, , .		5
147	A Note on Small Universal Spiking Neural P Systems. Lecture Notes in Computer Science, 2010, , 436-447.	1.3	16
148	Matrix Representation of Spiking Neural P Systems. Lecture Notes in Computer Science, 2010, , 377-391.	1.3	24
149	Homogeneous Spiking Neural P Systems. Fundamenta Informaticae, 2009, 97, 275-294.	0.4	54
150	On languages generated by asynchronous spiking neural P systems. Theoretical Computer Science, 2009, 410, 2478-2488.	0.9	37
151	A weakly universal spiking neural P system. , 2009, , .		1
152	On string languages generated by spiking neural P systems with exhaustive use of rules. Natural Computing, 2008, 7, 535-549.	3.0	51