Xiufen Zou

List of Publications by Year
in descending order

85 papers	1,414 citations	430874 18 h-index	395702 33 g-index
86 all docs	86 docs citations	86 times ranked	1425 citing authors

#	Article	IF	Citations
1	scLRTD : A Novel Low Rank Tensor Decomposition Method for Imputing Missing Values in Single-Cell Multi-Omics Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1144-1153.	3.0	5
2	Data-driven mathematical modeling and quantitative analysis of cell dynamics in the tumor microenvironment. Computers and Mathematics With Applications, 2022, 113, 300-314.	2.7	1
3	Identifying optimal adaptive therapeutic schedules for prostate cancer through combining mathematical modeling and dynamic optimization. Applied Mathematical Modelling, 2022, 107, 688-700.	4.2	4
4	Control Strategies for a Tumor-Immune System with Impulsive Drug Delivery under a Random Environment. Acta Mathematica Scientia, 2022, 42, 1141-1159.	1.0	4
5	SCCLRR: A Robust Computational Method for Accurate Clustering Single Cell RNA-Seq Data. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 247-256.	6.3	17
6	A network-based computational framework to predict and differentiate functions for gene isoforms using exon-level expression data. Methods, 2021, 189, 54-64.	3.8	2
7	Dynamic Host Immune and Transcriptomic Responses to Respiratory Syncytial Virus Infection in a Vaccination-Challenge Mouse Model. Virologica Sinica, 2021, 36, 1327-1340.	3.0	3
8	scASK: A Novel Ensemble Framework for Classifying Cell Types Based on Single-cell RNA-seq Data. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 3230-3239.	6.3	1
9	Data-Driven Mathematical Modeling and Dynamical Analysis for SARS-CoV-2 Coinfection with Bacteria. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2021, 31, 2150163.	1.7	6
10	Quantitative integration of radiomic and genomic data improves survival prediction of low-grade glioma patients. Mathematical Biosciences and Engineering, 2021, 18, 727-744.	1.9	6
11	Data-driven multi-scale mathematical modeling of SARS-CoV-2 infection reveals heterogeneity among COVID-19 patients. PLoS Computational Biology, 2021, 17, e1009587.	3.2	11
12	Identification of Intercellular Signaling Changes Across Conditions and Their Influence on Intracellular Signaling Response From Multiple Single-Cell Datasets. Frontiers in Genetics, 2021, 12, 751158.	2.3	7
13	DNA Methylation Basis in the Effect of White Matter Integrity Deficits on Cognitive Impairments and Psychopathological Symptoms in Drug-Naive First-Episode Schizophrenia. Frontiers in Psychiatry, 2021, 12, 777407.	2.6	7
14	Predicting Essential Proteins by Integrating Network Topology, Subcellular Localization Information, Gene Expression Profile and GO Annotation Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2053-2061.	3.0	21
15	Tensor-based mathematical framework and new centralities for temporal multilayer networks. Information Sciences, 2020, 512, 563-580.	6.9	13
16	scRCMF: Identification of Cell Subpopulations and Transition States From Single-Cell Transcriptomes. IEEE Transactions on Biomedical Engineering, 2020, 67, 1418-1428.	4.2	13
17	scPADGRN: A preconditioned ADMM approach for reconstructing dynamic gene regulatory network using single-cell RNA sequencing data. PLoS Computational Biology, 2020, 16, e1007471.	3.2	9
18	Microglia depletion exacerbates demyelination and impairs remyelination in a neurotropic coronavirus infection. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24464-24474.	7.1	54

#	Article	IF	Citations
19	A general index for linear and nonlinear correlations for high dimensional genomic data. BMC Genomics, 2020, 21, 846.	2.8	2
20	Hepatitis B Virus Core Particles Containing a Conserved Region of the G Protein Combined with Interleukin-35 Protected Mice against Respiratory Syncytial Virus Infection without Vaccine-Enhanced Immunopathology. Journal of Virology, 2020, 94, .	3.4	10
21	Oligodendrocytes that survive acute coronavirus infection induce prolonged inflammatory responses in the CNS. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15902-15910.	7.1	32
22	Control of multilayer biological networks and applied to target identification of complex diseases. BMC Bioinformatics, 2019, 20, 271.	2.6	7
23	Integrating network topology, gene expression data and GO annotation information for protein complex prediction. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950001.	0.8	8
24	Inferring Large-Scale Gene Regulatory Networks Using a Randomized Algorithm Based on Singular Value Decomposition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1997-2008.	3.0	8
25	A New Model System for Exploring Assembly Mechanisms of the HIV-1 Immature Capsid In Vivo. Bulletin of Mathematical Biology, 2019, 81, 1506-1526.	1.9	4
26	Single-cell data-driven mathematical model reveals possible molecular mechanisms of embryonic stem-cell differentiation. Mathematical Biosciences and Engineering, 2019, 16, 5877-5896.	1.9	3
27	Trajectory Control in Nonlinear Networked Systems and Its Applications to Complex Biological Systems. SIAM Journal on Applied Mathematics, 2018, 78, 629-649.	1.8	14
28	Detecting Essential Proteins Based on Network Topology, Gene Expression Data, and Gene Ontology Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 109-116.	3.0	44
29	A new centrality measure of nodes in multilayer networks under the framework of tensor computation. Applied Mathematical Modelling, 2018, 54, 46-63.	4.2	30
30	Mathematical modeling of HIV-like particle assembly in vitro. Mathematical Biosciences, 2017, 288, 46-51.	1.9	6
31	Identifying key nodes in multilayer networks based on tensor decomposition. Chaos, 2017, 27, 063108.	2.5	42
32	CONTROL ENERGY AND CONTROLLABILITY OF MULTILAYER NETWORKS. International Journal of Modeling, Simulation, and Scientific Computing, 2017, 20, 1750008.	1.4	12
33	Inference of Biochemical S-Systems via Mixed-Variable Multiobjective Evolutionary Optimization. Computational and Mathematical Methods in Medicine, 2017, 2017, 1-9.	1.3	2
34	Several Indicators of Critical Transitions for Complex Diseases Based on Stochastic Analysis. Computational and Mathematical Methods in Medicine, 2017, 2017, 1-10.	1.3	2
35	A new two-stage method for revealing missing parts of edges in protein-protein interaction networks. PLoS ONE, 2017, 12, e0177029.	2.5	1
36	Reverse-engineering of gene networks for regulating early blood development from single-cell measurements. BMC Medical Genomics, 2017, 10, 72.	1.5	16

#	Article	IF	Citations
37	Domain control of nonlinear networked systems and applications to complex disease networks. Discrete and Continuous Dynamical Systems - Series B, 2017, 22, 2169-2206.	0.9	11
38	Mathematical modeling and quantitative analysis of HIV-1 Gag trafficking and polymerization. PLoS Computational Biology, 2017, 13, e1005733.	3.2	2
39	Inference of genetic regulatory network for stem cell using single cells expression data. , 2016, , .		3
40	Qualitative Analysis of Critical Transitions in Complex Disease Propagation from a Dynamical Systems Perspective. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2016, 26, 1650239.	1.7	4
41	Optimization of controllability and robustness of complex networks by edge directionality. European Physical Journal B, 2016, 89, 1.	1.5	7
42	Identifying disease modules and components of viral infections based on multi-layer networks. Science China Information Sciences, 2016, 59, 1.	4.3	14
43	Crosstalk between pathways enhances the controllability of signalling networks. IET Systems Biology, 2016, 10, 2-9.	1.5	10
44	A New Method for Identifying Essential Proteins by Measuring Co-Expression and Functional Similarity. IEEE Transactions on Nanobioscience, 2016, 15, 939-945.	3.3	10
45	Optimal Control Strategy for Abnormal Innate Immune Response. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-16.	1.3	15
46	Mathematical modeling reveals the mechanisms of feedforward regulation in cell fate decisions in budding yeast. Quantitative Biology, 2015, 3, 55-68.	0.5	3
47	Negative feedback contributes to the stochastic expression of the interferon-β gene in virus-triggered type I interferon signaling pathways. Mathematical Biosciences, 2015, 265, 12-27.	1.9	8
48	Modeling HIV-1 viral capsid nucleation by dynamical systems. Mathematical Biosciences, 2015, 270, 95-105.	1.9	7
49	Mathematical modeling for intracellular transport and binding of HIV-1 Gag proteins. Mathematical Biosciences, 2015, 262, 198-205.	1.9	11
50	A New Method for Detecting Protein Complexes based on the Three Node Cliques. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 879-886.	3.0	16
51	The linear interplay of intrinsic and extrinsic noises ensures a high accuracy of cell fate selection in budding yeast. Scientific Reports, 2015, 4, 5764.	3.3	25
52	Deciphering deterioration mechanisms of complex diseases based on the construction of dynamic networks and systems analysis. Scientific Reports, 2015, 5, 9283.	3.3	48
53	ESTIMATION OF CONTROL ENERGY AND CONTROL STRATEGIES FOR COMPLEX NETWORKS. International Journal of Modeling, Simulation, and Scientific Computing, 2015, 18, 1550018.	1.4	10
54	Mathematical Modeling and Nonlinear Dynamical Analysis of Cell Growth in Response to Antibiotics. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2015, 25, 1540007.	1.7	12

#	Article	IF	Citations
55	A binary differential evolution algorithm learning from explored solutions. Neurocomputing, 2015, 149, 1038-1047.	5.9	93
56	A New Asynchronous Parallel Algorithm for Inferring Large-Scale Gene Regulatory Networks. PLoS ONE, 2015, 10, e0119294.	2.5	10
57	Characterizing and controlling the inflammatory network during influenza A virus infection. Scientific Reports, 2014, 4, 3799.	3.3	61
58	Systematic Analysis of the Mechanisms of Virus-Triggered Type I IFN Signaling Pathways through Mathematical Modeling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 771-779.	3.0	10
59	How can surrogates influence the convergence of evolutionary algorithms?. Swarm and Evolutionary Computation, 2013, 12, 18-23.	8.1	9
60	Identification of the Molecular Mechanisms for Cell-Fate Selection in Budding Yeast through Mathematical Modeling. Biophysical Journal, 2013, 104, 2282-2294.	0.5	9
61	Diversity-maintained differential evolution embedded with gradient-based local search. Soft Computing, 2013, 17, 1511-1535.	3.6	19
62	COMPLEX DYNAMICAL ANALYSIS OF A COUPLED NETWORK FROM INNATE IMMUNE RESPONSES. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2013, 23, 1350180.	1.7	20
63	Construction of the influenza A virus infection-induced cell-specific inflammatory regulatory network based on mutual information and optimization. BMC Systems Biology, 2013, 7, 105.	3.0	6
64	Modeling and Dynamical Analysis of Virus-Triggered Innate Immune Signaling Pathways. PLoS ONE, 2012, 7, e48114.	2.5	22
65	Synchronization feature of coupled cell-cycle oscillators. , 2011, , .		1
66	Convergence of multi-objective evolutionary algorithms to a uniformly distributed representation of the Pareto front. Information Sciences, 2011, 181, 3336-3355.	6.9	25
67	Drift conditions for estimating the first hitting times of evolutionary algorithms. International Journal of Computer Mathematics, 2011, 88, 37-50.	1.8	9
68	Understanding inhibition of viral proteins on type I IFN signaling pathways with modeling and optimization. Journal of Theoretical Biology, 2010, 265, 691-703.	1.7	11
69	Notice of Retraction: Searching for robust optimal solutions by an evolutionary algorithm. , 2010, , .		0
70	Several Dynamic Models of Large-Scale Insect Cell Infection at Low Multiplicity of Infection. , 2009, , .		0
71	A parallel evolutionary algorithm for optimal pulse-width modulation technique in power systems. , 2009, , .		0
72	A niche-based evolutionary Tabu search algorithm for optimal coordination of protection relays in power networks. Wuhan University Journal of Natural Sciences, 2009, 14, 215-222.	0.4	0

#	Article	IF	Citations
73	Performance assessment of DMOEA-DD with CEC 2009 MOEA competition test instances. , 2009, , .		57
74	Modeling specificity in the yeast MAPK signaling networks. Journal of Theoretical Biology, 2008, 250, 139-155.	1.7	26
75	Robustness analysis of EGFR signaling network with a multi-objective evolutionary algorithm. BioSystems, 2008, 91, 245-261.	2.0	5
76	A New Evolutionary Algorithm for Solving Many-Objective Optimization Problems. IEEE Transactions on Systems, Man, and Cybernetics, 2008, 38, 1402-1412.	5.0	266
77	Optimal coordination of protection relays using new hybrid evolutionary algorithm. , 2008, , .		7
78	Robustness Analysis of EGFR Signaling Network Based on Evolutionary Algorithm. , 2008, , .		1
79	Mathematical Models of Specificity in Cell Signaling. Biophysical Journal, 2007, 92, 3425-3441.	0.5	64
80	Fast annealing genetic algorithm for multi-objective optimization problems. International Journal of Computer Mathematics, 2005, 82, 931-940.	1.8	5
81	A new dynamical evolutionary algorithm based on statistical mechanics. Journal of Computer Science and Technology, 2003, 18, 361-368.	1.5	23
82	An efficient dynamical evolutionary algorithm for global optimization. International Journal of Computer Mathematics, 2003, 80, 1429-1436.	1.8	3
83	A dynamical evolutionary algorithm for constrained optimization problems. , 0, , .		4
84	Solving global optimal problems by using a dynamical evolutionary algorithm. , 0, , .		4
85	Evolutionary optimization based on chaotic sequence in dynamic environments. , 0, , .		1