

Tianhai Tian

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

1,885
citations

471509

17
h-index

265206

42
g-index

75
all docs

75
docs citations

75
times ranked

1940
citing authors

#	ARTICLE	IF	CITATIONS
1	Plasma membrane nanoswitches generate high-fidelity Ras signal transduction. <i>Nature Cell Biology</i> , 2007, 9, 905-914.	10.3	372
2	Oscillatory Regulation of Hes1: Discrete Stochastic Delay Modelling and Simulation. <i>PLoS Computational Biology</i> , 2006, 2, e117.	3.2	232
3	Stochastic models for regulatory networks of the genetic toggle switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8372-8377.	7.1	221
4	The origins of cancer robustness and evolvability. <i>Integrative Biology (United Kingdom)</i> , 2011, 3, 17-30.	1.3	144
5	Stochastic delay differential equations for genetic regulatory networks. <i>Journal of Computational and Applied Mathematics</i> , 2007, 205, 696-707.	2.0	141
6	Simulated maximum likelihood method for estimating kinetic rates in gene expression. <i>Bioinformatics</i> , 2007, 23, 84-91.	4.1	94
7	Implicit Taylor methods for stiff stochastic differential equations. <i>Applied Numerical Mathematics</i> , 2001, 38, 167-185.	2.1	84
8	Development of stock correlation networks using mutual information and financial big data. <i>PLoS ONE</i> , 2018, 13, e0195941.	2.5	51
9	A clustering-based ensemble approach with improved pigeon-inspired optimization and extreme learning machine for air quality prediction. <i>Applied Soft Computing Journal</i> , 2019, 85, 105827.	7.2	38
10	Spatial Correlation Network and Regional Differences for the Development of Digital Economy in China. <i>Entropy</i> , 2021, 23, 1575.	2.2	36
11	Mathematical Modelling of the MAP Kinase Pathway Using Proteomic Datasets. <i>PLoS ONE</i> , 2012, 7, e42230.	2.5	35
12	Approximate method for stochastic chemical kinetics with two-time scales by chemical Langevin equations. <i>Journal of Chemical Physics</i> , 2016, 144, 174112.	3.0	34
13	Mathematical modeling of GATA-switching for regulating the differentiation of hematopoietic stem cell. <i>BMC Systems Biology</i> , 2014, 8, S8.	3.0	28
14	A new model of time scheme for progression of colorectal cancer. <i>BMC Systems Biology</i> , 2014, 8, S2.	3.0	22
15	Approximate Bayesian computation schemes for parameter inference of discrete stochastic models using simulated likelihood density. <i>BMC Bioinformatics</i> , 2014, 15, S3.	2.6	21
16	Development of Stock Networks Using Part Mutual Information and Australian Stock Market Data. <i>Entropy</i> , 2020, 22, 773.	2.2	20
17	A continuous optimization approach for inferring parameters in mathematical models of regulatory networks. <i>BMC Bioinformatics</i> , 2014, 15, 256.	2.6	18
18	Online Identification of Nonlinear Stochastic Spatiotemporal System With Multiplicative Noise by Robust Optimal Control-Based Kernel Learning Method. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2019, 30, 389-404.	11.3	18

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19	Reverse-engineering of gene networks for regulating early blood development from single-cell measurements. BMC Medical Genomics, 2017, 10, 72.	1.5	16
20	Stochastic models for inferring genetic regulation from microarray gene expression data. BioSystems, 2010, 99, 192-200.	2.0	15
21	Mathematical modeling and dynamic analysis of anti-tumor immune response. Journal of Applied Mathematics and Computing, 2020, 62, 473-488.	2.5	15
22	Quantitative model for inferring dynamic regulation of the tumour suppressor gene p53. BMC Bioinformatics, 2010, 11, 36.	2.6	14
23	An integrated approach to infer dynamic protein-gene interactions “ A case study of the human P53 protein. Methods, 2016, 110, 3-13.	3.8	12
24	Stochastic modelling of multistage carcinogenesis and progression of human lung cancer. Journal of Theoretical Biology, 2019, 479, 81-89.	1.7	12
25	SCOUT: A new algorithm for the inference of pseudo-time trajectory using single-cell data. Computational Biology and Chemistry, 2019, 80, 111-120.	2.3	12
26	The impact of radiation on the development of lung cancer. Journal of Theoretical Biology, 2017, 428, 147-152.	1.7	11
27	A mathematical model of cell-mediated immune response to tumor. Mathematical Biosciences and Engineering, 2021, 18, 373-385.	1.9	11
28	Chemical Memory Reactions Induced Bursting Dynamics in Gene Expression. PLoS ONE, 2013, 8, e52029.	2.5	10
29	How MAP kinase modules function as robust, yet adaptable, circuits. Cell Cycle, 2014, 13, 2379-2390.	2.6	10
30	MultiStep Ahead Forecasting for Hourly PM10 and PM2.5 Based on Two-Stage Decomposition Embedded Sample Entropy and Group Teacher Optimization Algorithm. Atmosphere, 2021, 12, 64.	2.3	10
31	Mutation Mechanisms of Human Breast Cancer. Journal of Computational Biology, 2018, 25, 396-404.	1.6	9
32	Inference of model parameters using particle filter algorithm and Copula distributions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	8
33	Mutation Mechanisms of Breast Cancer among the Female Population in China. Current Bioinformatics, 2020, 15, 253-259.	1.5	8
34	A Weight-based Information Filtration Algorithm for Stock-correlation Networks. Physica A: Statistical Mechanics and Its Applications, 2021, 563, 125489.	2.6	7
35	A robust method for designing multistable systems by embedding bistable subsystems. Npj Systems Biology and Applications, 2022, 8, 10.	3.0	7
36	DTFLOW: Inference and Visualization of Single-cell Pseudotime Trajectory Using Diffusion Propagation. Genomics, Proteomics and Bioinformatics, 2021, 19, 306-318.	6.9	6

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37	Risk of lung cancer due to external environmental factor and epidemiological data analysis. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 6079-6094.	1.9	6
38	Mathematical Modeling and Analysis of Tumor Chemotherapy. <i>Symmetry</i> , 2022, 14, 704.	2.2	6
39	Mathematical modelling the pathway of genomic instability in lung cancer. <i>Scientific Reports</i> , 2019, 9, 14136.	3.3	5
40	Online Kernel Learning With Adaptive Bandwidth by Optimal Control Approach. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2021, 32, 1920-1934.	11.3	5
41	Breast Cancer Detection Based on Modified Harris Hawks Optimization and Extreme Learning Machine Embedded with Feature Weighting. <i>Neural Processing Letters</i> , 2023, 55, 3631-3654.	3.2	5
42	Sensitivity and Robustness Analysis for Stochastic Model of Nanog Gene Regulatory Network. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2015, 25, 1540009.	1.7	4
43	Control-based algorithms for high dimensional online learning. <i>Journal of the Franklin Institute</i> , 2020, 357, 1909-1942.	3.4	4
44	Multi-likelihood methods for developing relationship networks using stock market data. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2022, 585, 126421.	2.6	4
45	A non-linear reverse-engineering method for inferring genetic regulatory networks. <i>PeerJ</i> , 2020, 8, e9065.	2.0	4
46	Balance of positive and negative regulation for trade-off between efficiency and resilience of high-dimensional networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2022, 603, 127879.	2.6	4
47	Stochastic modelling of biochemical systems of multi-step reactions using a simplified two-variable model. <i>BMC Systems Biology</i> , 2013, 7, S14.	3.0	3
48	Inference of genetic regulatory network for stem cell using single cells expression data. , 2016, , .		3
49	Stochastic modeling of biochemical systems with multistep reactions using state-dependent time delay. <i>Scientific Reports</i> , 2016, 6, 31909.	3.3	3
50	Instantaneous mutation rate in cancer initiation and progression. <i>BMC Systems Biology</i> , 2018, 12, 110.	3.0	3
51	Robust Online Learning Method Based on Dynamical Linear Quadratic Regulator. <i>IEEE Access</i> , 2019, 7, 117780-117795.	4.2	3
52	The Cost-Effectiveness Analysis and Optimal Strategy of the Tobacco Control. <i>Computational and Mathematical Methods in Medicine</i> , 2019, 2019, 1-15.	1.3	3
53	Integrated Inference of Asymmetric Protein Interaction Networks Using Dynamic Model and Individual Patient Proteomics Data. <i>Symmetry</i> , 2021, 13, 1097.	2.2	3
54	Estimation of Kinetic Rates of MAP Kinase Activation from Experimental Data. , 2009, , .		2

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55	Mathematical modelling for variations of inbreeding populations fitness with single and polygenic traits. BMC Genomics, 2017, 18, 196.	2.8	2
56	Using Particle Swarm Optimization Algorithm to Calibrate the Term Structure Model. Mathematical Problems in Engineering, 2021, 2021, 1-11.	1.1	2
57	Deterministic implicit two-step Milstein methods for stochastic differential equations. Statistics and Probability Letters, 2021, 179, 109208.	0.7	2
58	Inference Method for Reconstructing Regulatory Networks Using Statistical Path-Consistency Algorithm and Mutual Information. Lecture Notes in Computer Science, 2020, , 45-56.	1.3	2
59	Approximate Bayesian computation for estimating rate constants in biochemical reaction systems. , 2013, , .		1
60	Bayesian Computation Methods for Inferring Regulatory Network Models Using Biomedical Data. Advances in Experimental Medicine and Biology, 2016, 939, 289-307.	1.6	1
61	A Bayesian framework for inferring heterogeneity of cellular processes using single-cell data. , 2021, , .		1
62	Integrated Pipelines for Inferring Gene Regulatory Networks from Single-Cell Data. Current Bioinformatics, 2022, 17, .	1.5	1
63	Generalized fluctuation-dissipation theorem for non-Markovian reaction networks. Physical Review E, 2022, 105, .	2.1	1
64	Systems Biology Studies of Gene Network and Cell Signaling Pathway in Cancer Research. Translational Bioinformatics, 2013, , 109-129.	0.0	0
65	A New Cost-Profit Model for Measuring the Optimal Scale of China's Foreign Exchange Reserve. Mathematical Problems in Engineering, 2016, 2016, 1-10.	1.1	0
66	Copula particle filter algorithm for inferring parameters of regulatory network models with noisy observation data. , 2016, , .		0
67	Inference Method for Developing Mathematical Models of Cell Signaling Pathways Using Proteomic Datasets. Methods in Molecular Biology, 2017, 1526, 329-344.	0.9	0
68	Inference of protein-protein networks for triple-negative breast cancer using single-patient proteomic data. , 2018, , .		0
69	Mathematical Modelling of Genetic Network for Regulating the Fate Determination of Hematopoietic Stem Cells. , 2018, , .		0
70	Approximate Bayesian Computational Methods for the Inference of Unknown Parameters. MATRIX Book Series, 2019, , 515-529.	0.2	0
71	Bayesian inference of stochastic dynamic models using early-rejection methods based on sequential stochastic simulations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	0
72	Inference of Molecular Regulatory Systems Using Statistical Path-Consistency Algorithm. Entropy, 2022, 24, 693.	2.2	0

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73	Mathematical modeling for mutator phenotype and clonal selection advantage in the risk analysis of lung cancer. <i>Theory in Biosciences</i> , 0, , .	1.4	0
74	The Linear Relationship Model with LASSO for Studying Stock Networks. <i>Entropy</i> , 2022, 24, 808.	2.2	0