Shihua Zhang

List of Publications by Year
in descending order

92 papers	3,593 citations	186265 28 h-index	144013 57 g-index
102 all docs	102 docs citations	102 times ranked	3925 citing authors

#	Article	IF	Citations
1	Adversarial Information Bottleneck. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 221-230.	11.3	0
2	Learnable Graph-Regularization for Matrix Decomposition. ACM Transactions on Knowledge Discovery From Data, 2023, 17, 1-20.	3.5	0
3	Distributed Bayesian Matrix Decomposition for Big Data Mining and Clustering. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 3701-3713.	5.7	6
4	Disease category-specific annotation of variants using an ensemble learning framework. Briefings in Bioinformatics, 2022, 23, .	6.5	7
5	A Novel Sparse Graph-Regularized Singular Value Decomposition Model and Its Application to Genomic Data Analysis. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 3842-3856.	11.3	4
6	Deciphering spatial domains from spatially resolved transcriptomics with an adaptive graph attention auto-encoder. Nature Communications, 2022, 13, 1739.	12.8	118
7	Prediction of the transcription factor binding sites with meta-learning. Methods, 2022, , .	3.8	2
8	VP-Detector: A 3D multi-scale dense convolutional neural network for macromolecule localization and classification in cryo-electron tomograms. Computer Methods and Programs in Biomedicine, 2022, 221, 106871.	4.7	10
9	Joint reconstruction of *cis*-regulatory interaction networks across multiple tissues using single-cell chromatin accessibility data. Briefings in Bioinformatics, 2021, 22, .	6.5	10
10	An Integrative Framework for Combining Sequence and Epigenomic Data to Predict Transcription Factor Binding Sites Using Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 355-364.	3.0	19
11	Imputing single-cell RNA-seq data by considering cell heterogeneity and prior expression of dropouts. Journal of Molecular Cell Biology, 2021, 13, 29-40.	3.3	21
12	Towards understanding residual and dilated dense neural networks via convolutional sparse coding. National Science Review, 2021, 8, nwaa159.	9.5	6
13	A kernel non-negative matrix factorization framework for single cell clustering. Applied Mathematical Modelling, 2021, 90, 875-888.	4.2	2
14	Bayesian Joint Matrix Decomposition for Data Integration with Heterogeneous Noise. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2021, 43, 1184-1196.	13.9	5
15	3D Genome of macaque fetal brain reveals evolutionary innovations during primate corticogenesis. Cell, 2021, 184, 723-740.e21.	28.9	76
16	TSCCA: A tensor sparse CCA method for detecting microRNA-gene patterns from multiple cancers. PLoS Computational Biology, 2021, 17, e1009044.	3.2	10
17	Robust Bayesian matrix decomposition with mixture of Gaussian noise. Neurocomputing, 2021, 449, 108-116.	5.9	4
18	Network diffusion for scalable embedding of massive single-cell ATAC-seq data. Science Bulletin, 2021, 66, 2271-2276.	9.0	7

#	ARTICLE	IF	CITATIONS
19	Prediction of transcription factor binding sites with an attention augmented convolutional neural network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	2
20	Approximate distance correlation for selecting highly interrelated genes across datasets. PLoS Computational Biology, 2021, 17, e1009548.	3.2	2
21	Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 657-667.	3.0	8
22	A General Joint Matrix Factorization Framework for Data Integration and Its Systematic Algorithmic Exploration. IEEE Transactions on Fuzzy Systems, 2020, 28, 1971-1983.	9.8	21
23	Prediction of enhancer–promoter interactions using the cross-cell type information and domain adversarial neural network. BMC Bioinformatics, 2020, 21, 507.	2.6	15
24	Sparse Partial Least Squares Methods for Joint Modular Pattern Discovery. Methods in Molecular Biology, 2020, 2082, 173-186.	0.9	0
25	MSTD for Detecting Topological Domains from 3D Genomic Maps. Methods in Molecular Biology, 2020, 2117, 79-92.	0.9	0
26	Comparison of computational methods for imputing single-cell RNA-sequencing data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	83
27	Group-sparse SVD Models via L_1- and L_0-norm Penalties and Their Applications in Biological Data. IEEE Transactions on Knowledge and Data Engineering, 2019, , 1-1.	5.7	6
28	Circular Trajectory Reconstruction Uncovers Cell‐Cycle Progression and Regulatory Dynamics from Single‐Cell Hi‐C Maps. Advanced Science, 2019, 6, 1900986.	11.2	10
29	Learning common and specific patterns from data of multiple interrelated biological scenarios with matrix factorization. Nucleic Acids Research, 2019, 47, 6606-6617.	14.5	28
30	Model-based understanding of single-cell CRISPR screening. Nature Communications, 2019, 10, 2233.	12.8	61
31	MSTD: an efficient method for detecting multi-scale topological domains from symmetric and asymmetric 3D genomic maps. Nucleic Acids Research, 2019, 47, e65-e65.	14.5	15
32	Simple tricks of convolutional neural network architectures improve DNA–protein binding prediction. Bioinformatics, 2019, 35, 1837-1843.	4.1	28
33	Computational Methods for Subtyping of Tumors and Their Applications for Deciphering Tumor Heterogeneity. Methods in Molecular Biology, 2019, 1878, 193-207.	0.9	0
34	Edge-group sparse PCA for network-guided high dimensional data analysis. Bioinformatics, 2018, 34, 3479-3487.	4.1	43
35	Network-Regularized Sparse Logistic Regression Models for Clinical Risk Prediction and Biomarker Discovery. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 944-953.	3.0	24
36	The Discovery of Mutated Driver Pathways in Cancer: Models and Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 988-998.	3.0	53

#	ARTICLE	IF	CITATIONS
37	Reveal cell type-specific regulatory elements and their characterized histone code classes via a hidden Markov model. BMC Genomics, 2018, 19, 903.	2.8	0
38	Sparse Weighted Canonical Correlation Analysis. Chinese Journal of Electronics, 2018, 27, 459-466.	1.5	6
39	Discovery of two-level modular organization from matched genomic data via joint matrix tri-factorization. Nucleic Acids Research, 2018, 46, 5967-5976.	14.5	27
40	Matrix Integrative Analysis (MIA) of Multiple Genomic Data for Modular Patterns. Frontiers in Genetics, 2018, 9, 194.	2.3	3
41	BMTK: a toolkit for determining modules in biological bipartite networks. Quantitative Biology, 2018, 6, 186-192.	0.5	0
42	Omics tools for the needle out of haystack?. Journal of Genetics and Genomics, 2018, 45, 343-344.	3.9	0
43	Discovery of cancer common and specific driver gene sets. Nucleic Acids Research, 2017, 45, e86-e86.	14.5	55
44	Integrative cancer genomics: models, algorithms and analysis. Frontiers of Computer Science, 2017, 11, 392-406.	2.4	3
45	Large-scale determination and characterization of cell type-specific regulatory elements in the human genome. Journal of Molecular Cell Biology, 2017, 9, 463-476.	3.3	6
46	Integrative Analysis of Transcription Factor Combinatorial Interactions Using a Bayesian Tensor Factorization Approach. Frontiers in Genetics, 2017, 8, 140.	2.3	2
47	High-dimensional genomic data bias correction and data integration using MANCIE. Nature Communications, 2016, 7, 11305.	12.8	52
48	An integrative and comparative study of pan-cancer transcriptomes reveals distinct cancer common and specific signatures. Scientific Reports, 2016, 6, 33398.	3.3	31
49	Quantitative function and algorithm for community detection in bipartite networks. Information Sciences, 2016, 367-368, 874-889.	6.9	35
50	Comparative pan-cancer DNA methylation analysis reveals cancer common and specific patterns. Briefings in Bioinformatics, 2016, 18, bbw063.	6.5	119
51	An effective sequence-alignment-free superpositioning of pairwise or multiple structures with missing data. Algorithms for Molecular Biology, 2016, 11, 18.	1.2	3
52	A Two-Stage Method to Identify Joint Modules From Matched MicroRNA and mRNA Expression Data. IEEE Transactions on Nanobioscience, 2016, 15, 362-370.	3.3	10
53	DrugE-Rank: improving drug–target interaction prediction of new candidate drugs or targets by ensemble learning to rank. Bioinformatics, 2016, 32, i18-i27.	4.1	115
54	Integrative analysis for identifying joint modular patterns of gene-expression and drug-response data. Bioinformatics, 2016, 32, 1724-1732.	4.1	75

#	ARTICLE	IF	CITATIONS
55	Local community extraction in directed networks. Physica A: Statistical Mechanics and Its Applications, 2016, 452, 258-265.	2.6	9
56	Network Analysis, Integration and Methods in Computational Biology: A Brief Survey on Recent Advances. Understanding Complex Systems, 2016, , 459-482.	0.6	0
57	Systematic DNA methylation analysis of multiple cell lines reveals common and specific patterns within and across tissues of origin. Human Molecular Genetics, 2015, 24, 4374-4384.	2.9	39
58	Guest Editorial for Special Section on ISB/TBC 2014. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1074-1075.	3.0	0
59	Tumor characterization and stratification by integrated molecular profiles reveals essential pan-cancer features. BMC Genomics, 2015, 16, 503.	2.8	32
60	Breast tumor subgroups reveal diverse clinical prognostic power. Scientific Reports, 2015, 4, 4002.	3.3	54
61	Toward a systematic understanding of cancers: a survey of the pan-cancer study. Frontiers in Genetics, 2014, 5, 194.	2.3	22
62	Profiling the transcription factor regulatory networks of human cell types. Nucleic Acids Research, 2014, 42, 12380-12387.	14.5	19
63	Discovery of co-occurring driver pathways in cancer. BMC Bioinformatics, 2014, 15, 271.	2.6	99
64	Matrix Factorization Methods for Integrative Cancer Genomics. Methods in Molecular Biology, 2014, 1176, 229-242.	0.9	8
65	Identification of mutated core cancer modules by integrating somatic mutation, copy number variation, and gene expression data. BMC Systems Biology, 2013, 7, S4.	3.0	36
66	Detect taxonomy-specific pathway associations with environmental factors using metagenomic data. , 2013, , .		1
67	Discovery of cell-type specific regulatory elements in the human genome using differential chromatin modification analysis. Nucleic Acids Research, 2013, 41, 9230-9242.	14.5	19
68	Discovering Link Communities in Complex Networks by an Integer Programming Model and a Genetic Algorithm. PLoS ONE, 2013, 8, e83739.	2.5	17
69	Integrating Multiple Types of Data to Identify MicroRNAâ€"Gene Co-modules. Methods in Molecular Biology, 2013, 1049, 215-229.	0.9	0
70	Identifying multi-layer gene regulatory modules from multi-dimensional genomic data. Bioinformatics, 2012, 28, 2458-2466.	4.1	123
71	Common community structure in time-varying networks. Physical Review E, 2012, 85, 056110.	2.1	15
72	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. Nucleic Acids Research, 2012, 40, 9379-9391.	14.5	305

#	Article	IF	Citations
73	Efficient methods for identifying mutated driver pathways in cancer. Bioinformatics, 2012, 28, 2940-2947.	4.1	155
74	Identifying mutated core modules in glioblastoma by integrative network analysis. , 2012, , .		0
75	A Querying Method with Feedback Mechanism for Protein Interaction Network. , 2011, , .		5
76	A dynamical method to extract communities induced by low or middle-degree nodes. , 2011, , .		0
77	A novel computational framework for simultaneous integration of multiple types of genomic data to identify microRNA-gene regulatory modules. Bioinformatics, 2011, 27, i401-i409.	4.1	212
78	Detecting community structure: From parsimony to weighted parsimony. Journal of Systems Science and Complexity, 2010, 23, 1024-1036.	2.8	2
79	Determining modular organization of protein interaction networks by maximizing modularity density. BMC Systems Biology, 2010, 4, S10.	3.0	34
80	A fast mathematical programming procedure for simultaneous fitting of assembly components into cryoEM density maps. Bioinformatics, 2010, 26, i261-i268.	4.1	21
81	A hybrid graph-theoretic method for mining overlapping functional modules in large sparse protein interaction networks. International Journal of Data Mining and Bioinformatics, 2009, 3, 68.	0.1	11
82	Fuzzy System Methods in Modeling Gene Expression and Analyzing Protein Networks. Studies in Fuzziness and Soft Computing, 2009, , 165-189.	0.8	3
83	Clustering complex networks and biological networks by nonnegative matrix factorization with various similarity measures. Neurocomputing, 2008, 72, 134-141.	5.9	54
84	Quantitative function for community detection. Physical Review E, 2008, 77, 036109.	2.1	295
85	Uncovering fuzzy community structure in complex networks. Physical Review E, 2007, 76, 046103.	2.1	111
86	Identification of overlapping community structure in complex networks using fuzzy -means clustering. Physica A: Statistical Mechanics and Its Applications, 2007, 374, 483-490.	2.6	445
87	Discovering functions and revealing mechanisms at molecular level from biological networks. Proteomics, 2007, 7, 2856-2869.	2.2	110
88	Identifying Modules in Complex Networks by a Graph-Theoretical Method and Its Application in Protein Interaction Networks. Lecture Notes in Computer Science, 2007, , 1090-1101.	1.3	1
89	Identification of functional modules in a PPI network by clique percolation clustering. Computational Biology and Chemistry, 2006, 30, 445-451.	2.3	65
90	A New Approach of Information Discrepancy to Analysis of Questionnaire Data. Communications in Statistics - Theory and Methods, 2003, 32, 435-457.	1.0	0

#	Article	IF	Citations
91	Convergence of algorithms used for principal component analysis. Science in China Series D: Earth Sciences, 1997, 40, 597-604.	0.9	4
92	Deciphering the Spatial Modular Patterns of Tissues by Integrating Spatial and Single-Cell Transcriptomic Data. Journal of Computational Biology, 0, , .	1.6	5