

# Shihua Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Identification of overlapping community structure in complex networks using fuzzy -means clustering. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 374, 483-490.	2.6	445
2	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. <i>Nucleic Acids Research</i> , 2012, 40, 9379-9391.	14.5	305
3	Quantitative function for community detection. <i>Physical Review E</i> , 2008, 77, 036109.	2.1	295
4	A novel computational framework for simultaneous integration of multiple types of genomic data to identify microRNA-gene regulatory modules. <i>Bioinformatics</i> , 2011, 27, i401-i409.	4.1	212
5	Efficient methods for identifying mutated driver pathways in cancer. <i>Bioinformatics</i> , 2012, 28, 2940-2947.	4.1	155
6	Identifying multi-layer gene regulatory modules from multi-dimensional genomic data. <i>Bioinformatics</i> , 2012, 28, 2458-2466.	4.1	123
7	Comparative pan-cancer DNA methylation analysis reveals cancer common and specific patterns. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw063.	6.5	119
8	Deciphering spatial domains from spatially resolved transcriptomics with an adaptive graph attention auto-encoder. <i>Nature Communications</i> , 2022, 13, 1739.	12.8	118
9	DrugE-Rank: improving drug-target interaction prediction of new candidate drugs or targets by ensemble learning to rank. <i>Bioinformatics</i> , 2016, 32, i18-i27.	4.1	115
10	Uncovering fuzzy community structure in complex networks. <i>Physical Review E</i> , 2007, 76, 046103.	2.1	111
11	Discovering functions and revealing mechanisms at molecular level from biological networks. <i>Proteomics</i> , 2007, 7, 2856-2869.	2.2	110
12	Discovery of co-occurring driver pathways in cancer. <i>BMC Bioinformatics</i> , 2014, 15, 271.	2.6	99
13	Comparison of computational methods for imputing single-cell RNA-sequencing data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	83
14	3D Genome of macaque fetal brain reveals evolutionary innovations during primate corticogenesis. <i>Cell</i> , 2021, 184, 723-740.e21.	28.9	76
15	Integrative analysis for identifying joint modular patterns of gene-expression and drug-response data. <i>Bioinformatics</i> , 2016, 32, 1724-1732.	4.1	75
16	Identification of functional modules in a PPI network by clique percolation clustering. <i>Computational Biology and Chemistry</i> , 2006, 30, 445-451.	2.3	65
17	Model-based understanding of single-cell CRISPR screening. <i>Nature Communications</i> , 2019, 10, 2233.	12.8	61
18	Discovery of cancer common and specific driver gene sets. <i>Nucleic Acids Research</i> , 2017, 45, e86-e86.	14.5	55

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19	Clustering complex networks and biological networks by nonnegative matrix factorization with various similarity measures. <i>Neurocomputing</i> , 2008, 72, 134-141.	5.9	54
20	Breast tumor subgroups reveal diverse clinical prognostic power. <i>Scientific Reports</i> , 2015, 4, 4002.	3.3	54
21	The Discovery of Mutated Driver Pathways in Cancer: Models and Algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 988-998.	3.0	53
22	High-dimensional genomic data bias correction and data integration using MANCIE. <i>Nature Communications</i> , 2016, 7, 11305.	12.8	52
23	Edge-group sparse PCA for network-guided high dimensional data analysis. <i>Bioinformatics</i> , 2018, 34, 3479-3487.	4.1	43
24	Systematic DNA methylation analysis of multiple cell lines reveals common and specific patterns within and across tissues of origin. <i>Human Molecular Genetics</i> , 2015, 24, 4374-4384.	2.9	39
25	Identification of mutated core cancer modules by integrating somatic mutation, copy number variation, and gene expression data. <i>BMC Systems Biology</i> , 2013, 7, S4.	3.0	36
26	Quantitative function and algorithm for community detection in bipartite networks. <i>Information Sciences</i> , 2016, 367-368, 874-889.	6.9	35
27	Determining modular organization of protein interaction networks by maximizing modularity density. <i>BMC Systems Biology</i> , 2010, 4, S10.	3.0	34
28	Tumor characterization and stratification by integrated molecular profiles reveals essential pan-cancer features. <i>BMC Genomics</i> , 2015, 16, 503.	2.8	32
29	An integrative and comparative study of pan-cancer transcriptomes reveals distinct cancer common and specific signatures. <i>Scientific Reports</i> , 2016, 6, 33398.	3.3	31
30	Learning common and specific patterns from data of multiple interrelated biological scenarios with matrix factorization. <i>Nucleic Acids Research</i> , 2019, 47, 6606-6617.	14.5	28
31	Simple tricks of convolutional neural network architectures improve DNA-protein binding prediction. <i>Bioinformatics</i> , 2019, 35, 1837-1843.	4.1	28
32	Discovery of two-level modular organization from matched genomic data via joint matrix tri-factorization. <i>Nucleic Acids Research</i> , 2018, 46, 5967-5976.	14.5	27
33	Network-Regularized Sparse Logistic Regression Models for Clinical Risk Prediction and Biomarker Discovery. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 944-953.	3.0	24
34	Toward a systematic understanding of cancers: a survey of the pan-cancer study. <i>Frontiers in Genetics</i> , 2014, 5, 194.	2.3	22
35	A fast mathematical programming procedure for simultaneous fitting of assembly components into cryoEM density maps. <i>Bioinformatics</i> , 2010, 26, i261-i268.	4.1	21
36	A General Joint Matrix Factorization Framework for Data Integration and Its Systematic Algorithmic Exploration. <i>IEEE Transactions on Fuzzy Systems</i> , 2020, 28, 1971-1983.	9.8	21

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37	Imputing single-cell RNA-seq data by considering cell heterogeneity and prior expression of dropouts. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 29-40.	3.3	21
38	Discovery of cell-type specific regulatory elements in the human genome using differential chromatin modification analysis. <i>Nucleic Acids Research</i> , 2013, 41, 9230-9242.	14.5	19
39	Profiling the transcription factor regulatory networks of human cell types. <i>Nucleic Acids Research</i> , 2014, 42, 12380-12387.	14.5	19
40	An Integrative Framework for Combining Sequence and Epigenomic Data to Predict Transcription Factor Binding Sites Using Deep Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 355-364.	3.0	19
41	Discovering Link Communities in Complex Networks by an Integer Programming Model and a Genetic Algorithm. <i>PLoS ONE</i> , 2013, 8, e83739.	2.5	17
42	Common community structure in time-varying networks. <i>Physical Review E</i> , 2012, 85, 056110.	2.1	15
43	MSTD: an efficient method for detecting multi-scale topological domains from symmetric and asymmetric 3D genomic maps. <i>Nucleic Acids Research</i> , 2019, 47, e65-e65.	14.5	15
44	Prediction of enhancer-promoter interactions using the cross-cell type information and domain adversarial neural network. <i>BMC Bioinformatics</i> , 2020, 21, 507.	2.6	15
45	A hybrid graph-theoretic method for mining overlapping functional modules in large sparse protein interaction networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 68.	0.1	11
46	A Two-Stage Method to Identify Joint Modules From Matched MicroRNA and mRNA Expression Data. <i>IEEE Transactions on Nanobioscience</i> , 2016, 15, 362-370.	3.3	10
47	Circular Trajectory Reconstruction Uncovers Cell Cycle Progression and Regulatory Dynamics from Single-Cell Hi-C Maps. <i>Advanced Science</i> , 2019, 6, 1900986.	11.2	10
48	Joint reconstruction of <i>cis</i> -regulatory interaction networks across multiple tissues using single-cell chromatin accessibility data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	10
49	TSCCA: A tensor sparse CCA method for detecting microRNA-gene patterns from multiple cancers. <i>PLoS Computational Biology</i> , 2021, 17, e1009044.	3.2	10
50	VP-Detector: A 3D multi-scale dense convolutional neural network for macromolecule localization and classification in cryo-electron tomograms. <i>Computer Methods and Programs in Biomedicine</i> , 2022, 221, 106871.	4.7	10
51	Local community extraction in directed networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2016, 452, 258-265.	2.6	9
52	Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 657-667.	3.0	8
53	Matrix Factorization Methods for Integrative Cancer Genomics. <i>Methods in Molecular Biology</i> , 2014, 1176, 229-242.	0.9	8
54	Disease category-specific annotation of variants using an ensemble learning framework. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	7

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55	Network diffusion for scalable embedding of massive single-cell ATAC-seq data. Science Bulletin, 2021, 66, 2271-2276.	9.0	7
56	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
57	Sparse Weighted Canonical Correlation Analysis. Chinese Journal of Electronics, 2018, 27, 459-466.	1.5	6
58	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
59	Distributed Bayesian Matrix Decomposition for Big Data Mining and Clustering. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 3701-3713.	5.7	6
60	Towards understanding residual and dilated dense neural networks via convolutional sparse coding. National Science Review, 2021, 8, nwaal159.	9.5	6
61	A Querying Method with Feedback Mechanism for Protein Interaction Network. , 2011, , .		5
62	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
63	Deciphering the Spatial Modular Patterns of Tissues by Integrating Spatial and Single-Cell Transcriptomic Data. Journal of Computational Biology, 0, , .	1.6	5
64	Convergence of algorithms used for principal component analysis. Science in China Series D: Earth Sciences, 1997, 40, 597-604.	0.9	4
65	Robust Bayesian matrix decomposition with mixture of Gaussian noise. Neurocomputing, 2021, 449, 108-116.	5.9	4
66	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
67	Fuzzy System Methods in Modeling Gene Expression and Analyzing Protein Networks. Studies in Fuzziness and Soft Computing, 2009, , 165-189.	0.8	3
68	An effective sequence-alignment-free superpositioning of pairwise or multiple structures with missing data. Algorithms for Molecular Biology, 2016, 11, 18.	1.2	3
69	Integrative cancer genomics: models, algorithms and analysis. Frontiers of Computer Science, 2017, 11, 392-406.	2.4	3
70	Matrix Integrative Analysis (MIA) of Multiple Genomic Data for Modular Patterns. Frontiers in Genetics, 2018, 9, 194.	2.3	3
71	Detecting community structure: From parsimony to weighted parsimony. Journal of Systems Science and Complexity, 2010, 23, 1024-1036.	2.8	2
72	Integrative Analysis of Transcription Factor Combinatorial Interactions Using a Bayesian Tensor Factorization Approach. Frontiers in Genetics, 2017, 8, 140.	2.3	2

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73	A kernel non-negative matrix factorization framework for single cell clustering. Applied Mathematical Modelling, 2021, 90, 875-888.	4.2	2
74	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
75	Approximate distance correlation for selecting highly interrelated genes across datasets. PLoS Computational Biology, 2021, 17, e1009548.	3.2	2
76	Prediction of the transcription factor binding sites with meta-learning. Methods, 2022, , .	3.8	2
77	Detect taxonomy-specific pathway associations with environmental factors using metagenomic data. , 2013, , .		1
78	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
79	A New Approach of Information Discrepancy to Analysis of Questionnaire Data. Communications in Statistics - Theory and Methods, 2003, 32, 435-457.	1.0	0
80	A dynamical method to extract communities induced by low or middle-degree nodes. , 2011, , .		0
81	Identifying mutated core modules in glioblastoma by integrative network analysis. , 2012, , .		0
82	Guest Editorial for Special Section on ISB/TBC 2014. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1074-1075.	3.0	0
83	Network Analysis, Integration and Methods in Computational Biology: A Brief Survey on Recent Advances. Understanding Complex Systems, 2016, , 459-482.	0.6	0
84	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
85	BMTK: a toolkit for determining modules in biological bipartite networks. Quantitative Biology, 2018, 6, 186-192.	0.5	0
86	Omics tools for the needle out of haystack?. Journal of Genetics and Genomics, 2018, 45, 343-344.	3.9	0
87	Computational Methods for Subtyping of Tumors and Their Applications for Deciphering Tumor Heterogeneity. Methods in Molecular Biology, 2019, 1878, 193-207.	0.9	0
88	Integrating Multiple Types of Data to Identify MicroRNAâ€“Gene Co-modules. Methods in Molecular Biology, 2013, 1049, 215-229.	0.9	0
89	Sparse Partial Least Squares Methods for Joint Modular Pattern Discovery. Methods in Molecular Biology, 2020, 2082, 173-186.	0.9	0
90	MSTD for Detecting Topological Domains from 3D Genomic Maps. Methods in Molecular Biology, 2020, 2117, 79-92.	0.9	0

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91	Adversarial Information Bottleneck. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 221-230.	11.3	0
92	Learnable Graph-Regularization for Matrix Decomposition. ACM Transactions on Knowledge Discovery From Data, 2023, 17, 1-20.	3.5	0