

Jingyi Jessica Li

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

18,930
citations

279798

23
h-index

149698

56
g-index

91
all docs

91
docs citations

91
times ranked

38027
citing authors

#	ARTICLE	IF	CITATIONS
1	Simulating Single-Cell Gene Expression Count Data with Preserved Gene Correlations by scDesign2. <i>Journal of Computational Biology</i> , 2022, 29, 23-26.	1.6	3
2	Statistics or biology: the zero-inflation controversy about scRNA-seq data. <i>Genome Biology</i> , 2022, 23, 31.	8.8	302
3	Exaggerated false positives by popular differential expression methods when analyzing human population samples. <i>Genome Biology</i> , 2022, 23, 79.	8.8	88
4	The interplay between translational efficiency, poly(A) tails, microRNAs, and neuronal activation. <i>Rna</i> , 2022, 28, 808-831.	3.5	2
5	scSampler: fast diversity-preserving subsampling of large-scale single-cell transcriptomic data. <i>Bioinformatics</i> , 2022, 38, 3126-3127.	4.1	1
6	Single-cell generalized trend model (scGTM): a flexible and interpretable model of gene expression trend along cell pseudotime. <i>Bioinformatics</i> , 2022, 38, 3927-3934.	4.1	2
7	A new bioinformatics tool to recover missing gene expression in single-cell RNA sequencing data. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 1-2.	3.3	1
8	Benchmarking Computational Doublet-Detection Methods for Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2021, 12, 176-194.e6.	6.2	99
9	Bipartite tight spectral clustering (BiTSC) algorithm for identifying conserved gene co-clusters in two species. <i>Bioinformatics</i> , 2021, 37, 1225-1233.	4.1	3
10	Cellular Heterogeneityâ€Adjusted clonal Methylation (CHALM) improves prediction of gene expression. <i>Nature Communications</i> , 2021, 12, 400.	12.8	13
11	Network Modeling in Biology: Statistical Methods for Gene and Brain Networks. <i>Statistical Science</i> , 2021, 36, 89-108.	2.8	6
12	RAD: a web application to identify region associated differentially expressed genes. <i>Bioinformatics</i> , 2021, 37, 2741-2743.	4.1	11
13	Postoperative Admission of Adult Craniotomy Patients to the Neuroscience Ward Reduces Length of Stay and Cost. <i>Neurosurgery</i> , 2021, 89, 85-93.	1.1	3
14	PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data. <i>Genome Biology</i> , 2021, 22, 124.	8.8	26
15	scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. <i>Genome Biology</i> , 2021, 22, 163.	8.8	48
16	Identifying the combinatorial control of signal-dependent transcription factors. <i>PLoS Computational Biology</i> , 2021, 17, e1009095.	3.2	15
17	mblmpute: an accurate and robust imputation method for microbiome data. <i>Genome Biology</i> , 2021, 22, 192.	8.8	23
18	scPNMF: sparse gene encoding of single cells to facilitate gene selection for targeted gene profiling. <i>Bioinformatics</i> , 2021, 37, i358-i366.	4.1	9

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19	Protocol for executing and benchmarking eight computational doublet-detection methods in single-cell RNA sequencing data analysis. STAR Protocols, 2021, 2, 100699.	1.2	12
20	The concurrence of DNA methylation and demethylation is associated with transcription regulation. Nature Communications, 2021, 12, 5285.	12.8	29
21	Clipper: p-value-free FDR control on high-throughput data from two conditions. Genome Biology, 2021, 22, 288.	8.8	20
22	A flexible model-free prediction-based framework for feature ranking.. Journal of Machine Learning Research, 2021, 22, .	62.4	0
23	Integrin-Src-YAP1 signaling mediates the melanoma acquired resistance to MAPK and PI3K/mTOR dual targeted therapy. Molecular Biomedicine, 2020, 1, 12.	4.4	16
24	DORGE: Discovery of Oncogenes and tumor suppressor genes using Genetic and Epigenetic features. Science Advances, 2020, 6, .	10.3	34
25	Statistical Hypothesis Testing versus Machine Learning Binary Classification: Distinctions and Guidelines. Patterns, 2020, 1, 100115.	5.9	24
26	A Bootstrap Lasso + Partial Ridge Method to Construct Confidence Intervals for Parameters in High-dimensional Sparse Linear Models. Statistica Sinica, 2020, , .	0.3	5
27	Quantitative principles of cis-translational control by general mRNA sequence features in eukaryotes. Genome Biology, 2019, 20, 162.	8.8	29
28	A statistical simulator scDesign for rational scRNA-seq experimental design. Bioinformatics, 2019, 35, i41-i50.	4.1	48
29	AIDE: annotation-assisted isoform discovery with high precision. Genome Research, 2019, 29, 2056-2072.	5.5	10
30	EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. Nucleic Acids Research, 2019, 47, e77-e77.	14.5	6
31	Word and Sentence Embedding Tools to Measure Semantic Similarity of Gene Ontology Terms by Their Definitions. Journal of Computational Biology, 2019, 26, 38-52.	1.6	16
32	Neyman-Pearson classification algorithms and NP receiver operating characteristics. Science Advances, 2018, 4, eaao1659.	10.3	46
33	Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1069-E1074.	7.1	51
34	Spliceosome Profiling Visualizes Operations of a Dynamic RNP at Nucleotide Resolution. Cell, 2018, 173, 1014-1030.e17.	28.9	39
35	MSIQ: Joint modeling of multiple RNA-seq samples for accurate isoform quantification. Annals of Applied Statistics, 2018, 12, 510-539.	1.1	5
36	An accurate and robust imputation method scImpute for single-cell RNA-seq data. Nature Communications, 2018, 9, 997.	12.8	495

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37	Understanding patterns and correlates of daily pain using the Sickle cell disease Mobile Application to Record Symptoms via Technology (<scp>SMART</scp>). <i>British Journal of Haematology</i> , 2018, 183, 306-308.	2.5	3
38	Modeling and analysis of RNA-seq data: a review from a statistical perspective. <i>Quantitative Biology</i> , 2018, 6, 195-209.	0.5	49
39	Large-scale mapping of mammalian transcriptomes identifies conserved genes associated with different cell states. <i>Nucleic Acids Research</i> , 2017, 45, gkw1256.	14.5	10
40	TROM: A Testing-Based Method for Finding Transcriptomic Similarity of Biological Samples. <i>Statistics in Biosciences</i> , 2017, 9, 105-136.	1.2	16
41	Hybrid Statistical and Mechanistic Mathematical Model Guides Mobile Health Intervention for Chronic Pain. <i>Journal of Computational Biology</i> , 2017, 24, 675-688.	1.6	3
42	Correspondence of <i>D. melanogaster</i> and <i>C. elegans</i> developmental stages revealed by alternative splicing characteristics of conserved exons. <i>BMC Genomics</i> , 2017, 18, 234.	2.8	3
43	Quantitating translational control: mRNA abundance-dependent and independent contributions and the mRNA sequences that specify them. <i>Nucleic Acids Research</i> , 2017, 45, 11821-11836.	14.5	28
44	Genomic Applications of the Neyman-Pearson Classification Paradigm. , 2016, , 145-167.		2
45	NMFP: a non-negative matrix factorization based preselection method to increase accuracy of identifying mRNA isoforms from RNA-seq data. <i>BMC Genomics</i> , 2016, 17, 11.	2.8	10
46	Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. <i>BMC Genomics</i> , 2016, 17, 10.	2.8	7
47	A quantitative proteomic analysis of cellular responses to high glucose media in Chinese hamster ovary cells. <i>Biotechnology Progress</i> , 2015, 31, 1026-1038.	2.6	30
48	TRANSCRIPTOME ANALYSIS USING NEXT-GENERATION SEQUENCING. , 2015, , 915-936.		1
49	Statistics requantitates the central dogma. <i>Science</i> , 2015, 347, 1066-1067.	12.6	155
50	Comparison of <i>D. melanogaster</i> and <i>C. elegans</i> developmental stages, tissues, and cells by modENCODE RNA-seq data. <i>Genome Research</i> , 2014, 24, 1086-1101.	5.5	88
51	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	27.8	289
52	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	27.8	184
53	System wide analyses have underestimated protein abundances and the importance of transcription in mammals. <i>PeerJ</i> , 2014, 2, e270.	2.0	255
54	DNA regions bound at low occupancy by transcription factors do not drive patterned reporter gene expression in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21330-21335.	7.1	141

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55	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
56	Bi-clustering of Li near P-attens In Gene Expression Data. <i>Journal of Computational Biology</i> , 2012, 19, 619-631.	1.6	9
57	Oct4 was a novel target of Wnt signaling pathway. <i>Molecular and Cellular Biochemistry</i> , 2012, 362, 233-240.	3.1	49
58	Sparse linear modeling of next-generation mRNA sequencing (RNA-Seq) data for isoform discovery and abundance estimation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19867-19872.	7.1	135
59	Developmental roles of 21 <i>Drosophila</i> transcription factors are determined by quantitative differences in binding to an overlapping set of thousands of genomic regions. <i>Genome Biology</i> , 2009, 10, R80.	9.6	313