

Ziv Bar-Joseph

List of Publications by Year in descending order

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Version: 2024-02-01

148
papers

14,344
citations

50566

48
h-index

25230

113
g-index

176
all docs

176
docs citations

176
times ranked

20441
citing authors

#	ARTICLE	IF	CITATIONS
1	Clustering spatial transcriptomics data. <i>Bioinformatics</i> , 2022, 38, 997-1004.	1.8	25
2	Temporal modelling using single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2022, 23, 355-368.	7.7	65
3	TraSig: inferring cell-cell interactions from pseudotime ordering of scRNA-Seq data. <i>Genome Biology</i> , 2022, 23, 73.	3.8	6
4	Integrating longitudinal clinical and microbiome data to predict growth faltering in preterm infants. <i>Journal of Biomedical Informatics</i> , 2022, 128, 104031.	2.5	3
5	Interactive single-cell data analysis using Cellar. <i>Nature Communications</i> , 2022, 13, 1998.	5.8	11
6	Membrane marker selection for segmenting single cell spatial proteomics data. <i>Nature Communications</i> , 2022, 13, 1999.	5.8	11
7	scSTEM: clustering pseudotime ordered single-cell data. <i>Genome Biology</i> , 2022, 23, .	3.8	3
8	Dhaka: variational autoencoder for unmasking tumor heterogeneity from single cell genomic data. <i>Bioinformatics</i> , 2021, 37, 1535-1543.	1.8	38
9	Identifying signaling genes in spatial single-cell expression data. <i>Bioinformatics</i> , 2021, 37, 968-975.	1.8	33
10	Dynamic Bayesian Networks for Integrating Multi-omics Time Series Microbiome Data. <i>MSystems</i> , 2021, 6, .	1.7	19
11	Deep learning of gene relationships from single cell time-course expression data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	15
12	Supervised Adversarial Alignment of Single-Cell RNA-seq Data. <i>Journal of Computational Biology</i> , 2021, 28, 501-513.	0.8	18
13	Computational tools for analyzing single-cell data in pluripotent cell differentiation studies. <i>Cell Reports Methods</i> , 2021, 1, 100087.	1.4	3
14	Analysis of time-series regulatory networks. <i>Current Opinion in Systems Biology</i> , 2020, 21, 16-24.	1.3	11
15	GCNG: graph convolutional networks for inferring gene interaction from spatial transcriptomics data. <i>Genome Biology</i> , 2020, 21, 300.	3.8	83
16	Single-cell lineage tracing by integrating CRISPR-Cas9 mutations with transcriptomic data. <i>Nature Communications</i> , 2020, 11, 3055.	5.8	41
17	Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , 2020, 6, 290-302.	4.7	145
18	Inferring TF activation order in time series scRNA-Seq studies. <i>PLoS Computational Biology</i> , 2020, 16, e1007644.	1.5	9

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19	Reconstructed Single-Cell Fate Trajectories Define Lineage Plasticity Windows during Differentiation of Human PSC-Derived Distal Lung Progenitors. <i>Cell Stem Cell</i> , 2020, 26, 593-608.e8.	5.2	114
20	Supervised Adversarial Alignment of Single-Cell RNA-seq Data. <i>Lecture Notes in Computer Science</i> , 2020, , 72-87.	1.0	6
21	Iterative point set registration for aligning scRNA-seq data. <i>PLoS Computational Biology</i> , 2020, 16, e1007939.	1.5	3
22	Iterative point set registration for aligning scRNA-seq data. , 2020, 16, e1007939.		0
23	Iterative point set registration for aligning scRNA-seq data. , 2020, 16, e1007939.		0
24	Iterative point set registration for aligning scRNA-seq data. , 2020, 16, e1007939.		0
25	Iterative point set registration for aligning scRNA-seq data. , 2020, 16, e1007939.		0
26	Control of cytokinesis by β_2 -adrenergic receptors indicates an approach for regulating cardiomyocyte endowment. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	73
27	Integrating multiomics longitudinal data to reconstruct networks underlying lung development. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2019, 317, L556-L568.	1.3	19
28	Adjustment in tumbling rates improves bacterial chemotaxis on obstacle-laden terrains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11770-11775.	3.3	12
29	Continuous-state HMMs for modeling time-series single-cell RNA-Seq data. <i>Bioinformatics</i> , 2019, 35, 4707-4715.	1.8	34
30	Protein interaction disruption in cancer. <i>BMC Cancer</i> , 2019, 19, 370.	1.1	7
31	A bacterial based distributed gradient descent model for mass scale evacuations. <i>Swarm and Evolutionary Computation</i> , 2019, 46, 97-103.	4.5	3
32	Cell lineage inference from SNP and scRNA-Seq data. <i>Nucleic Acids Research</i> , 2019, 47, e56-e56.	6.5	21
33	Dynamic interaction network inference from longitudinal microbiome data. <i>Microbiome</i> , 2019, 7, 54.	4.9	59
34	Network-guided prediction of aromatase inhibitor response in breast cancer. <i>PLoS Computational Biology</i> , 2019, 15, e1006730.	1.5	5
35	Deep learning for inferring gene relationships from single-cell expression data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 27151-27158.	3.3	141
36	Construction of integrated microRNA and mRNA immune cell signatures to predict survival of patients with breast and ovarian cancer. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 34-42.	1.5	9

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37	Integration of Heterogeneous Experimental Data Improves Global Map of Human Protein Complexes. , 2019, 2019, 144-153.		1
38	Transcriptional regulatory model of fibrosis progression in the human lung. JCI Insight, 2019, 4, .	2.3	113
39	Reconstructing differentiation networks and their regulation from time series single-cell expression data. Genome Research, 2018, 28, 383-395.	2.4	39
40	Network Design and the Brain. Trends in Cognitive Sciences, 2018, 22, 64-78.	4.0	30
41	AAweb server for comparative analysis of single-cell RNA-seq data. Nature Communications, 2018, 9, 4768.	5.8	48
42	Predicting protein targets for drug-like compounds using transcriptomics. PLoS Computational Biology, 2018, 14, e1006651.	1.5	51
43	Single-Cell Transcriptomic Analysis of Cardiac Differentiation from Human PSCs Reveals HOPX-Dependent Cardiomyocyte Maturation. Cell Stem Cell, 2018, 23, 586-598.e8.	5.2	215
44	Hercules: a profile HMM-based hybrid error correction algorithm for long reads. Nucleic Acids Research, 2018, 46, e125.	6.5	23
45	iDREM: Interactive visualization of dynamic regulatory networks. PLoS Computational Biology, 2018, 14, e1006019.	1.5	29
46	TASIC: determining branching models from time series single cell data. Bioinformatics, 2017, 33, 2504-2512.	1.8	33
47	Validation of a 52-gene risk profile for outcome prediction in patients with idiopathic pulmonary fibrosis: an international, multicentre, cohort study. Lancet Respiratory Medicine,the, 2017, 5, 857-868.	5.2	115
48	Using neural networks for reducing the dimensions of single-cell RNA-Seq data. Nucleic Acids Research, 2017, 45, e156-e156.	6.5	181
49	MethRaFo: MeDIP-seq methylation estimate using a Random Forest Regressor. Bioinformatics, 2017, 33, 3477-3479.	1.8	11
50	Transcriptome analyses identify key cellular factors associated with HIV-1-associated neuropathogenesis in infected men. Aids, 2017, 31, 623-633.	1.0	9
51	Reconstructing cancer drug response networks using multitask learning. BMC Systems Biology, 2017, 11, 96.	3.0	5
52	Selecting the most appropriate time points to profile in high-throughput studies. ELife, 2017, 6, .	2.8	27
53	Tradeoffs between Dense and Replicate Sampling Strategies for High-Throughput Time Series Experiments. Cell Systems, 2016, 3, 35-42.	2.9	39
54	Genome wide predictions of miRNA regulation by transcription factors. Bioinformatics, 2016, 32, i746-i754.	1.8	9

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55	A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , 2016, 354, .	6.0	394
56	Reconstructing the temporal progression of HIV-1 immune response pathways. <i>Bioinformatics</i> , 2016, 32, i253-i261.	1.8	14
57	The SDREM Method for Reconstructing Signaling and Regulatory Response Networks: Applications for Studying Disease Progression. <i>Methods in Molecular Biology</i> , 2016, 1303, 493-506.	0.4	4
58	Temporal transcriptional response to latency reversing agents identifies specific factors regulating HIV-1 viral transcriptional switch. <i>Retrovirology</i> , 2015, 12, 85.	0.9	14
59	De novo ChIP-seq analysis. <i>Genome Biology</i> , 2015, 16, 205.	3.8	10
60	Decreasing-Rate Pruning Optimizes the Construction of Efficient and Robust Distributed Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004347.	1.5	43
61	Unbiased, High-Throughput Electron Microscopy Analysis of Experience-Dependent Synaptic Changes in the Neocortex. <i>Journal of Neuroscience</i> , 2015, 35, 16450-16462.	1.7	23
62	cDREM: Inferring Dynamic Combinatorial Gene Regulation. <i>Journal of Computational Biology</i> , 2015, 22, 324-333.	0.8	10
63	Distributed information processing in biological and computational systems. <i>Communications of the ACM</i> , 2015, 58, 94-102.	3.3	68
64	MassExodus: modeling evolving networks in harsh environments. <i>Data Mining and Knowledge Discovery</i> , 2015, 29, 1211-1232.	2.4	3
65	ModuleBlast: identifying activated sub-networks within and across species. <i>Nucleic Acids Research</i> , 2015, 43, e20-e20.	6.5	12
66	SMARTS: reconstructing disease response networks from multiple individuals using time series gene expression data. <i>Bioinformatics</i> , 2015, 31, 1250-1257.	1.8	18
67	Gene Expression in Relation to Exhaled Nitric Oxide Identifies Novel Asthma Phenotypes with Unique Biomolecular Pathways. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014, 190, 1363-1372.	2.5	162
68	Multitask Learning of Signaling and Regulatory Networks with Application to Studying Human Response to Flu. <i>PLoS Computational Biology</i> , 2014, 10, e1003943.	1.5	12
69	Topological properties of robust biological and computational networks. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140283.	1.5	26
70	Future Directions in Idiopathic Pulmonary Fibrosis Research. An NHLBI Workshop Report. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014, 189, 214-222.	2.5	199
71	MicroRNA regulation and its effects on cellular transcriptome in Human Immunodeficiency Virus-1 (HIV-1) infected individuals with distinct viral load and CD4 cell counts. <i>BMC Infectious Diseases</i> , 2013, 13, 250.	1.3	63
72	Beeping a maximal independent set. <i>Distributed Computing</i> , 2013, 26, 195-208.	0.7	45

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73	Carbon catabolite repression correlates with the maintenance of near invariant molecular crowding in proliferating E. coli cells. BMC Systems Biology, 2013, 7, 138.	3.0	13
74	ExpressionBlast: mining large, unstructured expression databases. Nature Methods, 2013, 10, 925-926.	9.0	30
75	Linking the signaling cascades and dynamic regulatory networks controlling stress responses. Genome Research, 2013, 23, 365-376.	2.4	71
76	A high-throughput framework to detect synapses in electron microscopy images. Bioinformatics, 2013, 29, i9-i17.	1.8	14
77	Integrating sequence, expression and interaction data to determine condition-specific miRNA regulation. Bioinformatics, 2013, 29, i89-i97.	1.8	43
78	Identifying proteins controlling key disease signaling pathways. Bioinformatics, 2013, 29, i227-i236.	1.8	28
79	Probabilistic error correction for RNA sequencing. Nucleic Acids Research, 2013, 41, e109-e109.	6.5	68
80	Reconstructing dynamic microRNA-regulated interaction networks. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15686-15691.	3.3	59
81	Predicting tissue specific transcription factor binding sites. BMC Genomics, 2013, 14, 796.	1.2	25
82	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. ELife, 2013, 2, e00675.	2.8	379
83	Matching experiments across species using expression values and textual information. Bioinformatics, 2012, 28, i258-i264.	1.8	4
84	DREM 2.0: Improved reconstruction of dynamic regulatory networks from time-series expression data. BMC Systems Biology, 2012, 6, 104.	3.0	118
85	Studying and modelling dynamic biological processes using time-series gene expression data. Nature Reviews Genetics, 2012, 13, 552-564.	7.7	424
86	The sirtuin SIRT6 regulates lifespan in male mice. Nature, 2012, 483, 218-221.	13.7	910
87	A Network-based Approach for Predicting Missing Pathway Interactions. PLoS Computational Biology, 2012, 8, e1002640.	1.5	34
88	Algorithms in nature: the convergence of systems biology and computational thinking. Molecular Systems Biology, 2011, 7, 546.	3.2	93
89	DECOD: fast and accurate discriminative DNA motif finding. Bioinformatics, 2011, 27, 2361-2367.	1.8	38
90	Large Scale Comparison of Innate Responses to Viral and Bacterial Pathogens in Mouse and Macaque. PLoS ONE, 2011, 6, e22401.	1.1	24

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91	Biological interaction networks are conserved at the module level. BMC Systems Biology, 2011, 5, 134.	3.0	32
92	Preface. Journal of Computational Biology, 2011, 18, 131-131.	0.8	1
93	Discriminative Motif Finding for Predicting Protein Subcellular Localization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 441-451.	1.9	32
94	A Biological Solution to a Fundamental Distributed Computing Problem. Science, 2011, 331, 183-185.	6.0	117
95	Discovering pathways by orienting edges in protein interaction networks. Nucleic Acids Research, 2011, 39, e22-e22.	6.5	95
96	Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. Journal of Computational Biology, 2011, 18, 1709-1722.	0.8	3
97	Beeping a Maximal Independent Set. Lecture Notes in Computer Science, 2011, , 32-50.	1.0	22
98	Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. Lecture Notes in Computer Science, 2011, , 204-221.	1.0	0
99	Combination of genomic approaches with functional genetic experiments reveals two modes of repression of yeast middle-phase meiosis genes. BMC Genomics, 2010, 11, 478.	1.2	10
100	Integrating multiple evidence sources to predict transcription factor binding in the human genome. Genome Research, 2010, 20, 526-536.	2.4	85
101	Cross-species queries of large gene expression databases. Bioinformatics, 2010, 26, 2416-2423.	1.8	33
102	Computational Methods for Analyzing Dynamic Regulatory Networks. Methods in Molecular Biology, 2010, 674, 419-441.	0.4	7
103	Evolutionary divergence in the fungal response to fluconazole revealed by soft clustering. Genome Biology, 2010, 11, R77.	13.9	38
104	Cross Species Expression Analysis of Innate Immune Response. Journal of Computational Biology, 2010, 17, 253-268.	0.8	10
105	Backup in gene regulatory networks explains differences between binding and knockout results. Molecular Systems Biology, 2009, 5, 276.	3.2	76
106	Schools Anxiously Await NRC Program Rankings. Science, 2009, 324, 1140-1141.	6.0	0
107	Modeling spatial and temporal variation in motion data. , 2009, , .		5
108	Budding Yeast <i>SSD1-V</i> Regulates Transcript Levels of Many Longevity Genes and Extends Chronological Life Span in Purified Quiescent Cells. Molecular Biology of the Cell, 2009, 20, 3851-3864.	0.9	46

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109	Modeling spatial and temporal variation in motion data. <i>ACM Transactions on Graphics</i> , 2009, 28, 1-10.	4.9	54
110	Systematic prediction of human membrane receptor interactions. <i>Proteomics</i> , 2009, 9, 5243-5255.	1.3	22
111	A Combined Expression-Interaction Model for Inferring the Temporal Activity of Transcription Factors. <i>Journal of Computational Biology</i> , 2009, 16, 1035-1049.	0.8	14
112	Cross species analysis of microarray expression data. <i>Bioinformatics</i> , 2009, 25, 1476-1483.	1.8	104
113	IL-3 and Oncogenic Abl Regulate the Myeloblast Transcriptome by Altering mRNA Stability. <i>PLoS ONE</i> , 2009, 4, e7469.	1.1	9
114	Cross Species Expression Analysis of Innate Immune Response. <i>Lecture Notes in Computer Science</i> , 2009, , 90-107.	1.0	0
115	Impact of the solvent capacity constraint on <i>E. coli</i> metabolism. <i>BMC Systems Biology</i> , 2008, 2, 7.	3.0	106
116	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008, 9, S2.	13.9	214
117	Extracting Dynamics from Static Cancer Expression Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 172-182.	1.9	31
118	Alignment and classification of time series gene expression in clinical studies. <i>Bioinformatics</i> , 2008, 24, i147-i155.	1.8	53
119	A Semi-Supervised Method for Predicting Transcription Factor-Gene Interactions in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2008, 4, e1000044.	1.5	85
120	A probabilistic generative model for GO enrichment analysis. <i>Nucleic Acids Research</i> , 2008, 36, e109-e109.	6.5	74
121	Genome-wide transcriptional analysis of the human cell cycle identifies genes differentially regulated in normal and cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 955-960.	3.3	145
122	Protein complex identification by supervised graph local clustering. <i>Bioinformatics</i> , 2008, 24, i250-i268.	1.8	121
123	A Combined Expression-Interaction Model for Inferring the Temporal Activity of Transcription Factors. , 2008, , 82-97.		0
124	Intracellular crowding defines the mode and sequence of substrate uptake by <i>Escherichia coli</i> and constrains its metabolic activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12663-12668.	3.3	338
125	Inferring pairwise regulatory relationships from multiple time series datasets. <i>Bioinformatics</i> , 2007, 23, 755-763.	1.8	30
126	A Patient-Gene Model for Temporal Expression Profiles in Clinical Studies. <i>Journal of Computational Biology</i> , 2007, 14, 324-338.	0.8	12

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127	Continuous hidden process model for time series expression experiments. <i>Bioinformatics</i> , 2007, 23, i459-i467.	1.8	15
128	Reconstructing dynamic regulatory maps. <i>Molecular Systems Biology</i> , 2007, 3, 74.	3.2	183
129	Combined analysis reveals a core set of cycling genes. <i>Genome Biology</i> , 2007, 8, R146.	13.9	36
130	A mixture of feature experts approach for protein-protein interaction prediction. <i>BMC Bioinformatics</i> , 2007, 8, S6.	1.2	53
131	Evaluation of different biological data and computational classification methods for use in protein interaction prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 490-500.	1.5	299
132	STEM: a tool for the analysis of short time series gene expression data. <i>BMC Bioinformatics</i> , 2006, 7, 191.	1.2	1,309
133	Identifying cycling genes by combining sequence homology and expression data. <i>Bioinformatics</i> , 2006, 22, e314-e322.	1.8	15
134	Combined static and dynamic analysis for determining the quality of time-series expression profiles. <i>Nature Biotechnology</i> , 2005, 23, 1503-1508.	9.4	32
135	Clustering short time series gene expression data. <i>Bioinformatics</i> , 2005, 21, i159-i168.	1.8	411
136	Random forest similarity for protein-protein interaction prediction from multiple sources. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 531-42.	0.7	47
137	Deconvolving cell cycle expression data with complementary information. <i>Bioinformatics</i> , 2004, 20, i23-i30.	1.8	45
138	Analyzing time series gene expression data. <i>Bioinformatics</i> , 2004, 20, 2493-2503.	1.8	385
139	RANDOM FOREST SIMILARITY FOR PROTEIN-PROTEIN INTERACTION PREDICTION FROM MULTIPLE SOURCES. , 2004, , .		78
140	Hierarchical Context-based Pixel Ordering. <i>Computer Graphics Forum</i> , 2003, 22, 349-358.	1.8	6
141	Computational discovery of gene modules and regulatory networks. <i>Nature Biotechnology</i> , 2003, 21, 1337-1342.	9.4	528
142	Comparing the continuous representation of time-series expression profiles to identify differentially expressed genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10146-10151.	3.3	109
143	Continuous Representations of Time-Series Gene Expression Data. <i>Journal of Computational Biology</i> , 2003, 10, 341-356.	0.8	216
144	K-ary clustering with optimal leaf ordering for gene expression data. <i>Bioinformatics</i> , 2003, 19, 1070-1078.	1.8	95

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145	Transcriptional Regulatory Networks in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 298, 799-804.	6.0	2,706
146	K-ary Clustering with Optimal Leaf Ordering for Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2002, , 506-520.	1.0	4
147	Texture mixing and texture movie synthesis using statistical learning. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2001, 7, 120-135.	2.9	167
148	Cardiac Directed Differentiation Using Small Molecule WNT Modulation at Single-Cell Resolution. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0