

Minghua Deng

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

3,651
citations

186265

28
h-index

144013

57
g-index

101
all docs

101
docs citations

101
times ranked

4645
citing authors

#	ARTICLE	IF	CITATIONS
1	CLEAR: Cluster-Enhanced Contrast for Self-Supervised Graph Representation Learning. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 899-912.	11.3	11
2	A Survey on Deep Hashing Methods. ACM Transactions on Knowledge Discovery From Data, 2023, 17, 1-50.	3.5	27
3	scMRA: a robust deep learning method to annotate scRNA-seq data with multiple reference datasets. Bioinformatics, 2022, 38, 738-745.	4.1	17
4	Rare variant association tests for ancestry-matched case-control data based on conditional logistic regression. Briefings in Bioinformatics, 2022, , .	6.5	2
5	Profiling transcription factor activity dynamics using intronic reads in time-series transcriptome data. PLoS Computational Biology, 2022, 18, e1009762.	3.2	5
6	scNAME: neighborhood contrastive clustering with ancillary mask estimation for scRNA-seq data. Bioinformatics, 2022, 38, 1575-1583.	4.1	18
7	Improve Deep Unsupervised Hashing via Structural and Intrinsic Similarity Learning. IEEE Signal Processing Letters, 2022, 29, 602-606.	3.6	4
8	Uncovering the Dominant Motion Modes of Allosteric Regulation Improves Allosteric Site Prediction. Journal of Chemical Information and Modeling, 2022, 62, 187-195.	5.4	14
9	GHNN: Graph Harmonic Neural Networks for semi-supervised graph-level classification. Neural Networks, 2022, 151, 70-79.	5.9	23
10	Statistical Methods for Microbiome Compositional Data Network Inference: A Survey. Journal of Computational Biology, 2022, , .	1.6	5
11	DHWP: Learning High-Quality Short Hash Codes Via Weight Pruning. , 2022, , .		1
12	Single-cell RNA-seq data semi-supervised clustering and annotation via structural regularized domain adaptation. Bioinformatics, 2021, 37, 775-784.	4.1	28
13	DNA-GCN: Graph Convolutional Networks for Predicting DNA-Protein Binding. Lecture Notes in Computer Science, 2021, , 458-466.	1.3	4
14	Yeast cell fate control by temporal redundancy modulation of transcription factor paralogs. Nature Communications, 2021, 12, 3145.	12.8	12
15	An Interpretation of Convolutional Neural Networks for Motif Finding from the View of Probability. , 2021, , .		0
16	Expectation pooling: an effective and interpretable pooling method for predicting DNA-protein binding. Bioinformatics, 2020, 36, 1405-1412.	4.1	22
17	International Workshop on Applications of Probability and Statistics to Biology, July 11-13, 2019 - In Honor of Professor Mingping Qian's 80th Birthday. Quantitative Biology, 2020, 8, 177-186.	0.5	0
18	Integrating Deep Supervised, Self-Supervised and Unsupervised Learning for Single-Cell RNA-seq Clustering and Annotation. Genes, 2020, 11, 792.	2.4	23

#	ARTICLE	IF	CITATIONS
19	Direct interaction network inference for compositional data via codaloss. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050037.	0.8	0
20	Deep soft K-means clustering with self-training for single-cell RNA sequence data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa039.	3.2	48
21	Sparsity-Penalized Stacked Denoising Autoencoders for Imputing Single-Cell RNA-seq Data. <i>Genes</i> , 2020, 11, 532.	2.4	8
22	Single-Cell Transcriptome Data Clustering via Multinomial Modeling and Adaptive Fuzzy K-Means Algorithm. <i>Frontiers in Genetics</i> , 2020, 11, 295.	2.3	15
23	scRMD: imputation for single cell RNA-seq data via robust matrix decomposition. <i>Bioinformatics</i> , 2020, 36, 3156-3161.	4.1	42
24	Direct interaction network and differential network inference from compositional data via lasso penalized D-trace loss. <i>PLoS ONE</i> , 2019, 14, e0207731.	2.5	6
25	Detecting virus integration sites based on multiple related sequencing data by VirTect. <i>BMC Medical Genomics</i> , 2019, 12, 19.	1.5	27
26	Compositional data network analysis via lasso penalized D-trace loss. <i>Bioinformatics</i> , 2019, 35, 3404-3411.	4.1	11
27	Predicting protein inter-residue contacts using composite likelihood maximization and deep learning. <i>BMC Bioinformatics</i> , 2019, 20, 537.	2.6	6
28	Deepprune: Learning Efficient and Interpretable Convolutional Networks Through Weight Pruning for Predicting DNA-Protein Binding. <i>Frontiers in Genetics</i> , 2019, 10, 1145.	2.3	13
29	A Novel Noninvasive Program for Staging Liver Fibrosis in Untreated Patients With Chronic Hepatitis B. <i>Clinical and Translational Gastroenterology</i> , 2019, 10, e00033.	2.5	5
30	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. <i>Environmental Microbiology</i> , 2018, 20, 734-754.	3.8	53
31	Inferring Gene-Disease Association by an Integrative Analysis of eQTL Genome-Wide Association Study and Protein-Protein Interaction Data. <i>Human Heredity</i> , 2018, 83, 117-129.	0.8	9
32	RaptorX-Angle: real-value prediction of protein backbone dihedral angles through a hybrid method of clustering and deep learning. <i>BMC Bioinformatics</i> , 2018, 19, 100.	2.6	44
33	gCoda: Conditional Dependence Network Inference for Compositional Data. <i>Journal of Computational Biology</i> , 2017, 24, 699-708.	1.6	40
34	VCNet: vector-based gene co-expression network construction and its application to RNA-seq data. <i>Bioinformatics</i> , 2017, 33, 2173-2181.	4.1	9
35	SVmine improves structural variation detection by integrative mining of predictions from multiple algorithms. <i>Bioinformatics</i> , 2017, 33, 3348-3354.	4.1	6
36	Pysim-sv: a package for simulating structural variation data with GC-biases. <i>BMC Bioinformatics</i> , 2017, 18, 53.	2.6	22

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37	Cell Culture System for Analysis of Genetic Heterogeneity Within Hepatocellular Carcinomas and Response to Pharmacologic Agents. <i>Gastroenterology</i> , 2017, 152, 232-242.e4.	1.3	107
38	Differential network analysis via lasso penalized D-trace loss. <i>Biometrika</i> , 2017, 104, 755-770.	2.4	49
39	Inferring the progression of multifocal liver cancer from spatial and temporal genomic heterogeneity. <i>Oncotarget</i> , 2016, 7, 2867-2877.	1.8	38
40	Improving residue-residue contact prediction via low-rank and sparse decomposition of residue correlation matrix. <i>Biochemical and Biophysical Research Communications</i> , 2016, 472, 217-222.	2.1	19
41	A microscopic landscape of the invasive breast cancer genome. <i>Scientific Reports</i> , 2016, 6, 27545.	3.3	33
42	Insights into the transmission of respiratory infectious diseases through empirical human contact networks. <i>Scientific Reports</i> , 2016, 6, 31484.	3.3	16
43	A network based covariance test for detecting multivariate eQTL in <i>saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2016, 10, 8.	3.0	1
44	Inference of Markovian properties of molecular sequences from NGS data and applications to comparative genomics. <i>Bioinformatics</i> , 2016, 32, 993-1000.	4.1	25
45	Low-Rank and Sparse Matrix Decomposition for Genetic Interaction Data. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	3
46	CCLasso: correlation inference for compositional data through Lasso. <i>Bioinformatics</i> , 2015, 31, 3172-3180.	4.1	133
47	Estimation of isoform expression using hierarchical Bayesian model by RNA-seq. , 2015, , .		0
48	CD4 T-cell transcriptome analysis reveals aberrant regulation of STAT3 and Wnt signaling pathways in rheumatoid arthritis: evidence from a case-control study. <i>Arthritis Research and Therapy</i> , 2015, 17, 76.	3.5	45
49	Estimation of isoform expression in RNA-seq data using a hierarchical Bayesian model. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1542001.	0.8	4
50	RNA Editome in Rhesus Macaque Shaped by Purifying Selection. <i>PLoS Genetics</i> , 2014, 10, e1004274.	3.5	71
51	New developments of alignment-free sequence comparison: measures, statistics and next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2014, 15, 343-353.	6.5	126
52	Using graphical adaptive lasso approach to construct transcription factor and microRNA's combinatorial regulatory network in breast cancer. <i>IET Systems Biology</i> , 2014, 8, 87-95.	1.5	3
53	Imputing missing values for genetic interaction data. <i>Methods</i> , 2014, 67, 269-277.	3.8	5
54	Adjustment method for microarray data generated using two-cycle RNA labeling protocol. <i>BMC Genomics</i> , 2013, 14, 31.	2.8	6

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55	Alignment-Free Sequence Comparison Based on Next-Generation Sequencing Reads. <i>Journal of Computational Biology</i> , 2013, 20, 64-79.	1.6	76
56	Multiple alignment-free sequence comparison. <i>Bioinformatics</i> , 2013, 29, 2690-2698.	4.1	11
57	Statistical Analysis Reveals Co-Expression Patterns of Many Pairs of Genes in Yeast Are Jointly Regulated by Interacting Loci. <i>PLoS Genetics</i> , 2013, 9, e1003414.	3.5	17
58	Integrative Approaches for microRNA Target Prediction: Combining Sequence Information and the Paired mRNA and miRNA Expression Profiles. <i>Current Bioinformatics</i> , 2013, 8, 37-45.	1.5	0
59	Integrative Approaches for microRNA Target Prediction: Combining Sequence Information and the Paired mRNA and miRNA Expression Profiles. <i>Current Bioinformatics</i> , 2013, 8, 37-45.	1.5	16
60	Comparison of metagenomic samples using sequence signatures. <i>BMC Genomics</i> , 2012, 13, 730.	2.8	74
61	Hybridization and amplification rate correction for affymetrix SNP arrays. <i>BMC Medical Genomics</i> , 2012, 5, 24.	1.5	4
62	Etiologic Diagnosis of Lower Respiratory Tract Bacterial Infections Using Sputum Samples and Quantitative Loop-Mediated Isothermal Amplification. <i>PLoS ONE</i> , 2012, 7, e38743.	2.5	24
63	Comparison and evaluation of network clustering algorithms applied to genetic interaction networks. <i>Frontiers in Bioscience - Elite</i> , 2012, E4, 2150.	1.8	2
64	Alignment-Free Sequence Comparison Based on Next Generation Sequencing Reads: Extended Abstract. <i>Lecture Notes in Computer Science</i> , 2012, , 272-285.	1.3	2
65	Predicting MicroRNA targets by integrating sequence and expression data in cancer. , 2011, , .		4
66	A study of biases of DNA copy number estimation based on PICR model. <i>Frontiers of Mathematics in China</i> , 2011, 6, 1203-1216.	0.7	2
67	Integrating multiple types of data to predict novel cell cycle-related genes. <i>BMC Systems Biology</i> , 2011, 5, S9.	3.0	5
68	A Lasso regression model for the construction of microRNA-target regulatory networks. <i>Bioinformatics</i> , 2011, 27, 2406-2413.	4.1	110
69	Modular analysis of the probabilistic genetic interaction network. <i>Bioinformatics</i> , 2011, 27, 853-859.	4.1	10
70	Systematic identification of conserved motif modules in the human genome. <i>BMC Genomics</i> , 2010, 11, 567.	2.8	28
71	Combinatorial regulation of transcription factors and microRNAs. <i>BMC Systems Biology</i> , 2010, 4, 150.	3.0	37
72	Prediction of Protein Functions from Protein-Protein Interaction Data Based on a New Measure of Network Betweenness. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings]</i> International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0

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73	Binding Energy Landscape Analysis Helps to Discriminate True Hits from High-Scoring Decoys in Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 1855-1864.	5.4	23
74	A hybridization model for tiling array analysis. , 2010, , .		0
75	Predicting kinase functional sites using hierarchical stochastic language modelling. <i>Statistics and Its Interface</i> , 2010, 3, 523-531.	0.3	0
76	Pathway Detection Based on Hierarchical LASSO Regression Model. , 2009, , .		0
77	Feature-Based Causal Structure Discovery in Protein and Gene Expression Data with Bayesian Network. , 2009, , .		0
78	REMAS: a new regression model to identify alternative splicing events from exon array data. <i>BMC Bioinformatics</i> , 2009, 10, S18.	2.6	4
79	Searching for bidirectional promoters in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2009, 10, S29.	2.6	45
80	Transcription and splicing regulation in human umbilical vein endothelial cells under hypoxic stress conditions by exon array. <i>BMC Genomics</i> , 2009, 10, 126.	2.8	47
81	Nonlinear cooperation of p53-ING1-induced bax expression and protein S-nitrosylation in GSNO-induced thymocyte apoptosis: a quantitative approach with cross-platform validation. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2009, 14, 236-245.	4.9	5
82	A Robust Empirical Bayesian Method for Detecting Differentially Expressed Genes. , 2009, , .		0
83	Conservation and implications of eukaryote transcriptional regulatory regions across multiple species. <i>BMC Genomics</i> , 2008, 9, 623.	2.8	7
84	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008, 9, S2.	9.6	214
85	On Design of Oligonucleotide SNP Arrays and Methods for Genotype Calling. , 2008, , .		0
86	Diffusion Kernel-Based Logistic Regression Models for Protein Function Prediction. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 40-55.	2.0	90
87	Stochastic model of yeast cell-cycle network. <i>Physica D: Nonlinear Phenomena</i> , 2006, 219, 35-39.	2.8	67
88	An integrated approach to the prediction of domain-domain interactions. <i>BMC Bioinformatics</i> , 2006, 7, 269.	2.6	102
89	Using a Stochastic AdaBoost Algorithm to Discover Interactome Motif Pairs from Sequences. <i>Lecture Notes in Computer Science</i> , 2006, , 622-630.	1.3	2
90	Detecting differentially expressed genes by relative entropy. <i>Journal of Theoretical Biology</i> , 2005, 234, 395-402.	1.7	31

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91	An Integrated Probabilistic Model for Functional Prediction of Proteins. Journal of Computational Biology, 2004, 11, 463-475.	1.6	134
92	Mapping gene ontology to proteins based on protein-protein interaction data. Bioinformatics, 2004, 20, 895-902.	4.1	149
93	Prediction of Protein Function Using Protein-Protein Interaction Data. Journal of Computational Biology, 2003, 10, 947-960.	1.6	274
94	Assessment of the reliability of protein-protein interactions and protein function prediction. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2003, , 140-51.	0.7	39
95	A dynamic programming algorithm for haplotype block partitioning. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7335-7339.	7.1	312
96	Inferring Domain-Domain Interactions From Protein-Protein Interactions. Genome Research, 2002, 12, 1540-1548.	5.5	376
97	Prediction of protein function using protein-protein interaction data. Proceedings, 2002, 1, 197-206.	0.1	11
98	Prediction of protein function using protein-protein interaction data. , 0, , .		31