

# Bo Liao

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

1,401  
citations

293460

24  
h-index

425179

34  
g-index

63  
all docs

63  
docs citations

63  
times ranked

1497  
citing authors

#	ARTICLE	IF	CITATIONS
1	Local-View-Assisted Discriminative Band Selection With Hypergraph Autolearning for Hyperspectral Image Classification. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2020, 58, 2042-2055.	2.7	15
2	Scalable One-Pass Self-Representation Learning for Hyperspectral Band Selection. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2019, 57, 4360-4374.	2.7	32
3	Prediction of Protein Subcellular Localization Based on Fusion of Multi-view Features. <i>Molecules</i> , 2019, 24, 919.	1.7	21
4	Improved Pre-miRNAs Identification Through Mutual Information of Pre-miRNA Sequences and Structures. <i>Frontiers in Genetics</i> , 2019, 10, 119.	1.1	28
5	Global Similarity Method Based on a Two-tier Random Walk for the Prediction of microRNA-Disease Association. <i>Scientific Reports</i> , 2018, 8, 6481.	1.6	31
6	The Advances and Challenges of Deep Learning Application in Biological Big Data Processing. <i>Current Bioinformatics</i> , 2018, 13, 352-359.	0.7	91
7	New 3D graphical representation for RNA structure analysis and its application in the pre-miRNA identification of plants. <i>RSC Advances</i> , 2018, 8, 30833-30841.	1.7	6
8	A novel information diffusion method based on network consistency for identifying disease related microRNAs. <i>RSC Advances</i> , 2018, 8, 36675-36690.	1.7	14
9	Predicting Influenza Antigenicity by Matrix Completion With Antigen and Antiserum Similarity. <i>Frontiers in Microbiology</i> , 2018, 9, 2500.	1.5	16
10	Computational Tools for Investigating Pathogen, Pathogen-Host Interaction, and Infectious Disease. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2018, 2018, 1-2.	0.7	0
11	Gene function prediction based on combining gene ontology hierarchy with multi-instance multi-label learning. <i>RSC Advances</i> , 2018, 8, 28503-28509.	1.7	5
12	BPL LDA: Predicting lncRNA-Disease Associations Based on Simple Paths With Limited Lengths in a Heterogeneous Network. <i>Frontiers in Genetics</i> , 2018, 9, 411.	1.1	52
13	Fisher Discrimination Regularized Robust Coding Based on a Local Center for Tumor Classification. <i>Scientific Reports</i> , 2018, 8, 9152.	1.6	2
14	Semi-Supervised Maximum Discriminative Local Margin for Gene Selection. <i>Scientific Reports</i> , 2018, 8, 8619.	1.6	10
15	Matrix-Based Margin-Maximization Band Selection With Data-Driven Diversity for Hyperspectral Image Classification. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2018, 56, 7294-7309.	2.7	9
16	Predicting Drug-Target Interactions with Neighbor Interaction Information and Discriminative Low-rank Representation. <i>Current Protein and Peptide Science</i> , 2018, 19, 455-467.	0.7	3
17	New multilocus linkage disequilibrium measure for tag SNP selection. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750001.	0.3	6
18	Maxdenominator Reweighted Sparse Representation for Tumor Classification. <i>Scientific Reports</i> , 2017, 7, 46030.	1.6	9

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19	Predicting influenza antigenicity from Hemagglutinin sequence data based on a joint random forest method. <i>Scientific Reports</i> , 2017, 7, 1545.	1.6	40
20	Matrix completion with side information and its applications in predicting the antigenicity of influenza viruses. <i>Bioinformatics</i> , 2017, 33, 3195-3201.	1.8	33
21	Subcellular localization prediction of apoptosis proteins based on evolutionary information and support vector machine. <i>Artificial Intelligence in Medicine</i> , 2017, 78, 41-46.	3.8	29
22	Global network random walk for predicting potential human lncRNA-disease associations. <i>Scientific Reports</i> , 2017, 7, 12442.	1.6	89
23	Improving gene regulatory network structure using redundancy reduction in the MRNET algorithm. <i>RSC Advances</i> , 2017, 7, 23222-23233.	1.7	11
24	A novel information fusion strategy based on a regularized framework for identifying disease-related microRNAs. <i>RSC Advances</i> , 2017, 7, 44447-44455.	1.7	10
25	Network-based collaborative filtering recommendation model for inferring novel disease-related miRNAs. <i>RSC Advances</i> , 2017, 7, 44961-44971.	1.7	10
26	Screening drug-target interactions with positive-unlabeled learning. <i>Scientific Reports</i> , 2017, 7, 8087.	1.6	35
27	Improved low-rank matrix recovery method for predicting miRNA-disease association. <i>Scientific Reports</i> , 2017, 7, 6007.	1.6	21
28	Seeksv: an accurate tool for somatic structural variation and virus integration detection. <i>Bioinformatics</i> , 2017, 33, 184-191.	1.8	64
29	An Improved Binary Differential Evolution Algorithm to Infer Tumor Phylogenetic Trees. <i>BioMed Research International</i> , 2017, 2017, 1-13.	0.9	4
30	Gene Regulatory Network Inferences Using a Maximum-Relevance and Maximum-Significance Strategy. <i>PLoS ONE</i> , 2016, 11, e0166115.	1.1	7
31	Network Consistency Projection for Human miRNA-Disease Associations Inference. <i>Scientific Reports</i> , 2016, 6, 36054.	1.6	89
32	Uncover miRNA-Disease Association by Exploiting Global Network Similarity. <i>PLoS ONE</i> , 2016, 11, e0166509.	1.1	16
33	A Hierarchical Clustering Method of Selecting Kernel SNP to Unify Informative SNP and Tag SNP. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 113-122.	1.9	10
34	A new technique for generating pathogenic barcodes in breast cancer susceptibility analysis. <i>Journal of Theoretical Biology</i> , 2015, 366, 84-90.	0.8	5
35	A co-expression modules based gene selection for cancer recognition. <i>Journal of Theoretical Biology</i> , 2014, 362, 75-82.	0.8	13
36	Gene Selection Using Locality Sensitive Laplacian Score. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1146-1156.	1.9	47

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37	Using Multi-Instance Hierarchical Clustering Learning System to Predict Yeast Gene Function. PLoS ONE, 2014, 9, e90962.	1.1	6
38	Learning a Weighted Meta-Sample Based Parameter Free Sparse Representation Classification for Microarray Data. PLoS ONE, 2014, 9, e104314.	1.1	13
39	A new graphical coding of DNA sequence and its similarity calculation. Physica A: Statistical Mechanics and Its Applications, 2013, 392, 4663-4667.	1.2	30
40	Subcellular localization prediction of apoptosis proteins based on the data mining for amino acid index database. , 2013, , .		1
41	Informative SNPs Selection Based on Two-Locus and Multilocus Linkage Disequilibrium: Criteria of Max-Correlation and Min-Redundancy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 688-695.	1.9	12
42	Accelerating processing speed in pathway research based on GPU. , 2013, , .		0
43	Incorporating Secondary Structural Features into Sequence Information for Predicting Protein Structural Class. Protein and Peptide Letters, 2013, 20, 1079-1087.	0.4	2
44	Incorporating Secondary Features into the General form of Chou's PseAAC for Predicting Protein Structural Class. Protein and Peptide Letters, 2012, 19, 1133-1138.	0.4	36
45	A Novel Method to Select Informative SNPs and Their Application in Genetic Association Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1529-1534.	1.9	9
46	Multiple ant colony algorithm method for selecting tag SNPs. Journal of Biomedical Informatics, 2012, 45, 931-937.	2.5	14
47	A novel feature selection method based on CFS in cancer recognition. , 2012, , .		20
48	Predicting Apoptosis Protein Subcellular Location with PseAAC by Incorporating Tripeptide Composition. Protein and Peptide Letters, 2011, 18, 1086-1092.	0.4	30
49	RNA secondary structure alignment based on an extended binary coding method. International Journal of Quantum Chemistry, 2011, 111, 978-982.	1.0	1
50	A novel graphical representation of protein sequences and its application. Journal of Computational Chemistry, 2011, 32, 2539-2544.	1.5	25
51	A Novel method for similarity analysis and protein sub-cellular localization prediction. Bioinformatics, 2010, 26, 2678-2683.	1.8	43
52	A binary coding method of RNA secondary structure and its application. Journal of Computational Chemistry, 2009, 30, 2205-2212.	1.5	7
53	A 2D graphical representation of DNA sequence based on dual nucleotides and its application. International Journal of Quantum Chemistry, 2009, 109, 948-958.	1.0	26
54	A group of 3D graphical representation of DNA sequences based on dual nucleotides. International Journal of Quantum Chemistry, 2008, 108, 1485-1490.	1.0	34

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55	Novel method for analyzing proteome. International Journal of Quantum Chemistry, 2007, 107, 1295-1300.	1.0	8
56	On the Similarity of DNA Primary Sequences Based on 5-D Representation. Journal of Mathematical Chemistry, 2007, 42, 47-57.	0.7	39
57	On a four-dimensional representation of RNA secondary structures. Journal of Mathematical Chemistry, 2007, 42, 1015-1022.	0.7	10
58	RNA secondary structure 2D graphical representation without degeneracy. International Journal of Quantum Chemistry, 2006, 106, 1749-1755.	1.0	21
59	A graphical method to construct a phylogenetic tree. International Journal of Quantum Chemistry, 2006, 106, 1998-2005.	1.0	10
60	Coronavirus phylogeny based on triplets of nucleic acids bases. Chemical Physics Letters, 2006, 421, 313-318.	1.2	24
61	RNA Secondary Structure 3D Graphical Representation Without Degeneracy. Journal of Mathematical Chemistry, 2006, 39, 629-636.	0.7	10
62	Coronavirus phylogeny based on 2D graphical representation of DNA sequence. Journal of Computational Chemistry, 2006, 27, 1196-1202.	1.5	45
63	Graphical approach to analyzing DNA sequences. Journal of Computational Chemistry, 2005, 26, 1519-1523.	1.5	42