Yadong Wang

List of Publications by Year in Descending Order

117 papers	2,834 citations	20 h-index	52 g-index
141 ext. papers	3,975 ext. citations	5.5 avg, IF	5.54 L-index

#	Paper	IF	Citations
117	M2PP: a novel computational model for predicting drug-targeted pathogenic proteins.. *BMC Bioinformatics*, **2022**, 23, 7	3.6	
116	Prediction of the disease causal genes based on heterogeneous network and multi-feature combination method.. *Computational Biology and Chemistry*, **2022**, 97, 107639	3.6	0
115	Explore potential disease related metabolites based on latent factor model.. *BMC Genomics*, **2022**, 23, 269	4.5	1
114	OTUCD: Unsupervised GCN based metagenomics non-overlapping community detection.. *Computational Biology and Chemistry*, **2022**, 98, 107670	3.6	
113	Prediction performance of twelve tumor mutation burden panels in melanoma and non-small cell lung cancer.. *Critical Reviews in Oncology/Hematology*, **2021**, 169, 103573	7	2
112	A deep learning approach for filtering structural variants in short read sequencing data. *Briefings in Bioinformatics*, **2021**, 22,	13.4	9
111	abPOA: an SIMD-based C library for fast partial order alignment using adaptive band. *Bioinformatics* , **2021**, 37, 2209-2211	7.2	5
110	Factor graph-aggregated heterogeneous network embedding for disease-gene association prediction. *BMC Bioinformatics*, **2021**, 22, 165	3.6	1
109	Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. *Frontiers in Genetics*, **2021**, 12, 658352	4.5	1
108	Fast and Accurate Classification of Meta-Genomics Long Reads With deSAMBA. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 643645	5.7	
107	IIMLP: integrated information-entropy-based method for LncRNA prediction. *BMC Bioinformatics*, **2021**, 22, 243	3.6	0
106	Pan-Cancer Metastasis Prediction Based on Graph Deep Learning Method. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 675978	5.7	0
105	ScGSLC: An unsupervised graph similarity learning framework for single-cell RNA-seq data clustering. *Computational Biology and Chemistry*, **2021**, 90, 107415	3.6	2
104	isoCirc catalogs full-length circular RNA isoforms in human transcriptomes. *Nature Communications*, **2021**, 12, 266	17.4	33
103	Identification of Parkinsonâs Disease-Causing Genes via Omics Data. *Frontiers in Genetics*, **2021**, 12, 712164	4.5	2
102	Fast and SNP-aware short read alignment with SALT. *BMC Bioinformatics*, **2021**, 22, 172	3.6	
101	PanSVR: Pan-Genome Augmented Short Read Realignment for Sensitive Detection of Structural Variations. *Frontiers in Genetics*, **2021**, 12, 731515	4.5	0

100	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. *BMC Bioinformatics*, **2021**, 22, 403	3.6	5
99	Enhancing discoveries of molecular QTL studies with small sample size using summary statistic imputation. *Briefings in Bioinformatics*, **2021**,	13.4	5
98	Differentially Expressed Mutant Genes Reveal Potential Prognostic Markers For Lung Adenocarcinoma **2021**,		1
97	DRBin: Metagenomic binning based on deep representation learning.. *Journal of Genetics and Genomics*, **2021**,	4	1
96	Evaluating individual genome similarity with a topic model. *Bioinformatics*, **2020**, 36, 4757-4764	7.2	1
95	Identifying Protein Biomarkers in Blood for Alzheimerâs Disease. *Frontiers in Cell and Developmental Biology*, **2020**, 8, 472	5.7	6
94	Prognostic prediction of carcinoma by a differential-regulatory-network-embedded deep neural network. *Computational Biology and Chemistry*, **2020**, 88, 107317	3.6	2
93	Identifying and removing haplotypic duplication in primary genome assemblies. *Bioinformatics*, **2020**, 36, 2896-2898	7.2	222
92	Contents, Construction Methods, Data Resources, and Functions Comparative Analysis of Bacteria Databases. *International Journal of Biological Sciences*, **2020**, 16, 838-848	11.2	1
91	PGsim: A Comprehensive and Highly Customizable Personal Genome Simulator. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 28	5.8	1
90	PmDNE: Prediction of miRNA-Disease Association Based on Network Embedding and Network Similarity Analysis. *BioMed Research International*, **2020**, 2020, 6248686	3	2
89	SpliVert: A Protein Multiple Sequence Alignment Refinement Method Based on Splitting-Splicing Vertically. *Protein and Peptide Letters*, **2020**, 27, 295-302	1.9	4
88	An Information Gain-based Method for Evaluating the Classification Power of Features Towards Identifying Enhancers. *Current Bioinformatics*, **2020**, 15, 574-580	4.7	5
87	Disease Module Identification Based on Representation Learning of Complex Networks Integrated From GWAS, eQTL Summaries, and Human Interactome. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 418	5.8	6
86	MGMIN: A Normalization Method for Correcting Probe Design Bias in Illumina Infinium HumanMethylation450 BeadChips. *Frontiers in Genetics*, **2020**, 11, 538492	4.5	2
85	Filtering de novo indels in parent-offspring trios. *BMC Bioinformatics*, **2020**, 21, 547	3.6	
84	Short Read Alignment Based on Maximal Approximate Match Seeds. *Frontiers in Molecular Biosciences*, **2020**, 7, 572934	5.6	
83	Pan-Cancer Classification Based on Self-Normalizing Neural Networks and Feature Selection. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 766	5.8	6

82	Long-read-based human genomic structural variation detection with cuteSV. *Genome Biology*, **2020**, 21, 189	18.3	35
81	FSM: Fast and scalable network motif discovery for exploring higher-order network organizations. *Methods*, **2020**, 173, 83-93	4.6	11
80	Predicting circRNA-Disease Associations Based on circRNA Expression Similarity and Functional Similarity. *Frontiers in Genetics*, **2019**, 10, 832	4.5	11
79	Joint detection of germline and somatic copy number events in matched tumor-normal sample pairs. *Bioinformatics*, **2019**, 35, 4955-4961	7.2	
78	Integrated entropy-based approach for analyzing exons and introns in DNA sequences. *BMC Bioinformatics*, **2019**, 20, 283	3.6	5
77	CDL4CDRP: A Collaborative Deep Learning Approach for Clinical Decision and Risk Prediction. *Processes*, **2019**, 7, 265	2.9	8
76	An improved advanced fragment analysis-based classification and risk stratification of pediatric acute lymphoblastic leukemia. *Cancer Cell International*, **2019**, 19, 110	6.4	0
75	A Pipeline for Reconstructing Somatic Copy Number Alternations Subclonal Population-Based Next-Generation Sequencing Data. *Frontiers in Genetics*, **2019**, 10, 1374	4.5	1
74	eQTLMAPT: Fast and Accurate eQTL Mediation Analysis With Efficient Permutation Testing Approaches. *Frontiers in Genetics*, **2019**, 10, 1309	4.5	9
73	A network-based pathway-extending approach using DNA methylation and gene expression data to identify altered pathways. *Scientific Reports*, **2019**, 9, 11853	4.9	3
72	TideHunter: efficient and sensitive tandem repeat detection from noisy long-reads using seed-and-chain. *Bioinformatics*, **2019**, 35, i200-i207	7.2	11
71	Integrate GWAS, eQTL, and mQTL Data to Identify Alzheimers Disease-Related Genes. *Frontiers in Genetics*, **2019**, 10, 1021	4.5	27
70	An Approximate Bufferless Network-on-Chip. *IEEE Access*, **2019**, 7, 141516-141532	3.5	5
69	Identifying Alzheimers Disease-related miRNA Based on Semi-clustering. *Current Gene Therapy*, **2019**, 19, 216-223	4.3	6
68	A Bipartite Network Module-Based Project to Predict Pathogen-Host Association. *Frontiers in Genetics*, **2019**, 10, 1357	4.5	0
67	rMETL: sensitive mobile element insertion detection with long read realignment. *Bioinformatics*, **2019**, 35, 3484-3486	7.2	4
66	An automated quality control pipeline for eQTL analysis with RNA-seq data **2019**,		4
65	deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. *Genome Biology*, **2019**, 20, 274	18.3	17

64	ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function. *BMC Bioinformatics*, **2019**, 20, 573	3.6	8
63	Prioritizing candidate diseases-related metabolites based on literature and functional similarity. *BMC Bioinformatics*, **2019**, 20, 574	3.6	7
62	Extracting a biologically latent space of lung cancer epigenetics with variational autoencoders. *BMC Bioinformatics*, **2019**, 20, 568	3.6	11
61	Human mitochondrial genome compression using machine learning techniques. *Human Genomics*, **2019**, 13, 49	6.8	3
60	IBI: Identification of Biomarker Genes in Individual Tumor Samples. *Frontiers in Genetics*, **2019**, 10, 1236	4.5	1
59	LncDisAP: a computation model for LncRNA-disease association prediction based on multiple biological datasets. *BMC Bioinformatics*, **2019**, 20, 582	3.6	5
58	MeDReaders: a database for transcription factors that bind to methylated DNA. *Nucleic Acids Research*, **2018**, 46, D146-D151	20.1	64
57	A framework for analyzing DNA methylation data from Illumina Infinium HumanMethylation450 BeadChip. *BMC Bioinformatics*, **2018**, 19, 115	3.6	18
56	3D surface voxel tracing corrector for accurate bone segmentation. *International Journal of Computer Assisted Radiology and Surgery*, **2018**, 13, 1549-1563	3.9	4
55	DeepDNA: a hybrid convolutional and recurrent neural network for compressing human mitochondrial genomes **2018**,		6
54	Exploring DNA Methylation Data of Lung Cancer Samples with Variational Autoencoders **2018**,		8
53	Identifying Candidate Diseases-related Metabolites Based on Disease Similarity **2018**,		1
52	Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks **2018**,		1
51	Fast variation-aware read alignment with deBGA-VARA **2018**,		1
50	Analysis for Early Seizure Detection System Based on Deep Learning Algorithm **2018**,		1
49	ProbPFP: A Multiple Sequence Alignment Algorithm Combining Partition Function and Hidden Markov Model with Particle Swarm Optimization **2018**,		7
48	Optimizing gene set annotations combining GO structure and gene expression data. *BMC Systems Biology*, **2018**, 12, 133	3.5	
47	deSPI: efficient classification of metagenomics reads with lightweight de Bruijn graph-based reference indexing **2018**,		3

46	An online tool for measuring and visualizing phenotype similarities using HPO. *BMC Genomics*, **2018**, 19, 571	4.5	3
45	Prediction for High Risk Clinical Symptoms of Epilepsy Based on Deep Learning Algorithm. *IEEE Access*, **2018**, 6, 77596-77605	3.5	18
44	Review of Drug Repositioning Approaches and Resources. *International Journal of Biological Sciences*, **2018**, 14, 1232-1244	11.2	246
43	Predicting disease-related genes using integrated biomedical networks. *BMC Genomics*, **2017**, 18, 1043	4.5	29
42	Low-rank and sparse decomposition based shape model and probabilistic atlas for automatic pathological organ segmentation. *Medical Image Analysis*, **2017**, 38, 30-49	15.4	46
41	regSNPs-splicing: a tool for prioritizing synonymous single-nucleotide substitution. *Human Genetics*, **2017**, 136, 1279-1289	6.3	15
40	rMFilter: acceleration of long read-based structure variation calling by chimeric read filtering. *Bioinformatics*, **2017**, 33, 2750-2752	7.2	
39	DisSetSim: an online system for calculating similarity between disease sets. *Journal of Biomedical Semantics*, **2017**, 8, 28	2.2	14
38	Identifying term relations cross different gene ontology categories. *BMC Bioinformatics*, **2017**, 18, 573	3.6	36
37	FNSemSim: An improved disease similarity method based on network fusion **2017**,		6
36	WDNfinder: A method for minimum driver node set detection and analysis in directed and weighted biological network. *Journal of Bioinformatics and Computational Biology*, **2017**, 15, 1750021	1	6
35	Finding disagreement pathway signatures and constructing an ensemble model for cancer classification. *Scientific Reports*, **2017**, 7, 10044	4.9	2
34	DTWscore: differential expression and cell clustering analysis for time-series single-cell RNA-seq data. *BMC Bioinformatics*, **2017**, 18, 270	3.6	9
33	InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology. *BMC Genomics*, **2016**, 17 Suppl 5, 530	4.5	20
32	Improving alignment accuracy on homopolymer regions for semiconductor-based sequencing technologies. *BMC Genomics*, **2016**, 17 Suppl 7, 521	4.5	13
31	Shape-intensity prior level set combining probabilistic atlas and probability map constrains for automatic liver segmentation from abdominal CT images. *International Journal of Computer Assisted Radiology and Surgery*, **2016**, 11, 817-26	3.9	43
30	Joint detection of copy number variations in parent-offspring trios. *Bioinformatics*, **2016**, 32, 1130-7	7.2	8
29	Extending gene ontology with gene association networks. *Bioinformatics*, **2016**, 32, 1185-94	7.2	37

28	Annotating the Function of the Human Genome with Gene Ontology and Disease Ontology. *BioMed Research International*, **2016**, 2016, 4130861	3	13
27	Statistical Approaches for the Construction and Interpretation of Human Protein-Protein Interaction Network. *BioMed Research International*, **2016**, 2016, 5313050	3	8
26	Identifying Liver Cancer-Related Enhancer SNPs by Integrating GWAS and Histone Modification ChIP-seq Data. *BioMed Research International*, **2016**, 2016, 2395341	3	7
25	Measuring phenotype semantic similarity using Human Phenotype Ontology **2016**,		4
24	A network-based pathway-expanding approach for pathway analysis. *BMC Bioinformatics*, **2016**, 17, 536	3.6	4
23	Comparison among dimensionality reduction techniques based on Random Projection for cancer classification. *Computational Biology and Chemistry*, **2016**, 65, 165-172	3.6	23
22	Measuring semantic similarities by combining gene ontology annotations and gene co-function networks. *BMC Bioinformatics*, **2015**, 16, 44	3.6	30
21	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. *Nucleic Acids Research*, **2015**, 43, D193-6	20.1	104
20	Hidden Markov induced Dynamic Bayesian Network for recovering time evolving gene regulatory networks. *Scientific Reports*, **2015**, 5, 17841	4.9	7
19	Analyzing large-scale samples confirms the association between the rs1051730 polymorphism and lung cancer susceptibility. *Scientific Reports*, **2015**, 5, 15642	4.9	10
18	Understanding Transcription Factor Regulation by Integrating Gene Expression and DNase I Hypersensitive Sites. *BioMed Research International*, **2015**, 2015, 757530	3	6
17	A generalized topological entropy for analyzing the complexity of DNA sequences. *PLoS ONE*, **2014**, 9, e88519	3.7	14
16	SemFunSim: a new method for measuring disease similarity by integrating semantic and gene functional association. *PLoS ONE*, **2014**, 9, e99415	3.7	83
15	PERGA: a paired-end read guided de novo assembler for extending contigs using SVM and look ahead approach. *PLoS ONE*, **2014**, 9, e114253	3.7	12
14	Automatic centerline detection of small three-dimensional vessel structures. *Journal of Electronic Imaging*, **2014**, 23, 013007	0.7	2
13	A gradient-boosting approach for filtering de novo mutations in parent-offspring trios. *Bioinformatics*, **2014**, 30, 1830-6	7.2	24
12	TF2LncRNA: identifying common transcription factors for a list of lncRNA genes from ChIP-Seq data. *BioMed Research International*, **2014**, 2014, 317642	3	35
11	Segmentation of the hip joint in CT volumes using adaptive thresholding classification and normal direction correction **2013**, 36, 1059-1072		3

10	Predicting human microRNA-disease associations based on support vector machine. *International Journal of Data Mining and Bioinformatics*, **2013**, 8, 282-93	0.5	160
9	Modelling non-stationary gene regulatory process with hidden Markov Dynamic Bayesian Network **2012**,		1
8	Privacy-Preserving Data Mining Based on Sample Selection and Singular Value Decomposition **2011** ,		4
7	Weighted Network-Based Inference of Human MicroRNA-Disease Associations **2010**,		10
6	Predicting human microRNA-disease associations based on support vector machine **2010**,		11
5	An approach for prioritizing disease-related microRNAs based on genomic data integration **2010**,		17
4	miR2Disease: a manually curated database for microRNA deregulation in human disease. *Nucleic Acids Research*, **2009**, 37, D98-104	20.1	1041
3	Reconstruct gene regulatory network using slice pattern model. *BMC Genomics*, **2009**, 10 Suppl 1, S2	4.5	3
2	The minimum feature subset selection problem. *Journal of Computer Science and Technology*, **1997**, 12, 145-153	1.7	6
1	Back propagation based on selective attention for fast convergence of training neural network		4