Junwei Luo

List of Publications by Year
in descending order

35 papers	811 citations	623734 14 h-index	526287 27 g-index
36 all docs	36 docs citations	36 times ranked	684 citing authors

#	Article	IF	Citations
1	A Novel Feature Selection Method Based on MRMR and Enhanced Flower Pollination Algorithm for High Dimensional Biomedical Data. Current Bioinformatics, 2022, 17, 133-149.	1.5	6
2	MultiGATAE: A Novel Cancer Subtype Identification Method Based on Multi-Omics and Attention Mechanism. Frontiers in Genetics, 2022, 13, 855629.	2.3	7
3	A Distributed Attribute Reduction Algorithm for High-Dimensional Data under the Spark Framework. International Journal of Computational Intelligence Systems, 2022, 15, 1.	2.7	2
4	MAMnet: detecting and genotyping deletions and insertions based on long reads and a deep learning approach. Briefings in Bioinformatics, 2022, 23, .	6.5	4
5	Tumor detection for whole slide image of liver based on patch-based convolutional neural network. Multimedia Tools and Applications, 2021, 80, 17429-17440.	3.9	7
6	Deletion Detection Method Using the Distribution of Insert Size and a Precise Alignment Strategy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1070-1081.	3.0	0
7	A comprehensive review of scaffolding methods in genome assembly. Briefings in Bioinformatics, 2021, 22, .	6.5	16
8	SIns: A Novel Insertion Detection Approach Based on Soft-Clipped Reads. Frontiers in Genetics, 2021, 12, 665812.	2.3	1
9	Predicting Drug-Disease Association Based on Ensemble Strategy. Frontiers in Genetics, 2021, 12, 666575.	2.3	10
10	MI_DenseNetCAM: A Novel Pan-Cancer Classification and Prediction Method Based on Mutual Information and Deep Learning Model. Frontiers in Genetics, 2021, 12, 670232.	2.3	3
11	BreakNet: detecting deletions using long reads and a deep learning approach. BMC Bioinformatics, 2021, 22, 577.	2.6	5
12	GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 877-886.	3.0	11
13	MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 847-857.	3.0	17
14	Improving de novo Assembly Based on Read Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 177-188.	3.0	19
15	LROD: An Overlap Detection Algorithm for Long Reads Based on k-mer Distribution. Frontiers in Genetics, 2020, 11, 632.	2.3	2
16	D-MSCD: Mean-Standard Deviation Curve Descriptor Based on Deep Learning. IEEE Access, 2020, 8, 204509-204517.	4.2	2
17	Multi-Label Classification of Fundus Images With EfficientNet. IEEE Access, 2020, 8, 212499-212508.	4.2	76
18	Influential node identification in a constrained greedy way. Physica A: Statistical Mechanics and Its Applications, 2020, 557, 124887.	2.6	8

#	Article	IF	Citations
19	Feature Selection for Microarray Data Classification Using Hybrid Information Gain and a Modified Binary Krill Herd Algorithm. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 288-301.	3.6	45
20	A Novel Drug Repositioning Approach Based on Integrative Multiple Similarity Measures. Current Molecular Medicine, 2020, 20, 442-451.	1.3	3
21	A Novel Scaffolding Algorithm Based on Contig Error Correction and Path Extension. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 764-773.	3.0	8
22	EPGA-SC : A framework for de novo assembly of single-cell sequencing reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	3.0	3
23	SLR: a scaffolding algorithm based on long reads and contig classification. BMC Bioinformatics, 2019, 20, 539.	2.6	17
24	A Novel Feature Selection Method for High-Dimensional Biomedical Data Based on an Improved Binary Clonal Flower Pollination Algorithm. Human Heredity, 2019, 84, 34-46.	0.8	22
25	Computational Drug Repositioning with Random Walk on a Heterogeneous Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1890-1900.	3.0	47
26	ISEA: Iterative Seed-Extension Algorithm for De Novo Assembly Using Paired-End Information and Insert Size Distribution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 916-925.	3.0	20
27	PECC: Correcting contigs based on paired-end read distribution. Computational Biology and Chemistry, 2017, 69, 178-184.	2.3	17
28	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. Bioinformatics, 2017, 33, 169-176.	4.1	33
29	MEC: Misassembly error correction in contigs using a combination of paired-end reads and GC-contents. , 2017, , .		2
30	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. Bioinformatics, 2016, 32, 2664-2671.	4.1	311
31	Sprites: detection of deletions from sequencing data by re-aligning split reads. Bioinformatics, 2016, 32, 1788-1796.	4.1	23
32	An efficient method to identify essential proteins for different species by integrating protein subcellular localization information. , 2015, , .		16
33	EPGA2: memory-efficient <i>de novo</i> assembler. Bioinformatics, 2015, 31, 3988-3990.	4.1	19
34	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. Bioinformatics, 2015, 31, 825-833.	4.1	25
35	Performance analysis of an improved variable tap-length LMS algorithm. , 2009, , .		4