

Xiguo Yuan

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

697
citations

687363

13
h-index

610901

24
g-index

51
all docs

51
docs citations

51
times ranked

643
citing authors

#	ARTICLE	IF	CITATIONS
1	An Overview of Population Genetic Data Simulation. <i>Journal of Computational Biology</i> , 2012, 19, 42-54.	1.6	72
2	Inferring subgroup-specific driver genes from heterogeneous cancer samples via subspace learning with subgroup indication. <i>Bioinformatics</i> , 2020, 36, 1855-1863.	4.1	53
3	IntSIM: An Integrated Simulator of Next-Generation Sequencing Data. <i>IEEE Transactions on Biomedical Engineering</i> , 2017, 64, 441-451.	4.2	47
4	FHSA-SED: Two-Locus Model Detection for Genome-Wide Association Study with Harmony Search Algorithm. <i>PLoS ONE</i> , 2016, 11, e0150669.	2.5	45
5	CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples using Sequence Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	3.0	42
6	Comparative study of whole exome sequencing-based copy number variation detection tools. <i>BMC Bioinformatics</i> , 2020, 21, 97.	2.6	40
7	CNV_IFTV: An Isolation Forest and Total Variation-Based Detection of CNVs from Short-Read Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 539-549.	3.0	38
8	Niche harmony search algorithm for detecting complex disease associated high-order SNP combinations. <i>Scientific Reports</i> , 2017, 7, 11529.	3.3	36
9	Genome-wide identification of significant aberrations in cancer genome. <i>BMC Genomics</i> , 2012, 13, 342.	2.8	34
10	Detection of Significant Copy Number Variations From Multiple Samples in Next-Generation Sequencing Data. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 12-20.	3.3	25
11	A Local Outlier Factor-Based Detection of Copy Number Variations From NGS Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1811-1820.	3.0	24
12	Improving the prediction accuracy of protein structural class: Approached with alternating word frequency and normalized Lempel-Ziv complexity. <i>Journal of Theoretical Biology</i> , 2014, 341, 71-77.	1.7	20
13	Simulating Linkage Disequilibrium Structures in a Human Population for SNP Association Studies. <i>Biochemical Genetics</i> , 2011, 49, 395-409.	1.7	16
14	Stratification of Breast Cancer by Integrating Gene Expression Data and Clinical Variables. <i>Molecules</i> , 2019, 24, 631.	3.8	16
15	SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1082-1091.	3.0	13
16	MFCNV: A New Method to Detect Copy Number Variations From Next-Generation Sequencing Data. <i>Frontiers in Genetics</i> , 2020, 11, 434.	2.3	13
17	Network based stratification of major cancers by integrating somatic mutation and gene expression data. <i>PLoS ONE</i> , 2017, 12, e0177662.	2.5	13
18	NeuroTIS: Enhancing the prediction of translation initiation sites in mRNA sequences via a hybrid dependency network and deep learning framework. <i>Knowledge-Based Systems</i> , 2021, 212, 106459.	7.1	12

#	ARTICLE	IF	CITATIONS
19	Comparative Analysis of Methods for Identifying Recurrent Copy Number Alterations in Cancer. PLoS ONE, 2012, 7, e52516.	2.5	11
20	Random Subspace Aggregation for Cancer Prediction with Gene Expression Profiles. BioMed Research International, 2016, 2016, 1-10.	1.9	11
21	ALSAIC: a software suite for accurate identification of significant aberrations in cancers. Bioinformatics, 2014, 30, 431-433.	4.1	10
22	A new differential evolution algorithm for solving multimodal optimization problems with high dimensionality. Soft Computing, 2018, 22, 4361-4388.	3.6	10
23	Integrating Somatic Mutations for Breast Cancer Survival Prediction Using Machine Learning Methods. Frontiers in Genetics, 2020, 11, 632901.	2.3	10
24	BagGMM: Calling copy number variation by bagging multiple Gaussian mixture models from tumor and matched normal next-generation sequencing data. , 2019, 88, 90-100.		8
25	Accurate Inference of Tumor Purity and Absolute Copy Numbers From High-Throughput Sequencing Data. Frontiers in Genetics, 2020, 11, 458.	2.3	8
26	KNNCNV: A K-Nearest Neighbor Based Method for Detection of Copy Number Variations Using NGS Data. Frontiers in Cell and Developmental Biology, 2021, 9, 796249.	3.7	8
27	lhybCNV: An intra-hybrid approach for CNV detection from next-generation sequencing data. , 2022, 121, 103304.		6
28	Enhancing the prediction of protein coding regions in biological sequence via a deep learning framework with hybrid encoding. , 2022, 123, 103430.		6
29	DINTD: Detection and Inference of Tandem Duplications From Short Sequencing Reads. Frontiers in Genetics, 2020, 11, 924.	2.3	5
30	RKDOSCNV: A Local Kernel Density-Based Approach to the Detection of Copy Number Variations by Using Next-Generation Sequencing Data. Frontiers in Genetics, 2020, 11, 569227.	2.3	5
31	STIC: Predicting Single Nucleotide Variants and Tumor Purity in Cancer Genome. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2692-2701.	3.0	5
32	HBOS-CNV: A New Approach to Detect Copy Number Variations From Next-Generation Sequencing Data. Frontiers in Genetics, 2021, 12, 642473.	2.3	5
33	SM-RCNV: a statistical method to detect recurrent copy number variations in sequenced samples. Genes and Genomics, 2019, 41, 529-536.	1.4	4
34	Novel method of mining classification information for SVM training. Wuhan University Journal of Natural Sciences, 2011, 16, 475-480.	0.4	3
35	Mutual information and linkage disequilibrium based SNP association study by grouping case-control. Genes and Genomics, 2011, 33, 65-73.	1.4	3
36	Analysis of breast cancer subtypes by AP-ISA biclustering. BMC Bioinformatics, 2017, 18, 481.	2.6	3

#	ARTICLE	IF	CITATIONS
37	Identification of PIWI-interacting RNA modules by weighted correlation network analysis. Cluster Computing, 2019, 22, 707-717.	5.0	3
38	A Density Peak-Based Method to Detect Copy Number Variations From Next-Generation Sequencing Data. Frontiers in Genetics, 2020, 11, 632311.	2.3	3
39	TAGCNA: A Method to Identify Significant Consensus Events of Copy Number Alterations in Cancer. PLoS ONE, 2012, 7, e41082.	2.5	3
40	Probability Theory-Based SNP Association Study Method for Identifying Susceptibility Loci and Genetic Disease Models in Human Case-Control Data. IEEE Transactions on Nanobioscience, 2010, 9, 232-241.	3.3	2
41	CRSCNV: A Cross-Model-Based Statistical Approach to Detect Copy Number Variations in Sequence Data. IEEE Access, 2020, 8, 2302-2312.	4.2	2
42	ERINS: Novel Sequence Insertion Detection by Constructing an Extended Reference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1893-1901.	3.0	1
43	dpGMM: A Dirichlet Process Gaussian Mixture Model for Copy Number Variation Detection in Low-Coverage Whole-Genome Sequencing Data. IEEE Access, 2020, 8, 27973-27985.	4.2	1
44	Detection of copy number variations from NGS data by using an adaptive kernel density estimation-based outlier factor. , 2022, 126, 103524.		1
45	WAVECNV: A New Approach for Detecting Copy Number Variation by Wavelet Clustering. Mathematics, 2022, 10, 2151.	2.2	1
46	A new statistical method to detect risk SNPs. , 2017, , .		0
47	Detection of False-Positive Deletions from the Database of Genomic Variants. BioMed Research International, 2019, 2019, 1-8.	1.9	0
48	Detection of Pathogenic Microbe Composition Using Next-Generation Sequencing Data. Frontiers in Genetics, 2020, 11, 603093.	2.3	0
49	Detection and inference of interspersed duplicated insertions from paired-end reads. , 2021, 111, 102959.		0
50	svBreak: A New Approach for the Detection of Structural Variant Breakpoints Based on Convolutional Neural Network. BioMed Research International, 2022, 2022, 1-8.	1.9	0