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	IhybCNV: An intra-hybrid approach for CNV detection from next-generation sequencing data. , 2022, 121, 103304.		6
2	Enhancing the prediction of protein coding regions in biological sequence via a deep learning framework with hybrid encoding. , 2022, 123, 103430.		6
3	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
4	Detection of copy number variations from NGS data by using an adaptive kernel density estimation-based outlier factor. , 2022, 126, 103524.		1
5	WAVECNV: A New Approach for Detecting Copy Number Variation by Wavelet Clustering. Mathematics, 2022, 10, 2151.	2.2	1
6	A Local Outlier Factor-Based Detection of Copy Number Variations From NGS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1811-1820.	3.0	24
7	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
8	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
9	CNV_IFTV: An Isolation Forest and Total Variation-Based Detection of CNVs from Short-Read Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 539-549.	3.0	38
10	NeuroTIS: Enhancing the prediction of translation initiation sites in mRNA sequences via a hybrid dependency network and deep learning framework. Knowledge-Based Systems, 2021, 212, 106459.	7.1	12
11	Detection and inference of interspersed duplicated insertions from paired-end reads. , 2021, 111, 102959.		0
12	HBOS-CNV: A New Approach to Detect Copy Number Variations From Next-Generation Sequencing Data. Frontiers in Genetics, 2021, 12, 642473.	2.3	5
13	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
14	Inferring subgroup-specific driver genes from heterogeneous cancer samples via subspace learning with subgroup indication. Bioinformatics, 2020, 36, 1855-1863.	4.1	53
15	SVSR: A Program to Simulate Structural Variations and Generate Sequencing Reads for Multiple Platforms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1082-1091.	3.0	13
16	DINTD: Detection and Inference of Tandem Duplications From Short Sequencing Reads. Frontiers in Genetics, 2020, 11, 924.	2.3	5
17	Detection of Pathogenic Microbe Composition Using Next-Generation Sequencing Data. Frontiers in Genetics, 2020, 11, 603093.	2.3	0
18	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

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19	Accurate Inference of Tumor Purity and Absolute Copy Numbers From High-Throughput Sequencing Data. Frontiers in Genetics, 2020, 11, 458.	2.3	8
20	Comparative study of whole exome sequencing-based copy number variation detection tools. BMC Bioinformatics, 2020, 21, 97.	2.6	40
21	CRSCNV: A Cross-Model-Based Statistical Approach to Detect Copy Number Variations in Sequence Data. IEEE Access, 2020, 8, 2302-2312.	4.2	2
22	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
23	MFCNV: A New Method to Detect Copy Number Variations From Next-Generation Sequencing Data. Frontiers in Genetics, 2020, 11, 434.	2.3	13
24	A Density Peak-Based Method to Detect Copy Number Variations From Next-Generation Sequencing Data. Frontiers in Genetics, 2020, 11, 632311.	2.3	3
25	Integrating Somatic Mutations for Breast Cancer Survival Prediction Using Machine Learning Methods. Frontiers in Genetics, 2020, 11, 632901.	2.3	10
26	Detection of False-Positive Deletions from the Database of Genomic Variants. BioMed Research International, 2019, 2019, 1-8.	1.9	0
27	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
28	Stratification of Breast Cancer by Integrating Gene Expression Data and Clinical Variables. Molecules, 2019, 24, 631.	3.8	16
29	SM-RCNV: a statistical method to detect recurrent copy number variations in sequenced samples. Genes and Genomics, 2019, 41, 529-536.	1.4	4
30	Identification of PIWI-interacting RNA modules by weighted correlation network analysis. Cluster Computing, 2019, 22, 707-717.	5.0	3
31	Detection of Significant Copy Number Variations From Multiple Samples in Next-Generation Sequencing Data. IEEE Transactions on Nanobioscience, 2018, 17, 12-20.	3.3	25
32	A new differential evolution algorithm for solving multimodal optimization problems with high dimensionality. Soft Computing, 2018, 22, 4361-4388.	3.6	10
33	CONDEL: Detecting Copy Number Variation and Genotyping Deletion Zygosity from Single Tumor Samples using Sequence Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	42
34	IntSIM: An Integrated Simulator of Next-Generation Sequencing Data. IEEE Transactions on Biomedical Engineering, 2017, 64, 441-451.	4.2	47
35	Niche harmony search algorithm for detecting complex disease associated high-order SNP combinations. Scientific Reports, 2017, 7, 11529.	3.3	36
36	A new statistical method to detect risk SNPs. , 2017, , .		0

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37	Analysis of breast cancer subtypes by AP-ISA biclustering. BMC Bioinformatics, 2017, 18, 481.	2.6	3
38	Network based stratification of major cancers by integrating somatic mutation and gene expression data. PLoS ONE, 2017, 12, e0177662.	2.5	13
39	Random Subspace Aggregation for Cancer Prediction with Gene Expression Profiles. BioMed Research International, 2016, 2016, 1-10.	1.9	11
40	FHSA-SED: Two-Locus Model Detection for Genome-Wide Association Study with Harmony Search Algorithm. PLoS ONE, 2016, 11, e0150669.	2.5	45
41	AISAIC: a software suite for accurate identification of significant aberrations in cancers. Bioinformatics, 2014, 30, 431-433.	4.1	10
42	Improving the prediction accuracy of protein structural class: Approached with alternating word frequency and normalized Lempelâ€“Ziv complexity. Journal of Theoretical Biology, 2014, 341, 71-77.	1.7	20
43	An Overview of Population Genetic Data Simulation. Journal of Computational Biology, 2012, 19, 42-54.	1.6	72
44	Genome-wide identification of significant aberrations in cancer genome. BMC Genomics, 2012, 13, 342.	2.8	34
45	Comparative Analysis of Methods for Identifying Recurrent Copy Number Alterations in Cancer. PLoS ONE, 2012, 7, e52516.	2.5	11
46	TAGCNA: A Method to Identify Significant Consensus Events of Copy Number Alterations in Cancer. PLoS ONE, 2012, 7, e41082.	2.5	3
47	Novel method of mining classification information for SVM training. Wuhan University Journal of Natural Sciences, 2011, 16, 475-480.	0.4	3
48	Simulating Linkage Disequilibrium Structures in a Human Population for SNP Association Studies. Biochemical Genetics, 2011, 49, 395-409.	1.7	16
49	Mutual information and linkage disequilibrium based SNP association study by grouping case-control. Genes and Genomics, 2011, 33, 65-73.	1.4	3
50	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