

Pierre Neuvial

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

9,780
citations

471509

17
h-index

501196

28
g-index

31
all docs

31
docs citations

31
times ranked

17302
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	27.8	6,541
2	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	16.8	2,078
3	Subtype and pathway specific responses to anticancer compounds in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2724-2729.	7.1	417
4	VAMP: Visualization and analysis of array-CGH, transcriptome and other molecular profiles. <i>Bioinformatics</i> , 2006, 22, 2066-2073.	4.1	106
5	Parent-specific copy number in paired tumor-normal studies using circular binary segmentation. <i>Bioinformatics</i> , 2011, 27, 2038-2046.	4.1	100
6	Spatial normalization of array-CGH data. <i>BMC Bioinformatics</i> , 2006, 7, 264.	2.6	71
7	More power via graph-structured tests for differential expression of gene networks. <i>Annals of Applied Statistics</i> , 2012, 6, .	1.1	67
8	High-Resolution Mapping of DNA Breakpoints to Define True Recurrences Among Ipsilateral Breast Cancers. <i>Journal of the National Cancer Institute</i> , 2008, 100, 48-58.	6.3	61
9	TumorBoost: Normalization of allele-specific tumor copy numbers from a single pair of tumor-normal genotyping microarrays. <i>BMC Bioinformatics</i> , 2010, 11, 245.	2.6	49
10	LICORN: learning cooperative regulation networks from gene expression data. <i>Bioinformatics</i> , 2007, 23, 2407-2414.	4.1	40
11	CAPweb: a bioinformatics CGH array Analysis Platform. <i>Nucleic Acids Research</i> , 2006, 34, W477-W481.	14.5	32
12	Post hoc confidence bounds on false positives using reference families. <i>Annals of Statistics</i> , 2020, 48, .	2.6	24
13	Performance of a blockwise approach in variable selection using linkage disequilibrium information. <i>BMC Bioinformatics</i> , 2015, 16, 148.	2.6	23
14	Adjacency-constrained hierarchical clustering of a band similarity matrix with application to genomics. <i>Algorithms for Molecular Biology</i> , 2019, 14, 22.	1.2	21
15	Applicability and Interpretability of Ward's Hierarchical Agglomerative Clustering With or Without Contiguity Constraints. <i>Journal of Classification</i> , 2021, 38, 363-389.	2.2	21
16	On false discovery rate thresholding for classification under sparsity. <i>Annals of Statistics</i> , 2012, 40, .	2.6	20
17	Performance evaluation of DNA copy number segmentation methods. <i>Briefings in Bioinformatics</i> , 2015, 16, 600-615.	6.5	19
18	Asymptotic properties of false discovery rate controlling procedures under independence. <i>Electronic Journal of Statistics</i> , 2008, 2, .	0.7	18

#	ARTICLE	IF	CITATIONS
19	Estimation of a non-parametric variable importance measure of a continuous exposure. <i>Electronic Journal of Statistics</i> , 2012, 6, 1059-1099.	0.7	17
20	CalMaTe: a method and software to improve allele-specific copy number of SNP arrays for downstream segmentation. <i>Bioinformatics</i> , 2012, 28, 1793-1794.	4.1	16
21	On the post selection inference constant under restricted isometry properties. <i>Electronic Journal of Statistics</i> , 2018, 12, .	0.7	8
22	New insight for pharmacogenomics studies from the transcriptional analysis of two large-scale cancer cell line panels. <i>Scientific Reports</i> , 2017, 7, 15126.	3.3	7
23	Post hoc false positive control for structured hypotheses. <i>Scandinavian Journal of Statistics</i> , 2020, 47, 1114-1148.	1.4	6
24	A model for gene deregulation detection using expression data. <i>BMC Systems Biology</i> , 2015, 9, S6.	3.0	5
25	Statistical Analysis of Single Nucleotide Polymorphism Microarrays in Cancer Studies. , 2011, , 225-255.		4
26	tmle.npvi: targeted, integrative search of associations between DNA copy number and gene expression, accounting for DNA methylation: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 3054-3056.	4.1	3
27	Corrigendum to "Asymptotic properties of false discovery rate controlling procedures under independence" <i>Electronic Journal of Statistics</i> , 2009, 3, .	0.7	2
28	Identification of deregulation mechanisms specific to cancer subtypes. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2140003.	0.8	2
29	Stability-Based Comparison of Class Discovery Methods for DNA Copy Number Profiles. <i>PLoS ONE</i> , 2013, 8, e81458.	2.5	1