Pierre Neuvial

List of Publications by Year
in descending order

		471509	501196
29	9,780	17	28
papers	citations	h-index	g-index
31	31	31	17302
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Applicability and Interpretability of Ward's Hierarchical Agglomerative Clustering With or Without Contiguity Constraints. Journal of Classification, 2021, 38, 363-389.	2.2	21
2	Identification of deregulation mechanisms specific to cancer subtypes. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140003.	0.8	2
3	Post hoc false positive control for structured hypotheses. Scandinavian Journal of Statistics, 2020, 47, 1114-1148.	1.4	6
4	Post hoc confidence bounds on false positives using reference families. Annals of Statistics, 2020, 48, .	2.6	24
5	Adjacency-constrained hierarchical clustering of a band similarity matrix with application to genomics. Algorithms for Molecular Biology, 2019, 14, 22.	1.2	21
6	On the post selection inference constant under restricted isometry properties. Electronic Journal of Statistics, 2018, 12, .	0.7	8
7	New insight for pharmacogenomics studies from the transcriptional analysis of two large-scale cancer cell line panels. Scientific Reports, 2017, 7, 15126.	3.3	7
8	A model for gene deregulation detection using expression data. BMC Systems Biology, 2015, 9, S6.	3.0	5
9	Performance of a blockwise approach in variable selection using linkage disequilibrium information. BMC Bioinformatics, 2015, 16, 148.	2.6	23
10	tmle.npvi: targeted, integrative search of associations between DNA copy number and gene expression, accounting for DNA methylation: Fig. 1.. Bioinformatics, 2015, 31, 3054-3056.	4.1	3
11	Performance evaluation of DNA copy number segmentation methods. Briefings in Bioinformatics, 2015, 16, 600-615.	6.5	19
12	Stability-Based Comparison of Class Discovery Methods for DNA Copy Number Profiles. PLoS ONE, 2013, 8, e81458.	2.5	1
13	CalMaTe: a method and software to improve allele-specific copy number of SNP arrays for downstream segmentation. Bioinformatics, 2012, 28, 1793-1794.	4.1	16
14	Estimation of a non-parametric variable importance measure of a continuous exposure. Electronic Journal of Statistics, 2012, 6, 1059-1099.	0.7	17
15	More power via graph-structured tests for differential expression of gene networks. Annals of Applied Statistics, 2012, 6, .	1.1	67
16	On false discovery rate thresholding for classification under sparsity. Annals of Statistics, 2012, 40, .	2.6	20
17	Subtype and pathway specific responses to anticancer compounds in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2724-2729.	7.1	417
18	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541

#	Article	IF	Citations
19	Parent-specific copy number in paired tumor–normal studies using circular binary segmentation. Bioinformatics, 2011, 27, 2038-2046.	4.1	100
20	Statistical Analysis of Single Nucleotide Polymorphism Microarrays in Cancer Studies. , 2011, , 225-255.		4
21	TumorBoost: Normalization of allele-specific tumor copy numbers from a single pair of tumor-normal genotyping microarrays. BMC Bioinformatics, 2010, 11, 245.	2.6	49
22	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	16.8	2,078
23	Corrigendum to "Asymptotic properties of false discovery rate controlling procedures under independence". Electronic Journal of Statistics, 2009, 3, .	0.7	2
24	High-Resolution Mapping of DNA Breakpoints to Define True Recurrences Among Ipsilateral Breast Cancers. Journal of the National Cancer Institute, 2008, 100, 48-58.	6.3	61
25	Asymptotic properties of false discovery rate controlling procedures under independence. Electronic Journal of Statistics, 2008, 2, .	0.7	18
26	LICORN: learning cooperative regulation networks from gene expression data. Bioinformatics, 2007, 23, 2407-2414.	4.1	40
27	Spatial normalization of array-CGH data. BMC Bioinformatics, 2006, 7, 264.	2.6	71
28	VAMP: Visualization and analysis of array-CGH, transcriptome and other molecular profiles. Bioinformatics, 2006, 22, 2066-2073.	4.1	106
29	CAPweb: a bioinformatics CGH array Analysis Platform. Nucleic Acids Research, 2006, 34, W477-W481.	14.5	32