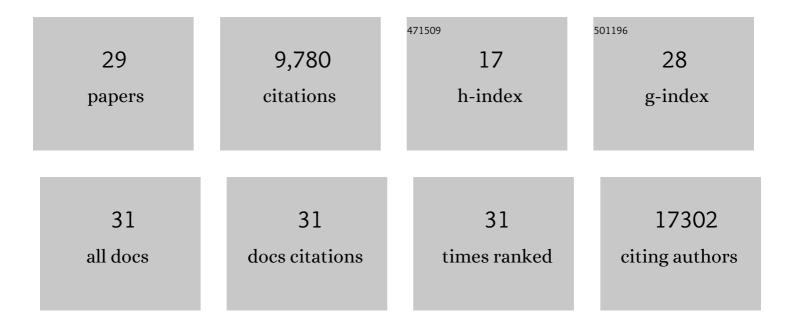
Pierre Neuvial

List of Publications by Year in descending order

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

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#	Article	IF	CITATIONS
19	Estimation of a non-parametric variable importance measure of a continuous exposure. Electronic Journal of Statistics, 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. Bioinformatics, 2012, 28, 1793-1794.	4.1	16
21	On the post selection inference constant under restricted isometry properties. Electronic Journal of Statistics, 2018, 12, .	0.7	8
22	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
23	Post hoc false positive control for structured hypotheses. Scandinavian Journal of Statistics, 2020, 47, 1114-1148.	1.4	6
24	A model for gene deregulation detection using expression data. BMC Systems Biology, 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 Bioinformatics, 2015, 31, 3054-3056.	4.1	3
27	Corrigendum to "Asymptotic properties of false discovery rate controlling procedures under independence― Electronic Journal of Statistics, 2009, 3, .	0.7	2
28	Identification of deregulation mechanisms specific to cancer subtypes. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140003.	0.8	2
29	Stability-Based Comparison of Class Discovery Methods for DNA Copy Number Profiles. PLoS ONE, 2013, 8, e81458.	2.5	1