

StÃ©phane Robin

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

1,395
citations

933447

10
h-index

1199594

12
g-index

12
all docs

12
docs citations

12
times ranked

2372
citing authors

#	ARTICLE	IF	CITATIONS
1	A factor model approach for the joint segmentation with between-series correlation. <i>Scandinavian Journal of Statistics</i> , 2019, 46, 686-705.	1.4	2
2	SegCorr a statistical procedure for the detection of genomic regions of correlated expression. <i>BMC Bioinformatics</i> , 2017, 18, 333.	2.6	5
3	Hidden Markov Models with mixtures as emission distributions. <i>Statistics and Computing</i> , 2014, 24, 493-504.	1.5	42
4	Segmentor3lsBack: an R package for the fast and exact segmentation of Seq-data. <i>Algorithms for Molecular Biology</i> , 2014, 9, 6.	1.2	21
5	Genomic Instability: A Stronger Prognostic Marker Than Proliferation for Early Stage Luminal Breast Carcinomas. <i>PLoS ONE</i> , 2013, 8, e76496.	2.5	16
6	Joint segmentation, calling, and normalization of multiple CGH profiles. <i>Biostatistics</i> , 2011, 12, 413-428.	1.5	88
7	Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. <i>EMBO Journal</i> , 2011, 30, 1928-1938.	7.8	600
8	The MatP/matS Site-Specific System Organizes the Terminus Region of the E. coli Chromosome into a Macrodomain. <i>Cell</i> , 2008, 135, 475-485.	28.9	252
9	ChIPmix: mixture model of regressions for two-color ChIP-chip analysis. <i>Bioinformatics</i> , 2008, 24, i181-i186.	4.1	22
10	Identification of DNA Motifs Implicated in Maintenance of Bacterial Core Genomes by Predictive Modeling. <i>PLoS Genetics</i> , 2007, 3, e153.	3.5	63
11	Statistical tests to compare motif count exceptionalities. <i>BMC Bioinformatics</i> , 2007, 8, 84.	2.6	28
12	A statistical approach for array CGH data analysis. <i>BMC Bioinformatics</i> , 2005, 6, 27.	2.6	256