Julien Chiquet

List of Publications by Year
in descending order

35 papers	2,681 citations	623734 14 h-index	395702 33 g-index
42 all docs	42 docs citations	42 times ranked	3019 citing authors

#	Article	IF	Citations
1	Early allopolyploid evolution in the post-Neolithic *Brassica napus* oilseed genome. Science, 2014, 345, 950-953.	12.6	2,089
2	Learning Ecological Networks from Next-Generation Sequencing Data. Advances in Ecological Research, 2016, , 1-39.	2.7	68
3	Inferring multiple graphical structures. Statistics and Computing, 2011, 21, 537-553.	1.5	50
4	Weighted-LASSO for Structured Network Inference from Time Course Data. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 15.	0.6	44
5	Piecewise deterministic Markov processes applied to fatigue crack growth modelling. Journal of Statistical Planning and Inference, 2009, 139, 1657-1667.	0.6	43
6	Prevalence of gene expression additivity in genetically stable wheat allohexaploids. New Phytologist, 2013, 197, 730-736.	7.3	36
7	SIMoNe: Statistical Inference for MOdular NEtworks. Bioinformatics, 2009, 25, 417-418.	4.1	35
8	Variational inference for probabilistic Poisson PCA. Annals of Applied Statistics, 2018, 12, .	1.1	35
9	Inferring sparse Gaussian graphical models with latent structure. Electronic Journal of Statistics, 2009, 3, .	0.7	29
10	A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication. Cell, 2019, 179, 432-447.e21.	28.9	23
11	A method to compute the transition function of a piecewise deterministic Markov process with application to reliability. Statistics and Probability Letters, 2008, 78, 1397-1403.	0.7	22
12	Sparsity with sign-coherent groups of variables via the cooperative-Lasso. Annals of Applied Statistics, 2012, 6, .	1.1	21
13	Structured regularization for conditional Gaussian graphical models. Statistics and Computing, 2017, 27, 789-804.	1.5	18
14	The Poisson-Lognormal Model as a Versatile Framework for the Joint Analysis of Species Abundances. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	18
15	Variational Inference for Stochastic Block Models From Sampled Data. Journal of the American Statistical Association, 2020, 115, 455-466.	3.1	15
16	Fast tree aggregation for consensus hierarchical clustering. BMC Bioinformatics, 2020, 21, 120.	2.6	11
17	Estimating Stochastic Dynamical Systems Driven by a Continuous-Time Jump Markov Process. Methodology and Computing in Applied Probability, 2006, 8, 431-447.	1.2	10
18	Modelling and estimating the reliability of stochastic dynamical systems with Markovian switching. Reliability Engineering and System Safety, 2008, 93, 1801-1808.	8.9	10

#	Article	IF	Citations
19	Fast Tree Inference With Weighted Fusion Penalties. Journal of Computational and Graphical Statistics, 2017, 26, 205-216.	1.7	9
20	Variable selection in multivariate linear models with high-dimensional covariance matrix estimation. Journal of Multivariate Analysis, 2018, 166, 78-97.	1.0	9
21	Harnessing multivariate, penalized regression methods for genomic prediction and QTL detection of drought-related traits in grapevine. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	9
22	Joint species distributions reveal the combined effects of host plants, abiotic factors and species competition as drivers of species abundances in fruit flies. Ecology Letters, 2021, 24, 1905-1916.	6.4	8
23	A Multiattribute Gaussian Graphical Model for Inferring Multiscale Regulatory Networks: An Application in Breast Cancer. Methods in Molecular Biology, 2019, 1883, 143-160.	0.9	8
24	Combining a relaxed EM algorithm with Occam's razor for Bayesian variable selection in high-dimensional regression. Journal of Multivariate Analysis, 2016, 146, 177-190.	1.0	7
25	A model for gene deregulation detection using expression data. BMC Systems Biology, 2015, 9, S6.	3.0	5
26	A variable selection approach in the multivariate linear model: an application to LC-MS metabolomics data. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	5
27	Coupling ecological network analysis with high-throughput sequencing-based surveys: Lessons from the next-generation biomonitoring project. Advances in Ecological Research, 2021, 65, 367-430.	2.7	5
28	Fast computation of genome-metagenome interaction effects. Algorithms for Molecular Biology, 2020, 15, 13.	1.2	2
29	Identification of deregulation mechanisms specific to cancer subtypes. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140003.	0.8	2
30	Dynamical Systems with Semi-Markovian Perturbations and Their Use in Structural Reliability. Springer Series in Reliability Engineering, 2013, , 191-218.	0.5	2
31	Efficient block boundaries estimation in block-wise constant matrices: An application to HiC data. Electronic Journal of Statistics, 2017, 11, .	0.7	1
32	Identification of Deregulated Transcription Factors Involved in Specific Bladder Cancer Subtypes. , 0, , .		1
33	A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication. SSRN Electronic Journal, 0, , .	0.4	1
34	Network Inference in Breast Cancer with Gaussian Graphical Models and Extensions. , 2014, , 121-146.		0
35	Fast Detection of Block Boundaries in Block-Wise Constant Matrices. Lecture Notes in Computer Science, 2016, , 214-228.	1.3	0