Vincent Miele

List of Publications by Year in descending order

26 papers	1,232 citations	16 h-index 516710	25 g-index 580821
29 all docs	29 docs citations	29 times ranked	2116 citing authors

#	Article	IF	Citations
1	Ultra-fast sequence clustering from similarity networks with SiLiX. BMC Bioinformatics, 2011, 12, 116.	2.6	271
2	Statistical Clustering of Temporal Networks Through a Dynamic Stochastic Block Model. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2017, 79, 1119-1141.	2.2	175
3	How Structured Is the Entangled Bank? The Surprisingly Simple Organization of Multiplex Ecological Networks Leads to Increased Persistence and Resilience. PLoS Biology, 2016, 14, e1002527.	5.6	154
4	DNA physical properties determine nucleosome occupancy from yeast to fly. Nucleic Acids Research, 2008, 36, 3746-3756.	14.5	125
5	Fast online graph clustering via ErdÅ's–RÃ©nyi mixture. Pattern Recognition, 2008, 41, 3592-3599.	8.1	74
6	Diversity indices for ecological networks: a unifying framework using Hill numbers. Ecology Letters, 2019, 22, 737-747.	6.4	49
7	Global survey of mobile DNA horizontal transfer in arthropods reveals Lepidoptera as a prime hotspot. PLoS Genetics, 2019, 15, e1007965.	3.5	41
8	High-quality sequence clustering guided by network topology and multiple alignment likelihood. Bioinformatics, 2012, 28, 1078-1085.	4.1	39
9	Ecological networks to unravel the routes to horizontal transposon transfers. PLoS Biology, 2017, 15, e2001536.	5.6	39
10	Core–periphery dynamics in a plant–pollinator network. Journal of Animal Ecology, 2020, 89, 1670-1677.	2.8	36
11	Deciphering the connectivity structure of biological networks using MixNet. BMC Bioinformatics, 2009, 10, S17.	2.6	26
12	Fruiting Strategies of Perennial Plants: A Resource Budget Model to Couple Mast Seeding to Pollination Efficiency and Resource Allocation Strategies. American Naturalist, 2016, 188, 66-75.	2.1	26
13	Nine quick tips for analyzing network data. PLoS Computational Biology, 2019, 15, e1007434.	3.2	23
14	DNA Physical Properties and Nucleosome Positions Are Major Determinants of HIV-1 Integrase Selectivity. PLoS ONE, 2015, 10, e0129427.	2.5	21
15	Spatially constrained clustering of ecological networks. Methods in Ecology and Evolution, 2014, 5, 771-779.	5.2	20
16	Strategies for online inference of model-based clustering in large and growing networks. Annals of Applied Statistics, 2010, 4, .	1.1	19
17	Non-trophic interactions strengthen the diversity–functioning relationship in an ecological bioenergetic network model. PLoS Computational Biology, 2019, 15, e1007269.	3.2	19
18	Playing hide and seek with repeats in local and global de novo transcriptome assembly of short RNA-seq reads. Algorithms for Molecular Biology, 2017, 12, 2.	1.2	18

#	Article	IF	Citations
19	Revealing the hidden structure of dynamic ecological networks. Royal Society Open Science, 2017, 4, 170251.	2.4	16
20	Revisiting animal photo‐identification using deep metric learning and network analysis. Methods in Ecology and Evolution, 2021, 12, 863-873.	5.2	14
21	seq++: analyzing biological sequences with a range of Markov-related models. Bioinformatics, 2005, 21, 2783-2784.	4.1	6
22	An appraisal of graph embeddings for comparing trophic network architectures. Methods in Ecology and Evolution, 2022, 13, 203-216.	5.2	5
23	A Reversible Jump Markov Chain Monte Carlo Algorithm for Bacterial Promoter Motifs Discovery. Journal of Computational Biology, 2006, 13, 651-667.	1.6	4
24	Colib'read on galaxy: a tools suite dedicated to biological information extraction from raw NGS reads. GigaScience, 2016, 5, 9.	6.4	2
25	Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96.	1.3	2
26	Fast and Parallel Algorithm for Population-Based Segmentation of Copy-Number Profiles. Lecture Notes in Computer Science, 2014, , 248-258.	1.3	0