Vincent Miele

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	An appraisal of graph embeddings for comparing trophic network architectures. Methods in Ecology and Evolution, 2022, 13, 203-216.	5.2	5
2	Revisiting animal photoâ€identification using deep metric learning and network analysis. Methods in Ecology and Evolution, 2021, 12, 863-873.	5.2	14
3	Core–periphery dynamics in a plant–pollinator network. Journal of Animal Ecology, 2020, 89, 1670-1677.	2.8	36
4	Non-trophic interactions strengthen the diversity—functioning relationship in an ecological bioenergetic network model. PLoS Computational Biology, 2019, 15, e1007269.	3.2	19
5	Diversity indices for ecological networks: a unifying framework using Hill numbers. Ecology Letters, 2019, 22, 737-747.	6.4	49
6	Global survey of mobile DNA horizontal transfer in arthropods reveals Lepidoptera as a prime hotspot. PLoS Genetics, 2019, 15, e1007965.	3.5	41
7	Nine quick tips for analyzing network data. PLoS Computational Biology, 2019, 15, e1007434.	3.2	23
8	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
9	Revealing the hidden structure of dynamic ecological networks. Royal Society Open Science, 2017, 4, 170251.	2.4	16
10	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
11	Ecological networks to unravel the routes to horizontal transposon transfers. PLoS Biology, 2017, 15, e2001536.	5.6	39
12	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
13	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
14	Colib'read on galaxy: a tools suite dedicated to biological information extraction from raw NGS reads. GigaScience, 2016, 5, 9.	6.4	2
15	DNA Physical Properties and Nucleosome Positions Are Major Determinants of HIV-1 Integrase Selectivity. PLoS ONE, 2015, 10, e0129427.	2.5	21
16	Spatially constrained clustering of ecological networks. Methods in Ecology and Evolution, 2014, 5, 771-779.	5.2	20
17	Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96.	1.3	2
18	Fast and Parallel Algorithm for Population-Based Segmentation of Copy-Number Profiles. Lecture Notes in Computer Science, 2014, , 248-258.	1.3	0

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19	High-quality sequence clustering guided by network topology and multiple alignment likelihood. Bioinformatics, 2012, 28, 1078-1085.	4.1	39
20	Ultra-fast sequence clustering from similarity networks with SiLiX. BMC Bioinformatics, 2011, 12, 116.	2.6	271
21	Strategies for online inference of model-based clustering in large and growing networks. Annals of Applied Statistics, 2010, 4, .	1.1	19
22	Deciphering the connectivity structure of biological networks using MixNet. BMC Bioinformatics, 2009, 10, S17.	2.6	26
23	Fast online graph clustering via Erdős–Rényi mixture. Pattern Recognition, 2008, 41, 3592-3599.	8.1	74
24	DNA physical properties determine nucleosome occupancy from yeast to fly. Nucleic Acids Research, 2008, 36, 3746-3756.	14.5	125
25	A Reversible Jump Markov Chain Monte Carlo Algorithm for Bacterial Promoter Motifs Discovery. Journal of Computational Biology, 2006, 13, 651-667.	1.6	4
26	seq++: analyzing biological sequences with a range of Markov-related models. Bioinformatics, 2005, 21, 2783-2784.	4.1	6