Jerome Kelleher

List of Publications by Year
in descending order

29 papers	1,959 citations	516710 16 h-index	610901 24 g-index
44 all docs	44 docs citations	44 times ranked	2158 citing authors

#	Article	IF	Citations
1	Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. PLoS Computational Biology, 2016, 12, e1004842.	3.2	547
2	Inferring whole-genome histories in large population datasets. Nature Genetics, 2019, 51, 1330-1338.	21.4	187
3	Tree‑sequence recording in SLiM opens new horizons for forward‑time simulation of whole genomes. Molecular Ecology Resources, 2019, 19, 552-566.	4.8	154
4	Efficient ancestry and mutation simulation with msprime 1.0. Genetics, 2022, 220, .	2.9	133
5	Efficient pedigree recording for fast population genetics simulation. PLoS Computational Biology, 2018, 14, e1006581.	3.2	130
6	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	6.0	112
7	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
8	A unified genealogy of modern and ancient genomes. Science, 2022, 375, eabi8264.	12.6	59
9	A NEW MODEL FOR EXTINCTION AND RECOLONIZATION IN TWO DIMENSIONS: QUANTIFYING PHYLOGEOGRAPHY. Evolution; International Journal of Organic Evolution, 2010, 64, 2701-2715.	2.3	57
10	Efficiently Summarizing Relationships in Large Samples: A General Duality Between Statistics of Genealogies and Genomes. Genetics, 2020, 215, 779-797.	2.9	51
11	Genetic hitchhiking in spatially extended populations. Theoretical Population Biology, 2013, 87, 75-89.	1.1	49
12	Accounting for long-range correlations in genome-wide simulations of large cohorts. PLoS Genetics, 2020, 16, e1008619.	3.5	43
13	Inference in two dimensions: Allele frequencies versus lengths of shared sequence blocks. Theoretical Population Biology, 2013, 87, 105-119.	1.1	36
14	Coalescent simulation in continuous space: Algorithms for large neighbourhood size. Theoretical Population Biology, 2014, 95, 13-23.	1.1	27
15	An Accurate and Scalable Collaborative Recommender. Artificial Intelligence Review, 2004, 21, 193-213.	15.7	24
16	Coalescent simulation in continuous space. Bioinformatics, 2013, 29, 955-956.	4.1	24
17	htsget: a protocol for securely streaming genomic data. Bioinformatics, 2019, 35, 119-121.	4.1	23
18	Lessons Learned from Bugs in Models of Human History. American Journal of Human Genetics, 2020, 107, 583-588.	6.2	23

#	Article	IF	Citations
19	Coalescent Simulation with msprime. Methods in Molecular Biology, 2020, 2090, 191-230.	0.9	23
20	Spread of pedigree versus genetic ancestry in spatially distributed populations. Theoretical Population Biology, 2016, 108, 1-12.	1.1	18
21	Bayesian inference of ancestral recombination graphs. PLoS Computational Biology, 2022, 18, e1009960.	3.2	12
22	Processing genome scale tabular data with wormtable. BMC Bioinformatics, 2013, 14, 356.	2.6	11
23	Measuring the degree of starshape in genealogies â€" summary statistics and demographic inference. Genetical Research, 2009, 91, 281-292.	0.9	6
24	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
25	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
26	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
27	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
28	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
29	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0