

Jerome Kelleher

List of Publications by Year in descending order

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Version: 2024-02-01

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	A unified genealogy of modern and ancient genomes. <i>Science</i> , 2022, 375, eabi8264.	12.6	59
2	Bayesian inference of ancestral recombination graphs. <i>PLoS Computational Biology</i> , 2022, 18, e1009960.	3.2	12
3	Efficient ancestry and mutation simulation with msprime 1.0. <i>Genetics</i> , 2022, 220, .	2.9	133
4	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	6.5	94
5	Lessons Learned from Bugs in Models of Human History. <i>American Journal of Human Genetics</i> , 2020, 107, 583-588.	6.2	23
6	Efficiently Summarizing Relationships in Large Samples: A General Duality Between Statistics of Genealogies and Genomes. <i>Genetics</i> , 2020, 215, 779-797.	2.9	51
7	Accounting for long-range correlations in genome-wide simulations of large cohorts. <i>PLoS Genetics</i> , 2020, 16, e1008619.	3.5	43
8	Coalescent Simulation with msprime. <i>Methods in Molecular Biology</i> , 2020, 2090, 191-230.	0.9	23
9	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, .	6.0	112
10	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
11	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
12	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
13	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
14	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
15	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
16	htsget: a protocol for securely streaming genomic data. <i>Bioinformatics</i> , 2019, 35, 119-121.	4.1	23
17	Inferring whole-genome histories in large population datasets. <i>Nature Genetics</i> , 2019, 51, 1330-1338.	21.4	187
18	Treeâ€ sequence recording in SLiM opens new horizons for forwardâ€ time simulation of whole genomes. <i>Molecular Ecology Resources</i> , 2019, 19, 552-566.	4.8	154

#	ARTICLE	IF	CITATIONS
19	Efficient pedigree recording for fast population genetics simulation. PLoS Computational Biology, 2018, 14, e1006581.	3.2	130
20	Spread of pedigree versus genetic ancestry in spatially distributed populations. Theoretical Population Biology, 2016, 108, 1-12.	1.1	18
21	Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. PLoS Computational Biology, 2016, 12, e1004842.	3.2	547
22	Coalescent simulation in continuous space: Algorithms for large neighbourhood size. Theoretical Population Biology, 2014, 95, 13-23.	1.1	27
23	Genetic hitchhiking in spatially extended populations. Theoretical Population Biology, 2013, 87, 75-89.	1.1	49
24	Processing genome scale tabular data with wormtable. BMC Bioinformatics, 2013, 14, 356.	2.6	11
25	Inference in two dimensions: Allele frequencies versus lengths of shared sequence blocks. Theoretical Population Biology, 2013, 87, 105-119.	1.1	36
26	Coalescent simulation in continuous space. Bioinformatics, 2013, 29, 955-956.	4.1	24
27	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
28	Measuring the degree of starshape in genealogies – summary statistics and demographic inference. Genetical Research, 2009, 91, 281-292.	0.9	6
29	An Accurate and Scalable Collaborative Recommender. Artificial Intelligence Review, 2004, 21, 193-213.	15.7	24