

Michael G B Blum

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

6,743
citations

136740

32
h-index

149479

56
g-index

72
all docs

72
docs citations

72
times ranked

10653
citing authors

#	ARTICLE	IF	CITATIONS
1	Approximate Bayesian Computation (ABC) in practice. <i>Trends in Ecology and Evolution</i> , 2010, 25, 410-418.	4.2	943
2	<i>pcadapt</i> : an R package to perform genome scans for selection based on principal component analysis. <i>Molecular Ecology Resources</i> , 2017, 17, 67-77.	2.2	647
3	abc: an R package for approximate Bayesian computation (ABC). <i>Methods in Ecology and Evolution</i> , 2012, 3, 475-479.	2.2	617
4	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	9.4	466
5	Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. <i>Science</i> , 2012, 338, 374-379.	6.0	364
6	Non-linear regression models for Approximate Bayesian Computation. <i>Statistics and Computing</i> , 2010, 20, 63-73.	0.8	331
7	The goat domestication process inferred from large-scale mitochondrial DNA analysis of wild and domestic individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17659-17664.	3.3	279
8	A Comparative Review of Dimension Reduction Methods in Approximate Bayesian Computation. <i>Statistical Science</i> , 2013, 28, .	1.6	232
9	Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. <i>Bioinformatics</i> , 2018, 34, 2781-2787.	1.8	217
10	Demographic History of European Populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000075.	1.5	182
11	Which Random Processes Describe the Tree of Life? A Large-Scale Study of Phylogenetic Tree Imbalance. <i>Systematic Biology</i> , 2006, 55, 685-691.	2.7	154
12	Approximate Bayesian Computation: A Nonparametric Perspective. <i>Journal of the American Statistical Association</i> , 2010, 105, 1178-1187.	1.8	153
13	Performing Highly Efficient Genome Scans for Local Adaptation with R Package pcadapt Version 4. <i>Molecular Biology and Evolution</i> , 2020, 37, 2153-2154.	3.5	133
14	Integrating deep learning CT-scan model, biological and clinical variables to predict severity of COVID-19 patients. <i>Nature Communications</i> , 2021, 12, 634.	5.8	126
15	Detecting Genomic Signatures of Natural Selection with Principal Component Analysis: Application to the 1000 Genomes Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 1082-1093.	3.5	123
16	Making the Most of Clumping and Thresholding for Polygenic Scores. <i>American Journal of Human Genetics</i> , 2019, 105, 1213-1221.	2.6	123
17	Evaluation of redundancy analysis to identify signatures of local adaptation. <i>Molecular Ecology Resources</i> , 2018, 18, 1223-1233.	2.2	118
18	apTreeshape: statistical analysis of phylogenetic tree shape. <i>Bioinformatics</i> , 2006, 22, 363-364.	1.8	109

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19	Genome Scans for Detecting Footprints of Local Adaptation Using a Bayesian Factor Model. <i>Molecular Biology and Evolution</i> , 2014, 31, 2483-2495.	3.5	94
20	On statistical tests of phylogenetic tree imbalance: The Sackin and other indices revisited. <i>Mathematical Biosciences</i> , 2005, 195, 141-153.	0.9	93
21	Inferring population size changes with sequence and SNP data: lessons from human bottlenecks. <i>Heredity</i> , 2013, 110, 409-419.	1.2	84
22	Low Levels of Genetic Divergence across Geographically and Linguistically Diverse Populations from India. <i>PLoS Genetics</i> , 2006, 2, e215.	1.5	82
23	Unravelling the invasion history of the Asian tiger mosquito in Europe. <i>Molecular Ecology</i> , 2019, 28, 2360-2377.	2.0	82
24	Efficient toolkit implementing best practices for principal component analysis of population genetic data. <i>Bioinformatics</i> , 2020, 36, 4449-4457.	1.8	76
25	Loter: A Software Package to Infer Local Ancestry for a Wide Range of Species. <i>Molecular Biology and Evolution</i> , 2018, 35, 2318-2326.	3.5	70
26	The mean, variance and limiting distribution of two statistics sensitive to phylogenetic tree balance. <i>Annals of Applied Probability</i> , 2006, 16, 2195.	0.6	69
27	HIV with contact tracing: a case study in approximate Bayesian computation. <i>Biostatistics</i> , 2010, 11, 644-660.	0.9	60
28	Deep Divergences of Human Gene Trees and Models of Human Origins. <i>Molecular Biology and Evolution</i> , 2011, 28, 889-898.	3.5	60
29	Identification of a new recurrent Aurora kinase C mutation in both European and African men with macrozoospermia. <i>Human Reproduction</i> , 2012, 27, 3337-3346.	0.4	52
30	Efficient Implementation of Penalized Regression for Genetic Risk Prediction. <i>Genetics</i> , 2019, 212, 65-74.	1.2	51
31	Resequencing Data Provide No Evidence for a Human Bottleneck in Africa during the Penultimate Glacial Period. <i>Molecular Biology and Evolution</i> , 2012, 29, 1851-1860.	3.5	43
32	NONSTATIONARY PATTERNS OF ISOLATION BY DISTANCE: INFERRING MEASURES OF LOCAL GENETIC DIFFERENTIATION WITH BAYESIAN KRIGING. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1110-1123.	1.1	42
33	Identifying outlier loci in admixed and in continuous populations using ancestral population differentiation statistics. <i>Molecular Ecology</i> , 2016, 25, 5029-5042.	2.0	38
34	Diagnostic tools for approximate Bayesian computation using the coverage property. <i>Australian and New Zealand Journal of Statistics</i> , 2014, 56, 309-329.	0.4	37
35	Anisotropic Isolation by Distance: The Main Orientations of Human Genetic Differentiation. <i>Molecular Biology and Evolution</i> , 2013, 30, 513-525.	3.5	35
36	Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. <i>BMC Bioinformatics</i> , 2020, 21, 16.	1.2	34

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37	Fine-scale human genetic structure in Western France. <i>European Journal of Human Genetics</i> , 2015, 23, 831-836.	1.4	31
38	Matrilineal Fertility Inheritance Detected in Hunter-Gatherer Populations Using the Imbalance of Gene Genealogies. <i>PLoS Genetics</i> , 2006, 2, e122.	1.5	30
39	Minimal clade size and external branch length under the neutral coalescent. <i>Advances in Applied Probability</i> , 2005, 37, 647-662.	0.4	29
40	Cold adaptation in the Asian tiger mosquito's native range precedes its invasion success in temperate regions. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1793-1808.	1.1	28
41	Predicting the success of an invader: Niche shift versus niche conservatism. <i>Ecology and Evolution</i> , 2019, 9, 12658-12675.	0.8	20
42	Reimagining Electronic Clinical Communication in the Post-Pager, Smartphone Era. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 21.	3.8	16
43	Choosing the Summary Statistics and the Acceptance Rate in Approximate Bayesian Computation. , 2010, , 47-56.		13
44	Invalid arguments against ABC: Reply to A.R. Templeton. <i>Trends in Ecology and Evolution</i> , 2010, 25, 490-491.	4.2	12
45	Hepatitis C virus whole genome sequencing: Current methods/issues and future challenges. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2016, 53, 341-351.	2.7	12
46	POPS: A Software for Prediction of Population Genetic Structure Using Latent Regression Models. <i>Journal of Statistical Software</i> , 2015, 68, .	1.8	11
47	Brownian models and coalescent structures. <i>Theoretical Population Biology</i> , 2004, 65, 249-261.	0.5	10
48	Prediction of group patterns in social mammals based on a coalescent model. <i>Journal of Theoretical Biology</i> , 2007, 249, 262-270.	0.8	10
49	Predictions of Native American Population Structure Using Linguistic Covariates in a Hidden Regression Framework. <i>PLoS ONE</i> , 2011, 6, e16227.	1.1	9
50	Estimating the Number of Ancestral Lineages Using a Maximum-Likelihood Method Based on Rejection Sampling. <i>Genetics</i> , 2007, 176, 1741-1757.	1.2	8
51	Sampling properties of homozygosity-based statistics for linkage disequilibrium. <i>Mathematical Biosciences</i> , 2007, 208, 33-47.	0.9	8
52	HaploPOP: a software that improves population assignment by combining markers into haplotypes. <i>BMC Bioinformatics</i> , 2015, 16, 242.	1.2	8
53	Can secondary contact following range expansion be distinguished from barriers to gene flow?. <i>PeerJ</i> , 2018, 6, e5325.	0.9	8
54	A deterministic model of admixture and genetic introgression: The case of Neanderthal and Cro-Magnon. <i>Mathematical Biosciences</i> , 2008, 216, 71-76.	0.9	6

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55	Ultradeep Pyrosequencing of NS3 To Predict Response to Triple Therapy with Protease Inhibitors in Previously Treated Chronic Hepatitis C Patients. <i>Journal of Clinical Microbiology</i> , 2015, 53, 389-397.	1.8	6
56	Ultradeep sequencing of B and non-B HIV-1 subtypes: Viral diversity and drug resistance mutations before and after one month of antiretroviral therapy in naive patients. <i>Journal of Clinical Virology</i> , 2017, 95, 13-19.	1.6	4
57	Individuality of breathing during volitional moderate hyperventilation. <i>European Journal of Applied Physiology</i> , 2016, 116, 217-225.	1.2	2