

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

136950

32
h-index

149698

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. | 8.7 | 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. | 4.8 | 647 |
| 3 | abc: an R package for approximate Bayesian computation (ABC). <i>Methods in Ecology and Evolution</i> , 2012, 3, 475-479. | 5.2 | 617 |
| 4 | Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249. | 21.4 | 466 |
| 5 | Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. <i>Science</i> , 2012, 338, 374-379. | 12.6 | 364 |
| 6 | Non-linear regression models for Approximate Bayesian Computation. <i>Statistics and Computing</i> , 2010, 20, 63-73. | 1.5 | 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. | 7.1 | 279 |
| 8 | A Comparative Review of Dimension Reduction Methods in Approximate Bayesian Computation. <i>Statistical Science</i> , 2013, 28, . | 2.8 | 232 |
| 9 | Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. <i>Bioinformatics</i> , 2018, 34, 2781-2787. | 4.1 | 217 |
| 10 | Demographic History of European Populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000075. | 3.5 | 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. | 5.6 | 154 |
| 12 | Approximate Bayesian Computation: A Nonparametric Perspective. <i>Journal of the American Statistical Association</i> , 2010, 105, 1178-1187. | 3.1 | 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. | 8.9 | 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. | 12.8 | 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. | 8.9 | 123 |
| 16 | Making the Most of Clumping and Thresholding for Polygenic Scores. <i>American Journal of Human Genetics</i> , 2019, 105, 1213-1221. | 6.2 | 123 |
| 17 | Evaluation of redundancy analysis to identify signatures of local adaptation. <i>Molecular Ecology Resources</i> , 2018, 18, 1223-1233. | 4.8 | 118 |
| 18 | apTreeshape: statistical analysis of phylogenetic tree shape. <i>Bioinformatics</i> , 2006, 22, 363-364. | 4.1 | 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. | 8.9 | 94 |
| 20 | On statistical tests of phylogenetic tree imbalance: The Sackin and other indices revisited. <i>Mathematical Biosciences</i> , 2005, 195, 141-153. | 1.9 | 93 |
| 21 | Inferring population size changes with sequence and SNP data: lessons from human bottlenecks. <i>Heredity</i> , 2013, 110, 409-419. | 2.6 | 84 |
| 22 | Low Levels of Genetic Divergence across Geographically and Linguistically Diverse Populations from India. <i>PLoS Genetics</i> , 2006, 2, e215. | 3.5 | 82 |
| 23 | Unravelling the invasion history of the Asian tiger mosquito in Europe. <i>Molecular Ecology</i> , 2019, 28, 2360-2377. | 3.9 | 82 |
| 24 | Efficient toolkit implementing best practices for principal component analysis of population genetic data. <i>Bioinformatics</i> , 2020, 36, 4449-4457. | 4.1 | 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. | 8.9 | 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. | 1.3 | 69 |
| 27 | HIV with contact tracing: a case study in approximate Bayesian computation. <i>Biostatistics</i> , 2010, 11, 644-660. | 1.5 | 60 |
| 28 | Deep Divergences of Human Gene Trees and Models of Human Origins. <i>Molecular Biology and Evolution</i> , 2011, 28, 889-898. | 8.9 | 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. | 0.9 | 52 |
| 30 | Efficient Implementation of Penalized Regression for Genetic Risk Prediction. <i>Genetics</i> , 2019, 212, 65-74. | 2.9 | 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. | 8.9 | 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. | 2.3 | 42 |
| 33 | Identifying outlier loci in admixed and in continuous populations using ancestral population differentiation statistics. <i>Molecular Ecology</i> , 2016, 25, 5029-5042. | 3.9 | 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. | 0.9 | 37 |
| 35 | Anisotropic Isolation by Distance: The Main Orientations of Human Genetic Differentiation. <i>Molecular Biology and Evolution</i> , 2013, 30, 513-525. | 8.9 | 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. | 2.6 | 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. | 2.8 | 31 |
| 38 | Matrilineal Fertility Inheritance Detected in Hunter-Gatherer Populations Using the Imbalance of Gene Genealogies. <i>PLoS Genetics</i> , 2006, 2, e122. | 3.5 | 30 |
| 39 | Minimal clade size and external branch length under the neutral coalescent. <i>Advances in Applied Probability</i> , 2005, 37, 647-662. | 0.7 | 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. | 2.3 | 28 |
| 41 | Predicting the success of an invader: Niche shift versus niche conservatism. <i>Ecology and Evolution</i> , 2019, 9, 12658-12675. | 1.9 | 20 |
| 42 | Reimagining Electronic Clinical Communication in the Post-Pager, Smartphone Era. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 21. | 7.4 | 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. | 8.7 | 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. | 6.1 | 12 |
| 46 | POPS: A Software for Prediction of Population Genetic Structure Using Latent Regression Models. <i>Journal of Statistical Software</i> , 2015, 68, . | 3.7 | 11 |
| 47 | Brownian models and coalescent structures. <i>Theoretical Population Biology</i> , 2004, 65, 249-261. | 1.1 | 10 |
| 48 | Prediction of group patterns in social mammals based on a coalescent model. <i>Journal of Theoretical Biology</i> , 2007, 249, 262-270. | 1.7 | 10 |
| 49 | Predictions of Native American Population Structure Using Linguistic Covariates in a Hidden Regression Framework. <i>PLoS ONE</i> , 2011, 6, e16227. | 2.5 | 9 |
| 50 | Estimating the Number of Ancestral Lineages Using a Maximum-Likelihood Method Based on Rejection Sampling. <i>Genetics</i> , 2007, 176, 1741-1757. | 2.9 | 8 |
| 51 | Sampling properties of homozygosity-based statistics for linkage disequilibrium. <i>Mathematical Biosciences</i> , 2007, 208, 33-47. | 1.9 | 8 |
| 52 | HaploPOP: a software that improves population assignment by combining markers into haplotypes. <i>BMC Bioinformatics</i> , 2015, 16, 242. | 2.6 | 8 |
| 53 | Can secondary contact following range expansion be distinguished from barriers to gene flow?. <i>PeerJ</i> , 2018, 6, e5325. | 2.0 | 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. | 1.9 | 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. | 3.9 | 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. | 3.1 | 4 |
| 57 | Individuality of breathing during volitional moderate hyperventilation. <i>European Journal of Applied Physiology</i> , 2016, 116, 217-225. | 2.5 | 2 |