

Brian R Moore

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,800
citations

361413

20
h-index

580821

25
g-index

28
all docs

28
docs citations

28
times ranked

4446
citing authors

#	ARTICLE	IF	CITATIONS
1	A LIKELIHOOD FRAMEWORK FOR INFERRING THE EVOLUTION OF GEOGRAPHIC RANGE ON PHYLOGENETIC TREES. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2299-2311.	2.3	698
2	Bayesian Analysis of Biogeography when the Number of Areas is Large. <i>Systematic Biology</i> , 2013, 62, 789-804.	5.6	622
3	RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language. <i>Systematic Biology</i> , 2016, 65, 726-736.	5.6	538
4	Critically evaluating the theory and performance of Bayesian analysis of macroevolutionary mixtures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9569-9574.	7.1	272
5	Toward an Integrative Historical Biogeography. <i>Integrative and Comparative Biology</i> , 2003, 43, 261-270.	2.0	250
6	Correlates of Diversification in the Plant Clade Dipsacales: Geographic Movement and Evolutionary Innovations. <i>American Naturalist</i> , 2007, 170, S28-S55.	2.1	197
7	A likelihood framework for inferring the evolution of geographic range on phylogenetic trees. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2299-311.	2.3	142
8	Rapid Global Spread of wRi-like Wolbachia across Multiple <i>Drosophila</i> . <i>Current Biology</i> , 2018, 28, 963-971.e8.	3.9	127
9	TESS: an R package for efficiently simulating phylogenetic trees and performing Bayesian inference of lineage diversification rates. <i>Bioinformatics</i> , 2016, 32, 789-791.	4.1	114
10	SYMMETREE: whole-tree analysis of differential diversification rates. <i>Bioinformatics</i> , 2005, 21, 1709-1710.	4.1	105
11	Whole-Tree Methods for Detecting Differential Diversification Rates. <i>Systematic Biology</i> , 2002, 51, 855-865.	5.6	96
12	A Bayesian approach for detecting the impact of mass extinction events on molecular phylogenies when rates of lineage diversification may vary. <i>Methods in Ecology and Evolution</i> , 2016, 7, 947-959.	5.2	94
13	Heterostyly accelerates diversification via reduced extinction in primroses. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140075.	2.6	84
14	Detecting Diversification Rate Variation in Supertrees. <i>Computational Biology</i> , 2004, , 487-533.	0.2	79
15	A Bayesian approach for evaluating the impact of historical events on rates of diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4307-4312.	7.1	74
16	A critical appraisal of the use of microRNA data in phylogenetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3659-68.	7.1	63
17	The Dawn of Open Access to Phylogenetic Data. <i>PLoS ONE</i> , 2014, 9, e110268.	2.5	46
18	How Well Can We Detect Lineage-Specific Diversification-Rate Shifts? A Simulation Study of Sequential AIC Methods. <i>Systematic Biology</i> , 2016, 65, 1076-1084.	5.6	39

#	ARTICLE	IF	CITATIONS
19	A Bayesian Approach for Inferring the Impact of a Discrete Character on Rates of Continuous-Character Evolution in the Presence of Background-Rate Variation. <i>Systematic Biology</i> , 2020, 69, 530-544.	5.6	28
20	Increasing Data Transparency and Estimating Phylogenetic Uncertainty in Supertrees: Approaches Using Nonparametric Bootstrapping. <i>Systematic Biology</i> , 2006, 55, 662-676.	5.6	25
21	Accounting for Mode of Speciation Increases Power and Realism of Tests of Phylogenetic Asymmetry. <i>American Naturalist</i> , 1999, 153, 332-346.	2.1	20
22	A LIKELIHOOD FRAMEWORK FOR INFERRING THE EVOLUTION OF GEOGRAPHIC RANGE ON PHYLOGENETIC TREES. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2299.	2.3	20
23	Phylodynamics of H5N1 Highly Pathogenic Avian Influenza in Europe, 2005â€“2010: Potential for Molecular Surveillance of New Outbreaks. <i>Viruses</i> , 2015, 7, 3310-3328.	3.3	18
24	A hierarchical Bayesian mixture model for inferring the expression state of genes in transcriptomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19339-19346.	7.1	16
25	A Comparative Analysis of Herbivory and Amniote Diversification in Modern Terrestrial Ecosystems. <i>The Paleontological Society Special Publications</i> , 1996, 8, 280-280.	0.0	1
26	Exploring the â€œEgg/Plant Questionâ€: What Best Explains the Patterns of Amniote Diversification?. <i>The Paleontological Society Special Publications</i> , 1996, 8, 322-322.	0.0	0