

David Bryant

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

15,254
citations

516215

16
h-index

454577

30
g-index

34
all docs

34
docs citations

34
times ranked

21080
citing authors

#	ARTICLE	IF	CITATIONS
1	Bayesian Inference of Species Trees using Diffusion Models. <i>Systematic Biology</i> , 2021, 70, 145-161.	2.7	21
2	Negative-Type Diversities, a Multi-dimensional Analogue of Negative-Type Metrics. <i>Journal of Geometric Analysis</i> , 2021, 31, 1703-1720.	0.5	1
3	V-Spline: An Adaptive Smoothing Spline for Trajectory Reconstruction. <i>Sensors</i> , 2021, 21, 3215.	2.1	5
4	Microbial Phylogenetic Context Using Phylogenetic Outlines. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
5	Discrete coalescent trees. <i>Journal of Mathematical Biology</i> , 2021, 83, 60.	0.8	4
6	An $O(n \log n)$ Time Algorithm for Computing the Path-Length Distance Between Trees. <i>Algorithmica</i> , 2019, 81, 3692-3706.	1.0	1
7	Failure to Recover Major Events of Gene Flux in Real Biological Data Due to Method Misapplication. <i>Genome Biology and Evolution</i> , 2018, 10, 1198-1209.	1.1	4
8	How disturbance and dispersal influence intraspecific structure. <i>Journal of Ecology</i> , 2018, 106, 1298-1306.	1.9	24
9	The dimensionality of niche space allows bounded and unbounded processes to jointly influence diversification. <i>Nature Communications</i> , 2018, 9, 4258.	5.8	16
10	Can We "Future-Proof" Consensus Trees?. <i>Systematic Biology</i> , 2017, 66, 611-619.	2.7	30
11	A Universal Separable Diversity. <i>Analysis and Geometry in Metric Spaces</i> , 2017, 5, 138-151.	0.2	6
12	The probability of monophyly of a sample of gene lineages on a species tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8002-8009.	3.3	15
13	Efficient Recycled Algorithms for Quantitative Trait Models on Phylogenies. <i>Genome Biology and Evolution</i> , 2016, 8, 1338-1350.	1.1	13
14	Constant Distortion Embeddings of Symmetric Diversities. <i>Analysis and Geometry in Metric Spaces</i> , 2016, 4, .	0.2	3
15	<scp>popart</scp>: full-featured software for haplotype network construction. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1110-1116.	2.2	4,199
16	Flexible methods for estimating genetic distances from single nucleotide polymorphisms. <i>Methods in Ecology and Evolution</i> , 2015, 6, 938-948.	2.2	38
17	Monte Carlo Strategies for Selecting Parameter Values in Simulation Experiments. <i>Systematic Biology</i> , 2015, 64, 741-751.	2.7	21
18	Endosymbiotic origin and differential loss of eukaryotic genes. <i>Nature</i> , 2015, 524, 427-432.	13.7	251

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19	Origins of major archaeal clades correspond to gene acquisitions from bacteria. <i>Nature</i> , 2015, 517, 77-80.	13.7	238
20	Statistical flaws undermine pre-Columbian chicken debate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3584.	3.3	5
21	Forty Years of Model-Based Phylogeography. <i>Computational Biology</i> , 2013, , 17-28.	0.1	0
22	Inferring Species Trees Directly from Biallelic Genetic Markers: Bypassing Gene Trees in a Full Coalescent Analysis. <i>Molecular Biology and Evolution</i> , 2012, 29, 1917-1932.	3.5	828
23	Hyperconvexity and tight-span theory for diversities. <i>Advances in Mathematics</i> , 2012, 231, 3172-3198.	0.5	19
24	Investigating the Global Dispersal of Chickens in Prehistory Using Ancient Mitochondrial DNA Signatures. <i>PLoS ONE</i> , 2012, 7, e39171.	1.1	111
25	â€œBureaucraticâ€™ set systems, and their role in phylogenetics. <i>Applied Mathematics Letters</i> , 2012, 25, 1148-1152.	1.5	0
26	The link between segregation and phylogenetic diversity. <i>Journal of Mathematical Biology</i> , 2012, 64, 149-162.	0.8	2
27	Species delimitation and phylogeny of a New Zealand plant species radiation. <i>BMC Evolutionary Biology</i> , 2009, 9, 111.	3.2	47
28	Continuous and tractable models for the variation of evolutionary rates. <i>Mathematical Biosciences</i> , 2006, 199, 216-233.	0.9	52
29	Application of Phylogenetic Networks in Evolutionary Studies. <i>Molecular Biology and Evolution</i> , 2006, 23, 254-267.	3.5	7,402
30	Neighbor-Net: An Agglomerative Method for the Construction of Phylogenetic Networks. <i>Molecular Biology and Evolution</i> , 2003, 21, 255-265.	3.5	1,675
31	A classification of consensus methods for phylogenetics. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 2003, , 163-183.	0.0	173
32	Hunting for Trees in Binary Character Sets: Efficient Algorithms for Extraction, Enumeration, and Optimization. <i>Journal of Computational Biology</i> , 1996, 3, 275-288.	0.8	14
33	FRAËSSÄ% LIMITS FOR RELATIONAL METRIC STRUCTURES. <i>Journal of Symbolic Logic</i> , 0, , 1-22.	0.4	1