

Remco R Bouckaert

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

12,687
citations

377584

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445137

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docs citations

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times ranked

18368
citing authors

#	ARTICLE	IF	CITATIONS
1	Multidimensional Phylogenetic Metrics Identify Class I Aminoacyl-tRNA Synthetase Evolutionary Mosaicity and Inter-Modular Coupling. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1520.	1.8	5
2	StarBeast3: Adaptive Parallelized Bayesian Inference under the Multispecies Coalescent. <i>Systematic Biology</i> , 2022, 71, 901-916.	2.7	29
3	An Efficient Coalescent Epoch Model for Bayesian Phylogenetic Inference. <i>Systematic Biology</i> , 2022, 71, 1549-1560.	2.7	19
4	Detecting contact in language trees: a Bayesian phylogenetic model with horizontal transfer. <i>Humanities and Social Sciences Communications</i> , 2022, 9, .	1.3	9
5	Bayesian Inference of Species Trees using Diffusion Models. <i>Systematic Biology</i> , 2021, 70, 145-161.	2.7	21
6	Adaptive dating and fast proposals: Revisiting the phylogenetic relaxed clock model. <i>PLoS Computational Biology</i> , 2021, 17, e1008322.	1.5	60
7	Phylodynamics reveals the role of human travel and contact tracing in controlling the first wave of COVID-19 in four island nations. <i>Virus Evolution</i> , 2021, 7, veab052.	2.2	35
8	Real-Time Genomics for Tracking Severe Acute Respiratory Syndrome Coronavirus 2 Border Incursions after Virus Elimination, New Zealand. <i>Emerging Infectious Diseases</i> , 2021, 27, 2361-2368.	2.0	27
9	Bayesian phylogenetic analysis of linguistic data using BEAST. <i>Journal of Language Evolution</i> , 2021, 6, 119-135.	0.4	9
10	Combinatorial perspectives on Dollo-k characters in phylogenetics. <i>Advances in Applied Mathematics</i> , 2021, 131, 102252.	0.4	1
11	Triangulation supports agricultural spread of the Transeurasian languages. <i>Nature</i> , 2021, 599, 616-621.	13.7	58
12	OBAMA: OBAMA for Bayesian amino-acid model averaging. <i>PeerJ</i> , 2020, 8, e9460.	0.9	11
13	Adaptive Metropolis-coupled MCMC for BEAST 2. <i>PeerJ</i> , 2020, 8, e9473.	0.9	28
14	Phylodynamic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , 2019, 68, 358-364.	2.7	25
15	Model Selection and Parameter Inference in Phylogenetics Using Nested Sampling. <i>Systematic Biology</i> , 2019, 68, 219-233.	2.7	138
16	Bayesian phylodynamics of avian influenza A virus H9N2 in Asia with time-dependent predictors of migration. <i>PLoS Computational Biology</i> , 2019, 15, e1007189.	1.5	22
17	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	1.5	2,484
18	A Bayesian phylogenetic study of the Dravidian language family. <i>Royal Society Open Science</i> , 2018, 5, 171504.	1.1	54

#	ARTICLE	IF	CITATIONS
19	The origin and expansion of PamañNyungan languages across Australia. <i>Nature Ecology and Evolution</i> , 2018, 2, 741-749.	3.4	54
20	Bayesian Phylogenetic Estimation of Clade Ages Supports Trans-Atlantic Dispersal of Cichlid Fishes. <i>Systematic Biology</i> , 2017, 66, syw076.	2.7	86
21	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2101-2114.	3.5	371
22	bModelTest: Bayesian phylogenetic site model averaging and model comparison. <i>BMC Evolutionary Biology</i> , 2017, 17, 42.	3.2	609
23	Tracing hepatitis B virus (HBV) genotype B5 (formerly B6) evolutionary history in the circumpolar Arctic through phylogeographic modelling. <i>PeerJ</i> , 2017, 5, e3757.	0.9	29
24	Phylogeography by diffusion on a sphere: whole world phylogeography. <i>PeerJ</i> , 2016, 4, e2406.	0.9	37
25	BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003537.	1.5	5,301
26	Species Delimitation using Genome-Wide SNP Data. <i>Systematic Biology</i> , 2014, 63, 534-542.	2.7	390
27	Looking for trees in the forest: summary tree from posterior samples. <i>BMC Evolutionary Biology</i> , 2013, 13, 221.	3.2	131
28	Evolutionary Rates and Hbv: Issues of Rate Estimation with Bayesian Molecular Methods. <i>Antiviral Therapy</i> , 2013, 18, 497-504.	0.6	68
29	Mapping the Origins and Expansion of the Indo-European Language Family. <i>Science</i> , 2012, 337, 957-960.	6.0	549
30	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
31	DensiTree: making sense of sets of phylogenetic trees. <i>Bioinformatics</i> , 2010, 26, 1372-1373.	1.8	565
32	Racing algorithms for conditional independence inference. <i>International Journal of Approximate Reasoning</i> , 2007, 45, 386-401.	1.9	12
33	A modified simulation scheme for inference in Bayesian networks. <i>International Journal of Approximate Reasoning</i> , 1996, 14, 55-80.	1.9	27