

Bret Larget

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12168353/publications.pdf>

Version: 2024-02-01

25
papers

23,692
citations

430874

18
h-index

677142

22
g-index

26
all docs

26
docs citations

26
times ranked

25896
citing authors

#	ARTICLE	IF	CITATIONS
1	BayesCAT: Bayesian Co-estimation of Alignment and Tree. <i>Biometrics</i> , 2018, 74, 270-279.	1.4	3
2	Phantom species: adjusting estimates of colonization and extinction for pseudo-turnover. <i>Oikos</i> , 2018, 127, 1605-1618.	2.7	6
3	Statistical evidence for common ancestry: Application to primates. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1354-1363.	2.3	8
4	Exploring Tree-Like and Non-Tree-Like Patterns Using Genome Sequences: An Example Using the Inbreeding Plant Species <i>Arabidopsis thaliana</i> (L.) Heynh. <i>Systematic Biology</i> , 2015, 64, 809-823.	5.6	57
5	Bayesian estimation of the phylogeography of African gorillas with genome-differentiated population trees. <i>Biometrics</i> , 2014, 70, 683-694.	1.4	0
6	The Estimation of Tree Posterior Probabilities Using Conditional Clade Probability Distributions. <i>Systematic Biology</i> , 2013, 62, 501-511.	5.6	35
7	Ecosystem respiration: Drivers of daily variability and background respiration in lakes around the globe. <i>Limnology and Oceanography</i> , 2013, 58, 849-866.	3.1	195
8	MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. <i>Systematic Biology</i> , 2012, 61, 539-542.	5.6	20,458
9	Efficiency of Markov Chain Monte Carlo Tree Proposals in Bayesian Phylogenetics. <i>Systematic Biology</i> , 2008, 57, 86-103.	5.6	146
10	A Bayesian Model of AFLP Marker Evolution and Phylogenetic Inference. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007, 6, Article11.	0.6	22
11	Bayesian Estimation of Concordance among Gene Trees. <i>Molecular Biology and Evolution</i> , 2006, 24, 412-426.	8.9	420
12	Comment on "Phylogenetic MCMC Algorithms Are Misleading on Mixtures of Trees". <i>Science</i> , 2006, 312, 367a-367a.	12.6	19
13	A Bayesian approach to the estimation of ancestral genome arrangements. <i>Molecular Phylogenetics and Evolution</i> , 2005, 36, 214-223.	2.7	37
14	A Bayesian Analysis of Metazoan Mitochondrial Genome Arrangements. <i>Molecular Biology and Evolution</i> , 2005, 22, 486-495.	8.9	78
15	Hastings Ratio of the LOCAL Proposal Used in Bayesian Phylogenetics. <i>Systematic Biology</i> , 2005, 54, 961-965.	5.6	41
16	Introduction to Markov Chain Monte Carlo Methods in Molecular Evolution. , 2005, , 45-62.		6
17	Bayesian Phylogenetic Model Selection Using Reversible Jump Markov Chain Monte Carlo. <i>Molecular Biology and Evolution</i> , 2004, 21, 1123-1133.	8.9	502
18	Potential Applications and Pitfalls of Bayesian Inference of Phylogeny. <i>Systematic Biology</i> , 2002, 51, 673-688.	5.6	721

#	ARTICLE	IF	CITATIONS
19	Bayesian phylogenetic inference from animal mitochondrial genome arrangements. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2002, 64, 681-693.	2.2	49
20	Statistical Analysis of DOE EML QAP Data from 1982 to 1998. Journal of Chemical Information and Computer Sciences, 2001, 41, 1099-1105.	2.8	0
21	Phylogenetic Inference from Mitochondrial Genome Arrangement Data. Lecture Notes in Computer Science, 2001, , 1022-1028.	1.3	2
22	A BAYESIAN FRAMEWORK FOR THE ANALYSIS OF COSPECIATION. Evolution; International Journal of Organic Evolution, 2000, 54, 352-364.	2.3	111
23	A Compound Poisson Process for Relaxing the Molecular Clock. Genetics, 2000, 154, 1879-1892.	2.9	290
24	Markov chain Monte Carlo for the Bayesian analysis of evolutionary trees from aligned molecular sequences. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 1999, 33, 143-162.	1.0	26
25	Bayesian Phylogenetic Inference via Markov Chain Monte Carlo Methods. Biometrics, 1999, 55, 1-12.	1.4	460