

Vladimir N Minin

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

3,363
citations

270111

25
h-index

190340

53
g-index

65
all docs

65
docs citations

65
times ranked

6139
citing authors

#	ARTICLE	IF	CITATIONS
1	A linear noise approximation for stochastic epidemic models fit to partially observed incidence counts. <i>Biometrics</i> , 2022, 78, 1530-1541.	0.8	13
2	Optimal experimental design for mathematical models of haematopoiesis. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20200729.	1.5	5
3	Predictors of Test Positivity, Mortality, and Seropositivity during the Early Coronavirus Disease Epidemic, Orange County, California, USA. <i>Emerging Infectious Diseases</i> , 2021, 27, 2604-2618.	2.0	12
4	19 Dubious Ways to Compute the Marginal Likelihood of a Phylogenetic Tree Topology. <i>Systematic Biology</i> , 2020, 69, 209-220.	2.7	40
5	Rejoinder for discussion on "Horseshoe"-based Bayesian nonparametric estimation of effective population size trajectories". <i>Biometrics</i> , 2020, 76, 695-699.	0.8	2
6	A Bayesian phylogenetic hidden Markov model for B cell receptor sequence analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1008030.	1.5	20
7	Horseshoe"-based Bayesian nonparametric estimation of effective population size trajectories. <i>Biometrics</i> , 2020, 76, 677-690.	0.8	16
8	Estimating effective population size changes from preferentially sampled genetic sequences. <i>PLoS Computational Biology</i> , 2020, 16, e1007774.	1.5	14
9	Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts. <i>PLoS Computational Biology</i> , 2020, 16, e1007999.	1.5	30
10	Survival analysis of DNA mutation motifs with penalized proportional hazards. <i>Annals of Applied Statistics</i> , 2019, 13, 1268-1294.	0.5	8
11	Marginal Likelihoods in Phylogenetics: A Review of Methods and Applications. <i>Systematic Biology</i> , 2019, 68, 681-697.	2.7	26
12	Spatio-Temporal Analysis of Surveillance Data. , 2019, , 455-475.		8
13	Statistical inference for partially observed branching processes with application to cell lineage tracking of in vivo hematopoiesis. <i>Annals of Applied Statistics</i> , 2019, 13, .	0.5	6
14	Using Genotype Abundance to Improve Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2018, 35, 1253-1265.	3.5	55
15	Introduction to the Special Section on Inference for Infectious Disease Dynamics. <i>Statistical Science</i> , 2018, 33, .	1.6	2
16	Birth/birth-death processes and their computable transition probabilities with biological applications. <i>Journal of Mathematical Biology</i> , 2018, 76, 911-944.	0.8	28
17	Recombination-independent rapid convergent evolution of the gastric pathogen <i>Helicobacter pylori</i> . <i>BMC Genomics</i> , 2018, 19, 835.	1.2	3
18	Predicting B cell receptor substitution profiles using public repertoire data. <i>PLoS Computational Biology</i> , 2018, 14, e1006388.	1.5	8

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19	Locally Adaptive Smoothing with Markov Random Fields and Shrinkage Priors. <i>Bayesian Analysis</i> , 2018, 13, 225-252.	1.6	39
20	Calculating Higher-Order Moments of Phylogenetic Stochastic Mapping Summaries in Linear Time. <i>Journal of Computational Biology</i> , 2017, 24, 377-399.	0.8	1
21	Efficient Data Augmentation for Fitting Stochastic Epidemic Models to Prevalence Data. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 918-929.	0.9	13
22	Myosin-independent cytokinesis in <i>Giardia</i> utilizes flagella to coordinate force generation and direct membrane trafficking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5854-E5863.	3.3	56
23	<code>scp</code> phylodyn: an R package for phylodynamic simulation and inference. <i>Molecular Ecology Resources</i> , 2017, 17, 96-100.	2.2	53
24	Predictive modeling of cholera outbreaks in Bangladesh. <i>Annals of Applied Statistics</i> , 2016, 10, 575-595.	0.5	17
25	Detecting the Anomaly Zone in Species Trees and Evidence for a Misleading Signal in Higher-Level Skink Phylogeny (Squamata: Scincidae). <i>Systematic Biology</i> , 2016, 65, 465-477.	2.7	85
26	Quantifying and Mitigating the Effect of Preferential Sampling on Phylodynamic Inference. <i>PLoS Computational Biology</i> , 2016, 12, e1004789.	1.5	45
27	Stochastic Modeling of Hematopoietic Stem and Progenitor Cell Barcoding Data from Rhesus Macaques Challenges the Classic Model of Hematopoiesis. <i>Blood</i> , 2016, 128, 2643-2643.	0.6	0
28	Likelihood-Based Inference for Discretely Observed Birth-Death-Shift Processes, with Applications to Evolution of Mobile Genetic Elements. <i>Biometrics</i> , 2015, 71, 1009-1021.	0.8	11
29	An efficient Bayesian inference framework for coalescent-based nonparametric phylodynamics. <i>Bioinformatics</i> , 2015, 31, 3282-3289.	1.8	34
30	Synonymous and nonsynonymous distances help untangle convergent evolution and recombination. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 375-89.	0.2	5
31	Quantifying evolutionary constraints on B-cell affinity maturation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140244.	1.8	45
32	A Joint Model for Multistate Disease Processes and Random Informative Observation Times, with Applications to Electronic Medical Records Data. <i>Biometrics</i> , 2015, 71, 90-101.	0.8	33
33	Efficient Transition Probability Computation for Continuous-Time Branching Processes via Compressed Sensing. <i>Uncertainty in artificial intelligence : proceedings of the ... conference.</i> , 2015, 2015, 952-961.	0.9	1
34	Predictable transcriptome evolution in the convergent and complex bioluminescent organs of squid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4736-42.	3.3	77
35	Phylogenetic Stochastic Mapping Without Matrix Exponentiation. <i>Journal of Computational Biology</i> , 2014, 21, 676-690.	0.8	9
36	Estimation for General Birth-Death Processes. <i>Journal of the American Statistical Association</i> , 2014, 109, 730-747.	1.8	32

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37	Species Delimitation using Genome-Wide SNP Data. <i>Systematic Biology</i> , 2014, 63, 534-542.	2.7	390
38	Heritability estimation of osteoarthritis in the pig-tailed macaque (<i>Macaca nemestrina</i>) with a look toward future data collection. <i>PeerJ</i> , 2014, 2, e373.	0.9	2
39	Phylogeography of the Trans-Volcanic bunchgrass lizard (<i>Sceloporus bicanthalis</i>) across the highlands of south-eastern Mexico. <i>Biological Journal of the Linnean Society</i> , 2013, 110, 852-865.	0.7	23
40	rbrothers: R Package for Bayesian Multiple Change-Point Recombination Detection. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11945.	0.6	2
41	Fitting and interpreting continuous-time latent Markov models for panel data. <i>Statistics in Medicine</i> , 2013, 32, 4581-4595.	0.8	18
42	Gaussian Process-Based Bayesian Nonparametric Inference of Population Size Trajectories from Gene Genealogies. <i>Biometrics</i> , 2013, 69, 8-18.	0.8	37
43	Fitting birth-death processes to panel data with applications to bacterial DNA fingerprinting. <i>Annals of Applied Statistics</i> , 2013, 7, 2315-2335.	0.5	11
44	A counting renaissance: combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection. <i>Bioinformatics</i> , 2012, 28, 3248-3256.	1.8	75
45	A statistical approach to peptide identification from clustered tandem mass spectrometry data. , 2012, , 648-653.		4
46	Measuring Microsatellite Conservation in Mammalian Evolution with a Phylogenetic Birth-Death Model. <i>Genome Biology and Evolution</i> , 2012, 4, 636-647.	1.1	30
47	Recombination Between Variants from Genital Tract and Plasma: Evolution of Multidrug-Resistant HIV Type 1. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1766-1774.	0.5	10
48	Imputation Estimators Partially Correct for Model Misspecification. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	1
49	Learning to Count: Robust Estimates for Labeled Distances between Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2009, 26, 801-814.	3.5	102
50	High frequency of hotspot mutations in core genes of <i>Escherichia coli</i> due to short-term positive selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12412-12417.	3.3	95
51	Smooth Skyride through a Rough Skyline: Bayesian Coalescent-Based Inference of Population Dynamics. <i>Molecular Biology and Evolution</i> , 2008, 25, 1459-1471.	3.5	626
52	Fast, accurate and simulation-free stochastic mapping. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3985-3995.	1.8	149
53	cBrother: relaxing parental tree assumptions for Bayesian recombination detection. <i>Bioinformatics</i> , 2007, 23, 507-508.	1.8	16
54	Phylogenetic Mapping of Recombination Hotspots in Human Immunodeficiency Virus via Spatially Smoothed Change-Point Processes. <i>Genetics</i> , 2007, 175, 1773-1785.	1.2	29

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55	Hot and Cold: Spatial Fluctuation in HIV-1 Recombination Rates. , 2007, , .		2
56	Counting labeled transitions in continuous-time Markov models of evolution. Journal of Mathematical Biology, 2007, 56, 391-412.	0.8	235
57	Accounting for Uncertainty in the Tree Topology Has Little Effect on the Decision-Theoretic Approach to Model Selection in Phylogeny Estimation. Molecular Biology and Evolution, 2005, 22, 691-703.	3.5	68
58	Dual multiple change-point model leads to more accurate recombination detection. Bioinformatics, 2005, 21, 3034-3042.	1.8	136
59	Statistical Methods for Analyzing Tissue Microarray Data. Journal of Biopharmaceutical Statistics, 2004, 14, 671-685.	0.4	57
60	Performance-Based Selection of Likelihood Models for Phylogeny Estimation. Systematic Biology, 2003, 52, 674-683.	2.7	386