

Vladimir N Minin

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

3,363
citations

236925

25
h-index

161849

54
g-index

65
all docs

65
docs citations

65
times ranked

5510
citing authors

#	ARTICLE	IF	CITATIONS
1	Smooth Skyride through a Rough Skyline: Bayesian Coalescent-Based Inference of Population Dynamics. <i>Molecular Biology and Evolution</i> , 2008, 25, 1459-1471.	8.9	626
2	Species Delimitation using Genome-Wide SNP Data. <i>Systematic Biology</i> , 2014, 63, 534-542.	5.6	390
3	Performance-Based Selection of Likelihood Models for Phylogeny Estimation. <i>Systematic Biology</i> , 2003, 52, 674-683.	5.6	386
4	Counting labeled transitions in continuous-time Markov models of evolution. <i>Journal of Mathematical Biology</i> , 2007, 56, 391-412.	1.9	235
5	Fast, accurate and simulation-free stochastic mapping. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3985-3995.	4.0	149
6	Dual multiple change-point model leads to more accurate recombination detection. <i>Bioinformatics</i> , 2005, 21, 3034-3042.	4.1	136
7	Learning to Count: Robust Estimates for Labeled Distances between Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2009, 26, 801-814.	8.9	102
8	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.	7.1	95
9	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.	5.6	85
10	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.	7.1	77
11	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.	4.1	75
12	Accounting for Uncertainty in the Tree Topology Has Little Effect on the Decision-Theoretic Approach to Model Selection in Phylogeny Estimation. <i>Molecular Biology and Evolution</i> , 2005, 22, 691-703.	8.9	68
13	Statistical Methods for Analyzing Tissue Microarray Data. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 671-685.	0.8	57
14	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.	7.1	56
15	Using Genotype Abundance to Improve Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2018, 35, 1253-1265.	8.9	55
16	<sc>phylodyn</sc>: an R package for phylodynamic simulation and inference. <i>Molecular Ecology Resources</i> , 2017, 17, 96-100.	4.8	53
17	Quantifying evolutionary constraints on B-cell affinity maturation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140244.	4.0	45
18	Quantifying and Mitigating the Effect of Preferential Sampling on Phylodynamic Inference. <i>PLoS Computational Biology</i> , 2016, 12, e1004789.	3.2	45

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19	19 Dubious Ways to Compute the Marginal Likelihood of a Phylogenetic Tree Topology. <i>Systematic Biology</i> , 2020, 69, 209-220.	5.6	40
20	Locally Adaptive Smoothing with Markov Random Fields and Shrinkage Priors. <i>Bayesian Analysis</i> , 2018, 13, 225-252.	3.0	39
21	Gaussian Process-Based Bayesian Nonparametric Inference of Population Size Trajectories from Gene Genealogies. <i>Biometrics</i> , 2013, 69, 8-18.	1.4	37
22	An efficient Bayesian inference framework for coalescent-based nonparametric phylodynamics. <i>Bioinformatics</i> , 2015, 31, 3282-3289.	4.1	34
23	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.	1.4	33
24	Estimation for General Birth-Death Processes. <i>Journal of the American Statistical Association</i> , 2014, 109, 730-747.	3.1	32
25	Measuring Microsatellite Conservation in Mammalian Evolution with a Phylogenetic Birth-Death Model. <i>Genome Biology and Evolution</i> , 2012, 4, 636-647.	2.5	30
26	Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts. <i>PLoS Computational Biology</i> , 2020, 16, e1007999.	3.2	30
27	Phylogenetic Mapping of Recombination Hotspots in Human Immunodeficiency Virus via Spatially Smoothed Change-Point Processes. <i>Genetics</i> , 2007, 175, 1773-1785.	2.9	29
28	Birth/birth-death processes and their computable transition probabilities with biological applications. <i>Journal of Mathematical Biology</i> , 2018, 76, 911-944.	1.9	28
29	Marginal Likelihoods in Phylogenetics: A Review of Methods and Applications. <i>Systematic Biology</i> , 2019, 68, 681-697.	5.6	26
30	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.	1.6	23
31	A Bayesian phylogenetic hidden Markov model for B cell receptor sequence analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1008030.	3.2	20
32	Fitting and interpreting continuous-time latent Markov models for panel data. <i>Statistics in Medicine</i> , 2013, 32, 4581-4595.	1.6	18
33	Predictive modeling of cholera outbreaks in Bangladesh. <i>Annals of Applied Statistics</i> , 2016, 10, 575-595.	1.1	17
34	cBrother: relaxing parental tree assumptions for Bayesian recombination detection. <i>Bioinformatics</i> , 2007, 23, 507-508.	4.1	16
35	Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories. <i>Biometrics</i> , 2020, 76, 677-690.	1.4	16
36	Estimating effective population size changes from preferentially sampled genetic sequences. <i>PLoS Computational Biology</i> , 2020, 16, e1007774.	3.2	14

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37	Efficient Data Augmentation for Fitting Stochastic Epidemic Models to Prevalence Data. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 918-929.	1.7	13
38	A linear noise approximation for stochastic epidemic models fit to partially observed incidence counts. <i>Biometrics</i> , 2022, 78, 1530-1541.	1.4	13
39	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.	4.3	12
40	Fitting birth–death processes to panel data with applications to bacterial DNA fingerprinting. <i>Annals of Applied Statistics</i> , 2013, 7, 2315-2335.	1.1	11
41	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.	1.4	11
42	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.	1.1	10
43	Phylogenetic Stochastic Mapping Without Matrix Exponentiation. <i>Journal of Computational Biology</i> , 2014, 21, 676-690.	1.6	9
44	Predicting B cell receptor substitution profiles using public repertoire data. <i>PLoS Computational Biology</i> , 2018, 14, e1006388.	3.2	8
45	Survival analysis of DNA mutation motifs with penalized proportional hazards. <i>Annals of Applied Statistics</i> , 2019, 13, 1268-1294.	1.1	8
46	Spatio-Temporal Analysis of Surveillance Data. , 2019, , 455-475.		8
47	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, .	1.1	6
48	Synonymous and nonsynonymous distances help untangle convergent evolution and recombination. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 375-89.	0.6	5
49	Optimal experimental design for mathematical models of haematopoiesis. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20200729.	3.4	5
50	A statistical approach to peptide identification from clustered tandem mass spectrometry data. , 2012, , 648-653.		4
51	Recombination-independent rapid convergent evolution of the gastric pathogen <i>Helicobacter pylori</i> . <i>BMC Genomics</i> , 2018, 19, 835.	2.8	3
52	Hot and Cold: Spatial Fluctuation in HIV-1 Recombination Rates. , 2007, , .		2
53	rbrothers: R Package for Bayesian Multiple Change-Point Recombination Detection. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11945.	1.2	2
54	Introduction to the Special Section on Inference for Infectious Disease Dynamics. <i>Statistical Science</i> , 2018, 33, .	2.8	2

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55	Rejoinder for discussion on "Horseshoe"-based Bayesian nonparametric estimation of effective population size trajectories. <i>Biometrics</i> , 2020, 76, 695-699.	1.4	2
56	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.	2.0	2
57	Imputation Estimators Partially Correct for Model Misspecification. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.6	1
58	Calculating Higher-Order Moments of Phylogenetic Stochastic Mapping Summaries in Linear Time. <i>Journal of Computational Biology</i> , 2017, 24, 377-399.	1.6	1
59	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
60	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.	1.4	0