Vladimir N Minin

List of Publications by Year
in descending order

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	A linear noise approximation for stochastic epidemic models fit to partially observed incidence counts. Biometrics, 2022, 78, 1530-1541.	1.4	13
2	Optimal experimental design for mathematical models of haematopoiesis. Journal of the Royal Society Interface, 2021, 18, 20200729.	3.4	5
3	Predictors of Test Positivity, Mortality, and Seropositivity during the Early Coronavirus Disease Epidemic, Orange County, California, USA. Emerging Infectious Diseases, 2021, 27, 2604-2618.	4.3	12
4	19 Dubious Ways to Compute the Marginal Likelihood of a Phylogenetic Tree Topology. Systematic Biology, 2020, 69, 209-220.	5.6	40
5	Rejoinder for discussion on â€œHorseshoeâ€based Bayesian nonparametric estimation of effective population size trajectoriesâ€. Biometrics, 2020, 76, 695-699.	1.4	2
6	A Bayesian phylogenetic hidden Markov model for B cell receptor sequence analysis. PLoS Computational Biology, 2020, 16, e1008030.	3.2	20
7	Horseshoeâ€based Bayesian nonparametric estimation of effective population size trajectories. Biometrics, 2020, 76, 677-690.	1.4	16
8	Estimating effective population size changes from preferentially sampled genetic sequences. PLoS Computational Biology, 2020, 16, e1007774.	3.2	14
9	Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts. PLoS Computational Biology, 2020, 16, e1007999.	3.2	30
10	Survival analysis of DNA mutation motifs with penalized proportional hazards. Annals of Applied Statistics, 2019, 13, 1268-1294.	1.1	8
11	Marginal Likelihoods in Phylogenetics: A Review of Methods and Applications. Systematic Biology, 2019, 68, 681-697.	5.6	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. Annals of Applied Statistics, 2019, 13, .	1.1	6
14	Using Genotype Abundance to Improve Phylogenetic Inference. Molecular Biology and Evolution, 2018, 35, 1253-1265.	8.9	55
15	Introduction to the Special Section on Inference for Infectious Disease Dynamics. Statistical Science, 2018, 33, .	2.8	2
16	Birth/birth-death processes and their computable transition probabilities with biological applications. Journal of Mathematical Biology, 2018, 76, 911-944.	1.9	28
17	Recombination-independent rapid convergent evolution of the gastric pathogen Helicobacter pylori. BMC Genomics, 2018, 19, 835.	2.8	3
18	Predicting B cell receptor substitution profiles using public repertoire data. PLoS Computational Biology, 2018, 14, e1006388.	3.2	8

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19	Locally Adaptive Smoothing with Markov Random Fields and Shrinkage Priors. Bayesian Analysis, 2018, 13, 225-252.	3.0	39
20	Calculating Higher-Order Moments of Phylogenetic Stochastic Mapping Summaries in Linear Time. Journal of Computational Biology, 2017, 24, 377-399.	1.6	1
21	Efficient Data Augmentation for Fitting Stochastic Epidemic Models to Prevalence Data. Journal of Computational and Graphical Statistics, 2017, 26, 918-929.	1.7	13
22	Myosin-independent cytokinesis in *Giardia* utilizes flagella to coordinate force generation and direct membrane trafficking. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5854-E5863.	7.1	56
23	<scp>phylodyn</scp>: an R package for phylodynamic simulation and inference. Molecular Ecology Resources, 2017, 17, 96-100.	4.8	53
24	Predictive modeling of cholera outbreaks in Bangladesh. Annals of Applied Statistics, 2016, 10, 575-595.	1.1	17
25	Detecting the Anomaly Zone in Species Trees and Evidence for a Misleading Signal in Higher-Level Skink Phylogeny (Squamata: Scincidae).. Systematic Biology, 2016, 65, 465-477.	5.6	85
26	Quantifying and Mitigating the Effect of Preferential Sampling on Phylodynamic Inference. PLoS Computational Biology, 2016, 12, e1004789.	3.2	45
27	Stochastic Modeling of Hematopoietic Stem and Progenitor Cell Barcoding Data from Rhesus Macaques Challenges the Classic Model of Hematopoiesis. Blood, 2016, 128, 2643-2643.	1.4	0
28	Likelihood-Based Inference for Discretely Observed Birthâ€"Death-Shift Processes, with Applications to Evolution of Mobile Genetic Elements. Biometrics, 2015, 71, 1009-1021.	1.4	11
29	An efficient Bayesian inference framework for coalescent-based nonparametric phylodynamics. Bioinformatics, 2015, 31, 3282-3289.	4.1	34
30	Synonymous and nonsynonymous distances help untangle convergent evolution and recombination. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 375-89.	0.6	5
31	Quantifying evolutionary constraints on B-cell affinity maturation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140244.	4.0	45
32	A Joint Model for Multistate Disease Processes and Random Informative Observation Times, with Applications to Electronic Medical Records Data. Biometrics, 2015, 71, 90-101.	1.4	33
33	Efficient Transition Probability Computation for Continuous-Time Branching Processes via Compressed Sensing. Uncertainty in artificial intelligence : proceedings of the ... conference., 2015, 2015, 952-961.	0.9	1
34	Predictable transcriptome evolution in the convergent and complex bioluminescent organs of squid. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4736-42.	7.1	77
35	Phylogenetic Stochastic Mapping Without Matrix Exponentiation. Journal of Computational Biology, 2014, 21, 676-690.	1.6	9
36	Estimation for General Birth-Death Processes. Journal of the American Statistical Association, 2014, 109, 730-747.	3.1	32

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37	Species Delimitation using Genome-Wide SNP Data. Systematic Biology, 2014, 63, 534-542.	5.6	390
38	Heritability estimation of osteoarthritis in the pig-tailed macaque (*Macaca nemestrina*) with a look toward future data collection. PeerJ, 2014, 2, e373.	2.0	2
39	Phylogeography of the Trans-Volcanic bunchgrass lizard (*Sceloporus bicanthalis*) across the highlands of south-eastern Mexico. Biological Journal of the Linnean Society, 2013, 110, 852-865.	1.6	23
40	rbrothers: R Package for Bayesian Multiple Change-Point Recombination Detection. Evolutionary Bioinformatics, 2013, 9, EBO.S11945.	1.2	2
41	Fitting and interpreting continuous-time latent Markov models for panel data. Statistics in Medicine, 2013, 32, 4581-4595.	1.6	18
42	Gaussian Process-Based Bayesian Nonparametric Inference of Population Size Trajectories from Gene Genealogies. Biometrics, 2013, 69, 8-18.	1.4	37
43	Fitting birth-death processes to panel data with applications to bacterial DNA fingerprinting. Annals of Applied Statistics, 2013, 7, 2315-2335.	1.1	11
44	A counting renaissance: combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection. Bioinformatics, 2012, 28, 3248-3256.	4.1	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. Genome Biology and Evolution, 2012, 4, 636-647.	2.5	30
47	Recombination Between Variants from Genital Tract and Plasma: Evolution of Multidrug-Resistant HIV Type 1. AIDS Research and Human Retroviruses, 2012, 28, 1766-1774.	1.1	10
48	Imputation Estimators Partially Correct for Model Misspecification. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	1
49	Learning to Count: Robust Estimates for Labeled Distances between Molecular Sequences. Molecular Biology and Evolution, 2009, 26, 801-814.	8.9	102
50	High frequency of hotspot mutations in core genes of Escherichia coli due to short-term positive selection. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12412-12417.	7.1	95
51	Smooth Skyride through a Rough Skyline: Bayesian Coalescent-Based Inference of Population Dynamics. Molecular Biology and Evolution, 2008, 25, 1459-1471.	8.9	626
52	Fast, accurate and simulation-free stochastic mapping. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 3985-3995.	4.0	149
53	cBrother: relaxing parental tree assumptions for Bayesian recombination detection. Bioinformatics, 2007, 23, 507-508.	4.1	16
54	Phylogenetic Mapping of Recombination Hotspots in Human Immunodeficiency Virus via Spatially Smoothed Change-Point Processes. Genetics, 2007, 175, 1773-1785.	2.9	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.	1.9	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.	8.9	68
58	Dual multiple change-point model leads to more accurate recombination detection. Bioinformatics, 2005, 21, 3034-3042.	4.1	136
59	Statistical Methods for Analyzing Tissue Microarray Data. Journal of Biopharmaceutical Statistics, 2004, 14, 671-685.	0.8	57
60	Performance-Based Selection of Likelihood Models for Phylogeny Estimation. Systematic Biology, 2003, 52, 674-683.	5.6	386