

Tanja Stadler

List of Publications by Year in descending order

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Version: 2024-02-01

146
papers

17,808
citations

41627

51
h-index

22488

117
g-index

200
all docs

200
docs citations

200
times ranked

22613
citing authors

#	ARTICLE	IF	CITATIONS
1	CoV-Spectrum: analysis of globally shared SARS-CoV-2 data to identify and characterize new variants. <i>Bioinformatics</i> , 2022, 38, 1735-1737.	1.8	191
2	Joint Inference of Migration and Reassortment Patterns for Viruses with Segmented Genomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
3	DeepSARS: simultaneous diagnostic detection and genomic surveillance of SARS-CoV-2. <i>BMC Genomics</i> , 2022, 23, 289.	1.2	5
4	SARS-CoV-2 Vaccine Alpha and Delta Variant Breakthrough Infections Are Rare and Mild but Can Happen Relatively Early after Vaccination. <i>Microorganisms</i> , 2022, 10, 857.	1.6	8
5	Advancing genomic epidemiology by addressing the bioinformatics bottleneck: Challenges, design principles, and a Swiss example. <i>Epidemics</i> , 2022, , 100576.	1.5	3
6	Wastewater-Based Estimation of the Effective Reproductive Number of SARS-CoV-2. <i>Environmental Health Perspectives</i> , 2022, 130, .	2.8	92
7	The Occurrence Birth-Death Process for Combined-Evidence Analysis in Macroevolution and Epidemiology. <i>Systematic Biology</i> , 2022, 71, 1440-1452.	2.7	10
8	Early detection and surveillance of SARS-CoV-2 genomic variants in wastewater using COJAC. <i>Nature Microbiology</i> , 2022, 7, 1151-1160.	5.9	69
9	Plasmid- and strain-specific factors drive variation in ESBL-plasmid spread in vitro and in vivo. <i>ISME Journal</i> , 2021, 15, 862-878.	4.4	66
10	The probability distribution of the ancestral population size conditioned on the reconstructed phylogenetic tree with occurrence data. <i>Journal of Theoretical Biology</i> , 2021, 509, 110400.	0.8	12
11	Phylodynamics for cell biologists. <i>Science</i> , 2021, 371, .	6.0	51
12	The origin and early spread of SARS-CoV-2 in Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	83
13	Detection and Genome Sequencing of SARS-CoV-2 in a Domestic Cat with Respiratory Signs in Switzerland. <i>Viruses</i> , 2021, 13, 496.	1.5	53
14	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , 2021, 6, 121.	0.9	115
15	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712.	13.7	363
16	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales. <i>Systematic Biology</i> , 2021, 71, 208-220.	2.7	9
17	Quantifying transmission fitness costs of multi-drug resistant tuberculosis. <i>Epidemics</i> , 2021, 36, 100471.	1.5	13
18	What can phylodynamics bring to animal health research?. <i>Trends in Ecology and Evolution</i> , 2021, 36, 837-847.	4.2	9

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19	Quantification of the spread of SARS-CoV-2 variant B.1.1.7 in Switzerland. <i>Epidemics</i> , 2021, 37, 100480.	1.5	34
20	The probability distribution of the reconstructed phylogenetic tree with occurrence data. <i>Journal of Theoretical Biology</i> , 2020, 488, 110115.	0.8	13
21	Fast likelihood calculation for multivariate Gaussian phylogenetic models with shifts. <i>Theoretical Population Biology</i> , 2020, 131, 66-78.	0.5	31
22	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	3.5	81
23	Identification of a Cluster of Extended-spectrum Beta-Lactamase-Producing <i>Klebsiella pneumoniae</i> Sequence Type 101 Isolated From Food and Humans. <i>Clinical Infectious Diseases</i> , 2020, 73, 332-335.	2.9	3
24	A transmissible cancer shifts from emergence to endemism in Tasmanian devils. <i>Science</i> , 2020, 370, .	6.0	24
25	Inter- and intraspecies comparison of phylogenetic fingerprints and sequence diversity of immunoglobulin variable genes. <i>Immunogenetics</i> , 2020, 72, 279-294.	1.2	5
26	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
27	PIQMEE: Bayesian Phylodynamic Method for Analysis of Large Data Sets with Duplicate Sequences. <i>Molecular Biology and Evolution</i> , 2020, 37, 3061-3075.	3.5	12
28	IgM Antibody Repertoire Fingerprints in Mice Are Personalized but Robust to Viral Infection Status. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 254.	1.8	5
29	Ignoring Fossil Age Uncertainty Leads to Inaccurate Topology and Divergence Time Estimates in Time Calibrated Tree Inference. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	35
30	Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17104-17111.	3.3	35
31	A Multitype Birth-Death Model for Bayesian Inference of Lineage-Specific Birth and Death Rates. <i>Systematic Biology</i> , 2020, 69, 973-986.	2.7	44
32	Quantitative and Qualitative Analysis of Humoral Immunity Reveals Continued and Personalized Evolution in Chronic Viral Infection. <i>Cell Reports</i> , 2020, 30, 997-1012.e6.	2.9	34
33	Assessing the impact of incomplete species sampling on estimates of speciation and extinction rates. <i>Paleobiology</i> , 2020, 46, 137-157.	1.3	30
34	Practical considerations for measuring the effective reproductive number, Rt. <i>PLoS Computational Biology</i> , 2020, 16, e1008409.	1.5	343
35	Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. <i>PLoS Pathogens</i> , 2020, 16, e1008984.	2.1	17
36	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	186

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37	Reproductive number of the COVID-19 epidemic in Switzerland with a focus on the Cantons of Basel-Stadt and Basel-Landschaft. <i>Swiss Medical Weekly</i> , 2020, 150, w20271.	0.8	64
38	Phylogenetic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , 2019, 68, 358-364.	2.7	25
39	Automatic generation of evolutionary hypotheses using mixed Gaussian phylogenetic models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16921-16926.	3.3	31
40	Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations. <i>Virus Evolution</i> , 2019, 5, vez030.	2.2	20
41	Swapping Birth and Death: Symmetries and Transformations in Phylogenetic Models. <i>Systematic Biology</i> , 2019, 68, 852-858.	2.7	10
42	Evaluation of two workflows for whole genome sequencing-based typing of influenza A viruses. <i>Journal of Virological Methods</i> , 2019, 266, 30-33.	1.0	9
43	Ignoring stratigraphic age uncertainty leads to erroneous estimates of species divergence times under the fossilized birth-death process. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190685.	1.2	50
44	Species-specific diversification. <i>Nature Ecology and Evolution</i> , 2019, 3, 1003-1004.	3.4	2
45	Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816.	3.5	39
46	Earlier Initiation of Antiretroviral Treatment Coincides With an Initial Control of the HIV-1 Sub-Subtype F1 Outbreak Among Men-Having-Sex-With-Men in Flanders, Belgium. <i>Frontiers in Microbiology</i> , 2019, 10, 613.	1.5	21
47	Asymmetric division events promote variability in cell cycle duration in animal cells and <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 1901.	5.8	6
48	Exploring the power of Bayesian birth-death skyline models to detect mass extinction events from phylogenies with only extant taxa. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1133-1150.	1.1	12
49	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	1.5	2,484
50	Parallel likelihood calculation for phylogenetic comparative models: The <code>SPLITT</code> C++ library. <i>Methods in Ecology and Evolution</i> , 2019, 10, 493-506.	2.2	7
51	Identification of influenza urban transmission patterns by geographical, epidemiological and whole genome sequencing data: protocol for an observational study. <i>BMJ Open</i> , 2019, 9, e030913.	0.8	7
52	Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. <i>ELife</i> , 2019, 8, .	2.8	18
53	Transmission of ESBL-producing Enterobacteriaceae and their mobile genetic elements—identification of sources by whole genome sequencing: study protocol for an observational study in Switzerland. <i>BMJ Open</i> , 2018, 8, e021823.	0.8	32
54	Impact of the tree prior on estimating clock rates during epidemic outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4200-4205.	3.3	35

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55	Bayesian Inference of Species Networks from Multilocus Sequence Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 504-517.	3.5	158
56	The fossilized birth-death model for the analysis of stratigraphic range data under different speciation modes. <i>Journal of Theoretical Biology</i> , 2018, 447, 41-55.	0.8	83
57	Taming the BEAST – A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	2.7	79
58	<i>TreeSim</i> : Simulating phylogenetic trees under general Bellman-Harris models with lineage-specific shifts of speciation and extinction in R. <i>Methods in Ecology and Evolution</i> , 2018, 9, 754-760.	2.2	19
59	On the statistical analysis of single cell lineage trees. <i>Journal of Theoretical Biology</i> , 2018, 439, 160-165.	0.8	15
60	Tracking external introductions of HIV using phylodynamics reveals a major source of infections in rural KwaZulu-Natal, South Africa. <i>Virus Evolution</i> , 2018, 4, vey037.	2.2	22
61	The influence of phylodynamic model specifications on parameter estimates of the Zika virus epidemic. <i>Virus Evolution</i> , 2018, 4, vex044.	2.2	31
62	Closing the gap between palaeontological and neontological speciation and extinction rate estimates. <i>Nature Communications</i> , 2018, 9, 5237.	5.8	72
63	Detection of HIV transmission clusters from phylogenetic trees using a multi-state birth-death model. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180512.	1.5	22
64	Tracing Antibody Repertoire Evolution by Systems Phylogeny. <i>Frontiers in Immunology</i> , 2018, 9, 2149.	2.2	26
65	The relationship between transmission time and clustering methods in <i>Mycobacterium tuberculosis</i> epidemiology. <i>EBioMedicine</i> , 2018, 37, 410-416.	2.7	106
66	MASCOT: parameter and state inference under the marginal structured coalescent approximation. <i>Bioinformatics</i> , 2018, 34, 3843-3848.	1.8	78
67	A Practical Guide to Estimating the Heritability of Pathogen Traits. <i>Molecular Biology and Evolution</i> , 2018, 35, 756-772.	3.5	18
68	Tuberculosis outbreak investigation using phylodynamic analysis. <i>Epidemics</i> , 2018, 25, 47-53.	1.5	19
69	Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. <i>PLoS Pathogens</i> , 2018, 14, e1006895.	2.1	53
70	Bayesian Total-Evidence Dating Reveals the Recent Crown Radiation of Penguins. <i>Systematic Biology</i> , 2017, 66, syw060.	2.7	255
71	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	3.5	53
72	Mathematical Models for the Epidemiology and Evolution of <i>Mycobacterium tuberculosis</i> . <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 281-307.	0.8	1

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73	The Structured Coalescent and Its Approximations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2970-2981.	3.5	98
74	Comparison of methods for phylogenetic B-cell lineage inference using time-resolved antibody repertoire simulations (AbSim). <i>Bioinformatics</i> , 2017, 33, 3938-3946.	1.8	50
75	Vaccination of dogs in an African city interrupts rabies transmission and reduces human exposure. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	87
76	Phylodynamics on local sexual contact networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005448.	1.5	16
77	Assessment of Overlap of Phylogenetic Transmission Clusters and Communities in Simple Sexual Contact Networks: Applications to HIV-1. <i>PLoS ONE</i> , 2016, 11, e0148459.	1.1	28
78	Phylodynamics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 2102-2116.	3.5	131
79	Outbreak investigation for toxigenic <i>Corynebacterium diphtheriae</i> wound infections in refugees from Northeast Africa and Syria in Switzerland and Germany by whole genome sequencing. <i>Clinical Microbiology and Infection</i> , 2016, 22, 1003.e1-1003.e8.	2.8	70
80	Estimating shifts in diversification rates based on higher-level phylogenies. <i>Biology Letters</i> , 2016, 12, 20160273.	1.0	6
81	Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. <i>Infection, Genetics and Evolution</i> , 2016, 46, 200-208.	1.0	23
82	Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?. <i>Systematic Biology</i> , 2016, 65, 628-639.	2.7	18
83	Bayesian phylogenetic estimation of fossil ages. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150129.	1.8	34
84	Quantifying Age-dependent Extinction from Species Phylogenies. <i>Systematic Biology</i> , 2016, 65, 35-50.	2.7	31
85	Total-Evidence Dating under the Fossilized Birth–Death Process. <i>Systematic Biology</i> , 2016, 65, 228-249.	2.7	304
86	How well can the exponential-growth coalescent approximate constant-rate birth–death population dynamics?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150420.	1.2	29
87	Mathematical and Computational Evolutionary Biology (2013). <i>Systematic Biology</i> , 2015, 64, 1-2.	2.7	52
88	Getting to the root of epidemic spread with phylodynamic analysis of genomic data. <i>Trends in Microbiology</i> , 2015, 23, 383-386.	3.5	36
89	Age-Dependent Speciation Can Explain the Shape of Empirical Phylogenies. <i>Systematic Biology</i> , 2015, 64, 432-440.	2.7	63
90	Inferring Epidemiological Dynamics with Bayesian Coalescent Inference: The Merits of Deterministic and Stochastic Models. <i>Genetics</i> , 2015, 199, 595-607.	1.2	30

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91	Phylogenetics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	1.5	51
92	Finding the best resolution for the Kingman's Tajima coalescent: theory and applications. <i>Journal of Mathematical Biology</i> , 2015, 70, 1207-1247.	0.8	16
93	The contrasting phylogenetics of human influenza B viruses. <i>ELife</i> , 2015, 4, e05055.	2.8	166
94	The fossilized birth-death process for coherent calibration of divergence-time estimates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2957-66.	3.3	612
95	Inference of Epidemiological Dynamics Based on Simulated Phylogenies Using Birth-Death and Coalescent Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003913.	1.5	58
96	Bayesian Inference of Sampled Ancestor Trees for Epidemiology and Fossil Calibration. <i>PLoS Computational Biology</i> , 2014, 10, e1003919.	1.5	276
97	Using an Epidemiological Model for Phylogenetic Inference Reveals Density Dependence in HIV Transmission. <i>Molecular Biology and Evolution</i> , 2014, 31, 6-17.	3.5	55
98	On Age and Species Richness of Higher Taxa. <i>American Naturalist</i> , 2014, 184, 447-455.	1.0	44
99	Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth-death SIR model. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20131106.	1.5	104
100	Phylogenetic analysis accounting for age-dependent death and sampling with applications to epidemics. <i>Journal of Theoretical Biology</i> , 2014, 352, 60-70.	0.8	8
101	Social Meets Molecular: Combining Phylogenetic and Latent Class Analyses to Understand HIV-1 Transmission in Switzerland. <i>American Journal of Epidemiology</i> , 2014, 179, 1514-1525.	1.6	25
102	FOSSILS AND A LARGE MOLECULAR PHYLOGENY SHOW THAT THE EVOLUTION OF SPECIES RICHNESS, GENERIC DIVERSITY, AND TURNOVER RATES ARE DISCONNECTED. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2821-2832.	1.1	70
103	Exact vs. Approximate Computation: Reconciling Different Estimates of <i>Mycobacterium tuberculosis</i> Epidemiological Parameters. <i>Genetics</i> , 2014, 196, 1227-1230.	1.2	17
104	Epiphytic leafy liverworts diversified in angiosperm-dominated forests. <i>Scientific Reports</i> , 2014, 4, 5974.	1.6	104
105	Insights into the Early Epidemic Spread of Ebola in Sierra Leone Provided by Viral Sequence Data. <i>PLOS Currents</i> , 2014, 6, .	1.4	71
106	Dating Phylogenies with Sequentially Sampled Tips. <i>Systematic Biology</i> , 2013, 62, 674-688.	2.7	79
107	Birth-death models and coalescent point processes: The shape and probability of reconstructed phylogenies. <i>Theoretical Population Biology</i> , 2013, 90, 113-128.	0.5	107
108	Estimating Speciation and Extinction Rates for Phylogenies of Higher Taxa. <i>Systematic Biology</i> , 2013, 62, 220-230.	2.7	40

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109	How Can We Improve Accuracy of Macroevolutionary Rate Estimates?. <i>Systematic Biology</i> , 2013, 62, 321-329.	2.7	99
110	The abrupt climate change at the Eocene–Oligocene boundary and the emergence of South-East Asia triggered the spread of sapindaceous lineages. <i>Annals of Botany</i> , 2013, 112, 151-160.	1.4	46
111	Uncovering epidemiological dynamics in heterogeneous host populations using phylogenetic methods. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120198.	1.8	117
112	Birth–death skyline plot reveals temporal changes of epidemic spread in HIV and hepatitis C virus (HCV). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 228-233.	3.3	454
113	On the Need for Mechanistic Models in Computational Genomics and Metagenomics. <i>Genome Biology and Evolution</i> , 2013, 5, 2008-2018.	1.1	40
114	Recovering speciation and extinction dynamics based on phylogenies. <i>Journal of Evolutionary Biology</i> , 2013, 26, 1203-1219.	0.8	116
115	Estimating the Basic Reproductive Number from Viral Sequence Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 347-357.	3.5	206
116	Branch Lengths on Birth–Death Trees and the Expected Loss of Phylogenetic Diversity. <i>Systematic Biology</i> , 2012, 61, 195-203.	2.7	67
117	Inferring Epidemic Contact Structure from Phylogenetic Trees. <i>PLoS Computational Biology</i> , 2012, 8, e1002413.	1.5	85
118	Response to Comment on “Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification”. <i>Science</i> , 2012, 337, 34-34.	6.0	2
119	Diversity-dependence brings molecular phylogenies closer to agreement with the fossil record. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1300-1309.	1.2	281
120	A Characterization of the Set of Species Trees that Produce Anomalous Ranked Gene Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1558-1568.	1.9	15
121	A New Method for Handling Missing Species in Diversification Analysis Applicable to Randomly or Nonrandomly Sampled Phylogenies. <i>Systematic Biology</i> , 2012, 61, 785-792.	2.7	62
122	The probability distribution of ranked gene trees on a species tree. <i>Mathematical Biosciences</i> , 2012, 235, 45-55.	0.9	44
123	A polynomial time algorithm for calculating the probability of a ranked gene tree given a species tree. <i>Algorithms for Molecular Biology</i> , 2012, 7, 7.	0.3	11
124	Macroevolutionary Dynamics and Historical Biogeography of Primate Diversification Inferred from a Species Supermatrix. <i>PLoS ONE</i> , 2012, 7, e49521.	1.1	447
125	UNEXPECTEDLY MANY EXTINCT HOMININS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2969-2974.	1.1	16
126	Distribution of branch lengths and phylogenetic diversity under homogeneous speciation models. <i>Journal of Theoretical Biology</i> , 2012, 297, 33-40.	0.8	52

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127	Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification. <i>Science</i> , 2011, 334, 521-524.	6.0	1,264
128	Inferring Epidemiological Parameters on the Basis of Allele Frequencies. <i>Genetics</i> , 2011, 188, 663-672.	1.2	24
129	Origins of Biodiversityâ€”Response. <i>Science</i> , 2011, 331, 399-400.	6.0	23
130	Inferring speciation and extinction processes from extant species data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16145-16146.	3.3	54
131	Inferring Speciation and Extinction Rates under Different Sampling Schemes. <i>Molecular Biology and Evolution</i> , 2011, 28, 2577-2589.	3.5	144
132	Mammalian phylogeny reveals recent diversification rate shifts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6187-6192.	3.3	387
133	Simulating Trees with a Fixed Number of Extant Species. <i>Systematic Biology</i> , 2011, 60, 676-684.	2.7	241
134	Amazonia Through Time: Andean Uplift, Climate Change, Landscape Evolution, and Biodiversity. <i>Science</i> , 2010, 330, 927-931.	6.0	1,826
135	Analyzing and reconstructing reticulation networks under timing constraints. <i>Journal of Mathematical Biology</i> , 2010, 61, 715-737.	0.8	10
136	Sampling-through-time in birthâ€”death trees. <i>Journal of Theoretical Biology</i> , 2010, 267, 396-404.	0.8	379
137	Testing the spatial and temporal framework of speciation in an ancient lake species flock: the leech genus <i>Dina</i> (Hirudinea: Erpobdellidae) in Lake Ohrid. <i>Biogeosciences</i> , 2010, 7, 3387-3402.	1.3	40
138	Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. <i>PLoS Pathogens</i> , 2010, 6, e1001123.	2.1	108
139	Sampling Trees from Evolutionary Models. <i>Systematic Biology</i> , 2010, 59, 465-476.	2.7	75
140	A Method for Investigating Relative Timing Information on Phylogenetic Trees. <i>Systematic Biology</i> , 2009, 58, 167-183.	2.7	30
141	On incomplete sampling under birthâ€”death models and connections to the sampling-based coalescent. <i>Journal of Theoretical Biology</i> , 2009, 261, 58-66.	0.8	330
142	Stochastic properties of generalised Yule models, with biodiversity applications. <i>Journal of Mathematical Biology</i> , 2008, 57, 713-735.	0.8	47
143	New Analytic Results for Speciation Times in Neutral Models. <i>Bulletin of Mathematical Biology</i> , 2008, 70, 1082-1097.	0.9	60
144	The conditioned reconstructed process. <i>Journal of Theoretical Biology</i> , 2008, 253, 769-778.	0.8	845

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145	Lineages-through-time plots of neutral models for speciation. <i>Mathematical Biosciences</i> , 2008, 216, 163-171.	0.9	35
146	Estimating the Relative Order of Speciation or Coalescence Events on a Given Phylogeny. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	3