

Alexei J. Drummond

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

79,573
citations

21215

62
h-index

37326

100
g-index

113
all docs

113
docs citations

113
times ranked

63658
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary history of cotranscriptional editing in the paramyxoviral phosphoprotein gene. <i>Virus Evolution</i> , 2021, 7, veab028.	2.2	18
2	Genomic Evidence of In-Flight Transmission of SARS-CoV-2 Despite Predeparture Testing. <i>Emerging Infectious Diseases</i> , 2021, 27, 687-693.	2.0	58
3	Use of Genomics to Track Coronavirus Disease Outbreaks, New Zealand. <i>Emerging Infectious Diseases</i> , 2021, 27, 1317-1322.	2.0	28
4	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. <i>Nature Communications</i> , 2020, 11, 6351.	5.8	100
5	Bayesian inference and comparison of stochastic transcription elongation models. <i>PLoS Computational Biology</i> , 2020, 16, e1006717.	1.5	8
6	Phylogenetic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , 2019, 68, 358-364.	2.7	25
7	Bayesian phylodynamics of avian influenza A virus H9N2 in Asia with time-dependent predictors of migration. <i>PLoS Computational Biology</i> , 2019, 15, e1007189.	1.5	22
8	Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816.	3.5	39
9	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. <i>Virus Evolution</i> , 2019, 5, vez003.	2.2	26
10	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	1.5	2,484
11	Estimating the biodiversity of terrestrial invertebrates on a forested island using DNA barcodes and metabarcoding data. <i>Ecological Applications</i> , 2019, 29, e01877.	1.8	37
12	Impacts of DNA extraction and PCR on DNA metabarcoding estimates of soil biodiversity. <i>Methods in Ecology and Evolution</i> , 2019, 10, 120-133.	2.2	62
13	Bayesian Inference of Species Networks from Multilocus Sequence Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 504-517.	3.5	158
14	Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. <i>Systematic Biology</i> , 2018, 67, 901-904.	2.7	6,726
15	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
16	Taming the BEAST – A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	2.7	79
17	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018, 4, vey016.	2.2	2,401
18	Bayesian Total-Evidence Dating Reveals the Recent Crown Radiation of Penguins. <i>Systematic Biology</i> , 2017, 66, syw060.	2.7	255

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19	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2101-2114.	3.5	371
20	Inferring Ancestral Recombination Graphs from Bacterial Genomic Data. <i>Genetics</i> , 2017, 205, 857-870.	1.2	45
21	bModelTest: Bayesian phylogenetic site model averaging and model comparison. <i>BMC Evolutionary Biology</i> , 2017, 17, 42.	3.2	609
22	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
23	The space of ultrametric phylogenetic trees. <i>Journal of Theoretical Biology</i> , 2016, 403, 197-208.	0.8	32
24	Bayesian phylogenetic estimation of fossil ages. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150129.	1.8	34
25	Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. <i>Systematic Biology</i> , 2016, 65, 381-396.	2.7	107
26	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
27	Calibrated Birth–Death Phylogenetic Time-Tree Priors for Bayesian Inference. <i>Systematic Biology</i> , 2015, 64, 369-383.	2.7	48
28	Inferring Epidemiological Dynamics with Bayesian Coalescent Inference: The Merits of Deterministic and Stochastic Models. <i>Genetics</i> , 2015, 199, 595-607.	1.2	30
29	Evaluating a multigene environmental DNA approach for biodiversity assessment. <i>GigaScience</i> , 2015, 4, 46.	3.3	122
30	Efficient Bayesian inference under the structured coalescent. <i>Bioinformatics</i> , 2014, 30, 2272-2279.	1.8	118
31	The Genealogical Population Dynamics of HIV-1 in a Large Transmission Chain: Bridging within and among Host Evolutionary Rates. <i>PLoS Computational Biology</i> , 2014, 10, e1003505.	1.5	79
32	BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003537.	1.5	5,301
33	Bayesian Inference of Sampled Ancestor Trees for Epidemiology and Fossil Calibration. <i>PLoS Computational Biology</i> , 2014, 10, e1003919.	1.5	276
34	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
35	Report of the 14th Genomic Standards Consortium Meeting, Oxford, UK, September 17-21, 2012.. <i>Standards in Genomic Sciences</i> , 2014, 9, 1236-1250.	1.5	1
36	Simulating gene trees under the multispecies coalescent and time-dependent migration. <i>BMC Evolutionary Biology</i> , 2013, 13, 44.	3.2	55

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37	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	2.1	83
38	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
39	A Stochastic Simulator of Birth-Death Master Equations with Application to Phylodynamics. <i>Molecular Biology and Evolution</i> , 2013, 30, 1480-1493.	3.5	73
40	Bayesian Selection of Nucleotide Substitution Models and Their Site Assignments. <i>Molecular Biology and Evolution</i> , 2013, 30, 669-688.	3.5	37
41	Recursive algorithms for phylogenetic tree counting. <i>Algorithms for Molecular Biology</i> , 2013, 8, 26.	0.3	10
42	Estimating the Basic Reproductive Number from Viral Sequence Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 347-357.	3.5	206
43	Guided Tree Topology Proposals for Bayesian Phylogenetic Inference. <i>Systematic Biology</i> , 2012, 61, 1-11.	2.7	190
44	Accurate Model Selection of Relaxed Molecular Clocks in Bayesian Phylogenetics. <i>Molecular Biology and Evolution</i> , 2012, 30, 239-243.	3.5	538
45	Model Averaging and Bayes Factor Calculation of Relaxed Molecular Clocks in Bayesian Phylogenetics. <i>Molecular Biology and Evolution</i> , 2012, 29, 751-761.	3.5	129
46	Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. <i>Bioinformatics</i> , 2012, 28, 1647-1649.	1.8	16,096
47	Bayesian Phylogenetics with BEAUti and the BEAST 1.7. <i>Molecular Biology and Evolution</i> , 2012, 29, 1969-1973.	3.5	9,040
48	Calibrated Tree Priors for Relaxed Phylogenetics and Divergence Time Estimation. <i>Systematic Biology</i> , 2012, 61, 138-149.	2.7	275
49	Mapping the Origins and Expansion of the Indo-European Language Family. <i>Science</i> , 2012, 337, 957-960.	6.0	549
50	Within-host demographic fluctuations and correlations in early retroviral infection. <i>Journal of Theoretical Biology</i> , 2012, 295, 86-99.	0.8	6
51	A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. <i>Molecular Biology and Evolution</i> , 2011, 28, 879-887.	3.5	119
52	Phylogenetic and epidemic modeling of rapidly evolving infectious diseases. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1825-1841.	1.0	70
53	Joint Inference of Microsatellite Mutation Models, Population History and Genealogies Using Transdimensional Markov Chain Monte Carlo. <i>Genetics</i> , 2011, 188, 151-164.	1.2	51
54	A retrodictive stochastic simulation algorithm. <i>Journal of Computational Physics</i> , 2010, 229, 3777-3791.	1.9	0

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55	Bayesian random local clocks, or one rate to rule them all. <i>BMC Biology</i> , 2010, 8, 114.	1.7	367
56	How Accurate and Robust Are the Phylogenetic Estimates of Austronesian Language Relationships?. <i>PLoS ONE</i> , 2010, 5, e9573.	1.1	37
57	Bayesian Inference of Species Trees from Multilocus Data. <i>Molecular Biology and Evolution</i> , 2010, 27, 570-580.	3.5	2,246
58	Extinction Times in Autocatalytic Systems. <i>Journal of Physical Chemistry A</i> , 2010, 114, 10481-10491.	1.1	21
59	Epidemic Dynamics Revealed in Dengue Evolution. <i>Molecular Biology and Evolution</i> , 2010, 27, 811-818.	3.5	92
60	Accommodating the Effect of Ancient DNA Damage on Inferences of Demographic Histories. <i>Molecular Biology and Evolution</i> , 2009, 26, 245-248.	3.5	86
61	The evolutionary history of the extinct ratite moa and New Zealand Neogene paleogeography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20646-20651.	3.3	150
62	Bayesian Phylogeography Finds Its Roots. <i>PLoS Computational Biology</i> , 2009, 5, e1000520.	1.5	1,519
63	Bayesian coalescent inference of major human mitochondrial DNA haplogroup expansions in Africa. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 367-373.	1.2	83
64	Language Phylogenies Reveal Expansion Pulses and Pauses in Pacific Settlement. <i>Science</i> , 2009, 323, 479-483.	6.0	675
65	Fully Bayesian tests of neutrality using genealogical summary statistics. <i>BMC Genetics</i> , 2008, 9, 68.	2.7	27
66	Bayesian inference of population size history from multiple loci. <i>BMC Evolutionary Biology</i> , 2008, 8, 289.	3.2	658
67	mtDNA Variation Predicts Population Size in Humans and Reveals a Major Southern Asian Chapter in Human Prehistory. <i>Molecular Biology and Evolution</i> , 2008, 25, 468-474.	3.5	221
68	Evidence of the Recombinant Origin of a Bat Severe Acute Respiratory Syndrome (SARS)-Like Coronavirus and Its Implications on the Direct Ancestor of SARS Coronavirus. <i>Journal of Virology</i> , 2008, 82, 1819-1826.	1.5	197
69	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. <i>PLoS Computational Biology</i> , 2007, 3, e29.	1.5	152
70	Phylogenetic Evidence for Deleterious Mutation Load in RNA Viruses and Its Contribution to Viral Evolution. <i>Molecular Biology and Evolution</i> , 2007, 24, 845-852.	3.5	133
71	Evidence for Time Dependency of Molecular Rate Estimates. <i>Systematic Biology</i> , 2007, 56, 515-522.	2.7	257
72	The Evolutionary Genetics of Viral Emergence. <i>Current Topics in Microbiology and Immunology</i> , 2007, 315, 51-66.	0.7	58

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73	BEAST: Bayesian evolutionary analysis by sampling trees. <i>BMC Evolutionary Biology</i> , 2007, 7, 214.	3.2	11,072
74	Divergence time estimates for major cephalopod groups: evidence from multiple genes. <i>Cladistics</i> , 2006, 22, 89-96.	1.5	82
75	Population genetic estimation of the loss of genetic diversity during horizontal transmission of HIV-1. <i>BMC Evolutionary Biology</i> , 2006, 6, 28.	3.2	67
76	Evolution of the Human Immunodeficiency Virus Envelope Gene Is Dominated by Purifying Selection. <i>Genetics</i> , 2006, 174, 1441-1453.	1.2	64
77	A Virus Reveals Population Structure and Recent Demographic History of Its Carnivore Host. <i>Science</i> , 2006, 311, 538-541.	6.0	138
78	Phylogenetic Analysis Reveals a Correlation between the Expansion of Very Virulent Infectious Bursal Disease Virus and Reassortment of Its Genome Segment B. <i>Journal of Virology</i> , 2006, 80, 8503-8509.	1.5	100
79	Choosing Appropriate Substitution Models for the Phylogenetic Analysis of Protein-Coding Sequences. <i>Molecular Biology and Evolution</i> , 2006, 23, 7-9.	3.5	695
80	Relaxed Phylogenetics and Dating with Confidence. <i>PLoS Biology</i> , 2006, 4, e88.	2.6	5,566
81	Molecular phylogeny of coleoid cephalopods (Mollusca: Cephalopoda) using a multigene approach; the effect of data partitioning on resolving phylogenies in a Bayesian framework. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 426-441.	1.2	125
82	Bayesian coestimation of phylogeny and sequence alignment. <i>BMC Bioinformatics</i> , 2005, 6, 83.	1.2	169
83	Tree measures and the number of segregating sites in time-structured population samples. <i>BMC Genetics</i> , 2005, 6, 35.	2.7	4
84	Accuracy of Rate Estimation Using Relaxed-Clock Models with a Critical Focus on the Early Metazoan Radiation. <i>Molecular Biology and Evolution</i> , 2005, 22, 1355-1363.	3.5	169
85	Bayesian Coalescent Inference of Past Population Dynamics from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2005, 22, 1185-1192.	3.5	2,782
86	Post-mortem DNA damage hotspots in Bison (<i>Bison bison</i>) provide evidence for both damage and mutational hotspots in human mitochondrial DNA. <i>Journal of Archaeological Science</i> , 2005, 32, 1053-1060.	1.2	25
87	Time Dependency of Molecular Rate Estimates and Systematic Overestimation of Recent Divergence Times. <i>Molecular Biology and Evolution</i> , 2005, 22, 1561-1568.	3.5	933
88	Statistical Alignment: Recent Progress, New Applications, and Challenges. , 2005, , 375-405.		20
89	The Molecular Population Genetics of HIV-1 Group O. <i>Genetics</i> , 2004, 167, 1059-1068.	1.2	105
90	Neotenus origins for pelagic octopuses. <i>Current Biology</i> , 2004, 14, R300-R301.	1.8	34

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91	Ancient DNA: Would the Real Neandertal Please Stand up?. <i>Current Biology</i> , 2004, 14, R431-R433.	1.8	19
92	Rise and Fall of the Beringian Steppe Bison. <i>Science</i> , 2004, 306, 1561-1565.	6.0	601
93	Genealogies from Time-Stamped Sequence Data. <i>Lecture Notes in Statistics</i> , 2004, , 149-171.	0.1	6
94	Extreme reversed sexual size dimorphism in the extinct New Zealand moa <i>Dinornis</i> . <i>Nature</i> , 2003, 425, 172-175.	13.7	151
95	Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , 2003, 18, 481-488.	4.2	371
96	Inference of Viral Evolutionary Rates from Molecular Sequences. <i>Advances in Parasitology</i> , 2003, 54, 331-358.	1.4	161
97	Epidemiology, Genetic Diversity, and Evolution of Endemic Feline Immunodeficiency Virus in a Population of Wild Cougars. <i>Journal of Virology</i> , 2003, 77, 9578-9589.	1.5	74
98	The Epidemiology and Iatrogenic Transmission of Hepatitis C Virus in Egypt: A Bayesian Coalescent Approach. <i>Molecular Biology and Evolution</i> , 2003, 20, 381-387.	3.5	225
99	Inferring Evolutionary Rates Using Serially Sampled Sequences from Several Populations. <i>Molecular Biology and Evolution</i> , 2003, 20, 2010-2018.	3.5	15
100	Rates of Evolution in Ancient DNA from Adelie Penguins. <i>Science</i> , 2002, 295, 2270-2273.	6.0	274
101	The Inference of Stepwise Changes in Substitution Rates Using Serial Sequence Samples. <i>Molecular Biology and Evolution</i> , 2001, 18, 1365-1371.	3.5	51
102	Reconstructing Genealogies of Serial Samples Under the Assumption of a Molecular Clock Using Serial-Sample UPGMA. <i>Molecular Biology and Evolution</i> , 2000, 17, 1807-1815.	3.5	90