Alexei J. Drummond

List of Publications by Citations

110 papers	57,777 citations	61 h-index	113 g-index
113 ext. papers	71,533 ext. citations	7.8 avg, IF	8.18 L-index

#	Paper	IF	Citations
110	Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*, **2012**, 28, 1647-9	7.2	11253
109	BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evolutionary Biology*, **2007**, 7, 214	3	9349
108	Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Molecular Biology and Evolution*, **2012**, 29, 1969-73	8.3	7409
107	Relaxed phylogenetics and dating with confidence. *PLoS Biology*, **2006**, 4, e88	9.7	4483
106	BEAST 2: a software platform for Bayesian evolutionary analysis. *PLoS Computational Biology*, **2014**, 10, e1003537	5	3659
105	Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. *Systematic Biology*, **2018**, 67, 901-904	6.4	3267
104	Bayesian coalescent inference of past population dynamics from molecular sequences. *Molecular Biology and Evolution*, **2005**, 22, 1185-92	8.3	2280
103	Bayesian inference of species trees from multilocus data. *Molecular Biology and Evolution*, **2010**, 27, 570-80	8.3	1880
102	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. *Virus Evolution*, **2018**, 4, vey016	3.7	1199
101	Bayesian phylogeography finds its roots. *PLoS Computational Biology*, **2009**, 5, e1000520	5	1101
100	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. *PLoS Computational Biology*, **2019**, 15, e1006650	5	1014
99	Time dependency of molecular rate estimates and systematic overestimation of recent divergence times. *Molecular Biology and Evolution*, **2005**, 22, 1561-8	8.3	840
98	Choosing appropriate substitution models for the phylogenetic analysis of protein-coding sequences. *Molecular Biology and Evolution*, **2006**, 23, 7-9	8.3	562
97	Bayesian inference of population size history from multiple loci. *BMC Evolutionary Biology*, **2008**, 8, 289	3	526
96	Language phylogenies reveal expansion pulses and pauses in Pacific settlement. *Science*, **2009**, 323, 479-83	33.3	522
95	Rise and fall of the Beringian steppe bison. *Science*, **2004**, 306, 1561-5	33.3	518
94	Accurate model selection of relaxed molecular clocks in bayesian phylogenetics. *Molecular Biology and Evolution*, **2013**, 30, 239-43	8.3	416

#	Reference		
93	Mapping the origins and expansion of the Indo-European language family. *Science*, **2012**, 337, 957-60	33.3	368
92	bModelTest: Bayesian phylogenetic site model averaging and model comparison. *BMC Evolutionary Biology*, **2017**, 17, 42	3	337
91	Measurably evolving populations. *Trends in Ecology and Evolution*, **2003**, 18, 481-488	10.9	300
90	Birth-death skyline plot reveals temporal changes of epidemic spread in HIV and hepatitis C virus (HCV). *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 228-33	11.5	295
89	Bayesian random local clocks, or one rate to rule them all. *BMC Biology*, **2010**, 8, 114	7.3	283
88	Rates of evolution in ancient DNA from Adélie penguins. *Science*, **2002**, 295, 2270-3	33.3	255
87	Bayesian Evolutionary Analysis with BEAST **2015**,		237
86	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. *Molecular Biology and Evolution*, **2017**, 34, 2101-2114	8.3	229
85	Evidence for time dependency of molecular rate estimates. *Systematic Biology*, **2007**, 56, 515-22	8.4	222
84	Calibrated tree priors for relaxed phylogenetics and divergence time estimation. *Systematic Biology*, **2012**, 61, 138-49	8.4	204
83	The epidemiology and iatrogenic transmission of hepatitis C virus in Egypt: a Bayesian coalescent approach. *Molecular Biology and Evolution*, **2003**, 20, 381-7	8.3	202
82	mtDNA variation predicts population size in humans and reveals a major Southern Asian chapter in human prehistory. *Molecular Biology and Evolution*, **2008**, 25, 468-74	8.3	189
81	Bayesian inference of sampled ancestor trees for epidemiology and fossil calibration. *PLoS Computational Biology*, **2014**, 10, e1003919	5	179
80	Bayesian Total-Evidence Dating Reveals the Recent Crown Radiation of Penguins. *Systematic Biology*, **2017**, 66, 57-73	8.4	170
79	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. *Journal of Virology*, **2008**, 82, 1819-26	6.6	152
78	Guided tree topology proposals for Bayesian phylogenetic inference. *Systematic Biology*, **2012**, 61, 1-11	8.4	143
77	Synonymous substitution rates predict HIV disease progression as a result of underlying replication dynamics. *PLoS Computational Biology*, **2007**, 3, e29	5	138
76	Accuracy of rate estimation using relaxed-clock models with a critical focus on the early metazoan radiation. *Molecular Biology and Evolution*, **2005**, 22, 1355-63	8.3	138

75	Estimating the basic reproductive number from viral sequence data. *Molecular Biology and Evolution*, **2012**, 29, 347-57	8.3	136
74	Extreme reversed sexual size dimorphism in the extinct New Zealand moa Dinornis. *Nature*, **2003**, 425, 172-5	50.4	134
73	The evolutionary history of the extinct ratite moa and New Zealand Neogene paleogeography. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 20646-51	11.5	131
72	Inference of viral evolutionary rates from molecular sequences. *Advances in Parasitology*, **2003**, 54, 331-58	3.2	127
71	A virus reveals population structure and recent demographic history of its carnivore host. *Science*, **2006**, 311, 538-41	33.3	122
70	Phylogenetic evidence for deleterious mutation load in RNA viruses and its contribution to viral evolution. *Molecular Biology and Evolution*, **2007**, 24, 845-52	8.3	119
69	Bayesian coestimation of phylogeny and sequence alignment. *BMC Bioinformatics*, **2005**, 6, 83	3.6	119
68	Molecular phylogeny of coleoid cephalopods (Mollusca: Cephalopoda) using a multigene approach; the effect of data partitioning on resolving phylogenies in a Bayesian framework. *Molecular Phylogenetics and Evolution*, **2005**, 37, 426-41	4.1	105
67	A Bayesian phylogenetic method to estimate unknown sequence ages. *Molecular Biology and Evolution*, **2011**, 28, 879-87	8.3	98
66	Evaluating a multigene environmental DNA approach for biodiversity assessment. *GigaScience*, **2015**, 4, 46	7.6	97
65	Bayesian Inference of Species Networks from Multilocus Sequence Data. *Molecular Biology and Evolution*, **2018**, 35, 504-517	8.3	94
64	Phylogenetic analysis reveals a correlation between the expansion of very virulent infectious bursal disease virus and reassortment of its genome segment B. *Journal of Virology*, **2006**, 80, 8503-9	6.6	91
63	The molecular population genetics of HIV-1 group O. *Genetics*, **2004**, 167, 1059-68	4	89
62	Model averaging and Bayes factor calculation of relaxed molecular clocks in Bayesian phylogenetics. *Molecular Biology and Evolution*, **2012**, 29, 751-61	8.3	88
61	Epidemic dynamics revealed in dengue evolution. *Molecular Biology and Evolution*, **2010**, 27, 811-8	8.3	85
60	Efficient Bayesian inference under the structured coalescent. *Bioinformatics*, **2014**, 30, 2272-9	7.2	78
59	Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth-death SIR model. *Journal of the Royal Society Interface*, **2014**, 11, 20131106	4.1	78
58	Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. *Systematic Biology*, **2016**, 65, 381-96	8.4	77

57	Accommodating the effect of ancient DNA damage on inferences of demographic histories. *Molecular Biology and Evolution*, **2009**, 26, 245-8	8.3	77
56	Reconstructing genealogies of serial samples under the assumption of a molecular clock using serial-sample UPGMA. *Molecular Biology and Evolution*, **2000**, 17, 1807-15	8.3	76
55	Phylodynamics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. *Molecular Biology and Evolution*, **2016**, 33, 2102-16	8.3	71
54	Influenza a virus migration and persistence in North American wild birds. *PLoS Pathogens*, **2013**, 9, e1003570	7.6	69
53	Epidemiology, genetic diversity, and evolution of endemic feline immunodeficiency virus in a population of wild cougars. *Journal of Virology*, **2003**, 77, 9578-89	6.6	68
52	The genealogical population dynamics of HIV-1 in a large transmission chain: bridging within and among host evolutionary rates. *PLoS Computational Biology*, **2014**, 10, e1003505	5	66
51	Bayesian coalescent inference of major human mitochondrial DNA haplogroup expansions in Africa. *Proceedings of the Royal Society B: Biological Sciences*, **2009**, 276, 367-73	4.4	66
50	Divergence time estimates for major cephalopod groups: evidence from multiple genes. *Cladistics*, **2006**, 22, 89-96	3.5	63
49	Evolution of the human immunodeficiency virus envelope gene is dominated by purifying selection. *Genetics*, **2006**, 174, 1441-53	4	58
48	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. *Nature Communications*, **2020**, 11, 6351	17.4	57
47	Population genetic estimation of the loss of genetic diversity during horizontal transmission of HIV-1. *BMC Evolutionary Biology*, **2006**, 6, 28	3	55
46	Phylogenetic and epidemic modeling of rapidly evolving infectious diseases. *Infection, Genetics and Evolution*, **2011**, 11, 1825-41	4.5	51
45	The evolutionary genetics of viral emergence. *Current Topics in Microbiology and Immunology*, **2007**, 315, 51-66	3.3	50
44	The fossilized birth-death model for the analysis of stratigraphic range data under different speciation modes. *Journal of Theoretical Biology*, **2018**, 447, 41-55	2.3	45
43	The inference of stepwise changes in substitution rates using serial sequence samples. *Molecular Biology and Evolution*, **2001**, 18, 1365-71	8.3	45
42	Taming the BEAST-A Community Teaching Material Resource for BEAST 2. *Systematic Biology*, **2018**, 67, 170-174	8.4	43
41	A stochastic simulator of birth-death master equations with application to phylodynamics. *Molecular Biology and Evolution*, **2013**, 30, 1480-93	8.3	43
40	Joint inference of microsatellite mutation models, population history and genealogies using transdimensional Markov Chain Monte Carlo. *Genetics*, **2011**, 188, 151-64	4	43

39	Calibrated birth-death phylogenetic time-tree priors for bayesian inference. *Systematic Biology*, **2015**, 64, 369-83	8.4	34
38	Simulating gene trees under the multispecies coalescent and time-dependent migration. *BMC Evolutionary Biology*, **2013**, 13, 44	3	34
37	Genomic Evidence of In-Flight Transmission of SARS-CoV-2 Despite Predeparture Testing. *Emerging Infectious Diseases*, **2021**, 27, 687-693	10.2	30
36	Bayesian selection of nucleotide substitution models and their site assignments. *Molecular Biology and Evolution*, **2013**, 30, 669-88	8.3	27
35	Impacts of DNA extraction and PCR on DNA metabarcoding estimates of soil biodiversity. *Methods in Ecology and Evolution*, **2019**, 10, 120-133	7.7	27
34	Inferring Ancestral Recombination Graphs from Bacterial Genomic Data. *Genetics*, **2017**, 205, 857-870	4	26
33	Neotenous origins for pelagic octopuses. *Current Biology*, **2004**, 14, R300-1	6.3	26
32	How accurate and robust are the phylogenetic estimates of Austronesian language relationships?. *PLoS ONE*, **2010**, 5, e9573	3.7	23
31	Bayesian phylogenetic estimation of fossil ages. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2016**, 371,	5.8	22
30	Post-mortem DNA damage hotspots in Bison (Bison bison) provide evidence for both damage and mutational hotspots in human mitochondrial DNA. *Journal of Archaeological Science*, **2005**, 32, 1053-1060	2.9	22
29	Fully Bayesian tests of neutrality using genealogical summary statistics. *BMC Genetics*, **2008**, 9, 68	2.6	21
28	Extinction times in autocatalytic systems. *Journal of Physical Chemistry A*, **2010**, 114, 10481-91	2.8	20
27	Estimating the biodiversity of terrestrial invertebrates on a forested island using DNA barcodes and metabarcoding data. *Ecological Applications*, **2019**, 29, e01877	4.9	19
26	How well can the exponential-growth coalescent approximate constant-rate birth-death population dynamics?. *Proceedings of the Royal Society B: Biological Sciences*, **2015**, 282, 20150420	4.4	19
25	Estimating Epidemic Incidence and Prevalence from Genomic Data. *Molecular Biology and Evolution*, **2019**, 36, 1804-1816	8.3	17
24	The space of ultrametric phylogenetic trees. *Journal of Theoretical Biology*, **2016**, 403, 197-208	2.3	17
23	Inferring epidemiological dynamics with Bayesian coalescent inference: the merits of deterministic and stochastic models. *Genetics*, **2015**, 199, 595-607	4	16
22	Statistical Alignment: Recent Progress, New Applications, and Challenges **2005**, 375-405		16

21	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. *Virus Evolution*, **2019**, 5, vez003	3.7	15
20	Ancient DNA: would the real Neandertal please stand up?. *Current Biology*, **2004**, 14, R431-3	6.3	15
19	Inferring evolutionary rates using serially sampled sequences from several populations. *Molecular Biology and Evolution*, **2003**, 20, 2010-8	8.3	13
18	Bayesian phylodynamics of avian influenza A virus H9N2 in Asia with time-dependent predictors of migration. *PLoS Computational Biology*, **2019**, 15, e1007189	5	11
17	Use of Genomics to Track Coronavirus Disease Outbreaks, New Zealand. *Emerging Infectious Diseases*, **2021**, 27, 1317-1322	10.2	11
16	Phylodynamic Model Adequacy Using Posterior Predictive Simulations. *Systematic Biology*, **2019**, 68, 358-364	8.4	10
15	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales		9
14	Recursive algorithms for phylogenetic tree counting. *Algorithms for Molecular Biology*, **2013**, 8, 26	1.8	7
13	Joint inference of species histories and gene flow		7
12	Within-host demographic fluctuations and correlations in early retroviral infection. *Journal of Theoretical Biology*, **2012**, 295, 86-99	2.3	5
11	Genealogies from Time-Stamped Sequence Data. *Lecture Notes in Statistics*, **2004**, 149-171	2.9	5
10	bModelTest: Bayesian phylogenetic site model averaging and model comparison		4
9	Bayesian inference and comparison of stochastic transcription elongation models. *PLoS Computational Biology*, **2020**, 16, e1006717	5	3
8	StarBEAST2 brings faster species tree inference and accurate estimates of substitution rates		3
7	Scalable total-evidence inference from molecular and continuous characters in a Bayesian framework		3
6	Tree measures and the number of segregating sites in time-structured population samples. *BMC Genetics*, **2005**, 6, 35	2.6	2
5	Evolutionary history of cotranscriptional editing in the paramyxoviral phosphoprotein gene. *Virus Evolution*, **2021**, 7, veab028	3.7	2
4	Report of the 14th Genomic Standards Consortium Meeting, Oxford, UK, September 17-21, 2012.. *Standards in Genomic Sciences*, **2014**, 9, 1236-1250		1