

Alexei J. Drummond

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

79,573
citations

18479

62
h-index

32838

100
g-index

113
all docs

113
docs citations

113
times ranked

57899
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. <i>Bioinformatics</i> , 2012, 28, 1647-1649. | 4.1 | 16,096 |
| 2 | BEAST: Bayesian evolutionary analysis by sampling trees. <i>BMC Evolutionary Biology</i> , 2007, 7, 214. | 3.2 | 11,072 |
| 3 | Bayesian Phylogenetics with BEAUti and the BEAST 1.7. <i>Molecular Biology and Evolution</i> , 2012, 29, 1969-1973. | 8.9 | 9,040 |
| 4 | Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. <i>Systematic Biology</i> , 2018, 67, 901-904. | 5.6 | 6,726 |
| 5 | Relaxed Phylogenetics and Dating with Confidence. <i>PLoS Biology</i> , 2006, 4, e88. | 5.6 | 5,566 |
| 6 | BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003537. | 3.2 | 5,301 |
| 7 | Bayesian Coalescent Inference of Past Population Dynamics from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2005, 22, 1185-1192. | 8.9 | 2,782 |
| 8 | BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650. | 3.2 | 2,484 |
| 9 | Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018, 4, vey016. | 4.9 | 2,401 |
| 10 | Bayesian Inference of Species Trees from Multilocus Data. <i>Molecular Biology and Evolution</i> , 2010, 27, 570-580. | 8.9 | 2,246 |
| 11 | Bayesian Phylogeography Finds Its Roots. <i>PLoS Computational Biology</i> , 2009, 5, e1000520. | 3.2 | 1,519 |
| 12 | Time Dependency of Molecular Rate Estimates and Systematic Overestimation of Recent Divergence Times. <i>Molecular Biology and Evolution</i> , 2005, 22, 1561-1568. | 8.9 | 933 |
| 13 | Choosing Appropriate Substitution Models for the Phylogenetic Analysis of Protein-Coding Sequences. <i>Molecular Biology and Evolution</i> , 2006, 23, 7-9. | 8.9 | 695 |
| 14 | Language Phylogenies Reveal Expansion Pulses and Pauses in Pacific Settlement. <i>Science</i> , 2009, 323, 479-483. | 12.6 | 675 |
| 15 | Bayesian inference of population size history from multiple loci. <i>BMC Evolutionary Biology</i> , 2008, 8, 289. | 3.2 | 658 |
| 16 | bModelTest: Bayesian phylogenetic site model averaging and model comparison. <i>BMC Evolutionary Biology</i> , 2017, 17, 42. | 3.2 | 609 |
| 17 | Rise and Fall of the Beringian Steppe Bison. <i>Science</i> , 2004, 306, 1561-1565. | 12.6 | 601 |
| 18 | Mapping the Origins and Expansion of the Indo-European Language Family. <i>Science</i> , 2012, 337, 957-960. | 12.6 | 549 |

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|----|--|------|-----------|
| 19 | Accurate Model Selection of Relaxed Molecular Clocks in Bayesian Phylogenetics. <i>Molecular Biology and Evolution</i> , 2012, 30, 239-243. | 8.9 | 538 |
| 20 | Birthâ€“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. | 7.1 | 454 |
| 21 | Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , 2003, 18, 481-488. | 8.7 | 371 |
| 22 | StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2101-2114. | 8.9 | 371 |
| 23 | Bayesian random local clocks, or one rate to rule them all. <i>BMC Biology</i> , 2010, 8, 114. | 3.8 | 367 |
| 24 | Bayesian Inference of Sampled Ancestor Trees for Epidemiology and Fossil Calibration. <i>PLoS Computational Biology</i> , 2014, 10, e1003919. | 3.2 | 276 |
| 25 | Calibrated Tree Priors for Relaxed Phylogenetics and Divergence Time Estimation. <i>Systematic Biology</i> , 2012, 61, 138-149. | 5.6 | 275 |
| 26 | Rates of Evolution in Ancient DNA from Adelie Penguins. <i>Science</i> , 2002, 295, 2270-2273. | 12.6 | 274 |
| 27 | Evidence for Time Dependency of Molecular Rate Estimates. <i>Systematic Biology</i> , 2007, 56, 515-522. | 5.6 | 257 |
| 28 | Bayesian Total-Evidence Dating Reveals the Recent Crown Radiation of Penguins. <i>Systematic Biology</i> , 2017, 66, syw060. | 5.6 | 255 |
| 29 | 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. | 8.9 | 225 |
| 30 | 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. | 8.9 | 221 |
| 31 | Estimating the Basic Reproductive Number from Viral Sequence Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 347-357. | 8.9 | 206 |
| 32 | 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. | 3.4 | 197 |
| 33 | Guided Tree Topology Proposals for Bayesian Phylogenetic Inference. <i>Systematic Biology</i> , 2012, 61, 1-11. | 5.6 | 190 |
| 34 | Bayesian coestimation of phylogeny and sequence alignment. <i>BMC Bioinformatics</i> , 2005, 6, 83. | 2.6 | 169 |
| 35 | 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. | 8.9 | 169 |
| 36 | Inference of Viral Evolutionary Rates from Molecular Sequences. <i>Advances in Parasitology</i> , 2003, 54, 331-358. | 3.2 | 161 |

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|----|--|------|-----------|
| 37 | Bayesian Inference of Species Networks from Multilocus Sequence Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 504-517. | 8.9 | 158 |
| 38 | Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. <i>PLoS Computational Biology</i> , 2007, 3, e29. | 3.2 | 152 |
| 39 | Extreme reversed sexual size dimorphism in the extinct New Zealand moa <i>Dinornis</i> . <i>Nature</i> , 2003, 425, 172-175. | 27.8 | 151 |
| 40 | 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. | 7.1 | 150 |
| 41 | A Virus Reveals Population Structure and Recent Demographic History of Its Carnivore Host. <i>Science</i> , 2006, 311, 538-541. | 12.6 | 138 |
| 42 | 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. | 8.9 | 133 |
| 43 | Phylodynamics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 2102-2116. | 8.9 | 131 |
| 44 | Model Averaging and Bayes Factor Calculation of Relaxed Molecular Clocks in Bayesian Phylogenetics. <i>Molecular Biology and Evolution</i> , 2012, 29, 751-761. | 8.9 | 129 |
| 45 | 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. | 2.7 | 125 |
| 46 | Evaluating a multigene environmental DNA approach for biodiversity assessment. <i>GigaScience</i> , 2015, 4, 46. | 6.4 | 122 |
| 47 | A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. <i>Molecular Biology and Evolution</i> , 2011, 28, 879-887. | 8.9 | 119 |
| 48 | Efficient Bayesian inference under the structured coalescent. <i>Bioinformatics</i> , 2014, 30, 2272-2279. | 4.1 | 118 |
| 49 | Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. <i>Systematic Biology</i> , 2016, 65, 381-396. | 5.6 | 107 |
| 50 | The Molecular Population Genetics of HIV-1 Group O. <i>Genetics</i> , 2004, 167, 1059-1068. | 2.9 | 105 |
| 51 | 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. | 3.4 | 104 |
| 52 | 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. | 3.4 | 100 |
| 53 | Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. <i>Nature Communications</i> , 2020, 11, 6351. | 12.8 | 100 |
| 54 | Epidemic Dynamics Revealed in Dengue Evolution. <i>Molecular Biology and Evolution</i> , 2010, 27, 811-818. | 8.9 | 92 |

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|----|---|-----|-----------|
| 55 | 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. | 8.9 | 90 |
| 56 | Accommodating the Effect of Ancient DNA Damage on Inferences of Demographic Histories. <i>Molecular Biology and Evolution</i> , 2009, 26, 245-248. | 8.9 | 86 |
| 57 | 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. | 2.6 | 83 |
| 58 | Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570. | 4.7 | 83 |
| 59 | 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. | 1.7 | 83 |
| 60 | Divergence time estimates for major cephalopod groups: evidence from multiple genes. <i>Cladistics</i> , 2006, 22, 89-96. | 3.3 | 82 |
| 61 | 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. | 3.2 | 79 |
| 62 | Taming the BEAST—A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174. | 5.6 | 79 |
| 63 | 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. | 3.4 | 74 |
| 64 | A Stochastic Simulator of Birth-Death Master Equations with Application to Phylodynamics. <i>Molecular Biology and Evolution</i> , 2013, 30, 1480-1493. | 8.9 | 73 |
| 65 | Phylogenetic and epidemic modeling of rapidly evolving infectious diseases. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1825-1841. | 2.3 | 70 |
| 66 | 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 |
| 67 | Evolution of the Human Immunodeficiency Virus Envelope Gene Is Dominated by Purifying Selection. <i>Genetics</i> , 2006, 174, 1441-1453. | 2.9 | 64 |
| 68 | Impacts of DNA extraction and PCR on DNA metabarcoding estimates of soil biodiversity. <i>Methods in Ecology and Evolution</i> , 2019, 10, 120-133. | 5.2 | 62 |
| 69 | The Evolutionary Genetics of Viral Emergence. <i>Current Topics in Microbiology and Immunology</i> , 2007, 315, 51-66. | 1.1 | 58 |
| 70 | Genomic Evidence of In-Flight Transmission of SARS-CoV-2 Despite Predeparture Testing. <i>Emerging Infectious Diseases</i> , 2021, 27, 687-693. | 4.3 | 58 |
| 71 | Simulating gene trees under the multispecies coalescent and time-dependent migration. <i>BMC Evolutionary Biology</i> , 2013, 13, 44. | 3.2 | 55 |
| 72 | The Inference of Stepwise Changes in Substitution Rates Using Serial Sequence Samples. <i>Molecular Biology and Evolution</i> , 2001, 18, 1365-1371. | 8.9 | 51 |

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|----|--|-----|-----------|
| 73 | Joint Inference of Microsatellite Mutation Models, Population History and Genealogies Using Transdimensional Markov Chain Monte Carlo. <i>Genetics</i> , 2011, 188, 151-164. | 2.9 | 51 |
| 74 | Calibrated Birth-Death Phylogenetic Time-Tree Priors for Bayesian Inference. <i>Systematic Biology</i> , 2015, 64, 369-383. | 5.6 | 48 |
| 75 | Inferring Ancestral Recombination Graphs from Bacterial Genomic Data. <i>Genetics</i> , 2017, 205, 857-870. | 2.9 | 45 |
| 76 | Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816. | 8.9 | 39 |
| 77 | How Accurate and Robust Are the Phylogenetic Estimates of Austronesian Language Relationships?. <i>PLoS ONE</i> , 2010, 5, e9573. | 2.5 | 37 |
| 78 | Bayesian Selection of Nucleotide Substitution Models and Their Site Assignments. <i>Molecular Biology and Evolution</i> , 2013, 30, 669-688. | 8.9 | 37 |
| 79 | Estimating the biodiversity of terrestrial invertebrates on a forested island using DNA barcodes and metabarcoding data. <i>Ecological Applications</i> , 2019, 29, e01877. | 3.8 | 37 |
| 80 | Neotenus origins for pelagic octopuses. <i>Current Biology</i> , 2004, 14, R300-R301. | 3.9 | 34 |
| 81 | Bayesian phylogenetic estimation of fossil ages. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150129. | 4.0 | 34 |
| 82 | The space of ultrametric phylogenetic trees. <i>Journal of Theoretical Biology</i> , 2016, 403, 197-208. | 1.7 | 32 |
| 83 | Inferring Epidemiological Dynamics with Bayesian Coalescent Inference: The Merits of Deterministic and Stochastic Models. <i>Genetics</i> , 2015, 199, 595-607. | 2.9 | 30 |
| 84 | 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. | 2.6 | 29 |
| 85 | Use of Genomics to Track Coronavirus Disease Outbreaks, New Zealand. <i>Emerging Infectious Diseases</i> , 2021, 27, 1317-1322. | 4.3 | 28 |
| 86 | Fully Bayesian tests of neutrality using genealogical summary statistics. <i>BMC Genetics</i> , 2008, 9, 68. | 2.7 | 27 |
| 87 | SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. <i>Virus Evolution</i> , 2019, 5, vez003. | 4.9 | 26 |
| 88 | 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. | 2.4 | 25 |
| 89 | Phylogenetic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , 2019, 68, 358-364. | 5.6 | 25 |
| 90 | Bayesian phylodynamics of avian influenza A virus H9N2 in Asia with time-dependent predictors of migration. <i>PLoS Computational Biology</i> , 2019, 15, e1007189. | 3.2 | 22 |

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|-----|---|-----|-----------|
| 91 | Extinction Times in Autocatalytic Systems. <i>Journal of Physical Chemistry A</i> , 2010, 114, 10481-10491. | 2.5 | 21 |
| 92 | Statistical Alignment: Recent Progress, New Applications, and Challenges. , 2005, , 375-405. | | 20 |
| 93 | Ancient DNA: Would the Real Neandertal Please Stand up?. <i>Current Biology</i> , 2004, 14, R431-R433. | 3.9 | 19 |
| 94 | Evolutionary history of cotranscriptional editing in the paramyxoviral phosphoprotein gene. <i>Virus Evolution</i> , 2021, 7, veab028. | 4.9 | 18 |
| 95 | Inferring Evolutionary Rates Using Serially Sampled Sequences from Several Populations. <i>Molecular Biology and Evolution</i> , 2003, 20, 2010-2018. | 8.9 | 15 |
| 96 | Recursive algorithms for phylogenetic tree counting. <i>Algorithms for Molecular Biology</i> , 2013, 8, 26. | 1.2 | 10 |
| 97 | Bayesian inference and comparison of stochastic transcription elongation models. <i>PLoS Computational Biology</i> , 2020, 16, e1006717. | 3.2 | 8 |
| 98 | Genealogies from Time-Stamped Sequence Data. <i>Lecture Notes in Statistics</i> , 2004, , 149-171. | 0.2 | 6 |
| 99 | Within-host demographic fluctuations and correlations in early retroviral infection. <i>Journal of Theoretical Biology</i> , 2012, 295, 86-99. | 1.7 | 6 |
| 100 | Tree measures and the number of segregating sites in time-structured population samples. <i>BMC Genetics</i> , 2005, 6, 35. | 2.7 | 4 |
| 101 | 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 |
| 102 | A retrodictive stochastic simulation algorithm. <i>Journal of Computational Physics</i> , 2010, 229, 3777-3791. | 3.8 | 0 |