

Bruce Rannala

List of Publications by Year in Descending Order

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Version: 2024-04-29

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

87
papers

13,955
citations

42
h-index

92
g-index

92
ext. papers

16,073
ext. citations

7.4
avg, IF

7.05
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 87 | The cost of ectoparasitism in Cliff Swallows declines over 35 years. <i>Ecological Monographs</i> , 2021 , 91, e01446 | 9 | 6 |
| 86 | The Impact of Cross-Species Gene Flow on Species Tree Estimation. <i>Systematic Biology</i> , 2020 , 69, 830-848 | 8.4 | 12 |
| 85 | A Bayesian Implementation of the Multispecies Coalescent Model with Introgression for Phylogenomic Analysis. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1211-1223 | 8.3 | 33 |
| 84 | Haplotype analysis of the internationally distributed BRCA1 c.3331_3334delCAAG founder mutation reveals a common ancestral origin in Iberia. <i>Breast Cancer Research</i> , 2020 , 22, 108 | 8.3 | 0 |
| 83 | The Spectre of Too Many Species. <i>Systematic Biology</i> , 2019 , 68, 168-181 | 8.4 | 105 |
| 82 | Species Tree Inference with BPP Using Genomic Sequences and the Multispecies Coalescent. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2585-2593 | 8.3 | 132 |
| 81 | Bayesian species identification under the multispecies coalescent provides significant improvements to DNA barcoding analyses. <i>Molecular Ecology</i> , 2017 , 26, 3028-3036 | 5.7 | 48 |
| 80 | Efficient Bayesian Species Tree Inference under the Multispecies Coalescent. <i>Systematic Biology</i> , 2017 , 66, 823-842 | 8.4 | 84 |
| 79 | Conceptual issues in Bayesian divergence time estimation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371, | 5.8 | 20 |
| 78 | A Glance at Recombination Hotspots in the Domestic Cat. <i>PLoS ONE</i> , 2016 , 11, e0148710 | 3.7 | |
| 77 | Critically evaluating the theory and performance of Bayesian analysis of macroevolutionary mixtures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9569-74 | 11.5 | 190 |
| 76 | The art and science of species delimitation. <i>Environmental Epigenetics</i> , 2015 , 61, 846-853 | 2.4 | 91 |
| 75 | The influence of gene flow on species tree estimation: a simulation study. <i>Systematic Biology</i> , 2014 , 63, 17-30 | 8.4 | 210 |
| 74 | Bayesian species delimitation can be robust to guide-tree inference errors. <i>Systematic Biology</i> , 2014 , 63, 993-1004 | 8.4 | 44 |
| 73 | Unguided species delimitation using DNA sequence data from multiple Loci. <i>Molecular Biology and Evolution</i> , 2014 , 31, 3125-35 | 8.3 | 337 |
| 72 | The functional significance of common polymorphisms in zinc finger transcription factors. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1647-55 | 3.2 | 6 |
| 71 | Bayesian inference of shared recombination hotspots between humans and chimpanzees. <i>Genetics</i> , 2014 , 198, 1621-8 | 4 | 5 |

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| 70 | Improved reversible jump algorithms for Bayesian species delimitation. <i>Genetics</i> , 2013 , 194, 245-53 | 4 | 178 |
| 69 | Meiotic gene-conversion rate and tract length variation in the human genome. <i>European Journal of Human Genetics</i> , 2013 , | 5.3 | 15 |
| 68 | Robustness of compound Dirichlet priors for Bayesian inference of branch lengths. <i>Systematic Biology</i> , 2012 , 61, 779-84 | 8.4 | 42 |
| 67 | Molecular phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2012 , 13, 303-14 | 30.1 | 403 |
| 66 | Tail paradox, partial identifiability, and influential priors in Bayesian branch length inference. <i>Molecular Biology and Evolution</i> , 2012 , 29, 325-35 | 8.3 | 63 |
| 65 | Bayesian population genomic inference of crossing over and gene conversion. <i>Genetics</i> , 2011 , 189, 607-19 | 3 | 3 |
| 64 | The accuracy of species tree estimation under simulation: a comparison of methods. <i>Systematic Biology</i> , 2011 , 60, 126-37 | 8.4 | 190 |
| 63 | Bayesian species delimitation using multilocus sequence data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9264-9 | 11.5 | 918 |
| 62 | Population genomic inference of recombination rates and hotspots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6215-9 | 11.5 | 21 |
| 61 | Identification and analysis of evolutionary selection pressures acting at the molecular level in five forkhead subfamilies. <i>BMC Evolutionary Biology</i> , 2008 , 8, 261 | 3 | 13 |
| 60 | TP53 gene mutations of lung cancer patients in upper northern Thailand and environmental risk factors. <i>Cancer Genetics and Cytogenetics</i> , 2008 , 185, 20-7 | | 28 |
| 59 | Phylogenetic inference using whole genomes. <i>Annual Review of Genomics and Human Genetics</i> , 2008 , 9, 217-31 | 9.7 | 138 |
| 58 | Bayesian inference of fine-scale recombination rates using population genomic data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008 , 363, 3921-30 | 5.8 | 36 |
| 57 | Inferring speciation times under an episodic molecular clock. <i>Systematic Biology</i> , 2007 , 56, 453-66 | 8.4 | 304 |
| 56 | Summarizing a posterior distribution of trees using agreement subtrees. <i>Systematic Biology</i> , 2007 , 56, 578-90 | 8.4 | 26 |
| 55 | Inferring somatic mutation rates using the stop-enhanced green fluorescent protein mouse. <i>Genetics</i> , 2007 , 177, 9-16 | 4 | 3 |
| 54 | Inferring complex DNA substitution processes on phylogenies using uniformization and data augmentation. <i>Systematic Biology</i> , 2006 , 55, 259-69 | 8.4 | 29 |
| 53 | Bayesian estimation of species divergence times under a molecular clock using multiple fossil calibrations with soft bounds. <i>Molecular Biology and Evolution</i> , 2006 , 23, 212-26 | 8.3 | 559 |

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|----|--|------|------|
| 52 | In silico analysis of disease-association mapping strategies using the coalescent process and incorporating ascertainment and selection. <i>American Journal of Human Genetics</i> , 2005 , 76, 1066-73 | 11 | 16 |
| 51 | Evidence from the stop-EGFP mouse supports a niche-sharing model of epidermal proliferative units. <i>Experimental Dermatology</i> , 2005 , 14, 838-43 | 4 | 23 |
| 50 | Branch-length prior influences Bayesian posterior probability of phylogeny. <i>Systematic Biology</i> , 2005 , 54, 455-70 | 8.4 | 155 |
| 49 | Frequentist properties of Bayesian posterior probabilities of phylogenetic trees under simple and complex substitution models. <i>Systematic Biology</i> , 2004 , 53, 904-13 | 8.4 | 669 |
| 48 | A novel solution for the time-dependent probability of gene fixation or loss under natural selection. <i>Genetics</i> , 2004 , 168, 1081-4 | 4 | 11 |
| 47 | The Bayesian revolution in genetics. <i>Nature Reviews Genetics</i> , 2004 , 5, 251-61 | 30.1 | 328 |
| 46 | A stop-EGFP transgenic mouse to detect clonal cell lineages generated by mutation. <i>EMBO Reports</i> , 2004 , 5, 914-20 | 6.5 | 40 |
| 45 | Simulating a Coalescent Process with Recombination and Ascertainment. <i>Lecture Notes in Computer Science</i> , 2004 , 84-95 | 0.9 | 1 |
| 44 | DETECTING CORRELATION BETWEEN CHARACTERS IN A COMPARATIVE ANALYSIS WITH UNCERTAIN PHYLOGENY. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 1237 | 3.8 | 8 |
| 43 | Bayesian inference of recent migration rates using multilocus genotypes. <i>Genetics</i> , 2003 , 163, 1177-91 | 4 | 1284 |
| 42 | Bayes estimation of species divergence times and ancestral population sizes using DNA sequences from multiple loci. <i>Genetics</i> , 2003 , 164, 1645-56 | 4 | 755 |
| 41 | Likelihood models of somatic mutation and codon substitution in cancer genes. <i>Genetics</i> , 2003 , 165, 695-705 | 30 | |
| 40 | DMLE+: Bayesian linkage disequilibrium gene mapping. <i>Bioinformatics</i> , 2002 , 18, 894-5 | 7.2 | 108 |
| 39 | Disease surveillance in recombining pathogens: multilocus genotypes identify sources of human <i>Coccidioides</i> infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9067-71 | 11.5 | 43 |
| 38 | Identifiability of parameters in MCMC Bayesian inference of phylogeny. <i>Systematic Biology</i> , 2002 , 51, 754-60 | 8.4 | 125 |
| 37 | Using linked markers to infer the age of a mutation. <i>Human Mutation</i> , 2001 , 18, 87-100 | 4.7 | 57 |
| 36 | Methylation patterns and mathematical models reveal dynamics of stem cell turnover in the human colon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 10519-21 | 11.5 | 42 |
| 35 | High-resolution multipoint linkage-disequilibrium mapping in the context of a human genome sequence. <i>American Journal of Human Genetics</i> , 2001 , 69, 159-78 | 11 | 104 |

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|----|---|------|------|
| 34 | Finding genes influencing susceptibility to complex diseases in the post-genome era. <i>Molecular Diagnosis and Therapy</i> , 2001 , 1, 203-21 | | 59 |
| 33 | Methods for multipoint disease mapping using linkage disequilibrium. <i>Genetic Epidemiology</i> , 2000 , 19 Suppl 1, S71-7 | 2.6 | 18 |
| 32 | A Bayesian framework for the analysis of cospeciation. <i>Evolution; International Journal of Organic Evolution</i> , 2000 , 54, 352-64 | 3.8 | 98 |
| 31 | Estimating allele age. <i>Annual Review of Genomics and Human Genetics</i> , 2000 , 1, 225-49 | 9.7 | 171 |
| 30 | Accommodating phylogenetic uncertainty in evolutionary studies. <i>Science</i> , 2000 , 288, 2349-50 | 33.3 | 261 |
| 29 | Methods for estimating gene frequencies and detecting selection in bacterial populations. <i>Genetics</i> , 2000 , 155, 499-508 | 4 | 12 |
| 28 | Methods for multipoint disease mapping using linkage disequilibrium. <i>Genetic Epidemiology</i> , 2000 , 19, S71-S77 | 2.6 | 3 |
| 27 | INSIGHT INTO SPECIATION FROM HISTORICAL DEMOGRAPHY IN THE PHYTOPHAGOUS BEETLE GENUS OPHRAELLA. <i>Evolution; International Journal of Organic Evolution</i> , 1999 , 53, 1846-1856 | 3.8 | 36 |
| 26 | Likelihood analysis of disequilibrium mapping, and related problems. <i>American Journal of Human Genetics</i> , 1998 , 62, 459-73 | 11 | 79 |
| 25 | Taxon sampling and the accuracy of large phylogenies. <i>Systematic Biology</i> , 1998 , 47, 702-10 | 8.4 | 184 |
| 24 | Using rare mutations to estimate population divergence times: a maximum likelihood approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 15452-7 | 11.5 | 6 |
| 23 | Bayesian phylogenetic inference using DNA sequences: a Markov Chain Monte Carlo Method. <i>Molecular Biology and Evolution</i> , 1997 , 14, 717-24 | 8.3 | 926 |
| 22 | Detecting immigration by using multilocus genotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 9197-201 | 11.5 | 1699 |
| 21 | STATISTICAL TESTS OF HOST-PARASITE COSPECIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 410-419 | 3.8 | 47 |
| 20 | Statistical Tests of Host-Parasite Cospeciation. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 410 | 3.8 | 44 |
| 19 | On the genealogy of a rare allele. <i>Theoretical Population Biology</i> , 1997 , 52, 216-23 | 1.2 | 7 |
| 18 | Maximum likelihood estimation of phylogeny using stratigraphic data. <i>Paleobiology</i> , 1997 , 23, 174-180 | 2.6 | 67 |
| 17 | Gene genealogy in a population of variable size. <i>Heredity</i> , 1997 , 78 (Pt 4), 417-23 | 3.6 | 27 |

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|----|--|------|------|
| 16 | Phylogenetic methods come of age: testing hypotheses in an evolutionary context. <i>Science</i> , 1997 , 276, 227-32 | 33.3 | 696 |
| 15 | The sampling distribution of disease-associated alleles. <i>Genetics</i> , 1997 , 147, 1855-61 | 4 | 9 |
| 14 | The Sampling Theory of Neutral Alleles in an Island Population of Fluctuating Size. <i>Theoretical Population Biology</i> , 1996 , 50, 91-104 | 1.2 | 36 |
| 13 | Estimating gene flow in island populations. <i>Genetical Research</i> , 1996 , 67, 147-58 | 1.1 | 60 |
| 12 | Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. <i>Journal of Molecular Evolution</i> , 1996 , 43, 304-11 | 3.1 | 1190 |
| 11 | Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference 1996 , 43, 304 | | 21 |
| 10 | Colony choice in birds: models based on temporally invariant site quality. <i>Behavioral Ecology and Sociobiology</i> , 1995 , 36, 221-228 | 2.5 | 31 |
| 9 | Polymorphic Characters and Phylogenetic Analysis: A Statistical Perspective. <i>Systematic Biology</i> , 1995 , 44, 421 | 8.4 | 2 |
| 8 | Polymorphic Characters and Phylogenetic Analysis: A Statistical Perspective. <i>Systematic Biology</i> , 1995 , 44, 421-429 | 8.4 | 10 |
| 7 | Relatedness and conflict over optimal group size. <i>Trends in Ecology and Evolution</i> , 1994 , 9, 117-9 | 10.9 | 28 |
| 6 | Comparative evolutionary genetics of trematode parasites (Plagiorchiidae) and their anuran hosts. <i>Canadian Journal of Zoology</i> , 1992 , 70, 993-1000 | 1.5 | 14 |
| 5 | A Bayesian implementation of the multispecies coalescent model with introgression for comparative genomic analysis | | 1 |
| 4 | Gene genealogy in a population of variable size | | 1 |
| 3 | Species Identification by Bayesian Fingerprinting: A Powerful Alternative to DNA Barcoding | | 3 |
| 2 | The Spectre of Too Many Species | | 3 |
| 1 | The Impact of Cross-Species Gene Flow on Species Tree Estimation | | 2 |