

John P Huelsenbeck

List of Publications by Citations

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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.

82

papers

68,735

citations

53

h-index

83

g-index

83

ext. papers

77,361

ext. citations

8.7

avg, IF

8.28

L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 82 | MrBayes 3: Bayesian phylogenetic inference under mixed models. <i>Bioinformatics</i> , 2003 , 19, 1572-4 | 7.2 | 23258 |
| 81 | MRBAYES: Bayesian inference of phylogenetic trees. <i>Bioinformatics</i> , 2001 , 17, 754-5 | 7.2 | 17826 |
| 80 | MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. <i>Systematic Biology</i> , 2012 , 61, 539-42 | 8.4 | 14368 |
| 79 | Bayesian phylogenetic analysis of combined data. <i>Systematic Biology</i> , 2004 , 53, 47-67 | 8.4 | 1437 |
| 78 | Parallel Metropolis coupled Markov chain Monte Carlo for Bayesian phylogenetic inference. <i>Bioinformatics</i> , 2004 , 20, 407-15 | 7.2 | 803 |
| 77 | PHYLOGENY ESTIMATION AND HYPOTHESIS TESTING USING MAXIMUM LIKELIHOOD. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 1997 , 28, 437-466 | | 710 |
| 76 | 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 |
| 75 | Combining data in phylogenetic analysis. <i>Trends in Ecology and Evolution</i> , 1996 , 11, 152-8 | 10.9 | 660 |
| 74 | Potential applications and pitfalls of Bayesian inference of phylogeny. <i>Systematic Biology</i> , 2002 , 51, 673-84 | | 657 |
| 73 | Stochastic mapping of morphological characters. <i>Systematic Biology</i> , 2003 , 52, 131-58 | 8.4 | 590 |
| 72 | Performance of Phylogenetic Methods in Simulation. <i>Systematic Biology</i> , 1995 , 44, 17-48 | 8.4 | 447 |
| 71 | Bayesian analysis of biogeography when the number of areas is large. <i>Systematic Biology</i> , 2013 , 62, 789-804 | | 411 |
| 70 | 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 | 11.5 | 402 |
| 69 | BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. <i>Systematic Biology</i> , 2012 , 61, 170-3 | 8.4 | 374 |
| 68 | Bayesian phylogenetic model selection using reversible jump Markov chain Monte Carlo. <i>Molecular Biology and Evolution</i> , 2004 , 21, 1123-33 | 8.3 | 373 |
| 67 | RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language. <i>Systematic Biology</i> , 2016 , 65, 726-36 | 8.4 | 295 |
| 66 | Alignment uncertainty and genomic analysis. <i>Science</i> , 2008 , 319, 473-6 | 33.3 | 286 |

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| 65 | Bias in Phylogenetic Estimation and Its Relevance to the Choice between Parsimony and Likelihood Methods. <i>Systematic Biology</i> , 2001 , 50, 525-539 | 8.4 | 276 |
| 64 | Is the Felsenstein zone a fly trap?. <i>Systematic Biology</i> , 1997 , 46, 69-74 | 8.4 | 240 |
| 63 | A compound poisson process for relaxing the molecular clock. <i>Genetics</i> , 2000 , 154, 1879-92 | 4 | 227 |
| 62 | Inference of population structure under a Dirichlet process model. <i>Genetics</i> , 2007 , 175, 1787-802 | 4 | 208 |
| 61 | Empirical and Hierarchical Bayesian Estimation of Ancestral States. <i>Systematic Biology</i> , 2001 , 50, 351-366 | 8.4 | 199 |
| 60 | 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 |
| 59 | Taxon sampling and the accuracy of large phylogenies. <i>Systematic Biology</i> , 1998 , 47, 702-10 | 8.4 | 184 |
| 58 | A Likelihood Ratio Test to Detect Conflicting Phylogenetic Signal. <i>Systematic Biology</i> , 1996 , 45, 92-98 | 8.4 | 174 |
| 57 | Comparing the stratigraphic record to estimates of phylogeny. <i>Paleobiology</i> , 1994 , 20, 470-483 | 2.6 | 167 |
| 56 | Inferring the root of a phylogenetic tree. <i>Systematic Biology</i> , 2002 , 51, 32-43 | 8.4 | 161 |
| 55 | Rates and patterns in the evolution of snake-like body form in squamate reptiles: evidence for repeated re-evolution of lost digits and long-term persistence of intermediate body forms. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 2042-64 | 3.8 | 155 |
| 54 | Statistical assignment of DNA sequences using Bayesian phylogenetics. <i>Systematic Biology</i> , 2008 , 57, 750-7 | 8.4 | 151 |
| 53 | Hobgoblin of phylogenetics?. <i>Nature</i> , 1994 , 369, 363-4 | 50.4 | 149 |
| 52 | Testing a covariotide model of DNA substitution. <i>Molecular Biology and Evolution</i> , 2002 , 19, 698-707 | 8.3 | 147 |
| 51 | When are Fossils better than Extant Taxa in Phylogenetic Analysis?. <i>Systematic Zoology</i> , 1991 , 40, 458 | | 138 |
| 50 | Modeling the site-specific variation of selection patterns along lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 12957-62 | 11.5 | 132 |
| 49 | Bayesian Analysis of Molecular Evolution Using MrBayes 2005 , 183-226 | | 127 |
| 48 | A Likelihood-Ratio Test of Monophyly. <i>Systematic Biology</i> , 1996 , 45, 546-558 | 8.4 | 124 |

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| 47 | Bias in Phylogenetic Estimation and Its Relevance to the Choice between Parsimony and Likelihood Methods. <i>Systematic Biology</i> , 2001 , 50, 525-539 | 8.4 | 113 |
| 46 | Performance of Phylogenetic Methods in Simulation. <i>Systematic Biology</i> , 1995 , 44, 17 | 8.4 | 106 |
| 45 | Bayesian inference of the metazoan phylogeny; a combined molecular and morphological approach. <i>Current Biology</i> , 2004 , 14, 1644-9 | 6.3 | 100 |
| 44 | Geographic origin of human mitochondrial DNA: accommodating phylogenetic uncertainty and model comparison. <i>Systematic Biology</i> , 2002 , 51, 155-65 | 8.4 | 99 |
| 43 | A Bayesian framework for the analysis of cospeciation. <i>Evolution; International Journal of Organic Evolution</i> , 2000 , 54, 352-64 | 3.8 | 98 |
| 42 | Efficiency of Markov chain Monte Carlo tree proposals in Bayesian phylogenetics. <i>Systematic Biology</i> , 2008 , 57, 86-103 | 8.4 | 94 |
| 41 | Structurama: bayesian inference of population structure. <i>Evolutionary Bioinformatics</i> , 2011 , 7, 55-9 | 1.9 | 82 |
| 40 | BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019 , 68, 1052-1061 | 8.4 | 71 |
| 39 | Detecting correlation between characters in a comparative analysis with uncertain phylogeny. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 1237-47 | 3.8 | 69 |
| 38 | Maximum likelihood estimation of phylogeny using stratigraphic data. <i>Paleobiology</i> , 1997 , 23, 174-180 | 2.6 | 67 |
| 37 | A dirichlet process prior for estimating lineage-specific substitution rates. <i>Molecular Biology and Evolution</i> , 2012 , 29, 939-55 | 8.3 | 64 |
| 36 | Phylogeny, genome evolution, and host specificity of single-stranded RNA bacteriophage (family Leviviridae). <i>Journal of Molecular Evolution</i> , 2001 , 52, 117-28 | 3.1 | 64 |
| 35 | Probabilistic graphical model representation in phylogenetics. <i>Systematic Biology</i> , 2014 , 63, 753-71 | 8.4 | 63 |
| 34 | A Dirichlet process model for detecting positive selection in protein-coding DNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 6263-8 | 11.5 | 63 |
| 33 | Bayesian estimation of positively selected sites. <i>Journal of Molecular Evolution</i> , 2004 , 58, 661-72 | 3.1 | 62 |
| 32 | Comparative performance of Bayesian and AIC-based measures of phylogenetic model uncertainty. <i>Systematic Biology</i> , 2006 , 55, 89-96 | 8.4 | 57 |
| 31 | Support for dental HIV transmission. <i>Nature</i> , 1994 , 369, 24-5 | 50.4 | 54 |
| 30 | Clonal interference is alleviated by high mutation rates in large populations. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1397-406 | 8.3 | 53 |

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|----|--|------|----|
| 29 | DO PHYLOGENETIC METHODS PRODUCE TREES WITH BIASED SHAPES?. <i>Evolution; International Journal of Organic Evolution</i> , 1996 , 50, 1418-1424 | 3.8 | 48 |
| 28 | STATISTICAL TESTS OF HOST-PARASITE COSPECIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 410-419 | 3.8 | 47 |
| 27 | A nonparametric method for accommodating and testing across-site rate variation. <i>Systematic Biology</i> , 2007 , 56, 975-87 | 8.4 | 47 |
| 26 | Parallel genetic evolution within and between bacteriophage species of varying degrees of divergence. <i>Genetics</i> , 2009 , 181, 225-34 | 4 | 46 |
| 25 | Statistical Tests of Host-Parasite Cospeciation. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 410 | 3.8 | 44 |
| 24 | Effect of nonindependent substitution on phylogenetic accuracy. <i>Systematic Biology</i> , 1999 , 48, 317-28 | 8.4 | 44 |
| 23 | Bayesian analysis of amino acid substitution models. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008 , 363, 3941-53 | 5.8 | 39 |
| 22 | Strepsiptera, phylogenomics and the long branch attraction problem. <i>PLoS ONE</i> , 2014 , 9, e107709 | 3.7 | 38 |
| 21 | Frequent inconsistency of parsimony under a simple model of cladogenesis. <i>Systematic Biology</i> , 2003 , 52, 641-8 | 8.4 | 37 |
| 20 | Base compositional bias and phylogenetic analyses: a test of the "flying DNA" hypothesis. <i>Molecular Phylogenetics and Evolution</i> , 1998 , 10, 408-16 | 4.1 | 34 |
| 19 | MAXIMUM-LIKELIHOOD ESTIMATION OF POPULATION DIVERGENCE TIMES AND POPULATION PHYLOGENY IN MODELS WITHOUT MUTATION. <i>Evolution; International Journal of Organic Evolution</i> , 1998 , 52, 669-677 | 3.8 | 34 |
| 18 | Quantifying the impact of dependent evolution among sites in phylogenetic inference. <i>Systematic Biology</i> , 2011 , 60, 60-73 | 8.4 | 24 |
| 17 | Biologically inspired phylogenetic models strongly outperform the no common mechanism model. <i>Systematic Biology</i> , 2011 , 60, 225-32 | 8.4 | 22 |
| 16 | A Bayesian perspective on a non-parsimonious parsimony model. <i>Systematic Biology</i> , 2008 , 57, 406-19 | 8.4 | 21 |
| 15 | Assessing Uncertainty in the Rooting of the SARS-CoV-2 Phylogeny. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1537-1543 | 8.3 | 19 |
| 14 | Comment on "Phylogenetic MCMC algorithms are misleading on mixtures of trees". <i>Science</i> , 2006 , 312, 367; author reply 367 | 33.3 | 15 |
| 13 | Bayesian Supertrees. <i>Computational Biology</i> , 2004 , 193-224 | 0.7 | 14 |
| 12 | Reply from j.p. Huelsenbeck, j.j. Bull and C.w. Cunningham. <i>Trends in Ecology and Evolution</i> , 1996 , 11, 335 | 10.9 | 12 |

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| 11 | A Bayesian Approach for Estimating Branch-Specific Speciation and Extinction Rates | | 12 |
| 10 | A phylogenetic model for the detection of epistatic interactions. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2197-208 | 8.3 | 10 |
| 9 | Using Parsimony-Guided Tree Proposals to Accelerate Convergence in Bayesian Phylogenetic Inference. <i>Systematic Biology</i> , 2020 , 69, 1016-1032 | 8.4 | 10 |
| 8 | Assessing uncertainty in the rooting of the SARS-CoV-2 phylogeny | | 9 |
| 7 | Reply to Nakov et al.: Model choice requires biological insight when studying the ancestral habitat of photosynthetic eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E10608-E10609 | 11.5 | 6 |
| 6 | Parallel power posterior analyses for fast computation of marginal likelihoods in phylogenetics | | 6 |
| 5 | Parallel power posterior analyses for fast computation of marginal likelihoods in phylogenetics. <i>PeerJ</i> , 2021 , 9, e12438 | 3.1 | 1 |
| 4 | Assessment of fungal diversity in soil rhizosphere associated with <i>Rhazya stricta</i> and some desert plants using metagenomics. <i>Archives of Microbiology</i> , 2021 , 203, 1211-1219 | 3 | 1 |
| 3 | Phylogeny Estimation Using Likelihood-Based Methods 2019 , 177-40 | | 1 |
| 2 | Stratigraphic Data and Estimates of Phylogenies: Contrasting the Efficiency of Different Methods Using Simulations. <i>The Paleontological Society Special Publications</i> , 1996 , 8, 184-184 | | |
| 1 | Rates of evolution and fossils in phylogenetic analysis: a computer simulation approach. <i>The Paleontological Society Special Publications</i> , 1992 , 6, 140-140 | | |