# Ziheng Yang

List of Publications by Year
in descending order

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|---|---|---|---|
| 126 papers | 48,114 citations | 12330<br>69 h-index | 17592<br>121 g-index |
| 145 all docs | 145 docs citations | 145 times ranked | 34419 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | PAML 4: Phylogenetic Analysis by Maximum Likelihood. Molecular Biology and Evolution, 2007, 24, 1586-1591. | 8.9 | 11,130 |
| 2 | PAML: a program package for phylogenetic analysis by maximum likelihood. Bioinformatics, 1997, 13, 555-556. | 4.1 | 3,510 |
| 3 | Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: Approximate methods. Journal of Molecular Evolution, 1994, 39, 306-314. | 1.8 | 2,657 |
| 4 | Bayes Empirical Bayes Inference of Amino Acid Sites Under Positive Selection. Molecular Biology and Evolution, 2005, 22, 1107-1118. | 8.9 | 2,095 |
| 5 | Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449. | 2.9 | 2,064 |
| 6 | Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference. Journal of Molecular Evolution, 1996, 43, 304-311. | 1.8 | 1,486 |
| 7 | Likelihood Models for Detecting Positively Selected Amino Acid Sites and Applications to the HIV-1 Envelope Gene. Genetics, 1998, 148, 929-936. | 2.9 | 1,419 |
| 8 | Codon-Substitution Models for Detecting Molecular Adaptation at Individual Sites Along Specific Lineages. Molecular Biology and Evolution, 2002, 19, 908-917. | 8.9 | 1,238 |
| 9 | Bayesian species delimitation using multilocus sequence data. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9264-9269. | 7.1 | 1,154 |
| 10 | Among-site rate variation and its impact on phylogenetic analyses. Trends in Ecology and Evolution, 1996, 11, 367-372. | 8.7 | 1,091 |
| 11 | Bayes Estimation of Species Divergence Times and Ancestral Population Sizes Using DNA Sequences From Multiple Loci. Genetics, 2003, 164, 1645-1656. | 2.9 | 946 |
| 12 | Estimating the pattern of nucleotide substitution. Journal of Molecular Evolution, 1994, 39, 105-11. | 1.8 | 939 |
| 13 | Bayesian Estimation of Species Divergence Times Under a Molecular Clock Using Multiple Fossil Calibrations with Soft Bounds. Molecular Biology and Evolution, 2006, 23, 212-226. | 8.9 | 742 |
| 14 | Accuracy and Power of the Likelihood Ratio Test in Detecting Adaptive Molecular Evolution. Molecular Biology and Evolution, 2001, 18, 1585-1592. | 8.9 | 658 |
| 15 | The timescale of early land plant evolution. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2274-E2283. | 7.1 | 654 |
| 16 | Synonymous and nonsynonymous rate variation in nuclear genes of mammals. Journal of Molecular Evolution, 1998, 46, 409-418. | 1.8 | 619 |
| 17 | Best Practices for Justifying Fossil Calibrations. Systematic Biology, 2012, 61, 346-359. | 5.6 | 616 |
| 18 | Molecular phylogenetics: principles and practice. Nature Reviews Genetics, 2012, 13, 303-314. | 16.3 | 572 |

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|---|---------|----|-----------|
| 19 | The BPP program for species tree estimation and species delimitation. Environmental Epigenetics, 2015, 61, 854-865. | 1.8 | 568 |
| 20 | Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 3491-3500. | 2.6 | 449 |
| 21 | Unguided Species Delimitation Using DNA Sequence Data from Multiple Loci. Molecular Biology and Evolution, 2014, 31, 3125-3135. | 8.9 | 449 |
| 22 | Estimation of Primate Speciation Dates Using Local Molecular Clocks. Molecular Biology and Evolution, 2000, 17, 1081-1090. | 8.9 | 441 |
| 23 | Inferring Speciation Times under an Episodic Molecular Clock. Systematic Biology, 2007, 56, 453-466. | 5.6 | 388 |
| 24 | Maximum-likelihood models for combined analyses of multiple sequence data. Journal of Molecular Evolution, 1996, 42, 587-596. | 1.8 | 387 |
| 25 | Uncertainty in the Timing of Origin of Animals and the Limits of Precision in Molecular Timescales. Current Biology, 2015, 25, 2939-2950. | 3.9 | 370 |
| 26 | Codon-Substitution Models to Detect Adaptive Evolution that Account for Heterogeneous Selective Pressures Among Site Classes. Molecular Biology and Evolution, 2002, 19, 49-57. | 8.9 | 343 |
| 27 | Comparison of Likelihood and Bayesian Methods for Estimating Divergence Times Using Multiple Gene Loci and Calibration Points, with Application to a Radiation of Cute-Looking Mouse Lemur Species. Systematic Biology, 2003, 52, 705-716. | 5.6 | 327 |
| 28 | The Influence of Gene Flow on Species Tree Estimation: A Simulation Study. Systematic Biology, 2014, 63, 17-30. | 5.6 | 308 |
| 29 | Mutation-Selection Models of Codon Substitution and Their Use to Estimate Selective Strengths on Codon Usage. Molecular Biology and Evolution, 2008, 25, 568-579. | 8.9 | 304 |
| 30 | Approximate Likelihood Calculation on a Phylogeny for Bayesian Estimation of Divergence Times. Molecular Biology and Evolution, 2011, 28, 2161-2172. | 8.9 | 303 |
| 31 | Statistical Properties of the Branch-Site Test of Positive Selection. Molecular Biology and Evolution, 2011, 28, 1217-1228. | 8.9 | 289 |
| 32 | Phylogenetic analysis using parsimony and likelihood methods. Journal of Molecular Evolution, 1996, 42, 294-307. | 1.8 | 277 |
| 33 | Species Tree Inference with BPP Using Genomic Sequences and the Multispecies Coalescent. Molecular Biology and Evolution, 2018, 35, 2585-2593. | 8.9 | 265 |
| 34 | On the Best Evolutionary Rate for Phylogenetic Analysis. Systematic Biology, 1998, 47, 125-133. | 5.6 | 259 |
| 35 | Improved Reversible Jump Algorithms for Bayesian Species Delimitation. Genetics, 2013, 194, 245-253. | 2.9 | 251 |
| 36 | The Effect of Insertions, Deletions, and Alignment Errors on the Branch-Site Test of Positive Selection. Molecular Biology and Evolution, 2010, 27, 2257-2267. | 8.9 | 249 |

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|---|---------|-----|-----------|
| 37 | The Impact of the Representation of Fossil Calibrations on Bayesian Estimation of Species Divergence Times. Systematic Biology, 2010, 59, 74-89. | 5.6 | 247 |
| 38 | Bayesian molecular clock dating of species divergences in the genomics era. Nature Reviews Genetics, 2016, 17, 71-80. | 16.3 | 244 |
| 39 | Evaluation of a Bayesian Coalescent Method of Species Delimitation. Systematic Biology, 2011, 60, 747-761. | 5.6 | 242 |
| 40 | Maximum Likelihood Trees from DNA Sequences: A Peculiar Statistical Estimation Problem. Systematic Biology, 1995, 44, 384-399. | 5.6 | 239 |
| 41 | Phylogenetic tree building in the genomic age. Nature Reviews Genetics, 2020, 21, 428-444. | 16.3 | 226 |
| 42 | Exploring uncertainty in the calibration of the molecular clock. Biology Letters, 2012, 8, 156-159. | 2.3 | 206 |
| 43 | Maximum Likelihood Estimation on Large Phylogenies and Analysis of Adaptive Evolution in Human Influenza Virus A. Journal of Molecular Evolution, 2000, 51, 423-432. | 1.8 | 202 |
| 44 | Branch-Length Prior Influences Bayesian Posterior Probability of Phylogeny. Systematic Biology, 2005, 54, 455-470. | 5.6 | 196 |
| 45 | Dating Primate Divergences through an Integrated Analysis of Palaeontological and Molecular Data. Systematic Biology, 2011, 60, 16-31. | 5.6 | 195 |
| 46 | The Spectre of Too Many Species. Systematic Biology, 2019, 68, 168-181. | 5.6 | 189 |
| 47 | Estimation of the Transition/Transversion Rate Bias and Species Sampling. Journal of Molecular Evolution, 1999, 48, 274-283. | 1.8 | 186 |
| 48 | Likelihood and Bayes Estimation of Ancestral Population Sizes in Hominoids Using Data From Multiple Loci. Genetics, 2002, 162, 1811-1823. | 2.9 | 186 |
| 49 | Inference of selection from multiple species alignments. Current Opinion in Genetics and Development, 2002, 12, 688-694. | 3.3 | 183 |
| 50 | Estimation of Hominoid Ancestral Population Sizes under Bayesian Coalescent Models Incorporating Mutation Rate Variation and Sequencing Errors. Molecular Biology and Evolution, 2008, 25, 1979-1994. | 8.9 | 177 |
| 51 | Phylogenetic Inference Using Whole Genomes. Annual Review of Genomics and Human Genetics, 2008, 9, 217-231. | 6.2 | 159 |
| 52 | A biologist's guide to Bayesian phylogenetic analysis. Nature Ecology and Evolution, 2017, 1, 1446-1454. | 7.8 | 154 |
| 53 | Maximum likelihood methods for detecting adaptive evolution after gene duplication. Journal of Structural and Functional Genomics, 2003, 3, 201-212. | 1.2 | 152 |
| 54 | Efficient Bayesian Species Tree Inference under the Multispecies Coalescent. Systematic Biology, 2017, 66, 823-842. | 5.6 | 151 |

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|---|---------|-----|-----------|
| 55 | Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution. New Phytologist, 2018, 218, 819-834. | 7.3 | 149 |
| 56 | Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case. Systematic Biology, 2018, 67, 594-615. | 5.6 | 143 |
| 57 | An Empirical Examination of the Utility of Codon-Substitution Models in Phylogeny Reconstruction. Systematic Biology, 2005, 54, 808-818. | 5.6 | 142 |
| 58 | In defence of model-based inference in phylogeography. Molecular Ecology, 2010, 19, 436-446. | 3.9 | 141 |
| 59 | Challenges in Species Tree Estimation Under the Multispecies Coalescent Model. Genetics, 2016, 204, 1353-1368. | 2.9 | 137 |
| 60 | The unbearable uncertainty of Bayesian divergence time estimation. Journal of Systematics and Evolution, 2013, 51, 30-43. | 3.1 | 130 |
| 61 | A Bayesian Implementation of the Multispecies Coalescent Model with Introgression for Phylogenomic Analysis. Molecular Biology and Evolution, 2020, 37, 1211-1223. | 8.9 | 109 |
| 62 | MtZoa: A general mitochondrial amino acid substitutions model for animal evolutionary studies. Molecular Phylogenetics and Evolution, 2009, 52, 268-272. | 2.7 | 105 |
| 63 | Tail Paradox, Partial Identifiability, and Influential Priors in Bayesian Branch Length Inference. Molecular Biology and Evolution, 2012, 29, 325-335. | 8.9 | 92 |
| 64 | The power of phylogenetic comparison in revealing protein function. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3179-3180. | 7.1 | 89 |
| 65 | Neither phylogenomic nor palaeontological data support a Palaeogene origin of placental mammals. Biology Letters, 2014, 10, 20131003. | 2.3 | 87 |
| 66 | Probability Distribution of Molecular Evolutionary Trees: A New Method of Phylogenetic Inference. Journal of Molecular Evolution, 1996, 43, 304-311. | 1.8 | 84 |
| 67 | A species-level timeline of mammal evolution integrating phylogenomic data. Nature, 2022, 602, 263-267. | 27.8 | 84 |
| 68 | Complexity of the simplest phylogenetic estimation problem. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 109-116. | 2.6 | 81 |
| 69 | Maximum Likelihood Implementation of an Isolation-with-Migration Model with Three Species for Testing Speciation with Gene Flow. Molecular Biology and Evolution, 2012, 29, 3131-3142. | 8.9 | 81 |
| 70 | Dating Phylogenies with Sequentially Sampled Tips. Systematic Biology, 2013, 62, 674-688. | 5.6 | 79 |
| 71 | The evolution of methods for establishing evolutionary timescales. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20160020. | 4.0 | 79 |
| 72 | The Impact of the Rate Prior on Bayesian Estimation of Divergence Times with Multiple Loci. Systematic Biology, 2014, 63, 555-565. | 5.6 | 78 |

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| 73 | Molecular evolution of the hepatitis B virus genome. Journal of Molecular Evolution, 1995, 41, 587-96. | 1.8 | 77 |
| 74 | Coalescent Analysis of Phylogenomic Data Confidently Resolves the Species Relationships in the Anopheles gambiae Species Complex. Molecular Biology and Evolution, 2018, 35, 2512-2527. | 8.9 | 76 |
| 75 | Rates of Nucleotide Substitution and Mammalian Nuclear Gene Evolution: Approximate and Maximum-Likelihood Methods Lead to Different Conclusions. Genetics, 2000, 156, 1299-1308. | 2.9 | 75 |
| 76 | Substitution Rates in Drosophila Nuclear Genes: Implications for Translational Selection. Genetics, 2001, 157, 295-305. | 2.9 | 74 |
| 77 | Bayesian species identification under the multispecies coalescent provides significant improvements to <scp>DNA</scp> barcoding analyses. Molecular Ecology, 2017, 26, 3028-3036. | 3.9 | 73 |
| 78 | Characterization of the Uncertainty of Divergence Time Estimation under Relaxed Molecular Clock Models Using Multiple Loci. Systematic Biology, 2015, 64, 267-280. | 5.6 | 70 |
| 79 | A Likelihood Ratio Test of Speciation with Gene Flow Using Genomic Sequence Data. Genome Biology and Evolution, 2010, 2, 200-211. | 2.5 | 69 |
| 80 | Coalescent-Based Analyses of Genomic Sequence Data Provide a Robust Resolution of Phylogenetic Relationships among Major Groups of Gibbons. Molecular Biology and Evolution, 2018, 35, 159-179. | 8.9 | 69 |
| 81 | STATISTICAL TESTS OF HOST-PARASITE COSPECIATION. Evolution; International Journal of Organic Evolution, 1997, 51, 410-419. | 2.3 | 67 |
| 82 | Fair-Balance Paradox, Star-tree Paradox, and Bayesian Phylogenetics. Molecular Biology and Evolution, 2007, 24, 1639-1655. | 8.9 | 66 |
| 83 | Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824. | 9.5 | 65 |
| 84 | Searching for efficient Markov chain Monte Carlo proposal kernels. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19307-19312. | 7.1 | 64 |
| 85 | Bayesian selection of misspecified models is overconfident and may cause spurious posterior probabilities for phylogenetic trees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1854-1859. | 7.1 | 61 |
| 86 | On the estimation of ancestral population sizes of modern humans. Genetical Research, 1997, 69, 111-116. | 0.9 | 54 |
| 87 | Bayesian Species Delimitation Can Be Robust to Guide-Tree Inference Errors. Systematic Biology, 2014, 63, 993-1004. | 5.6 | 52 |
| 88 | Testing the molecular clock using mechanistic models of fossil preservation and molecular evolution. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170227. | 2.6 | 51 |
| 89 | Comparison of different strategies for using fossil calibrations to generate the time prior in Bayesian molecular clock dating. Molecular Phylogenetics and Evolution, 2017, 114, 386-400. | 2.7 | 46 |
| 90 | Molecular and morphological evidence on the phylogeny of the Elephantidae. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 2493-2500. | 2.6 | 45 |

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| 91 | Maximum Likelihood Implementation of an Isolation-with-Migration Model for Three Species. Systematic Biology, 2017, 66, syw063. | 5.6 | 45 |
| 92 | Prevalence of cryptic species in morphologically uniform taxa â€" Fast speciation and evolutionary radiation in Asian frogs. Molecular Phylogenetics and Evolution, 2018, 127, 723-731. | 2.7 | 45 |
| 93 | Multilocus estimation of divergence times and ancestral effective population sizes of <i><scp>O</scp>ryza</i> species and implications for the rapid diversification of the genus. New Phytologist, 2013, 198, 1155-1164. | 7.3 | 43 |
| 94 | Maximum Likelihood Trees from DNA Sequences: A Peculiar Statistical Estimation Problem. Systematic Biology, 1995, 44, 384. | 5.6 | 41 |
| 95 | Evaluation of Ancestral Sequence Reconstruction Methods to Infer Nonstationary Patterns of Nucleotide Substitution. Genetics, 2015, 200, 873-890. | 2.9 | 37 |
| 96 | The Impact of Cross-Species Gene Flow on Species Tree Estimation. Systematic Biology, 2020, 69, 830-847. | 5.6 | 37 |
| 97 | Multispecies coalescent and its applications to infer species phylogenies and cross-species gene flow. National Science Review, 2021, 8, nwab127. | 9.5 | 36 |
| 98 | Empirical evaluation of a prior for Bayesian phylogenetic inference. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 4031-4039. | 4.0 | 35 |
| 99 | Bayesian Molecular Clock Dating Using Genome-Scale Datasets. Methods in Molecular Biology, 2019, 1910, 309-330. | 0.9 | 33 |
| 100 | An Evaluation of Different Partitioning Strategies for Bayesian Estimation of Species Divergence Times. Systematic Biology, 2018, 67, 61-77. | 5.6 | 32 |
| 101 | Molecular Clocks without Rocks: New Solutions for Old Problems. Trends in Genetics, 2020, 36, 845-856. | 6.7 | 32 |
| 102 | Rapid morphological evolution in placental mammals post-dates the origin of the crown group. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182418. | 2.6 | 29 |
| 103 | Defining Species When There is Gene Flow. Systematic Biology, 2021, 70, 108-119. | 5.6 | 29 |
| 104 | On the general reversible Markov process model of nucleotide substitution: A reply to Saccone et al.. Journal of Molecular Evolution, 1995, 41, 254. | 1.8 | 27 |
| 105 | Phylogeny and species delimitation of the Câ€genome diploid species in <i>Oryza</i>. Journal of Systematics and Evolution, 2011, 49, 386-395. | 3.1 | 27 |
| 106 | Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters. Systematic Biology, 2019, 68, 967-986. | 5.6 | 27 |
| 107 | Complexity of the simplest species tree problem. Molecular Biology and Evolution, 2021, 38, 3993-4009. | 8.9 | 22 |
| 108 | A Simulation Study to Examine the Information Content in Phylogenomic Data Sets under the Multispecies Coalescent Model. Molecular Biology and Evolution, 2020, 37, 3211-3224. | 8.9 | 20 |

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| 109 | A simulation study to examine the impact of recombination on phylogenomic inferences under the multispecies coalescent model. Molecular Ecology, 2022, 31, 2814-2829. | 3.9 | 20 |
| 110 | Full-Likelihood Genomic Analysis Clarifies a Complex History of Species Divergence and Introgression: The Example of the *erato-sara* Group of *Heliconius* Butterflies. Systematic Biology, 2022, 71, 1159-1177. | 5.6 | 16 |
| 111 | Reply to Hedges et al.: Accurate timetrees do indeed require accurate calibrations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9512-E9513. | 7.1 | 15 |
| 112 | MAXIMUM LIKELIHOOD ANALYSIS OF ADAPTIVE EVOLUTION IN HIV-1 GP120 ENV GENE. , 2000, , . | | 15 |
| 113 | Genome-Scale Data Reveal Deep Lineage Divergence and a Complex Demographic History in the Texas Horned Lizard (*Phrynosoma cornutum*) throughout the Southwestern and Central United States. Genome Biology and Evolution, 2022, 14, . | 2.5 | 15 |
| 114 | Bayesian Estimation of Nonsynonymous/Synonymous Rate Ratios for Pairwise Sequence Comparisons. Molecular Biology and Evolution, 2014, 31, 1902-1913. | 8.9 | 13 |
| 115 | SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model. , 2012, , . | | 12 |
| 116 | Phase Resolution of Heterozygous Sites in Diploid Genomes is Important to Phylogenomic Analysis under the Multispecies Coalescent Model. Systematic Biology, 2022, 71, 334-352. | 5.6 | 11 |
| 117 | Estimation of Cross-Species Introgression Rates Using Genomic Data Despite Model Unidentifiability. Molecular Biology and Evolution, 2022, 39, . | 8.9 | 10 |
| 118 | On the Varied Pattern of Evolution of 2 Fungal Genomes: A Critique of Hughes and Friedman. Molecular Biology and Evolution, 2006, 23, 2279-2282. | 8.9 | 8 |
| 119 | Dating species divergences using rocks and clocks. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150126. | 4.0 | 8 |
| 120 | Functional and Adaptive Significance of Promoter Mutations That Affect Divergent Myocardial Expressions of *TRIM72* in Primates. Molecular Biology and Evolution, 2021, 38, 2930-2945. | 8.9 | 6 |
| 121 | The Asymptotic Behavior of Bootstrap Support Values in Molecular Phylogenetics. Systematic Biology, 2021, 70, 774-785. | 5.6 | 6 |
| 122 | RELATING PHYSICOCHEMMICAL PROPERTIES OF AMINO ACIDS TO VARIABLE NUCLEOTIDE SUBSTITUTION PATTERNS AMONG SITES. , 1999, , . | | 3 |
| 123 | A discrete–beta model for testing gene flow after speciation. Methods in Ecology and Evolution, 2015, 6, 715-724. | 5.2 | 2 |
| 124 | Ambiguity Coding Allows Accurate Inference of Evolutionary Parameters from Alignments in an Aggregated State-Space. Systematic Biology, 2021, 70, 21-32. | 5.6 | 1 |
| 125 | A. W.ÂF. Edwards and the Origin of Bayesian Phylogenetics. , 0, , 352-362. | | 0 |
| 126 | Proteins: Structure, Function and Evolution. , 2001, , . | | 0 |