

CITATION REPORT

List of articles citing

Effects of nucleotide composition bias on the success of the parsimony criterion in phylogenetic inference

DOI: 10.1093/oxfordjournals.molbev.a003874
Molecular Biology and Evolution, 2001, 18, 1024-33.

Source: <https://exaly.com/paper-pdf/33319095/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
64	Evolutionary rate differences in trypanosomes. <i>Infection, Genetics and Evolution</i> , 2001 , 1, 143-50	4.5	48
63	Group II introns as phylogenetic tools: structure, function, and evolutionary constraints. <i>American Journal of Botany</i> , 2002 , 89, 1651-69	2.7	104
62	Examining Basal avian divergences with mitochondrial sequences: model complexity, taxon sampling, and sequence length. <i>Systematic Biology</i> , 2002 , 51, 614-25	8.4	69
61	Troubleshooting Molecular Phylogenetic Analyses. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2002 , 33, 49-72		206
60	Phylogenetics and sequence analysis--some problems for the unwary. <i>Trends in Parasitology</i> , 2003 , 19, 582-8	6.4	13
59	Evolutionary processes in the genus <i>Coreocarpus</i> : insights from molecular phylogenetics. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 52-61	3.8	18
58	EVOLUTIONARY PROCESSES IN THE GENUS COREOCARPUS: INSIGHTS FROM MOLECULAR PHYLOGENETICS. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 52	3.8	2
57	Heterogeneity of nucleotide frequencies among evolutionary lineages and phylogenetic inference. <i>Molecular Biology and Evolution</i> , 2003 , 20, 610-21	8.3	76
56	Modeling compositional heterogeneity. <i>Systematic Biology</i> , 2004 , 53, 485-95	8.4	335
55	Tracing the decay of the historical signal in biological sequence data. <i>Systematic Biology</i> , 2004 , 53, 623-38	8.4	127
54	Biogeography of the <i>Pistia</i> clade (Araceae): based on chloroplast and mitochondrial DNA sequences and Bayesian divergence time inference. <i>Systematic Biology</i> , 2004 , 53, 422-32	8.4	58
53	The biasing effect of compositional heterogeneity on phylogenetic estimates may be underestimated. <i>Systematic Biology</i> , 2004 , 53, 638-43	8.4	199
52	Gene phylogenies and protein-protein interactions: possible artifacts resulting from shared protein interaction partners. <i>Journal of Theoretical Biology</i> , 2004 , 231, 197-202	2.3	8
51	Relative character-state space, amount of potential phylogenetic information, and heterogeneity of nucleotide and amino acid characters*1. <i>Molecular Phylogenetics and Evolution</i> , 2004 , 32, 913-913	4.1	
50	Multiple data sets, high homoplasy, and the phylogeny of softshell turtles (Testudines: Trionychidae). <i>Systematic Biology</i> , 2004 , 53, 693-710	8.4	87
49	Relative character-state space, amount of potential phylogenetic information, and heterogeneity of nucleotide and amino acid characters. <i>Molecular Phylogenetics and Evolution</i> , 2004 , 32, 913-26	4.1	38
48	Does elision account for molecular saturation: case study based on mitochondrial ribosomal DNA among Characiform fishes (Teleostei: Ostariophysii). <i>Molecular Phylogenetics and Evolution</i> , 2005 , 35, 300-8	4.1	13

47	Nonhomogeneous model of sequence evolution indicates independent origins of primary endosymbionts within the enterobacteriales (gamma-Proteobacteria). <i>Molecular Biology and Evolution</i> , 2005 , 22, 520-32	8.3	51
46	Peracarid monophyly and interordinal phylogeny inferred from nuclear small-subunit ribosomal DNA sequences (Crustacea: Malacostraca: Peracarida). <i>Proceedings of the Biological Society of Washington</i> , 2005 , 118, 117-157	0.2	49
45	Phylogenetic analyses of parasites in the new millennium. <i>Advances in Parasitology</i> , 2006 , 63, 1-124	3.2	25
44	The systematics of Australian <i>Daphnia</i> and <i>Daphniopsis</i> (Crustacea: Cladocera): a shared phylogenetic history transformed by habitat-specific rates of evolution. <i>Biological Journal of the Linnean Society</i> , 2006 , 89, 469-488	1.9	29
43	Quantification of the success of phylogenetic inference in simulations. <i>Cladistics</i> , 2006 , 22, 249-255	3.5	24
42	Phylogenetic invariants for stationary base composition. <i>Journal of Symbolic Computation</i> , 2006 , 41, 138-180	1.8	8
41	Generation of the Exact Distribution and Simulation of Matched Nucleotide Sequences on a Phylogenetic Tree. <i>Mathematical Modelling and Algorithms</i> , 2006 , 5, 291-308		21
40	Vertical Transmission of a Pentatomid Caeca-Associated Symbiont. <i>Annals of the Entomological Society of America</i> , 2006 , 99, 577-585	2	89
39	Phylogenetic analysis of Tylenchida Thorne, 1949 as inferred from D2 and D3 expansion fragments of the 28S rRNA gene sequences. <i>Nematology</i> , 2006 , 8, 455-474	0.9	175
38	A reversible jump method for Bayesian phylogenetic inference with a nonhomogeneous substitution model. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1286-99	8.3	42
37	Base-compositional heterogeneity in the RAG1 locus among didelphid marsupials: implications for phylogenetic inference and the evolution of GC content. <i>Systematic Biology</i> , 2007 , 56, 83-96	8.4	44
36	Estimation of phylogeny and invariant sites under the general Markov model of nucleotide sequence evolution. <i>Systematic Biology</i> , 2007 , 56, 155-62	8.4	28
35	Phylogenetic Methods for the Analysis of Parasites and Pathogens. 265-297		
34	Species boundaries and phylogenetic relationships within the green algal genus <i>Codium</i> (Bryopsidales) based on plastid DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2007 , 44, 240-54	4.1	74
33	Phylogeny of "core Gruiformes" (Aves: Grues) and resolution of the Limpkin-Sungrebe problem. <i>Molecular Phylogenetics and Evolution</i> , 2007 , 43, 515-29	4.1	60
32	Detecting and overcoming systematic errors in genome-scale phylogenies. <i>Systematic Biology</i> , 2007 , 56, 389-99	8.4	241
31	Building trees of algae: some advances in phylogenetic and evolutionary analysis. <i>European Journal of Phycology</i> , 2008 , 43, 229-252	2.2	42
30	A fuzzy classifier to taxonomically group DNA fragments within a metagenome. 2008 ,		3

29	Nonstationary evolution and compositional heterogeneity in beetle mitochondrial phylogenomics. <i>Systematic Biology</i> , 2009 , 58, 381-94	8.4	134
28	A broadscale phylogenetic analysis of group II intron RNAs and intron-encoded reverse transcriptases. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2795-808	8.3	31
27	Evolution of prokaryotic SPFH proteins. <i>BMC Evolutionary Biology</i> , 2009 , 9, 10	3	39
26	16S and 28S rDNA Sequences in Phylogenetic Analyses of Freshwater Prawns (<i>Macrobrachium</i> Bate, 1868) from Taiwan. <i>Journal of Crustacean Biology</i> , 2009 , 29, 400-412	0.8	4
25	From reptilian phylogenomics to reptilian genomes: analyses of c-Jun and DJ-1 proto-oncogenes. <i>Cytogenetic and Genome Research</i> , 2009 , 127, 79-93	1.9	14
24	SeqVis: a tool for detecting compositional heterogeneity among aligned nucleotide sequences. <i>Methods in Molecular Biology</i> , 2009 , 537, 65-91	1.4	8
23	Comparative evolution of the mitochondrial cytochrome b gene and nuclear S7 ribosomal protein gene intron 1 in sinipercid fishes and their relatives. <i>Hydrobiologia</i> , 2010 , 649, 139-156	2.4	6
22	An evaluation of phylogenetic informativeness profiles and the molecular phylogeny of diplazontinae (Hymenoptera, Ichneumonidae). <i>Systematic Biology</i> , 2010 , 59, 226-41	8.4	55
21	Phylogenetic relationships between Sophophora and Lordiphosa, with proposition of a hypothesis on the vicariant divergences of tropical lineages between the Old and New Worlds in the family Drosophilidae. <i>Molecular Phylogenetics and Evolution</i> , 2011 , 60, 98-107	4.1	21
20	RY-Coding and Non-Homogeneous Models Can Ameliorate the Maximum-Likelihood Inferences From Nucleotide Sequence Data with Parallel Compositional Heterogeneity. <i>Evolutionary Bioinformatics</i> , 2012 , 8, 357-71	1.9	18
19	The impact of taxon sampling on phylogenetic inference: a review of two decades of controversy. <i>Briefings in Bioinformatics</i> , 2012 , 13, 122-34	13.4	121
18	Addressing gene tree discordance and non-stationarity to resolve a multi-locus phylogeny of the flatfishes (Teleostei: Pleuronectiformes). <i>Systematic Biology</i> , 2013 , 62, 763-85	8.4	94
17	Relaxed phylogenetics and the palaeoptera problem: resolving deep ancestral splits in the insect phylogeny. <i>Systematic Biology</i> , 2013 , 62, 285-97	8.4	45
16	Shaking the Diptera tree of life: performance analysis of nuclear and mitochondrial sequence data partitions. <i>Systematic Entomology</i> , 2013 , 38, 93-103	3.4	20
15	Coalescent versus concatenation methods and the placement of Amborella as sister to water lilies. <i>Systematic Biology</i> , 2014 , 63, 919-32	8.4	132
14	A Genome-Scale Investigation of How Sequence, Function, and Tree-Based Gene Properties Influence Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016 , 8, 2565-80	3.9	37
13	Testing heterogeneous base composition as potential cause for conflicting phylogenetic signal between mitochondrial and nuclear DNA in the land snail genus <i>Theba</i> Risso 1826 (Gastropoda: Stylommatophora: Helicoidea). <i>Organisms Diversity and Evolution</i> , 2016 , 16, 835-846	1.7	5
12	Relative benefits of amino-acid, codon, degeneracy, DNA, and purine-pyrimidine character coding for phylogenetic analyses of exons. <i>Journal of Systematics and Evolution</i> , 2017 , 55, 85-109	2.9	18

11	Phylogenetic position of the coral symbiont <i>Ostreobium</i> (Ulvophyceae) inferred from chloroplast genome data. <i>Journal of Phycology</i> , 2017 , 53, 790-803	3	17
10	Biogeography of the freshwater fishes of the Guianas using a partitioned parsimony analysis of endemism with reappraisal of ecoregional boundaries. <i>Cladistics</i> , 2019 , 35, 106-124	3.5	9
9	Phylogenomics of Auchenorrhyncha (Insecta: Hemiptera) using transcriptomes: examining controversial relationships via degeneracy coding and interrogation of gene conflict. <i>Systematic Entomology</i> , 2020 , 45, 85-113	3.4	16
8	Whole genome phylogeny of <i>Gallus</i> : introgression and data-type effects. <i>Avian Research</i> , 2020 , 11,	2	10
7	A multigene phylogeny and timeline for Trichoptera (Insecta). <i>Systematic Entomology</i> , 2020 , 45, 670-686	3.4	16
6	Inferring the Deep Past from Molecular Data. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	6
5	Phylogenetic model evaluation. <i>Methods in Molecular Biology</i> , 2008 , 452, 331-64	1.4	30
4	Sources of signal in 62 protein-coding nuclear genes for higher-level phylogenetics of arthropods. <i>PLoS ONE</i> , 2011 , 6, e23408	3.7	40
3	The Interaction between Base Compositional Heterogeneity and Among-Site Rate Variation in Models of Molecular Evolution. 2013 , 2013, 1-8		3
2	Fuzzy Genome Sequence Assembly for Single and Environmental Genomes. <i>Studies in Fuzziness and Soft Computing</i> , 2009 , 19-44	0.7	
1	Protein Structure, Models of Sequence Evolution, and Data Type Effects in Phylogenetic Analyses of Mitochondrial Data: A Case Study in Birds. <i>Diversity</i> , 2021 , 13, 555	2.5	2