

# Concatenation versus coalescence versus $\hat{\rho}$ -concatenation

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Phylogenetics: Bats United, Microbats Divided. <i>Current Biology</i> , 2013, 23, R999-R1001.	1.8	19
2	Reply to Gatesy and Springer: The multispecies coalescent model can effectively handle recombination and gene tree heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1180.	3.3	26
3	Phylogenetic relationships and character evolution in <i>Heuchera</i> (Saxifragaceae) on the basis of multiple nuclear loci. <i>American Journal of Botany</i> , 2014, 101, 1532-1550.	0.8	28
4	Land plant origins and coalescence confusion. <i>Trends in Plant Science</i> , 2014, 19, 267-269.	4.3	61
5	Phylogenetic analysis at deep timescales: Unreliable gene trees, bypassed hidden support, and the coalescence/concatalescence conundrum. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 231-266.	1.2	286
6	An Introduction to Supertree Construction (and Partitioned Phylogenetic Analyses) with a View Toward the Distinction Between Gene Trees and Species Trees. , 2014, , 49-76.		10
7	A multilocus phylogeny reveals deep lineages within African galagids (Primates: Galagidae). <i>BMC Evolutionary Biology</i> , 2014, 14, 72.	3.2	80
8	Dubious resolution and support from published sparse supermatrices: The importance of thorough tree searches. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 334-348.	1.2	26
9	Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer. <i>BMC Genomics</i> , 2015, 16, S1.	1.2	57
10	The BPP program for species tree estimation and species delimitation. <i>Environmental Epigenetics</i> , 2015, 61, 854-865.	0.9	568
11	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015, 1360, 36-53.	1.8	165
12	Likelihood-based tree reconstruction on a concatenation of aligned sequence data sets can be statistically inconsistent. <i>Theoretical Population Biology</i> , 2015, 100, 56-62.	0.5	218
13	Disentangling the complex evolutionary history of the Western Palearctic blue tits ( <i>Cyanistes</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf isolation. <i>Molecular Ecology</i> , 2015, 24, 2477-2494.	2.0	39
14	Genes with minimal phylogenetic information are problematic for coalescent analyses when gene tree estimation is biased. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 63-71.	1.2	104
15	Multilocus Species Trees Show the Recent Adaptive Radiation of the Mimetic Heliconius Butterflies. <i>Systematic Biology</i> , 2015, 64, 505-524.	2.7	204
16	Convergence of multiple markers and analysis methods defines the genetic distinctiveness of cryptic pitvipers. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 266-279.	1.2	9
17	On the Robustness to Gene Tree Estimation Error (or lack thereof) of Coalescent-Based Species Tree Methods. <i>Systematic Biology</i> , 2015, 64, 663-676.	2.7	161
18	Phylogenetic analysis of <i>scp</i> RAD data: examining the influence of gene genealogy conflict on analysis of concatenated data. <i>Cladistics</i> , 2016, 32, 672-681.	1.5	39

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19	Incomplete Lineage Sorting in Mammalian Phylogenomics. <i>Systematic Biology</i> , 2017, 66, syw082.	2.7	88
20	Accounting for Uncertainty in Gene Tree Estimation: Summary-Coalescent Species Tree Inference in a Challenging Radiation of Australian Lizards. <i>Systematic Biology</i> , 2017, 66, syw089.	2.7	56
21	Ancestral Gene Flow and Parallel Organellar Genome Capture Result in Extreme Phylogenomic Discord in a Lineage of Angiosperms. <i>Systematic Biology</i> , 2017, 66, syw083.	2.7	132
22	Consensus Methods, <i>Phylogenetic.</i> , 2016, , 341-346.		0
23	A performance study of the impact of recombination on species tree analysis. <i>BMC Genomics</i> , 2016, 17, 785.	1.2	15
24	Mammal madness: is the mammal tree of life not yet resolved?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150140.	1.8	216
25	Analysis of a Rapid Evolutionary Radiation Using Ultraconserved Elements: Evidence for a Bias in Some Multispecies Coalescent Methods. <i>Systematic Biology</i> , 2016, 65, 612-627.	2.7	137
26	Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. <i>Systematic Biology</i> , 2016, 65, 381-396.	2.7	107
27	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 447-462.	1.2	321
28	The gene tree delusion. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 1-33.	1.2	259
29	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2101-2114.	3.5	371
30	Assessing the potential of RAD-sequencing to resolve phylogenetic relationships within species radiations: The fly genus <i>Chiastocheta</i> (Diptera: Anthomyiidae) as a case study. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 189-198.	1.2	18
31	Systematics and biogeography of the <i>Automolus infuscatus</i> complex (Aves; Furnariidae): Cryptic diversity reveals western Amazonia as the origin of a transcontinental radiation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 503-515.	1.2	22
32	Talpid Mole Phylogeny Unites Shrew Moles and Illuminates Overlooked Cryptic Species Diversity. <i>Molecular Biology and Evolution</i> , 2017, 34, 78-87.	3.5	36
33	Resolution of a concatenation/coalescence kerfuffle: partitioned coalescence support and a robust family-level tree for Mammalia. <i>Cladistics</i> , 2017, 33, 295-332.	1.5	70
34	Phylogenomics of tubeworms (Siboglinidae, Annelida) and comparative performance of different reconstruction methods. <i>Zoologica Scripta</i> , 2017, 46, 200-213.	0.7	33
35	Phylogenomic analyses reveal a deep history of hybridization and polyploidy in the Neotropical genus <i>Lachemilla</i> (Rosaceae). <i>New Phytologist</i> , 2018, 218, 1668-1684.	3.5	141
36	Bayesian Divergence-Time Estimation with Genome-Wide Single-Nucleotide Polymorphism Data of Sea Catfishes (Ariidae) Supports Miocene Closure of the Panamanian Isthmus. <i>Systematic Biology</i> , 2018, 67, 681-699.	2.7	137

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37	Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (Vitaceae). <i>Cladistics</i> , 2018, 34, 57-77.	1.5	44
38	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. <i>Systematic Biology</i> , 2018, 67, 400-412.	2.7	85
39	Pinniped Diphly and Bat Triphyly: More Homology Errors Drive Conflicts in the Mammalian Tree. <i>Journal of Heredity</i> , 2018, 109, 297-307.	1.0	13
40	Incomplete lineage sorting impacts the inference of macroevolutionary regimes from molecular phylogenies when concatenation is employed: An analysis based on Cetacea. <i>Ecology and Evolution</i> , 2018, 8, 6965-6971.	0.8	5
41	Delimiting Coalescence Genes (C-Genes) in Phylogenomic Data Sets. <i>Genes</i> , 2018, 9, 123.	1.0	30
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49	Parameters of Classification: <i>Ordo Ab Chao</i> . , 2020, , 153-212.		0
51	Modern Artificial Methods and Raw Data. , 2020, , 215-236.		0
52	How to Study Classification. , 2020, , 273-286.		0
53	How to Study Classification. , 2020, , 287-350.		0
54	Further Myths and More Misunderstandings. , 2020, , 396-429.		0
56	Introduction: Carving Nature at Its Joints, or Why Birds Are Not Dinosaurs and Men Are Not Apes. , 2020, , 1-10.		0
57	Intragenic Conflict in Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2020, 37, 3380-3388.	3.5	5
59	The Separation of Classification and Phylogenetics. , 2020, , 369-395.		0

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62	Beyond Classification: How to Study Phylogeny. , 2020, , 353-368.		0
64	How to Study Classification: Consensus Techniques and General Classifications. , 2020, , 237-252.		0
65	How to Study Classification: "Total Evidence"™ vs. "Consensus"™, Character Congruence vs. Taxonomic Congruence, Simultaneous Analysis vs. Partitioned Data. , 2020, , 253-272.		0
68	From Summary Statistics to Gene Trees: Methods for Inferring Positive Selection. Trends in Genetics, 2020, 36, 243-258.	2.9	28
69	Phylogenomics and the Genetic Architecture of the Placental Mammal Radiation. Annual Review of Animal Biosciences, 2021, 9, 29-53.	3.6	32
70	Gene Tree Discord, Simplex Plots, and Statistical Tests under the Coalescent. Systematic Biology, 2022, 71, 929-942.	2.7	14
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72	Rampant Genome-Wide Admixture across the <i>Heliconius</i> Radiation. Genome Biology and Evolution, 2021, 13, .	1.1	31
73	Defining Coalescent Genes: Theory Meets Practice in Organelle Phylogenomics. Systematic Biology, 2022, 71, 476-489.	2.7	47
75	Gene Tree Estimation Error with Ultraconserved Elements: An Empirical Study on <i>Pseudapis</i> Bees. Systematic Biology, 2021, 70, 803-821.	2.7	25
82	Concatenation Analyses in the Presence of Incomplete Lineage Sorting. PLOS Currents, 2015, 7, .	1.4	31
83	Can Single Protein and Protein Family Phylogenies be Resolved Better?. Journal of Phylogenetics & Evolutionary Biology, 2015, 03, .	0.2	4
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91	Phylogenetic Relationships Within the Hyper-Diverse Genus <i>Eugenia</i> (Myrtaceae: Myrteae) Based on Target Enrichment Sequencing. Frontiers in Plant Science, 2021, 12, 759460.	1.7	5
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