John A Rhodes

List of Publications by Year
in descending order

44 papers	1,430 citations	471509 17 h-index	361022 35 g-index
47 all docs	47 docs citations	47 times ranked	888 citing authors

#	ARTICLE	IF	CITATIONS
1	Testing Multispecies Coalescent Simulators Using Summary Statistics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1613-1618.	3.0	2
2	Gene Tree Discord, Simplex Plots, and Statistical Tests under the Coalescent. Systematic Biology, 2022, 71, 929-942.	5.6	14
3	Identifiability of species network topologies from genomic sequences using the logDet distance. Journal of Mathematical Biology, 2022, 84, 35.	1.9	6
4	MSCquartets 1.0: quartet methods for species trees and networks under the multispecies coalescent model in R. Bioinformatics, 2021, 37, 1766-1768.	4.1	24
5	Parameter Identifiability for a Profile Mixture Model of Protein Evolution. Journal of Computational Biology, 2021, 28, 570-586.	1.6	4
6	Topological Metrizations of Trees, and New Quartet Methods of Tree Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2107-2118.	3.0	15
7	Inferring Metric Trees from Weighted Quartets via an Intertaxon Distance. Bulletin of Mathematical Biology, 2020, 82, 97.	1.9	4
8	Species Tree Inference from Genomic Sequences Using the Log-Det Distance. SIAM Journal on Applied Algebra and Geometry, 2019, 3, 107-127.	1.4	16
9	NANUQ: a method for inferring species networks from gene trees under the coalescent model. Algorithms for Molecular Biology, 2019, 14, 24.	1.2	36
10	Algebraic Methods in Phylogenetics. Bulletin of Mathematical Biology, 2019, 81, 313-315.	1.9	1
11	Hypothesis testing near singularities and boundaries. Electronic Journal of Statistics, 2019, 13, 2150-2193.	0.7	15
12	Species Tree Inference from Gene Splits by Unrooted STAR Methods. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 337-342.	3.0	32
13	Split Probabilities and Species Tree Inference Under the Multispecies Coalescent Model. Bulletin of Mathematical Biology, 2018, 80, 64-103.	1.9	4
14	Split Scores: A Tool to Quantify Phylogenetic Signal in Genome-Scale Data. Systematic Biology, 2017, 66, syw103.	5.6	21
15	Phylogenetic trees and Euclidean embeddings. Journal of Mathematical Biology, 2017, 74, 99-111.	1.9	6
16	Statistically Consistent k-mer Methods for Phylogenetic Tree Reconstruction. Journal of Computational Biology, 2017, 24, 153-171.	1.6	19
17	There are no caterpillars in a wicked forest. Theoretical Population Biology, 2015, 105, 17-23.	1.1	10
18	Parameter Identifiability of Discrete Bayesian Networks with Hidden Variables. Journal of Causal Inference, 2015, 3, 189-205.	1.2	2

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19	Tensors of nonnegative rank two. Linear Algebra and Its Applications, 2015, 473, 37-53.	0.9	17
20	A Semialgebraic Description of the General Markov Model on Phylogenetic Trees. SIAM Journal on Discrete Mathematics, 2014, 28, 736-755.	0.8	12
21	Tensor Rank, Invariants, Inequalities, and Applications. SIAM Journal on Matrix Analysis and Applications, 2013, 34, 1014-1045.	1.4	58
22	Species Tree Inference by the STAR Method and Its Generalizations. Journal of Computational Biology, 2013, 20, 50-61.	1.6	17
23	When Do Phylogenetic Mixture Models Mimic Other Phylogenetic Models?. Systematic Biology, 2012, 61, 1049-1059.	5.6	12
24	Identifiability of Large Phylogenetic Mixture Models. Bulletin of Mathematical Biology, 2012, 74, 212-231.	1.9	34
25	Identifiability of Two-Tree Mixtures for Group-Based Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 710-722.	3.0	28
26	Determining species tree topologies from clade probabilities under the coalescent. Journal of Theoretical Biology, 2011, 289, 96-106.	1.7	26
27	Identifying the rooted species tree from the distribution of unrooted gene trees under the coalescent. Journal of Mathematical Biology, 2011, 62, 833-862.	1.9	124
28	Parameter identifiability in a class of random graph mixture models. Journal of Statistical Planning and Inference, 2011, 141, 1719-1736.	0.6	22
29	Estimating trees from filtered data: Identifiability of models for morphological phylogenetics. Journal of Theoretical Biology, 2010, 263, 108-119.	1.7	17
30	A concise proof of Kruskal's theorem on tensor decomposition. Linear Algebra and Its Applications, 2010, 432, 1818-1824.	0.9	30
31	Trees, Fast and Accurate. Science, 2010, 327, 1334-1335.	12.6	5
32	The Identifiability of Covarion Models in Phylogenetics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 76-88.	3.0	19
33	Identifiability of parameters in latent structure models with many observed variables. Annals of Statistics, 2009, 37, .	2.6	278
34	Phylogenetic ideals and varieties for the general Markov model. Advances in Applied Mathematics, 2008, 40, 127-148.	0.7	83
35	Identifying evolutionary trees and substitution parameters for the general Markov model with invariable sites. Mathematical Biosciences, 2008, 211, 18-33.	1.9	41
36	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. Advances in Applied Probability, 2008, 40, 229-249.	0.7	63

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37	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. Advances in Applied Probability, 2008, 40, 229-249.	0.7	17
38	Phylogenetic invariants for stationary base composition. Journal of Symbolic Computation, 2006, 41, 138-150.	0.8	10
39	The Identifiability of Tree Topology for Phylogenetic Models, Including Covarion and Mixture Models. Journal of Computational Biology, 2006, 13, 1101-1113.	1.6	72
40	Title is missing!. Applied Mathematics Research EXpress, 2004, 2004, 107.	1.0	14
41	Relativistic velocity space, Wigner rotation, and Thomas precession. American Journal of Physics, 2004, 72, 943-960.	0.7	75
42	Rationality theorems for Hecke operators on GLn. Journal of Number Theory, 2003, 102, 278-297.	0.4	3
43	Phylogenetic invariants for the general Markov model of sequence mutation. Mathematical Biosciences, 2003, 186, 113-144.	1.9	71
44	Automorphic Forms, Definite Quaternion Algebras, and Atkinâ€"Lehner Theory on Trees. Journal of Number Theory, 2001, 86, 210-243.	0.4	1