

# John A Rhodes

## List of Publications by Year in descending order

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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	Identifiability of parameters in latent structure models with many observed variables. <i>Annals of Statistics</i> , 2009, 37, .	2.6	278
2	Identifying the rooted species tree from the distribution of unrooted gene trees under the coalescent. <i>Journal of Mathematical Biology</i> , 2011, 62, 833-862.	1.9	124
3	Phylogenetic ideals and varieties for the general Markov model. <i>Advances in Applied Mathematics</i> , 2008, 40, 127-148.	0.7	83
4	Relativistic velocity space, Wigner rotation, and Thomas precession. <i>American Journal of Physics</i> , 2004, 72, 943-960.	0.7	75
5	The Identifiability of Tree Topology for Phylogenetic Models, Including Covarion and Mixture Models. <i>Journal of Computational Biology</i> , 2006, 13, 1101-1113.	1.6	72
6	Phylogenetic invariants for the general Markov model of sequence mutation. <i>Mathematical Biosciences</i> , 2003, 186, 113-144.	1.9	71
7	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. <i>Advances in Applied Probability</i> , 2008, 40, 229-249.	0.7	63
8	Tensor Rank, Invariants, Inequalities, and Applications. <i>SIAM Journal on Matrix Analysis and Applications</i> , 2013, 34, 1014-1045.	1.4	58
9	Identifying evolutionary trees and substitution parameters for the general Markov model with invariable sites. <i>Mathematical Biosciences</i> , 2008, 211, 18-33.	1.9	41
10	NANUQ: a method for inferring species networks from gene trees under the coalescent model. <i>Algorithms for Molecular Biology</i> , 2019, 14, 24.	1.2	36
11	Identifiability of Large Phylogenetic Mixture Models. <i>Bulletin of Mathematical Biology</i> , 2012, 74, 212-231.	1.9	34
12	Species Tree Inference from Gene Splits by Unrooted STAR Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 337-342.	3.0	32
13	A concise proof of Kruskal's theorem on tensor decomposition. <i>Linear Algebra and Its Applications</i> , 2010, 432, 1818-1824.	0.9	30
14	Identifiability of Two-Tree Mixtures for Group-Based Models. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 710-722.	3.0	28
15	Determining species tree topologies from clade probabilities under the coalescent. <i>Journal of Theoretical Biology</i> , 2011, 289, 96-106.	1.7	26
16	MSCquartets 1.0: quartet methods for species trees and networks under the multispecies coalescent model in R. <i>Bioinformatics</i> , 2021, 37, 1766-1768.	4.1	24
17	Parameter identifiability in a class of random graph mixture models. <i>Journal of Statistical Planning and Inference</i> , 2011, 141, 1719-1736.	0.6	22
18	Split Scores: A Tool to Quantify Phylogenetic Signal in Genome-Scale Data. <i>Systematic Biology</i> , 2017, 66, syw103.	5.6	21

#	ARTICLE	IF	CITATIONS
19	The Identifiability of Covarion Models in Phylogenetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 76-88.	3.0	19
20	Statistically Consistent $k$ -mer Methods for Phylogenetic Tree Reconstruction. <i>Journal of Computational Biology</i> , 2017, 24, 153-171.	1.6	19
21	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. <i>Advances in Applied Probability</i> , 2008, 40, 229-249.	0.7	17
22	Estimating trees from filtered data: Identifiability of models for morphological phylogenetics. <i>Journal of Theoretical Biology</i> , 2010, 263, 108-119.	1.7	17
23	Species Tree Inference by the STAR Method and Its Generalizations. <i>Journal of Computational Biology</i> , 2013, 20, 50-61.	1.6	17
24	Tensors of nonnegative rank two. <i>Linear Algebra and Its Applications</i> , 2015, 473, 37-53.	0.9	17
25	Species Tree Inference from Genomic Sequences Using the Log-Det Distance. <i>SIAM Journal on Applied Algebra and Geometry</i> , 2019, 3, 107-127.	1.4	16
26	Topological Metrizations of Trees, and New Quartet Methods of Tree Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 2107-2118.	3.0	15
27	Hypothesis testing near singularities and boundaries. <i>Electronic Journal of Statistics</i> , 2019, 13, 2150-2193.	0.7	15
28	Title is missing!. <i>Applied Mathematics Research EXpress</i> , 2004, 2004, 107.	1.0	14
29	Gene Tree Discord, Simplex Plots, and Statistical Tests under the Coalescent. <i>Systematic Biology</i> , 2022, 71, 929-942.	5.6	14
30	When Do Phylogenetic Mixture Models Mimic Other Phylogenetic Models?. <i>Systematic Biology</i> , 2012, 61, 1049-1059.	5.6	12
31	A Semialgebraic Description of the General Markov Model on Phylogenetic Trees. <i>SIAM Journal on Discrete Mathematics</i> , 2014, 28, 736-755.	0.8	12
32	Phylogenetic invariants for stationary base composition. <i>Journal of Symbolic Computation</i> , 2006, 41, 138-150.	0.8	10
33	There are no caterpillars in a wicked forest. <i>Theoretical Population Biology</i> , 2015, 105, 17-23.	1.1	10
34	Phylogenetic trees and Euclidean embeddings. <i>Journal of Mathematical Biology</i> , 2017, 74, 99-111.	1.9	6
35	Identifiability of species network topologies from genomic sequences using the logDet distance. <i>Journal of Mathematical Biology</i> , 2022, 84, 35.	1.9	6
36	Trees, Fast and Accurate. <i>Science</i> , 2010, 327, 1334-1335.	12.6	5

#	ARTICLE	IF	CITATIONS
37	Split Probabilities and Species Tree Inference Under the Multispecies Coalescent Model. <i>Bulletin of Mathematical Biology</i> , 2018, 80, 64-103.	1.9	4
38	Inferring Metric Trees from Weighted Quartets via an Intertaxon Distance. <i>Bulletin of Mathematical Biology</i> , 2020, 82, 97.	1.9	4
39	Parameter Identifiability for a Profile Mixture Model of Protein Evolution. <i>Journal of Computational Biology</i> , 2021, 28, 570-586.	1.6	4
40	Rationality theorems for Hecke operators on $GL_n$ . <i>Journal of Number Theory</i> , 2003, 102, 278-297.	0.4	3
41	Parameter Identifiability of Discrete Bayesian Networks with Hidden Variables. <i>Journal of Causal Inference</i> , 2015, 3, 189-205.	1.2	2
42	Testing Multispecies Coalescent Simulators Using Summary Statistics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1613-1618.	3.0	2
43	Automorphic Forms, Definite Quaternion Algebras, and Atkin's Lehner Theory on Trees. <i>Journal of Number Theory</i> , 2001, 86, 210-243.	0.4	1
44	Algebraic Methods in Phylogenetics. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 313-315.	1.9	1