

James H Degnan

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

3,432
citations

623734

14
h-index

552781

26
g-index

30
all docs

30
docs citations

30
times ranked

3930
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene tree discordance, phylogenetic inference and the multispecies coalescent. <i>Trends in Ecology and Evolution</i> , 2009, 24, 332-340.	8.7	1,500
2	Discordance of Species Trees with Their Most Likely Gene Trees. <i>PLoS Genetics</i> , 2006, 2, e68.	3.5	761
3	GENE TREE DISTRIBUTIONS UNDER THE COALESCENT PROCESS. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 24-37.	2.3	296
4	Properties of Consensus Methods for Inferring Species Trees from Gene Trees. <i>Systematic Biology</i> , 2009, 58, 35-54.	5.6	135
5	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
6	Gene tree distributions under the coalescent process. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 24-37.	2.3	106
7	Modeling Hybridization Under the Network Multispecies Coalescent. <i>Systematic Biology</i> , 2018, 67, 786-799.	5.6	97
8	GENE TREE DISTRIBUTIONS UNDER THE COALESCENT PROCESS. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 24.	2.3	91
9	Anomalous Unrooted Gene Trees. <i>Systematic Biology</i> , 2013, 62, 574-590.	5.6	64
10	The probability distribution of ranked gene trees on a species tree. <i>Mathematical Biosciences</i> , 2012, 235, 45-55.	1.9	44
11	Displayed Trees Do Not Determine Distinguishability Under the Network Multispecies Coalescent. <i>Systematic Biology</i> , 2017, 66, syw097.	5.6	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	Hybrid-Lambda: simulation of multiple merger and Kingman gene genealogies in species networks and species trees. <i>BMC Bioinformatics</i> , 2015, 16, 292.	2.6	30
14	Genomics and genome-wide association studies: An integrative approach to expression QTL mapping. <i>Genomics</i> , 2008, 92, 129-133.	2.9	18
15	Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?. <i>Systematic Biology</i> , 2016, 65, 628-639.	5.6	18
16	An initiative to implement immediate postpartum long-acting reversible contraception in rural New Mexico. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, S911.e1-S911.e7.	1.3	18
17	A Characterization of the Set of Species Trees that Produce Anomalous Ranked Gene Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1558-1568.	3.0	15
18	Inferring rooted species trees from unrooted gene trees using approximate Bayesian computation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 13-24.	2.7	12

#	ARTICLE	IF	CITATIONS
19	There are no caterpillars in a wicked forest. <i>Theoretical Population Biology</i> , 2015, 105, 17-23.	1.1	10
20	Performance of Matrix Representation with Parsimony for Inferring Species from Gene Trees. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.6	8
21	PRANC: ML species tree estimation from the ranked gene trees under coalescence. <i>Bioinformatics</i> , 2020, 36, 4819-4821.	4.1	7
22	Split Probabilities and Species Tree Inference Under the Multispecies Coalescent Model. <i>Bulletin of Mathematical Biology</i> , 2018, 80, 64-103.	1.9	4
23	Probabilities of Unranked and Ranked Anomaly Zones under Birth-Death Models. <i>Molecular Biology and Evolution</i> , 2020, 37, 1480-1494.	8.9	3
24	Evaluating variations on the STAR algorithm for relative efficiency and sample sizes needed to reconstruct species trees. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 262-72.	0.7	2
25	Meng and Kubatko (2009): Modeling hybridization with coalescence. <i>Theoretical Population Biology</i> , 2020, 133, 36-37.	1.1	1
26	Statistical inconsistency of the unrooted minimize deep coalescence criterion. <i>PLoS ONE</i> , 2021, 16, e0251107.	2.5	1
27	EVALUATING VARIATIONS ON THE STAR ALGORITHM FOR RELATIVE EFFICIENCY AND SAMPLE SIZES NEEDED TO RECONSTRUCT SPECIES TREES. , 2012, , .		1
28	Heuristics for unrooted, unranked, and ranked anomaly zones under birth-death models. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107162.	2.7	0
29	Trying out a million genes to find the perfect pair with <i>RTIST</i> . <i>Bioinformatics</i> , 2022, 38, 3565-3573.	4.1	0