

Oliver Eulenstein

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

632
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759233

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38
docs citations

38
times ranked

463
citing authors

#	ARTICLE	IF	CITATIONS
1	RF-Net 2: fast inference of virus reassortment and hybridization networks. <i>Bioinformatics</i> , 2022, 38, 2144-2152.	4.1	5
2	Quartet-based inference is statistically consistent under the unified duplication-loss-coalescence model. <i>Bioinformatics</i> , 2021, 37, 4064-4074.	4.1	21
3	Taming the Duplication-Loss-Coalescence Model with Integer Linear Programming. <i>Journal of Computational Biology</i> , 2021, 28, 758-773.	1.6	2
4	Exact median-tree inference for unrooted reconciliation costs. <i>BMC Evolutionary Biology</i> , 2020, 20, 136.	3.2	0
5	Finding orthologous gene blocks in bacteria: the computational hardness of the problem and novel methods to address it. <i>Bioinformatics</i> , 2020, 36, i668-i674.	4.1	0
6	The Unconstrained Diameters of the Duplication-Loss Cost and the Loss Cost. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	0
7	Consensus of all Solutions for Intractable Phylogenetic Tree Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	3
8	Tracing the ancestry of operons in bacteria. <i>Bioinformatics</i> , 2019, 35, 2998-3004.	4.1	7
9	Cophenetic Median Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1459-1470.	3.0	0
10	Efficient Local Search for Euclidean Path-Difference Median Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1374-1385.	3.0	1
11	Computing Manhattan Path-Difference Median Trees: A Practical Local Search Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1063-1076.	3.0	1
12	Robinson-Foulds Reticulation Networks. , 2019, , .		6
13	Bijjective Diameters of Gene Tree Parsimony Costs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1-1.	3.0	2
14	Unconstrained Diameters for Deep Coalescence. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1002-1012.	3.0	2
15	Synthesizing large-scale species trees using the strict consensus approach. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1740002.	0.8	3
16	Phylogenetic Tree Reconciliation: Mean Values for Fixed Gene Trees. <i>Lecture Notes in Computer Science</i> , 2017, , 234-245.	1.3	0
17	Manhattan Path-Difference Median Trees. , 2016, , .		2
18	Robinson-Foulds Median Trees. , 2016, , .		0

#	ARTICLE	IF	CITATIONS
19	Consensus properties and their large-scale applications for the gene duplication problem. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1642005.	0.8	5
20	Path-Difference Median Trees. <i>Lecture Notes in Computer Science</i> , 2016, , 211-223.	1.3	5
21	Gene Tree Diameter for Deep Coalescence. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 155-165.	3.0	5
22	Maximizing Deep Coalescence Cost. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 231-242.	3.0	12
23	Duplication Cost Diameters. <i>Lecture Notes in Computer Science</i> , 2014, , 212-223.	1.3	5
24	Unrooted Tree Reconciliation: A Unified Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 522-536.	3.0	39
25	EXACT SOLUTIONS FOR SPECIES TREE INFERENCE FROM DISCORDANT GENE TREES. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1342005.	0.8	21
26	Consensus properties for the deep coalescence problem and their application for scalable tree search. <i>BMC Bioinformatics</i> , 2012, 13, S12.	2.6	17
27	Invited: Reconciled gene trees and their applications. , 2011, , .		0
28	An ILP solution for the gene duplication problem. <i>BMC Bioinformatics</i> , 2011, 12, S14.	2.6	19
29	iGTP: A software package for large-scale gene tree parsimony analysis. <i>BMC Bioinformatics</i> , 2010, 11, 574.	2.6	79
30	Efficient genome-scale phylogenetic analysis under the duplication-loss and deep coalescence cost models. <i>BMC Bioinformatics</i> , 2010, 11, S42.	2.6	53
31	Robinson-Foulds Supertrees. <i>Algorithms for Molecular Biology</i> , 2010, 5, 18.	1.2	88
32	Triplet supertree heuristics for the tree of life. <i>BMC Bioinformatics</i> , 2009, 10, S8.	2.6	20
33	Groves of Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2009, 13, 139-167.	0.6	8
34	Improved Heuristics for Minimum-Flip Supertree Construction. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	1.2	32
35	The Shape of Supertrees to Come: Tree Shape Related Properties of Fourteen Supertree Methods. <i>Systematic Biology</i> , 2005, 54, 419-431.	5.6	88
36	Performance of Flip Supertree Construction with a Heuristic Algorithm. <i>Systematic Biology</i> , 2004, 53, 299-308.	5.6	57