Ran Libeskind-Hadas

List of Publications by Year in descending order

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PAN LIBESKIND-HADAS

#	Article	IF	CITATIONS
1	Jane: a new tool for the cophylogeny reconstruction problem. Algorithms for Molecular Biology, 2010, 5, 16.	1.2	335
2	An Extreme Case of Plant–Insect Codiversification: Figs and Fig-Pollinating Wasps. Systematic Biology, 2012, 61, 1029-1047.	5.6	319
3	Discordant phylogenies suggest repeated host shifts in the Fusarium–Euwallacea ambrosia beetle mutualism. Fungal Genetics and Biology, 2015, 82, 277-290.	2.1	121
4	Increasing women's participation in computing at Harvey Mudd College. ACM Inroads, 2012, 3, 55-64.	0.6	105
5	Pareto-optimal phylogenetic tree reconciliation. Bioinformatics, 2014, 30, i87-i95.	4.1	59
6	On the Computational Complexity of the Reticulate Cophylogeny Reconstruction Problem. Journal of Computational Biology, 2009, 16, 105-117.	1.6	57
7	eMPRess: a systematic cophylogeny reconciliation tool. Bioinformatics, 2021, 37, 2481-2482.	4.1	53
8	Invasive Asian Fusarium – Euwallacea ambrosia beetle mutualists pose a serious threat to forests, urban landscapes and the avocado industry. Phytoparasitica, 2016, 44, 435-442.	1.2	52
9	On edge-disjoint spanning trees in hypercubes. Information Processing Letters, 1999, 70, 13-16.	0.6	30
10	Origin-based fault-tolerant routing in the mesh. Future Generation Computer Systems, 1995, 11, 603-615.	7.5	27
11	A first course in computing with applications to biology. Briefings in Bioinformatics, 2013, 14, 610-617.	6.5	23
12	Event-Based Cophylogenetic Comparative Analysis. , 2014, , 465-480.		13
13	Hierarchical clustering of maximum parsimony reconciliations. BMC Bioinformatics, 2019, 20, 612.	2.6	13
14	Multiple Optimal Reconciliations Under the Duplication-Loss-Coalescence Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2144-2156.	3.0	11
15	The Computational Complexity of Motion Planning. SIAM Review, 2003, 45, 543-557.	9.5	9
16	Evaluating a breadth-first cs 1 for scientists. SIGCSE Bulletin, 2008, 40, 266-270.	0.1	9
17	Computing the Diameter of the Space of Maximum Parsimony Reconciliations in the Duplication-Transfer-Loss Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 14-22.	3.0	9
18	An efficient exact algorithm for computing all pairwise distances between reconciliations in the duplication-transfer-loss model. BMC Bioinformatics, 2019, 20, 636.	2.6	8

#	Article	IF	CITATIONS
19	On the computational complexity of the maximum parsimony reconciliation problem in the duplication-loss-coalescence model. Algorithms for Molecular Biology, 2017, 12, 6.	1.2	7
20	DTL reconciliation repair. BMC Bioinformatics, 2017, 18, 76.	2.6	7
21	Inferring Pareto-optimal reconciliations across multiple event costs under the duplication-loss-coalescence model. BMC Bioinformatics, 2019, 20, 639.	2.6	7
22	Reconciliation Reconsidered: In Search of a Most Representative Reconciliation in the Duplication-Transfer-Loss Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	3.0	5
23	A Polynomial-Time Algorithm for Minimizing the Deep Coalescence Cost for Level-1 Species Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2642-2653.	3.0	5
24	Competitive Analysis of Online Traffic Grooming in WDM Rings. IEEE/ACM Transactions on Networking, 2008, 16, 984-997.	3.8	3
25	Tree Reconciliation Methods for Host-Symbiont Cophylogenetic Analyses. Life, 2022, 12, 443.	2.4	3
26	Maximum parsimony reconciliation in the DTLOR model. BMC Bioinformatics, 2021, 22, 394.	2.6	2
27	Approximation Algorithms: Good Solutions to Hard Problems. American Mathematical Monthly, 1995, 102, 57.	0.3	0
28	Sorting in Parallel. American Mathematical Monthly, 1998, 105, 238-245.	0.3	0
29	Sorting in Parallel. American Mathematical Monthly, 1998, 105, 238.	0.3	0