

Pawel Gorecki

List of Publications by Year in descending order

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50
papers

1,912
citations

932766

10
h-index

329751

37
g-index

50
all docs

50
docs citations

50
times ranked

2768
citing authors

#	ARTICLE	IF	CITATIONS
1	Embedding gene trees into phylogenetic networks by conflict resolution algorithms. Algorithms for Molecular Biology, 2022, 17, 11.	0.3	3
2	Taming the Duplication-Loss-Coalescence Model with Integer Linear Programming. Journal of Computational Biology, 2021, 28, 758-773.	0.8	2
3	Novel genomic duplication models through integer linear programming. , 2021, , .		0
4	Exact median-tree inference for unrooted reconciliation costs. BMC Evolutionary Biology, 2020, 20, 136.	3.2	0
5	Minimizing genomic duplication episodes. Computational Biology and Chemistry, 2020, 89, 107260.	1.1	3
6	Integer Linear Programming Formulation for the Unified Duplication-Loss-Coalescence Model. Lecture Notes in Computer Science, 2020, , 229-242.	1.0	0
7	The Unconstrained Diameters of the Duplication-Loss Cost and the Loss Cost. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	0
8	Consensus of all Solutions for Intractable Phylogenetic Tree Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	3
9	Mathematical properties of the gene duplication cost. Discrete Applied Mathematics, 2019, 258, 114-122.	0.5	0
10	Credibility of Evolutionary Events in Gene Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 713-726.	1.9	2
11	Feasibility Algorithms for the Duplication-Loss Cost. Lecture Notes in Computer Science, 2019, , 206-218.	1.0	0
12	High-Throughput BCR Sequencing and Single-Cell Transcriptomics Reveal Distinct Transcriptional Profiles Associated with Subclonal Evolution of Follicular Lymphoma. Blood, 2019, 134, 298-298.	0.6	1
13	Bijjective Diameters of Gene Tree Parsimony Costs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1-1.	1.9	2
14	Efficient Algorithms for Genomic Duplication Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1-1.	1.9	8
15	Inferring gene-species assignments in the presence of horizontal gene transfer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1-1.	1.9	5
16	Inferring time-consistent and well-supported horizontal gene transfers. , 2018, , .		2
17	Phylogenetic Consensus for Exact Median Trees. , 2018, , .		2
18	Minimizing the deep coalescence cost. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840021.	0.3	1

#	ARTICLE	IF	CITATIONS
19	Locus-aware decomposition of gene trees with respect to polytomous species trees. Algorithms for Molecular Biology, 2018, 13, 11.	0.3	1
20	Inferring duplication episodes from unrooted gene trees. BMC Genomics, 2018, 19, 288.	1.2	5
21	Cophenetic Distances: A Near-Linear Time Algorithmic Framework. Lecture Notes in Computer Science, 2018, , 168-179.	1.0	0
22	Unconstrained Diameters for Deep Coalescence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1002-1012.	1.9	2
23	New Algorithms for the Genomic Duplication Problem. Lecture Notes in Computer Science, 2017, , 101-115.	1.0	2
24	Phylogenetic Tree Reconciliation: Mean Values for Fixed Gene Trees. Lecture Notes in Computer Science, 2017, , 234-245.	1.0	0
25	Genomic duplication problems for unrooted gene trees. BMC Genomics, 2016, 17, 15.	1.2	8
26	Bootstrapping Algorithms for Gene Duplication and Speciation Events. Lecture Notes in Computer Science, 2016, , 106-118.	1.0	1
27	Mean Values of Gene Duplication and Loss Cost Functions. Lecture Notes in Computer Science, 2016, , 189-199.	1.0	1
28	Gene Tree Diameter for Deep Coalescence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 155-165.	1.9	5
29	Fast Algorithms for Inferring Gene-Species Associations. Lecture Notes in Computer Science, 2015, , 36-47.	1.0	7
30	Unconstrained gene tree diameters for deep coalescence. , 2014, , .		3
31	DrML: Probabilistic Modeling of Gene Duplications. Journal of Computational Biology, 2014, 21, 89-98.	0.8	11
32	Maximizing Deep Coalescence Cost. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 231-242.	1.9	12
33	Refining discordant gene trees. BMC Bioinformatics, 2014, 15, S3.	1.2	4
34	Duplication Cost Diameters. Lecture Notes in Computer Science, 2014, , 212-223.	1.0	5
35	Unrooted Tree Reconciliation: A Unified Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 522-536.	1.9	39
36	EXACT SOLUTIONS FOR SPECIES TREE INFERENCE FROM DISCORDANT GENE TREES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1342005.	0.3	21

#	ARTICLE	IF	CITATIONS
37	Deep Coalescence Reconciliation with Unrooted Gene Trees: Linear Time Algorithms. Lecture Notes in Computer Science, 2012, , 531-542.	1.0	9
38	Inferring Evolutionary Scenarios in the Duplication, Loss and Horizontal Gene Transfer Model. Lecture Notes in Computer Science, 2012, , 83-105.	1.0	4
39	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. Science, 2012, 336, 1715-1719.	6.0	1,424
40	Algorithms: simultaneous error-correction and rooting for gene tree reconciliation and the gene duplication problem. BMC Bioinformatics, 2012, 13, S14.	1.2	28
41	GTP Supertrees from Unrooted Gene Trees: Linear Time Algorithms for NNI Based Local Searches. Lecture Notes in Computer Science, 2012, , 102-114.	1.0	11
42	A Robinson-Foulds Measure to Compare Unrooted Trees with Rooted Trees. Lecture Notes in Computer Science, 2012, , 115-126.	1.0	7
43	Maximum likelihood models and algorithms for gene tree evolution with duplications and losses. BMC Bioinformatics, 2011, 12, S15.	1.2	35
44	A Linear Time Algorithm for Error-Corrected Reconciliation of Unrooted Gene Trees. Lecture Notes in Computer Science, 2011, , 148-159.	1.0	14
45	H-trees: a Model of Evolutionary Scenarios with Horizontal Gene Transfer. Fundamenta Informaticae, 2010, 103, 105-128.	0.3	7
46	UIRec: a system for unrooted reconciliation. Bioinformatics, 2007, 23, 511-512.	1.8	31
47	Inferring phylogeny from whole genomes. Bioinformatics, 2007, 23, e116-e122.	1.8	34
48	DLS-trees: A model of evolutionary scenarios. Theoretical Computer Science, 2006, 359, 378-399.	0.5	115
49	On the Structure of Reconciliations. Lecture Notes in Computer Science, 2005, , 42-54.	1.0	5
50	Reconciliation problems for duplication, loss and horizontal gene transfer. , 2004, , .		27