

Mareike Fischer

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

233
citations

1163117

8
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1125743

13
g-index

41
all docs

41
docs citations

41
times ranked

209
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence length bounds for resolving a deep phylogenetic divergence. <i>Journal of Theoretical Biology</i> , 2009, 256, 247-252.	1.7	25
2	On the Maximum Parsimony Distance Between Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2016, 20, 87-113.	0.6	21
3	On Computing the Maximum Parsimony Score of a Phylogenetic Network. <i>SIAM Journal on Discrete Mathematics</i> , 2015, 29, 559-585.	0.8	17
4	Application of YOLOv4 for Detection and Motion Monitoring of Red Foxes. <i>Animals</i> , 2021, 11, 1723.	2.3	17
5	On the Complexity of Computing MP Distance Between Binary Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2017, 21, 573-604.	0.6	11
6	Maximum parsimony on subsets of taxa. <i>Journal of Theoretical Biology</i> , 2009, 260, 290-293.	1.7	10
7	Revisiting an Equivalence Between Maximum Parsimony and Maximum Likelihood Methods in Phylogenetics. <i>Bulletin of Mathematical Biology</i> , 2010, 72, 208-220.	1.9	10
8	On the minimum value of the Colless index and the bifurcating trees that achieve it. <i>Journal of Mathematical Biology</i> , 2020, 80, 1993-2054.	1.9	9
9	Reduction rules for the maximum parsimony distance on phylogenetic trees. <i>Theoretical Computer Science</i> , 2016, 646, 1-15.	0.9	8
10	On the quirks of maximum parsimony and likelihood on phylogenetic networks. <i>Journal of Theoretical Biology</i> , 2017, 417, 100-108.	1.7	8
11	Phylogenetic diversity and biodiversity indices on phylogenetic networks. <i>Mathematical Biosciences</i> , 2018, 298, 80-90.	1.9	8
12	Comparing the rankings obtained from two biodiversity indices: the Fair Proportion Index and the Shapley Value. <i>Journal of Theoretical Biology</i> , 2017, 430, 207-214.	1.7	7
13	How tree-based is my network? Proximity measures for unrooted phylogenetic networks. <i>Discrete Applied Mathematics</i> , 2020, 283, 98-114.	0.9	6
14	Classes of tree-based networks. <i>Visual Computing for Industry, Biomedicine, and Art</i> , 2020, 3, 12.	3.7	6
15	Hierarchical Structures in Livestock Trade Networks – A Stochastic Block Model of the German Cattle Trade Network. <i>Frontiers in Veterinary Science</i> , 2020, 7, 281.	2.2	5
16	Computer Vision for Detection of Body Posture and Behavior of Red Foxes. <i>Animals</i> , 2022, 12, 233.	2.3	5
17	Perfectly Misleading Distances from Ternary Characters. <i>Systematic Biology</i> , 2008, 57, 540-543.	5.6	4
18	Mathematical Aspects of Phylogenetic Groves. <i>Annals of Combinatorics</i> , 2013, 17, 295-310.	0.6	4

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19	Automatic classification of farms and traders in the pig production chain. Preventive Veterinary Medicine, 2018, 150, 86-92.	1.9	4
20	LVQ-KNN: Composition-based DNA/RNA binning of short nucleotide sequences utilizing a prototype-based k-nearest neighbor approach. Virus Research, 2018, 258, 55-63.	2.2	4
21	Unrooted non-binary tree-based phylogenetic networks. Discrete Applied Mathematics, 2021, 294, 10-30.	0.9	4
22	Extremal Values of the Sackin Tree Balance Index. Annals of Combinatorics, 2021, 25, 515-541.	0.6	4
23	Measuring tree balance using symmetry nodes "A new balance index and its extremal properties. Mathematical Biosciences, 2021, 341, 108690.	1.9	4
24	Discrete coalescent trees. Journal of Mathematical Biology, 2021, 83, 60.	1.9	4
25	Ancestral Sequence Reconstruction with Maximum Parsimony. Bulletin of Mathematical Biology, 2017, 79, 2865-2886.	1.9	3
26	On the Accuracy of Ancestral Sequence Reconstruction for Ultrametric Trees with Parsimony. Bulletin of Mathematical Biology, 2018, 80, 864-879.	1.9	3
27	On the Shapley Value of Unrooted Phylogenetic Trees. Bulletin of Mathematical Biology, 2019, 81, 618-638.	1.9	3
28	On the Balance of Unrooted Trees. Journal of Graph Algorithms and Applications, 2021, 25, 133-150.	0.4	3
29	Phylogenetic Diversity Rankings in the Face of Extinctions: The Robustness of the Fair Proportion Index. Systematic Biology, 2023, 72, 606-615.	5.6	3
30	Non-hereditary Maximum Parsimony trees. Journal of Mathematical Biology, 2012, 65, 293-308.	1.9	2
31	The most parsimonious tree for random data. Molecular Phylogenetics and Evolution, 2014, 80, 165-168.	2.7	2
32	A Linear Bound on the Number of States in Optimal Convex Characters for Maximum Parsimony Distance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 472-477.	3.0	2
33	On the uniqueness of the maximum parsimony tree for data with up to two substitutions: An extension of the classic Buneman theorem in phylogenetics. Molecular Phylogenetics and Evolution, 2019, 137, 127-137.	2.7	2
34	On the information content of discrete phylogenetic characters. Journal of Mathematical Biology, 2018, 77, 527-544.	1.9	1
35	Combinatorial views on persistent characters in phylogenetics. Advances in Applied Mathematics, 2020, 119, 102046.	0.7	1
36	The Space of Tree-Based Phylogenetic Networks. Bulletin of Mathematical Biology, 2020, 82, 70.	1.9	1

#	ARTICLE	IF	CITATIONS
37	Combinatorial perspectives on Dollo-k characters in phylogenetics. <i>Advances in Applied Mathematics</i> , 2021, 131, 102252.	0.7	1
38	Expected Anomalies in the Fossil Record. <i>Evolutionary Bioinformatics</i> , 2008, 4, EBO.S555.	1.2	0
39	Statistical Inconsistency of Maximum Parsimony for k-Tuple-Site Data. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 1173-1200.	1.9	0