

Mareike Fischer

List of Publications by Year in descending order

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39
papers

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1163117

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docs citations

41
times ranked

209
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic Diversity Rankings in the Face of Extinctions: The Robustness of the Fair Proportion Index. <i>Systematic Biology</i> , 2023, 72, 606-615.	5.6	3
2	Computer Vision for Detection of Body Posture and Behavior of Red Foxes. <i>Animals</i> , 2022, 12, 233.	2.3	5
3	Unrooted non-binary tree-based phylogenetic networks. <i>Discrete Applied Mathematics</i> , 2021, 294, 10-30.	0.9	4
4	Extremal Values of the Sackin Tree Balance Index. <i>Annals of Combinatorics</i> , 2021, 25, 515-541.	0.6	4
5	Application of YOLOv4 for Detection and Motion Monitoring of Red Foxes. <i>Animals</i> , 2021, 11, 1723.	2.3	17
6	Measuring tree balance using symmetry nodes "A new balance index and its extremal properties. <i>Mathematical Biosciences</i> , 2021, 341, 108690.	1.9	4
7	Combinatorial perspectives on Dollo-k characters in phylogenetics. <i>Advances in Applied Mathematics</i> , 2021, 131, 102252.	0.7	1
8	On the Balance of Unrooted Trees. <i>Journal of Graph Algorithms and Applications</i> , 2021, 25, 133-150.	0.4	3
9	Discrete coalescent trees. <i>Journal of Mathematical Biology</i> , 2021, 83, 60.	1.9	4
10	Combinatorial views on persistent characters in phylogenetics. <i>Advances in Applied Mathematics</i> , 2020, 119, 102046.	0.7	1
11	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
12	The Space of Tree-Based Phylogenetic Networks. <i>Bulletin of Mathematical Biology</i> , 2020, 82, 70.	1.9	1
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	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
15	Classes of tree-based networks. <i>Visual Computing for Industry, Biomedicine, and Art</i> , 2020, 3, 12.	3.7	6
16	On the uniqueness of the maximum parsimony tree for data with up to two substitutions: An extension of the classic Buneman theorem in phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 127-137.	2.7	2
17	Statistical Inconsistency of Maximum Parsimony for k-Tuple-Site Data. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 1173-1200.	1.9	0
18	On the Shapley Value of Unrooted Phylogenetic Trees. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 618-638.	1.9	3

#	ARTICLE	IF	CITATIONS
19	Phylogenetic diversity and biodiversity indices on phylogenetic networks. <i>Mathematical Biosciences</i> , 2018, 298, 80-90.	1.9	8
20	On the Accuracy of Ancestral Sequence Reconstruction for Ultrametric Trees with Parsimony. <i>Bulletin of Mathematical Biology</i> , 2018, 80, 864-879.	1.9	3
21	On the information content of discrete phylogenetic characters. <i>Journal of Mathematical Biology</i> , 2018, 77, 527-544.	1.9	1
22	Automatic classification of farms and traders in the pig production chain. <i>Preventive Veterinary Medicine</i> , 2018, 150, 86-92.	1.9	4
23	LVQ-KNN: Composition-based DNA/RNA binning of short nucleotide sequences utilizing a prototype-based k-nearest neighbor approach. <i>Virus Research</i> , 2018, 258, 55-63.	2.2	4
24	A Linear Bound on the Number of States in Optimal Convex Characters for Maximum Parsimony Distance. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 472-477.	3.0	2
25	On the quirks of maximum parsimony and likelihood on phylogenetic networks. <i>Journal of Theoretical Biology</i> , 2017, 417, 100-108.	1.7	8
26	Ancestral Sequence Reconstruction with Maximum Parsimony. <i>Bulletin of Mathematical Biology</i> , 2017, 79, 2865-2886.	1.9	3
27	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
28	On the Complexity of Computing MP Distance Between Binary Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2017, 21, 573-604.	0.6	11
29	Reduction rules for the maximum parsimony distance on phylogenetic trees. <i>Theoretical Computer Science</i> , 2016, 646, 1-15.	0.9	8
30	On the Maximum Parsimony Distance Between Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2016, 20, 87-113.	0.6	21
31	On Computing the Maximum Parsimony Score of a Phylogenetic Network. <i>SIAM Journal on Discrete Mathematics</i> , 2015, 29, 559-585.	0.8	17
32	The most parsimonious tree for random data. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 165-168.	2.7	2
33	Mathematical Aspects of Phylogenetic Groves. <i>Annals of Combinatorics</i> , 2013, 17, 295-310.	0.6	4
34	Non-hereditary Maximum Parsimony trees. <i>Journal of Mathematical Biology</i> , 2012, 65, 293-308.	1.9	2
35	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
36	Sequence length bounds for resolving a deep phylogenetic divergence. <i>Journal of Theoretical Biology</i> , 2009, 256, 247-252.	1.7	25

#	ARTICLE	IF	CITATIONS
37	Maximum parsimony on subsets of taxa. <i>Journal of Theoretical Biology</i> , 2009, 260, 290-293.	1.7	10
38	Perfectly Misleading Distances from Ternary Characters. <i>Systematic Biology</i> , 2008, 57, 540-543.	5.6	4
39	Expected Anomalies in the Fossil Record. <i>Evolutionary Bioinformatics</i> , 2008, 4, EBO.S555.	1.2	0