

Steven Kelk

List of Publications by Year in descending order

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46
papers

707
citations

687363

13
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580821

25
g-index

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all docs

47
docs citations

47
times ranked

482
citing authors

#	ARTICLE	IF	CITATIONS
1	Reflections on kernelizing and computing unrooted agreement forests. <i>Annals of Operations Research</i> , 2022, 309, 425-451.	4.1	5
2	Maximum parsimony distance on phylogenetic trees: A linear kernel and constant factor approximation algorithm. <i>Journal of Computer and System Sciences</i> , 2021, 117, 165-181.	1.2	4
3	Applicability of several rooted phylogenetic network algorithms for representing the evolutionary history of SARS-CoV-2. <i>Bmc Ecology and Evolution</i> , 2021, 21, 220.	1.6	2
4	New Reduction Rules for the Tree Bisection and Reconnection Distance. <i>Annals of Combinatorics</i> , 2020, 24, 475-502.	0.6	4
5	A Machine Learning Approach to Algorithm Selection for Exact Computation of Treewidth. <i>Algorithms</i> , 2019, 12, 200.	2.1	0
6	Integrality gaps for colorful matchings. <i>Discrete Optimization</i> , 2019, 32, 73-92.	0.9	1
7	Deciding the existence of a cherry-picking sequence is hard on two trees. <i>Discrete Applied Mathematics</i> , 2019, 260, 131-143.	0.9	5
8	A Third Strike Against Perfect Phylogeny. <i>Systematic Biology</i> , 2019, 68, 814-827.	5.6	2
9	A Tight Kernel for Computing the Tree Bisection and Reconnection Distance between Two Phylogenetic Trees. <i>SIAM Journal on Discrete Mathematics</i> , 2019, 33, 1556-1574.	0.8	7
10	Finding a most parsimonious or likely tree in a network with respect to an alignment. <i>Journal of Mathematical Biology</i> , 2019, 78, 527-547.	1.9	1
11	Treewidth of display graphs: bounds, brambles and applications. <i>Journal of Graph Algorithms and Applications</i> , 2019, 23, 715-743.	0.4	4
12	Treewidth distance on phylogenetic trees. <i>Theoretical Computer Science</i> , 2018, 731, 99-117.	0.9	3
13	On Unrooted and Root-Uncertain Variants of Several Well-Known Phylogenetic Network Problems. <i>Algorithmica</i> , 2018, 80, 2993-3022.	1.3	14
14	A Resolution of the Static Formulation Question for the Problem of Computing the History Bound. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 404-417.	3.0	1
15	On the challenge of reconstructing level-1 phylogenetic networks from triplets and clusters. <i>Journal of Mathematical Biology</i> , 2017, 74, 1729-1751.	1.9	8
16	A note on convex characters, Fibonacci numbers and exponential-time algorithms. <i>Advances in Applied Mathematics</i> , 2017, 84, 34-46.	0.7	6
17	ToTo: An open database for computation, storage and retrieval of tree decompositions. <i>Discrete Applied Mathematics</i> , 2017, 217, 389-393.	0.9	2
18	On the Complexity of Computing MP Distance Between Binary Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2017, 21, 573-604.	0.6	11

#	ARTICLE	IF	CITATIONS
19	Reduction rules for the maximum parsimony distance on phylogenetic trees. Theoretical Computer Science, 2016, 646, 1-15.	0.9	8
20	Do Branch Lengths Help to Locate a Tree in a Phylogenetic Network?. Bulletin of Mathematical Biology, 2016, 78, 1773-1795.	1.9	8
21	Hybridization Number on Three Rooted Binary Trees is EPT. SIAM Journal on Discrete Mathematics, 2016, 30, 1607-1631.	0.8	11
22	On the Maximum Parsimony Distance Between Phylogenetic Trees. Annals of Combinatorics, 2016, 20, 87-113.	0.6	21
23	Kernelizations for the hybridization number problem on multiple nonbinary trees. Journal of Computer and System Sciences, 2016, 82, 1075-1089.	1.2	11
24	Phylogenetic incongruence through the lens of Monadic Second Order logic. Journal of Graph Algorithms and Applications, 2016, 20, 189-215.	0.4	10
25	On Computing the Maximum Parsimony Score of a Phylogenetic Network. SIAM Journal on Discrete Mathematics, 2015, 29, 559-585.	0.8	17
26	On Low Treewidth Graphs and Supertrees. Journal of Graph Algorithms and Applications, 2015, 19, 325-343.	0.4	4
27	Approximation Algorithms for Nonbinary Agreement Forests. SIAM Journal on Discrete Mathematics, 2014, 28, 49-66.	0.8	12
28	Constructing Minimal Phylogenetic Networks from Softwired Clusters is Fixed Parameter Tractable. Algorithmica, 2014, 68, 886-915.	1.3	16
29	A practical approximation algorithm for solving massive instances of hybridization number for binary and nonbinary trees. BMC Bioinformatics, 2014, 15, 127.	2.6	9
30	The agreement problem for unrooted phylogenetic trees is FPT. Journal of Graph Algorithms and Applications, 2014, 18, 385-392.	0.4	7
31	Networks: expanding evolutionary thinking. Trends in Genetics, 2013, 29, 439-441.	6.7	176
32	Phylogenetic Networks: Concepts, Algorithms and Applications. Systematic Biology, 2012, 61, 174-175.	5.6	4
33	Cycle Killer...Qu'est-ce que c'est? On the Comparative Approximability of Hybridization Number and Directed Feedback Vertex Set. SIAM Journal on Discrete Mathematics, 2012, 26, 1635-1656.	0.8	18
34	On the Elusiveness of Clusters. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 517-534.	3.0	10
35	A Practical Approximation Algorithm for Solving Massive Instances of Hybridization Number. Lecture Notes in Computer Science, 2012, , 430-440.	1.3	1
36	Constructing the Simplest Possible Phylogenetic Network from Triplets. Algorithmica, 2011, 60, 207-235.	1.3	35

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37	When two trees go to war. <i>Journal of Theoretical Biology</i> , 2011, 269, 245-255.	1.7	18
38	Worst-case optimal approximation algorithms for maximizing triplet consistency within phylogenetic networks. <i>Journal of Discrete Algorithms</i> , 2010, 8, 65-75.	0.7	22
39	Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. <i>Bioinformatics</i> , 2010, 26, i124-i131.	4.1	47
40	Constructing Level-2 Phylogenetic Networks from Triplets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 667-681.	3.0	51
41	UNIQUENESS, INTRACTABILITY AND EXACT ALGORITHMS: REFLECTIONS ON LEVEL-K PHYLOGENETIC NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 597-623.	0.8	27
42	Shorelines of Islands of Tractability: Algorithms for Parsimony and Minimum Perfect Phylogeny Haplotyping Problems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 301-312.	3.0	9
43	Prefix Reversals on Binary and Ternary Strings. <i>SIAM Journal on Discrete Mathematics</i> , 2007, 21, 592-611.	0.8	15
44	The Complexity of the Single Individual SNP Haplotyping Problem. <i>Algorithmica</i> , 2007, 49, 13-36.	1.3	45
45	The Complexity of Choosing an H-Coloring (Nearly) Uniformly at Random. <i>SIAM Journal on Computing</i> , 2004, 33, 416-432.	1.0	13
46	New FPT Algorithms for Finding the Temporal Hybridization Number for Sets of Phylogenetic Trees. <i>Algorithmica</i> , 0, , .	1.3	1