Jesper Jansson

List of Publications by Year in descending order

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96	980	471509	501196
papers	citations	17 h-index	28 g-index

102	102	102	454
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Online and Approximate Network Construction from Bounded Connectivity Constraints. Lecture Notes in Computer Science, 2021, , 314-325.	1.3	0
2	Graph Orientation with Edge Modifications. International Journal of Foundations of Computer Science, 2021, 32, 209-233.	1.1	0
3	Computing the Rooted Triplet Distance Between Phylogenetic Networks. Algorithmica, 2021, 83, 1786-1828.	1.3	0
4	Pushing the Online Boolean Matrix-vector Multiplication conjecture off-line and identifying its easy cases. Journal of Computer and System Sciences, 2021, 118, 108-118.	1.2	0
5	New and improved algorithms for unordered tree inclusion. Theoretical Computer Science, 2021, 883, 83-98.	0.9	3
6	Upper and Lower Degree-Constrained Graph Orientation with Minimum Penalty. Theoretical Computer Science, 2021, 900, 53-53.	0.9	1
7	Graph orientation with splits. Theoretical Computer Science, 2020, 844, 16-25.	0.9	0
8	Exact algorithms for the repetition-bounded longest common subsequence problem. Theoretical Computer Science, 2020, 838, 238-249.	0.9	3
9	Better Link Prediction for Protein-Protein Interaction Networks. , 2020, , .		6
10	Computing the Rooted Triplet Distance Between Phylogenetic Networks. Lecture Notes in Computer Science, 2019, , 290-303.	1.3	2
11	Editorial: Special Issue on Efficient Data Structures. Algorithms, 2019, 12, 136.	2.1	0
12	An Efficient Algorithm for the Rooted Triplet Distance Between Galled Trees. Journal of Computational Biology, 2019, 26, 893-907.	1.6	1
13	Pushing the Online Matrix-Vector Conjecture Off-Line and Identifying Its Easy Cases. Lecture Notes in Computer Science, 2019, , 156-169.	1.3	0
14	The approximability of maximum rooted triplets consistency with fan triplets and forbidden triplets. Discrete Applied Mathematics, 2019, 257, 101-114.	0.9	2
15	Graph Orientation with Edge Modifications. Lecture Notes in Computer Science, 2019, , 38-50.	1.3	0
16	Exact Algorithms for the Bounded Repetition Longest Common Subsequence Problem. Lecture Notes in Computer Science, 2019, , 1-12.	1.3	0
17	Algorithms for the Majority Rule (+) Consensus Tree and the Frequency Difference Consensus Tree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 15-26.	3.0	4
18	3D Rectangulations and Geometric Matrix Multiplication. Algorithmica, 2018, 80, 136-154.	1.3	8

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19	Determining the Consistency of Resolved Triplets and Fan Triplets. Journal of Computational Biology, 2018, 25, 740-754.	1.6	1
20	Graph Orientation with Splits. Lecture Notes in Computer Science, 2018, , 52-63.	1.3	2
21	Determining the minimum number of protein-protein interactions required to support known protein complexes. PLoS ONE, 2018, 13, e0195545.	2.5	13
22	Minimal Phylogenetic Supertrees and Local Consensus Trees. AIMS Medical Science, 2018, 5, 181-203.	0.4	1
23	On the parameterized complexity of associative and commutative unification. Theoretical Computer Science, 2017, 660, 57-74.	0.9	0
24	On finding the Adams consensus tree. Information and Computation, 2017, 256, 334-347.	0.7	4
25	A More Practical Algorithm for the Rooted Triplet Distance. Journal of Computational Biology, 2017, 24, 106-126.	1.6	7
26	An Efficient Algorithm for the Rooted Triplet Distance Between Galled Trees. Lecture Notes in Computer Science, 2017, , 115-126.	1.3	1
27	Determining the Consistency of Resolved Triplets and Fan Triplets. Lecture Notes in Computer Science, 2017, , 82-98.	1.3	4
28	Similar subtree search using extended tree inclusion. , 2016, , .		0
29	Faster Algorithms for Computing the R* Consensus Tree. Algorithmica, 2016, 76, 1224-1244.	1.3	0
30	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network. , 2016, , 48-52.		27
31	Improved Algorithms for Constructing Consensus Trees. Journal of the ACM, 2016, 63, 1-24.	2.2	16
32	Degree-Constrained Graph Orientation: Maximum Satisfaction and Minimum Violation. Theory of Computing Systems, 2016, 58, 60-93.	1.1	8
33	Maximum Agreement Supertree. , 2016, , 1224-1227.		0
34	Similar Subtree Search Using Extended Tree Inclusion. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 3360-3373.	5.7	1
35	Linked Dynamic Tries with Applications to LZ-Compression in Sublinear Time and Space. Algorithmica, 2015, 71, 969-988.	1.3	24
36	A More Practical Algorithm for the Rooted Triplet Distance. Lecture Notes in Computer Science, 2015, , 109-125.	1.3	2

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37	Graph Orientations Optimizing the Number of Light or Heavy Vertices. Journal of Graph Algorithms and Applications, 2015, 19, 441-465.	0.4	6
38	The Approximability of Maximum Rooted Triplets Consistency with Fan Triplets and Forbidden Triplets. Lecture Notes in Computer Science, 2015, , 272-283.	1.3	2
39	Maximum Agreement Supertree. , 2015, , 1-5.		0
40	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network. , 2015, , 1-6.		0
41	Computing the rooted triplet distance between galled trees by counting triangles. Journal of Discrete Algorithms, 2014, 25, 66-78.	0.7	11
42	Fast relative Lempelâ€“Ziv self-index for similar sequences. Theoretical Computer Science, 2014, 532, 14-30.	0.9	34
43	Faster Algorithms for Computing theÂR*ÂConsensusÂTree. Lecture Notes in Computer Science, 2014, , 414-425.	1.3	2
44	Constructing the R* Consensus Tree of Two Trees in Subcubic Time. Algorithmica, 2013, 66, 329-345.	1.3	7
45	Algorithms for the Majority Rule (+) Consensus Tree and the Frequency Difference Consensus Tree. Lecture Notes in Computer Science, 2013, , 141-155.	1.3	0
46	Special Issue on Graph Algorithms. Algorithms, 2013, 6, 457-458.	2.1	1
47	Improved Algorithms for Constructing Consensus Trees. , 2013, , .		4
48	An Optimal Algorithm for Building the Majority Rule Consensus Tree. Lecture Notes in Computer Science, 2013, , 88-99.	1.3	1
49	Polynomial-Time Algorithms for Building a Consensus MUL-Tree. Journal of Computational Biology, 2012, 19, 1073-1088.	1.6	13
50	The Complexity of Inferring a Minimally Resolved Phylogenetic Supertree. SIAM Journal on Computing, 2012, 41, 272-291.	1.0	16
51	More efficient periodic traversal in anonymous undirected graphs. Theoretical Computer Science, 2012, 444, 60-76.	0.9	11
52	Inferring a graph from path frequency. Discrete Applied Mathematics, 2012, 160, 1416-1428.	0.9	19
53	Faster computation of the Robinsonâ€“Foulds distance between phylogenetic networks. Information Sciences, 2012, 197, 77-90.	6.9	3
54	Ultra-succinct representation of ordered trees with applications. Journal of Computer and System Sciences, 2012, 78, 619-631.	1.2	44

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55	Fast Relative Lempel-Ziv Self-index for Similar Sequences. Lecture Notes in Computer Science, 2012, , 291-302.	1.3	9
56	Asymptotic Limits of a New Type of Maximization Recurrence with an Application to Bioinformatics. Lecture Notes in Computer Science, 2012, , 177-188.	1.3	2
57	CRAM: Compressed Random Access Memory. Lecture Notes in Computer Science, 2012, , 510-521.	1.3	15
58	Graph Orientations Optimizing the Number of Light or Heavy Vertices. Lecture Notes in Computer Science, 2012, , 332-343.	1.3	2
59	Computing the Rooted Triplet Distance between Galled Trees by Counting Triangles. Lecture Notes in Computer Science, 2012, , 385-398.	1.3	0
60	Computing a Smallest Multilabeled Phylogenetic Tree from Rooted Triplets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1141-1147.	3.0	9
61	Approximation algorithms for the graph orientation minimizing the maximum weighted outdegree. Journal of Combinatorial Optimization, 2011, 22, 78-96.	1.3	27
62	Algorithms for Finding a Most Similar Subforest. Theory of Computing Systems, 2011, 48, 865-887.	1.1	2
63	Flexible taxonomic assignment of ambiguous sequencing reads. BMC Bioinformatics, 2011, 12, 8.	2.6	26
64	APPROXIMATION ALGORITHMS FOR BUY-AT-BULK GEOMETRIC NETWORK DESIGN. International Journal of Foundations of Computer Science, 2011, 22, 1949-1969.	1.1	2
65	GRAPH ORIENTATION TO MAXIMIZE THE MINIMUM WEIGHTED OUTDEGREE. International Journal of Foundations of Computer Science, 2011, 22, 583-601.	1.1	11
66	Algorithms for Building Consensus MUL-trees. Lecture Notes in Computer Science, 2011, , 744-753.	1.3	0
67	New results on optimizing rooted triplets consistency. Discrete Applied Mathematics, 2010, 158, 1136-1147.	0.9	43
68	Linear-time protein 3-D structure searching with insertions and deletions. Algorithms for Molecular Biology, 2010, 5, 7.	1.2	9
69	Faster Computation of the Robinson-Foulds Distance between Phylogenetic Networks. Lecture Notes in Computer Science, 2010, , 190-201.	1.3	3
70	The Complexity of Inferring a Minimally Resolved Phylogenetic Supertree. Lecture Notes in Computer Science, 2010, , 262-273.	1.3	1
71	More Efficient Periodic Traversal in Anonymous Undirected Graphs. Lecture Notes in Computer Science, 2010, , 167-181.	1.3	4
72	ACCURATE TAXONOMIC ASSIGNMENT OF SHORT PYROSEQUENCING READS. , 2009, , 3-9.		13

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73	Linear-Time Protein 3-D Structure Searching with Insertions and Deletions. Lecture Notes in Computer Science, 2009, , 310-320.	1.3	1
74	Computing a Smallest Multi-labeled Phylogenetic Tree from Rooted Triplets. Lecture Notes in Computer Science, 2009, , 1205-1214.	1.3	1
75	Approximation Algorithms for Buy-at-Bulk Geometric Network Design. Lecture Notes in Computer Science, 2009, , 168-180.	1.3	1
76	New Results on Optimizing Rooted Triplets Consistency. Lecture Notes in Computer Science, 2008, , 484-495.	1.3	4
77	ONLINE AND DYNAMIC RECOGNITION OF SQUAREFREE STRINGS. International Journal of Foundations of Computer Science, 2007, 18, 401-414.	1.1	4
78	ON THE APPROXIMABILITY OF MAXIMUM AND MINIMUM EDGE CLIQUE PARTITION PROBLEMS. International Journal of Foundations of Computer Science, 2007, 18, 217-226.	1.1	21
79	Polynomial-Time Algorithms for the Ordered Maximum Agreement Subtree Problem. Algorithmica, 2007, 48, 233-248.	1.3	1
80	Local Gapped Subforest Alignment and Its Application in Finding RNA Structural Motifs. Journal of Computational Biology, 2006, 13, 702-718.	1.6	8
81	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network. SIAM Journal on Computing, 2006, 35, 1098-1121.	1.0	88
82	Inferring a level-1 phylogenetic network from a dense set of rooted triplets. Theoretical Computer Science, 2006, 363, 60-68.	0.9	60
83	A Faster and More Space-Efficient Algorithm for Inferring Arc-Annotations of RNA Sequences through Alignment. Algorithmica, 2006, 46, 223-245.	1.3	7
84	RECONSTRUCTING AN ULTRAMETRIC GALLED PHYLOGENETIC NETWORK FROM A DISTANCE MATRIX. Journal of Bioinformatics and Computational Biology, 2006, 04, 807-832.	0.8	19
85	INFERRING PHYLOGENETIC RELATIONSHIPS AVOIDING FORBIDDEN ROOTED TRIPLETS. Journal of Bioinformatics and Computational Biology, 2006, 04, 59-74.	0.8	27
86	Algorithms for Finding a Most Similar Subforest. Lecture Notes in Computer Science, 2006, , 377-388.	1.3	4
87	Computing the maximum agreement of phylogenetic networks. Theoretical Computer Science, 2005, 335, 93-107.	0.9	66
88	Rooted Maximum Agreement Supertrees. Algorithmica, 2005, 43, 293-307.	1.3	43
89	Finding Short Right-Hand-on-the-Wall Walks in Graphs. Lecture Notes in Computer Science, 2005, , 127-139.	1.3	17
90	Computing the Maximum Agreement of Phylogenetic Networks. Electronic Notes in Theoretical Computer Science, 2004, 91, 134-147.	0.9	8

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91	Semi-Balanced Colorings of Graphs: Generalized 2-Colorings Based on a Relaxed Discrepancy Condition. Graphs and Combinatorics, 2004, 20, 205-222.	0.4	2
92	Approximation algorithms for Hamming clustering problems. Journal of Discrete Algorithms, 2004, 2, 289-301.	0.7	19
93	Inferring a Level-1 Phylogenetic Network from a Dense Set of Rooted Triplets. Lecture Notes in Computer Science, 2004, , 462-471.	1.3	13
94	Local Gapped Subforest Alignment and Its Application in Finding RNA Structural Motifs. Lecture Notes in Computer Science, 2004, , 569-580.	1.3	4
95	On the Complexity of Inferring Rooted Evolutionary Trees. Electronic Notes in Discrete Mathematics, 2001, 7, 50-53.	0.4	18
96	On the Complexity of Constructing Evolutionary Trees. Journal of Combinatorial Optimization, 1999, 3, 183-197.	1.3	47