

Solon Pp Pissis

List of Publications by Year in descending order

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84
papers

596
citations

759190

12
h-index

888047

17
g-index

86
all docs

86
docs citations

86
times ranked

330
citing authors

#	ARTICLE	IF	CITATIONS
1	MARS: improving multiple circular sequence alignment using refined sequences. BMC Genomics, 2017, 18, 86.	2.8	35
2	Linear-time computation of minimal absent words using suffix array. BMC Bioinformatics, 2014, 15, 388.	2.6	30
3	Fast algorithms for approximate circular string matching. Algorithms for Molecular Biology, 2014, 9, 9.	1.2	26
4	REAL. , 2010, , .		24
5	MoTeX-II: structured MoTif eXtraction from large-scale datasets. BMC Bioinformatics, 2014, 15, 235.	2.6	21
6	On avoided words, absent words, and their application to biological sequence analysis. Algorithms for Molecular Biology, 2017, 12, 5.	1.2	19
7	Enhanced string covering. Theoretical Computer Science, 2013, 506, 102-114.	0.9	18
8	Circular sequence comparison: algorithms and applications. Algorithms for Molecular Biology, 2016, 11, 12.	1.2	17
9	Linear-time superbubble identification algorithm for genome assembly. Theoretical Computer Science, 2016, 609, 374-383.	0.9	16
10	Alignment-free sequence comparison using absent words. Information and Computation, 2018, 262, 57-68.	0.7	16
11	Fast Algorithm for Partial Covers in Words. Algorithmica, 2015, 73, 217-233.	1.3	15
12	Fast phylogenetic inference from typing data. Algorithms for Molecular Biology, 2018, 13, 4.	1.2	14
13	Absent words in a sliding window with applications. Information and Computation, 2020, 270, 104461.	0.7	14
14	Average-Case Optimal Approximate Circular String Matching. Lecture Notes in Computer Science, 2015, , 85-96.	1.3	13
15	Dynamic and Internal Longest Common Substring. Algorithmica, 2020, 82, 3707-3743.	1.3	12
16	Mapping uniquely occurring short sequences derived from high throughput technologies to a reference genome. , 2009, , .		11
17	Global and local sequence alignment with a bounded number of gaps. Theoretical Computer Science, 2015, 582, 1-16.	0.9	11
18	Parallelising the Computation of Minimal Absent Words. Lecture Notes in Computer Science, 2016, , 243-253.	1.3	10

#	ARTICLE	IF	CITATIONS
19	emMAW: computing minimal absent words in external memory. <i>Bioinformatics</i> , 2017, 33, 2746-2749.	4.1	10
20	Accurate and Efficient Methods to Improve Multiple Circular Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2015, , 247-258.	1.3	10
21	Linear-Time Sequence Comparison Using Minimal Absent Words & Applications. <i>Lecture Notes in Computer Science</i> , 2016, , 334-346.	1.3	10
22	MoTeX. , 2013, , .		9
23	A faster and more accurate heuristic for cyclic edit distance computation. <i>Pattern Recognition Letters</i> , 2017, 88, 81-87.	4.2	9
24	Pattern Matching and Consensus Problems on Weighted Sequences and Profiles. <i>Theory of Computing Systems</i> , 2019, 63, 506-542.	1.1	9
25	Approximate pattern matching on elastic-degenerate text. <i>Theoretical Computer Science</i> , 2020, 812, 109-122.	0.9	9
26	Efficient Pattern Matching in Elastic-Degenerate Texts. <i>Lecture Notes in Computer Science</i> , 2017, , 131-142.	1.3	9
27	GapMis: a Tool for Pairwise Sequence Alignment with a Single Gap. <i>Recent Patents on DNA & Gene Sequences</i> , 2013, 7, 84-95.	0.7	9
28	libgapmis: extending short-read alignments. <i>BMC Bioinformatics</i> , 2013, 14, S4.	2.6	8
29	Optimal computation of all tandem repeats in a weighted sequence. <i>Algorithms for Molecular Biology</i> , 2014, 9, 21.	1.2	8
30	Linear-time computation of prefix table for weighted strings & applications. <i>Theoretical Computer Science</i> , 2016, 656, 160-172.	0.9	8
31	Efficient algorithms for shortest partial seeds in words. <i>Theoretical Computer Science</i> , 2018, 710, 139-147.	0.9	8
32	Longest Common Prefixes with k-Errors and Applications. <i>Lecture Notes in Computer Science</i> , 2018, , 27-41.	1.3	8
33	Indexing weighted sequences: Neat and efficient. <i>Information and Computation</i> , 2020, 270, 104462.	0.7	7
34	IUPACpal: efficient identification of inverted repeats in IUPAC-encoded DNA sequences. <i>BMC Bioinformatics</i> , 2021, 22, 51.	2.6	7
35	On Extended Special Factors of a Word. <i>Lecture Notes in Computer Science</i> , 2018, , 131-138.	1.3	7
36	libFLASM: a software library for fixed-length approximate string matching. <i>BMC Bioinformatics</i> , 2016, 17, 454.	2.6	6

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37	Fast circular dictionary-matching algorithm. <i>Mathematical Structures in Computer Science</i> , 2017, 27, 143-156.	0.6	6
38	Fast Average-Case Pattern Matching on Weighted Sequences. <i>International Journal of Foundations of Computer Science</i> , 2018, 29, 1331-1343.	1.1	6
39	On-Line Pattern Matching on Uncertain Sequences and Applications. <i>Lecture Notes in Computer Science</i> , 2016, , 547-562.	1.3	6
40	Longest Common Factor After One Edit Operation. <i>Lecture Notes in Computer Science</i> , 2017, , 14-26.	1.3	6
41	Faster Algorithms for 1-Mappability of a Sequence. <i>Lecture Notes in Computer Science</i> , 2017, , 109-121.	1.3	6
42	Minimal Absent Words in a Sliding Window and Applications to On-Line Pattern Matching. <i>Lecture Notes in Computer Science</i> , 2017, , 164-176.	1.3	6
43	Longest Common Prefixes with k-Mismatches and Applications. <i>Lecture Notes in Computer Science</i> , 2018, , 636-649.	1.3	6
44	A Parallel Algorithm for Fixed-Length Approximate String-Matching with k-mismatches. <i>Lecture Notes in Computer Science</i> , 2010, , 92-101.	1.3	5
45	Generalised Implementation for Fixed-Length Approximate String Matching under Hamming Distance and Applications. , 2015, , .		4
46	Comparing Degenerate Strings. <i>Fundamenta Informaticae</i> , 2020, 175, 41-58.	0.4	4
47	Reverse-Safe Data Structures for Text Indexing. , 2020, , 199-213.		4
48	Combinatorial Algorithms for String Sanitization. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2021, 15, 1-34.	3.5	4
49	Efficient pattern matching in elastic-degenerate strings. <i>Information and Computation</i> , 2021, 279, 104616.	0.7	4
50	Accelerating String Matching on MIC Architecture for Motif Extraction. <i>Lecture Notes in Computer Science</i> , 2014, , 258-267.	1.3	4
51	Property Suffix Array with Applications in Indexing Weighted Sequences. <i>Journal of Experimental Algorithmics</i> , 2020, 25, 1-16.	1.0	4
52	Crochemore's Partitioning on Weighted Strings and Applications. <i>Algorithmica</i> , 2018, 80, 496-514.	1.3	3
53	On-line weighted pattern matching. <i>Information and Computation</i> , 2019, 266, 49-59.	0.7	3
54	Efficient Data Structures for Range Shortest Unique Substring Queries. <i>Algorithms</i> , 2020, 13, 276.	2.1	3

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55	Maximal Motif Discovery in a Sliding Window. Lecture Notes in Computer Science, 2018, , 191-205.	1.3	3
56	Efficient Computation of Sequence Mappability. Lecture Notes in Computer Science, 2018, , 12-26.	1.3	3
57	String Sanitization: A Combinatorial Approach. Lecture Notes in Computer Science, 2020, , 627-644.	1.3	3
58	Internal shortest absent word queries in constant time and linear space. Theoretical Computer Science, 2022, 922, 271-282.	0.9	3
59	Elastic-Degenerate String Matching via Fast Matrix Multiplication. SIAM Journal on Computing, 2022, 51, 549-576.	1.0	3
60	Tree template matching in ranked ordered trees by pushdown automata. Journal of Discrete Algorithms, 2012, 17, 15-23.	0.7	2
61	Searching and Indexing Circular Patterns. , 2017, , 77-90.		2
62	Constructing Antidictionaries in Output-Sensitive Space. , 2019, , .		2
63	On overabundant words and their application to biological sequence analysis. Theoretical Computer Science, 2019, 792, 85-95.	0.9	2
64	Longest property-preserved common factor: A new string-processing framework. Theoretical Computer Science, 2020, 812, 244-251.	0.9	2
65	Beyond the BEST Theorem: Fast Assessment of Eulerian Trails. Lecture Notes in Computer Science, 2021, , 162-175.	1.3	2
66	How to Answer a Small Batch of RMQs or LCA Queries in Practice. Lecture Notes in Computer Science, 2018, , 343-355.	1.3	2
67	Circular Pattern Matching with k Mismatches. Lecture Notes in Computer Science, 2019, , 213-228.	1.3	2
68	Constructing Antidictionaries of Long Texts in Output-Sensitive Space. Theory of Computing Systems, 2021, 65, 777-797.	1.1	2
69	Tree template matching in unranked ordered trees. Journal of Discrete Algorithms, 2013, 20, 51-60.	0.7	1
70	Efficient Enumeration of Non-Equivalent Squares in Partial Words with Few Holes. Lecture Notes in Computer Science, 2017, , 99-111.	1.3	1
71	Efficient Computation of Palindromes in Sequences with Uncertainties. Communications in Computer and Information Science, 2017, , 620-629.	0.5	1
72	Property Suffix Array with Applications. Lecture Notes in Computer Science, 2018, , 290-302.	1.3	1

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73	Faster algorithms for 1-mappability of a sequence. Theoretical Computer Science, 2020, 812, 2-12.	0.9	1
74	Clustering Demographics and Sequences of Diagnosis Codes. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 2351-2359.	6.3	1
75	Optimal Computation of Avoided Words. Lecture Notes in Computer Science, 2016, , 1-13.	1.3	0
76	Efficient enumeration of non-equivalent squares in partial words with few holes. Journal of Combinatorial Optimization, 2019, 37, 501-522.	1.3	0
77	Circular pattern matching with k mismatches. Journal of Computer and System Sciences, 2021, 115, 73-85.	1.2	0
78	Influence maximization in the presence of vulnerable nodes: A ratio perspective. Theoretical Computer Science, 2021, 852, 84-103.	0.9	0
79	Reverse-Safe Text Indexing. Journal of Experimental Algorithmics, 2021, 26, 1-26.	1.0	0
80	Weighted Shortest Common Supersequence Problem Revisited. Lecture Notes in Computer Science, 2019, , 221-238.	1.3	0
81	Comparing Degenerate Strings. , 2020, , .		0
82	Clustering sequence graphs. Data and Knowledge Engineering, 2022, 138, 101981.	3.4	0
83	Efficient Computation of Sequence Mappability. Algorithmica, 0, , 1.	1.3	0
84	All-pairs suffix/prefix in optimal time using Aho-Corasick space. Information Processing Letters, 2022, , 106275.	0.6	0