

Solon Pp Pissis

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3087252/publications.pdf>

Version: 2024-02-01

84
papers

596
citations

858243

12
h-index

993246

17
g-index

86
all docs

86
docs citations

86
times ranked

361
citing authors

#	ARTICLE	IF	CITATIONS
1	Clustering Demographics and Sequences of Diagnosis Codes. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 2351-2359.	3.9	1
2	Clustering sequence graphs. Data and Knowledge Engineering, 2022, 138, 101981.	2.1	0
3	Internal shortest absent word queries in constant time and linear space. Theoretical Computer Science, 2022, 922, 271-282.	0.5	3
4	All-pairs suffix/prefix in optimal time using Aho-Corasick space. Information Processing Letters, 2022, , 106275.	0.4	0
5	Elastic-Degenerate String Matching via Fast Matrix Multiplication. SIAM Journal on Computing, 2022, 51, 549-576.	0.8	3
6	Circular pattern matching with k mismatches. Journal of Computer and System Sciences, 2021, 115, 73-85.	0.9	0
7	Influence maximization in the presence of vulnerable nodes: A ratio perspective. Theoretical Computer Science, 2021, 852, 84-103.	0.5	0
8	Beyond the BEST Theorem: Fast Assessment of Eulerian Trails. Lecture Notes in Computer Science, 2021, , 162-175.	1.0	2
9	Combinatorial Algorithms for String Sanitization. ACM Transactions on Knowledge Discovery From Data, 2021, 15, 1-34.	2.5	4
10	IUPACpal: efficient identification of inverted repeats in IUPAC-encoded DNA sequences. BMC Bioinformatics, 2021, 22, 51.	1.2	7
11	Reverse-Safe Text Indexing. Journal of Experimental Algorithmics, 2021, 26, 1-26.	0.7	0
12	Efficient pattern matching in elastic-degenerate strings. Information and Computation, 2021, 279, 104616.	0.5	4
13	Constructing Antidictionaries of Long Texts in Output-Sensitive Space. Theory of Computing Systems, 2021, 65, 777-797.	0.7	2
14	Indexing weighted sequences: Neat and efficient. Information and Computation, 2020, 270, 104462.	0.5	7
15	Approximate pattern matching on elastic-degenerate text. Theoretical Computer Science, 2020, 812, 109-122.	0.5	9
16	Absent words in a sliding window with applications. Information and Computation, 2020, 270, 104461.	0.5	14
17	Faster algorithms for 1-mappability of a sequence. Theoretical Computer Science, 2020, 812, 2-12.	0.5	1
18	Dynamic and Internal Longest Common Substring. Algorithmica, 2020, 82, 3707-3743.	1.0	12

#	ARTICLE	IF	CITATIONS
19	Comparing Degenerate Strings. <i>Fundamenta Informaticae</i> , 2020, 175, 41-58.	0.3	4
20	Longest property-preserved common factor: A new string-processing framework. <i>Theoretical Computer Science</i> , 2020, 812, 244-251.	0.5	2
21	Efficient Data Structures for Range Shortest Unique Substring Queries. <i>Algorithms</i> , 2020, 13, 276.	1.2	3
22	Reverse-Safe Data Structures for Text Indexing. , 2020, , 199-213.		4
23	Property Suffix Array with Applications in Indexing Weighted Sequences. <i>Journal of Experimental Algorithmics</i> , 2020, 25, 1-16.	0.7	4
24	String Sanitization: A Combinatorial Approach. <i>Lecture Notes in Computer Science</i> , 2020, , 627-644.	1.0	3
25	Comparing Degenerate Strings. , 2020, , .		0
26	Constructing Antidictionaries in Output-Sensitive Space. , 2019, , .		2
27	Efficient enumeration of non-equivalent squares in partial words with few holes. <i>Journal of Combinatorial Optimization</i> , 2019, 37, 501-522.	0.8	0
28	On-line weighted pattern matching. <i>Information and Computation</i> , 2019, 266, 49-59.	0.5	3
29	Pattern Matching and Consensus Problems on Weighted Sequences and Profiles. <i>Theory of Computing Systems</i> , 2019, 63, 506-542.	0.7	9
30	On overabundant words and their application to biological sequence analysis. <i>Theoretical Computer Science</i> , 2019, 792, 85-95.	0.5	2
31	Weighted Shortest Common Supersequence Problem Revisited. <i>Lecture Notes in Computer Science</i> , 2019, , 221-238.	1.0	0
32	Circular Pattern Matching with k Mismatches. <i>Lecture Notes in Computer Science</i> , 2019, , 213-228.	1.0	2
33	Efficient algorithms for shortest partial seeds in words. <i>Theoretical Computer Science</i> , 2018, 710, 139-147.	0.5	8
34	Crochemore's Partitioning on Weighted Strings and Applications. <i>Algorithmica</i> , 2018, 80, 496-514.	1.0	3
35	Fast Average-Case Pattern Matching on Weighted Sequences. <i>International Journal of Foundations of Computer Science</i> , 2018, 29, 1331-1343.	0.8	6
36	Alignment-free sequence comparison using absent words. <i>Information and Computation</i> , 2018, 262, 57-68.	0.5	16

#	ARTICLE	IF	CITATIONS
37	Fast phylogenetic inference from typing data. Algorithms for Molecular Biology, 2018, 13, 4.	0.3	14
38	Property Suffix Array with Applications. Lecture Notes in Computer Science, 2018, , 290-302.	1.0	1
39	Maximal Motif Discovery in a Sliding Window. Lecture Notes in Computer Science, 2018, , 191-205.	1.0	3
40	Longest Common Prefixes with k-Errors and Applications. Lecture Notes in Computer Science, 2018, , 27-41.	1.0	8
41	How to Answer a Small Batch of RMQs or LCA Queries in Practice. Lecture Notes in Computer Science, 2018, , 343-355.	1.0	2
42	Longest Common Prefixes with k-Mismatches and Applications. Lecture Notes in Computer Science, 2018, , 636-649.	1.0	6
43	Efficient Computation of Sequence Mappability. Lecture Notes in Computer Science, 2018, , 12-26.	1.0	3
44	On Extended Special Factors of a Word. Lecture Notes in Computer Science, 2018, , 131-138.	1.0	7
45	A faster and more accurate heuristic for cyclic edit distance computation. Pattern Recognition Letters, 2017, 88, 81-87.	2.6	9
46	emMAW: computing minimal absent words in external memory. Bioinformatics, 2017, 33, 2746-2749.	1.8	10
47	On avoided words, absent words, and their application to biological sequence analysis. Algorithms for Molecular Biology, 2017, 12, 5.	0.3	19
48	Searching and Indexing Circular Patterns. , 2017, , 77-90.		2
49	Efficient Enumeration of Non-Equivalent Squares in Partial Words with Few Holes. Lecture Notes in Computer Science, 2017, , 99-111.	1.0	1
50	Efficient Computation of Palindromes in Sequences with Uncertainties. Communications in Computer and Information Science, 2017, , 620-629.	0.4	1
51	Fast circular dictionary-matching algorithm. Mathematical Structures in Computer Science, 2017, 27, 143-156.	0.5	6
52	MARS: improving multiple circular sequence alignment using refined sequences. BMC Genomics, 2017, 18, 86.	1.2	35
53	Efficient Pattern Matching in Elastic-Degenerate Texts. Lecture Notes in Computer Science, 2017, , 131-142.	1.0	9
54	Longest Common Factor After One Edit Operation. Lecture Notes in Computer Science, 2017, , 14-26.	1.0	6

#	ARTICLE	IF	CITATIONS
55	Faster Algorithms for 1-Mappability of a Sequence. Lecture Notes in Computer Science, 2017, , 109-121.	1.0	6
56	Minimal Absent Words in a Sliding Window and Applications to On-Line Pattern Matching. Lecture Notes in Computer Science, 2017, , 164-176.	1.0	6
57	libFLASM: a software library for fixed-length approximate string matching. BMC Bioinformatics, 2016, 17, 454.	1.2	6
58	Circular sequence comparison: algorithms and applications. Algorithms for Molecular Biology, 2016, 11, 12.	0.3	17
59	Parallelising the Computation of Minimal Absent Words. Lecture Notes in Computer Science, 2016, , 243-253.	1.0	10
60	Linear-time computation of prefix table for weighted strings & applications. Theoretical Computer Science, 2016, 656, 160-172.	0.5	8
61	Optimal Computation of Avoided Words. Lecture Notes in Computer Science, 2016, , 1-13.	1.0	0
62	Linear-time superbubble identification algorithm for genome assembly. Theoretical Computer Science, 2016, 609, 374-383.	0.5	16
63	On-Line Pattern Matching on Uncertain Sequences and Applications. Lecture Notes in Computer Science, 2016, , 547-562.	1.0	6
64	Linear-Time Sequence Comparison Using Minimal Absent Words & Applications. Lecture Notes in Computer Science, 2016, , 334-346.	1.0	10
65	Fast Algorithm for Partial Covers in Words. Algorithmica, 2015, 73, 217-233.	1.0	15
66	Global and local sequence alignment with a bounded number of gaps. Theoretical Computer Science, 2015, 582, 1-16.	0.5	11
67	Generalised Implementation for Fixed-Length Approximate String Matching under Hamming Distance and Applications. , 2015, , .		4
68	Average-Case Optimal Approximate Circular String Matching. Lecture Notes in Computer Science, 2015, , 85-96.	1.0	13
69	Accurate and Efficient Methods to Improve Multiple Circular Sequence Alignment. Lecture Notes in Computer Science, 2015, , 247-258.	1.0	10
70	Linear-time computation of minimal absent words using suffix array. BMC Bioinformatics, 2014, 15, 388.	1.2	30
71	Optimal computation of all tandem repeats in a weighted sequence. Algorithms for Molecular Biology, 2014, 9, 21.	0.3	8
72	MoTeX-II: structured MoTif eXtraction from large-scale datasets. BMC Bioinformatics, 2014, 15, 235.	1.2	21

#	ARTICLE	IF	CITATIONS
73	Fast algorithms for approximate circular string matching. Algorithms for Molecular Biology, 2014, 9, 9.	0.3	26
74	Accelerating String Matching on MIC Architecture for Motif Extraction. Lecture Notes in Computer Science, 2014, , 258-267.	1.0	4
75	Enhanced string covering. Theoretical Computer Science, 2013, 506, 102-114.	0.5	18
76	libgapmis: extending short-read alignments. BMC Bioinformatics, 2013, 14, S4.	1.2	8
77	Tree template matching in unranked ordered trees. Journal of Discrete Algorithms, 2013, 20, 51-60.	0.7	1
78	MoTeX. , 2013, , .		9
79	GapMis: a Tool for Pairwise Sequence Alignment with a Single Gap. Recent Patents on DNA & Gene Sequences, 2013, 7, 84-95.	0.7	9
80	Tree template matching in ranked ordered trees by pushdown automata. Journal of Discrete Algorithms, 2012, 17, 15-23.	0.7	2
81	REAL. , 2010, , .		24
82	A Parallel Algorithm for Fixed-Length Approximate String-Matching with k-mismatches. Lecture Notes in Computer Science, 2010, , 92-101.	1.0	5
83	Mapping uniquely occurring short sequences derived from high throughput technologies to a reference genome. , 2009, , .		11
84	Efficient Computation of Sequence Mappability. Algorithmica, 0, , 1.	1.0	0