

Paola Bonizzoni

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1095731/publications.pdf>

Version: 2024-02-01

99
papers

1,475
citations

361413

20
h-index

434195

31
g-index

125
all docs

125
docs citations

125
times ranked

1039
citing authors

#	ARTICLE	IF	CITATIONS
1	The Haplotyping problem: An overview of computational models and solutions. Journal of Computer Science and Technology, 2003, 18, 675-688.	1.5	104
2	The complexity of multiple sequence alignment with SP-score that is a metric. Theoretical Computer Science, 2001, 259, 63-79.	0.9	91
3	Reconciling a gene tree to a species tree under the duplication cost model. Theoretical Computer Science, 2005, 347, 36-53.	0.9	71
4	The binary perfect phylogeny with persistent characters. Theoretical Computer Science, 2012, 454, 51-63.	0.9	57
5	Beyond Perfect Phylogeny. , 2017, , .		42
6	Explaining evolution via constrained persistent perfect phylogeny. BMC Genomics, 2014, 15, S10.	2.8	40
7	H _{ap} C _{ol} : accurate and memory-efficient haplotype assembly from long reads. Bioinformatics, 2016, 32, 1610-1617.	4.1	40
8	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. Nucleic Acids Research, 2011, 39, D80-D85.	14.5	38
9	Inferring cancer progression from Single-Cell Sequencing while allowing mutation losses. Bioinformatics, 2021, 37, 326-333.	4.1	35
10	Variants of constrained longest common subsequence. Information Processing Letters, 2010, 110, 877-881.	0.6	33
11	ASPIC: a novel method to predict the exon-intron structure of a gene that is optimally compatible to a set of transcript sequences. BMC Bioinformatics, 2005, 6, 244.	2.6	32
12	Exemplar Longest Common Subsequence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 535-543.	3.0	30
13	Overlap graphs and <i>de Bruijn</i> graphs: data structures for <i>de novo</i> genome assembly in the big data era. Quantitative Biology, 2019, 7, 278-292.	0.5	30
14	On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. Journal of Computational Biology, 2016, 23, 718-736.	1.6	29
15	On the Approximation of Correlation Clustering and Consensus Clustering. Journal of Computer and System Sciences, 2008, 74, 671-696.	1.2	28
16	ASPIC: a web resource for alternative splicing prediction and transcript isoforms characterization. Nucleic Acids Research, 2006, 34, W440-W443.	14.5	27
17	MALVA: Genotyping by Mapping-free ALlele Detection of Known VARIants. IScience, 2019, 18, 20-27.	4.1	27
18	ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events. BMC Bioinformatics, 2018, 19, 444.	2.6	26

#	ARTICLE	IF	CITATIONS
19	Separating some splicing models. Information Processing Letters, 2001, 79, 255-259.	0.6	25
20	Experimenting an approximation algorithm for the LCS. Discrete Applied Mathematics, 2001, 110, 13-24.	0.9	23
21	Detecting Alternative Gene Structures from Spliced ESTs: A Computational Approach. Journal of Computational Biology, 2009, 16, 43-66.	1.6	23
22	An approximation algorithm for the shortest common supersequence problem. , 2001, , .		22
23	The structure of reflexive regular splicing languages via Sch $\frac{1}{4}$ tzenberger constants. Theoretical Computer Science, 2005, 334, 71-98.	0.9	22
24	A Linear-Time Algorithm for the Perfect Phylogeny Haplotype Problem. Algorithmica, 2007, 48, 267-285.	1.3	22
25	Modeling Alternative Splicing Variants from RNA-Seq Data with Isoform Graphs. Journal of Computational Biology, 2014, 21, 16-40.	1.6	22
26	Further Steps in TANGO: improved taxonomic assignment in metagenomics. Bioinformatics, 2014, 30, 17-23.	4.1	22
27	Computational graph pangénomics: a tutorial on data structures and their applications. Natural Computing, 2022, 21, 81-108.	3.0	22
28	On the parameterized complexity of the repetition free longest common subsequence problem. Information Processing Letters, 2012, 112, 272-276.	0.6	19
29	Regular splicing languages and subclasses. Theoretical Computer Science, 2005, 340, 349-363.	0.9	16
30	Computational methods for alternative splicing prediction. Briefings in Functional Genomics & Proteomics, 2006, 5, 46-51.	3.8	16
31	Anonymizing binary and small tables is \hat{A} hard \hat{A} approximate. Journal of Combinatorial Optimization, 2011, 22, 97-119.	1.3	14
32	LSG: An External-Memory Tool to Compute String Graphs for Next-Generation Sequencing Data Assembly. Journal of Computational Biology, 2016, 23, 137-149.	1.6	14
33	Inverse Lyndon words and inverse Lyndon factorizations of words. Advances in Applied Mathematics, 2018, 101, 281-319.	0.7	14
34	Does Relaxing the Infinite Sites Assumption Give Better Tumor Phylogenies? An ILP-Based Comparative Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1410-1423.	3.0	14
35	Correlation Clustering and Consensus Clustering. Lecture Notes in Computer Science, 2005, , 226-235.	1.3	14
36	Triplet-based similarity score for fully multilabeled trees with poly-occurring labels. Bioinformatics, 2021, 37, 178-184.	4.1	13

#	ARTICLE	IF	CITATIONS
37	Circular splicing and regularity. <i>RAIRO - Theoretical Informatics and Applications</i> , 2004, 38, 189-228.	0.5	12
38	FSG: Fast String Graph Construction for De Novo Assembly. <i>Journal of Computational Biology</i> , 2017, 24, 953-968.	1.6	12
39	A colored graph approach to perfect phylogeny with persistent characters. <i>Theoretical Computer Science</i> , 2017, 658, 60-73.	0.9	12
40	On the power of circular splicing. <i>Discrete Applied Mathematics</i> , 2005, 150, 51-66.	0.9	11
41	Decision Problems for Linear and Circular Splicing Systems. <i>Lecture Notes in Computer Science</i> , 2003, , 78-92.	1.3	11
42	A characterization of (regular) circular languages generated by monotone complete splicing systems. <i>Theoretical Computer Science</i> , 2010, 411, 4149-4161.	0.9	10
43	Maximum Disjoint Paths on Edge-Colored Graphs: Approximability and Tractability. <i>Algorithms</i> , 2013, 6, 1-11.	2.1	10
44	Existence of constants in regular splicing languages. <i>Information and Computation</i> , 2015, 242, 340-353.	0.7	10
45	gpps: an ILP-based approach for inferring cancer progression with mutation losses from single cell data. <i>BMC Bioinformatics</i> , 2020, 21, 413.	2.6	10
46	DNA and circular splicing?. <i>Lecture Notes in Computer Science</i> , 2001, , 117-129.	1.3	10
47	Primitive 2-structures with the $(n \hat{=} 2)$ -property. <i>Theoretical Computer Science</i> , 1994, 132, 151-178.	0.9	9
48	An Efficient Algorithm for Haplotype Inference on Pedigrees with Recombinations and Mutations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 12-25.	3.0	9
49	An External-Memory Algorithm for String Graph Construction. <i>Algorithmica</i> , 2017, 78, 394-424.	1.3	9
50	On the regularity of circular splicing languages: a survey and new developments. <i>Natural Computing</i> , 2010, 9, 397-420.	3.0	8
51	Plntron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. <i>BMC Bioinformatics</i> , 2012, 13, S2.	2.6	8
52	On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction Problem. <i>Lecture Notes in Computer Science</i> , 2015, , 100-113.	1.3	8
53	HapCHAT: adaptive haplotype assembly for efficiently leveraging high coverage in long reads. <i>BMC Bioinformatics</i> , 2018, 19, 252.	2.6	8
54	Multithread Multistring Burrowsâ€Wheeler Transform and Longest Common Prefix Array. <i>Journal of Computational Biology</i> , 2019, 26, 948-961.	1.6	8

#	ARTICLE	IF	CITATIONS
55	Shark: fishing relevant reads in an RNA-Seq sample. <i>Bioinformatics</i> , 2021, 37, 464-472.	4.1	8
56	Effective Clustering for Single Cell Sequencing Cancer Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 4068-4078.	6.3	8
57	Regular Splicing Languages Must Have a Constant. <i>Lecture Notes in Computer Science</i> , 2011, , 82-92.	1.3	7
58	Haplotype-based prediction of gene alleles using pedigrees and SNP genotypes. , 2013, , .		6
59	Covering Pairs in Directed Acyclic Graphs. <i>Computer Journal</i> , 2015, 58, 1673-1686.	2.4	6
60	Regular Languages Generated by Reflexive Finite Splicing Systems. <i>Lecture Notes in Computer Science</i> , 2003, , 134-145.	1.3	6
61	Parameterized complexity of k-anonymity: hardness and tractability. <i>Journal of Combinatorial Optimization</i> , 2013, 26, 19-43.	1.3	5
62	Complexity insights of the Minimum Duplication problem. <i>Theoretical Computer Science</i> , 2014, 530, 66-79.	0.9	5
63	On the longest common prefix of suffixes in an inverse Lyndon factorization and other properties. <i>Theoretical Computer Science</i> , 2021, 862, 24-41.	0.9	5
64	Comparative genome analysis using sample-specific string detection in accurate long reads. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	5
65	Constructing String Graphs in External Memory. <i>Lecture Notes in Computer Science</i> , 2014, , 311-325.	1.3	5
66	Complexity Insights of the Minimum Duplication Problem. <i>Lecture Notes in Computer Science</i> , 2012, , 153-164.	1.3	5
67	APPROXIMATING THE MAXIMUM ISOMORPHIC AGREEMENT SUBTREE IS HARD. <i>International Journal of Foundations of Computer Science</i> , 2000, 11, 579-590.	1.1	4
68	Linear splicing and syntactic monoid. <i>Discrete Applied Mathematics</i> , 2006, 154, 452-470.	0.9	4
69	Constants and label-equivalence: A decision procedure for reflexive regular splicing languages. <i>Theoretical Computer Science</i> , 2010, 411, 865-877.	0.9	4
70	Pure Parsimony Xor Haplotyping. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 598-610.	3.0	4
71	A Clustering Algorithm for Planning the Integration Process of a Large Number of Conceptual Schemas. <i>Journal of Computer Science and Technology</i> , 2015, 30, 214-224.	1.5	4
72	Finding Maximal Exact Matches Using the r-Index. <i>Journal of Computational Biology</i> , 2022, 29, 188-194.	1.6	4

#	ARTICLE	IF	CITATIONS
73	GPPS: an ILP-based approach for inferring cancer progression with mutation losses from single cell data. , 2018, , .		3
74	Computing the multi-string BWT and LCP array in external memory. Theoretical Computer Science, 2021, 862, 42-58.	0.9	3
75	A Decision Procedure for Reflexive Regular Splicing Languages. Lecture Notes in Computer Science, 2006, , 315-326.	1.3	3
76	Picture Languages Generated by Assembling Tiles. Lecture Notes in Computer Science, 2009, , 224-235.	1.3	2
77	Fingerprint Clustering with Bounded Number of Missing Values. Algorithmica, 2010, 58, 282-303.	1.3	1
78	Reconstructing isoform graphs from RNA-Seq data. , 2012, , .		1
79	A fast and practical approach to genotype phasing and imputation on a pedigree with erroneous and incomplete information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1582-1594.	3.0	1
80	A randomized PTAS for the minimum Consensus Clustering with a fixed number of clusters. Theoretical Computer Science, 2012, 429, 36-45.	0.9	1
81	Restricted and Swap Common Superstring: A Multivariate Algorithmic Perspective. Algorithmica, 2015, 72, 914-939.	1.3	1
82	FSG: Fast String Graph Construction for De Novo Assembly of Reads Data. Lecture Notes in Computer Science, 2016, , 27-39.	1.3	1
83	Transcriptome Assembly and Alternative Splicing Analysis. Methods in Molecular Biology, 2015, 1269, 173-188.	0.9	1
84	Circular Languages Generated by Complete Splicing Systems and Pure Unitary Languages. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 9, 22-31.	0.8	1
85	Recombinant DNA ,Gene Splicing as Generative Devices of Formal Languages. Lecture Notes in Computer Science, 2005, , 65-67.	1.3	1
86	Exemplar Longest Common Subsequence. Lecture Notes in Computer Science, 2006, , 622-629.	1.3	1
87	Restricted and Swap Common Superstring: A Parameterized View. Lecture Notes in Computer Science, 2012, , 49-60.	1.3	1
88	Nesting of prime substructures in k-ary relations. Theoretical Computer Science, 2001, 259, 341-357.	0.9	0
89	Plntron: A fast method for gene structure prediction via maximal pairings of a pattern and a text. , 2011, , .		0
90	Picture Languages Generated by Assembling Tiles. Fundamenta Informaticae, 2011, 110, 77-93.	0.4	0

#	ARTICLE	IF	CITATIONS
91	A fast and practical approach to genotype phasing and imputation on a pedigree with erroneous and incomplete information. , 2012, , .		0
92	Species-Driven Persistent Phylogeny. Fundamenta Informaticae, 2017, 154, 47-63.	0.4	0
93	Incomplete Directed Perfect Phylogeny in Linear Time. Lecture Notes in Computer Science, 2021, , 172-185.	1.3	0
94	Fingerprint Clustering with Bounded Number of Missing Values. Lecture Notes in Computer Science, 2006, , 106-116.	1.3	0
95	Finite Splicing: Generative Capacity, New Models and Complexity Aspects. Natural Computing Series, 2009, , 313-329.	2.2	0
96	Pure Parsimony Xor Haplotyping. Lecture Notes in Computer Science, 2009, , 186-197.	1.3	0
97	Haplotype Inference on Pedigrees with Recombinations and Mutations. Lecture Notes in Computer Science, 2010, , 148-161.	1.3	0
98	Covering Pairs in Directed Acyclic Graphs. Lecture Notes in Computer Science, 2014, , 126-137.	1.3	0
99	Automata and Formal Languages for Next Generation Sequencing Data. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 252, 1-2.	0.8	0