Giuseppe Lancia

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/154863/publications.pdf

Version: 2024-02-01

56
papers

1,632
citations

411340
20
h-index

355658
38
g-index

60
all docs

60
docs citations

60
times ranked

952
citing authors

#	Article	IF	Citations
1	Computational Complexity and ILP Models for Pattern Problems in the Logical Analysis of Data. Algorithms, 2021, 14, 235.	1.2	3
2	Finding the Best 3-OPT Move in Subcubic Time. Algorithms, 2020, 13, 306.	1.2	2
3	Finding the largest triangle in a graph in expected quadratic time. European Journal of Operational Research, 2020, 286, 458-467.	3.5	4
4	Using Integer Programming to Search for Counterexamples: A Case Study. Lecture Notes in Computer Science, 2020, , 69-84.	1.0	4
5	FASTSET: A Fast Data Structure for the Representation of Sets of Integers. Algorithms, 2019, 12, 91.	1.2	1
6	Speeding-Up the Dynamic Programming Procedure for the Edit Distance of Two Strings. Communications in Computer and Information Science, 2019, , 59-66.	0.4	0
7	Compact Extended Linear Programming Models. EURO Advanced Tutorials on Operational Research, 2018, , .	0.6	34
8	A Facility Location Model for Air Pollution Detection. Mathematical Problems in Engineering, 2018, 2018, 1-8.	0.6	5
9	New Modeling Ideas for the Exact Solution of the Closest String Problem. Communications in Computer and Information Science, 2018, , 105-114.	0.4	0
10	Separating sets of strings by finding matching patterns is almost always hard. Theoretical Computer Science, 2017, 665, 73-86.	0.5	5
11	Algorithmic approaches for the single individual haplotyping problem. RAIRO - Operations Research, 2016, 50, 331-340.	1.0	13
12	Deriving compact extended formulations via LP-based separation techniques. Annals of Operations Research, 2016, 240, 321-350.	2.6	0
13	The Complexity of Some Pattern Problems in the Logical Analysis of Large Genomic Data Sets. Lecture Notes in Computer Science, 2016, , 3-12.	1.0	2
14	Perfect Phylogeny Haplotyping. , 2016, , 1553-1557.		0
15	Local search inequalities. Discrete Optimization, 2015, 16, 76-89.	0.6	4
16	Estimating the strength of poker hands by integer linear programming techniques. Central European Journal of Operations Research, 2015, 23, 625-640.	1.1	5
17	A Unified Integer Programming Model for Genome Rearrangement Problems. Lecture Notes in Computer Science, 2015, , 491-502.	1.0	4
18	Deriving compact extended formulations via LP-based separation techniques. 4or, 2014, 12, 201-234.	1.0	12

#	Article	IF	Citations
19	Ramsey theory and integrality gap for the independent set problem. Operations Research Letters, 2014, 42, 137-139.	0.5	2
20	A time-indexed LP-based approach for min-sum job-shop problems. Annals of Operations Research, 2011, 186, 175-198.	2.6	9
21	An effective compact formulation of the max cut problem on sparse graphs. Electronic Notes in Discrete Mathematics, 2011, 37, 111-116.	0.4	6
22	CollHaps: A Heuristic Approach to Haplotype Inference by Parsimony. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 511-523.	1.9	15
23	A Set-Covering Approach with Column Generation for Parsimony Haplotyping. INFORMS Journal on Computing, 2009, 21, 151-166.	1.0	8
24	The phasing of heterozygous traits: Algorithms and complexity. Computers and Mathematics With Applications, 2008, 55, 960-969.	1.4	10
25	Logic classification and feature selection for biomedical data. Computers and Mathematics With Applications, 2008, 55, 889-899.	1.4	26
26	FLIPPING LETTERS TO MINIMIZE THE SUPPORT OF A STRING. International Journal of Foundations of Computer Science, 2008, 19, 5-17.	0.8	0
27	Haplotyping for Disease Association: A Combinatorial Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 245-251.	1.9	1
28	Mathematical Programming in Computational Biology: an Annotated Bibliography. Algorithms, 2008, 1, 100-129.	1.2	39
29	Perfect Phylogeny Haplotyping. , 2008, , 647-650.		0
30	Articles selected from posters presented at the Tenth Annual International Conference on Research in Computational Biology â€“ Preface. BMC Bioinformatics, 2007, 8, S1.	1.2	2
31	The approximability of the String Barcoding problem. Algorithms for Molecular Biology, 2006, 1, 12.	0.3	3
32	A polynomial case of the parsimony haplotyping problem. Operations Research Letters, 2006, 34, 289-295.	0.5	37
33	Computational Molecular Biology. , 2006, , 373-425.		0
34	Polynomial and APX-hard cases of the individual haplotyping problem. Theoretical Computer Science, 2005, 335, 109-125.	0.5	50
35	The String Barcoding Problem is NP-Hard. Lecture Notes in Computer Science, 2005, , 88-96.	1.0	1
36	Opportunities for Combinatorial Optimization in Computational Biology. INFORMS Journal on Computing, 2004, 16, 211-231.	1.0	101

#	ARTICLE	IF	CITATIONS
37	Haplotyping Populations by Pure Parsimony: Complexity of Exact and Approximation Algorithms. INFORMS Journal on Computing, 2004, 16, 348-359.	1.0	105
38	Integer programming models for computational biology problems. Journal of Computer Science and Technology, 2004, 19, 60-77.	0.9	39
39	1001 Optimal PDB Structure Alignments: Integer Programming Methods for Finding the Maximum Contact Map Overlap. Journal of Computational Biology, 2004, 11, 27-52.	0.8	138
40	Haplotyping as Perfect Phylogeny. Lecture Notes in Computer Science, 2004, , 131-131.	1.0	0
41	Haplotyping as Perfect Phylogeny: A Direct Approach. Journal of Computational Biology, 2003, 10, 323-340.	0.8	115
42	Protein Structure Comparison: Algorithms and Applications. Lecture Notes in Computer Science, 2003, , 1-33.	1.0	25
43	Algorithmic strategies for the single nucleotide polymorphism haplotype assembly problem. Briefings in Bioinformatics, 2002, 3, 23-31.	3.2	187
44	Structural alignment of large---size proteins via lagrangian relaxation. , 2002, , .		50
45	Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem. Lecture Notes in Computer Science, 2002, , 29-43.	1.0	56
46	Exact algorithms for minimum routing cost trees. Networks, 2002, 39, 161-173.	1.6	35
47	Compact vs. exponential-size LP relaxations. Operations Research Letters, 2002, 30, 57-65.	0.5	21
48	Sorting Permutations by Reversals Through Branch-and-Price. INFORMS Journal on Computing, 2001, 13, 224-244.	1.0	20
49	101 optimal PDB structure alignments. , 2001, , .		66
50	Scheduling jobs with release dates and tails on two unrelated parallel machines to minimize the makespan. European Journal of Operational Research, 2000, 120, 277-288.	3.5	26
51	A Polynomial-Time Approximation Scheme for Minimum Routing Cost Spanning Trees. SIAM Journal on Computing, 2000, 29, 761-778.	0.8	103
52	GESTALT: Genomic Steiner Alignments. Lecture Notes in Computer Science, 1999, , 101-114.	1.0	14
53	A column-generation based branch-and-bound algorithm for sorting by reversals. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 1999, , 213-226.	0.0	14
54	Job Shop Scheduling With Deadlines. Journal of Combinatorial Optimization, 1998, 1, 329-353.	0.8	23

#	ARTICLE	IF	CITATIONS
55	Genotyping of pooled microsatellite markers by combinatorial optimization techniques. Discrete Applied Mathematics, 1998, 88, 291-314.	0.5	5
56	Banishing bias from consensus sequences. Lecture Notes in Computer Science, 1997, , 247-261.	1.0	43