

Giuseppe Lancia

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

1,632
citations

361388

20
h-index

315719

38
g-index

60
all docs

60
docs citations

60
times ranked

820
citing authors

#	ARTICLE	IF	CITATIONS
1	Algorithmic strategies for the single nucleotide polymorphism haplotype assembly problem. Briefings in Bioinformatics, 2002, 3, 23-31.	6.5	187
2	1001 Optimal PDB Structure Alignments: Integer Programming Methods for Finding the Maximum Contact Map Overlap. Journal of Computational Biology, 2004, 11, 27-52.	1.6	138
3	Haplotyping as Perfect Phylogeny: A Direct Approach. Journal of Computational Biology, 2003, 10, 323-340.	1.6	115
4	Haplotyping Populations by Pure Parsimony: Complexity of Exact and Approximation Algorithms. INFORMS Journal on Computing, 2004, 16, 348-359.	1.7	105
5	A Polynomial-Time Approximation Scheme for Minimum Routing Cost Spanning Trees. SIAM Journal on Computing, 2000, 29, 761-778.	1.0	103
6	Opportunities for Combinatorial Optimization in Computational Biology. INFORMS Journal on Computing, 2004, 16, 211-231.	1.7	101
7	101 optimal PDB structure alignments. , 2001, , .		66
8	Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem. Lecture Notes in Computer Science, 2002, , 29-43.	1.3	56
9	Structural alignment of large-size proteins via lagrangian relaxation. , 2002, , .		50
10	Polynomial and APX-hard cases of the individual haplotyping problem. Theoretical Computer Science, 2005, 335, 109-125.	0.9	50
11	Banishing bias from consensus sequences. Lecture Notes in Computer Science, 1997, , 247-261.	1.3	43
12	Integer programming models for computational biology problems. Journal of Computer Science and Technology, 2004, 19, 60-77.	1.5	39
13	Mathematical Programming in Computational Biology: an Annotated Bibliography. Algorithms, 2008, 1, 100-129.	2.1	39
14	A polynomial case of the parsimony haplotyping problem. Operations Research Letters, 2006, 34, 289-295.	0.7	37
15	Exact algorithms for minimum routing cost trees. Networks, 2002, 39, 161-173.	2.7	35
16	Compact Extended Linear Programming Models. EURO Advanced Tutorials on Operational Research, 2018, , .	0.6	34
17	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.	5.7	26
18	Logic classification and feature selection for biomedical data. Computers and Mathematics With Applications, 2008, 55, 889-899.	2.7	26

#	ARTICLE	IF	CITATIONS
19	Protein Structure Comparison: Algorithms and Applications. Lecture Notes in Computer Science, 2003, , 1-33.	1.3	25
20	Job Shop Scheduling With Deadlines. Journal of Combinatorial Optimization, 1998, 1, 329-353.	1.3	23
21	Compact vs. exponential-size LP relaxations. Operations Research Letters, 2002, 30, 57-65.	0.7	21
22	Sorting Permutations by Reversals Through Branch-and-Price. INFORMS Journal on Computing, 2001, 13, 224-244.	1.7	20
23	CollHaps: A Heuristic Approach to Haplotype Inference by Parsimony. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 511-523.	3.0	15
24	GESTALT: Genomic Steiner Alignments. Lecture Notes in Computer Science, 1999, , 101-114.	1.3	14
25	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
26	Algorithmic approaches for the single individual haplotyping problem. RAIRO - Operations Research, 2016, 50, 331-340.	1.8	13
27	Deriving compact extended formulations via LP-based separation techniques. 4or, 2014, 12, 201-234.	1.6	12
28	The phasing of heterozygous traits: Algorithms and complexity. Computers and Mathematics With Applications, 2008, 55, 960-969.	2.7	10
29	A time-indexed LP-based approach for min-sum job-shop problems. Annals of Operations Research, 2011, 186, 175-198.	4.1	9
30	A Set-Covering Approach with Column Generation for Parsimony Haplotyping. INFORMS Journal on Computing, 2009, 21, 151-166.	1.7	8
31	An effective compact formulation of the max cut problem on sparse graphs. Electronic Notes in Discrete Mathematics, 2011, 37, 111-116.	0.4	6
32	Genotyping of pooled microsatellite markers by combinatorial optimization techniques. Discrete Applied Mathematics, 1998, 88, 291-314.	0.9	5
33	Estimating the strength of poker hands by integer linear programming techniques. Central European Journal of Operations Research, 2015, 23, 625-640.	1.8	5
34	Separating sets of strings by finding matching patterns is almost always hard. Theoretical Computer Science, 2017, 665, 73-86.	0.9	5
35	A Facility Location Model for Air Pollution Detection. Mathematical Problems in Engineering, 2018, 2018, 1-8.	1.1	5
36	Local search inequalities. Discrete Optimization, 2015, 16, 76-89.	0.9	4

#	ARTICLE	IF	CITATIONS
37	Finding the largest triangle in a graph in expected quadratic time. <i>European Journal of Operational Research</i> , 2020, 286, 458-467.	5.7	4
38	Using Integer Programming to Search for Counterexamples: A Case Study. <i>Lecture Notes in Computer Science</i> , 2020, , 69-84.	1.3	4
39	A Unified Integer Programming Model for Genome Rearrangement Problems. <i>Lecture Notes in Computer Science</i> , 2015, , 491-502.	1.3	4
40	The approximability of the String Barcoding problem. <i>Algorithms for Molecular Biology</i> , 2006, 1, 12.	1.2	3
41	Computational Complexity and ILP Models for Pattern Problems in the Logical Analysis of Data. <i>Algorithms</i> , 2021, 14, 235.	2.1	3
42	Articles selected from posters presented at the Tenth Annual International Conference on Research in Computational Biology "Preface. <i>BMC Bioinformatics</i> , 2007, 8, S1.	2.6	2
43	Ramsey theory and integrality gap for the independent set problem. <i>Operations Research Letters</i> , 2014, 42, 137-139.	0.7	2
44	The Complexity of Some Pattern Problems in the Logical Analysis of Large Genomic Data Sets. <i>Lecture Notes in Computer Science</i> , 2016, , 3-12.	1.3	2
45	Finding the Best 3-OPT Move in Subcubic Time. <i>Algorithms</i> , 2020, 13, 306.	2.1	2
46	Haplotyping for Disease Association: A Combinatorial Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 245-251.	3.0	1
47	FASTSET: A Fast Data Structure for the Representation of Sets of Integers. <i>Algorithms</i> , 2019, 12, 91.	2.1	1
48	The String Barcoding Problem is NP-Hard. <i>Lecture Notes in Computer Science</i> , 2005, , 88-96.	1.3	1
49	Haplotyping as Perfect Phylogeny. <i>Lecture Notes in Computer Science</i> , 2004, , 131-131.	1.3	0
50	FLIPPING LETTERS TO MINIMIZE THE SUPPORT OF A STRING. <i>International Journal of Foundations of Computer Science</i> , 2008, 19, 5-17.	1.1	0
51	Deriving compact extended formulations via LP-based separation techniques. <i>Annals of Operations Research</i> , 2016, 240, 321-350.	4.1	0
52	Perfect Phylogeny Haplotyping. , 2008, , 647-650.		0
53	Perfect Phylogeny Haplotyping. , 2016, , 1553-1557.		0
54	New Modeling Ideas for the Exact Solution of the Closest String Problem. <i>Communications in Computer and Information Science</i> , 2018, , 105-114.	0.5	0

#	ARTICLE	IF	CITATIONS
55	Speeding-Up the Dynamic Programming Procedure for the Edit Distance of Two Strings. Communications in Computer and Information Science, 2019, , 59-66.	0.5	0
56	Computational Molecular Biology. , 2006, , 373-425.		0