

Gabriel Valiente

List of Publications by Year in descending order

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59
papers

1,388
citations

471509

17
h-index

414414

32
g-index

63
all docs

63
docs citations

63
times ranked

1340
citing authors

#	ARTICLE	IF	CITATIONS
1	Adjacency Maps and Efficient Graph Algorithms. Algorithms, 2022, 15, 67.	2.1	1
2	Graph Isomorphism. Texts in Computer Science, 2021, , 255-285.	0.7	0
3	Tree Isomorphism. Texts in Computer Science, 2021, , 113-180.	0.7	0
4	Algorithmic Techniques. Texts in Computer Science, 2021, , 45-83.	0.7	0
5	The Generalized Robinson-Foulds Distance for Phylogenetic Trees. Journal of Computational Biology, 2021, 28, 1181-1195.	1.6	6
6	AligNet: alignment of protein-protein interaction networks. BMC Bioinformatics, 2020, 21, 265.	2.6	8
7	Alignment of biological networks by integer linear programming: virus-host protein-protein interaction networks. BMC Bioinformatics, 2020, 21, 434.	2.6	3
8	Alignment of virus-host protein-protein interaction networks by integer linear programming: SARS-CoV-2. PLoS ONE, 2020, 15, e0236304.	2.5	3
9	A Generalized Robinson-Foulds Distance for Clonal Trees, Mutation Trees, and Phylogenetic Trees and Networks. , 2020, , .		2
10	Unbiased Taxonomic Annotation of Metagenomic Samples. Journal of Computational Biology, 2018, 25, 348-360.	1.6	12
11	Unbiased Taxonomic Annotation of Metagenomic Samples. Lecture Notes in Computer Science, 2017, , 162-173.	1.3	0
12	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. BMC Bioinformatics, 2015, 16, 203.	2.6	49
13	The Comparison of Tree-Sibling Time Consistent Phylogenetic Networks Is Graph Isomorphism-Complete. Scientific World Journal, The, 2014, 2014, 1-6.	2.1	4
14	Further Steps in TANGO: improved taxonomic assignment in metagenomics. Bioinformatics, 2014, 30, 17-23.	4.1	22
15	Reference databases for taxonomic assignment in metagenomics. Briefings in Bioinformatics, 2012, 13, 682-695.	6.5	82
16	Editorial. Briefings in Bioinformatics, 2012, 13, 645-645.	6.5	3
17	Faster computation of the Robinson-Foulds distance between phylogenetic networks. Information Sciences, 2012, 197, 77-90.	6.9	3
18	Comparison of Galled Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 410-427.	3.0	15

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19	Flexible taxonomic assignment of ambiguous sequencing reads. BMC Bioinformatics, 2011, 12, 8.	2.6	26
20	Computational challenges of sequence classification in microbiomic data. Briefings in Bioinformatics, 2011, 12, 614-625.	6.5	15
21	Nodal distances for rooted phylogenetic trees. Journal of Mathematical Biology, 2010, 61, 253-276.	1.9	26
22	An optimized TOPS+ comparison method for enhanced TOPS models. BMC Bioinformatics, 2010, 11, 138.	2.6	2
23	Characterization of phylogenetic networks with NetTest. BMC Bioinformatics, 2010, 11, 268.	2.6	11
24	Path lengths in tree-child time consistent hybridization networks. Information Sciences, 2010, 180, 366-383.	6.9	7
25	Faster Computation of the Robinson-Foulds Distance between Phylogenetic Networks. Lecture Notes in Computer Science, 2010, , 190-201.	1.3	3
26	Metrics for Phylogenetic Networks II: Nodal and Triplets Metrics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 454-469.	3.0	22
27	Metrics for Phylogenetic Networks I: Generalizations of the Robinson-Foulds Metric. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 46-61.	3.0	44
28	ACCURATE TAXONOMIC ASSIGNMENT OF SHORT PYROSEQUENCING READS. , 2009, , 3-9.		13
29	Optimized ancestral state reconstruction using Sankoff parsimony. BMC Bioinformatics, 2009, 10, 51.	2.6	11
30	Efficient Reconstruction of Metabolic Pathways by Bidirectional Chemical Search. Bulletin of Mathematical Biology, 2009, 71, 750-769.	1.9	3
31	An algebraic metric for phylogenetic trees. Applied Mathematics Letters, 2009, 22, 1320-1324.	2.7	15
32	All that glitters is not galled. Mathematical Biosciences, 2009, 221, 54-59.	1.9	17
33	Comparison of Tree-Child Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 552-569.	3.0	123
34	On Nakhleh's Metric for Reduced Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 629-638.	3.0	15
35	A perl package and an alignment tool for phylogenetic networks. BMC Bioinformatics, 2008, 9, 175.	2.6	13
36	Extended Newick: it is time for a standard representation of phylogenetic networks. BMC Bioinformatics, 2008, 9, 532.	2.6	82

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37	Tripartitions do not always discriminate phylogenetic networks. <i>Mathematical Biosciences</i> , 2008, 211, 356-370.	1.9	28
38	Seeded Tree Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 503-513.	3.0	11
39	A distance metric for a class of tree-sibling phylogenetic networks. <i>Bioinformatics</i> , 2008, 24, 1481-1488.	4.1	48
40	Characterization of Reticulate Networks Based on the Coalescent with Recombination. <i>Molecular Biology and Evolution</i> , 2008, 25, 2517-2520.	8.9	22
41	Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs. , 2008, , 372-395.		6
42	Phylogenetic reconstruction from non-genomic data. <i>Bioinformatics</i> , 2007, 23, e110-e115.	4.1	27
43	Linear structure of bipartite permutation graphs and the longest path problem. <i>Information Processing Letters</i> , 2007, 103, 71-77.	0.6	27
44	Compression-based classification of biological sequences and structures via the Universal Similarity Metric: experimental assessment. <i>BMC Bioinformatics</i> , 2007, 8, 252.	2.6	89
45	Validation of metabolic pathway databases based on chemical substructure search. <i>New Biotechnology</i> , 2007, 24, 327-335.	2.7	10
46	Efficient Algorithms on Trees and Graphs with Unique Node Labels. , 2007, , 137-149.		8
47	Seeded Tree Alignment and Planar Tanglegram Layout. <i>Lecture Notes in Computer Science</i> , 2007, , 98-110.	1.3	10
48	Reconstructing Metabolic Pathways by Bidirectional Chemical Search. <i>Lecture Notes in Computer Science</i> , 2007, , 217-232.	1.3	1
49	An algebraic view of the relation between largest common subtrees and smallest common supertrees. <i>Theoretical Computer Science</i> , 2006, 362, 33-53.	0.9	10
50	On the Ancestral Compatibility of Two Phylogenetic Trees with Nested Taxa. <i>Journal of Mathematical Biology</i> , 2006, 53, 340-364.	1.9	0
51	Constrained tree inclusion. <i>Journal of Discrete Algorithms</i> , 2005, 3, 431-447.	0.7	19
52	Chemical Graphs, Chemical Reaction Graphs, and Chemical Graph Transformation. <i>Electronic Notes in Theoretical Computer Science</i> , 2005, 127, 157-166.	0.9	15
53	An edit script for taxonomic classifications. <i>BMC Bioinformatics</i> , 2005, 6, 208.	2.6	10
54	Graph Transformation in Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2005, , 116-133.	1.3	21

#	ARTICLE	IF	CITATIONS
55	A Fast Algorithmic Technique for Comparing Large Phylogenetic Trees. Lecture Notes in Computer Science, 2005, , 370-375.	1.3	4
56	Trading uninitialized space for time. Information Processing Letters, 2004, 92, 9-13.	0.6	3
57	Analysis of Metabolic Pathways by Graph Transformation. Lecture Notes in Computer Science, 2004, , 70-82.	1.3	11
58	Algorithms on Trees and Graphs. , 2002, , .		171
59	A graph distance metric combining maximum common subgraph and minimum common supergraph. Pattern Recognition Letters, 2001, 22, 753-758.	4.2	161