Gabriel Valiente

List of Publications by Year
in descending order

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	Algorithms on Trees and Graphs. , 2002, , .		171
2	A graph distance metric combining maximum common subgraph and minimum common supergraph. Pattern Recognition Letters, 2001, 22, 753-758.	4.2	161
3	Comparison of Tree-Child Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 552-569.	3.0	123
4	Compression-based classification of biological sequences and structures via the Universal Similarity Metric: experimental assessment. BMC Bioinformatics, 2007, 8, 252.	2.6	89
5	Extended Newick: it is time for a standard representation of phylogenetic networks. BMC Bioinformatics, 2008, 9, 532.	2.6	82
6	Reference databases for taxonomic assignment in metagenomics. Briefings in Bioinformatics, 2012, 13, 682-695.	6.5	82
7	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. BMC Bioinformatics, 2015, 16, 203.	2.6	49
8	A distance metric for a class of tree-sibling phylogenetic networks. Bioinformatics, 2008, 24, 1481-1488.	4.1	48
9	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
10	Tripartitions do not always discriminate phylogenetic networks. Mathematical Biosciences, 2008, 211, 356-370.	1.9	28
11	Phylogenetic reconstruction from non-genomic data. Bioinformatics, 2007, 23, e110-e115.	4.1	27
12	Linear structure of bipartite permutation graphs and the longest path problem. Information Processing Letters, 2007, 103, 71-77.	0.6	27
13	Nodal distances for rooted phylogenetic trees. Journal of Mathematical Biology, 2010, 61, 253-276.	1.9	26
14	Flexible taxonomic assignment of ambiguous sequencing reads. BMC Bioinformatics, 2011, 12, 8.	2.6	26
15	Characterization of Reticulate Networks Based on the Coalescent with Recombination. Molecular Biology and Evolution, 2008, 25, 2517-2520.	8.9	22
16	Metrics for Phylogenetic Networks II: Nodal and Triplets Metrics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 454-469.	3.0	22
17	Further Steps in TANGO: improved taxonomic assignment in metagenomics. Bioinformatics, 2014, 30, 17-23.	4.1	22
18	Graph Transformation in Molecular Biology. Lecture Notes in Computer Science, 2005, , 116-133.	1.3	21

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19	Constrained tree inclusion. Journal of Discrete Algorithms, 2005, 3, 431-447.	0.7	19
20	All that glisters is not galled. Mathematical Biosciences, 2009, 221, 54-59.	1.9	17
21	Chemical Graphs, Chemical Reaction Graphs, and Chemical Graph Transformation. Electronic Notes in Theoretical Computer Science, 2005, 127, 157-166.	0.9	15
22	An algebraic metric for phylogenetic trees. Applied Mathematics Letters, 2009, 22, 1320-1324.	2.7	15
23	On Nakhleh's Metric for Reduced Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 629-638.	3.0	15
24	Comparison of Galled Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 410-427.	3.0	15
25	Computational challenges of sequence classification in microbiomic data. Briefings in Bioinformatics, 2011, 12, 614-625.	6.5	15
26	A perl package and an alignment tool for phylogenetic networks. BMC Bioinformatics, 2008, 9, 175.	2.6	13
27	ACCURATE TAXONOMIC ASSIGNMENT OF SHORT PYROSEQUENCING READS. , 2009, , 3-9.		13
28	Unbiased Taxonomic Annotation of Metagenomic Samples. Journal of Computational Biology, 2018, 25, 348-360.	1.6	12
29	Seeded Tree Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 503-513.	3.0	11
30	Optimized ancestral state reconstruction using Sankoff parsimony. BMC Bioinformatics, 2009, 10, 51.	2.6	11
31	Characterization of phylogenetic networks with NetTest. BMC Bioinformatics, 2010, 11, 268.	2.6	11
32	Analysis of Metabolic Pathways by Graph Transformation. Lecture Notes in Computer Science, 2004, , 70-82.	1.3	11
33	An edit script for taxonomic classifications. BMC Bioinformatics, 2005, 6, 208.	2.6	10
34	An algebraic view of the relation between largest common subtrees and smallest common supertrees. Theoretical Computer Science, 2006, 362, 33-53.	0.9	10
35	Validation of metabolic pathway databases based on chemical substructure search. New Biotechnology, 2007, 24, 327-335.	2.7	10
36	Seeded Tree Alignment and Planar Tanglegram Layout. Lecture Notes in Computer Science, 2007, , 98-110.	1.3	10

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37	AligNet: alignment of protein-protein interaction networks. BMC Bioinformatics, 2020, 21, 265.	2.6	8
38	Efficient Algorithms on Trees and Graphs with Unique Node Labels. , 2007, , 137-149.		8
39	Path lengths in tree-child time consistent hybridization networks. Information Sciences, 2010, 180, 366-383.	6.9	7
40	Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs. , 2008, , 372-395.		6
41	The Generalized Robinson-Foulds Distance for Phylogenetic Trees. Journal of Computational Biology, 2021, 28, 1181-1195.	1.6	6
42	The Comparison of Tree-Sibling Time Consistent Phylogenetic Networks Is Graph Isomorphism-Complete. Scientific World Journal, The, 2014, 2014, 1-6.	2.1	4
43	A Fast Algorithmic Technique for Comparing Large Phylogenetic Trees. Lecture Notes in Computer Science, 2005, , 370-375.	1.3	4
44	Trading uninitialized space for time. Information Processing Letters, 2004, 92, 9-13.	0.6	3
45	Efficient Reconstruction of Metabolic Pathways byÂBidirectional Chemical Search. Bulletin of Mathematical Biology, 2009, 71, 750-769.	1.9	3
46	Editorial. Briefings in Bioinformatics, 2012, 13, 645-645.	6.5	3
47	Faster computation of the Robinsonâ€"Foulds distance between phylogenetic networks. Information Sciences, 2012, 197, 77-90.	6.9	3
48	Alignment of biological networks by integer linear programming: virus-host protein-protein interaction networks. BMC Bioinformatics, 2020, 21, 434.	2.6	3
49	Faster Computation of the Robinson-Foulds Distance between Phylogenetic Networks. Lecture Notes in Computer Science, 2010, , 190-201.	1.3	3
50	Alignment of virus-host protein-protein interaction networks by integer linear programming: SARS-CoV-2. PLoS ONE, 2020, 15, e0236304.	2.5	3
51	An optimized TOPS+ comparison method for enhanced TOPS models. BMC Bioinformatics, 2010, 11, 138.	2.6	2
52	A Generalized Robinson-Foulds Distance for Clonal Trees, Mutation Trees, and Phylogenetic Trees and Networks. , 2020, , .		2
53	Reconstructing Metabolic Pathways by Bidirectional Chemical Search. Lecture Notes in Computer Science, 2007, , 217-232.	1.3	1
54	Adjacency Maps and Efficient Graph Algorithms. Algorithms, 2022, 15, 67.	2.1	1

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55	On the Ancestral Compatibility of Two Phylogenetic Trees with Nested Taxa. Journal of Mathematical Biology, 2006, 53, 340-364.	1.9	0
56	Graph Isomorphism. Texts in Computer Science, 2021, , 255-285.	0.7	0
57	Tree Isomorphism. Texts in Computer Science, 2021, , 113-180.	0.7	0
58	Algorithmic Techniques. Texts in Computer Science, 2021, , 45-83.	0.7	0
59	Unbiased Taxonomic Annotation of Metagenomic Samples. Lecture Notes in Computer Science, 2017, , 162-173.	1.3	0