

Bernard Me Moret

List of Publications by Year in descending order

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37
papers

1,894
citations

567281

15
h-index

414414

32
g-index

39
all docs

39
docs citations

39
times ranked

2286
citing authors

#	ARTICLE	IF	CITATIONS
1	How Many Bootstrap Replicates Are Necessary?. Journal of Computational Biology, 2010, 17, 337-354.	1.6	800
2	A Linear-Time Algorithm for Computing Inversion Distance between Signed Permutations with an Experimental Study. Journal of Computational Biology, 2001, 8, 483-491.	1.6	293
3	New approaches for reconstructing phylogenies from gene order data. Bioinformatics, 2001, 17, S165-S173.	4.1	104
4	Steps toward accurate reconstructions of phylogenies from gene-order data. Journal of Computer and System Sciences, 2002, 65, 508-525.	1.2	90
5	Efficiently Computing the Robinson-Foulds Metric. Journal of Computational Biology, 2007, 14, 724-735.	1.6	63
6	An Exact Algorithm to Compute the Double-Cut-and-Join Distance for Genomes with Duplicate Genes. Journal of Computational Biology, 2015, 22, 425-435.	1.6	61
7	Genomic Distances under Deletions and Insertions. Theoretical Computer Science, 2004, 325, 347-360.	0.9	56
8	Refining transcriptional regulatory networks using network evolutionary models and gene histories. Algorithms for Molecular Biology, 2010, 5, 1.	1.2	49
9	Comparing genomes with rearrangements and segmental duplications. Bioinformatics, 2015, 31, i329-i338.	4.1	41
10	A Fast and Exact Algorithm for the Exemplar Breakpoint Distance. Journal of Computational Biology, 2016, 23, 337-346.	1.6	35
11	On Computing Breakpoint Distances for Genomes with Duplicate Genes. Journal of Computational Biology, 2017, 24, 571-580.	1.6	33
12	Gene rearrangement analysis and ancestral order inference from chloroplast genomes with inverted repeat. BMC Genomics, 2008, 9, S25.	2.8	32
13	Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining. Journal of Algorithms, 2003, 48, 173-193.	0.9	31
14	Advances in Phylogeny Reconstruction from Gene Order and Content Data. Methods in Enzymology, 2005, 395, 673-700.	1.0	24
15	An Exact Algorithm to Compute the DCJ Distance for Genomes with Duplicate Genes. Lecture Notes in Computer Science, 2014, , 280-292.	1.3	20
16	Probabilistic partitioning methods to find significant patterns in ChIP-Seq data. Bioinformatics, 2014, 30, 2406-2413.	4.1	14
17	Heuristics for the inversion median problem. BMC Bioinformatics, 2010, 11, S30.	2.6	13
18	Sorting Signed Permutations by Inversions in $O(n \log n)$ Time. Journal of Computational Biology, 2010, 17, 489-501.	1.6	13

#	ARTICLE	IF	CITATIONS
19	A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses that Applies across Eukaryotes and Prokaryotes. <i>Journal of Computational Biology</i> , 2011, 18, 1055-1064.	1.6	13
20	Bootstrapping phylogenies inferred from rearrangement data. <i>Algorithms for Molecular Biology</i> , 2012, 7, 21.	1.2	13
21	Sorting genomes with rearrangements and segmental duplications through trajectory graphs. <i>BMC Bioinformatics</i> , 2013, 14, S9.	2.6	13
22	Estimating true evolutionary distances under rearrangements, duplications, and losses. <i>BMC Bioinformatics</i> , 2010, 11, S54.	2.6	12
23	Study of cell differentiation by phylogenetic analysis using histone modification data. <i>BMC Bioinformatics</i> , 2014, 15, 269.	2.6	12
24	Inversion-based genomic signatures. <i>BMC Bioinformatics</i> , 2009, 10, S7.	2.6	10
25	Refining Regulatory Networks through Phylogenetic Transfer of Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1032-1045.	3.0	8
26	The computational metaphor and quantum physics. <i>Communications of the ACM</i> , 1983, 26, 137-145.	4.5	7
27	Maximum independent sets of commuting and noninterfering inversions. <i>BMC Bioinformatics</i> , 2009, 10, S6.	2.6	7
28	A Transcript Perspective on Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1403-1411.	3.0	6
29	An Experimental Evaluation of Inversion-and Transposition-Based Genomic Distances through Simulations. , 2007, , .		4
30	Constructive complexity. <i>Discrete Applied Mathematics</i> , 1991, 34, 3-16.	0.9	3
31	Hurdles and Sorting by Inversions: Combinatorial, Statistical, and Experimental Results. <i>Journal of Computational Biology</i> , 2009, 16, 1339-1351.	1.6	3
32	Inferring Transcript Phylogenies. , 2011, , .		3
33	A new method for one-dimensional linear feature transformations. <i>Pattern Recognition</i> , 1990, 23, 745-752.	8.1	1
34	A method for the choice of smoothing parameter. <i>Mathematical and Computer Modelling</i> , 1990, 13, 1-16.	2.0	1
35	Using Phylogenetic Relationships to Improve the Inference of Transcriptional Regulatory Networks. , 2008, , .		1
36	FluRF, an automated flu virus reassortment finder based on phylogenetic trees. , 2010, , .		1

#	ARTICLE	IF	CITATIONS
37	New Genome Similarity Measures based on Conserved Gene Adjacencies. Journal of Computational Biology, 2017, 24, 616-634.	1.6	1