

Bernard Me Moret

List of Publications by Year in descending order

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37
papers

1,894
citations

567281

15
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414414

32
g-index

39
all docs

39
docs citations

39
times ranked

2286
citing authors

#	ARTICLE	IF	CITATIONS
1	New Genome Similarity Measures based on Conserved Gene Adjacencies. Journal of Computational Biology, 2017, 24, 616-634.	1.6	1
2	On Computing Breakpoint Distances for Genomes with Duplicate Genes. Journal of Computational Biology, 2017, 24, 571-580.	1.6	33
3	A Fast and Exact Algorithm for the Exemplar Breakpoint Distance. Journal of Computational Biology, 2016, 23, 337-346.	1.6	35
4	Comparing genomes with rearrangements and segmental duplications. Bioinformatics, 2015, 31, i329-i338.	4.1	41
5	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
6	Study of cell differentiation by phylogenetic analysis using histone modification data. BMC Bioinformatics, 2014, 15, 269.	2.6	12
7	Probabilistic partitioning methods to find significant patterns in ChIP-Seq data. Bioinformatics, 2014, 30, 2406-2413.	4.1	14
8	An Exact Algorithm to Compute the DCJ Distance for Genomes with Duplicate Genes. Lecture Notes in Computer Science, 2014, , 280-292.	1.3	20
9	Sorting genomes with rearrangements and segmental duplications through trajectory graphs. BMC Bioinformatics, 2013, 14, S9.	2.6	13
10	A Transcript Perspective on Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1403-1411.	3.0	6
11	Refining Regulatory Networks through Phylogenetic Transfer of Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1032-1045.	3.0	8
12	Bootstrapping phylogenies inferred from rearrangement data. Algorithms for Molecular Biology, 2012, 7, 21.	1.2	13
13	Inferring Transcript Phylogenies. , 2011, , .		3
14	A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses that Applies across Eukaryotes and Prokaryotes. Journal of Computational Biology, 2011, 18, 1055-1064.	1.6	13
15	Heuristics for the inversion median problem. BMC Bioinformatics, 2010, 11, S30.	2.6	13
16	Estimating true evolutionary distances under rearrangements, duplications, and losses. BMC Bioinformatics, 2010, 11, S54.	2.6	12
17	Refining transcriptional regulatory networks using network evolutionary models and gene histories. Algorithms for Molecular Biology, 2010, 5, 1.	1.2	49
18	FluRF, an automated flu virus reassortment finder based on phylogenetic trees. , 2010, , .		1

#	ARTICLE	IF	CITATIONS
19	How Many Bootstrap Replicates Are Necessary?. Journal of Computational Biology, 2010, 17, 337-354.	1.6	800
20	Sorting Signed Permutations by Inversions in $O(n \log n)$ Time. Journal of Computational Biology, 2010, 17, 489-501.	1.6	13
21	Maximum independent sets of commuting and noninterfering inversions. BMC Bioinformatics, 2009, 10, S6.	2.6	7
22	Inversion-based genomic signatures. BMC Bioinformatics, 2009, 10, S7.	2.6	10
23	Hurdles and Sorting by Inversions: Combinatorial, Statistical, and Experimental Results. Journal of Computational Biology, 2009, 16, 1339-1351.	1.6	3
24	Gene rearrangement analysis and ancestral order inference from chloroplast genomes with inverted repeat. BMC Genomics, 2008, 9, S25.	2.8	32
25	Using Phylogenetic Relationships to Improve the Inference of Transcriptional Regulatory Networks. , 2008, , .		1
26	An Experimental Evaluation of Inversion-and Transposition-Based Genomic Distances through Simulations. , 2007, , .		4
27	Efficiently Computing the Robinson-Foulds Metric. Journal of Computational Biology, 2007, 14, 724-735.	1.6	63
28	Advances in Phylogeny Reconstruction from Gene Order and Content Data. Methods in Enzymology, 2005, 395, 673-700.	1.0	24
29	Genomic Distances under Deletions and Insertions. Theoretical Computer Science, 2004, 325, 347-360.	0.9	56
30	Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining. Journal of Algorithms, 2003, 48, 173-193.	0.9	31
31	Steps toward accurate reconstructions of phylogenies from gene-order data. Journal of Computer and System Sciences, 2002, 65, 508-525.	1.2	90
32	New approaches for reconstructing phylogenies from gene order data. Bioinformatics, 2001, 17, S165-S173.	4.1	104
33	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
34	Constructive complexity. Discrete Applied Mathematics, 1991, 34, 3-16.	0.9	3
35	A new method for one-dimensional linear feature transformations. Pattern Recognition, 1990, 23, 745-752.	8.1	1
36	A method for the choice of smoothing parameter. Mathematical and Computer Modelling, 1990, 13, 1-16.	2.0	1

#	ARTICLE	IF	CITATIONS
37	The computational metaphor and quantum physics. Communications of the ACM, 1983, 26, 137-145.	4.5	7