Benny Chor

List of Publications by Year
in descending order

55	2,104	279798	243625
papers	citations	23	44
		h-index	g-index

58	58	58	1606
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	RSA and Rabin Functions: Certain Parts are as Hard as the Whole. SIAM Journal on Computing, 1988, 17, 194-209.	1.0	275
2	The Average Common Substring Approach to Phylogenomic Reconstruction. Journal of Computational Biology, 2006, 13, 336-350.	1.6	184
3	Genomic DNA k-mer spectra: models and modalities. Genome Biology, 2009, 10, R108.	9.6	165
4	On the power of two-point based sampling. Journal of Complexity, 1989, 5, 96-106.	1.3	146
5	A Zero-One Law for Boolean Privacy. SIAM Journal on Discrete Mathematics, 1991, 4, 36-47.	0.8	117
6	Multiple Maxima of Likelihood in Phylogenetic Trees: An Analytic Approach. Molecular Biology and Evolution, 2000, 17, 1529-1541.	8.9	115
7	A Geometric Approach to Betweenness. SIAM Journal on Discrete Mathematics, 1998, 11, 511-523.	0.8	75
8	Maximum likelihood of evolutionary trees: hardness and approximation. Bioinformatics, 2005, 21, i97-i106.	4.1	72
9	A deep neural network approach for learning intrinsic protein-RNA binding preferences. Bioinformatics, 2018, 34, i638-i646.	4.1	68
10	Computational Thinking in Life Science Education. PLoS Computational Biology, 2014, 10, e1003897.	3.2	64
11	Simple constant-time consensus protocols in realistic failure models. Journal of the ACM, 1989, 36, 591-614.	2.2	50
12	A communication-privacy tradeoff for modular addition. Information Processing Letters, 1993, 45, 205-210.	0.6	49
13	Molecular Clock Fork Phylogenies: Closed Form Analytic Maximum Likelihood Solutions. Systematic Biology, 2004, 53, 963-967.	5.6	44
14	Finding a maximum likelihood tree is hard. Journal of the ACM, 2006, 53, 722-744.	2.2	44
15	Genomic analysis of COP9 signalosome function in Drosophila melanogaster reveals a role in temporal regulation of gene expression. Molecular Systems Biology, 2007, 3, 108.	7.2	41
16	Wait-Free Consensus Using Asynchronous Hardware. SIAM Journal on Computing, 1994, 23, 701-712.	1.0	40
17	Maximum Likelihood Jukes-Cantor Triplets: Analytic Solutions. Molecular Biology and Evolution, 2006, 23, 626-632.	8.9	39
18	Maximum Likelihood of Evolutionary Trees Is Hard. Lecture Notes in Computer Science, 2005, , 296-310.	1.3	35

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19	On Constructing Radiation Hybrid Maps. Journal of Computational Biology, 1997, 4, 517-533.	1.6	34
20	Constructing Phylogenies from Quartets: Elucidation of Eutherian Superordinal Relationships. Journal of Computational Biology, 1998, 5, 377-390.	1.6	34
21	Secret sharing over infinite domains. Journal of Cryptology, 1993, 6, 87-95.	2.8	32
22	Inversion symmetry of DNA k-mer counts: validity and deviations. BMC Genomics, 2016, 17, 696.	2.8	32
23	Forbidden penta‐peptides. Protein Science, 2007, 16, 2251-2259.	7.6	26
24	RHO—Radiation Hybrid Ordering. Genome Research, 2000, 10, 365-378.	5.5	25
25	On the structure of the privacy hierarchy. Journal of Cryptology, 1994, 7, 53-60.	2.8	24
26	Private Computations over the Integers. SIAM Journal on Computing, 1995, 24, 376-386.	1.0	23
27	Analytic solutions for three taxon ML trees with variable rates across sites. Discrete Applied Mathematics, 2007, 155, 750-758.	0.9	21
28	ANCESTRAL MAXIMUM LIKELIHOOD OF EVOLUTIONARY TREES IS HARD. Journal of Bioinformatics and Computational Biology, 2004, 02, 257-271.	0.8	17
29	Extending partial haplotypes to full genome haplotypes using chromosome conformation capture data. Bioinformatics, 2016, 32, i559-i566.	4.1	17
30	String graph construction using incremental hashing. Bioinformatics, 2014, 30, 3515-3523.	4.1	16
31	BioNSi: A Discrete Biological Network Simulator Tool. Journal of Proteome Research, 2016, 15, 2871-2880.	3.7	16
32	Approximate Maximum Parsimony and Ancestral Maximum Likelihood. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 183-187.	3.0	15
33	A Phylogenetic Approach to Music Performance Analysis. Journal of New Music Research, 2012, 41, 195-222.	0.8	14
34	Biological Networks: Comparison, Conservation, and Evolution via Relative Description Length. Journal of Computational Biology, 2007, 14, 817-838.	1.6	12
35	Maximum likelihood on four taxa phylogenetic trees. , 2003, , .		12
36	Detecting Phylogenetic Signals in Eukaryotic Whole Genome Sequences. Journal of Computational Biology, 2012, 19, 945-956.	1.6	11

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37	Secret Sharing Over Infinite Domains. , 1989, , 299-306.		11
38	Solvability in Asynchronous Environments II: Finite Interactive Tasks. SIAM Journal on Computing, 1999, 29, 351-377.	1.0	8
39	The effective application of a discrete transition model to explore cell-cycle regulation in yeast. BMC Research Notes, 2013, 6, 311.	1.4	8
40	On Privacy and Partition Arguments. Information and Computation, 2001, 167, 2-9.	0.7	7
41	Maximum Likelihood Molecular Clock Comb: Analytic Solutions. Journal of Computational Biology, 2006, 13, 819-837.	1.6	7
42	The Bit Security of Modular Squaring given Partial Factorization of the Modulos. , 1985, , 448-457.		7
43	Information Theoretic Approaches to Whole Genome Phylogenies. Lecture Notes in Computer Science, 2005, , 283-295.	1.3	6
44	RSA/Rabin least significant bits are $$ \frac{1}{2} + \frac{1}{{poly \left({\log N} \right)}} $$ secure (Extended Abstract). , 1984, , 303-313.		6
45	The privacy of dense symmetric functions. Computational Complexity, 1995, 5, 43-59.	0.3	5
46	From Quartets to Phylogenetic Trees. Lecture Notes in Computer Science, 1998, , 36-53.	1.3	5
47	CRISPR Detection From Short Reads Using Partial Overlap Graphs. Journal of Computational Biology, 2016, 23, 461-471.	1.6	5
48	Analytic solutions of maximum likelihood on forks of four taxa. Mathematical Biosciences, 2007, 208, 347-358.	1.9	4
49	Representative Selection in Nonmetric Datasets. Applied Artificial Intelligence, 2015, 29, 807-838.	3.2	3
50	Hierarchical Partitioning of Metazoan Protein Conservation Profiles Provides New Functional Insights. PLoS ONE, 2014, 9, e90282.	2.5	1
51	Do tree split probabilities determine the branch lengths?. Journal of Theoretical Biology, 2015, 374, 54-59.	1.7	1
52	Cases in which ancestral maximum likelihood will be confusingly misleading. Journal of Theoretical Biology, 2017, 420, 318-323.	1.7	1
53	A High Quartet Distance Construction. Annals of Combinatorics, 2019, 23, 51-65.	0.6	1
54	Inter-chromosomal k-mer distances. BMC Genomics, 2021, 22, 644.	2.8	1

#	Article	IF	Citations
55	The Functional 3D Organization of Unicellular Genomes. Scientific Reports, 2019, 9, 12734.	3.3	0