Sagi Snir

List of Publications by Year
in descending order

67 papers	1,632 citations	361413 20 h-index	345221 36 g-index
69 all docs	69 docs citations	69 times ranked	1452 citing authors

#	Article	IF	Citations
1	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. Journal of Bacteriology, 2011, 193, 6039-6056.	2.2	358
2	Maximum likelihood of phylogenetic networks. Bioinformatics, 2006, 22, 2604-2611.	4.1	112
3	Quartet MaxCut: A fast algorithm for amalgamating quartet trees. Molecular Phylogenetics and Evolution, 2012, 62, 1-8.	2.7	85
4	Inferring Phylogenetic Networks by the Maximum Parsimony Criterion: A Case Study. Molecular Biology and Evolution, 2006, 24, 324-337.	8.9	74
5	Quartets MaxCut: A Divide and Conquer Quartets Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 704-718.	3.0	73
6	Detecting Horizontal Gene Transfer between Closely Related Taxa. PLoS Computational Biology, 2015, 11, e1004408.	3.2	60
7	Weighted Quartets Phylogenetics. Systematic Biology, 2015, 64, 233-242.	5.6	50
8	Human epigenetic ageing is logarithmic with time across the entire lifespan. Epigenetics, 2019, 14, 912-926.	2.7	47
9	Efficient parsimony-based methods for phylogenetic network reconstruction. Bioinformatics, 2007, 23, e123-e128.	4.1	46
10	Molecular Clock Fork Phylogenies: Closed Form Analytic Maximum Likelihood Solutions. Systematic Biology, 2004, 53, 963-967.	5.6	44
11	Convex recolorings of strings and trees: Definitions, hardness results and algorithms. Journal of Computer and System Sciences, 2008, 74, 850-869.	1.2	42
12	Universal Pacemaker of Genome Evolution. PLoS Computational Biology, 2012, 8, e1002785.	3.2	41
13	Is Evolution of Blind Mole Rats Determined by Climate Oscillations?. PLoS ONE, 2012, 7, e30043.	2.5	40
14	Maximum Likelihood Jukes-Cantor Triplets: Analytic Solutions. Molecular Biology and Evolution, 2006, 23, 626-632.	8.9	39
15	Efficient approximation of convex recolorings. Journal of Computer and System Sciences, 2007, 73, 1078-1089.	1.2	39
16	Stability along with Extreme Variability in Core Genome Evolution. Genome Biology and Evolution, 2013, 5, 1393-1402.	2.5	38
17	Using Max Cut to Enhance Rooted Trees Consistency. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 323-333.	3.0	37
18	Short Quartet Puzzling: A New Quartet-Based Phylogeny Reconstruction Algorithm. Journal of Computational Biology, 2008, 15, 91-103.	1.6	33

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19	Recovering the Treelike Trend of Evolution Despite Extensive Lateral Genetic Transfer: A Probabilistic Analysis. Journal of Computational Biology, 2013, 20, 93-112.	1.6	31
20	A Statistical Framework to Identify Deviation from Time Linearity in Epigenetic Aging. PLoS Computational Biology, 2016, 12, e1005183.	3.2	24
21	Hibernation slows epigenetic ageing in yellow-bellied marmots. Nature Ecology and Evolution, 2022, 6, 418-426.	7.8	23
22	Phylo SI: a new genome-wide approach for prokaryotic phylogeny. Nucleic Acids Research, 2014, 42, 2391-2404.	14.5	22
23	Universal Pacemaker of Genome Evolution in Animals and Fungi and Variation of Evolutionary Rates in Diverse Organisms. Genome Biology and Evolution, 2014, 6, 1268-1278.	2.5	21
24	Detecting horizontal gene transfer: a probabilistic approach. BMC Genomics, 2020, 21, 106.	2.8	20
25	The Epigenetic Pacemaker: modeling epigenetic states under an evolutionary framework. Bioinformatics, 2020, 36, 4662-4663.	4.1	19
26	Scorpion speciation in the Holy Land: Multilocus phylogeography corroborates diagnostic differences in morphology and burrowing behavior among Scorpio subspecies and justifies recognition as phylogenetic, ecological and biological species. Molecular Phylogenetics and Evolution, 2015, 91, 226-237.	2.7	18
27	An epigenetic pacemaker is detected via a fast conditional expectation maximization algorithm. Epigenomics, 2018, 10, 695-706.	2.1	14
28	Triplet MaxCut: a new toolkit for rooted supertree. Methods in Ecology and Evolution, 2016, 7, 1359-1365.	5.2	13
29	Fast and reliable reconstruction of phylogenetic trees with indistinguishable edges. Random Structures and Algorithms, 2012, 40, 350-384.	1.1	12
30	'Multi-SpaM': a maximum-likelihood approach to phylogeny reconstruction using multiple spaced-word matches and quartet trees. NAR Genomics and Bioinformatics, 2020, 2, lqz013.	3.2	12
31	A New Phylogenomic Approach For Quantifying Horizontal Gene Transfer Trends in Prokaryotes. Scientific Reports, 2020, 10, 12425.	3.3	10
32	Recovering the Tree-Like Trend of Evolution Despite Extensive Lateral Genetic Transfer: A Probabilistic Analysis. Lecture Notes in Computer Science, 2012, , 224-238.	1.3	10
33	Phylogenetic Profiling of Insertions and Deletions in Vertebrate Genomes. Lecture Notes in Computer Science, 2006, , 265-280.	1.3	9
34	Reconstructing Approximate Phylogenetic Trees from Quartet Samples. SIAM Journal on Computing, 2012, 41, 1466-1480.	1.0	8
35	On the number of genomic pacemakers: a geometric approach. Algorithms for Molecular Biology, 2014, 9, 26.	1.2	8
36	Synteny footprints provide clearer phylogenetic signal than sequence data for prokaryotic classification. Molecular Phylogenetics and Evolution, 2019, 136, 128-137.	2.7	8

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37	Maximum Likelihood Molecular Clock Comb: Analytic Solutions. Journal of Computational Biology, 2006, 13, 819-837.	1.6	7
38	Hadamard Conjugation for the Kimura 3ST Model: Combinatorial Proof Using Path Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 461-471.	3.0	5
39	Tracing the Most Parsimonious Indel History. Journal of Computational Biology, 2011, 18, 967-986.	1.6	5
40	Gene–Gene Interactions Detection Using a Two-stage Model. Journal of Computational Biology, 2015, 22, 563-576.	1.6	5
41	The Performance of Two Supertree Schemes Compared Using Synthetic and Real Data Quartet Input. Journal of Molecular Evolution, 2018, 86, 150-165.	1.8	5
42	Horizontal Gene Transfer Phylogenetics: A Random Walk Approach. Molecular Biology and Evolution, 2020, 37, 1470-1479.	8.9	5
43	Multi-SpaM: A Maximum-Likelihood Approach to Phylogeny Reconstruction Using Multiple Spaced-Word Matches and Quartet Trees. Lecture Notes in Computer Science, 2018, , 227-241.	1.3	5
44	Reconstructing approximate phylogenetic trees from quartet samples. , 2010, , .		5
45	Analytic solutions of maximum likelihood on forks of four taxa. Mathematical Biosciences, 2007, 208, 347-358.	1.9	4
46	A Linear Time Approximation Scheme for Maximum Quartet Consistency on Sparse Sampled Inputs. SIAM Journal on Discrete Mathematics, 2011, 25, 1722-1736.	0.8	4
47	On the Compatibility of Quartet Trees. SIAM Journal on Discrete Mathematics, 2014, 28, 1493-1507.	0.8	4
48	Inference of mutability landscapes of tumors from single cell sequencing data. PLoS Computational Biology, 2020, 16, e1008454.	3.2	4
49	Analysis of Point Mutations in Vertebrate Genomes. , 2005, , 375-386.		3
50	INCORPORATING HOMOLOGUES INTO SEQUENCE EMBEDDINGS FOR PROTEIN ANALYSIS. Journal of Bioinformatics and Computational Biology, 2007, 05, 717-738.	0.8	3
51	THE NET-HMM APPROACH: PHYLOGENETIC NETWORK INFERENCE BY COMBINING MAXIMUM LIKELIHOOD AND HIDDEN MARKOV MODELS. Journal of Bioinformatics and Computational Biology, 2009, 07, 625-644.	0.8	3
52	A phylogenomic study quantifies competing mechanisms for pseudogenization in prokaryotes—The Mycobacterium leprae case. PLoS ONE, 2018, 13, e0204322.	2.5	3
53	The effects of age, sex, weight, and breed on canid methylomes. Epigenetics, 2022, 17, 1497-1512.	2.7	3
54	Structural relatedness via flow networks in protein sequence space. Journal of Theoretical Biology, 2009, 260, 438-444.	1.7	2

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55	A Novel Technique for Detecting Putative Horizontal Gene Transfer in the Sequence Space. Journal of Computational Biology, 2010, 17, 1535-1548.	1.6	2
56	Convex recoloring as an evolutionary marker. Molecular Phylogenetics and Evolution, 2017, 107, 209-220.	2.7	2
57	Toxic genes present a unique phylogenetic signature. Molecular Phylogenetics and Evolution, 2017, 116, 141-148.	2.7	2
58	Prokaryotic evolutionary mechanisms accelerate learning. Discrete Applied Mathematics, 2019, 258, 222-234.	0.9	2
59	Lateral Transfer: A Survey and New Developments. Israel Journal of Ecology and Evolution, 2006, 52, 443-459.	0.6	1
60	Restricting SBH ambiguity via restriction enzymes. Discrete Applied Mathematics, 2007, 155, 857-867.	0.9	1
61	Ordered orthology as a tool in prokaryotic evolutionary inference. Mobile Genetic Elements, 2016, 6, e1120576.	1.8	1
62	Reconstruction of real and simulated phylogenies based on quartet plurality inference. BMC Genomics, 2018, 19, 570.	2.8	1
63	Bounds on Identification of Genome Evolution Pacemakers. Journal of Computational Biology, 2019, 26, 806-821.	1.6	1
64	A New Quartet-Based Statistical Method for Comparing Sets of Gene Trees Is Developed Using a Generalized Hoeffding Inequality. Journal of Computational Biology, 2019, 26, 27-37.	1.6	1
65	Extending the Evolvability Model to the Prokaryotic World: Simulations and Results on Real Data. Journal of Computational Biology, 2019, 26, 794-805.	1.6	1
66	Epigenetic pacemaker: closed form algebraic solutions. BMC Genomics, 2020, 21, 257.	2.8	1
67	On the quartet distance given partial information. Journal of Graph Theory, 0, , .	0.9	0