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	Hibernation slows epigenetic ageing in yellow-bellied marmots. Nature Ecology and Evolution, 2022, 6, 418-426.	7.8	23
2	The effects of age, sex, weight, and breed on canid methylomes. Epigenetics, 2022, 17, 1497-1512.	2.7	3
3	'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
4	Horizontal Gene Transfer Phylogenetics: A Random Walk Approach. Molecular Biology and Evolution, 2020, 37, 1470-1479.	8.9	5
5	A New Phylogenomic Approach For Quantifying Horizontal Gene Transfer Trends in Prokaryotes. Scientific Reports, 2020, 10, 12425.	3.3	10
6	Detecting horizontal gene transfer: a probabilistic approach. BMC Genomics, 2020, 21, 106.	2.8	20
7	The Epigenetic Pacemaker: modeling epigenetic states under an evolutionary framework. Bioinformatics, 2020, 36, 4662-4663.	4.1	19
8	Epigenetic pacemaker: closed form algebraic solutions. BMC Genomics, 2020, 21, 257.	2.8	1
9	Inference of mutability landscapes of tumors from single cell sequencing data. PLoS Computational Biology, 2020, 16, e1008454.	3.2	4
10	Bounds on Identification of Genome Evolution Pacemakers. Journal of Computational Biology, 2019, 26, 806-821.	1.6	1
11	Human epigenetic ageing is logarithmic with time across the entire lifespan. Epigenetics, 2019, 14, 912-926.	2.7	47
12	Prokaryotic evolutionary mechanisms accelerate learning. Discrete Applied Mathematics, 2019, 258, 222-234.	0.9	2
13	Synteny footprints provide clearer phylogenetic signal than sequence data for prokaryotic classification. Molecular Phylogenetics and Evolution, 2019, 136, 128-137.	2.7	8
14	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
15	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
16	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
17	Reconstruction of real and simulated phylogenies based on quartet plurality inference. BMC Genomics, 2018, 19, 570.	2.8	1
18	A phylogenomic study quantifies competing mechanisms for pseudogenization in prokaryotes—The Mycobacterium leprae case. PLoS ONE, 2018, 13, e0204322.	2.5	3

#	ARTICLE	IF	CITATIONS
19	An epigenetic pacemaker is detected via a fast conditional expectation maximization algorithm. Epigenomics, 2018, 10, 695-706.	2.1	14
20	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
21	Convex recoloring as an evolutionary marker. Molecular Phylogenetics and Evolution, 2017, 107, 209-220.	2.7	2
22	Toxic genes present a unique phylogenetic signature. Molecular Phylogenetics and Evolution, 2017, 116, 141-148.	2.7	2
23	Triplet MaxCut: a new toolkit for rooted supertree. Methods in Ecology and Evolution, 2016, 7, 1359-1365.	5.2	13
24	Ordered orthology as a tool in prokaryotic evolutionary inference. Mobile Genetic Elements, 2016, 6, e1120576.	1.8	1
25	A Statistical Framework to Identify Deviation from Time Linearity in Epigenetic Aging. PLoS Computational Biology, 2016, 12, e1005183.	3.2	24
26	Detecting Horizontal Gene Transfer between Closely Related Taxa. PLoS Computational Biology, 2015, 11, e1004408.	3.2	60
27	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
28	Weighted Quartets Phylogenetics. Systematic Biology, 2015, 64, 233-242.	5.6	50
29	Gene–Gene Interactions Detection Using a Two-stage Model. Journal of Computational Biology, 2015, 22, 563-576.	1.6	5
30	On the number of genomic pacemakers: a geometric approach. Algorithms for Molecular Biology, 2014, 9, 26.	1.2	8
31	On the Compatibility of Quartet Trees. SIAM Journal on Discrete Mathematics, 2014, 28, 1493-1507.	0.8	4
32	Phylo SI: a new genome-wide approach for prokaryotic phylogeny. Nucleic Acids Research, 2014, 42, 2391-2404.	14.5	22
33	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
34	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
35	Stability along with Extreme Variability in Core Genome Evolution. Genome Biology and Evolution, 2013, 5, 1393-1402.	2.5	38
36	Universal Pacemaker of Genome Evolution. PLoS Computational Biology, 2012, 8, e1002785.	3.2	41

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37	Reconstructing Approximate Phylogenetic Trees from Quartet Samples. SIAM Journal on Computing, 2012, 41, 1466-1480.	1.0	8
38	Quartet MaxCut: A fast algorithm for amalgamating quartet trees. Molecular Phylogenetics and Evolution, 2012, 62, 1-8.	2.7	85
39	Fast and reliable reconstruction of phylogenetic trees with indistinguishable edges. Random Structures and Algorithms, 2012, 40, 350-384.	1.1	12
40	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
41	Is Evolution of Blind Mole Rats Determined by Climate Oscillations?. PLoS ONE, 2012, 7, e30043.	2.5	40
42	Tracing the Most Parsimonious Indel History. Journal of Computational Biology, 2011, 18, 967-986.	1.6	5
43	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
44	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. Journal of Bacteriology, 2011, 193, 6039-6056.	2.2	358
45	A Novel Technique for Detecting Putative Horizontal Gene Transfer in the Sequence Space. Journal of Computational Biology, 2010, 17, 1535-1548.	1.6	2
46	Quartets MaxCut: A Divide and Conquer Quartets Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 704-718.	3.0	73
47	Reconstructing approximate phylogenetic trees from quartet samples. , 2010, , .		5
48	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
49	Structural relatedness via flow networks in protein sequence space. Journal of Theoretical Biology, 2009, 260, 438-444.	1.7	2
50	Convex recolorings of strings and trees: Definitions, hardness results and algorithms. Journal of Computer and System Sciences, 2008, 74, 850-869.	1.2	42
51	Short Quartet Puzzling: A New Quartet-Based Phylogeny Reconstruction Algorithm. Journal of Computational Biology, 2008, 15, 91-103.	1.6	33
52	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
53	INCORPORATING HOMOLOGUES INTO SEQUENCE EMBEDDINGS FOR PROTEIN ANALYSIS. Journal of Bioinformatics and Computational Biology, 2007, 05, 717-738.	0.8	3
54	Efficient parsimony-based methods for phylogenetic network reconstruction. Bioinformatics, 2007, 23, e123-e128.	4.1	46

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55	Analytic solutions of maximum likelihood on forks of four taxa. Mathematical Biosciences, 2007, 208, 347-358.	1.9	4
56	Restricting SBH ambiguity via restriction enzymes. Discrete Applied Mathematics, 2007, 155, 857-867.	0.9	1
57	Efficient approximation of convex recolorings. Journal of Computer and System Sciences, 2007, 73, 1078-1089.	1.2	39
58	Maximum Likelihood Molecular Clock Comb: Analytic Solutions. Journal of Computational Biology, 2006, 13, 819-837.	1.6	7
59	Inferring Phylogenetic Networks by the Maximum Parsimony Criterion: A Case Study. Molecular Biology and Evolution, 2006, 24, 324-337.	8.9	74
60	Maximum Likelihood Jukes-Cantor Triplets: Analytic Solutions. Molecular Biology and Evolution, 2006, 23, 626-632.	8.9	39
61	Maximum likelihood of phylogenetic networks. Bioinformatics, 2006, 22, 2604-2611.	4.1	112
62	Lateral Transfer: A Survey and New Developments. Israel Journal of Ecology and Evolution, 2006, 52, 443-459.	0.6	1
63	Using Max Cut to Enhance Rooted Trees Consistency. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 323-333.	3.0	37
64	Phylogenetic Profiling of Insertions and Deletions in Vertebrate Genomes. Lecture Notes in Computer Science, 2006, , 265-280.	1.3	9
65	Analysis of Point Mutations in Vertebrate Genomes. , 2005, , 375-386.		3
66	Molecular Clock Fork Phylogenies: Closed Form Analytic Maximum Likelihood Solutions. Systematic Biology, 2004, 53, 963-967.	5.6	44
67	On the quartet distance given partial information. Journal of Graph Theory, 0, , .	0.9	0