

Mukul S Bansal

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

8,115
citations

623734

14
h-index

501196

28
g-index

37
all docs

37
docs citations

37
times ranked

20933
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
3	Efficient algorithms for the reconciliation problem with gene duplication, horizontal transfer and loss. <i>Bioinformatics</i> , 2012, 28, i283-i291.	4.1	188
4	Genome-Scale Phylogenetics: Inferring the Plant Tree of Life from 18,896 Gene Trees. <i>Systematic Biology</i> , 2011, 60, 117-125.	5.6	110
5	TreeFix: Statistically Informed Gene Tree Error Correction Using Species Trees. <i>Systematic Biology</i> , 2013, 62, 110-120.	5.6	101
6	Robinson-Foulds Supertrees. <i>Algorithms for Molecular Biology</i> , 2010, 5, 18.	1.2	88
7	Improved gene tree error correction in the presence of horizontal gene transfer. <i>Bioinformatics</i> , 2015, 31, 1211-1218.	4.1	64
8	RANGER-DTL 2.0: rigorous reconstruction of gene-family evolution by duplication, transfer and loss. <i>Bioinformatics</i> , 2018, 34, 3214-3216.	4.1	64
9	Pareto-optimal phylogenetic tree reconciliation. <i>Bioinformatics</i> , 2014, 30, i87-i95.	4.1	59
10	Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss. <i>Journal of Computational Biology</i> , 2013, 20, 738-754.	1.6	55
11	Efficient genome-scale phylogenetic analysis under the duplication-loss and deep coalescence cost models. <i>BMC Bioinformatics</i> , 2010, 11, S42.	2.6	53
12	Systematic inference of highways of horizontal gene transfer in prokaryotes. <i>Bioinformatics</i> , 2013, 29, 571-579.	4.1	31
13	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
14	A Note on the Fixed Parameter Tractability of the Gene-Duplication Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 848-850.	3.0	19
15	Assessing the accuracy of phylogenetic rooting methods on prokaryotic gene families. <i>PLoS ONE</i> , 2020, 15, e0232950.	2.5	19
16	An Integrated Reconciliation Framework for Domain, Gene, and Species Level Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 63-76.	3.0	17
17	SaGePhy: an improved phylogenetic simulation framework for gene and subgene evolution. <i>Bioinformatics</i> , 2019, 35, 3496-3498.	4.1	17
18	Detecting Highways of Horizontal Gene Transfer. <i>Journal of Computational Biology</i> , 2011, 18, 1087-1114.	1.6	16

#	ARTICLE	IF	CITATIONS
19	PhyloFinder: An intelligent search engine for phylogenetic tree databases. BMC Evolutionary Biology, 2008, 8, 90.	3.2	14
20	Exact Algorithms for Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1077-1090.	3.0	14
21	On the impact of uncertain gene tree rooting on duplication-transfer-loss reconciliation. BMC Bioinformatics, 2018, 19, 290.	2.6	13
22	Systematic Detection of Large-Scale Multigene Horizontal Transfer in Prokaryotes. Molecular Biology and Evolution, 2021, 38, 2639-2659.	8.9	10
23	On Inferring Additive and Replacing Horizontal Gene Transfers Through Phylogenetic Reconciliation. , 2019, , .		8
24	TNet: Phylogeny-Based Inference of Disease Transmission Networks Using Within-Host Strain Diversity. Lecture Notes in Computer Science, 2020, , 203-216.	1.3	8
25	TNet: Transmission Network Inference Using Within-Host Strain Diversity and its Application to Geographical Tracking of COVID-19 Spread. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 230-242.	3.0	5
26	Simultaneous Multi-Domain-Multi-Gene Reconciliation Under the Domain-Gene-Species Reconciliation Model. Lecture Notes in Computer Science, 2019, , 73-86.	1.3	4
27	Improved Duplication-Transfer-Loss Reconciliation with Extinct and Unsourced Lineages. Algorithms, 2021, 14, 231.	2.1	3
28	TreeFix-TP: Phylogenetic Error-Correction for Infectious Disease Transmission Network Inference. , 2020, , .		3
29	TreeFix-TP: Phylogenetic Error-Correction for Infectious Disease Transmission Network Inference. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 119-130.	0.7	3
30	TreeSolve: Rapid Error-Correction of Microbial Gene Trees. Lecture Notes in Computer Science, 2020, , 125-139.	1.3	2
31	Linear-time algorithms for phylogenetic tree completion under Robinson&Foulds distance. Algorithms for Molecular Biology, 2020, 15, 6.	1.2	1
32	Phylogenetic uncertainty and transmission network inference: Lessons from phylogenetic reconciliation. , 2016, , .		0
33	A Supervised Machine Learning Approach for Distinguishing Between Additive and Replacing Horizontal Gene Transfers. , 2020, , .		0