Mukul S Bansal

List of Publications by Year
in descending order

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	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
2	Systematic Detection of Large-Scale Multigene Horizontal Transfer in Prokaryotes. Molecular Biology and Evolution, 2021, 38, 2639-2659.	8.9	10
3	Improved Duplication-Transfer-Loss Reconciliation with Extinct and Unsampled Lineages. Algorithms, 2021, 14, 231.	2.1	3
4	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
5	Assessing the accuracy of phylogenetic rooting methods on prokaryotic gene families. PLoS ONE, 2020, 15, e0232950.	2.5	19
6	Linear-time algorithms for phylogenetic tree completion under Robinson–Foulds distance. Algorithms for Molecular Biology, 2020, 15, 6.	1.2	1
7	TNet: Phylogeny-Based Inference of Disease Transmission Networks Using Within-Host Strain Diversity. Lecture Notes in Computer Science, 2020, , 203-216.	1.3	8
8	TreeSolve: Rapid Error-Correction of Microbial Gene Trees. Lecture Notes in Computer Science, 2020, , 125-139.	1.3	2
9	A Supervised Machine Learning Approach for Distinguishing Between Additive and Replacing Horizontal Gene Transfers. , 2020, , .		0
10	TreeFix-TP: Phylogenetic Error-Correction for Infectious Disease Transmission Network Inference. , 2020, , .		3
11	An Integrated Reconciliation Framework for Domain, Gene, and Species Level Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 63-76.	3.0	17
12	On Inferring Additive and Replacing Horizontal Gene Transfers Through Phylogenetic Reconciliation. , 2019, , .		8
13	SaGePhy: an improved phylogenetic simulation framework for gene and subgene evolution. Bioinformatics, 2019, 35, 3496-3498.	4.1	17
14	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
15	Simultaneous Multi-Domain-Multi-Gene Reconciliation Under the Domain-Gene-Species Reconciliation Model. Lecture Notes in Computer Science, 2019, , 73-86.	1.3	4
16	RANGER-DTL 2.0: rigorous reconstruction of gene-family evolution by duplication, transfer and loss. Bioinformatics, 2018, 34, 3214-3216.	4.1	64
17	On the impact of uncertain gene tree rooting on duplication-transfer-loss reconciliation. BMC Bioinformatics, 2018, 19, 290.	2.6	13
18	RecPhyloXML: a format for reconciled gene trees. Bioinformatics, 2018, 34, 3646-3652.	4.1	22

#	Article	IF	Citations
19	Phylogenetic uncertainty and transmission network inference: Lessons from phylogenetic reconciliation. , 2016, , .		0
20	Improved gene tree error correction in the presence of horizontal gene transfer. Bioinformatics, 2015, 31, 1211-1218.	4.1	64
21	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
22	Pareto-optimal phylogenetic tree reconciliation. Bioinformatics, 2014, 30, i87-i95.	4.1	59
23	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
24	Systematic inference of highways of horizontal gene transfer in prokaryotes. Bioinformatics, 2013, 29, 571-579.	4.1	31
25	Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss. Journal of Computational Biology, 2013, 20, 738-754.	1.6	55
26	TreeFix: Statistically Informed Gene Tree Error Correction Using Species Trees. Systematic Biology, 2013, 62, 110-120.	5.6	101
27	Efficient algorithms for the reconciliation problem with gene duplication, horizontal transfer and loss. Bioinformatics, 2012, 28, i283-i291.	4.1	188
28	Detecting Highways of Horizontal Gene Transfer. Journal of Computational Biology, 2011, 18, 1087-1114.	1.6	16
29	A Note on the Fixed Parameter Tractability of the Gene-Duplication Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 848-850.	3.0	19
30	Genome-Scale Phylogenetics: Inferring the Plant Tree of Life from 18,896 Gene Trees. Systematic Biology, 2011, 60, 117-125.	5.6	110
31	Efficient genome-scale phylogenetic analysis under the duplication-loss and deep coalescence cost models. BMC Bioinformatics, 2010, 11, S42.	2.6	53
32	Robinson-Foulds Supertrees. Algorithms for Molecular Biology, 2010, 5, 18.	1.2	88
33	PhyloFinder: An intelligent search engine for phylogenetic tree databases. BMC Evolutionary Biology, 2008, 8, 90.	3.2	14