Kris Varun Parag

List of Publications by Year
in descending order

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Version: 2024-02-01

40 papers	7,002 citations	516215 16 h-index	414034 32 g-index
69 all docs	69 docs citations	69 times ranked	12955 citing authors

#	Article	IF	Citations
1	Tracking the emergence of disparities in the subnational spread of COVID-19 in Brazil using an online application for real-time data visualisation: A longitudinal analysis. The Lancet Regional Health Americas, 2022, 5, 100119.	1.5	7
2	A computationally tractable birth-death model that combines phylogenetic and epidemiological data. PLoS Computational Biology, 2022, 18, e1009805.	1.5	7
3	Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India. Emerging Infectious Diseases, 2022, 28, 751-758.	2.0	4
4	Fundamental limits on inferring epidemic resurgence in real time using effective reproduction numbers. PLoS Computational Biology, 2022, 18, e1010004.	1.5	11
5	Are Epidemic Growth Rates More Informative than Reproduction Numbers?. Journal of the Royal Statistical Society Series A: Statistics in Society, 2022, 185, S5-S15.	0.6	23
6	Database of epidemic trends and control measures during the first wave of COVID-19 in mainland China. International Journal of Infectious Diseases, 2021, 102, 463-471.	1.5	12
7	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. Science, 2021, 371, 288-292.	6.0	412
8	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. Science, 2021, 371, 708-712.	6.0	335
9	Reduction in mobility and COVID-19 transmission. Nature Communications, 2021, 12, 1090.	5.8	394
10	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. Lancet, The, 2021, 397, 452-455.	6.3	720
11	Are Skyline Plot-Based Demographic Estimates Overly Dependent on Smoothing Prior Assumptions?. Systematic Biology, 2021, 71, 121-138.	2.7	10
12	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. Science, 2021, 373, 889-895.	6.0	142
13	Sub-spreading events limit the reliable elimination of heterogeneous epidemics. Journal of the Royal Society Interface, 2021, 18, 20210444.	1.5	15
14	Improved estimation of time-varying reproduction numbers at low case incidence and between epidemic waves. PLoS Computational Biology, 2021, 17, e1009347.	1.5	46
15	Deciphering early-warning signals of SARS-CoV-2 elimination and resurgence from limited data at multiple scales. Journal of the Royal Society Interface, 2021, 18, 20210569.	1.5	22
16	Potential impact of the COVID-19 pandemic on HIV, tuberculosis, and malaria in low-income and middle-income countries: a modelling study. The Lancet Global Health, 2020, 8, e1132-e1141.	2.9	573
17	State-level tracking of COVID-19 in the United States. Nature Communications, 2020, 11, 6189.	5.8	104
18	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. Nature Human Behaviour, 2020, 4, 856-865.	6.2	281

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19	Suppression of a SARS-CoV-2 outbreak in the Italian municipality of Voâ€™. Nature, 2020, 584, 425-429.	13.7	872
20	Key questions for modelling COVID-19 exit strategies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201405.	1.2	106
21	SARS-CoV-2 infection prevalence on repatriation flights from Wuhan City, China. Journal of Travel Medicine, 2020, 27, .	1.4	5
22	Adaptive Estimation for Epidemic Renewal and Phylogenetic Skyline Models. Systematic Biology, 2020, 69, 1163-1179.	2.7	30
23	Using information theory to optimise epidemic models for real-time prediction and estimation. PLoS Computational Biology, 2020, 16, e1007990.	1.5	41
24	Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. Molecular Biology and Evolution, 2020, 37, 2414-2429.	3.5	30
25	Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. Nature, 2020, 584, 257-261.	13.7	2,558
26	An exact method for quantifying the reliability of end-of-epidemic declarations in real time. PLoS Computational Biology, 2020, 16, e1008478.	1.5	22
27	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
28	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
29	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
30	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
31	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
32	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
33	On signalling and estimation limits for molecular birth-processes. Journal of Theoretical Biology, 2019, 480, 262-273.	0.8	6
34	Comparative micro-epidemiology of pathogenic avian influenza virus outbreaks in a wild bird population. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180259.	1.8	23
35	Robust Design for Coalescent Model Inference. Systematic Biology, 2019, 68, 730-743.	2.7	27
36	Exact Bayesian inference for phylogenetic birth-death models. Bioinformatics, 2018, 34, 3638-3645.	1.8	12

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37	Optimal point process filtering and estimation of the coalescent process. Journal of Theoretical Biology, 2017, 421, 153-167.	0.8	13
38	Point process analysis of noise in early invertebrate vision. PLoS Computational Biology, 2017, 13, e1005687.	1.5	15
39	Event triggered signalling codecs for molecular estimation. , 2013, , .		3
40	Single event molecular signalling for estimation and control. , 2013, , .		6