

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	Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. <i>Nature</i> , 2020, 584, 257-261.	13.7	2,558
2	Suppression of a SARS-CoV-2 outbreak in the Italian municipality of Voâ€™. <i>Nature</i> , 2020, 584, 425-429.	13.7	872
3	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet</i> , The, 2021, 397, 452-455.	6.3	720
4	Potential impact of the COVID-19 pandemic on HIV, tuberculosis, and malaria in low-income and middle-income countries: a modelling study. <i>The Lancet Global Health</i> , 2020, 8, e1132-e1141.	2.9	573
5	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , 2021, 371, 288-292.	6.0	412
6	Reduction in mobility and COVID-19 transmission. <i>Nature Communications</i> , 2021, 12, 1090.	5.8	394
7	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	6.0	335
8	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020, 4, 856-865.	6.2	281
9	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	6.0	142
10	Key questions for modelling COVID-19 exit strategies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201405.	1.2	106
11	State-level tracking of COVID-19 in the United States. <i>Nature Communications</i> , 2020, 11, 6189.	5.8	104
12	Improved estimation of time-varying reproduction numbers at low case incidence and between epidemic waves. <i>PLoS Computational Biology</i> , 2021, 17, e1009347.	1.5	46
13	Using information theory to optimise epidemic models for real-time prediction and estimation. <i>PLoS Computational Biology</i> , 2020, 16, e1007990.	1.5	41
14	Adaptive Estimation for Epidemic Renewal and Phylogenetic Skyline Models. <i>Systematic Biology</i> , 2020, 69, 1163-1179.	2.7	30
15	Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2020, 37, 2414-2429.	3.5	30
16	Robust Design for Coalescent Model Inference. <i>Systematic Biology</i> , 2019, 68, 730-743.	2.7	27
17	Comparative micro-epidemiology of pathogenic avian influenza virus outbreaks in a wild bird population. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180259.	1.8	23
18	Are Epidemic Growth Rates More Informative than Reproduction Numbers?. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 2022, 185, S5-S15.	0.6	23

#	ARTICLE	IF	CITATIONS
19	An exact method for quantifying the reliability of end-of-epidemic declarations in real time. PLoS Computational Biology, 2020, 16, e1008478.	1.5	22
20	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
21	Sub-spreading events limit the reliable elimination of heterogeneous epidemics. Journal of the Royal Society Interface, 2021, 18, 20210444.	1.5	15
22	Point process analysis of noise in early invertebrate vision. PLoS Computational Biology, 2017, 13, e1005687.	1.5	15
23	Optimal point process filtering and estimation of the coalescent process. Journal of Theoretical Biology, 2017, 421, 153-167.	0.8	13
24	Exact Bayesian inference for phylogenetic birth-death models. Bioinformatics, 2018, 34, 3638-3645.	1.8	12
25	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
26	Fundamental limits on inferring epidemic resurgence in real time using effective reproduction numbers. PLoS Computational Biology, 2022, 18, e1010004.	1.5	11
27	Are Skyline Plot-Based Demographic Estimates Overly Dependent on Smoothing Prior Assumptions?. Systematic Biology, 2021, 71, 121-138.	2.7	10
28	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
29	A computationally tractable birth-death model that combines phylogenetic and epidemiological data. PLoS Computational Biology, 2022, 18, e1009805.	1.5	7
30	Single event molecular signalling for estimation and control. , 2013, , .		6
31	On signalling and estimation limits for molecular birth-processes. Journal of Theoretical Biology, 2019, 480, 262-273.	0.8	6
32	SARS-CoV-2 infection prevalence on repatriation flights from Wuhan City, China. Journal of Travel Medicine, 2020, 27, .	1.4	5
33	Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India. Emerging Infectious Diseases, 2022, 28, 751-758.	2.0	4
34	Event triggered signalling codecs for molecular estimation. , 2013, , .		3
35	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
36	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0

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37	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
38	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
39	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0
40	Using information theory to optimise epidemic models for real-time prediction and estimation. , 2020, 16, e1007990.		0