

Nicola De Maio

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

5,223
citations

236925

25
h-index

377865

34
g-index

61
all docs

61
docs citations

61
times ranked

8708
citing authors

#	ARTICLE	IF	CITATIONS
1	phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets. PLoS Computational Biology, 2022, 18, e1010056.	3.2	13
2	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. Molecular Biology and Evolution, 2021, 38, 1608-1613.	8.9	79
3	The Cumulative Indel Model: Fast and Accurate Statistical Evolutionary Alignment. Systematic Biology, 2021, 70, 236-257.	5.6	8
4	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. PLoS Computational Biology, 2021, 17, e1008561.	3.2	48
5	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. Nature, 2021, 591, 30-33.	27.8	92
6	Genomic network analysis of environmental and livestock F-type plasmid populations. ISME Journal, 2021, 15, 2322-2335.	9.8	24
7	Short-range template switching in great ape genomes explored using pair hidden Markov models. PLoS Genetics, 2021, 17, e1009221.	3.5	11
8	Mutation Rates and Selection on Synonymous Mutations in SARS-CoV-2. Genome Biology and Evolution, 2021, 13, .	2.5	83
9	A phylogenetic approach for weighting genetic sequences. BMC Bioinformatics, 2021, 22, 285.	2.6	3
10	Ultrafast Sample placement on Existing tRees (USHER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. Nature Genetics, 2021, 53, 809-816.	21.4	264
11	Genetic Variability of the SARS-CoV-2 Pocketome. Journal of Proteome Research, 2021, 20, 4212-4215.	3.7	23
12	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. Virus Evolution, 2021, 7, veab065.	4.9	0
13	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. Molecular Biology and Evolution, 2021, 38, 5819-5824.	8.9	69
14	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	27.8	80
15	Accounting for spatial sampling patterns in Bayesian phylogeography. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	14
16	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. , 2021, 17, e1008561.		0
17	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. , 2021, 17, e1008561.		0
18	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. , 2021, 17, e1008561.		0

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19	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. , 2021, 17, e1008561.		0
20	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism calling pipelines. GigaScience, 2020, 9, .	6.4	92
21	Stability of SARS-CoV-2 phylogenies. PLoS Genetics, 2020, 16, e1009175.	3.5	92
22	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. PLoS Computational Biology, 2019, 15, e1006650.	3.2	2,484
23	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. Environmental Microbiomes, 2019, 14, 7.	5.0	69
24	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. Microbial Genomics, 2019, 5, .	2.0	171
25	Combining genomics and epidemiology to analyse bi-directional transmission of Mycobacterium bovis in a multi-host system. ELife, 2019, 8, .	6.0	63
26	Two Distinct Patterns of Clostridium difficile Diversity Across Europe Indicating Contrasting Routes of Spread. Clinical Infectious Diseases, 2018, 67, 1035-1044.	5.8	60
27	Bayesian reconstruction of transmission within outbreaks using genomic variants. PLoS Computational Biology, 2018, 14, e1006117.	3.2	69
28	Pneumococcal Capsule Synthesis Locus cps as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. Molecular Biology and Evolution, 2017, 34, 2537-2554.	8.9	65
29	The Bacterial Sequential Markov Coalescent. Genetics, 2017, 206, 333-343.	2.9	28
30	Covert dissemination of carbapenemase-producing Klebsiella pneumoniae (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission. Journal of Antimicrobial Chemotherapy, 2017, 72, 3025-3034.	3.0	73
31	SimBac: simulation of whole bacterial genomes with homologous recombination. Microbial Genomics, 2016, 2, .	2.0	33
32	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. PLoS Computational Biology, 2016, 12, e1005130.	3.2	104
33	Reversible polymorphism-aware phylogenetic models and their application to tree inference. Journal of Theoretical Biology, 2016, 407, 362-370.	1.7	70
34	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	4.1	289
35	PoMo: An Allele Frequency-Based Approach for Species Tree Estimation. Systematic Biology, 2015, 64, 1018-1031.	5.6	66
36	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. PLoS Genetics, 2015, 11, e1005421.	3.5	216

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37	VARIATION IN THERMAL PERFORMANCE AND REACTION NORMS AMONG POPULATIONS OF <i>DROSOPHILA MELANOGASTER</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3573-3587.	2.3	72
38	Estimating Empirical Codon Hidden Markov Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 725-736.	8.9	51
39	Linking Great Apes Genome Evolution across Time Scales Using Polymorphism-Aware Phylogenetic Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 2249-2262.	8.9	73