Nicola De Maio

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50 papers	2,356 citations	23 h-index	48 g-index
61 ext. papers	4,057 ext. citations	9.4 avg, IF	5.17 L-index

#	Paper	IF	Citations
50	phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets.. *PLoS Computational Biology*, **2022**, 18, e1010056	5	0
49	Genomic reconstruction of the SARS-CoV-2 epidemic in England. *Nature*, **2021**,	50.4	16
48	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. *Nature*, **2021**, 591, 30-33	50.4	27
47	phastSim: efficient simulation of sequence evolution for pandemic-scale datasets **2021**,		1
46	Genomic network analysis of environmental and livestock F-type plasmid populations. *ISME Journal*, **2021**, 15, 2322-2335	11.9	4
45	Short-range template switching in great ape genomes explored using pair hidden Markov models. *PLoS Genetics*, **2021**, 17, e1009221	6	3
44	Mutation Rates and Selection on Synonymous Mutations in SARS-CoV-2. *Genome Biology and Evolution*, **2021**, 13,	3.9	25
43	A daily-updated database and tools for comprehensive SARS-CoV-2 mutation-annotated trees **2021** ,		4
42	VGsim: scalable viral genealogy simulator for global pandemic **2021**,		2
41	A phylogenetic approach for weighting genetic sequences. *BMC Bioinformatics*, **2021**, 22, 285	3.6	0
40	Ultrafast Sample placement on Existing tRees (UShER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. *Nature Genetics*, **2021**, 53, 809-816	36.3	58
39	Genetic Variability of the SARS-CoV-2 Pocketome. *Journal of Proteome Research*, **2021**, 20, 4212-4215	5.6	2
38	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	8.3	36
37	The Cumulative Indel Model: Fast and Accurate Statistical Evolutionary Alignment. *Systematic Biology*, **2021**, 70, 236-257	8.4	2
36	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk. *PLoS Computational Biology*, **2021**, 17, e1008561	5	12
35	Mutation rates and selection on synonymous mutations in SARS-CoV-2 **2021**,		6
34	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. *Virus Evolution*, **2021**, 7, veab065	3.7	

33	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. *Molecular Biology and Evolution*, **2021**, 38, 5819-5824	8.3	12
32	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**, 17, e1008561		
31	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**, 17, e1008561		
30	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**, 17, e1008561		
29	Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk **2021**, 17, e1008561		
28	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism-calling pipelines. *GigaScience*, **2020**, 9,	7.6	42
27	Stability of SARS-CoV-2 phylogenies. *PLoS Genetics*, **2020**, 16, e1009175	6	43
26	Ultrafast Sample Placement on Existing Trees (UShER) Empowers Real-Time Phylogenetics for the SARS-CoV-2 Pandemic **2020**,		14
25	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. *PLoS Computational Biology*, **2019**, 15, e1006650	5	1014
24	Combining genomics and epidemiology to analyse bi-directional transmission of in a multi-host system. *ELife*, **2019**, 8,	8.9	33
23	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. *Microbial Genomics*, **2019**, 5,	4.4	93
22	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. *Environmental Microbiomes*, **2019**, 14, 7	5.6	24
21	Two Distinct Patterns of Clostridium difficile Diversity Across Europe Indicating Contrasting Routes of Spread. *Clinical Infectious Diseases*, **2018**, 67, 1035-1044	11.6	36
20	Bayesian reconstruction of transmission within outbreaks using genomic variants. *PLoS Computational Biology*, **2018**, 14, e1006117	5	37
19	Pneumococcal Capsule Synthesis Locus cps as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. *Molecular Biology and Evolution*, **2017**, 34, 2537-2554	8.3	42
18	The Bacterial Sequential Markov Coalescent. *Genetics*, **2017**, 206, 333-343	4	17
17	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	5.1	48
16	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. *MBio*, **2016**, 7, e02162	7.8	200

15	SimBac: simulation of whole bacterial genomes with homologous recombination. *Microbial Genomics*, **2016**, 2,	4.4	23
14	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. *PLoS Computational Biology*, **2016**, 12, e1005130	5	64
13	Reversible polymorphism-aware phylogenetic models and their application to tree inference. *Journal of Theoretical Biology*, **2016**, 407, 362-370	2.3	34
12	PoMo: An Allele Frequency-Based Approach for Species Tree Estimation. *Systematic Biology*, **2015**, 64, 1018-31	8.4	41
11	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. *PLoS Genetics*, **2015**, 11, e1005421	6	133
10	Variation in thermal performance and reaction norms among populations of Drosophila melanogaster. *Evolution; International Journal of Organic Evolution*, **2013**, 67, 3573-87	3.8	58
9	Estimating empirical codon hidden Markov models. *Molecular Biology and Evolution*, **2013**, 30, 725-36	8.3	43
8	Linking great apes genome evolution across time scales using polymorphism-aware phylogenetic models. *Molecular Biology and Evolution*, **2013**, 30, 2249-62	8.3	45
7	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples		1
6	A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages		16
5	Repeated global migrations on different plant hosts by the tropical pathogenPhytophthora palmivora		2
4	BEAST 2.5: An Advanced Software Platform for Bayesian Evolutionary Analysis		12
3	Genomic reconstruction of the SARS-CoV-2 epidemic in England		9
2	The SARS-CoV-2 replication-transcription complex is a priority target for broad-spectrum pan-coronavirus drugs		1
1	Pandemic-Scale Phylogenomics Reveals Elevated Recombination Rates in the SARS-CoV-2 Spike Region		16