

# CITATION REPORT

List of articles citing

Inferring epidemiological parameters from phylogenies using regression-ABC: A comparative study

DOI: 10.1371/journal.pcbi.1005416  
PLoS Computational Biology, 2017, 13, e1005416.

**Source:** <https://exaly.com/paper-pdf/68474867/citation-report.pdf>

**Version:** 2024-04-26

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
33	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. <i>BMC Evolutionary Biology</i> , <b>2018</b> , 18, 95	3	13
32	Can Machines Learn Respiratory Virus Epidemiology?: A Comparative Study of Likelihood-Free Methods for the Estimation of Epidemiological Dynamics. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 343	5.7	8
31	Phylogenetic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , <b>2019</b> , 68, 358-364	8.4	10
30	Tree shape-based approaches for the comparative study of cophylogeny. <i>Ecology and Evolution</i> , <b>2019</b> , 9, 6756-6771	2.8	8
29	Detecting within-host interactions from genotype combination prevalence data. <i>Epidemics</i> , <b>2019</b> , 29, 100349	5.1	6
28	Assessing biases in phylodynamic inferences in the presence of super-spreaders. <i>Veterinary Research</i> , <b>2019</b> , 50, 74	3.8	0
27	Calibrating an individual-based movement model to predict functional connectivity for little owls. <i>Ecological Applications</i> , <b>2019</b> , 29, e01873	4.9	11
26	ABC random forests for Bayesian parameter inference. <i>Bioinformatics</i> , <b>2019</b> , 35, 1720-1728	7.2	65
25	A review of approximate Bayesian computation methods via density estimation: Inference for simulator-models. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , <b>2020</b> , 12, e1486	1.4	5
24	How mechanistic modelling supports decision making for the control of enzootic infectious diseases. <i>Epidemics</i> , <b>2020</b> , 32, 100398	5.1	7
23	Squaring within the Colless index yields a better balance index. <i>Mathematical Biosciences</i> , <b>2021</b> , 331, 108503	3.9	1
22	Deep learning from phylogenies to uncover the transmission dynamics of epidemics.		0
21	Quantifying transmission dynamics of acute hepatitis C virus infections in a heterogeneous population using sequence data. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009916	7.6	2
20	PopART-IBM, a highly efficient stochastic individual-based simulation model of generalised HIV epidemics developed in the context of the HPTN 071 (PopART) trial. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009301	5	0
19	Random Forest Adjustment for Approximate Bayesian Computation. <i>Journal of Computational and Graphical Statistics</i> , 1-28	1.4	0
18	Polynomial Phylogenetic Analysis of Tree Shapes.		0
17	Simulating trajectories and phylogenies from population dynamics models with TiPS.		2

16	Phylogenetic model adequacy using posterior predictive simulations.		1
15	Tree Shape-based approaches for the Comparative study of Cophylogeny.		2
14	Network science inspires novel tree shape statistics.		0
13	Reconciling Pasteur and Darwin to control infectious diseases. <i>PLoS Biology</i> , <b>2018</b> , 16, e2003815	9.7	9
12	Detecting within-host interactions from genotype combination prevalence data.		1
11	Quantifying transmission dynamics of acute hepatitis C virus infections in a heterogeneous population using sequence data.		0
10	Identifying likely transmissions in Mycobacterium bovis infected populations of cattle and badgers using the Kolmogorov Forward Equations. <i>Scientific Reports</i> , <b>2020</b> , 10, 21980	4.9	1
9	Phylogenetics of hepatitis C virus reveals transmission dynamics within and between risk groups in Lyon. <i>Peer Community in Evolutionary Biology</i> ,		
8	Analyzing Phylogenetic Trees with a Tree Lattice Coordinate System and a Graph Polynomial.. <i>Systematic Biology</i> , <b>2022</b> ,	8.4	1
7	Evolution during primary HIV infection does not require adaptive immune selection.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119,	11.5	0
6	Network science inspires novel tree shape statistics.. <i>PLoS ONE</i> , <b>2021</b> , 16, e0259877	3.7	0
5	Statistical Challenges in Tracking the Evolution of SARS-CoV-2. <i>Statistical Science</i> , <b>2022</b> , 37,	2.4	1
4	Deep learning from phylogenies to uncover the epidemiological dynamics of outbreaks. <i>Nature Communications</i> , <b>2022</b> , 13,	17.4	0
3	Deep Learning from Phylogenies for Diversification Analyses.		0
2	TiPS : Rapidly simulating trajectories and phylogenies from compartmental models.		0
1	A Comparison of Deep Learning Architectures for Inferring Parameters of Diversification Models from Extant Phylogenies.		0