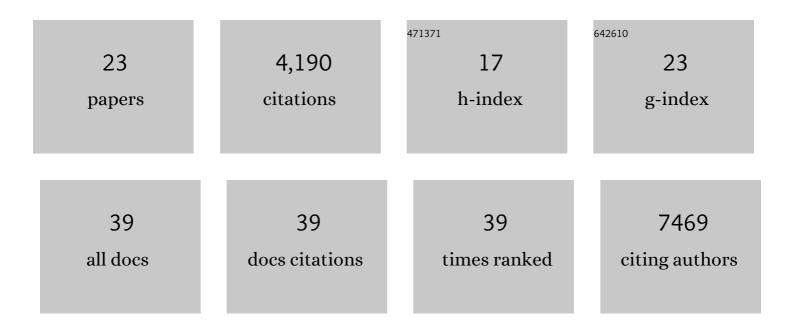
Timothy G Vaughan

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/583952/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Joint Inference of Migration and Reassortment Patterns for Viruses with Segmented Genomes. Molecular Biology and Evolution, 2022, 39, .	3.5	9
2	Epidemiological inference from pathogen genomes: A review of phylodynamic models and applications. Virus Evolution, 2022, 8, .	2.2	9
3	The origin and early spread of SARS-CoV-2 in Europe. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	83
4	Field validation of phylodynamic analytical methods for inference on epidemiological processes in wildlife. Transboundary and Emerging Diseases, 2021, , .	1.3	1
5	Infectious disease phylodynamics with occurrence data. Methods in Ecology and Evolution, 2021, 12, 1498-1507.	2.2	14
6	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. Nature, 2021, 595, 707-712.	13.7	363
7	Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17104-17111.	3.3	35
8	A Multitype Birth–Death Model for Bayesian Inference of Lineage-Specific Birth and Death Rates. Systematic Biology, 2020, 69, 973-986.	2.7	44
9	Estimating Epidemic Incidence and Prevalence from Genomic Data. Molecular Biology and Evolution, 2019, 36, 1804-1816.	3.5	39
10	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. PLoS Computational Biology, 2019, 15, e1006650.	1.5	2,484
11	Taming the BEAST—A Community Teaching Material Resource for BEAST 2. Systematic Biology, 2018, 67, 170-174.	2.7	79
12	Detection of HIV transmission clusters from phylogenetic trees using a multi-state birth–death model. Journal of the Royal Society Interface, 2018, 15, 20180512.	1.5	22
13	IcyTree: rapid browser-based visualization for phylogenetic trees and networks. Bioinformatics, 2017, 33, 2392-2394.	1.8	91
14	Inferring Ancestral Recombination Graphs from Bacterial Genomic Data. Genetics, 2017, 205, 857-870.	1.2	45
15	Phylodynamics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. Molecular Biology and Evolution, 2016, 33, 2102-2116.	3.5	131
16	How well can the exponential-growth coalescent approximate constant-rate birth–death population dynamics?. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150420.	1.2	29
17	Genetic diversity loss in a biodiversity hotspot: ancient <scp>DNA</scp> quantifies genetic decline and former connectivity in a critically endangered marsupial. Molecular Ecology, 2015, 24, 5813-5828.	2.0	48
18	Molecular Approaches to Understanding Transmission and Source Attribution in Nontyphoidal <i>Salmonella</i> and Their Application in Africa. Clinical Infectious Diseases, 2015, 61, S259-S265.	2.9	26

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#	Article	IF	CITATIONS
19	Efficient Bayesian inference under the structured coalescent. Bioinformatics, 2014, 30, 2272-2279.	1.8	118
20	Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth–death SIR model. Journal of the Royal Society Interface, 2014, 11, 20131106.	1.5	104
21	A Stochastic Simulator of Birth-Death Master Equations with Application to Phylodynamics. Molecular Biology and Evolution, 2013, 30, 1480-1493.	3.5	73
22	Within-host demographic fluctuations and correlations in early retroviral infection. Journal of Theoretical Biology, 2012, 295, 86-99.	0.8	6
23	Extinction Times in Autocatalytic Systems. Journal of Physical Chemistry A, 2010, 114, 10481-10491.	1.1	21