

Nicholas L Geard

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

749
citations

623734

14
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610901

24
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61
all docs

61
docs citations

61
times ranked

1172
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid assessment of the risk of SARS-CoV-2 importation: case study and lessons learned. <i>Epidemics</i> , 2022, 38, 100549.	3.0	5
2	Exploring automatic inconsistency detection for literature-based gene ontology annotation. <i>Bioinformatics</i> , 2022, 38, i273-i281.	4.1	0
3	COVID-19 in low-tolerance border quarantine systems: Impact of the Delta variant of SARS-CoV-2. <i>Science Advances</i> , 2022, 8, eabm3624.	10.3	10
4	The efficacy of sampling strategies for estimating scabies prevalence. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010456.	3.0	2
5	Modelling the effect of within-host dynamics on the diversity of a multi-strain pathogen. <i>Journal of Theoretical Biology</i> , 2022, 548, 111185.	1.7	0
6	PoLoBag: Polynomial Lasso Bagging for signed gene regulatory network inference from expression data. <i>Bioinformatics</i> , 2021, 36, 5187-5193.	4.1	10
7	Risk mapping for COVID-19 outbreaks in Australia using mobility data. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20200657.	3.4	40
8	Bow-tie architecture of gene regulatory networks in species of varying complexity. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210069.	3.4	2
9	Modelling testing and response strategies for COVID-19 outbreaks in remote Australian Aboriginal communities. <i>BMC Infectious Diseases</i> , 2021, 21, 929.	2.9	6
10	Mapping home internet activity during COVID-19 lockdown to identify occupation related inequalities. <i>Scientific Reports</i> , 2021, 11, 21054.	3.3	7
11	Automatic consistency assurance for literature-based gene ontology annotation. <i>BMC Bioinformatics</i> , 2021, 22, 565.	2.6	2
12	Longitudinal Analysis of Group A Streptococcus emm Types and emm Clusters in a High-Prevalence Setting: Relationship between Past and Future Infections. <i>Journal of Infectious Diseases</i> , 2020, 221, 1429-1437.	4.0	11
13	Proportional multistate lifetable modelling of preventive interventions: concepts, code and worked examples. <i>International Journal of Epidemiology</i> , 2020, 49, 1624-1636.	1.9	22
14	Modelling the household-level impact of a maternal respiratory syncytial virus (RSV) vaccine in a high-income setting. <i>BMC Medicine</i> , 2020, 18, 319.	5.5	8
15	Epidemiological consequences of enduring strain-specific immunity requiring repeated episodes of infection. <i>PLoS Computational Biology</i> , 2020, 16, e1007182.	3.2	2
16	A model of population dynamics with complex household structure and mobility: implications for transmission and control of communicable diseases. <i>PeerJ</i> , 2020, 8, e10203.	2.0	4
17	What can urban mobility data reveal about the spatial distribution of infection in a single city?. <i>BMC Public Health</i> , 2019, 19, 656.	2.9	18
18	Optimal timing of influenza vaccine during pregnancy: A systematic review and meta-analysis. <i>Influenza and Other Respiratory Viruses</i> , 2019, 13, 438-452.	3.4	49

#	ARTICLE	IF	CITATIONS
19	GEOFIL: A spatially-explicit agent-based modelling framework for predicting the long-term transmission dynamics of lymphatic filariasis in American Samoa. <i>Epidemics</i> , 2019, 27, 19-27.	3.0	14
20	Profiling Mycobacterium tuberculosis transmission and the resulting disease burden in the five highest tuberculosis burden countries. <i>BMC Medicine</i> , 2019, 17, 208.	5.5	20
21	Implications of asymptomatic carriers for infectious disease transmission and control. <i>Royal Society Open Science</i> , 2018, 5, 172341.	2.4	57
22	Investigation of group A Streptococcus immune responses in an endemic setting, with a particular focus on J8. <i>Vaccine</i> , 2018, 36, 7618-7624.	3.8	5
23	Quantity or quality? Assessing relationships between perceived social connectedness and recorded encounters. <i>PLoS ONE</i> , 2018, 13, e0208083.	2.5	2
24	Characterising pandemic severity and transmissibility from data collected during first few hundred studies. <i>Epidemics</i> , 2017, 19, 61-73.	3.0	36
25	Determining the Best Strategies for Maternally Targeted Pertussis Vaccination Using an Individual-Based Model. <i>American Journal of Epidemiology</i> , 2017, 186, 109-117.	3.4	9
26	A Synthetic Population for Modelling the Dynamics of Infectious Disease Transmission in American Samoa. <i>Scientific Reports</i> , 2017, 7, 16725.	3.3	25
27	Whoâ€™s holding the baby? A prospective diary study of the contact patterns of mothers with an infant. <i>BMC Infectious Diseases</i> , 2017, 17, 634.	2.9	10
28	Indigenous Australian household structure: a simple data collection tool and implications for close contact transmission of communicable diseases. <i>PeerJ</i> , 2017, 5, e3958.	2.0	33
29	Influence of Population Demography and Immunization History on the Impact of an Antenatal Pertussis Program. <i>Clinical Infectious Diseases</i> , 2016, 63, S213-S220.	5.8	5
30	Model-Informed Risk Assessment and Decision Making for an Emerging Infectious Disease in the Asia-Pacific Region. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005018.	3.0	9
31	Vaccination Programs for Endemic Infections: Modelling Real versus Apparent Impacts of Vaccine and Infection Characteristics. <i>Scientific Reports</i> , 2015, 5, 15468.	3.3	15
32	Social encounter profiles of greater Melbourne residents, by location â€“ a telephone survey. <i>BMC Infectious Diseases</i> , 2015, 15, 494.	2.9	15
33	The effects of demographic change on disease transmission and vaccine impact in a household structured population. <i>Epidemics</i> , 2015, 13, 56-64.	3.0	50
34	The Practice of Agent-Based Model Visualization. <i>Artificial Life</i> , 2014, 20, 271-289.	1.3	14
35	Self-organizing agent communities for autonomic resource management. <i>Adaptive Behavior</i> , 2013, 21, 3-28.	1.9	4
36	A Bayesian Approach to the Validation of Agent-Based Models. <i>Intelligent Systems Reference Library</i> , 2013, , 255-269.	1.2	5

#	ARTICLE	IF	CITATIONS
37	Synthetic Population Dynamics: A Model of Household Demography. <i>Jasss</i> , 2013, 16, .	1.8	48
38	Developmental motifs reveal complex structure in cell lineages. <i>Complexity</i> , 2011, 16, 48-57.	1.6	10
39	Stability in flux: community structure in dynamic networks. <i>Journal of the Royal Society Interface</i> , 2011, 8, 1031-1040.	3.4	27
40	Spatial embedding as an enabling constraint: Introduction to a special issue of complexity on the topic of "Spatial Organization". <i>Complexity</i> , 2010, 16, 8-10.	1.6	2
41	COMPETITION AND THE DYNAMICS OF GROUP AFFILIATION. <i>International Journal of Modeling, Simulation, and Scientific Computing</i> , 2010, 13, 501-517.	1.4	6
42	<i>Adaptive Networks: Theory, Models and Applications</i> . T. Gross and H. Sayama (Eds.). (2009), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 16, 329-331.	1.3	0
43	Dynamical approaches to modeling developmental gene regulatory networks. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009, 87, 131-142.	3.6	16
44	Autonomic Resource Management through Self-Organising Agent Communities. , 2008, , .		1
45	LinMap: Visualizing Complexity Gradients in Evolutionary Landscapes. <i>Artificial Life</i> , 2008, 14, 277-297.	1.3	2
46	A generative bias towards average complexity in artificial cell lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1741-1751.	2.6	12
47	Directed Evolution of an Artificial Cell Lineage. , 2007, , 144-155.		0
48	A Gene Network Model for Developing Cell Lineages. <i>Artificial Life</i> , 2005, 11, 249-267.	1.3	33
49	Maximally rugged NK landscapes contain the highest peaks. , 2005, , .		11
50	Towards more biological mutation operators in gene regulation studies. <i>BioSystems</i> , 2004, 76, 239-248.	2.0	26
51	A comparison of neutral landscapes - NK, NKp and NKq. , 0, , .		15
52	Diversity maintenance on neutral landscapes: an argument for recombination. , 0, , .		2
53	Structure and dynamics of a gene network model incorporating small RNAs. , 0, , .		4