Matt J Keeling

List of Publications by Year
in descending order

231 papers	19,689 citations	20817 60 h-index	18130 120 g-index
308 all docs	308 docs citations	308 times ranked	17129 citing authors

#	Article	IF	Citations
1	Networks and epidemic models. Journal of the Royal Society Interface, 2005, 2, 295-307.	3.4	1,403
2	Threats to an ecosystem service: pressures on pollinators. Frontiers in Ecology and the Environment, 2013, 11, 251-259.	4.0	980
3	Dynamics of the 2001 UK Foot and Mouth Epidemic: Stochastic Dispersal in a Heterogeneous Landscape. Science, 2001, 294, 813-817.	12.6	765
4	The effects of local spatial structure on epidemiological invasions. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 859-867.	2.6	672
5	Identification of 100 fundamental ecological questions. Journal of Ecology, 2013, 101, 58-67.	4.0	605
6	Vaccination and non-pharmaceutical interventions for COVID-19: a mathematical modelling study. Lancet Infectious Diseases, The, 2021, 21, 793-802.	9.1	453
7	Appropriate Models for the Management of Infectious Diseases. PLoS Medicine, 2005, 2, e174.	8.4	407
8	Disease Extinction and Community Size: Modeling the Persistence of Measles. Science, 1997, 275, 65-67.	12.6	383
9	Modeling dynamic and network heterogeneities in the spread of sexually transmitted diseases. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13330-13335.	7.1	376
10	Modelling vaccination strategies against foot-and-mouth disease. Nature, 2003, 421, 136-142.	27.8	375
11	Planning for smallpox outbreaks. Nature, 2003, 425, 681-685.	27.8	324
12	Contact tracing and disease control. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 2565-2571.	2.6	321
13	Networks and the Epidemiology of Infectious Disease. Interdisciplinary Perspectives on Infectious Diseases, 2011, 2011, 1-28.	1.4	299
14	The implications of network structure for epidemic dynamics. Theoretical Population Biology, 2005, 67, 1-8.	1.1	272
15	Efficacy of contact tracing for the containment of the 2019 novel coronavirus (COVID-19). Journal of Epidemiology and Community Health, 2020, 74, jech-2020-214051.	3.7	245
16	Seasonally forced disease dynamics explored as switching between attractors. Physica D: Nonlinear Phenomena, 2001, 148, 317-335.	2.8	217
17	Metapopulation dynamics of bubonic plague. Nature, 2000, 407, 903-906.	27.8	216
18	Optimal reactive vaccination strategies for a foot-and-mouth outbreak in the UK. Nature, 2006, 440, 83-86.	27.8	216

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19	Disease evolution on networks: the role of contact structure. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 699-708.	2.6	187
20	A dynamic model of bovine tuberculosis spread and control in Great Britain. Nature, 2014, 511, 228-231.	27.8	186
21	Correlation models for childhood epidemics. Proceedings of the Royal Society B: Biological Sciences, 1997, 264, 1149-1156.	2.6	184
22	Estimating spatial coupling in epidemiological systems: a mechanistic approach. Ecology Letters, 2002, 5, 20-29.	6.4	178
23	Individual-based Perspectives on R0. Journal of Theoretical Biology, 2000, 203, 51-61.	1.7	174
24	The Interplay between Determinism and Stochasticity in Childhood Diseases. American Naturalist, 2002, 159, 469-481.	2.1	174
25	On methods for studying stochastic disease dynamics. Journal of the Royal Society Interface, 2008, 5, 171-181.	3.4	164
26	Invasion, stability and evolution to criticality in spatially extended, artificial host—pathogen ecologies. Proceedings of the Royal Society B: Biological Sciences, 1995, 259, 55-63.	2.6	160
27	Insights from unifying modern approximations to infections on networks. Journal of the Royal Society Interface, 2011, 8, 67-73.	3.4	153
28	Indirect effects of childhood pneumococcal conjugate vaccination on invasive pneumococcal disease: a systematic review and meta-analysis. The Lancet Global Health, 2017, 5, e51-e59.	6.3	144
29	Modelling optimal vaccination strategy for SARS-CoV-2 in the UK. PLoS Computational Biology, 2021, 17, e1008849.	3.2	142
30	Models of foot-and-mouth disease. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 1195-1202.	2.6	136
31	Mathematical modelling of infectious diseases. British Medical Bulletin, 2009, 92, 33-42.	6.9	131
32	Individual identity and movement networks for disease metapopulations. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8866-8870.	7.1	130
33	Understanding the persistence of measles: reconciling theory, simulation and observation. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 335-343.	2.6	129
34	Foot-and-mouth disease under control in the UK. Nature, 2001, 411, 258-259.	27.8	125
35	Bubonic plague: a metapopulation model of a zoonosis. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 2219-2230.	2.6	122
36	Silent spread of H5N1 in vaccinated poultry. Nature, 2006, 442, 757-757.	27.8	121

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37	Representing the UK's cattle herd as static and dynamic networks. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 469-476.	2.6	117
38	Metapopulation moments: coupling, stochasticity and persistence. Journal of Animal Ecology, 2000, 69, 725-736.	2.8	106
39	Key questions for modelling COVID-19 exit strategies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201405.	2.6	106
40	Social encounter networks: characterizing Great Britain. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131037.	2.6	103
41	Dynamics of infectious diseases. Reports on Progress in Physics, 2014, 77, 026602.	20.1	103
42	Multiplicative Moments and Measures of Persistence in Ecology. Journal of Theoretical Biology, 2000, 205, 269-281.	1.7	100
43	Social encounter networks: collective properties and disease transmission. Journal of the Royal Society Interface, 2012, 9, 2826-2833.	3.4	95
44	Estimation of country-level basic reproductive ratios for novel Coronavirus (SARS-CoV-2/COVID-19) using synthetic contact matrices. PLoS Computational Biology, 2020, 16, e1008031.	3.2	95
45	Possible future waves of SARS-CoV-2 infection generated by variants of concern with a range of characteristics. Nature Communications, 2021, 12, 5730.	12.8	90
46	Implications of vaccination and waning immunity. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2071-2080.	2.6	89
47	Predictions of COVID-19 dynamics in the UK: Short-term forecasting and analysis of potential exit strategies. PLoS Computational Biology, 2021, 17, e1008619.	3.2	87
48	Quantitative evaluation of the strategy to eliminate human African trypanosomiasis in the Democratic Republic of Congo. Parasites and Vectors, 2015, 8, 532.	2.5	86
49	Impact of spatial clustering on disease transmission and optimal control. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1041-1046.	7.1	85
50	The role of pre-emptive culling in the control of foot-and-mouth disease. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 3239-3248.	2.6	84
51	Reinterpreting Space, Time Lags, and Functional Responses in Ecological Models. , 2000, 290, 1758-1761.		82
52	Herd size and bovine tuberculosis persistence in cattle farms in Great Britain. Preventive Veterinary Medicine, 2009, 92, 360-365.	1.9	82
53	Monogamous networks and the spread of sexually transmitted diseases. Mathematical Biosciences, 2004, 189, 115-130.	1.9	80
54	Quantitative analyses and modelling to support achievement of the 2020 goals for nine neglected tropical diseases. Parasites and Vectors, 2015, 8, 630.	2.5	80

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55	The invasion and coexistence of competing Wolbachia strains. Heredity, 2003, 91, 382-388.	2.6	77
56	Household structure and infectious disease transmission. Epidemiology and Infection, 2009, 137, 654-661.	2.1	77
57	The Impact of Contact Tracing in Clustered Populations. PLoS Computational Biology, 2010, 6, e1000721.	3.2	75
58	Eight challenges in modelling infectious livestock diseases. Epidemics, 2015, 10, 1-5.	3.0	72
59	Deterministic epidemic models with explicit household structure. Mathematical Biosciences, 2008, 213, 29-39.	1.9	70
60	Accuracy of models for the 2001 foot-and-mouth epidemic. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 1459-1468.	2.6	68
61	Stochastic dynamics and a power law for measles variability. Philosophical Transactions of the Royal Society B: Biological Sciences, 1999, 354, 769-776.	4.0	64
62	Predicting undetected infections during the 2007 foot-and-mouth disease outbreak. Journal of the Royal Society Interface, 2009, 6, 1145-1151.	3.4	63
63	Modelling the impact of local reactive school closures on critical care provision during an influenza pandemic. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 2753-2760.	2.6	62
64	COVID-19 transmission dynamics underlying epidemic waves in Kenya. Science, 2021, 374, 989-994.	12.6	62
65	The Impact of Movements and Animal Density on Continental Scale Cattle Disease Outbreaks in the United States. PLoS ONE, 2014, 9, e91724.	2.5	61
66	Effect of variability in infection period on the persistence and spatial spread of infectious diseases. Mathematical Biosciences, 1998, 147, 207-226.	1.9	59
67	Metapopulation Dynamics of Infectious Diseases. , 2004, , 415-445.		59
68	INFERENCE FOR INDIVIDUAL-LEVEL MODELS OF INFECTIOUS DISEASES IN LARGE POPULATIONS. Statistica Sinica, 2010, 20, 239-261.	0.3	57
69	Simple Stochastic Models and Their Power-Law Type Behaviour. Theoretical Population Biology, 2000, 58, 21-31.	1.1	56
70	Integrating stochasticity and network structure into an epidemic model. Journal of the Royal Society Interface, 2009, 6, 761-774.	3.4	56
71	Predicting the Impact of Intervention Strategies for Sleeping Sickness in Two High-Endemicity Health Zones of the Democratic Republic of Congo. PLoS Neglected Tropical Diseases, 2017, 11, e0005162.	3.0	53
72	Predicting the spread of the Asian hornet (Vespa velutina) following its incursion into Great Britain. Scientific Reports, 2017, 7, 6240.	3.3	52

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73	Modelling the persistence of measles. Trends in Microbiology, 1997, 5, 513-518.	7.7	51
74	The effects of demographic change on disease transmission and vaccine impact in a household structured population. Epidemics, 2015, 13, 56-64.	3.0	50
75	A Motif-Based Approach to Network Epidemics. Bulletin of Mathematical Biology, 2009, 71, 1693-1706.	1.9	48
76	Resolving the impact of waiting time distributions on the persistence of measles. Journal of the Royal Society Interface, 2010, 7, 623-640.	3.4	48
77	Optimal but unequitable prophylactic distribution of vaccine. Epidemics, 2012, 4, 78-85.	3.0	48
78	Host–parasite interactions between the local and the mean-field: How and when does spatial population structure matter?. Journal of Theoretical Biology, 2007, 249, 140-152.	1.7	47
79	Real-time decision-making during emergency disease outbreaks. PLoS Computational Biology, 2018, 14, e1006202.	3.2	46
80	Endemic cattle diseases: comparative epidemiology and governance. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 1975-1986.	4.0	43
81	A spatial model of COVID-19 transmission in England and Wales: early spread, peak timing and the impact of seasonality. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200272.	4.0	43
82	Patterns of density dependence in measles dynamics. Proceedings of the Royal Society B: Biological Sciences, 1998, 265, 753-762.	2.6	42
83	Is a good predictor of final epidemic size: Foot-and-mouth disease in the UK. Journal of Theoretical Biology, 2009, 258, 623-629.	1.7	42
84	Targeting vaccination against novel infections: risk, age and spatial structure for pandemic influenza in Great Britain. Journal of the Royal Society Interface, 2011, 8, 661-670.	3.4	42
85	Modeling the spread and control of foot-and-mouth disease in Pennsylvania following its discovery and options for control. Preventive Veterinary Medicine, 2012, 104, 224-239.	1.9	42
86	The impact of temperature changes on vector-borne disease transmission: *Culicoides* midges and bluetongue virus. Journal of the Royal Society Interface, 2017, 14, 20160481.	3.4	42
87	The role of routine versus random movements on the spread of disease in Great Britain. Epidemics, 2009, 1, 250-258.	3.0	41
88	The impact of school reopening on the spread of COVID-19 in England. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200261.	4.0	41
89	Characteristic length scales of spatial models in ecology via fluctuation analysis. Philosophical Transactions of the Royal Society B: Biological Sciences, 1997, 352, 1589-1601.	4.0	40
90	Using conservation of pattern to estimate spatial parameters from a single snapshot. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9155-9160.	7.1	40

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91	Calculation of Disease Dynamics in a Population of Households. PLoS ONE, 2010, 5, e9666.	2.5	40
92	Neighbourhood control policies and the spread of infectious diseases. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 1659-1666.	2.6	39
93	Data-driven models to predict the elimination of sleeping sickness in former Equateur province of DRC. Epidemics, 2017, 18, 101-112.	3.0	39
94	Deterministic Limits to Stochastic Spatial Models of Natural Enemies. American Naturalist, 2002, 159, 57-80.	2.1	38
95	Spatiotemporal patterns and risks of herd breakdowns in pigs with postweaning multisystemic wasting syndrome. Veterinary Record, 2007, 160, 751-762.	0.3	38
96	Epidemic prediction and control in clustered populations. Journal of Theoretical Biology, 2011, 272, 1-7.	1.7	38
97	Assessing the cost-effectiveness of HPV vaccination strategies for adolescent girls and boys in the UK. BMC Infectious Diseases, 2019, 19, 552.	2.9	38
98	Using individual-based simulations to test the Levins metapopulation paradigm. Journal of Animal Ecology, 2002, 71, 270-279.	2.8	37
99	Topographic determinants of foot and mouth disease transmission in the UK 2001 epidemic. BMC Veterinary Research, 2006, 2, 3.	1.9	37
100	The Epidemiology of Rift Valley Fever in Mayotte: Insights and Perspectives from 11 Years of Data. PLoS Neglected Tropical Diseases, 2016, 10, e0004783.	3.0	37
101	Assessing Strategies Against Gambiense Sleeping Sickness Through Mathematical Modeling. Clinical Infectious Diseases, 2018, 66, S286-S292.	5.8	37
102	Evolutionary tradeâ€"offs at two timeâ€"scales: competition versus persistence. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 385-391.	2.6	36
103	Invasion dynamics of Asian hornet, Vespa velutina (Hymenoptera: Vespidae): a case study of a commune in south-west France. Applied Entomology and Zoology, 2017, 52, 221-229.	1.2	36
104	Correlation equations for endemic diseases: externally imposed and internally generated heterogeneity. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 953-960.	2.6	35
105	Ocean-scale patterns of Â«biodiversityÂ» of Atlantic asteroids determined from taxonomic distinctness and other measures. Biological Journal of the Linnean Society, 1999, 66, 187-203.	1.6	35
106	Seasonal influenza: Modelling approaches to capture immunity propagation. PLoS Computational Biology, 2019, 15, e1007096.	3.2	35
107	The effectiveness of social bubbles as part of a Covid-19 lockdown exit strategy, a modelling study. Wellcome Open Research, 2020, 5, 213.	1.8	35
108	The effectiveness of social bubbles as part of a Covid-19 lockdown exit strategy, a modelling study. Wellcome Open Research, 2020, 5, 213.	1.8	33

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109	Estimation of outbreak severity and transmissibility: Influenza A(H1N1)pdm09 in households. BMC Medicine, 2012, 10, 117.	5.5	32
110	Epidemiological consequences of household-based antiviral prophylaxis for pandemic influenza. Journal of the Royal Society Interface, 2013, 10, 20121019.	3.4	32
111	Village-scale persistence and elimination of gambiense human African trypanosomiasis. PLoS Neglected Tropical Diseases, 2019, 13, e0007838.	3.0	31
112	Disease evolution across a range of spatio-temporal scales. Theoretical Population Biology, 2006, 70, 201-213.	1.1	30
113	Modelling foot-and-mouth disease: A comparison between the UK and Denmark. Preventive Veterinary Medicine, 2008, 85, 107-124.	1.9	29
114	An in-host model of acute infection: Measles as a case study. Theoretical Population Biology, 2008, 73, 134-147.	1.1	29
115	Hospital bed capacity and usage across secondary healthcare providers in England during the first wave of the COVID-19 pandemic: a descriptive analysis. BMJ Open, 2021, 11, e042945.	1.9	29
116	A Spatial Mechanism for the Evolution and Maintenance of Sexual Reproduction. Oikos, 1995, 74, 414.	2.7	28
117	Predicting the impact of COVID-19 interruptions on transmission of *gambiense* human African trypanosomiasis in two health zones of the Democratic Republic of Congo. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2021, 115, 245-252.	1.8	28
118	Mathematical Models of Human African Trypanosomiasis Epidemiology. Advances in Parasitology, 2015, 87, 53-133.	3.2	27
119	Modelling the spread of American foulbrood in honeybees. Journal of the Royal Society Interface, 2013, 10, 20130650.	3.4	26
120	Screening Strategies for a Sustainable Endpoint for Gambiense Sleeping Sickness. Journal of Infectious Diseases, 2020, 221, S539-S545.	4.0	25
121	Ocean-scale patterns of 'biodiversity' of Atlantic asteroids determined from taxonomic distinctness and other measures. Biological Journal of the Linnean Society, 1999, 66, 187-203.	1.6	24
122	Modelling the many-wrongs principle: The navigational advantages of aggregation in nomadic foragers. Journal of Theoretical Biology, 2006, 240, 302-310.	1.7	24
123	Exact and approximate moment closures for non-Markovian network epidemics. Journal of Theoretical Biology, 2015, 382, 160-177.	1.7	24
124	The Interaction between Vector Life History and Short Vector Life in Vector-Borne Disease Transmission and Control. PLoS Computational Biology, 2016, 12, e1004837.	3.2	24
125	Developing a Framework for Public Involvement in Mathematical and Economic Modelling: Bringing New Dynamism to Vaccination Policy Recommendations. Patient, 2021, 14, 435-445.	2.7	24
126	Mapping social distancing measures to the reproduction number for COVID-19. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200276.	4.0	24

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127	Quantifying pupil-to-pupil SARS-CoV-2 transmission and the impact of lateral flow testing in English secondary schools. Nature Communications, 2022, 13, 1106.	12.8	24
128	Age- and bite-structured models for vector-borne diseases. Epidemics, 2015, 12, 20-29.	3.0	23
129	Incorporating household structure and demography into models of endemic disease. Journal of the Royal Society Interface, 2019, 16, 20190317.	3.4	23
130	Towards personalized guidelines: using machine-learning algorithms to guide antimicrobial selection. Journal of Antimicrobial Chemotherapy, 2020, 75, 2677-2680.	3.0	23
131	Assessing the impact of aggregating disease stage data in model predictions of human African trypanosomiasis transmission and control activities in Bandundu province (DRC). PLoS Neglected Tropical Diseases, 2020, 14, e0007976.	3.0	23
132	Quantifying epidemiological drivers of gambiense human African Trypanosomiasis across the Democratic Republic of Congo. PLoS Computational Biology, 2021, 17, e1008532.	3.2	23
133	Coexistence and Specialization of Pathogen Strains on Contact Networks. American Naturalist, 2006, 168, 230-241.	2.1	22
134	An Inter-Laboratory Validation of a Real Time PCR Assay to Measure Host Excretion of Bacterial Pathogens, Particularly of Mycobacterium bovis. PLoS ONE, 2011, 6, e27369.	2.5	22
135	Impact of regulatory perturbations to disease spread through cattle movements in Great Britain. Preventive Veterinary Medicine, 2012, 105, 110-117.	1.9	22
136	Fitting to the UK COVID-19 outbreak, short-term forecasts and estimating the reproductive number. Statistical Methods in Medical Research, 2022, 31, 1716-1737.	1.5	22
137	Drivers for Rift Valley fever emergence in Mayotte: A Bayesian modelling approach. PLoS Neglected Tropical Diseases, 2017, 11, e0005767.	3.0	21
138	Accelerator beam energy calibration with the 27Al(p, n) and 27Al(p, γ) reactions. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 1994, 340, 436-441.	1.6	20
139	Spatially extended host–parasite interactions: The role of recovery and immunity. Theoretical Population Biology, 2007, 71, 251-266.	1.1	20
140	Systematic Approximations to Susceptible-Infectious-Susceptible Dynamics on Networks. PLoS Computational Biology, 2016, 12, e1005296.	3.2	20
141	Estimating the distribution of time to extinction of infectious diseases in mean-field approaches. Journal of the Royal Society Interface, 2020, 17, 20200540.	3.4	19
142	Disentangling the influence of livestock vs. farm density on livestock disease epidemics. Ecosphere, 2018, 9, e02294.	2.2	18
143	Effect of data quality on estimates of farm infectiousness trends in the UK 2001 foot-and-mouth disease epidemic. Journal of the Royal Society Interface, 2007, 4, 235-241.	3.4	17
144	The role of movement restrictions in limiting the economic impact of livestock infections. Nature Sustainability, 2019, 2, 834-840.	23.7	17

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145	An analysis of school absences in England during the COVID-19 pandemic. BMC Medicine, 2021, 19, 137.	5.5	17
146	Modelling SARS-CoV-2 transmission in a UK university setting. Epidemics, 2021, 36, 100476.	3.0	17
147	Quantifying the Value of Perfect Information in Emergency Vaccination Campaigns. PLoS Computational Biology, 2017, 13, e1005318.	3.2	16
148	An individual based model of bearded pig abundance. Ecological Modelling, 2005, 181, 123-137.	2.5	14
149	Contingency planning for a deliberate release of smallpox in Great Britain - the role of geographical scale and contact structure. BMC Infectious Diseases, 2010, 10, 25.	2.9	14
150	Efficient methods for studying stochastic disease and population dynamics. Theoretical Population Biology, 2009, 75, 133-141.	1.1	13
151	Modelling to explore the potential impact of asymptomatic human infections on transmission and dynamics of African sleeping sickness. PLoS Computational Biology, 2021, 17, e1009367.	3.2	13
152	Comparison between one and two dose SARS-CoV-2 vaccine prioritization for a fixed number of vaccine doses. Journal of the Royal Society Interface, 2021, 18, 20210214.	3.4	13
153	Reducing respiratory syncytial virus (RSV) hospitalization in a lower-income country by vaccinating mothers-to-be and their households. ELife, 2020, 9, .	6.0	13
154	Stochasticity generates an evolutionary instability for infectious disease. Ecology Letters, 2007, 10, 818-827.	6.4	12
155	Contact structure and Salmonella control in the network of pig movements in France. Preventive Veterinary Medicine, 2011, 102, 30-40.	1.9	12
156	Policy implications of the potential use of a novel vaccine to prevent infection with Schistosoma mansoni with or without mass drug administration. Vaccine, 2020, 38, 4379-4386.	3.8	12
157	A network modelling approach to assess non-pharmaceutical disease controls in a worker population: An application to SARS-CoV-2. PLoS Computational Biology, 2021, 17, e1009058.	3.2	12
158	The colour of noise in short ecological time series data. Mathematical Medicine and Biology, 2004, 21, 63-72.	1.2	11
159	Fractal measures of spatial pattern as a heuristic for return rate in vegetative systems. Royal Society Open Science, 2016, 3, 150519.	2.4	11
160	Capturing sexual contact patterns in modelling the spread of sexually transmitted infections: Evidence using Natsal-3. PLoS ONE, 2018, 13, e0206501.	2.5	11
161	Concurrency of partnerships, consistency with data, and control of sexually transmitted infections. Epidemics, 2018, 25, 35-46.	3.0	11
162	Assessing the impact of lateral flow testing strategies on within-school SARS-CoV-2 transmission and absences: A modelling study. PLoS Computational Biology, 2022, 18, e1010158.	3.2	11

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163	The role of spatial population structure on the evolution of parasites with acquired immunity and demography. Journal of Theoretical Biology, 2013, 324, 21-31.	1.7	10
164	The effect of clumped population structure on the variability of spreading dynamics. Journal of Theoretical Biology, 2014, 359, 45-53.	1.7	10
165	Aggregation dynamics explain vegetation patch-size distributions. Theoretical Population Biology, 2016, 108, 70-74.	1.1	10
166	Contrasting factors associated with COVID-19-related ICU admission and death outcomes in hospitalised patients by means of Shapley values. PLoS Computational Biology, 2021, 17, e1009121.	3.2	10
167	Evolutionary Dynamics in Spatial Host–Parasite Systems. , 2000, , 271-291.		9
168	Optimal prophylactic vaccination in segregated populations: When can we improve on the equalising strategy?. Epidemics, 2015, 11, 7-13.	3.0	9
169	An assessment of the vaccination of school-aged children in England against SARS-CoV-2. BMC Medicine, 2022, 20, 196.	5.5	9
170	Modelling livestock infectious disease control policy under differing social perspectives on vaccination behaviour. PLoS Computational Biology, 2022, 18, e1010235.	3.2	9
171	Estimating the kernel parameters of premises-based stochastic models of farmed animal infectious disease epidemics using limited, incomplete, or ongoing data. Theoretical Population Biology, 2010, 78, 46-53.	1.1	8
172	Vaccination or mass drug administration against schistosomiasis: a hypothetical cost-effectiveness modelling comparison. Parasites and Vectors, 2019, 12, 499.	2.5	8
173	Biting midge dynamics and bluetongue transmission: a multiscale model linking catch data with climate and disease outbreaks. Scientific Reports, 2021, 11, 1892.	3.3	8
174	Cost-effectiveness modelling to optimise active screening strategy for gambiense human African trypanosomiasis in endemic areas of the Democratic Republic of Congo. BMC Medicine, 2021, 19, 86.	5.5	8
175	The population attributable fraction of cases due to gatherings and groups with relevance to COVID-19 mitigation strategies. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200273.	4.0	8
176	Revealing the extent of the first wave of the COVID-19 pandemic in Kenya based on serological and PCR-test data. Wellcome Open Research, 0, 6, 127.	1.8	8
177	Modelling to Quantify the Likelihood that Local Elimination of Transmission has Occurred Using Routine Gambiense Human African Trypanosomiasis Surveillance Data. Clinical Infectious Diseases, 2021, 72, S146-S151.	5.8	8
178	Can Reactive School Closures help critical care provision during the current influenza pandemic?. PLOS Currents, 2009, 1, RRN1119.	1.4	8
179	Precautionary breaks: Planned, limited duration circuit breaks to control the prevalence of SARS-CoV2 and the burden of COVID-19 disease. Epidemics, 2021, 37, 100526.	3.0	8
180	A theoretical study of the role of spatial population structure in the evolution of parasite virulence. Theoretical Population Biology, 2013, 84, 36-45.	1.1	7

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181	Mental health stigmatisation in deployed UK Armed Forces: a principal components analysis. Journal of the Royal Army Medical Corps, 2015, 161, i69-i76.	0.8	7
182	Testing the hypothesis of preferential attachment in social network formation. EPJ Data Science, 2015, 4, 13.	2.8	7
183	Rapid simulation of spatial epidemics: A spectral method. Journal of Theoretical Biology, 2015, 370, 121-134.	1.7	7
184	Preserving privacy whilst maintaining robust epidemiological predictions. Epidemics, 2016, 17, 35-41.	3.0	7
185	Mathematical modeling of ovine footrot in the UK: the effect of Dichelobacter nodosus and Fusobacterium necrophorum on the disease dynamics. Epidemics, 2017, 21, 13-20.	3.0	7
186	Need for speed: An optimized gridding approach for spatially explicit disease simulations. PLoS Computational Biology, 2018, 14, e1006086.	3.2	7
187	Optimising age coverage of seasonal influenza vaccination in England: A mathematical and health economic evaluation. PLoS Computational Biology, 2020, 16, e1008278.	3.2	7
188	Cattle farmer psychosocial profiles and their association with control strategies for bovine viral diarrhea. Journal of Dairy Science, 2022, 105, 3559-3573.	3.4	7
189	Cost-effectiveness of sleeping sickness elimination campaigns in five settings of the Democratic Republic of Congo. Nature Communications, 2022, 13, 1051.	12.8	7
190	Vaccination strategies for foot-and-mouth disease (reply). Nature, 2007, 445, E12-E13.	27.8	6
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