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	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
2	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
3	Cost-effectiveness of sleeping sickness elimination campaigns in five settings of the Democratic Republic of Congo. Nature Communications, 2022, 13, 1051.	12.8	7
4	MetaWards: A flexible metapopulation framework for modelling disease spread. Journal of Open Source Software, 2022, 7, 3914.	4.6	0
5	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
6	Identifying regions for enhanced control of gambiense sleeping sickness in the Democratic Republic of Congo. Nature Communications, 2022, 13, 1448.	12.8	3
7	An assessment of the vaccination of school-aged children in England against SARS-CoV-2. BMC Medicine, 2022, 20, 196.	5.5	9
8	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
9	The effect of notification window length on the epidemiological impact of COVID-19 contact tracing mobile applications. Communications Medicine, 2022, 2, .	4.2	3
10	Modelling livestock infectious disease control policy under differing social perspectives on vaccination behaviour. PLoS Computational Biology, 2022, 18, e1010235.	3.2	9
11	Coevolution fails to maintain genetic variation in a hostâ€"parasite model with constant finite population size. Theoretical Population Biology, 2021, 137, 10-21.	1.1	4
12	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
13	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
14	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
15	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
16	Predicting the impact of COVID-19 interruptions on transmission of <i>gambiense</i> 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
17	Modelling Sand Fly Lutzomyia longipalpis Attraction to Host Odour: Synthetic Sex-Aggregation Pheromone Dominates the Response. Microorganisms, 2021, 9, 602.	3.6	4
18	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

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19	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
20	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
21	Modelling optimal vaccination strategy for SARS-CoV-2 in the UK. PLoS Computational Biology, 2021, 17, e1008849.	3.2	142
22	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
23	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
24	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
25	An analysis of school absences in England during the COVID-19 pandemic. BMC Medicine, 2021, 19, 137.	5.5	17
26	Vaccination and non-pharmaceutical interventions for COVID-19: a mathematical modelling study. Lancet Infectious Diseases, The, 2021, 21, 793-802.	9.1	453
27	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
28	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
29	Spatially resolved simulations of the spread of COVID-19 in three European countries. PLoS Computational Biology, 2021, 17, e1009090.	3.2	5
30	Impact of Strain Variation of Dichelobacter nodosus on Disease Severity and Presence in Sheep Flocks in England. Frontiers in Veterinary Science, 2021, 8, 713927.	2.2	6
31	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
32	Modelling the persistence and control of Rift Valley fever virus in a spatially heterogeneous landscape. Nature Communications, 2021, 12, 5593.	12.8	6
33	Modelling SARS-CoV-2 transmission in a UK university setting. Epidemics, 2021, 36, 100476.	3.0	17
34	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
35	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
36	Feedback between coevolution and epidemiology can help or hinder the maintenance of genetic variation in hostâ€parasite models. Evolution; International Journal of Organic Evolution, 2021, 75, 582-599.	2.3	4

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37	Quantifying epidemiological drivers of gambiense human African Trypanosomiasis across the Democratic Republic of Congo. PLoS Computational Biology, 2021, 17, e1008532.	3.2	23
38	COVID-19 transmission dynamics underlying epidemic waves in Kenya. Science, 2021, 374, 989-994.	12.6	62
39	Modelling <i>gambiense</i> human African trypanosomiasis infection in villages of the Democratic Republic of Congo using Kolmogorov forward equations. Journal of the Royal Society Interface, 2021, 18, 20210419.	3.4	0
40	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
41	Improving pairwise approximations for network models with susceptible-infected-susceptible dynamics. Journal of Theoretical Biology, 2020, 500, 110328.	1.7	1
42	Key questions for modelling COVID-19 exit strategies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201405.	2.6	106
43	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
44	Climate drivers of plague epidemiology in British India, 1898â€“1949. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200538.	2.6	4
45	Detecting HLA-infectious disease associations for multi-strain pathogens. Infection, Genetics and Evolution, 2020, 83, 104344.	2.3	3
46	Towards personalized guidelines: using machine-learning algorithms to guide antimicrobial selection. Journal of Antimicrobial Chemotherapy, 2020, 75, 2677-2680.	3.0	23
47	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
48	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
49	Screening Strategies for a Sustainable Endpoint for Gambiense Sleeping Sickness. Journal of Infectious Diseases, 2020, 221, S539-S545.	4.0	25
50	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
51	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
52	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
53	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
54	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

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55	Incorporating Vector Ecology and Life History into Disease Transmission Models: Insights from Tsetse (Glossina spp.). , 2020, , 175-188.		1
56	Optimising age coverage of seasonal influenza vaccination in England: A mathematical and health economic evaluation. PLoS Computational Biology, 2020, 16, e1008278.	3.2	7
57	Title is missing!. , 2020, 16, e1008031.		0
58	Title is missing!. , 2020, 16, e1008031.		0
59	Title is missing!. , 2020, 16, e1008031.		0
60	Title is missing!. , 2020, 16, e1008031.		0
61	Title is missing!. , 2020, 16, e1008278.		0
62	Title is missing!. , 2020, 16, e1008278.		0
63	Title is missing!. , 2020, 16, e1008278.		0
64	Title is missing!. , 2020, 16, e1008278.		0
65	The role of movement restrictions in limiting the economic impact of livestock infections. Nature Sustainability, 2019, 2, 834-840.	23.7	17
66	Seasonal influenza: Modelling approaches to capture immunity propagation. PLoS Computational Biology, 2019, 15, e1007096.	3.2	35
67	Village-scale persistence and elimination of gambiense human African trypanosomiasis. PLoS Neglected Tropical Diseases, 2019, 13, e0007838.	3.0	31
68	Vaccination or mass drug administration against schistosomiasis: a hypothetical cost-effectiveness modelling comparison. Parasites and Vectors, 2019, 12, 499.	2.5	8
69	Incorporating household structure and demography into models of endemic disease. Journal of the Royal Society Interface, 2019, 16, 20190317.	3.4	23
70	Correlations between stochastic endemic infection in multiple interacting subpopulations. Journal of Theoretical Biology, 2019, 483, 109991.	1.7	2
71	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
72	Correlations between stochastic epidemics in two interacting populations. Epidemics, 2019, 26, 58-67.	3.0	6

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73	Conservation of pattern as a tool for inference on spatial snapshots in ecological data. Scientific Reports, 2018, 8, 132.	3.3	3
74	Disentangling the influence of livestock vs. farm density on livestock disease epidemics. Ecosphere, 2018, 9, e02294.	2.2	18
75	Capturing sexual contact patterns in modelling the spread of sexually transmitted infections: Evidence using Natsal-3. PLoS ONE, 2018, 13, e0206501.	2.5	11
76	Dynamics of the 2004 avian influenza H5N1 outbreak in Thailand: The role of duck farming, sequential model fitting and control. Preventive Veterinary Medicine, 2018, 159, 171-181.	1.9	5
77	Assessing Strategies Against Gambiense Sleeping Sickness Through Mathematical Modeling. Clinical Infectious Diseases, 2018, 66, S286-S292.	5.8	37
78	Concurrency of partnerships, consistency with data, and control of sexually transmitted infections. Epidemics, 2018, 25, 35-46.	3.0	11
79	Real-time decision-making during emergency disease outbreaks. PLoS Computational Biology, 2018, 14, e1006202.	3.2	46
80	Need for speed: An optimized gridding approach for spatially explicit disease simulations. PLoS Computational Biology, 2018, 14, e1006086.	3.2	7
81	Absence of Evidence of Rift Valley Fever Infection in Eulemur fulvus (Brown Lemur) in Mayotte During an Interepidemic Period. Vector-Borne and Zoonotic Diseases, 2017, 17, 358-360.	1.5	4
82	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
83	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
84	Data-driven models to predict the elimination of sleeping sickness in former Equateur province of DRC. Epidemics, 2017, 18, 101-112.	3.0	39
85	The impact of temperature changes on vector-borne disease transmission: <i>Culicoides</i> midges and bluetongue virus. Journal of the Royal Society Interface, 2017, 14, 20160481.	3.4	42
86	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
87	Predicting the spread of the Asian hornet (Vespa velutina) following its incursion into Great Britain. Scientific Reports, 2017, 7, 6240.	3.3	52
88	Efficient use of sentinel sites: detection of invasive honeybee pests and diseases in the UK. Journal of the Royal Society Interface, 2017, 14, 20160908.	3.4	6
89	The impact of current infection levels on the cost-benefit of vaccination. Epidemics, 2017, 21, 56-62.	3.0	5
90	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

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91	Drivers for Rift Valley fever emergence in Mayotte: A Bayesian modelling approach. PLoS Neglected Tropical Diseases, 2017, 11, e0005767.	3.0	21
92	Quantifying the Value of Perfect Information in Emergency Vaccination Campaigns. PLoS Computational Biology, 2017, 13, e1005318.	3.2	16
93	Fractal measures of spatial pattern as a heuristic for return rate in vegetative systems. Royal Society Open Science, 2016, 3, 150519.	2.4	11
94	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
95	Systematic Approximations to Susceptible-Infectious-Susceptible Dynamics on Networks. PLoS Computational Biology, 2016, 12, e1005296.	3.2	20
96	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
97	Preserving privacy whilst maintaining robust epidemiological predictions. Epidemics, 2016, 17, 35-41.	3.0	7
98	Disease transmission promotes evolution of host spatial patterns. Journal of the Royal Society Interface, 2016, 13, 20160463.	3.4	4
99	UK support services for families of wounded, injured or sick Service personnel: the need for evaluation: TableÂ1. Journal of the Royal Army Medical Corps, 2016, 162, 324-325.	0.8	4
100	Aggregation dynamics explain vegetation patch-size distributions. Theoretical Population Biology, 2016, 108, 70-74.	1.1	10
101	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
102	Testing the hypothesis of preferential attachment in social network formation. EPJ Data Science, 2015, 4, 13.	2.8	7
103	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
104	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
105	Mathematical Models of Human African Trypanosomiasis Epidemiology. Advances in Parasitology, 2015, 87, 53-133.	3.2	27
106	Rapid simulation of spatial epidemics: A spectral method. Journal of Theoretical Biology, 2015, 370, 121-134.	1.7	7
107	Age- and bite-structured models for vector-borne diseases. Epidemics, 2015, 12, 20-29.	3.0	23
108	Exact and approximate moment closures for non-Markovian network epidemics. Journal of Theoretical Biology, 2015, 382, 160-177.	1.7	24

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109	Optimal prophylactic vaccination in segregated populations: When can we improve on the equalising strategy?. Epidemics, 2015, 11, 7-13.	3.0	9
110	The effects of demographic change on disease transmission and vaccine impact in a household structured population. Epidemics, 2015, 13, 56-64.	3.0	50
111	Eight challenges in modelling infectious livestock diseases. Epidemics, 2015, 10, 1-5.	3.0	72
112	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
113	Strategies for Controlling Non-Transmissible Infection Outbreaks Using a Large Human Movement Data Set. PLoS Computational Biology, 2014, 10, e1003809.	3.2	6
114	Dynamics of infectious diseases. Reports on Progress in Physics, 2014, 77, 026602.	20.1	103
115	A dynamic model of bovine tuberculosis spread and control in Great Britain. Nature, 2014, 511, 228-231.	27.8	186
116	The effect of clumped population structure on the variability of spreading dynamics. Journal of Theoretical Biology, 2014, 359, 45-53.	1.7	10
117	Identification of 100 fundamental ecological questions. Journal of Ecology, 2013, 101, 58-67.	4.0	605
118	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
119	Threats to an ecosystem service: pressures on pollinators. Frontiers in Ecology and the Environment, 2013, 11, 251-259.	4.0	980
120	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
121	Social encounter networks: characterizing Great Britain. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131037.	2.6	103
122	Epidemiological consequences of household-based antiviral prophylaxis for pandemic influenza. Journal of the Royal Society Interface, 2013, 10, 20121019.	3.4	32
123	Modelling the spread of American foulbrood in honeybees. Journal of the Royal Society Interface, 2013, 10, 20130650.	3.4	26
124	Social encounter networks: collective properties and disease transmission. Journal of the Royal Society Interface, 2012, 9, 2826-2833.	3.4	95
125	Estimation of outbreak severity and transmissibility: Influenza A(H1N1)pdm09 in households. BMC Medicine, 2012, 10, 117.	5.5	32
126	Optimal but unequitable prophylactic distribution of vaccine. Epidemics, 2012, 4, 78-85.	3.0	48

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127	Modelling the future of the Hawaiian honeycreeper: An ecological and epidemiological problem. Ecological Modelling, 2012, 235-236, 26-35.	2.5	6
128	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
129	Impact of regulatory perturbations to disease spread through cattle movements in Great Britain. Preventive Veterinary Medicine, 2012, 105, 110-117.	1.9	22
130	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
131	Contact structure and Salmonella control in the network of pig movements in France. Preventive Veterinary Medicine, 2011, 102, 30-40.	1.9	12
132	Epidemic prediction and control in clustered populations. Journal of Theoretical Biology, 2011, 272, 1-7.	1.7	38
133	Endemic cattle diseases: comparative epidemiology and governance. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 1975-1986.	4.0	43
134	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
135	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
136	Insights from unifying modern approximations to infections on networks. Journal of the Royal Society Interface, 2011, 8, 67-73.	3.4	153
137	Networks and the Epidemiology of Infectious Disease. Interdisciplinary Perspectives on Infectious Diseases, 2011, 2011, 1-28.	1.4	299
138	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
139	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
140	Calculation of Disease Dynamics in a Population of Households. PLoS ONE, 2010, 5, e9666.	2.5	40
141	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
142	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
143	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
144	The Impact of Contact Tracing in Clustered Populations. PLoS Computational Biology, 2010, 6, e1000721.	3.2	75

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145	INFERENCE FOR INDIVIDUAL-LEVEL MODELS OF INFECTIOUS DISEASES IN LARGE POPULATIONS. Statistica Sinica, 2010, 20, 239-261.	0.3	57
146	Implications of vaccination and waning immunity. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2071-2080.	2.6	89
147	Mathematical modelling of infectious diseases. British Medical Bulletin, 2009, 92, 33-42.	6.9	131
148	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
149	Integrating stochasticity and network structure into an epidemic model. Journal of the Royal Society Interface, 2009, 6, 761-774.	3.4	56
150	Predicting undetected infections during the 2007 foot-and-mouth disease outbreak. Journal of the Royal Society Interface, 2009, 6, 1145-1151.	3.4	63
151	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
152	Herd size and bovine tuberculosis persistence in cattle farms in Great Britain. Preventive Veterinary Medicine, 2009, 92, 360-365.	1.9	82
153	Efficient methods for studying stochastic disease and population dynamics. Theoretical Population Biology, 2009, 75, 133-141.	1.1	13
154	A Motif-Based Approach to Network Epidemics. Bulletin of Mathematical Biology, 2009, 71, 1693-1706.	1.9	48
155	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
156	The role of routine versus random movements on the spread of disease in Great Britain. Epidemics, 2009, 1, 250-258.	3.0	41
157	Household structure and infectious disease transmission. Epidemiology and Infection, 2009, 137, 654-661.	2.1	77
158	Can Reactive School Closures help critical care provision during the current influenza pandemic?. PLOS Currents, 2009, 1, RRN1119.	1.4	8
159	Modelling foot-and-mouth disease: A comparison between the UK and Denmark. Preventive Veterinary Medicine, 2008, 85, 107-124.	1.9	29
160	An in-host model of acute infection: Measles as a case study. Theoretical Population Biology, 2008, 73, 134-147.	1.1	29
161	On methods for studying stochastic disease dynamics. Journal of the Royal Society Interface, 2008, 5, 171-181.	3.4	164
162	Deterministic epidemic models with explicit household structure. Mathematical Biosciences, 2008, 213, 29-39.	1.9	70

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163	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
164	Chapter 7. Spatial Models. , 2008, , 232-290.		1
165	Spatiotemporal patterns and risks of herd breakdowns in pigs with postweaning multisystemic wasting syndrome. Veterinary Record, 2007, 160, 751-762.	0.3	38
166	Spatially extended hostâ€"parasite interactions: The role of recovery and immunity. Theoretical Population Biology, 2007, 71, 251-266.	1.1	20
167	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
168	Vaccination strategies for foot-and-mouth disease (reply). Nature, 2007, 445, E12-E13.	27.8	6
169	Stochasticity generates an evolutionary instability for infectious disease. Ecology Letters, 2007, 10, 818-827.	6.4	12
170	Hostâ€"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
171	A robustness metric integrating spatial and temporal information: application to coral reefs exposed to local and regional disturbances. Marine Ecology - Progress Series, 2007, 331, 101-108.	1.9	6
172	Disease evolution across a range of spatio-temporal scales. Theoretical Population Biology, 2006, 70, 201-213.	1.1	30
173	Topographic determinants of foot and mouth disease transmission in the UK 2001 epidemic. BMC Veterinary Research, 2006, 2, 3.	1.9	37
174	Silent spread of H5N1 in vaccinated poultry. Nature, 2006, 442, 757-757.	27.8	121
175	Optimal reactive vaccination strategies for a foot-and-mouth outbreak in the UK. Nature, 2006, 440, 83-86.	27.8	216
176	Modelling the many-wrongs principle: The navigational advantages of aggregation in nomadic foragers. Journal of Theoretical Biology, 2006, 240, 302-310.	1.7	24
177	Coexistence and Specialization of Pathogen Strains on Contact Networks. American Naturalist, 2006, 168, 230-241.	2.1	22
178	FMD control strategies. Veterinary Record, 2006, 158, 707-708.	0.3	1
179	An individual based model of bearded pig abundance. Ecological Modelling, 2005, 181, 123-137.	2.5	14
180	Models of foot-and-mouth disease. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 1195-1202.	2.6	136

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181	Appropriate Models for the Management of Infectious Diseases. PLoS Medicine, 2005, 2, e174.	8.4	407
182	The implications of network structure for epidemic dynamics. Theoretical Population Biology, 2005, 67, 1-8.	1.1	272
183	Networks and epidemic models. Journal of the Royal Society Interface, 2005, 2, 295-307.	3.4	1,403
184	EXTENSIONS TO MASS-ACTION MIXING. , 2005, , 107-142.		5
185	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
186	Metapopulation Dynamics of Infectious Diseases. , 2004, , 415-445.		59
187	The colour of noise in short ecological time series data. Mathematical Medicine and Biology, 2004, 21, 63-72.	1.2	11
188	Monogamous networks and the spread of sexually transmitted diseases. Mathematical Biosciences, 2004, 189, 115-130.	1.9	80
189	Modelling vaccination strategies against foot-and-mouth disease. Nature, 2003, 421, 136-142.	27.8	375
190	Planning for smallpox outbreaks. Nature, 2003, 425, 681-685.	27.8	324
191	The invasion and coexistence of competing Wolbachia strains. Heredity, 2003, 91, 382-388.	2.6	77
192	Contact tracing and disease control. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 2565-2571.	2.6	321
193	Neighbourhood control policies and the spread of infectious diseases. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 1659-1666.	2.6	39
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