Adrian Esterman

List of Publications by Year
in descending order

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72 papers	1,698 citations	279778 23 h-index	361001 35 g-index
75 all docs	75 docs citations	75 times ranked	1979 citing authors

#	Article	IF	Citations
1	On methods for studying stochastic disease dynamics. Journal of the Royal Society Interface, 2008, 5, 171-181.	3.4	164
2	Where did all the pangolins go? International CITES trade in pangolin species. Global Ecology and Conservation, 2016, 8, 241-253.	2.1	119
3	Key questions for modelling COVID-19 exit strategies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201405.	2.6	106
4	Infectious disease pandemic planning and response: Incorporating decision analysis. PLoS Medicine, 2020, 17, e1003018.	8.4	67
5	Simulation-based Bayesian inference for epidemic models. Computational Statistics and Data Analysis, 2014, 71, 434-447.	1.2	57
6	Integrating stochasticity and network structure into an epidemic model. Journal of the Royal Society Interface, 2009, 6, 761-774.	3.4	56
7	Measuring social networks in British primary schools through scientific engagement. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1467-1475.	2.6	54
8	Understanding the biological invasion risk posed by the global wildlife trade: propagule pressure drives the introduction and establishment of Nearctic turtles. Global Change Biology, 2015, 21, 1078-1091.	9.5	53
9	Locally Fixed Alleles: A method to localize gene drive to island populations. Scientific Reports, 2019, 9, 15821.	3.3	52
10	Interpreting scratch assays using pair density dynamics and approximate Bayesian computation. Open Biology, 2014, 4, 140097.	3.6	47
11	Quantifying the effect of experimental design choices for in vitro scratch assays. Journal of Theoretical Biology, 2016, 400, 19-31.	1.7	46
12	A Y-chromosome shredding gene drive for controlling pest vertebrate populations. ELife, 2019, 8, .	6.0	42
13	Calculation of Disease Dynamics in a Population of Households. PLoS ONE, 2010, 5, e9666.	2.5	40
14	On parameter estimation in population models. Theoretical Population Biology, 2006, 70, 498-510.	1.1	36
15	Characterising pandemic severity and transmissibility from data collected during first few hundred studies. Epidemics, 2017, 19, 61-73.	3.0	36
16	On parameter estimation in population models II: Multi-dimensional processes and transient dynamics. Theoretical Population Biology, 2009, 75, 123-132.	1.1	34
17	The Illegal Wildlife Trade Is a Likely Source of Alien Species. Conservation Letters, 2017, 10, 690-698.	5.7	34
18	Estimation for queues from queue length data. Queueing Systems, 2007, 55, 131-138.	0.9	32

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19	Epidemiological consequences of household-based antiviral prophylaxis for pandemic influenza. Journal of the Royal Society Interface, 2013, 10, 20121019.	3.4	32
20	Influencing public health policy with data-informed mathematical models of infectious diseases: Recent developments and new challenges. Epidemics, 2020, 32, 100393.	3.0	31
21	A stochastic metapopulation model accounting for habitat dynamics. Journal of Mathematical Biology, 2006, 52, 788-806.	1.9	29
22	Computation of epidemic final size distributions. Journal of Theoretical Biology, 2015, 367, 159-165.	1.7	28
23	A note on density dependence in population models. Ecological Modelling, 2009, 220, 3472-3474.	2.5	25
24	A data-driven model for influenza transmission incorporating media effects. Royal Society Open Science, 2016, 3, 160481.	2.4	24
25	Characterising seasonal influenza epidemiology using primary care surveillance data. PLoS Computational Biology, 2018, 14, e1006377.	3.2	21
26	Invasion of infectious diseases in finite homogeneous populations. Journal of Theoretical Biology, 2011, 289, 83-89.	1.7	20
27	Pest demography critically determines the viability of synthetic gene drives for population control. Mathematical Biosciences, 2018, 305, 160-169.	1.9	20
28	Statistical description of wetland hydrological connectivity to the River Murray in South Australia under both natural and regulated conditions. Journal of Hydrology, 2015, 531, 929-939.	5.4	19
29	Scabies in residential care homes: Modelling, inference and interventions for well-connected population sub-units. PLoS Computational Biology, 2018, 14, e1006046.	3.2	19
30	Temporal modelling of ballast water discharge and ship-mediated invasion risk to Australia. Royal Society Open Science, 2015, 2, 150039.	2.4	18
31	Stochastic models for mainland-island metapopulations in static and dynamic landscapes. Bulletin of Mathematical Biology, 2006, 68, 417-449.	1.9	16
32	Disturbance affects short-term facilitation, but not long-term saturation, of exotic plant invasion in New Zealand forest. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1457-1466.	2.6	16
33	Managing the risk of wildlife disease introduction: pathwayâ€level biosecurity for preventing the introduction of alien ranaviruses. Journal of Applied Ecology, 2017, 54, 234-241.	4.0	15
34	Estimating the basic reproductive number during the early stages of an emerging epidemic. Theoretical Population Biology, 2018, 119, 26-36.	1.1	15
35	Catastrophe management and inter-reserve distance for marine reserve networks. Ecological Modelling, 2007, 201, 82-88.	2.5	13
36	Efficient methods for studying stochastic disease and population dynamics. Theoretical Population Biology, 2009, 75, 133-141.	1.1	13

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37	Plight of the commons: 17Âyears of wildlife trafficking in Cambodia. Biological Conservation, 2020, 241, 108379.	4.1	13
38	A comparison of models for predicting population persistence. Ecological Modelling, 2007, 201, 19-26.	2.5	12
39	Predicting the Risk of Biological Invasions Using Environmental Similarity and Transport Network Connectedness. Risk Analysis, 2019, 39, 35-53.	2.7	12
40	Integrative Analysis of the Physical Transport Network into Australia. PLoS ONE, 2016, 11, e0148831.	2.5	11
41	Simple rules for ranking and optimally managing metapopulations. Ecological Modelling, 2010, 221, 2515-2520.	2.5	10
42	The effect of clumped population structure on the variability of spreading dynamics. Journal of Theoretical Biology, 2014, 359, 45-53.	1.7	10
43	Hybrid Markov chain models of Sâ€“Iâ€“R disease dynamics. Journal of Mathematical Biology, 2017, 75, 521-541.	1.9	10
44	The role of antimalarial quality in the emergence and transmission of resistance. Medical Hypotheses, 2018, 111, 49-54.	1.5	10
45	Estimating a Markovian Epidemic Model Using Household Serial Interval Data from the Early Phase of an Epidemic. PLoS ONE, 2013, 8, e73420.	2.5	10
46	On the derivation of approximations to cellular automata models and the assumption of independence. Mathematical Biosciences, 2014, 253, 63-71.	1.9	9
47	Incomplete penetrance: The role of stochasticity in developmental cell colonization. Journal of Theoretical Biology, 2015, 380, 309-314.	1.7	9
48	Optimal prophylactic vaccination in segregated populations: When can we improve on the equalising strategy?. Epidemics, 2015, 11, 7-13.	3.0	9
49	On the efficient determination of optimal Bayesian experimental designs using ABC: A case study in optimal observation of epidemics. Journal of Statistical Planning and Inference, 2016, 172, 1-15.	0.6	9
50	The probability of epidemic fade-out is non-monotonic in transmission rate for the Markovian SIR model with demography. Journal of Theoretical Biology, 2016, 393, 170-178.	1.7	9
51	An induced natural selection heuristic for finding optimal Bayesian experimental designs. Computational Statistics and Data Analysis, 2018, 126, 112-124.	1.2	9
52	On costs and decisions in population management. Ecological Modelling, 2007, 201, 60-66.	2.5	8
53	Contact tracing and antiviral prophylaxis in the early stages of a pandemic: the probability of a major outbreak. Mathematical Medicine and Biology, 2015, 32, 331-343.	1.2	8
54	On parameter estimation in population models III: Time-inhomogeneous processes and observation error. Theoretical Population Biology, 2012, 82, 1-17.	1.1	7

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55	Extinction times for a birthâ€“death process with two phases. Mathematical Biosciences, 2006, 202, 310-322.	1.9	6
56	Computationally exact methods for stochastic periodic dynamics: Spatiotemporal dispersal and temporally forced transmission. Journal of Theoretical Biology, 2010, 262, 14-22.	1.7	6
57	The Impact of Antimalarial Use on the Emergence and Transmission of Plasmodium falciparum Resistance: A Scoping Review of Mathematical Models. Tropical Medicine and Infectious Disease, 2017, 2, 54.	2.3	6
58	Designing group dose-response studies in the presence of transmission. Mathematical Biosciences, 2018, 304, 62-78.	1.9	6
59	Modelling population processes with random initial conditions. Mathematical Biosciences, 2010, 223, 142-150.	1.9	5
60	Optimal use of GPS transmitter for estimating species migration rate. Ecological Modelling, 2013, 249, 37-41.	2.5	5
61	The distribution of the time taken for an epidemic to spread between two communities. Mathematical Biosciences, 2018, 303, 139-147.	1.9	5
62	Inference of epidemiological parameters from household stratified data. PLoS ONE, 2017, 12, e0185910.	2.5	5
63	Modelling the impact of antimalarial quality on the transmission of sulfadoxine-pyrimethamine resistance in Plasmodium falciparum. Infectious Disease Modelling, 2017, 2, 161-187.	1.9	4
64	Development of an influenza pandemic decision support tool linking situational analytics to national response policy. Epidemics, 2021, 36, 100478.	3.0	4
65	Intervention to maximise the probability of epidemic fade-out. Mathematical Biosciences, 2017, 293, 1-10.	1.9	3
66	Bayesian model discrimination for partially-observed epidemic models. Mathematical Biosciences, 2019, 317, 108266.	1.9	3
67	Dataset of seized wildlife and their intended uses. Data in Brief, 2021, 39, 107531.	1.0	3
68	Approximating spatially exclusive invasion processes. Physical Review E, 2014, 89, 052709.	2.1	2
69	Choice of Antiviral Allocation Scheme for Pandemic Influenza Depends on Strain Transmissibility, Delivery Delay and Stockpile Size. Bulletin of Mathematical Biology, 2016, 78, 293-321.	1.9	2
70	Identification of the relative timing of infectiousness and symptom onset for outbreak control. Journal of Theoretical Biology, 2020, 486, 110079.	1.7	2
71	Elucidating user behaviours in a digital health surveillance system to correct prevalence estimates. Epidemics, 2020, 33, 100404.	3.0	2
72	Optimised prophylactic vaccination in metapopulations. Epidemics, 2021, 34, 100420.	3.0	2