Adrian Esterman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

| 73 | 1,237 citations | 2 O | 32 |
|-------------------|----------------------|-------------|-----------------|
| papers | | h-index | g-index |
| 75 ext. papers | 1,498 ext. citations | 3.8 avg, IF | 4.87 L-index |

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 73 | Dataset of seized wildlife and their intended uses. <i>Data in Brief</i> , 2021 , 39, 107531 | 1.2 | O |
| 72 | Optimised prophylactic vaccination in metapopulations. <i>Epidemics</i> , 2021 , 34, 100420 | 5.1 | О |
| 71 | Development of an influenza pandemic decision support tool linking situational analytics to national response policy. <i>Epidemics</i> , 2021 , 36, 100478 | 5.1 | O |
| 70 | Elucidating user behaviours in a digital health surveillance system to correct prevalence estimates. <i>Epidemics</i> , 2020 , 33, 100404 | 5.1 | О |
| 69 | Infectious disease pandemic planning and response: Incorporating decision analysis. <i>PLoS Medicine</i> , 2020 , 17, e1003018 | 11.6 | 37 |
| 68 | Plight of the commons: 17 years of wildlife trafficking in Cambodia. <i>Biological Conservation</i> , 2020 , 241, 108379 | 6.2 | 9 |
| 67 | Identification of the relative timing of infectiousness and symptom onset for outbreak control. <i>Journal of Theoretical Biology</i> , 2020 , 486, 110079 | 2.3 | 2 |
| 66 | Influencing public health policy with data-informed mathematical models of infectious diseases: Recent developments and new challenges. <i>Epidemics</i> , 2020 , 32, 100393 | 5.1 | 14 |
| 65 | Key questions for modelling COVID-19 exit strategies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020 , 287, 20201405 | 4.4 | 65 |
| 64 | Bayesian model discrimination for partially-observed epidemic models. <i>Mathematical Biosciences</i> , 2019 , 317, 108266 | 3.9 | 0 |
| 63 | A Y-chromosome shredding gene drive for controlling pest vertebrate populations. <i>ELife</i> , 2019 , 8, | 8.9 | 24 |
| 62 | Locally Fixed Alleles: A method to localize gene drive to island populations. <i>Scientific Reports</i> , 2019 , 9, 15821 | 4.9 | 29 |
| 61 | Predicting the Risk of Biological Invasions Using Environmental Similarity and Transport Network Connectedness. <i>Risk Analysis</i> , 2019 , 39, 35-53 | 3.9 | 6 |
| 60 | The role of antimalarial quality in the emergence and transmission of resistance. <i>Medical Hypotheses</i> , 2018 , 111, 49-54 | 3.8 | 6 |
| 59 | The distribution of the time taken for an epidemic to spread between two communities. <i>Mathematical Biosciences</i> , 2018 , 303, 139-147 | 3.9 | 3 |
| 58 | Characterising seasonal influenza epidemiology using primary care surveillance data. <i>PLoS Computational Biology</i> , 2018 , 14, e1006377 | 5 | 13 |
| 57 | Scabies in residential care homes: Modelling, inference and interventions for well-connected population sub-units. <i>PLoS Computational Biology</i> , 2018 , 14, e1006046 | 5 | 11 |

(2016-2018)

| 56 | Estimating the basic reproductive number during the early stages of an emerging epidemic. <i>Theoretical Population Biology</i> , 2018 , 119, 26-36 | 1.2 | 11 |
|----|---|--------------|----|
| 55 | Designing group dose-response studies in the presence of transmission. <i>Mathematical Biosciences</i> , 2018 , 304, 62-78 | 3.9 | 2 |
| 54 | Pest demography critically determines the viability of synthetic gene drives for population control. <i>Mathematical Biosciences</i> , 2018 , 305, 160-169 | 3.9 | 13 |
| 53 | An induced natural selection heuristic for finding optimal Bayesian experimental designs. <i>Computational Statistics and Data Analysis</i> , 2018 , 126, 112-124 | 1.6 | 7 |
| 52 | Characterising pandemic severity and transmissibility from data collected during first few hundred studies. <i>Epidemics</i> , 2017 , 19, 61-73 | 5.1 | 23 |
| 51 | Modelling the impact of antimalarial quality on the transmission of sulfadoxine-pyrimethamine resistance in. <i>Infectious Disease Modelling</i> , 2017 , 2, 161-187 | 15.7 | 2 |
| 50 | The Illegal Wildlife Trade Is a Likely Source of Alien Species. <i>Conservation Letters</i> , 2017 , 10, 690-698 | 6.9 | 18 |
| 49 | Hybrid Markov chain models of S-I-R disease dynamics. <i>Journal of Mathematical Biology</i> , 2017 , 75, 521-5 | 421 | 8 |
| 48 | Intervention to maximise the probability of epidemic fade-out. <i>Mathematical Biosciences</i> , 2017 , 293, 1-10 | 3.9 | 3 |
| 47 | Managing the risk of wildlife disease introduction: pathway-level biosecurity for preventing the introduction of alien ranaviruses. <i>Journal of Applied Ecology</i> , 2017 , 54, 234-241 | 5.8 | 11 |
| 46 | The Impact of Antimalarial Use on the Emergence and Transmission of Plasmodium falciparum Resistance: A Scoping Review of Mathematical Models. <i>Tropical Medicine and Infectious Disease</i> , 2017 , 2, | 3.5 | 5 |
| 45 | Inference of epidemiological parameters from household stratified data. <i>PLoS ONE</i> , 2017 , 12, e0185910 |) 3.7 | 5 |
| 44 | A data-driven model for influenza transmission incorporating media effects. <i>Royal Society Open Science</i> , 2016 , 3, 160481 | 3.3 | 18 |
| 43 | Choice of Antiviral Allocation Scheme for Pandemic Influenza Depends on Strain Transmissibility, Delivery Delay and Stockpile Size. <i>Bulletin of Mathematical Biology</i> , 2016 , 78, 293-321 | 2.1 | 2 |
| 42 | The probability of epidemic fade-out is non-monotonic in transmission rate for the Markovian SIR model with demography. <i>Journal of Theoretical Biology</i> , 2016 , 393, 170-8 | 2.3 | 5 |
| 41 | Integrative Analysis of the Physical Transport Network into Australia. <i>PLoS ONE</i> , 2016 , 11, e0148831 | 3.7 | 10 |
| 40 | Where did all the pangolins go? International CITES trade in pangolin species. <i>Global Ecology and Conservation</i> , 2016 , 8, 241-253 | 2.8 | 89 |
| 39 | On the efficient determination of optimal Bayesian experimental designs using ABC: A case study in optimal observation of epidemics. <i>Journal of Statistical Planning and Inference</i> , 2016 , 172, 1-15 | 0.8 | 6 |

| 38 | Quantifying the effect of experimental design choices for in vitro scratch assays. <i>Journal of Theoretical Biology</i> , 2016 , 400, 19-31 | 2.3 | 33 |
|----|---|------|----|
| 37 | Incomplete penetrance: The role of stochasticity in developmental cell colonization. <i>Journal of Theoretical Biology</i> , 2015 , 380, 309-14 | 2.3 | 7 |
| 36 | Optimal prophylactic vaccination in segregated populations: When can we improve on the equalising strategy?. <i>Epidemics</i> , 2015 , 11, 7-13 | 5.1 | 8 |
| 35 | Contact tracing and antiviral prophylaxis in the early stages of a pandemic: the probability of a major outbreak. <i>Mathematical Medicine and Biology</i> , 2015 , 32, 331-43 | 1.3 | 6 |
| 34 | Understanding the biological invasion risk posed by the global wildlife trade: propagule pressure drives the introduction and establishment of Nearctic turtles. <i>Global Change Biology</i> , 2015 , 21, 1078-91 | 11.4 | 33 |
| 33 | Statistical description of wetland hydrological connectivity to the River Murray in South Australia under both natural and regulated conditions. <i>Journal of Hydrology</i> , 2015 , 531, 929-939 | 6 | 13 |
| 32 | Temporal modelling of ballast water discharge and ship-mediated invasion risk to Australia. <i>Royal Society Open Science</i> , 2015 , 2, 150039 | 3.3 | 15 |
| 31 | Computation of epidemic final size distributions. <i>Journal of Theoretical Biology</i> , 2015 , 367, 159-165 | 2.3 | 20 |
| 30 | Simulation-based Bayesian inference for epidemic models. <i>Computational Statistics and Data Analysis</i> , 2014 , 71, 434-447 | 1.6 | 39 |
| 29 | On the derivation of approximations to cellular automata models and the assumption of independence. <i>Mathematical Biosciences</i> , 2014 , 253, 63-71 | 3.9 | 7 |
| 28 | The effect of clumped population structure on the variability of spreading dynamics. <i>Journal of Theoretical Biology</i> , 2014 , 359, 45-53 | 2.3 | 7 |
| 27 | Interpreting scratch assays using pair density dynamics and approximate Bayesian computation. <i>Open Biology</i> , 2014 , 4, 140097 | 7 | 31 |
| 26 | Approximating spatially exclusive invasion processes. <i>Physical Review E</i> , 2014 , 89, 052709 | 2.4 | 2 |
| 25 | Optimal use of GPS transmitter for estimating species migration rate. <i>Ecological Modelling</i> , 2013 , 249, 37-41 | 3 | 5 |
| 24 | Epidemiological consequences of household-based antiviral prophylaxis for pandemic influenza. Journal of the Royal Society Interface, 2013 , 10, 20121019 | 4.1 | 28 |
| 23 | Estimating a Markovian epidemic model using household serial interval data from the early phase of an epidemic. <i>PLoS ONE</i> , 2013 , 8, e73420 | 3.7 | 9 |
| 22 | On parameter estimation in population models III: time-inhomogeneous processes and observation error. <i>Theoretical Population Biology</i> , 2012 , 82, 1-17 | 1.2 | 7 |
| 21 | Invasion of infectious diseases in finite homogeneous populations. <i>Journal of Theoretical Biology</i> , 2011 , 289, 83-9 | 2.3 | 18 |

(2006-2011)

| 20 | Disturbance affects short-term facilitation, but not long-term saturation, of exotic plant invasion in New Zealand forest. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011 , 278, 1457-66 | 4.4 | 15 |
|----|--|--------------------|----------------|
| 19 | Measuring social networks in British primary schools through scientific engagement. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011 , 278, 1467-75 | 4.4 | 49 |
| 18 | Calculation of disease dynamics in a population of households. <i>PLoS ONE</i> , 2010 , 5, e9666 | 3.7 | 35 |
| 17 | Modelling population processes with random initial conditions. <i>Mathematical Biosciences</i> , 2010 , 223, 142-50 | 3.9 | 4 |
| 16 | Computationally exact methods for stochastic periodic dynamics: Spatiotemporal dispersal and temporally forced transmission. <i>Journal of Theoretical Biology</i> , 2010 , 262, 14-22 | 2.3 | 4 |
| 15 | Simple rules for ranking and optimally managing metapopulations. <i>Ecological Modelling</i> , 2010 , 221, 251 | 5 ₃ 252 | 0 ₇ |
| 14 | Integrating stochasticity and network structure into an epidemic model. <i>Journal of the Royal Society Interface</i> , 2009 , 6, 761-74 | 4.1 | 49 |
| 13 | On parameter estimation in population models II: multi-dimensional processes and transient dynamics. <i>Theoretical Population Biology</i> , 2009 , 75, 123-32 | 1.2 | 32 |
| 12 | Efficient methods for studying stochastic disease and population dynamics. <i>Theoretical Population Biology</i> , 2009 , 75, 133-41 | 1.2 | 11 |
| 11 | A note on density dependence in population models. <i>Ecological Modelling</i> , 2009 , 220, 3472-3474 | 3 | 20 |
| 10 | On methods for studying stochastic disease dynamics. <i>Journal of the Royal Society Interface</i> , 2008 , 5, 171-81 | 4.1 | 130 |
| 9 | A comparison of models for predicting population persistence. <i>Ecological Modelling</i> , 2007 , 201, 19-26 | 3 | 11 |
| 8 | On costs and decisions in population management. <i>Ecological Modelling</i> , 2007 , 201, 60-66 | 3 | 8 |
| 7 | Catastrophe management and inter-reserve distance for marine reserve networks. <i>Ecological Modelling</i> , 2007 , 201, 82-88 | 3 | 11 |
| 6 | Estimation for queues from queue length data. <i>Queueing Systems</i> , 2007 , 55, 131-138 | 1.7 | 26 |
| 5 | A stochastic metapopulation model accounting for habitat dynamics. <i>Journal of Mathematical Biology</i> , 2006 , 52, 788-806 | 2 | 26 |
| 4 | Stochastic models for mainland-island metapopulations in static and dynamic landscapes. <i>Bulletin of Mathematical Biology</i> , 2006 , 68, 417-49 | 2.1 | 15 |
| 3 | On parameter estimation in population models. <i>Theoretical Population Biology</i> , 2006 , 70, 498-510 | 1.2 | 32 |

 $\text{Extinction times for a birth-death process with two phases.} \textit{Mathematical Biosciences}, \textbf{2006}, 202, 310-22 \\ 3.9 \\ 5$

Connecting surveillance and population-level influenza incidence

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