Tim CD Lucas

PERSONAL INFORMATION

email	✉ timcdlucas@gmail.com
twitter	🐦 @timcdlucas @statsforbios
github	www.github.com/timcdlucas
scholar	Google scholar
phone	07415 863 536

PRESENT APPOINTMENT

2016–Present **University of Oxford, Malaria Atlas Project**

Post Doc. My current position is as a postdoctoral research scientist in geospatial epidemiology with the Malaria Atlas Project at the University of Oxford. I use spatial statistics and machine learning methods to map malaria risk.

PREVIOUS APPOINTMENTS

Jan–July 2016 **CBER, UCL**

Research Programmer I was the staff programmer for the Centre of Biodiversity and Environment Research at UCL. I worked on two main projects. I worked with the Madingley Model—an ecological model of all life, written in C# to enable this model to run on the *high performance cluster* at UCL. Secondly, I translated code from *Mathematica to R* for analyses of measurements of 3D objects used in *paleontological research*. I also provide technical support for the rest of the department.

EDUCATION

2012–2016 **University College London, CoMPLEX**

PhD *The role of population structure and size in determining bat pathogen richness*
I used *network epidemiological models* and phylogenetic statistical methods to study the epidemiology of bat-borne diseases. As bats carry a number of important *zoonotic diseases*, including Nipah and Ebola, understanding the spread of these diseases within bat population and how this affects spillover to humans and livestock is increasingly important. [pdf]
Supervisors: PROF. KATE JONES & DR HILDE HERBOTS

2011–2012 **University College London, CoMPLEX**

MRes *Modelling Biological Complexity* · **M**erit
Projects included adapting '*ideal gas*' models to acoustic data, analysing moment closures for a *pair-approximation* model of plant ecology and applying a novel *machine learning* method to a library of bat calls.

2006–2010 **University of Sheffield, Animal & Plant Sciences**

MBioSci *Zoology* · **First**
For my final project I used *wavelet* analysis to study multi-annual *cycles in malaria* incidence in Thailand.

OTHER RESEARCH EXPERIENCE

Internship

Autumn 2014   Zoön: An R package for reproducible SDMs

I wrote the first version of an R package for *reproducible* species distribution modelling. The package uses an online repository of user submitted 'modules' to allow the software to keep up with this fast moving field and allow analyses to be completely reproducible. [Github]

Volunteer Fieldwork

2011   Smithsonian Tropical Research Institute and Chiloé Silvestre, Chilé

Two months fieldwork in Panamá on two projects: studying *Anolis* dewlap evolution and studying gut length plasticity in Red-eyed tree frogs. I also spent two weeks trapping Darwin's foxes in Chilé to collect samples for geophylogenetics.

Summer Internship

August 2010   University of Sheffield

I studied the evolutionary response of plant communities to climate change with Dr Raj Whitlock. I collected, propagated and analysed plants collected from the field.

TRANSIT Internship

August 2009   University of York, YCCSA

I studied collective foraging behaviour by programming a *complex 3D foraging model* in Java and running large simulations. York Centre for Complex Systems Analysis.

OTHER APPOINTMENTS AND AFFILIATIONS

Peer Review   *Journals Reviewed for:*

Methods in Ecology and Evolution, PLoS Pathogens, Malaria Journal, ROpenSci, National Academy Science Letters

PEER-REVIEWED PUBLICATIONS

2019   Weiss DJ, **Lucas TCD**, Nguyen M, *et al.* (2019) *The global landscape of Plasmodium falciparum prevalence, incidence, and mortality 2000–2017.* The Lancet (In press)

Battle KE, **Lucas TCD**, Nguyen M, *et al.* (2019) *Mapping the global endemicity and clinical burden of Plasmodium vivax 2000–2017.* The Lancet (In press)

2018   Weiss DJ, Nelson A, Gibson HS *et al.* (2018) *A global map of travel time to cities to assess inequalities in accessibility in 2015.* Nature 553 (7688), 333 [pdf]

Pfeffer D, **Lucas TCD**, May D *et al.* (2018) *malariaAtlas: an R interface to global malariometric data hosted by the Malaria Atlas Project.* Malaria Journal 17:352 doi: 10.1186/s12936-018-2500-5 [pdf]

2017   **Lucas TCD**, Herbots HM, & Jones KE. *Role of inter-related population-level host traits in determining pathogen richness and zoonotic risk.* [preprint]

Redding D, **Lucas TCD**, Blackburn T & Jones KE. (2017) *Evaluating Bayesian spatial methods for modelling species distributions models with clumped and restricted data.* PLoS One [pdf]

Golding N, August TA, **Lucas TCD**, Gavaghan DJ, van Loon EE & McInerny G. (2017) *The zoon R package for reproducible and shareable species distribution modelling.* Methods in Ecology and Evolution. doi: 10.1111/2041-210X.12858 [pdf]

2015 **Lucas TCD**∗, Moorcroft EA∗, Freeman R, Rowcliffe MJ & Jones KE. (2015) *A generalised random encounter model for estimating animal density with remote sensor data.* Methods in Ecology and Evolution. doi: 10.1111/2041-210X.12346 [pdf]

2013 Walters CL, Collen A, **Lucas TCD**, Mroz K, Sayer CA and Jones KE. (2013) Challenges of Using Bioacoustics to Globally Monitor Bats. in *Bat Evolution, Ecology, and Conservation.* Springer New York. 479-499.

∗ Co-first authors.

GLOBAL BURDEN OF DISEASE PUBLICATIONS

2018 GBD 2017 Risk Factor Collaborators (2018) *Global, regional, and national comparative risk assessment of 84 behavioural, environmental and occupational, and metabolic risks or clusters of risks for 195 countries and territories, 1990–2017: a systematic analysis for the Global Burden of Disease Study 2017.* The Lancet, 392 [pdf]

GBD 2017 Disease and Injury Incidence and Prevalence Collaborators (2018) *Global, regional, and national incidence, prevalence, and years lived with disability for 354 diseases and injuries for 195 countries and territories, 1990–2017: a systematic analysis for the Global Burden of Disease Study 2017.* The Lancet, 392 [pdf]

GBD 2017 DALYs and HALE Collaborators (2018) *Global, regional, and national disability-adjusted life-years (DALYs) for 359 diseases and injuries and healthy life expectancy (HALE) for 195 countries and territories, 1990–2017: a systematic analysis for the Global Burden of Disease Study 2017.* The Lancet, 392 [pdf]

GBD 2017 Mortality Collaborators (2018) *Global, regional, and national age-sex-specific mortality and life expectancy, 1950–2017: a systematic analysis for the Global Burden of Disease Study 2017.* The Lancet, 392 [pdf]

GBD 2016 Healthcare Access and Quality Collaborators (2017) *Measuring performance on the Healthcare Access and Quality Index for 195 countries and territories and selected subnational locations: a systematic analysis from the Global Burden of Disease Study 2016.* The Lancet, 391 (10136) [pdf]

2017 GBD 2016 Disease and Injury Incidence and Prevalence Collaborators (2017) *Global, regional, and national incidence, prevalence, and years lived with disability for 328 diseases and injuries for 195 countries, 1990–2016: a systematic analysis for the Global Burden of Disease Study 2016.* The Lancet, 390 [pdf]

GBD 2016 Causes of Death Collaborators (2017) *Global, regional, and national age-sex specific mortality for 264 causes of death, 1980–2016: a systematic analysis for the Global Burden of Disease Study 2016.* The Lancet, 390 [pdf]

GBD 2016 DALYs and HALE Collaborators (2017) *Global, regional, and national disability-adjusted life-years (DALYs) for 333 diseases and injuries and healthy life expectancy (HALE) for 195 countries and territories, 1990–2016: a systematic analysis for the Global Burden of Disease Study 2016.* The Lancet, 390[pdf]

GBD 2016 SDG Collaborators (2017) *Measuring progress and projecting attainment on the basis of past trends of the health-related Sustainable Development Goals in 188 countries: an analysis from the Global Burden of Disease Study 2016.* The Lancet, 390 [pdf]

PEER-REVIEWED CONFERENCE PROCEEDINGS

2019 **Lucas TCD**, Nandi A, Nguyen M, *et al.* (2019) *Model ensembles with different response variables for base and meta models: malaria disaggregation regression combining prevalence and incidence data.* ISI World Statistics Congress Proceedings (In press)

2018 Law HC, Sejdinovic D, *et al.* (2018) *Variational learning on aggregate outputs with Gaussian processes.* Advances in Neural Information Processing Systems [pdf]

INVITED CONFERENCE TALKS

2017   *Predicting malaria risk from diverse and multilevel data.*
Plenary at SDCS2017, Springer

CONTRIBUTED CONFERENCE TALKS

2018   *Estimating global malaria risk maps from aggregated, multilevel data.*
Presentation at Young Statisticians Meeting

2016   *Using gas models to model camera trap and acoustic sensor surveys.*
Presentation at Statistical Ecology Research Festival, University of Kent

A comparative and computational study of the affects of population size and group size on pathogen richness in bats.
Presentation at the 12th EWDA conference

2015   *Comparative and computational studies of pathogen richness in bats.*
Presentation at Research in Progress, RSTMH

A comparative and computational study of population structure and pathogen richness in bats.
Presentation at Epidemics5 conference

An ideal gas model for estimating absolute abundances from bat detector data.
Presentation at the National Bat Conference. [slides]

Estimating abundance from camera traps and acoustic sensors.
Invited presentation at CEH, Wallingford seminar series.

2014   Presentation at id2oxford conference. [slides]

2013   Presentation at BritBats 2 [slides].

SOFTWARE ON CRAN

Pfeffer D, **Lucas TCD**, May D, Keddie S, Rozier J, Gibson H. *malariaAtlas: An R Interface to Open-Access Malaria Data, Hosted by the 'Malaria Atlas Project'.*
`www.github.com/malaria-atlas-project/malariaAtlas`

Lucas TCD, Python A, Redding D. *INLAutils: Utility Functions for 'INLA'.*
`www.github.com/timcdlucas/INLAutils`

Goswami A, **Lucas TCD**, Sivasubramaniam P, Finarelli J. *A Maximum Likelihood Approach to the Analysis of Modularity.* `www.github.com/timcdlucas/EMMLi`

Lucas TCD, Goswami A. *paleomorph: Geometric Morphometric Tools for Paleobiology.* `www.github.com/timcdlucas/paleomorph`

August T, **Lucas TCD**, Golding N, van Loon E, McInerny G. *Zoon: Reproducible, Accessible & Shareable Species Distribution Modelling.*
`www.github.com/zoonproject/zoon`

Lucas TCD. *palettetown: Use Pokemon Inspired Colour Palettes*
`www.github.com/timcdlucas/palettetown`

TEACHING

2017 · Wrote and gave a two day workshop 'Geospatial statistics with R and INLA' at UiTM, Malaysia.

2015 · Demonstrator for reproducible species distribution modelling workshop run by Quantitative Ecology special interest group at BES.

2013–2014 · Online tutor for SysMIC, a course for teaching quantitative skills to biologists.

COMPUTATIONAL SKILLS

Statistical methods	Geospatial statistics, machine learning, Bayesian inference.
Languages	R (eight years), Python, Matlab, Mathematica, Java, SQL.
OS	Comfortable with Windows, Mac or Linux.
Other	Experience in R package development, Git/Github, unit testing, continuous integration, LaTeX, web design, markdown, shell/ssh and high performance computing.

REFEREES

Prof. Kate Jones
Chair of Ecology and Biodiversity
Centre for Biodiversity and Environment
Research
University College London
Gower Street
London
United Kingdom
WC1E 6BT

Email: kate.e.jones@ucl.ac.uk
Tel: +44 (0)20 31084230

Dr Greg McInerny
Centre for Interdisciplinary
Methodologies
University of Warwick
Coventry
United Kingdom
CV4 7AL

Email: G.McInerny@warwick.ac.uk
Tel: +44 (0)2476 574710

May 13, 2019