

# Tim CD Lucas

## PERSONAL INFORMATION

|                |   |
|----------------|---|
| <i>email</i>   | ✉ <a href="mailto:timcdlucas@gmail.com">timcdlucas@gmail.com</a>          |
| <i>twitter</i> | 🐦 <a href="https://twitter.com/timcdlucas">@timcdlucas</a> @statsforbios  |
| <i>website</i> | <a href="http://www.ucl.ac.uk/~ucbptcl">www.ucl.ac.uk/~ucbptcl</a>        |
| <i>github</i>  | <a href="https://www.github.com/timcdlucas">www.github.com/timcdlucas</a> |
| <i>scholar</i> | <a href="#">Google scholar</a>  |
| <i>phone</i>   | 07415 863 536   |

## PRESENT APPOINTMENT

|                  |                     |   |
|------------------|---------------------|---|
|                  | <i>2016–Present</i> | University of Oxford, Malaria Atlas Project   |
| <i>Post Doc.</i> |                     | My current position is as a postdoctoral research scientist in geospatial epidemiology with the <a href="#">Malaria Atlas Project</a> at the University of Oxford. I use spatial statistics and machine learning methods to map infectious and vector borne diseases. |

## PREVIOUS APPOINTMENTS

|                            |                      |   |
|----------------------------|----------------------|---|
|                            | <i>Jan–July 2016</i> | CBER, UCL   |
| <i>Research Programmer</i> |                      | 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 <a href="#">Madingley Model</a> —an ecological model of all life, written in C# to enable this model to run on the <i>high performance cluster</i> at UCL. Secondly, I translated code from <i>Mathematica to R</i> for analyses of measurements of 3D objects used in <i>paleontological research</i> . I also provide technical support for the rest of the department. |

## EDUCATION

|                |                  |  |
|----------------|------------------|--|
|                | <i>2012–2016</i> | University College London, CoMPLEX   |
| <i>PhD</i>     |                  | <i>The role of population structure and size in determining bat pathogen richness</i><br>I used <i>network epidemiological models</i> and phylogenetic statistical methods to study the epidemiology of bat-borne diseases. As bats carry a number of important <i>zoonotic diseases</i> , 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. [ <a href="#">pdf</a> ]<br>Supervisors: PROF. KATE JONES & DR HILDE HERBOTS |
|                | <i>2011–2012</i> | University College London, CoMPLEX   |
| <i>MRes</i>    |                  | <i>Modelling Biological Complexity · Merit</i><br>Projects included adapting ‘ <i>ideal gas</i> ’ models to acoustic data, analysing moment closures for a <i>pair-approximation</i> model of plant ecology and applying a novel <i>machine learning</i> method to a library of bat calls.   |
|                | <i>2006–2010</i> | University of Sheffield, Animal & Plant Sciences   |
| <i>MBioSci</i> |                  | <i>Zoology · First</i><br>For my final project I used <i>wavelet</i> analysis to study multi-annual <i>cycles in malaria</i> incidence in Thailand.  |

## RESEARCH EXPERIENCE

|                     |             |  |   |
|---------------------|-------------|--|---|
| Internship          | Autumn 2014 | Zoön: An R package for reproducible SDMs | I wrote the first version of an R package for <i>reproducible</i> 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] |
|                     | August 2011 | Smithsonian Tropical Research Institute  | Two months fieldwork in Panamá on two projects: studying <i>Anolis dewlap</i> evolution and studying gut length plasticity in Red-eyed tree frogs.  |
| Volunteer Fieldwork | May 2011    | Chiloé Silvestre, Chile                  | I spent two weeks trapping Darwin's foxes in Chile to collect samples for geophylogenetics.   |
|                     | 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.  |
| Summer Internship   | August 2009 | University of York, YCCSA                | I studied collective foraging behaviour by programming a <i>complex 3D foraging model</i> in Java and running simulations on a cluster at the York Centre for Complex Systems Analysis.   |
| TRANSIT Internship  |             |  |   |

## OTHER APPOINTMENTS AND AFFILIATIONS

|             |  |
|-------------|--|
| Peer Review | Journals Reviewed for:   |
|             | · Methods in Ecology and Evolution, National Academy Science Letters |

## CONFERENCES

|      |  |
|------|--|
| 2016 | <i>Population structure and pathogen richness in bats.</i><br>Presentation at <i>Epidemics5</i> , Elsevier by <b>Lucas TCD</b>   |
|      | <i>Using gas models to model camera trap and acoustic sensor surveys.</i><br>Presentation at <i>Statistical Ecology Research Festival</i> , University of Kent by <b>Lucas TCD</b>   |
| 2015 | <i>The Zoön Project: Reproducible, Remixable and Shareable Species Distribution Modelling with R.</i><br>Presentation at <i>BES Annual Meeting</i> by August T, Golding N, <b>Lucas TCD</b> , Gavaghan D, Isaac N, O'Hara B, van Loon E & McInerny G |
|      | <i>Simple, Shareable and Reproducible Species Distribution Modelling with the Zoön R package.</i><br>Poster at <i>BES Annual Meeting</i> by Golding N, <b>Lucas TCD</b> , August T, Gavaghan D, Isaac N, O'Hara B, van Loon E & McInerny G           |
|      | <i>Comparative and computational studies of pathogen richness in bats.</i><br>Presentation at Research in Progress, <i>RSTMH</i> by <b>Lucas TCD</b> , Herbots H & Jones KE.   |
|      | <i>A comparative and computational study of population structure and pathogen richness in bats.</i><br>Presentation at <i>Epidemics5</i> conference by <b>Lucas TCD</b> , Herbots H & Jones KE.  |
|      | <i>An ideal gas model for estimating absolute abundances from bat detector data.</i><br>Presentation at the National Bat Conference. [slides]  |
|      | <i>Pathogen diversity and bat population structure.</i><br>Poster at British Parasitological Society Autumn Meeting.   |

*Estimating abundance from camera traps and acoustic sensors.*  
Presentation at CEH, Wallingford seminar series.

- 2014 Presentation at [id2oxford](#) conference. [[slides](#)]  
Poster at the CoMPLEX conference. [[pdf](#)]
- 2013 Presentation at BritBats 2 [[slides](#)].  
Invited attendance at [ecoVIZ](#) Tansley workshop.  
Poster at the CoMPLEX conference and id2 conference. [[pdf](#)]

## PUBLICATIONS

- 2017 **Lucas TCD**, Herbots HM, & Jones KE. *Role of inter-related population-level host traits in determining pathogen richness and zoonotic risk.* [[preprint](#)]
- Golding N, August TA, **Lucas TCD**, Gavaghan DJ, van Loon EE & McInerny G. *The zoon R package for reproducible and shareable species distribution modelling.* In Review [[GitHub](#)]
- Redding D, **Lucas TCD**, Blackburn T & Jones KE. *Evaluating Bayesian spatial methods for modelling species distributions models with clumped and restricted data.* [[preprint](#)]
- Curnick DJ, Koldewey HJ, **Lucas TCD**, Jones KE & Collen B. *Detecting changes in pelagic shark populations using remote cameras.* Submitted.
- 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.

## SOFTWARE

- On CRAN Goswami A, Lucas TCD, Sivasubramaniam P, Finarelli J (2016) *A Maximum Likelihood Approach to the Analysis of Modularity.*  
[www.github.com/timcdlucas/EMMLi](http://www.github.com/timcdlucas/EMMLi)
- Lucas TCD, Goswami A (2016) *paleomorph: Geometric Morphometric Tools for Paleobiology.* [www.github.com/timcdlucas/paleomorph](http://www.github.com/timcdlucas/paleomorph)
- Lucas TCD, Golding N, August T, McInerny G, van Loon E (2015) *Zoön: Reproducible, Accessible & Shareable Species Distribution Modelling.*  
[www.github.com/zoonproject/zoon](http://www.github.com/zoonproject/zoon)
- Lucas TCD (2015) *palettetown: Use Pokemon Inspired Colour Palettes*  
[www.github.com/timcdlucas/palettetown](http://www.github.com/timcdlucas/palettetown)

## TEACHING

- 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

|                            |   |
|----------------------------|---|
| <i>Statistical methods</i> | Geospatial statistics, machine learning, Bayesian inference.  |
| <i>Languages</i>           | R (eight years), Python, Matlab, Mathematica, Java, SQL.  |
| <i>OS</i>                  | Comfortable with Windows, Mac or Linux.   |
| <i>Other</i>               | 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](mailto: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](mailto:G.McInerny@warwick.ac.uk)  
 Tel: +44 (0)2476 574710

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