

# Tim CD Lucas

## PERSONAL INFORMATION

*email*  [timcdlucas@gmail.com](mailto:timcdlucas@gmail.com)  
*twitter*  [@timcdlucas @statsforbios](https://twitter.com/timcdlucas)  
*website* [www.ucl.ac.uk/~ucbptcl](http://www.ucl.ac.uk/~ucbptcl)  
*github* [www.github.com/timcdlucas](https://www.github.com/timcdlucas)  
*scholar* [Google scholar](#)  
*phone* 07415 863 536

## PUBLICATIONS

- 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 **Tim Lucas**, Nick Golding, Tom August, Greg McInerny, Emiel van Loon (2015) *Zoön: Reproducible, Accessible & Shareable Species Distribution Modelling*.  
[www.github.com/zoonproject/zoon](https://www.github.com/zoonproject/zoon)

**Tim Lucas** (2015) *palettetown: Use Pokemon Inspired Colour Palettes*  
[www.github.com/timcdlucas/palettetown](https://www.github.com/timcdlucas/palettetown)

## EDUCATION

2012–present University College London, CoMPLEX

PhD *Social structure and network epidemiology in bat zoonoses*  
Description: I am using *complex networks* to study the epidemiology of bat-borne diseases. As bats carry a number of important *zoonotic diseases*, understanding the spread of these diseases within the bat population and how this affects spillover to humans and livestock is increasingly important. The unusually social nature of bat populations will strongly affect how diseases spread.  
Supervisors: Prof. Kate JONES & Dr Hilde WILKINSON-HERBOT

2011–2012 University College London, CoMPLEX

MRes *Modelling Biological Complexity · Merit*  
Description: This was part of a combined MRes/PhD program. It was an interdisciplinary course applying *quantitative methods* to the life sciences.

2006–2010 University of Sheffield, Animal & Plant Sciences

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

## RESEARCH EXPERIENCE

Research Programmer	2016–present	CBER Programmer	I am currently the stuff programmer for the Centre of Biodiversity and Environment Research at UCL. I work on two main projects. I am working with the <i>Madingley Model</i> —an ecological model of all life, written in C#. My primary task is to get this model running on the <i>high performance cluster</i> at UCL. Secondly, I am translating code from <i>Mathematica to R</i> that performs statistical analyses for measurements of 3D objects used in <i>paleontological research</i> . I also provide technical support for the rest of the department.
Summer Project	Summer 2012	Estimating abundances using acoustic data	I adapted ' <i>ideal gas</i> ' models to acoustic data. I applied the model using R to a pan-European bat survey. We have worked on this project further, validating results with simulations, and the work is now published.
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. [ <a href="#">Github</a> ]
Summer Project	Summer 2012	Estimating abundances using acoustic data	I adapted ' <i>ideal gas</i> ' models to acoustic data. I applied the model using R to a pan-European bat survey. We have worked on this project further, validating results with simulations, and the work is now published.
Case Presentation	May 2012	Pair approximations in spatial biology	I compared a number of moment closures for a <i>pair-approximation</i> model of tree population growth to lattice simulations written in Mathematica. [ <a href="#">pdf</a> ]
Case Presentation	Dec. 2011	Gaussian processes for bat identification	I applied a novel <i>machine learning</i> method to a library of <i>bat calls</i> in Matlab. I compared the effectiveness of this method to standard machine learning methods applied in R. [ <a href="#">pdf</a> ]
Volunteer Fieldwork	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.
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 <i>complex 3D foraging simulation</i> in Java and running simulations on a cluster at the York Centre for Complex Systems Analysis.

## COMPUTER SKILLS

<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 Git/Github, unit testing, LaTeX, web design, markdown, R package development, shell/ssh and high performance computing.

## OTHER INFORMATION

<i>Meetings 2015</i>	<p><i>The Zoön Project: Reproducible, Remixable and Shareable Species Distribution Modelling with R.</i> Presentation at <b>BES Annual Meeting</b> by T. August, N. Golding, <b>T. Lucas</b>, D. Gavaghan, N. Isaac, B. O'Hara, E. van Loon &amp; G. McNerny</p> <p><i>Simple, Shareable and Reproducible Species Distribution Modelling with the Zoön R package.</i> Poster at <b>BES Annual Meeting</b> by N. Golding, <b>T. Lucas</b>, T. August, D. Gavaghan, N. Isaac, B. O'Hara, E. van Loon &amp; Greg McNerny</p> <p><i>Comparative and computational studies of pathogen richness in bats.</i> Presentation at Research in Progress, <b>RSTMH</b> by <b>T. Lucas</b>, H. Wilkinson-Herbot &amp; K. Jones.</p> <p><i>A comparative and computational study of population structure and pathogen richness in bats.</i> Presentation at <b>Epidemics5</b> conference by <b>T. Lucas</b>, H. Wilkinson-Herbot &amp; K. Jones.</p> <p><i>An ideal gas model for estimating absolute abundances from bat detector data.</i> Presentation at the National Bat Conference. [slides]</p> <p><i>Pathogen diversity and bat population structure.</i> Poster at British Parasitological Society Autumn Meeting.</p> <p><i>Estimating abundance from camera traps and acoustic sensors.</i> Presentation at CEH, Wallingford seminar series.</p>
<i>2014</i>	<p>Presentation at <b>id2oxford</b> conference. [slides]</p> <p>Poster at the CoMPLEX conference. [pdf]</p>
<i>2013</i>	<p>Presentation at BritBats 2 [slides].</p> <p>Invited attendance at <b>ecoVIZ</b> Tansley workshop.</p> <p>Poster at the CoMPLEX conference and id2 conference. [pdf]</p>
<i>Teaching</i>	<p>2015 · Demonstrator for reproducible species distribution modelling workshop run by Quantitative Ecology special interest group at BES.</p> <p>2013–2014 · Online tutor for <b>SysMIC</b>, a course for teaching quantitative skills to biologists.</p>
<i>Peer Review</i>	<p><i>Journals Reviewed for:</i></p> <ul style="list-style-type: none"> <li>· Methods in Ecology and Evolution</li> <li>· National Academy Science Letters</li> </ul>

February 24, 2016