Edward B. Baskerville

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Education

University of Michigan, Ann Arbor	Ann Arbor, MI
Ph.D. in Ecology & Evolutionary Biology and Scientific Computing	2008 – 2013
Thesis Advisor: Mercedes Pascual	

University of Michigan, Ann Arbor	Ann Arbor, MI
B.S.E. in Computer Science, *summa cum laude*, Minor in Mathematics	2000 – 2004

Research & Professional Experience

University of Chicago Department of Ecology & Evolution	Chicago, IL
Computational and Statistical Researcher, Cobey Lab	2013 – 2016, 2018 – present

Currently investigating how influenza exposure history affects protection and immune response. Previously worked on computational and statistical research projects related to the ecology and evolution of infectious disease. Built software tools for the lab. Mentored graduate students and postdoctoral researchers.

Mount Sinai School of Medicine	Redwood City, CA
Engineer and Researcher, Health Data and Design Innovation Lab (HD^{2}i)	2017

Prototyped a web application for conducting N-of-1 clinical trials in Flask and React. Worked on statistical methods for N-of-1 clinical trials.

Microsoft Research	Cambridge, UK
Consultant, Computational Ecology and Environmental Science Group	2007 – 2008

Developed software tools to model the spatial spread of invasive species.

Google Summer of Code	Ann Arbor, MI
University of Michigan Center for the Study of Complex Systems	2006 – 2007

Designed and implemented a software tool for running large-scale computer experiments on remote clusters.

University of Michigan	Ann Arbor, MI
Programmer & Research Assistant, Dept. of Ecology & Evolutionary Biology	2003 – 2006

Implemented computational models for ecological research on food-web networks and infectious disease.

Apple Computer, Inc.	Cupertino, CA
Technical Writer, Software Engineering	2002

Wrote technical documentation describing core Mac OS X programming frameworks.

Kinetic Books, Inc.	Seattle, WA
Utility Infielder	2001 – 2004

Wrote educational materials and built software prototypes for electronic physics and mathematics textbooks.

Honors & Awards

Computational Science Graduate Fellowship	2009 – 2013
United States Department of Energy and Krell Institute	

Distinguished Achievement Award, Computer Science	2003
University of Michigan College of Engineering	

Publications

Baskerville, E. B., Dobson, A. P., Bedford, T., Allesina, S., Anderson, T. M., and Pascual, M. 2011. Spatial guilds in the Serengeti food web revealed by a Bayesian group model. PLoS Computational Biology 7(12): e1002321. doi:10.1371/journal.pcbi.1002321

Baeza, A., Bouma, M. J., Dhiman, R. C., Baskerville, E. B., Ceccato, P., Yadav, R. S., and Pascual, M. 2013. Long-Lasting transition toward sustainable elimination of desert malaria under irrigation development. PNAS. doi:10.1073/pnas.1305728110

Rorick, M. M., Rask, T. S., Baskerville, E. B., Day, K. P, and Pascual, M. 2013. Homology blocks of Plasmodium falciparum var genes and clinically distinct forms of severe malaria in a local population. BMC Microbiology 2013 13: 244. doi:10.1186/1471-2180-13-244

Baskerville, E. B., Bedford, T., Reiner, R. C., and Pascual, M. 2013. Nonparametric Bayesian grouping methods for spatial time-series data. Preprint, arXiv:1306.5202 [q-bio.QM]

Zinder, D., Bedford, T., Baskerville, E. B., Woods, R. J., Roy, M., and Pascual, M. 2014. Seasonality in the migration and establishment of H3N2 lineages with epidemic growth and decline. BMC Evolutionary Biology 14: 272. doi:10.1186/s12862-014-0272-2

Childs, L. M., Baskerville, E. B., and Cobey, S. 2015. Trade-offs in antibody repertoires to complex antigens. Philosophical Transactions of the Royal Society B 370: 20140245. doi:10.1098/rstb.2014.0245

Cobey, S. and Baskerville, E. B. 2016. Limits to causal inference with state-space reconstruction for infectious disease. PLOS One. doi:10.1371/journal.pone.0169050

Baskerville, E. B. and Cobey, S. 2017. Does influenza drive absolute humidity? PNAS 114(12): E2270–E2271. doi:10.1073/pnas.1700369114

Ranjeva, S. L., Baskerville, E.B., Dukij, V., Villa, L. L., Lazcano-Ponce, E., Giuliano, A. R., Dwyer, G., and Cobey, S. 2017. Recurring infection with ecologically distinct HPV types can explain high prevalence and diversity. PNAS 114(51): 13573-13578. doi:10.1073/pnas.1714712114

He, Q, Pilosof, S., Tiedje, K. E., Ruybal-Pesántez, S., Artzy-Randrup, Y, Baskerville, E. B., Day, K. P., and Pascual, M. 2018. Nature Communications. doi:10.1038/s41467-018-04219-3

Rorick, M. M., Baskerville, E. B., Rask, T. S., Day, K. P, and Pascual, M. 2018. Identifying functional groups among the diverse, recombining antigenic var genes of the malaria parasite Plasmodium falciparum from a local community in Ghana. PLOS Computational Biology 14(6): e1006174. doi:10.1371/journal.pcbi.1006174

Percha, B., Baskerville, E. B., Johnson, M., Dudley, J. T., and Zimmerman, N. Designing robust N-of-1 studies for precision medicine. 2018. BMC Bioinformatics (submitted).