

## Education

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

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

## Research & Professional Experience

Research Consultant  
University of Chicago, Emory University, NYU, HD<sup>2</sup>i, and others  
Provided advice on computation and modeling, sometimes in the form of code, primarily for the Pascual and Cobey groups in Ecology & Evolution at the University of Chicago. Part time.  
San Francisco, CA  
2017 – present

Mount Sinai School of Medicine  
Research Consultant, Health Data and Design Innovation Lab (HD<sup>2</sup>i)  
Prototyped a full-stack web application for conducting N-of-1 clinical trials in Flask and React.  
Redwood City, CA  
2017

University of Chicago  
Research Programmer, Cobey Group, Ecology & Evolution  
Worked on research involving computation and modeling, including projects on antibody evolution and causal inference. Mentored graduate students and postdoctoral researchers.  
Chicago, IL  
2013 – 2016

Microsoft Research  
Consultant, Computational Ecology and Environmental Science Group  
Developed software tools to model the spatial spread of invasive species.  
Cambridge, UK  
2007 – 2008

Google Summer of Code  
University of Michigan Center for the Study of Complex Systems  
Designed and implemented a software tool for running large-scale computer experiments on clusters.  
Ann Arbor, MI  
2006 – 2007

University of Michigan  
Research Assistant, Ecology & Evolutionary Biology  
Implemented computational models for research on food-web networks and infectious disease.  
Ann Arbor, MI  
2003 – 2006

Apple Computer, Inc.  
Technical Writer, Software Engineering  
Wrote technical documentation describing core Mac OS X application and networking frameworks, including conceptual overviews, programming tutorials, and API reference documentation.  
Cupertino, CA  
2002

## Technical Skills

Languages: Python, Julia, R, Stan, SQL, Rust, C, C++, Objective-C, Java, JavaScript, Elm, HyperTalk  
Computation etc.: stochastic simulation, differential equations, Bayesian inference, agent-based models

## Honors & Awards

- Computational Science Graduate Fellowship 2009 – 2013  
United States Department of Energy, Krell Institute
- Distinguished Achievement Award, Computer Science 2003  
University of Michigan College of Engineering

## Selected 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. <https://doi.org/10.1371/journal.pcbi.1002321>
- 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]. <https://doi.org/10.48550/arXiv.1306.5202>
- 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. <https://doi.org/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. <https://doi.org/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*. <https://doi.org/10.1371/journal.pone.0169050>
- Baskerville, E. B. and Cobey, S. 2017. Does influenza drive absolute humidity? *PNAS* 114(12): E2270–E2271. <https://doi.org/10.1073/pnas.1700369114>
- He, Q., Pilosof, S., Tiedje, K. E., Ruybal-Pesantez, S., Artzy-Randrup, Y., E. B. Baskerville, Day, K. P., and Pascual, M. Networks of genetic similarity reveal non-neutral processes shape strain structure in *Plasmodium falciparum*. 2018. *Nature Communications* 9. <https://doi.org/10.1038/s41467-018-04219-3>
- Percha, B., Baskerville, E. B., Johnson, M., Dudley, J., and Zimmerman, N. Designing robust N-of-1 studies for precision medicine: simulation study and design recommendations. 2019. *Journal of Medical Internet Research* 21(4). <https://doi.org/10.2196/12641>
- Gostic, K. M., McGough, L., Baskerville, E. B., Abbott, S., Joshi, K., Tedijanto, C., Kahn, R., Niehus, R., Hay, J. A., De Salazar, P. M., Hellewell, J., Meakin, S., Munday, J. D., Bosse, N. I., Sherratt, K., Thompson, R. N., White, L. F., Huisman, J. S., Scire, J., Bonhoeffer, S., Stadler, T., Wallinga, J., Funk, S., Lipsitch, M., and Cobey, S. Practical considerations for measuring the effective reproductive number, Rt. 2020. *PLOS Computational Biology* 16(12): e1008409. <https://doi.org/10.1371/journal.pcbi.1008409>