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**Appointments:**

Postdoctoral Research Scholar; University of Georgia; Athens, GA; 2015–present  
Postdoctoral Fellow; Georgetown University; Washington, DC; 2013–2015

**Degrees:**

University of Texas at Austin; PhD in Ecology, Evolution and Behavior; 2013.  
Supervising professors: Lauren Meyers and Claus Wilke.  
Thesis: Analyses of infectious disease data with attention to heterogeneity.  
State University of New York at Geneseo, BS in Biology, 2008.

**Research interests:**

applied statistics, complex networks, disease dynamics, phylogenetics

**Papers:**

C. J. Dibble, E. B. O’Dea, A. W. Park, and J. M. Drake. Waiting time to infectious disease emergence. *Journal of the Royal Society Interface*. 19 October 2016.  
E. B. O’Dea, H. Snelson, and S. Bansal. Using heterogeneity in the population structure of U.S. swine farms to compare transmission models for porcine epidemic diarrhoea. *Scientific Reports*. 7 March 2016.  
E. B. O’Dea, K. M. Pepin, B. A. Lopman, and C. O. Wilke. Fitting outbreak models to data from many small norovirus outbreaks. *Epidemics*. March 2014.  
E. B. O’Dea and C. O. Wilke. Contact networks and phylodynamics: How host contact networks shape parasite evolutionary trees. *Interdisciplinary Perspectives in Infectious Disease*. 2011:238743.  
E. B. O’Dea, T. E. Keller, and C. O. Wilke. Does mutational robustness inhibit extinction by lethal mutagenesis in viral populations? *PLoS Computational Biology*. 10 June 2010.

**Talks:**

E. B. O’Dea. An R-based approach to global sensitivity analysis for moments of stochastic models. Computational Ecology & Epidemiology Study Group. UGA. Athens, GA. 3 February 2016.  
E. B. O’Dea. Introduction to Docker. Computational Ecology & Epidemiology Study Group. UGA. Athens, GA. 23 September 2015.  
E. B. O’Dea. Investigating the transmission pathways of porcine epidemic diarrhea virus (PEDV) using outbreak incidence and virus sequence data. USDA Veterinary Services Simulation and Modeling Seminar Series. Webinar. 20 January 2015.  
E. B. O’Dea and S. Bansal. Spreading patterns in the ongoing U.S. Porcine Epidemic Diarrhea Virus outbreak. Friday Biology Seminar at Georgetown University. Washington, DC. 15 November 2013.  
E. B. O’Dea and C. Leary. Degree-correlated scale-free networks and epidemics. Undergraduate Biomathematics Day, Niagara Falls, NY. April, 2008. SUNY Geneseo GREAT Day. Geneseo, NY. April 2008.

**Posters:**

E. B. O'Dea and J. M. Drake. Estimating the distance to the epidemic threshold. MIDAS Network Meeting. Reston, VA. May 2016.

E. B. O'Dea and S. Bansal. Learning patterns of transmission from the U.S. PEDV outbreak. Epidemics. Amsterdam, The Netherlands. November 2013.

E. B. O'Dea and C. Leary. Epidemic dynamics on randomized scale-free networks. The Joint Mathematics Meeting of the MAA and AMS. San Diego, CA. January 2008.

**Honors and awards:**

Phi Beta Kappa.

SUNY Geneseo College Honors Program.

**Teaching assistantships:**

Ecology.

Genetics.

Introduction to Computational Biology.

**Undergraduate mentoring assignments:**

David Schaffer. Localization of the source of an outbreak on weighted and directed networks. Summer 2014.

Sarah Kramer. Estimating effects of risk compensation due to antiviral HIV therapy. Spring 2014.

Yongjun Cho. The impact of population immunity on antigenic drift during large epidemics and small outbreaks. Journal of the Young Investigator. Volume 20. Issue 3. September 2010.

**Journals for which I have been a reviewer:**

BMC Evolutionary Biology.

Ecosphere.

Genetics.

JSTAT.

PeerJ.

PLoS Neglected Tropical Diseases.

PLoS One.

PLoS Pathogens.

PNAS.

**References:** References can be provided when necessary.