Eli Bogart

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Education

Ph.D., Physics, Cornell University, 2015. Minor field: computational biology.

M.S., Physics, Cornell University, 2012.

B.S., Physics, with distinction, Harvey Mudd College, 2005.

Publications

Bucci, V., B. Tzen, N. Li, M. Simmons, T. Tanoue, **E. Bogart**, L. Deng, V. Yeliseyev, M. L. Delaney, Q. Liu, B. Olle, R. R. Stein, K. Honda, L. Bry, and G. K. Gerber (2016). MDSINE: Microbial dynamical systems inference engine for microbiome time-series analyses. *Genome Biology* 17(1):121.

Allegretti, J. R., S. Kearny, N. Li, **E. Bogart**, K. Bullock, G. K. Gerber, L. Bry, C. B. Clish, E. Alm, and J. R. Korzenik (2016). Recurrent *Clostridium difficile* infection associates with distinct bile acid and microbiome profiles. *Alimentary Pharmacology and Therapeutics* 43(11):1142-53.

Bogart, E. and C. R. Myers (2016). Multiscale metabolic modeling of C4 plants: connecting nonlinear genome-scale models to leaf-scale metabolism in developing maize leaves. *PLoS ONE* 11(3): e0151722.

Franck, C., W. Ip, A. Bae, N. Franck, **E. Bogart**, and T. T. Le (2008). Contact-mediated cell-assisted cell proliferation in a model eukaryotic single-cell organism: an explanation for the lag phase in shaken cell culture. *Phys. Rev. E* 77: 041905.

In preparation: **Bogart, E.** and C. R. Myers. Genome-scale modeling of the evolutionary path to C4 photosynthesis.

Research experience

Brigham and Women's Hospital / Harvard Medical School, Boston, MA

Machine learning methods for microbiome data, 2015-

Developed a method to infer human-interpretable models that can predict host phenotypes or patient disease outcomes from microbiome time-series data, incorporating phylogenetic relationships among bacteria; implemented as software package with custom MCMC sampling scheme and interactive graphical visualization of results.

Analyzed 16S data from gnotobiotic mouse experiments to detect *in vivo* interactions among a consortium of bacteria with engineered metabolic interdependencies.

Contributed to experimental design and data analysis for *in vivo* studies of interactions between a defined community of commensal bacteria and *Clostridium difficile*.

Laboratory of Atomic and Solid State Physics, Cornell University, Ithaca, NY

Nonlinear constraint-based modeling of the function and evolution of C4 photosynthesis, 2010-2015

Developed software for incorporating nonlinear constraints into flux balance analysis models, allowing correct handling of competitive binding of oxygen and carbon dioxide to Rubisco active sites in photosynthetic organisms.

Developed a method for predicting metabolic fluxes from transcriptomic data and applied it to analyze RNAseq data from the developing maize leaf, using a novel genome-scale reconstruction of maize metabolism and a model incorporating interactions between mesophyll and bundle sheath cells and metabolite exchange through leaf veins.

Simulated metabolic shifts along the evolutionary transition between C3 and C4 photosynthesis.

Experimental studies of growth and chemotaxis in *Dictyostelium discoideum*, 2008-2009

Designed microfluidic devices for chemotaxis studies and analyzed imaging data from amoeba growth chamber experiments.

Department of Mathematics, University of Utah, Salt Lake City, UT

Numerical simulation of in vitro blood clotting experiments, 2007-2008

Developed a reaction-diffusion model of coagulation in human blood plasma and implemented a solver for the resulting system of partial differential equations.

University of Oregon Institute of Molecular Biology, Eugene, OR

DNA methylation in *Neurospora crassa*, summer 2002, summer 2003

Searched for genes involved in DNA methylation in *Neurospora* using post-transcriptional silencing experiments.

Software developed

mitre (2017) Python package for inferring rule-based predictive and classification models from microbiome time-series data, with with d3.js-based interactive visualization

fluxtools (2015) A Python package for the development and analysis of flux balance analysis models with general nonlinear constraints (`http://github.com/ebogart/fluxtools`)

pycyc (2012) A Python interface to the Pathway Tools metabolic pathway database system (`http://github.com/ebogart/pycyc`)

Conference presentations

Bogart, E. and G. Gerber. Predictive and interpretable Bayesian models for analyzing microbiome time-series data. 2nd Workshop in Statistical and Algorithmic Challenges in Microbiome Data Analysis, Cambridge, MA, Feb 16–17, 2017 (talk).

Bogart, E. and G. Gerber. Interpretable temporal rules for classification and prediction of host phenotype from microbiome dynamics. Computational Aspects of Biological Information 2016, Cambridge, MA, Nov 30, 2016 (poster).

Bogart, E. and C. R. Myers. Nonlinear constraint-based models of the function and evolution of C4 photosynthesis. 3rd Conference on Constraint-Based Reconstruction and Analysis (COBRA 2014), Charlottesville, VA, May 20–23, 2014 (poster).

Bogart, E. and C. R. Myers. A metabolic network plasticity approach to the evolution of C4 photosynthesis. 6th q-bio Conference, Santa Fe, NM, August 8–11, 2012 (poster).

Bogart, E. and C. R. Myers. Plasticity of metabolic networks and the evolution of C4 photosynthesis. APS March Meeting 2012, Boston, MA, February 29, 2012 (talk).

Bogart, E., S. Lau, A. Deshmukh, and C. Franck. Exploring cell-assisted cell growth. APS March Meeting 2009, Pittsburgh, PA, March 17, 2009 (talk).

Teaching

Harvard-MIT Health Sciences and Technology program, 2016: Co-instructor, HST 164, Molecular Diagnostics and Bioinformatics (hands-on introduction to bioinformatics algorithms and their implementation for medical students).

Department of Physics, Cornell University, Fall 2009–Spring 2010: Laboratory and discussion section instructor for PHYS 2213 (sophomore-level electricity and magnetism).

Related activities

Co-organizer, Cornell computational biology student team for DREAM8 Whole-Cell Parameter Estimation Challenge, 2013.