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.

Experience

Senior Scientist, Kintai Therapeutics, Cambridge, MA, 2017-present

Postdoctoral fellow, Brigham and Women's Hospital / Harvard Medical School, Boston, MA, 2015-2017

Machine learning methods for microbiome data

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*.

PhD student, Laboratory of Atomic and Solid State Physics, Cornell University, Ithaca, NY, 2008-2015

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

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*

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

Graduate student, Department of Mathematics, University of Utah, Salt Lake City, UT, 2007-2008

Numerical simulation of in vitro blood clotting experiments

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

Publications

Bogart, E. and G. K. Gerber. MITRE: predicting host status from microbiota time-series data. Submitted to *Nature Methods*.

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.

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 (`http://github.com/gerberlab/mitre`)

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.