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

Lead Scientist, Deep Genomics, Cambridge, MA / Toronto, ON, 2023-present
Research Scientist, Deep Genomics, Cambridge, MA / Toronto, ON, 2022-2023

Led cross-functional team of biologists, chemists, and computational scientists responsible for improving potency and efficacy of oligonucleotide therapeutics through chemistry and sequence optimization. Developed plan for oligo optimization research efforts through 2024, working closely with company leadership, other project teams, and external scientific advisors.

Designed *in vitro* studies to efficiently characterize relationships between oligonucleotide sequence and function, in collaboration with experimental biologists.

Implemented and tested new approaches to using RNA-seq data to train improved machine learning models for splicing prediction.

Data Scientist Lead, CAMP4 Therapeutics, Cambridge, MA, 2020-2022

Developed and applied machine learning models to infer the state of transcriptional regulatory processes from epigenomic data, supporting target prioritization and mechanism-of-action determination for oligonucleotide drug development.

Principal Scientist, Kintai Therapeutics, Cambridge, MA, 2019-2020
Senior Scientist, Kintai Therapeutics, Cambridge, MA, 2017-2019

Developed methods and pipelines for metagenomic data analysis, analyzed key datasets, and presented results to research team and company leadership. Built and maintained cloud computing infrastructure and interactive data visualization tools.

Led expansion of computational biology team from 1 to 3 FTE; mentored and supervised junior scientists and statisticians. Managed relationships with contract research organizations and consultants providing bioinformatics, statistical, sequencing, and *in vitro* assay services.

Developed company strategy for accelerated drug discovery through machine learning; initiated and led machine learning research projects involving cross-disciplinary teams within Kintai and external consultants.

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

Developed a machine learning 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; contributed to design and data analysis for *in vivo* studies of interactions among defined bacterial communities in gnotobiotic mice.

Publications

Bogart, E., R. Creswell, and G. K. Gerber (2019). MITRE: inferring features from microbiota time-series data linked to host status. *Genome Biology* 20:186.

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* 17:121.

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.

Patent applications

"Multibiotics Agents and Methods of Using the Same". Casey, John P; Berry, David; Castro, Alfredo; Taylor, Steven J.; Massari, Ferdinand E.; Proudfoot, John; Bogart, Elijah; Briggs, Timothy F. WO 2018/226732.

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`)

Last updated: August 5, 2023