Conner Kummerlowe, PhD

(206) 849-5046
Cambridge, MA
connerk@mit.edu
Github: github.com/connersk/
Website: conner-kummerlowe.netlify.app/
Linkedin: linkedin.com/in/conner-kummerlowe-0a3a919a

Skills

Machine learning	Deep learning, feature selection, dimensionality reduction, clustering, regression, classification
Programming languages	Python (NumPy, Pandas, Scikit-learn, PyTorch), R (tidyverse, ggplot2, etc), Bash
Computational tools	Cloud Computing (AWS EC2, AWS S3, Google Cloud), Git, Docker

Technical Experience

PhD and postdoc computational biology research **Sept. 2017 — Present**
MIT *Cambridge, MA*

- Developed a non-negative matrix factorization and regularized regression based model for deconvoluting signals driven by biological perturbations in multiplexed experiments with high- dimensional measurements. Applied this approach to nominate biological factors that drive pancreatic cancer.
- Conducted unsupervised machine learning analyses and statistical hypothesis testing to generate new therapeutic development targets from a novel high-dimensional data set of intestinal cells with Environmental Enteropathy - a disease contributing to childhood malnutrition in low- and middle-income countries.
- Mentored 5 undergraduate and graduate students, providing research and career advice on a weekly or bi-weekly basis.

Deep learning project for graduate machine learning course at MIT **Sept. 2017 — Dec. 2017**
MIT *Cambridge, MA*

- Implemented CNNs in PyTorch with optimized architectures for regression and classification applied to a computational biology research problem (predicting transcription factor binding to DNA).
- Improved classification validation average precision from 0.24 to 0.93 with undersampling in a highly imbalanced data set, outperforming the state of the art model (DeepBind).

Internship in computational biology software development **June 2017 — Aug. 2017**
Genestack *Cambridge, UK*

- Developed an automated tool for preprocessing and classifying measurements from a high-dimensional biological data type.
- Worked in an object-oriented software development environment

Undergraduate research in physical chemistry **May 2013 — May 2016**
Pomona College *Claremont, CA*

- Basic research on the physical chemistry of surfaces

Education

PhD in Computational & Systems Biology, *MIT* July 2022
MPhil in Computational Biology, *University of Cambridge* September 2017
BA in Chemsitry, *Pomona College* May 2016

Selected coursework: Graduate machine learning, probabilistic systems analysis and applied probability, scientific computing, principles of computer science, data structures and program development

Select publications

1. Conner Kummerlowe and et al. Single-cell profiling of environmental enteropathy reveals signatures of epithelial remodeling and immune activation in severe disease. *bioRxiv*, 2021

2. Benjamin E. Mead*, Conner Kummerlowe*, and et al. Compressed phenotypic screening for sample-limited assays and modelse. *Working Paper*, 2022

Awards

Downing Scholar,University of Cambridge 2016-2017
Top Organic Chemistry student award, Pomona College 2014
Jaeger Mathematics Prize, Pomona College 2013
Tileston Physics Prize, Pomona College 2013

Activities

MIT Outing Club Trip Leader 2018 - Present
PhD program graduate committee student liaison 2019 - 2022
Eagle Scout, Boy Scouts of America 2011