

Aidan McLoughlin

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EDUCATION

University of California, Berkeley

Biostatistics PhD Candidate

Designated Emphasis in Computational and Genomic Biology

Advisors: Haiyan Huang, Lexin Li

Berkeley, CA

2021 – Present

University of California, (UC) Berkeley

MA in Biostatistics

Thesis: Scaling the Shared Identified Differential Expression Measure for Single Cell RNA Sequencing Data.

Committee: Haiyan Huang, Lexin Li, Elizabeth Purdom

Coursework: mathematical statistics, probability theory, applied statistics, optimization, causal inference, deep learning, computational genomics, reinforcement learning, longitudinal analysis

Berkeley, CA

2019 – 2021

Northwestern University

Triple BA in Mathematics, Math in Social Sciences, Economics

Interdisciplinary Honors Thesis: Who Benefits from Early Decision? An analysis of college admissions strategy.

Evanston, IL

2013 – 2017

RESEARCH EXPERIENCE

Graduate Student Researcher, UC Berkeley

Advisors: Haiyan Huang, Lexin Li

- Develop integrative machine learning methods (variational autoencoder, sparse canonical correlation analysis) to study multi-omics sequencing and cancer cell line drug response data.
- Develop reinforcement learning methods for optimization of dynamic deep brain stimulation (DBS) therapies.
- Apply tensor regression methods to develop brain connectivity measures of symptom severity and DBS impact.

2021 – Present

Graduate Student Assistant, UC Berkeley

Remais Lab

- Research and develop R modules to apply optimization methods useful for assorted problem contexts arising in infectious disease modeling.
- Instructional presentations of optimization methods for the research team.

2020 – 2021

Research Analyst

The Brattle Group

- Collaborated in a small modeling team to accurately estimate financial damages from unfair practices in Blue Cross Blue Shield (BCBS) antitrust case. Translated complex counterfactual market simulations to expert litigation report. Case settled with \$2.7 billion in damages awarded to the class.
- Cleaned and transformed high-dimensional healthcare utilization data, performed exploratory analysis on utilization compositions across insurers, specified and tuned a zero-inflated model to predict individual expected healthcare costs.
- Compiled hospital data and discharge data to help construct a multinomial response model of hospital choice.
- Scraped pricing data and wrote scripts to create product choice suites for all consumers in the relevant market to determine relative importance of pricing, product quality metrics, and provider brand.

Boston, MA

2017 – 2019

TEACHING EXPERIENCE

University of California, Berkeley

Teaching Assistant: DATA C102: Data, Inference, and Decisions

Teaching Assistant: PB HLTH 241: Statistical Analysis of Categorical Data

Teaching Assistant: PB HLTH 142: Introduction to Statistics in Public Health

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Fall 2022

Spring 2021

Spring 2020

Fall 2019

The Brattle Group

Teaching Assistant: Fundamentals of casework analysis and presentation

Fall 2018

PUBLICATIONS

Applications

- [1] **A. McLoughlin**, H. Huang. Shared Differential Expression-Based Distance Reflects Global Cell Type Relationships in Single-Cell RNA Sequencing Data. *Journal of Computational Biology*. 2022. doi: 10.1089/cmb.2021.0652. URL <https://doi.org/10.1089/cmb.2021.0652>
- [2] Q. Cheng, P. Collender, A. Heaney, **A. McLoughlin**, Y. Yang, Y. Zhang, J. Head, R. Dasan, S. Liang, Q. Lv, Y. Liu, C. Yang, H. Chang, L. Waller, J. Zelner, J. Lewnard, J. Remais. Optimizing laboratory-based surveillance networks for monitoring multi-genotype or multi-serotype infections. *PLOS Computational Biology*. 2022. doi: 10.1371/journal.pcbi.1010575. URL <https://doi.org/10.1371/journal.pcbi.1010575>

In Preparation

- [1] **A. McLoughlin**, Y. Wang, J. Demmel, B. Erichson, H. Huang. Deep biclustering with sparse canonical correlation analysis connects cis-regulatory elements with putatively related gene groups. 2022+
- [2] Y. Wang, **A. McLoughlin**, B. Erichson, J. Demmel. Relaxed Sparse Canonical Correlation Analysis with Applications in High-Dimensional Genomics. 2022+
- [3] S. Shi, **A. McLoughlin**, H. Huang. Penalized dual variational autoencoders of compounds and bulk RNA seq connect genes and compound motifs implicated in cancer cell line viability.
- [4] **A. McLoughlin**, C. Shi, L. Li. Deep Nested Lasso: Order Selection for Deep Reinforcement Learning. 2022+

ADDITIONAL

Computing: R, Python, Git, Bash, TensorFlow/PyTorch/Keras, SQL, Excel, LaTeX

Service: Cal BASIS Program (*Scientific Presenter, 2021-2022*), Berkeley Scholars to Cal (*Tutor, 2020-2021*), TPlus Cambridge (*Tutor, 2017-19*), Supplies for Dreams (*Mentor, 2016-17*)

Interests: Hiking, Climbing, Skiing, Cooking, Piano, Tennis