

# Aidan McLoughlin

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## EDUCATION

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### 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

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### 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

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### 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

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### 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

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**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