

# Zachary Ryan McCaw

## Curriculum Vitae

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## Education

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### Stanford University

01/2021 – 06/2022

GRADUATE CERTIFICATE IN ARTIFICIAL INTELLIGENCE

- COURSEWORK: Computer Vision, Deep Learning, Reinforcement Learning.
- GPA: 4.05 of 4.00.

### Harvard University

08/2014 – 05/2019

PH.D. IN BIOSTATISTICS, A.M. IN BIOSTATISTICS

- DISSERTATION: Transformation and multivariate methods for improving power in genome-wide association studies.
  - Studied operating characteristics of the rank-based inverse normal transformation for genome-wide association studies of quantitative traits. [18]
  - Developed multivariate regression methodology for leveraging a correlated surrogate outcome to improve inference on a partially missing target outcome. [14, 9]
- ADVISORS: Xihong Lin, Ph.D.
- COMMITTEE: Martin Aryee, Ph.D. and Jeffrey Miller, Ph.D.
- GPA: 3.93 of 4.00.

### University of North Carolina at Chapel Hill

08/2009 – 05/2013

B.S.P.H. IN BIOSTATISTICS, B.S. IN QUANTITATIVE BIOLOGY

- Graduated with highest distinction.
- GPA: 4.00 of 4.00; Dean's List: 8 of 8 Semesters; Phi Beta Kappa.

## Technical Experience

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- **AI & ML:** Computer vision, clinical ML (survival and risk-prediction), deep learning, representation learning, self-supervised learning, time-series and sequence models.
- **Statistical Genetics:** Genome-wide association studies, fine-mapping, Mendelian randomization, polygenic scoring, rare-variant association testing.
- **Biostatistics & Causal Inference:** Causal inference, clinical trials, longitudinal and multivariate analysis, meta-analysis, regression modeling, survival analysis.
- **Software & Programming:** Python (PyTorch, TensorFlow), R (tidyverse), C++/Rcpp; Git; Cloud computing (AWS, GCP); Docker; Reproducible research, package development.

## Professional Experience

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### Voleon

01/2025 – Present

SENIOR MEMBER OF RESEARCH STAFF: 01/25 –

### Insitro

09/2021 – 01/2025

STAFF MACHINE LEARNING SCIENTIST: 04/23 – 01/25

- DEPARTMENT: Statistical Genetics and Clinical Machine Learning
- TEAM LEAD: Colm O'Dushlaine, Ph.D.
- PUBLICATIONS & PROJECTS:
  - Extending the coding-variant allelic series test to summary statistics. [2]
  - Causal considerations can determine the utility of machine learning assisted GWAS. [1]
  - EmbedGEM: a framework to evaluate the utility of embeddings for genetic discovery. [8]
  - Machine learning enabled prediction of digital biomarkers from whole slide histopathology images. [4]
  - Pitfalls in performing genome-wide association studies on ratio traits. [4]

SENIOR MACHINE LEARNING SCIENTIST: 09/21 – 03/23.

- DEPARTMENT: Statistical Genetics
- TEAM LEAD: Thomas Soare, Ph.D.
- PUBLICATIONS & PROJECTS:
  - An allelic series rare-variant test for candidate gene discovery. [12]
  - Identification of Parkinson's risk variants using MRI-derived proxy phenotypes.

### Google

09/2019 – 09/2021

DATA SCIENTIST

- DEPARTMENT: Health, Genomic Medicine Team.
- TEAM LEADS: Babak Alipanahi, Ph.D. and Cory McLean, Ph.D.
- PUBLICATIONS & PROJECTS:
  - Unsupervised representation learning improves genomic discovery for lung function and respiratory disease prediction [7].
  - Inference of chronic obstructive pulmonary disease with deep learning on raw spirograms identifies new genetic loci and improves risk models [13].
  - DeepNull: Modeling non-linear covariate effects improves phenotype prediction and association power. [15]
  - Large-scale machine learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology. [17]
  - Developed and implemented tools for GWAS analysis, including fine-mapping, locus formation, replication analysis, and winner's curse correction.
- DEPARTMENT: Core Developer, DevIntel Data Science Team.

- TEAM LEAD: Heng Liu, Ph.D.
- PROJECT: Causal inference to understand factors affecting developer productivity.
  - Developed and implemented methodology for estimating average causal effects from observational and longitudinal data.

## Broad Institute

06/2019 – 09/2019

### VISITING SCIENTIST

- DEPARTMENT: Medical and Population Genetics.
- PRINCIPAL INVESTIGATOR: Hilary Finucane, Ph.D.
- PROJECT: Cross-population fine-mapping to identify shared and population-specific causal effects.

## Publications

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### Statistical Genetics

- [1] S Mukherjee et al. “Causal considerations can determine the utility of machine learning assisted GWAS”. In: *Proceedings of the sixth Conference on Health, Inference, and Learning*. Vol. 287. Proceedings of Machine Learning Research. 2025, pp. 179–193. URL: <https://proceedings.mlr.press/v287/mukherjee25a.html>.
- [2] ZR McCaw et al. “A Scalable Framework for Identifying Allelic Series from Summary Statistics”. In: *American Journal of Human Genetics* 112.11 (Nov. 2025), pp. 2772–2788. DOI: [10.1016/j.ajhg.2025.09.012](https://doi.org/10.1016/j.ajhg.2025.09.012).
- [3] Y Zhou et al. “Applying multimodal AI to physiological waveforms improves genetic prediction of cardiovascular traits”. In: *American Journal of Human Genetics* (July 2025). DOI: [10.1016/j.ajhg.2025.05.015](https://doi.org/10.1016/j.ajhg.2025.05.015).
- [4] ZR McCaw et al. “Pitfalls in performing genome-wide association studies on ratio traits”. In: *Human Genetics and Genomics Advances* (Apr. 2025). DOI: [10.1016/j.xhgg.2025.100406](https://doi.org/10.1016/j.xhgg.2025.100406).
- [5] X Li, H Chen, MS Selvaraj, et al. “A statistical framework for powerful multi-trait rare variant analysis in large-scale whole-genome sequencing studies”. In: *Nature Computer Science* (Feb. 2025). DOI: [10.1038/s43588-024-00764-8](https://doi.org/10.1038/s43588-024-00764-8).
- [6] R Sun, ZR McCaw, and X Lin. “Testing a Large Number of Composite Null Hypotheses Using Conditionally Symmetric Multidimensional Gaussian Mixtures in Genome-Wide Studies”. In: *Journal of the American Statistical Association* (Oct. 2024). DOI: [10.1080/01621459.2024.2422124](https://doi.org/10.1080/01621459.2024.2422124).
- [7] T Yun et al. “Unsupervised representation learning improves genomic discovery for lung function and respiratory disease prediction”. In: *Nature Genetics* (July 2024). DOI: [10.1038/s41588-024-01831-6](https://doi.org/10.1038/s41588-024-01831-6).
- [8] S Mukherjee et al. “EmbedGEM: A framework to evaluate the utility of embeddings for genetic discovery”. In: *Bioinformatics Advances* 4.1 (July 2024), vbae135. DOI: [10.1093/bioadv/vbae135](https://doi.org/10.1093/bioadv/vbae135).

- [9] ZR McCaw et al. “Synthetic surrogates improve power for genome-wide association studies of partially missing phenotypes in population biobanks”. In: *Nature Genetics* (June 2024). DOI: [10.1038/s41588-024-01793-9](https://doi.org/10.1038/s41588-024-01793-9).
- [10] J Rossen et al. “MultiSuSiE improves multi-ancestry fine-mapping in All of Us whole-genome sequencing data”. In: *medRxiv* (May 2024). DOI: [10.1101/2024.05.13.24307291](https://doi.org/10.1101/2024.05.13.24307291).
- [11] AD Sherry, AW Hahn, ZR McCaw, et al. “Differential Treatment Effects of Subgroup Analyses in Phase 3 Oncology Trials From 2004 to 2020”. In: *JAMA Network Open* 7.3 (Mar. 2024), e243379. DOI: [10.1001/jamanetworkopen.2024.3379](https://doi.org/10.1001/jamanetworkopen.2024.3379).
- [12] ZR McCaw et al. “An allelic-series rare-variant association test for candidate-gene discovery”. In: *American Journal of Human Genetics* 110.8 (July 2023), pp. 1330–1342. DOI: [10.1016/j.ajhg.2023.07.001](https://doi.org/10.1016/j.ajhg.2023.07.001).
- [13] J Cosentino et al. “Inference of chronic obstructive pulmonary disease with deep learning on raw spiromgrams identifies new genetic loci and improves risk models”. In: *Nature Genetics* (Apr. 2023). DOI: [10.1038/s41588-023-01372-4](https://doi.org/10.1038/s41588-023-01372-4).
- [14] ZR McCaw et al. “Leveraging a surrogate outcome to improve inference on a partially missing target outcome”. In: *Biometrics* (Feb. 2022). DOI: [10.1111/biom.13629](https://doi.org/10.1111/biom.13629).
- [15] ZR McCaw et al. “DeepNull: Modeling non-linear covariate effects improves phenotype prediction and association power”. In: *Nature Communications* 13.1 (Jan. 2022), p. 241. DOI: [10.1038/s41467-021-27930-0](https://doi.org/10.1038/s41467-021-27930-0).
- [16] H Julienne et al. “Multitrait GWAS to connect disease variants and biological mechanisms”. In: *PLoS Genetics* 17.8 (Aug. 2021), e1009713. DOI: [10.1371/journal.pgen.1009713](https://doi.org/10.1371/journal.pgen.1009713).
- [17] B Alipanahi et al. “Large-scale machine learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology”. In: *American Journal of Human Genetics* (May 2021). DOI: [10.1016/j.ajhg.2021.05.004](https://doi.org/10.1016/j.ajhg.2021.05.004).
- [18] ZR McCaw et al. “Operating Characteristics of the Rank-Based Inverse Normal Transformation for Quantitative Trait Analysis in Genome-Wide Association Studies”. In: *Biometrics* (Dec. 2019). DOI: [10.1111/biom.13214](https://doi.org/10.1111/biom.13214).

## Applied Machine Learning

- [1] J Gao et al. “What Is Fair? Defining Fairness in Machine Learning for Health”. In: *Stat Med* 44.20-22 (Sept. 2025), e70234. DOI: [10.1002/sim.70234](https://doi.org/10.1002/sim.70234).
- [2] V Kanwar et al. “Multi-Artifact Detection and Filtering in Digital Pathology Using Intrinsic Image Properties”. In: *2024 IEEE International Symposium on Biomedical Imaging (ISBI)*. Aug. 2024, pp. 1–5. DOI: [10.1109/ISBI56570.2024.10635902](https://doi.org/10.1109/ISBI56570.2024.10635902).
- [3] A Woicik et al. “In Silico Optimization of Tissue Microarray Design for Machine Learning Analysis”. In: *2024 IEEE International Symposium on Biomedical Imaging (ISBI)*. Aug. 2024, pp. 1–5. DOI: [10.1109/ISBI56570.2024.10635208](https://doi.org/10.1109/ISBI56570.2024.10635208).

- [4] ZR McCaw et al. “Machine learning enabled prediction of digital biomarkers from whole slide histopathology images”. In: *medRxiv* (Jan. 2024). DOI: [10.1101/2024.01.06.24300926](https://doi.org/10.1101/2024.01.06.24300926).
- [5] C Angermueller, Z Mariet, B Jester, et al. “High-throughput ML-guided design of diverse single-domain antibodies against SARS-CoV-2”. In: *bioRxiv* (Dec. 2023). DOI: [10.1101/2023.12.01.569227](https://doi.org/10.1101/2023.12.01.569227).
- [6] ZR McCaw, H Julienne, and H Aschard. “Fitting Gaussian mixture models on incomplete data”. In: *BMC Bioinformatics* 23.1 (June 2022), p. 208. DOI: [10.1186/s12859-022-04740-9](https://doi.org/10.1186/s12859-022-04740-9).

## Biostatistics & Clinical Trials

- [1] S Armbruster, ZR McCaw, K Jering, et al. “Capturing Totality of Treatment Effects: A Model-Free Approach to Analyzing Multiple Event-Time Data From Heart Failure Studies”. In: *JACC Heart Failure* (Aug. 2025). DOI: [10.1016/j.jchf.2025.102605](https://doi.org/10.1016/j.jchf.2025.102605).
- [2] AD Sherry, P Msaouel, AM Miller, et al. “Reproducibility of statistically significant phase III oncology trials: An In Silico meta-epidemiological analysis”. In: *European Journal of Cancer* (Aug. 2025). DOI: [10.1016/j.ejca.2025.115596](https://doi.org/10.1016/j.ejca.2025.115596).
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- [4] AD Sherry, Y Liu, P Msaouel, et al. “Survival-inferred fragility of statistical significance in phase III oncology trials”. In: *NPJ Precision Oncology* (July 2025). DOI: [10.1038/s41698-025-01024-2](https://doi.org/10.1038/s41698-025-01024-2).
- [5] TJ Kleber, AD Sherry, AJ Arifin, et al. “Justification, margin values, and analysis populations for oncologic noninferiority and equivalence trials: a meta-epidemiological study”. In: *Journal of the National Cancer Institute* (May 2025). DOI: [10.1093/jnci/djae318](https://doi.org/10.1093/jnci/djae318).
- [6] J Gronsbell et al. “Exact Inference for Random Effects Meta-Analyses for Small, Sparse Data”. In: *Stats* 8.1 (Mar. 2025). DOI: [10.3390/stats8010005](https://doi.org/10.3390/stats8010005).
- [7] AD Sherry et al. “Evidenced-Based Prior for Estimating the Treatment Effect of Phase III Randomized Trials in Oncology”. In: *JCO Precision Oncology* 8 (Oct. 2024), e2400363. DOI: [10.1200/P0.24.00363](https://doi.org/10.1200/P0.24.00363).
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- [10] AD Sherry et al. “Improving the clinical meaning of surrogate endpoints: An empirical assessment of clinical progression in phase III oncology trials”. In: *International Journal of Cancer* (Aug. 2024). DOI: [10.1002/ijc.35129](https://doi.org/10.1002/ijc.35129).

- [11] TA Lin et al. “Proportional Hazards Violations in Phase 3 Cancer Clinical Trials: A Potential Source of Trial Misinterpretation”. In: *Clinical Cancer Research* (Aug. 2024). DOI: [10.1158/1078-0432.CCR-24-0566](https://doi.org/10.1158/1078-0432.CCR-24-0566).
- [12] AD Sherry et al. “Towards Treatment Effect Interpretability: A Bayesian Re-analysis of 194,129 Patient Outcomes Across 230 Oncology Trials”. In: *medRxiv* (July 2024). DOI: [10.1101/2024.07.23.24310891](https://doi.org/10.1101/2024.07.23.24310891).
- [13] EJ Hsu et al. “Association of differential censoring with survival and suboptimal control arms among oncology clinical trials”. In: *Journal of the National Cancer Institute* 116.6 (June 2024), pp. 990–994. DOI: [10.1093/jnci/djae028](https://doi.org/10.1093/jnci/djae028).
- [14] AD Sherry, P Msaouel, TA Lin, et al. “Postprogression therapy and confounding for the estimated treatment effect on overall survival in phase III oncology trials”. In: *BMJ Oncology* (Apr. 2024). DOI: [10.1136/bmjonc-2024-000322](https://doi.org/10.1136/bmjonc-2024-000322).
- [15] AD Sherry, P Msaouel, ZR McCaw, et al. “Prevalence and implications of significance testing for baseline covariate imbalance in randomised cancer clinical trials: The Table 1 Fallacy”. In: *European Journal of Cancer* 194 (Nov. 2023), p. 113357. DOI: [10.1016/j.ejca.2023.113357](https://doi.org/10.1016/j.ejca.2023.113357).
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- [17] PS Jhund et al. “Effect of Dapagliflozin on Total Heart Failure Events in Patients With Heart Failure With Mildly Reduced or Preserved Ejection Fraction: A Prespecified Analysis of the DELIVER Trial”. In: *JAMA Cardiology* (Apr. 2023). DOI: [10.1001/jamacardio.2023.0711](https://doi.org/10.1001/jamacardio.2023.0711).
- [18] A Das et al. “Assessment of Median and Mean Survival Time in Cancer Clinical Trials”. In: *JAMA Network Open* 6.4 (Apr. 2023), e236498. DOI: [10.1001/jamanetworkopen.2023.6498](https://doi.org/10.1001/jamanetworkopen.2023.6498).
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- [21] ZR McCaw, DH Kim, and LJ Wei. “Pitfall in the Design and Analysis of Comparative Oncology Trials With a Time-to-Event Endpoint and Recommendations”. In: *JNCI Cancer Spectrum* 6.1 (Feb. 2022), pkac007. DOI: [10.1093/jncics/pkac007](https://doi.org/10.1093/jncics/pkac007).
- [22] ZR McCaw et al. “Practical Recommendations on Quantifying and Interpreting Treatment Effects in the Presence of Terminal Competing Risks: A Review”. In: *JAMA Cardiology* (Dec. 2021). DOI: [10.1001/jamacardio.2021.4932](https://doi.org/10.1001/jamacardio.2021.4932).



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- [25] ZR McCaw et al. “Neoadjuvant chemotherapy in bladder cancer: Clinical benefit observed in prospective trials computed with restricted mean survival times”. In: *Urologic Oncology* S1078-1439.20 (Jan. 2021), pp. 30640–30642. DOI: [10.1016/j.urolonc.2020.12.012](https://doi.org/10.1016/j.urolonc.2020.12.012).
- [26] ZR McCaw et al. “Survival analysis of treatment efficacy in comparative COVID-19 studies”. In: *Clinical Infectious Diseases* (Oct. 2020). DOI: [10.1093/cid/ciaa1563](https://doi.org/10.1093/cid/ciaa1563).
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## Biology

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- [2] J Marzec et al. “Toll-like receptor 4-mediated respiratory syncytial virus disease and lung transcriptomics in differentially susceptible inbred mouse strains”. In: *Physiological Genomics* (Nov. 2019). DOI: [10.1152/physiolgenomics.00101.2019](https://doi.org/10.1152/physiolgenomics.00101.2019).

- [3] M High et al. “Determinants of host susceptibility to murine respiratory syncytial virus (RSV) disease identify a role for the innate immunity scavenger receptor MARCO gene in human infants”. In: *EBioMedicine* S2352-3964.16 (2016), pp. 30360–7. DOI: [10.1016/j.ebiom.2016.08.011](https://doi.org/10.1016/j.ebiom.2016.08.011).
- [4] JM Ciencewicki et al. “Effects of mannose-binding lectin on pulmonary gene expression and innate immune inflammatory response to ozone”. In: *American Journal of Physiology-Lung Cellular and Molecular Physiology* 311.2 (2016), pp. 280–91. DOI: [10.1152/ajplung.00205.2015](https://doi.org/10.1152/ajplung.00205.2015).
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- [6] KC Verhein et al. “Novel Roles for Notch3 and Notch4 Receptors in Gene Expression and Susceptibility to Ozone Induced Lung Inflammation in Mice”. In: *Environmental Health Perspectives* 123.8 (2015), pp. 799–805. DOI: [10.1289/ehp.1408852](https://doi.org/10.1289/ehp.1408852).
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## Correspondence

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- [2] ZR McCaw, L Tian, and LJ Wei. “Evaluating the Duration of Response With Mirvetuximab Soravtansine for Treating Platinum-Resistant Ovarian Cancer”. In: *Journal of Clinical Oncology* (Aug. 2023), JCO2300288. DOI: [10.1200/JCO.23.00288](https://doi.org/10.1200/JCO.23.00288).
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## Professional Activities

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- **ML4H Section Chair** 2025
- **Peer Review** 2025  
Journals: Bioinformatics, BMC Bioinformatics,  
BMC Medical Research Methodology, Cancers, Clinical Trials, EJMR,  
iScience, ISMB, Nature Aging, Nutrition  
Nature Communications, npj Health Systems
- **Peer Review** 2024  
Journals: Bioinformatics, Briefings in Bioinformatics, BMC Medical Research  
Methodology, ISCB, ISMB, Statistics in Medicine, Stats
- **Peer Review** 2023  
Journals: Current Cancer Drug Targets, ISCB, RECOMB
- **Peer Review** 2022  
Journals: Axioms, ISCB, Life, Statistics in Biopharmaceutical Research,  
Statistics in Medicine, TEST, Viruses
- **Peer Review** 2021  
Journals: Circulation: Cardiovascular Quality and Outcomes,  
Frontiers in Genetics, ISCB, Statistics in Medicine
- **Peer Review** 2020  
Journals: ISCB, Statistics in Medicine
- **JSM Section Chair** 2019  
Regression Methods for Longitudinal Data
- **JSM Section Chair** 2018  
Gene-Gene and Gene-Environment Interactions

## Conference Presentations

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- **American Society of Human Genetics** 11/2024  
Unveiling the power of allelic series: enhancements and applications of  
COAST.
- **American Association for Cancer Research** 04/2024  
Machine learning enabled prediction of digital biomarkers from whole  
slide histopathology images.
- **American Society of Human Genetics** 10/2023  
Synthetic slope analysis for progression GWAS.
- **American Association for Cancer Research** 04/2023  
Learned phenotypic embeddings enable scalable imputation of high-  
content molecular data elucidating prognostic chromatin signatures.
- **American Society of Human Genetics** 10/2022  
An allelic series rare variant association test for candidate gene discovery.
- **American Society of Human Genetics** 10/2019

Cross-population fine-mapping to identify shared and population-specific causal effects.

- **Joint Statistical Meeting** 07/2019  
Cross-tissue eQTL calling via surrogate expression analysis.
- **Harvard School of Public Health, Program in Quantitative Genomics** 11/2018  
Leveraging the UKB to empower association testing on scarce phenotypes.
- **Joint Statistical Meeting** 07/2018  
Leveraging surrogate phenotypes to improve inference on a partially missing target phenotype.
- **Joint Statistical Meeting** 07/2017  
Inverse normal transformation for genome-wide association testing of quantitative Traits.
- **American Thoracic Society** 05/2014  
Gene expression profiling predicts response to respiratory syncytial virus (RSV) in mice.
- **National Institute of Environmental Health Sciences** 07/2011  
Identifying candidate susceptibility genes for respiratory syncytial virus (RSV) disease severity.
- **National Institute of Environmental Health Sciences** 07/2010  
Characterization of transcriptional networks underlying Tlr4-mediated respiratory syncytial virus (RSV) disease in mice.

## Awards and Distinctions

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- **Distinguished Student Paper Award** 07/2019  
Joint Statistical Meeting, Section in Genetics and Genomics.
- **Stellar Abstract Award** 11/2018  
Harvard School of Public Health, Program in Quantitative Genomics
- **Ruth L. Kirschstein National Research Service Award (F31)** 03/2018  
[Innovations in Genome Wide Association Testing Inspired by Obstructive Sleep Apnea Phenotypes](#)
- **Teaching Fellow** 11/2017  
Global Initiative for Neuropsychiatric Genetic Education in Research
- **NIH Pre-Doctoral Training Grant** 08/2016  
Statistical and Quantitative Training in Big Data Health Science
- **NIH Pre-Doctoral Training Grant** 08/2014  
Interdisciplinary Training Grant in Biostatistics and Computational Biology
- **NIH Post-Baccalaureate Research Fellow** 09/2013  
National Institute of Environmental Health Sciences
- **Undergraduate Academic Achievement Award** 04/2013  
UNC Department of Biostatistics
- **Phi Beta Kappa National Honors Society** 11/2011
- **NIH Summer Internship** 05/2011  
National Institute of Environmental Health Sciences 05/2010

## Teaching Experience

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### The University of North Carolina at Chapel Hill

06/2023 – Present

ADJUNCT INSTRUCTOR: 06/23 –

- DEPARTMENT: MPH@UNC
- CLASSES: Section instructor for SPHG 711, Data Analysis for Public Health.

### UNC Chapel Hill

- CLASS: Data Analysis for Public Health (SPHG 711) 08/2024 - 12/2024  
08/2023 - 12/2023

### Harvard University

- CLASS: Inference II (BST 241) 02/2019 – 05/2019  
INSTRUCTOR: Rui Wang, Ph.D.
- CLASS: Introduction to Biostatistics 02/2019  
INSTRUCTOR: Lori Chibnik, Ph.D.  
LOCATION: University of KwaZulu-Natal, Durban, South Africa
- CLASS: Multivariate and Longitudinal Analysis (BST 245) 02/2018 – 05/2018  
INSTRUCTOR: Sebastien Haneuse, Ph.D.
- CLASS: Inference I (BST 231) 02/2017 – 05/2017  
INSTRUCTOR: Judith Lok, Ph.D.
- CLASS: Statistical Genetics (BST 227) 10/2016 – 12/2016  
INSTRUCTOR: Martin Aryee, Ph.D.
- CLASS: Computational Biology (STAT 215) 02/2016 – 05/2016  
INSTRUCTOR: X. Shirley Liu, Ph.D.

### UNC Chapel Hill

- CLASS: General Chemistry I (CHEM 101) 08/2012 – 12/2012  
INSTRUCTOR: Jennifer Krumper, Ph.D.
- CLASS: Organic Chemistry II (CHEM 262) 08/2011 – 12/2011  
INSTRUCTOR: Jennifer Krumper, Ph.D.