

Zachary Ryan McCaw

Curriculum Vitae

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Education

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

- **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

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

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 spirograms 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 Julianne, 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).
- [3] AD Sherry et al. "Bayesian Interim Analysis and Efficiency of Phase III Randomized Trials". In: *Br J Cancer* (Aug. 2025). DOI: [10.1038/s41416-025-03156-5](https://doi.org/10.1038/s41416-025-03156-5).
- [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).
- [8] AD Sherry et al. "Increasing Power in Phase III Oncology Trials With Multivariable Regression: An Empirical Assessment of 535 Primary End Point Analyses". In: *JCO Clinical Cancer Informatics* 8 (Sept. 2024), e2400102. DOI: [10.1200/CCI.24.00102](https://doi.org/10.1200/CCI.24.00102).
- [9] AD Sherry et al. "Off-Protocol Radiation Therapy in Phase 3 Metastatic Solid Tumor Trials". In: *Int J Radiat Oncol Biol Phys* (Aug. 2024). DOI: [10.1016/j.ijrobp.2024.05.033](https://doi.org/10.1016/j.ijrobp.2024.05.033).
- [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/bmjjonc-2024-000322](https://doi.org/10.1136/bmjjonc-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).
- [16] X Wang et al. “Using a Clinically Interpretable End Point Composed of Multiple Outcomes to Evaluate Totality of Treatment Effect in Comparative Oncology Studies”. In: *JAMA Network Open* 6.6 (June 2023), e2319055. DOI: [10.1001/jamanetworkopen.2023.19055](https://doi.org/10.1001/jamanetworkopen.2023.19055).
- [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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- [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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- [24] R Sun et al. “Moving beyond conventional stratified analysis to assess the treatment effect in a comparative oncology study”. In: *Journal for ImmunoTherapy of Cancer* 9.11 (Nov. 2021), e003323. DOI: [10.1136/jitc-2021-003323](https://doi.org/10.1136/jitc-2021-003323).
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- [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).
- [27] C Perego et al. “Utility of Restricted Mean Survival Time Analysis for Heart Failure Clinical Trial Evaluation and Interpretation”. In: *JACC Heart Failure* (Oct. 2020). DOI: [10.1016/j.jchf.2020.07.005](https://doi.org/10.1016/j.jchf.2020.07.005).
- [28] ZR McCaw et al. “Selecting Appropriate Endpoints for Assessing Treatment Effects in Comparative Clinical Studies for COVID-19”. In: *Contemporary Clinical Trials* (Sept. 2020). DOI: [10.1016/j.cct.2020.106145](https://doi.org/10.1016/j.cct.2020.106145).
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- [30] B Huang et al. “Analysis of Response Data for Assessing Treatment Effects in Comparative Clinical Studies”. In: *Annals of Internal Medicine* (July 2020). DOI: [10.7326/M20-0104](https://doi.org/10.7326/M20-0104).
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Biology

- [1] L Siraj et al. “Functional dissection of complex and molecular trait variants at single nucleotide resolution”. In: *bioRxiv* (May 2024). DOI: [10.1101/2024.05.05.592437](https://doi.org/10.1101/2024.05.05.592437).
- [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).
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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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- [6] ZR McCaw and LJ Wei. "Clinical Utility Assessment of Gonadotropin-Releasing Hormone Analogs Among Women Younger Than 35 Years". In: *JAMA Surgery* 8.6 (Apr. 2022), pp. 943–944. DOI: [10.1001/jamaoncol.2022.0488](https://doi.org/10.1001/jamaoncol.2022.0488).
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- [8] ZR McCaw, L Tian, and LJ Wei. "Quantifying the Effect of Lower vs Higher Positive End-Expiratory Pressure on Ventilator-Free Survival in ICU Patients". In: *JAMA* 325.15 (Apr. 2021), pp. 1566–1567. DOI: [10.1001/jama.2021.1700](https://doi.org/10.1001/jama.2021.1700).
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Professional Activities

- **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

- **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

• 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

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

UNC Chapel Hill

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