Zachary Ryan McCaw

Curriculum Vitae

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July 2024

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. [36]
  - Developed multivariate regression methodology for leveraging a correlated surrogate outcome to improve inference on a partially missing target outcome. [22, 3]
- 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

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

Technical Experience

- **Genetics**: Genome-wide association studies, fine-mapping, Mendelian randomization, polygenic scoring, rare-variant association testing.
- **Machine Learning**: Computer vision, representation learning, survival modeling.
- **Software**: AWS, Git, Python, PyTorch, R, SQL, Tensorflow.
- **Statistics**: Causal inference, clinical trials, competing risks, longitudinal and multivariate analysis, meta-analysis, regression modeling, survival analysis.

Professional Experience

Insitro
09/2021 – Present

Staff Machine Learning Scientist: 04/23 –

- Department: Clinical Machine Learning
- Team Lead: Colm O'Dushlaine, Ph.D.
- Projects:
  - **Machine learning enabled prediction of digital biomarkers from whole slide histopathology images** [9]
  - **Pitfalls in performing genome-wide association studies on ratio traits** [11]

Senior Machine Learning Scientist: 09/21 – 03/23.

- Department: Statistical Genetics
- Team Lead: Thomas Soare, Ph.D.
- Projects:
  - **Developed an allelic series rare-variant test for candidate gene discovery**. [14]
  - Identified Parkinson's risk variants using MRI-derived proxy phenotypes.

Google
09/2019 – 09/2021

Data Scientist

- Department: Health, Genomic Medicine Team.
- Scientific and Team Leads: Babak Alipanahi, Ph.D. and Cory McLean, Ph.D.
- Projects: **Genetic discovery for machine learning derived phenotypes**.
  - Contributed to representation learning for genetic discovery on low-dimensional embeddings (REGLE) [1].
  - Identified genetic variants associated with ML-derived COPD risk ascertained from volumetric flow curves via deep convolutional networks. [17]
  - Developed methodology (DeepNull) to adjust for non-linear covariate effects in GWAS via deep neural networks. [24]
  - Identified genetic variants associated with glaucoma features extracted from retinal fundus images using deep convolutional networks. [29]
  - 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, 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.**
  - Developed an extension of sum of single effects regression for multiple populations allowing for different causal architectures and correlated effect sizes.

Articles

[1] 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.

[2] AD Sherry et al. "Bayesian Interim Analysis and Efficiency of Phase III Randomized Trials". In: *medRxiv* (June 2024). DOI: 10.1101/2024.06.27.24309608.

[3] 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.

[4] 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.

[5] 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.

[6] 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.

[7] Y Zhou et al. "Utilizing multimodal AI to improve genetic analyses of cardiovascular traits". In: *medRxiv* (Mar. 2024). DOI: 10.1101/2024.03.19.24304547.

[8] 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.

[9] 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.

[10] 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.

[11] ZR McCaw et al. "Pitfalls in performing genome-wide association studies on ratio traits". In: *bioRxiv* (Nov. 2023). DOI: 10.1101/2023.10.27.564385.

[12] 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: *bioRxiv* (Nov. 2023). DOI: 10.1101/2023.10.30.564764.

[13] 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.

[14] 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.

[15] X Wang et al. "Using a Clinically Interpretable End Point Composed of Multiple Outcomes to Evaluate Totality of Treatment Effect in Comparative Oncology Studie". In: *JAMA Network Open* 6.6 (June 2023), e2319055. DOI: 10.1001/jamanetworkopen.2023.19055.

[16] 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.

[17] 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.

[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.

[19] HM Dehbi, A Embleton-Thirsk, and McCaw ZR. "Sample size calculation for randomized selection trials with a time-to-event endpoint and a margin of practical equivalence". In: *Statistics in Medicine* (June 2022). DOI: 10.1002/sim.9490.

[20] 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.

[21] BL Claggett et al. "Quantifying Treatment Effects in Trials with Multiple Event-Time Outcomes". In: *NEJM Evidence* 1.10 (June 2022). DOI: 10.1056/EVIDoa2200047.

[22] 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.

[23] 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.

[24] 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.

[25] 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..

[26] ZR McCaw et al. “Choosing clinically interpretable summary measures and robust analytic procedures for quantifying the treatment difference in comparative clinical studies”. In: *Statistics in Medicine* 40.28 (Dec. 2021), pp. 6235–6242. DOI: 10.1002/sim.8971.

[27] 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.

[28] 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.

[29] 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.

[30] 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.

[31] 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.

[32] 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.

[33] 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..

[34] ZR McCaw et al. “How to Quantify and Interpret Treatment Effects in Comparative Clinical Studies of COVID-19”. In: *Annals of Internal Medicine* (July 2020). DOI: 10.7326/M20-4044.

[35] 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.

[36] 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.

[37] 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.

[38] ZR McCaw, G Yin, and LJ Wei. “Using the Restricted Mean Survival Time Difference as an Alternative to the Hazard Ratio for Analyzing Clinical Cardiovascular Studies”. In: *Circulation* 140.17 (Oct. 2019), pp. 1366–1368. DOI: 10.1161/CIRCULATIONAHA.119.040680.

[39] ZR McCaw et al. "Applying Evidence-Based Medicine to Shared Decision Making: Value of Restricted Mean Survival Time". In: *The American Journal of Medicine* 132.1 (Jan. 2019), pp. 13–15. DOI: 10.1016/j.amjmed.2018.07.026.

[40] 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.

[41] 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.

[42] BP Kleinstiver et al. "Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells". In: *Nature Biotechnology* 34.8 (2016), pp. 869–74. DOI: 10.1038/nbt.3620.

[43] 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.

[44] J Krishnaswamy et al. "Coincidental loss of DOCK8 function in NLRP10-deficient and C3H/HeJ mice results in defective dendritic cell migration". In: *PNAS* 112.10 (2015), pp. 3056–61. DOI: 10.1073/pnas.1501554112.

[45] H Cho et al. "Association of Nrf2 polymorphism haplotypes with acute lung injury phenotypes in inbred strains of mice". In: *Antioxidants and Redox Signaling* 22.4 (2015), pp. 325–38. DOI: 10.1089/ars.2014.5942.

[46] KC Verhein et al. "Genetic Factors Involved in Susceptibility to Lung Disease". In: *The Lung Second Edition: Development, Aging and the Environment*. Ed. by Plopper CG Harding R Pinkerton KE. London: Academic Press, 2014.

Correspondence

[1] AD Sherry et al. "Interpretation of long-term survival data from MONARCH 3". In: *Annals of Oncology* S0923-7534.24 (June 2024), pp. 00718–X. DOI: 10.1016/j.annonc.2024.05.543.

[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.

[3] ZR McCaw, PG Richardson, and LJ Wei. "Assessing the Ability of Long Noncoding RNA Expression to Predict Patient Outcomes in Pediatric AML". In: *Journal of Clinical Oncology* (June 2023), JCO2300465. DOI: 10.1200/JCO.23.00465.

[4] TA Lin et al. "Determining the Efficacy of Pembrolizumab in Patients With Previously Treated Advanced Hepatocellular Carcinoma". In: *Journal of Clinical Oncology* (Apr. 2023). DOI: 10.1200/JCO.23.0007.

[5] ZR McCaw, EB Ludmir, and LJ Wei. "Assessing the Clinical Utility of Oral Paclitaxel Plus Encequidar Versus Intravenous Paclitaxel in Patients With Metastatic Breast Cancer". In: *Journal of Clinical Oncology* 41.6 (Feb. 2023), p. 1323. DOI: 10.1200/JCO.22.01759.

[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.

[7] ZR McCaw and LJ Wei. "Questions About a Risk Prediction Model of Mortality After Esophagectomy for Cancer". In: *JAMA Surgery* 157.3 (Nov. 2021), pp. 279–280. DOI: 10.1001/jamasurg.2021.5701.

[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.

[9] ZR McCaw, MA Liu, and LJ Wei. "Olaparib in Metastatic Castration-Resistant Prostate Cancer". In: *New England Journal of Medicine* 384.12 (Mar. 2021), p. 1174. DOI: 10.1056/NEJMc2100225.

[10] ZR McCaw, EB Ludmir, and LJ Wei. "Quantifying the Long-term Survival Benefit of Pembrolizumab for Patients With Advanced Gastric Cancer". In: *JAMA Oncology* 7.4 (Feb. 2021). DOI: 10.1001/jamaoncol.2020.8002.

[11] ZR McCaw, G Fitzmaurice, and LJ Wei. "The COMPASS Trial: Net Clinical Benefit of Low-Dose Rivaroxaban Plus Aspirin as Compared With Aspirin in Patients With Chronic Vascular Disease". In: *Circulation* 143.1 (Jan. 2021), e1–e2. DOI: 10.1161/CIRCULATIONAHA.120.050723.

[12] RR Patel et al. "Transparency in reporting of phase 3 cancer clinical trial results". In: *Acta Oncologica* 60.2 (Dec. 2020). DOI: 10.1080/0284186X.2020.1856410.

[13] EB Ludmir, ZR McCaw, and LJ Wei. "Interpreting the Effect of Ipilimumab Following Radiotherapy for Patients with Postdocetaxel Metastatic Castration-resistant Prostate Cancer". In: *European Urology* 79.1 (Oct. 2020), e10–e11. DOI: 10.1016/j.eururo.2020.09.049.

[14] ZR McCaw, L Tian, and LJ Wei. "What We Learned from Recent COVID-19 Clinical Studies Regarding Statistical Methodology". In: *Biopharmaceutical Report* 27.3 (Oct. 2020).

[15] ZR McCaw, L Tian, and LJ Wei. "Appropriate Analysis of Duration of Response Data in Cancer Trials". In: *JAMA Oncology* 6.12 (Oct. 2020), p. 1978. DOI: 10.1001/jamaoncol.2020.4657.

[16] EB Ludmir et al. "Progression-free survival in the ICON8 trial". In: *Lancet* 396.10253 (Sept. 2020), p. 756. DOI: 10.1016/S0140-6736(20)31175-2.

[17] ZR McCaw et al. "Further clinical interpretation and implications of KEYNOTE-048 findings". In: *Lancet* 396.10248 (Aug. 2020), pp. 378–379. DOI: 10.1016/S0140-6736(20)30904-1.

[18] ZR McCaw, DH Kim, and LJ Wei. "Remdesivir for the Treatment of Covid-19 - Preliminary Report". In: *New England Journal of Medicine* 383 (July 2020), pp. 992–994. DOI: 10.1056/NEJMc2022236.

[19] ZR McCaw, DH Kim, and LJ Wei. "Risk-Benefit Comparisons Between Shorter and Longer Durations of Adjuvant Chemotherapy in High-Risk Stage II Colorectal Cancer". In: *JAMA Oncology* 6.8 (June 2020), pp. 1301–1302. DOI: 10.1001/jamaoncol.2020.2256.

[20] EB Ludmir et al. "Fulvestrant plus capivasertib for metastatic breast cancer". In: *Lancet Oncology* 21.5 (May 2020), e233. DOI: 10.1016/S1470-2045(20)30228-X.

[21] ZR McCaw, LJ Wei, and EB Ludmir. "Interpreting the impact of apalutamide on overall survival among patients with non-metastatic castration-resistant prostate cancer". In: *Annals of Oncology* 31.3 (Mar. 2020), pp. 438–440. DOI: 10.1016/j.annonc.2019.11.020.

[22] D Li, ZR McCaw, and LJ Wei. "Interpreting the Benefit of Simvastatin-Ezetimibe in Patients 75 Years or Older". In: *JAMA Cardiology* 5.2 (Jan. 2020), p. 235. DOI: 10.1001/jamacardio.2019.5200.

[23] EB Ludmir et al. "Quantifying the Benefit of Non-small-cell lung Cancer Immunotherapy". In: *Lancet* 394.10212 (Nov. 2019), p. 1904. DOI: 10.1016/S0140-6736(19)32503-6.

[24] ZR McCaw and LJ Wei. "P2Y12 Inhibitor Monotherapy vs Dual Antiplatelet Therapy After Percutaneous Coronary Intervention". In: *JAMA* 322.16 (Oct. 2019), p. 1607. DOI: 0.1001/jama.2019.13159.

[25] ZR McCaw, Z Meng, and LJ Wei. "A Shorter Regimen for Rifampin-Resistant Tuberculosis". In: *New England Journal of Medicine* 381.11 (Sept. 2019), e22. DOI: 10.1056/NEJMc1905782.

[26] G Yin and ZR McCaw. "Design of Noninferiority Trials for Hypofractionated vs Conventional Radiotherapy Among Patients With Cancer". In: *JAMA Oncology* 5.10 (Aug. 2019). DOI: 10.1001/jamaoncol.2019.2391.

[27] ZR McCaw, DH Kim, and LJ Wei. "Analysis of Long-term Benefits of Intensive Blood Pressure Control". In: *JAMA* 322.2 (July 2019), pp. 169–170. DOI: 10.1001/jama.2019.5840.

[28] Z Yang, ZR McCaw, and G Yin. "Caplacizumab for Acquired Thrombotic Thrombocytopenic Purpura". In: *New England Journal of Medicine* 380.18 (May 2019), e32. DOI: 10.1056/NEJMc1902336.

[29] ZR McCaw, LJ Wei, and DH Kim. "Effects of Aspirin in the Healthy Elderly". In: *New England Journal of Medicine* 380.18 (May 2019), pp. 1775–1776. DOI: 10.1056/NEJMc1901774.

[30] Z Yang, ZR McCaw, and G Yin. "Radical Surgery or Watchful Waiting in Prostate Cancer". In: *New England Journal of Medicine* 380.11 (Mar. 2019), pp. 1083–1 084. DOI: 10.1056/NEJMc1900410.

[31] ZR McCaw and LJ Wei. "Interpreting the Survival Benefit From Neoadjuvant Chemoradiotherapy Before Surgery for Locally Advanced Squamous Cell Carcinoma of the Esophagus". In: *Journal of Clinical Oncology* 37.12 (Mar. 2019), pp. 1032–1033. DOI: 10.1200/JCO.18.01164.

[32] ZR McCaw, LJ Wei, and DH Kim. "Interpreting the Prognostic Value of Unrecognized Myocardial Infarction Among Older Adults". In: *JAMA Cardiology* 4.4 (Mar. 2019), p. 391. DOI: 10.1001/jamacardio.2019.0184.

[33] ZR McCaw, JL Vassy, and LJ Wei. "Palbociclib and Fulvestrant in Breast Cancer". In: *New England Journal of Medicine* 380.8 (Feb. 2019), p. 796. DOI: 10.1056/NEJMc1816595.

[34] ZR McCaw, DH Kim, and LJ Wei. "Evaluating Treatment Effect of Transcatheter Interatrial Shunt Device Using Heart Failure Event Rates". In: *JAMA Cardiology* 4.3 (Feb. 2019), p. 299. DOI: 10.1001/jamacardio.2019.0001.

[35] ZR McCaw et al. "Trifluridine/tipiracil in metastatic gastric cancer". In: *Lancet Oncology* 20.1 (Jan. 2019), e8. DOI: 10.1016/S1470-2045(18)30908-2.

[36] ZR McCaw, F Jiang, and LJ Wei. "Trastuzumab Therapy for 9 Weeks vs 1 Year for Human Epidermal Growth Factor Receptor 2-Positive Breast Cancer". In: *JAMA Oncology* 3.1 (Dec. 2018), pp. 117–118. DOI: 10.1001/jamaoncol.2018.5730.

[37] ZR McCaw et al. "Interpreting Clinical Benefits of Neoadjuvant Chemoradiation With Gemcitabine Versus Upfront Surgery in Patients With Borderline Resectable Pancreatic Cancer (BRPC)". In: *Annals of Surgery* 270.2 (Nov. 2018), e48–e50. DOI: 10.1097/SLA.0000000000003115.

[38] ZR McCaw, S Piantadosi, and LJ Wei. "Quantifying the Added Value of Low-Molecular-Weight Heparin to Intermittent Pneumatic Compression for Preventing Venous Thromboembolic Events Under the Risk-Benefit Perspective". In: *JAMA Surgery* 154.3 (Nov. 2018), pp. 270–271. DOI: 10.1001/jamasurg.2018.4294.

[39] ZR McCaw, D Liu, and LJ Wei. "Body Composition and Overall Survival in Patients With Nonmetastatic Breast Cancer". In: *JAMA Oncology* 5.1 (Nov. 2018), pp. 114–115. DOI: 10.1001/jamaoncol.2018.5290.

[40] ZR McCaw, LJ Wei, and DH Kim. "Gene Expression-Guided Adjuvant Chemotherapy in Breast Cancer". In: *New England Journal of Medicine* 379.17 (Oct. 2018), p. 1681. DOI: 10.1056/NEJMc1810515.

[41] BL Claggett et al. "Sex as a predictor of response to cancer immunotherapy". In: *Lancet Oncology* 19.8 (Aug. 2018), e377. DOI: 10.1016/S1470-2045(18)30517-5.

Professional Activities

- **Peer Review** 2024
  Journals: Bioinformatics, ISCB, Statistics in Medicine
- **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: ISCM, 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 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

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.