Bryce Rowland

Department of Biostatistics Gillings School of Global Public Health University of North Carolina at Chapel Hill Chapel Hill, NC 27514

Last updated: July, 2020 Email: bryce.rowland@unc.edu Research group: https://yunliweb.its.unc.edu Website: https://brycerowland.netlify.app

EDUCATION

2017-Present PhD Candidate in Biostatistics, University of North Carolina at Chapel

Hill

2017 BS in Mathematics Summa Cum Laude, Centre College

AWARDS & HONORS

National Science Foundation - Graduate Research Fellowship Program
Department of Biostatistics Student Travel Award to present at the ASHG Annual Meeting, Houston, TX, USA
Doctoral Merit Assistantship, University of North Carolina at Chapel Hill
Brown Fellows Scholarhip, Centre College

2017 Phi Beta Kappa

RESEARCH EXPERIENCE

2018–Present Graduate Researcher - Yun Li Lab

Developed statistical methods for analysis of bulk Hi-C data

Lead statistician for a transcriptome-wide association study (TWAS) of blood cell traits in UK Biobank

Contributed significantly to in-progress research on a wide range of statistical genetics topics including LD score regression, polygenic risk scores, 3D chromatin modeling, co-localization analyses, and genotype imputation

2017–2019 Graduate Researcher - Collaborative Studies Coordinating Center

Primary statistician on a manuscript investigating the relationship between diabetes prevalence and segregation in Hispanic communities.

Research assistant to Dr. Jianwen Cai in theoretical statistics research concerning the linear model when the response variable is a ratio.

2016–2017 Field Research Coordinator - Harvard University

Successfully led a team of Harvard graduate students to conduct one hundred and five interviews during a three week period in Montserrat.

Independently conducted field research in Montserrat consisting of formal interviews, information gathering, and logistical planning for future research.

PUBLICATIONS

IN PROGRESS

2020

Bryce Rowland, Ruth Huh, Ziyi Zoey Hou, Yun Li THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data

Jia Wen, Munan Xie, **Bryce Rowland**, Jonathan D. Rosen, Quan Sun, Huijun Qian, Madeline H. Kowalski, Annie Shan, Amanda L. Tapia, Kristin Young, Yongmei Liu, Jerome I. Rotter, Stephen S. Rich, Christy Avery, Chani Hodonsky, Ruth J.F. Loos, Stephanie A. Bien, Charles Kooperberg, Steve Buyske, Kari E. North, Myriam Fornage, Misa Graff, Maria Argos, Jee-Young Moon, Tao Wang, Eric Jorgenson, Hélène Choquet, Alexander P. Reiner, Laura M. Raffield, Yun Li Transcriptome-wide association study of blood cell traits in African American and Hispanic/Latino Populations

TEACHING

2020-Present

Instructor, Linear Algebra Biostatistics Bootcamp

Two-week short course designed to review linear algebra concepts necessary for PhD theory coursework in linear models. Created and taught online course for Fall 2020.

2020-Present

Teaching Assistant, BIOS 782: Statistical Methods in Genetic Association Studies

2019

Teaching Assistant, BIOS 511: Introduction to Statistical Computing and Data Management

Led weekly office hours and graded homeworks and lab assignments on introductory SAS programming. Taught two lectures on SAS macros.

PRESENTATIONS

2019

Bryce Rowland, Ruth Huh, Ziyi Zoey Hou, Yun Li THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data *Poster*, *ASHG 2019*, Houston, TX, USA.