

Education

PhD—Computer Science, **University of California, Berkeley**

Computational Approaches to Understanding the Genetic Architecture of Complex Traits

Fall 2016; NSF Graduate Research Fellow, Chancellor's Fellow

Advisors: Lior Pachter, Noah Zaitlen

BA—Computer Science, **BS**—Physics, **University of Virginia**

The Complexity of Computing the Density of States

Spring 2011; Highest Distinction, Second-year Honors, Echol's Scholar

Positions

Data Science Institute Fellow—Columbia University, August 2019-present

Postdoctoral Researcher—New York Genome Center, August 2019-present

Postdoctoral fellow jointly affiliated with the Columbia Data Science Institute and New York Genome Center. Advisors: David Knowles and Tuuli Lappalainen.

Computational Biologist—Verily Life Sciences, March 2017 - July 2019

Development and application of statistical machine learning models for integrative analysis of multi-omic and healthcare data

Publications

B.C. Brown*, C.L. Wang et al. (2022). Multiset correlation and factor analysis enables exploratory analysis of multi-omic data. *In preparation*

B.C. Brown* and D. A. Knowles (2021), Welch-weighted Egger regression reduces false positives due to correlated pleiotropy in Mendelian randomization. *The American Journal of Human Genetics*, 108 (12), p2319–2335, 2 December 2021

B.C. Brown* and D. A. Knowles (2020), Phenome-scale causal network discovery with bidirectional mediated Mendelian randomization. *bioRxiv*, 22 June 2020

M. Lam, C. Chen et al. (2019), Comparative genetic architectures of schizophrenia in East Asian and European populations. *Nature Genetics* 51, p1670–1678, 18 November 2019

B.C. Brown, N.L. Bray and L. Pachter (2018), Expression Reflects Population Structure. *PLOS Genetics* 14(12): e1007841 19 December 2018

K.J. Galinsky, Y.A. Reshef, H.K. Finucane, P. Loh, N. Zaitlen, N.J. Patterson, **B.C. Brown*** and A.L. Price (2018), Estimating cross-population genetic correlations of causal effect sizes. *Genetic Epidemiology* 25 November 2018

B.C. Brown*, AGEN-T2D, C. Ye, A.L. Price and N. Zaitlen (2016), Transethnic genetic correlation estimates from summary statistics. *The American Journal of Human Genetics*, 99 (1), p76–88, 7 July 2016

B.C. Brown*, A.L. Price, N.A. Patsopoulos and N. Zaitlen (2016), Local joint testing improves power and identifies both missing and spurious heritability in association studies. *Genetics*, 203, 1-12 July 2016

D. Park, **B.C. Brown**, C. Eng, S. Huntsman, D. Hu, D. Torgerson, E. Burchard and N. Zaitlen (2015) Adapt-Mix: Learning local genetic correlation structure improves summary statistics based analyses. *ISMB 2015 Proceedings*

J. R. Shewchuk and **B.C. Brown** (2013), Inserting a Segment into a Constrained Delaunay Triangulation in Expected Linear Time. *Computational Geometry Special Issue: Selected Papers from SoCG 2013*

B.C. Brown, S. T. Flammia, N. Schuch (2011), The Computational Difficulty of Computing the Density of States. *Physical Review Letters*, 107 (4), 22 July 2011

B.C. Brown (2008). Considerations for the Optimal Polarization of ^3He Targets. *SPIN PHYSICS: 18th International Spin Physics Symposium. AIP Conference Proceedings*, Volume 1149, pp. 895-898

*BCB is co-corresponding author

Invited seminars and selected platform talks

"Multi-set correlation and factor analysis of multi-omic data." Platform talk, CHARGE Philadelphia. April 2022

"Multi-set correlation and factor analysis of multi-omic data." Invited seminar, University of Chicago. March 2022

"Phenome-scale causal network discovery with bidirectional mediated Mendelian randomization." Platform Talk, Probabilistic Modeling in Genomics. April 2021

"Causal network discovery with Bi-directional mediated Mendelian randomization." Invited seminar, University of California Los Angeles. October 2020

"Transethnic genetic correlation estimates from summary statistics" Platform Talk, The 13th International Congress of Human Genetics. Kyoto, Japan. April 2016

"Adapt-Mix: Learning local genetic correlation structure improves summary statistics based analyses" Platform Talk, 23rd Annual International Conference on Intelligent Systems for Molecular Biology. July 2015

"A joint testing framework uncovers paradoxical SNPs, improves power, and identifies new sources of missing heritability in association studies." Platform Talk, The 64th Annual American Society of Human Genetics Meeting. October, 2014

"Beating GWAS via joint testing" Invited talk, University of Virginia Center for Public Health Genomics. September 2014

"Considerations for the Optimal Polarization of ^3He Targets." Platform Talk, 18th International Spin Physics Symposium. September 2008

Funding and Awards

NIH K99HG012373 (2022): "Perturbation-response approaches to determining the regulatory networks underlying human complex traits". *Impact score: 19*. Has received programmatic scheduling for funding.

Data Science Institute Fellowship (2019): one of four Columbia data science postdoctoral researchers selected for funding from the Data Science Institute

Genetics Journal Spotlight Award (2016): top paper in Statistical Genetics and Genomics

ASHG Reviewers Choice (Aug 2016): top 10% of abstracts at the ASHG meeting

NSF Graduate Research Fellowship – Spring 2011

UC Berkeley Chancellor's Fellowship for Graduate Study – Spring 2011

Internships

Career Development in the Physical Sciences—Rhumbix, UC Berkeley

Developed a random forest classifier for construction worker tasks from sparse real-time location system data using python (pandas, scikit-learn)

July 2016, Mentor: Michael Myers

Statistical Genetics Intern—23&Me Research Team

Methods for estimating the heritability of disease using hundreds of thousands of genotypes

May 2013 – August 2013, Mentor: Nick Eriksson

Teaching Experience

Summer Rising—University of California, Berkeley

Targeted tutoring and mentorship for undergraduates of color in STEM

Summer 2015, Graduate Student Instructor - Computer Science

CS 176 Algorithms for Computational Biology—University of California, Berkeley

Fall 2014, Graduate Student Instructor

CS 70 Discrete Mathematics and Probability Theory—University of California, Berkeley

Summer 2014, Graduate Student Instructor

The Science of Sound Quality—University of Virginia

Spring 2010, Instructor of Record

Residential College Short Course

Philosophical Implications of Modern Physics—University of Virginia

Spring 2009, Instructor of Record

Residential College Short Course

Tutoring and Mentoring

Intern Host—Verily Life Sciences

Abubakar Abid - Deep learning models for inference from transcriptional profiles.

Mentoring—Verily Life Sciences

Cindy Tian - Transcriptomic and epigenomic profiling of immune cells from cancer responders and non-responders.

Mentoring—University of California, Berkeley

Corey Short, Saaleha Bey, Angel Klyce, Haile Shavers, Aaron Stern, Jimmy Wu

Berkeley Science Network Summer Fellows Luncheon—UC Berkeley

Discussion Facilitator: "Getting started with academics: prelims, classes, & rotations" and "The mentoring connection; The benefit of being mentored and serving as a mentor", Summer 2014-2016

Berkeley Edge Conference—University of California, Berkeley

Graduate Student Panel: Fall 2013-2014

Berkeley Science Network Tutoring Program—University of California, Berkeley
Fall 2012-2016. Tutoring program aimed to increase diversity in the sciences
Courses: Discrete Mathematics and Probability Theory, Introduction to Machine Learning, Programming Systems

Center for Diversity in Engineering Tutoring—University of Virginia
Spring 2008 - Spring 2011. Courses: Differential Equations, Calculus I II and III, Discrete Math, Theory of Computation, Algorithms

Reviewing

Frontiers in Cardiovascular Medicine - May 2022
BMC Genomics - January 2022
Molecular Genetics and Genomics - April 2021
PLoS Computational Biology - Feb 2020
International Conference on Learning Representations - Oct 2019
Human Molecular Genetics - Nov 2016
ISBRA 2015 - Conference Reviewer

Software

WVER—Mendelian Randomization accounting for correlated pleiotropy.
<https://github.com/brielin/WVER/>

bimmer—Phenome-scale causal network discovery using genetic instruments
<https://github.com/brielin/bimmer/>

pcca—Uncovering population structure in gene expression data by combining PCA and CCA
github.com/pachterlab/pcca

taskcode—Predicting construction worker tasks from real time location systems
github.com/baxen/taskcode

popcorn—Transethnic genetic correlation from summary statistics
github.com/brielin/popcorn

jester—Fast local joint testing for GWAS
github.com/brielin/jester

avocado—A Variant Caller, Distibuted
github.com/bigdatagenomics/avocado

pylmm—A fast and lightweight python-based linear mixed-model solver for use in GWAS
<https://github.com/brielin/pylmm>

Skills

Comp bio: ATAC-seq, RNA-seq, eQTL analysis, GWAS methods, phasing/imputation

Statistics: point estimation, hypothesis testing, regression, mixed-models

Machine learning: neural networks, graphical models, classification, clustering, dimensionality reduction

Programming: python (tensorflow, numpy, scipy, pandas, scikit-learn, seaborn), R, C++, bash, SGE