BRIELIN C. BROWN

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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
NHGRI K99/R00 Fellow. 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*, J.A. Morris, T. Lappalainen, D.A. Knowles (2023). Large-scale causal discovery using interventional data sheds light on the regulatory network architecture of blood traits. *bioRxiv* 10.1101/2023.10.13.562293, 13 October 2023. Submitted *Nature Methods*

B.C. Brown*†, C. Wang†, S. Kasela, F. Aguet, D.C. Nachun, K.D. Taylor, R.P. Tracy, P. Durda, Y. Liu, W.C. Johnson, D. Van Den Berg, N. Gupta, S. Gabriel, J.D. Smith, R. Gerzsten, C. Clish, Q. Wong, G. Papanicolau, T.W. Blackwell, J.I. Rotter, S.S. Rich, R.G Barr, K.G. Ardlie, D.A. Knowles, and T. Lappalainen (2023). Multiset correlation and factor analysis enables exploratory analysis of multi-omic data. *Cell Genomics*, 3, 100359, 9 August 2023

S. Kasela, F. Aguet, S. Kim-Hellmuth, **B.C. Brown**, D.C. Nachun, R.P. Tracy, P. Durda, Y. Liu, K.D. Taylor, W.C. Johnson, D. Van Den Berg, S. Gabriel, N. Gupta, J.D. Smith, T.W. Blackwell, J.I. Rotter, K.G. Ardlie, A. Manichaikul, S.S. Rich, R.G. Barr and T Lappalainen (2023) Interaction molecular QTL mapping discovers cellular and environmental modifiers of genetic regulatory effects. *bioRxiv* 10.1101/2023.06.26.546528, 27 June 2023. In revision, *American Journal of Human Genetics*

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* 10.1101/2020.06.18.160176, 22 June 2020

M. Lam, C. Chen, Z. Li, A.R. Martin, J. Bryois, X. Ma, H. Gaspar, M. Ikeda, B. Benyamin, **B.C. Brown**, R. Liu, W. Zhou, L. Guan, Y. Kamatani, S. Kim, M. Kubo, A.A.A.A. Kusumawardhani, C. Liu, H. Ma, S. Periyasamy, A. Takahashi, Z. Xu, H. Yu, F. Zhu,

Schizophrenia Working Group of the Psychiatric Genomics Consortium, Indonesia Schizophrenia Consortium, Genetic REsearch on schizophreniA neTwork-China and the Netherlands (GREAT-CN), W.J. Chen, S. Faraone, S.J. Glatt, L. He, S.E. Hyman, H. Hwu, S.A. McCarroll, B.M. Neale, P. Sklar, D.B. Wildenauer, X. Yu, D. Zhang, B.J. Mowry, J. Lee, P. Holmans, S. Xu, P.F. Sullivan, S. Ripke, M.C. O'Donovan, M.J. Daly, S. Qin, P. Sham, N. Iwata, K.S. Hong, S.G. Schwab, W. Yue, M. Tsuang, J. Liu, X. Ma, R.S. Kahn, Y. Shi and H. Huang (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. Patsopolous 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 ^{3}He Targets. *SPIN PHYSICS: 18th International Spin Physics Symposium. AIP Conference Proceedings*, Volume 1149, pp. 895-898

*BCB is corresponding, †equal contributions

Invited seminars and selected talks

"Multi-set correlation and factor analysis of multi-omic data." Poster talk, *The Annual American Society of Human Genetics Meeting*. October 2022

"Applications and analysis of multi-omic data in multi-population cohorts" Institute for Human Genetics Work in Progress Seminar, *Mount Sinai School of Medicine*. October 2022

"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 ^{3}He Targets." Platform Talk, *18th International Spin Physics Symposium*. September 2008

Selected Funding and Awards

National Human Genome Research Institute K99/R00—2022-2027
"Perturbation-response approaches to determining the regulatory networks underlying human complex traits" K99HG012373

ASHG Reviewers Choice—Aug 2022
Top 10% of abstracts at the ASHG meeting

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 Choicc—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
Prestigious award for the top incoming graduate students across the university

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

Mentoring and service

Diversity, Equity and Inclusion Advisory Group—New York Genome Center
Co-lead of group working to increase opportunities for marginalized scientists and provide DEI training and education to the orginization.

Mentoring—New York Genome Center
Collin Wang - *Undergraduate, Columbia University*. Towards principled integration of multiple single cell genomics datasets with kernel CCA.
Aditya Sriram - *PhD Student, University of Pittsburgh*. Applications of network analysis to genome-wide perturb-seq.

Mentoring—Verily Life Sciences
Abubakar Abid - *PhD Student, Stanford University.* Deep learning models for inference from transcriptional profiles.
Cindy Tian - *PhD Student, New York University* Transcriptomic and epigenomic profiling of immune cells.

Berkeley Science Network—University of California, Berkeley
BSN was a campus-wide program designed to provide enrichment and support to marginalized students to improve diversity in the sciences.
Mentoring: Corey Short, Saaleha Bey, Angel Klyce, Haile Shavers, Aaron Stern, Jimmy Wu
Summer Fellows Luncheon: Discussion facilitator
Berkeley Edge Conference: Graduate student panel participant
Tutoring: Discrete Mathematics and Probability Theory, Introduction to Machine Learning, Programming Systems

Reviewing

Genome Biology - August 2023

Communications Biology - May 2023

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