

Arjun Bhattacharya
Postdoctoral Fellow at UCLA Computational Medicine

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EDUCATION

University of North Carolina

PhD, Biostatistics

Chapel Hill, NC
2015—2020

- Concentration in computational genomics, statistical genetics, and genetic epidemiology with an emphasis in breast cancer genomics

University of North Carolina

BS, Mathematical Decision Sciences; BS, Biology

Chapel Hill, NC
2011—2015

- Mackenzie Family Foundation Innovation Scholarship (full scholarship, 4 years)

RESEARCH AND WORK EXPERIENCE

UCLA Institute for Quantitative and Computational Biosciences

Fellow

Los Angeles, CA
July 2021—present

- Teaching workshops in quantitative methods to experimental researchers and clinicians
- Collaborating and consulting with experimental labs at UCLA for quantitative analyses

Department of Pathology and Laboratory Medicine

Postdoctoral Fellow

Los Angeles, CA
August 2020—present

- Developing methods for integration of genetic association studies and functional genomics
- Studying the biological contributions to cancer and neuropsychiatric disorders
- Advisors: Prof. Bogdan Pasaniuc and Prof. Michael Gandal

Carolina Breast Cancer Study

Research Assistant

Chapel Hill, NC
August 2017—August 2020

- Elucidated the relationship between germline genetics and breast cancer tumor biology to study racial disparities in breast cancer outcomes
- Developed methods for genetic association studies and transcriptomic data from targeted RNA panels
- Advisors: Prof. Michael Love and Prof. Melissa Troester

ELGAN-ECHO Research Study

Research Assistant

Chapel Hill, NC
August 2017—August 2020

- Analyzed placental multi-omic effects on etiology of autism, post-partum depression, and other non-communicable disorders in underserved and underrepresented populations
- Collaborators: Prof. Hudson Santos and Prof. Rebecca Fry

NC TraCS Institute

Research Assistant

Chapel Hill, NC
August 2017—July 2018

- Reviewed incoming grant for biostatistical support and provided statistical consultation for approved projects

Roche Innovation Center

Research Assistant

New York, NY
May 2016—August 2016

- Identified immunogenetic signatures from 'omic profiles to estimate immune infiltration across different cancer tumors in response to cancer drugs
- Internship in Data Science group of Translational Genomics at Roche, supervised by Dr. Francesca Milletti and Dr. Jurriaan Brouwer-Visser

AWARDS, GRANTS, AND HONORS

O'Malley Alumni Award for Publication Excellence in Population Sciences	2021
UCLA Bruin in Genomics Outstanding Mentorship Award	2021
International Society of Psychiatric Genetics Early Career Investigator Program Award	2021-2023
Fellow, UCLA Institute of Quantitative and Computational Biosciences	2021-present
SER Conference Scholarship	2021
Center for Environmental Health and Susceptibility Training Grant	2019—2020
Susan G. Komen Graduate Training Fellowship in Breast Cancer Disparities	2018—2019
UNC-CH Department of Biostatistics Tuition Award	2017—2018
Mackenzie Family Foundation Innovation Scholarship	2011—2015

PUBLICATIONS

Accepted manuscripts (* for equal contribution)

1. **A. Bhattacharya***, J. Hirbo*, D. Zhou, W. Zhou, J. Zheng, M. Kanai, the Global Biobank Meta-analysis Initiative, B. Pasaniuc, E. Gamazon, N. Cox. [Best practices of multi-ancestry, meta-analytic transcriptome-wide association studies: lessons from the Global Biobank Meta-analysis Initiative](#). Accepted in principle, **Cell Genomics**, 2022.
2. R. Johnson, Y. Ding, V. Venkateswaran, **A. Bhattacharya**, A. Chiu, T. Schwarz, M. Freund, L. Zhan, K. Burch, C. Caggiano, B. Hill, N. Rakocz, B. Balliu, J. Sul, N. Zaitlen, V. Arboleda, E. Halperin, S. Sankararaman, M. Butte, UCLA Precision Health Data Discovery Repository Working Group, UCLA Precision Health ATLAS Working Group, C. Lajonchere, D. Geschwind, B. Pasaniuc. [Leveraging genomic diversity for discovery in an EHR-linked biobank: the UCLA ATLAS Community Health Initiative](#). Accepted in principle, **Genome Medicine**, 2022.
3. W. Zhou, M. Kanai, K. Wu, R. Humaira, K. Tsuo, J. Hirbo, Y. Wang, **A. Bhattacharya**, ..., C. Willer, M. Daly, B. Neale for the Global Biobank Meta-analysis Initiative. [Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases](#). Accepted in principle, **Cell Genomics**, 2022. **Lead TWAS analyst for Global Biobank Meta-analysis Initiative**.
4. W. Liu, L. Huang, Q. Sun, **A. Bhattacharya**, X. Tan, K. Kuban, R. Joseph, T. O'Shea, R. Fry, Y. Li, H. Santos. [Innovative computational approaches shed light on genetic mechanisms underlying cognitive impairment among children born extremely preterm](#). **Journal of Neurodevelopmental Disorders**, 2022. Featured in Intellectual and Developmental Disabilities Research Centers Special Issue.
5. **A. Bhattacharya**, A. Freedman, V. Avula, R. Harris, W. Liu, Y. Li, R. Joseph, L. Smeester, H. Hartwell, K. Kuban, T. O'Shea, C. Marsit, R. Fry, and H. Santos. [Genetic control of fetal placental genomics contributes to development of health and disease](#). **Nature Communications**, 2022.
6. A. Patel, M. García-Closas, A. Olshan, C. Perou, M. Troester, M. Love, **A. Bhattacharya**. [Gene-level germline contributions to clinical risk of recurrence scores in Black and White breast cancer patients](#). **Cancer Research**, 2022.
7. G. Jones, K.A. Hoadley, H. Benefield, L. Olsson, A. Hamilton, **A. Bhattacharya**, E. Kirk,
8. H. Tipaldos, J. Fleming, K. Williams, M. Love, H. Nichols, A. Olshan, M. Troester. [Racial differences in breast cancer outcomes by hepatocyte growth factor pathway expression](#). **Breast Cancer Research and Treatment**, 2022.
9. K. Hou, **A. Bhattacharya**, R. Mester, K. Burch, B. Pasaniuc. [On power GWAS in admixed populations](#). **Nature Genetics**, 2021.
10. G. Jones, K. Hoadley, L. Olsson, A. Hamilton, **A. Bhattacharya**, E. Kirk, H. Tipaldos, J. Fleming, M. Love, H. Nichols, A. Olshan, M. Troester. [Hepatocyte Growth Factor pathway expression in breast cancer by race and subtype](#). **Breast Cancer Research**, 2021.
11. **A. Bhattacharya**, Y. Li, M. Love. [MOSTWAS: Multi-Omic Strategies for Transcriptome-Wise Association Studies](#). **PLOS Genetics**, 2021.
12. **A. Bhattacharya**, A. Hamilton, M. Troester, M. Love. [DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing](#). **Nucleic Acids Research**, 2021.
13. H. Santos, H. Adynski, R. Harris, **A. Bhattacharya**, A. Incollingo-Rodriguez, R. Cali, A. Torres Yabar, B. Nephew, C. Murgatroyd. [Biopsychosocial Correlates of Psychological Distress in Latina Mothers](#). **Journal of Affective Disorders**, 2020.
14. H. Santos*, **A. Bhattacharya***, R. Joseph, L. Smeester, K. Kuban, C. Marsit, T. O'Shea, R. Fry. [Evidence for the Placenta-Brain Axis: Multi-Omic Kernel Aggregation Predicts Intellectual and Social Impairment in Children Born Extremely Preterm](#). **Molecular Autism**, 2020.
15. **A. Bhattacharya***, A. Hamilton*, M. Troester, K. Hoadley, M. Love. [An approach for normalization and quality control for NanoString RNA expression data](#). **Briefings in Bioinformatics**, 2020.
16. **A. Bhattacharya**, M. Garca-Closas, A. Olshan, C. Perou, M. Troester, M. Love. [A framework for transcriptome-wide association studies in breast cancer in diverse study populations](#). **Genome Biology**, 2020. **Winner of 2021 O'Malley Alumni Award for Publication Excellence in Population Sciences**.

17. H. Santos, **A. Bhattacharya**, E. Martin, K. Addo, M. Psioda, L. Smeester, R. Joseph, S. Hooper, J. Frazier, K. Kuban, T. O'Shea, R. Fry. [Epigenome-Wide DNA Methylation in Placentas from Preterm Infants: Association with Maternal Socioeconomic Status](#). **Epigenetics**, 2019.
18. H. Santos, B. Nephew, **A. Bhattacharya**, X. Tan, L. Smith, R. Alyamani, E. Martin, K. Perreira, R. Fry, C. Murgatroyd. [Discrimination Exposure and DNA Methylation of Stress-Related Genes in Latina Mothers](#). **Psychoneuroendocrinology**, 2018.

Pre-prints and submitted papers

1. D. Levey, M. Galimberti, J. Deak, F. Wendt, **A. Bhattacharya**, D. Koller, K. Harrington, R. Quaden, E. Johnson, M. Cooke, V. Rajagopal, S. Empke, H. Zhou, Y. Nunez, H. Kranzler, H. Edenberg, A. Agrawal, J. Smoller, D. Demontis, VA Million Veteran Program, J. Gaziano, M. Gandal, R. Polimanti, M. Stein, J. Gelertner. *The genetic architecture of Cannabis Use Disorder yields insight into public health concerns*. In review, **Nature Medicine**. **Lead gene prioritization analyst**.
2. N. Cole, P. Lee, T. Schwarz, P. Zhang, M. Freedman, A. Gusev, S. Lindström, M. Gandal, B. Pasaniuc, **A. Bhattacharya**. [Distal gene regulation mediated by non-coding RNAs contributes to germline risk for breast and prostate cancer](#). Preprint, medRxiv. In review, **Nature Communications**, 2022.
3. M. Gandal*, J. Haney*, ..., **A. Bhattacharya**, ..., B. Pasaniuc, D. Geschwind. [Broad transcriptomic dysregulation across the cerebral cortex in ASD reflects a loss of cortical regional heterogeneity](#). Preprint, bioRxiv. In revision, **Nature**, 2022.
4. R. Johnson, Y. Ding, **A. Bhattacharya**, A. Chiu, C. Lajonchere, D. Geschwind, B. Pasaniuc. [The UCLA ATLAS Community Health Initiative: promoting precision health research in a diverse biobank](#). Preprint, medRxiv. In review, **Cell Genomics**, 2022.
5. H. Zhao, H. Rasheed, T. Nost, Y. Cho, Y. Liu, L. Bhatta, **A. Bhattacharya**, the Global Biobank Meta-analysis Initiative, G. Hemani, G. Davey Smith, B. Brumpton*, W. Zhou*, B. Neale*, T. Gaunt*, J. Zheng*. [Proteome-wide Mendelian randomization in global biobank meta-analysis reveals trans-ancestry drug targets for common diseases](#). Preprint, medRxiv. In review, **Cell Genomics**, 2022.
6. V. Lo Faro, **A. Bhattacharya**, W. Zhou, D. Zhou, Y. Wang, K. Läll, M. Kanai, E. Lopera-Maya, P. Straub, P. Pawar, R. Tao, X. Zhong, S. Namba, the Global Biobank Meta-analysis Initiative, S. Sanna, I.M. Nolte, Y. Okada, N. Ingold, S. MacGregor, H. Sneider, I. Surakka, C. Willer, A.R. Martin, M.A. Brantley Jr, E.R. Gamazon, N.M. Jansonius, K. Joos, N.J. Cox, J. Hirbo. [Genome-wide association meta-analysis identifies novel ancestry-specific primary open-angle glaucoma loci and shared biology with vascular mechanisms and cell proliferation](#). Preprint, medRxiv. In review, **Cell Genomics**, 2022.
7. H. Santos, J. Bangma, **A. Bhattacharya**, V. Zhabotynsky, K. Roell, C. Marsit, J. Rager, L. Smeester, T.M. O'Shea, B. Zou, F. Zou, R. Fry for the ELGAN Investigators. *Sexual Dimorphism in Placental DNA Methylation Predicts Positive Child Health Outcome at Age 10 Years*. In revision, **Epigenetics**, 2021.

Works in preparation

1. **A. Bhattacharya**, M. Kim, C. Wen, D. Vo, J. Hervoso, C. Jops, B. Pasaniuc*, M. Gandal*. *Isoform-level transcriptomic-wide association studies uncover genetic mechanisms underlying neuropsychiatric disorders*. Manuscript ready to submit, 2022.
2. A. Patel, M. García-Closas, A. Olshan, C. Perou, B. Pasaniuc, W. Zheng, the Breast Cancer Association Consortium, M. Troester, M. Love, **A. Bhattacharya**. *Divergent gene-level genetic associations support etiologic heterogeneity of breast cancer molecular subtypes*. In preparation, 2022.
3. A. Patel, M. García-Closas, A. Olshan, C. Perou, W. Zheng, the Breast Cancer Association Consortium, M. Love, M. Troester, **A. Bhattacharya**. *Differences in genetic associations with breast cancer mortality across race and molecular subtype*. In preparation, 2022.
4. A. Patel, M. García-Closas, A. Olshan, C. Perou, M. Troester, M. Love, **A. Bhattacharya**. *Local ancestry-aware analyses show differential germline regulation with breast tumor transcriptomics*. In preparation.
5. K. Hou, Y. Ding, Z. Xu, A. Wu, **A. Bhattacharya**, R. Mester, G. Belbin, J. Cai, D. Conti, M. Forange, C. Gignoux, X. Guo, C. Haiman, R. Kaplan, E. Kenny, M. Kim, C. Kooperberg, L. Lange, A. Manichaikul, K. North, N. Nudelman, U. Peter, L. Rasmussen-Torvik, S. Rich, J. Rotter, H. Wheeler, Y. Zhou, the PAGE Consortium, S. Sankararaman, B. Pasaniuc. *Causal effects on complex traits are similar across segments of different continental ancestries within admixed individuals*. In preparation.
6. V. Venkateswaran, **A. Bhattacharya**, K. Boulier, Y. Ding, R. Johnson, B. Pasaniuc. *Multi-ancestry phenome-wide associations with polygenic risk for tobacco use disorder reveal potential risk factors and sequelae of smoking*. In preparation.

SELECTED AND INVITED TALKS

Isoform-level transcriptome-wide association studies uncover novel biological mechanisms underlying genetic associations with five neuropsychiatric traits

1. **International Genetic Epidemiology Society Annual Meeting, September 2022.** Oral presentation. **Finalist for James V. Neel Award** for Outstanding Oral Presentation by a postdoctoral fellow.
2. **World Congress of Psychiatric Genetics, September 2022.** Oral presentation in Cross-Disorder and Comorbidity Session. Finalist for Outstanding Oral Presentation Award, 2022 Early Career Investigator Program.

Distal mediator-enriched, placental transcriptome-wide analyses of 40 traits suggest genetic mechanisms supporting the Developmental Origins of Health and Disease hypothesis

3. **UCLA QCBio Research Seminar Series, April 2021.** Invited talk.
4. **Society for Epidemiologic Research, June 2021.** Oral presentation in So Much More Than GWAS: How Genetics Can Strengthen Causal Inference session.
5. **Singapore Institute for Clinical Sciences Lecture Series, August 2021.** Invited talk.
6. **World Congress of Psychiatric Genetics, October 2021.** Oral presentation in Genome-wide Approach session. Selected for Early Career Investigator Program.
7. **American Society for Human Genetics Annual Meeting, October 2021.** Platform talk in Mechanisms of Fetal CNS Development session.
8. **US Developmental Origins of Health and Disease Society Annual Meeting, November 2021.** Junior investigator keynote in the Gene, Epigenetics, and Fetal Programming session.

DeCompress: tissue compartment deconvolution for targeted RNA panels using compressed sensing

9. **International Conference on Computational Advances in Bio- and medical Sciences, December 2020.** Invited talk at Computational Advances for Next Generation Sequencing Workshop.

MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies

10. **American Society for Human Genetics Annual Meeting, October 2020.** Platform talk in Rare Variants and Complex Disease session.
11. **Society for Epidemiologic Research, December 2020.** Oral presentation in Genetics in Epidemiology session.
12. **International Conference on Intelligent Systems for Molecular Biology, July 2020.** Oral presentation at VarL-COSI.

A framework for transcriptome-wide association studies in breast cancer in diverse populations.

13. **International Genetic Epidemiology Society Meeting, October 2019.** Talk and highlighted poster presentation. Winner of Best Poster Award.
14. **AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved, September 2019.** Talk and poster presentation.

SERVICE

Referee and Reviewer Experience

- Referee for *Nature Biotechnology*, *Nature Genetics*, *Nature Communications*, *American Journal of Human Genetics*, *PLOS Genetics*, *PLOS Computational Biology*, *Genetics*, *G3*, *British Journal of Cancer*, *npj Breast Cancer*
- Abstract reviewer for the Society for Epidemiologic Research Annual Meetings

Formal Mentorship

- Undergraduate students mentored:
 1. Nolan Cole (Mentored through Bruins-In-Genomics Summer Research Program; Current: Biostatistics PhD student at University at Washington)
- Graduate students mentored:
 1. Achal Patel (Mentored during his PhD in Epidemiology at UNC-Chapel Hill; Current: incoming Postdoctoral Scholar at USC Genetic Epidemiology)

TEACHING EXPERIENCE

UCLA QCB W5, *RNA-seq Analysis*

Fall 2021 to Fall 2022

BIOS 735, *Introduction to Data Science*

Spring 2019

BIOS 550, *Basic Elements of Probability and Statistical Inference*

Spring 2018

BIOS 673, *Probability and Statistics*

Spring 2017

COMPUTING SKILLS

- Advanced: R (preferred), SAS, LaTeX
- Intermediate: Python, C++, Matlab

SOFTWARE

I maintain several R packages, all available on Github:

1. [NanoNormIter](#): A package for iterative quality control and normalization of NanoString nCounter gene expression.
2. [MOSTWAS](#): A package for distal-mediator enriched transcriptome-wide association studies.
3. [DeCompress](#): A package for cell-type deconvolution of RNA expression from targeted panels.
4. [isotwas](#): A package for isoform-level transcriptome-wide association studies.