Arjun Bhattacharya

Postdoctoral Fellow at UCLA Computational Medicine

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Education

- **University of North Carolina** — Chapel Hill, NC
  Ph.D. Biostatistics — *2015 - 2020*
  - Concentration in computational genomics, statistical genetics, and genetic epidemiology with an emphasis in health disparities

- **University of North Carolina** — Chapel Hill, NC
  B.S. Mathematical Decision Sciences, B.S. Biology — *2011 - 2015*
  - Mackenzie Family Foundation Innovation Scholarship (full scholarship, 4 years)

Research and Work Experience

- **UCLA Institute for Quantitative and Computational Biosciences** — Los Angeles, CA
  Fellow — *July 2021 - present*
  - Teaching workshops in quantitative methods to biology researchers
  - Collaborating and consulting with experimental labs at UCLA for quantitative analyses

- **Department of Pathology and Laboratory Medicine** — Los Angeles, CA
  Postdoctoral Fellow — *August 2020 - present*
  - Developing methods for integration of genetic association studies and functional genomics
  - Studying the genetic and genomic contributions to neuropsychiatric disease and cancer etiology, progression, and disparities
  - With Prof. Bogdan Pasaniuc and Prof. Michael Gandal

- **Carolina Breast Cancer Study** — Chapel Hill, NC
  Research Assistant — *August 2017 - August 2020*
  - Elucidating the relationship between germline genetic variation and breast cancer tumor biology to study racial disparities in breast cancer outcomes
  - Developing methods for the deconvolution of bulk tumor RNA
  - With Prof. Michael Love and Prof. Melissa Troester

- **ELGAN-ECHO Research Study** — Chapel Hill, NC
  Research Assistant — *July 2017 - August 2020*
  - Analyzing the genetic and epigenetic effects in autism, post-partum depression, and non-communicable developmental disorders in underserved and underrepresented populations
  - Collaboration with Prof. Hudson Santos and Prof. Rebecca Fry

- **NC TraCS Institute** — Chapel Hill, NC
  Research Assistant — *August 2017 - July 2018*
  - Reviewed incoming grants for biostatistical support and provided statistical consultation for approved projects

- **Roche Innovation Center** — New York, NY
  Graduate Research Intern — *May 2016 - August 2016*
  - Identified immunogenetic signatures from omic profiles from clinical trials to estimate immune infiltration in breast cancer tumors in response to cancer drugs
  - Internship in the Data Science group of Translational Genomics at Roche, under the supervision of Dr. Francesca Milletti and Dr. Jurriaan Brouwer-Visser

- **CBKEN @ UNC** Chapel Hill, NC
  Research Assistant *October 2015 - December 2016*
  - Modeled knowledge exchange networks in community-based health centers to assess best methods in knowledge dissemination and health practices in underinsured and low-income areas
  - Presented findings to the North Carolina Department of Health and Human Services, October 2016
  - With Prof. Timothy Carney

Awards, Grants & Honors

UCLA Bruins in Genomics Outstanding Mentorship Award 2021
International Society of Psychiatric Genetics Early Career Investigator Program Award . . 2021-present
Fellow, UCLA Institute of Quantitative and Computational Biosciences 2021-present
SER Conference Scholarship 2021
Center of Environmental Health and Susceptability 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
NSF Research Experience for Undergraduates, UGA 2014
UNC-CH OUR Summer Undergraduate Research Fellowship ($5,000) 2013

Publications

Accepted manuscripts (* indicates first authorship)

1. 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*. Forthcoming, *Cancer Research*, 2021.
   https://www.medrxiv.org/content/10.1101/2021.03.19.21253983v3.

2. K. Hou, **A. Bhattacharya**, R. Mester, K.S. Burch, B. Pasaniuc. *Powerful GWAS in admixed populations when allelic effects are similar across ancestries*. Forthcoming, *Nature Genetics*, 2021.

3. G. Jones, K. Hoadley, L. Olsson, A. Hamilton, **A. Bhattacharya**, E. Kirk, H. Tipaldos, J. Fleming, M. Love, H. Nichols, A. Olshan, M. Troester. *Hepatoctye Growth Factor pathway expression in breast cancer by race and subtype. Breast Cancer Research*, 2021.

4. **A. Bhattacharya***, Y. Li, M. Love. *MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. PLOS Genetics*, 2021.
   https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1009398

5. **A. Bhattacharya***, Alina M. Hamilton, Melissa A. Troester, and Michael I. Love. *DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing. Nucleic Acids Research*, 2021.
   https://academic.oup.com/nar/advance-article/doi/10.1093/nar/gkab031/6125666?

6. 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.
   https://www.sciencedirect.com/science/article/abs/pii/S0165032720332833.

7. H. Santos*, **A. Bhattacharya***, R. Joseph, L. Smeester, K. Kuban, C. Marsit, T. O'Shea, and 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. https://molecularautism.biomedcentral.com/articles/10.1186/s13229-020-00402-w. Co-first author.

8. **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. https://academic.oup.com/bib/advance-article-abstract/doi/10.1093/bib/bbaa163/5891144. Co-first author.

9. **A. Bhattacharya**, M. García-Closas, A. Olshan, C. Perou, M. Troester, M. Love. *A framework for transcriptome-wide association studies in breast cancer*. *Genome Biology*, 2020. https://genomebiology.biomedcentral.com/articles/10.1186/s13059-020-1942-6.

10. 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 for the ELGAN Investigators. *Epigenome-Wide DNA Methylation in Placentas from Preterm Infants: Association with Maternal Socioeconomic Status*. *Epigenetics*, 2019. https://www.ncbi.nlm.nih.gov/pubmed/31062658.

11. H. Santos, B. Nephew, **A. Bhattacharya**, E. Martin, R. Fry, K. Perrerira, L. Smith, C. Murgatroyd, R. Alyamani, X. Tan. *Discrimination Exposure and DNA Methylation of Stress-Related Genes in Latina Mothers*. *Psychoneuroendocrinology*, 2018. https://www.ncbi.nlm.nih.gov/pubmed/30144780.

Pre-prints and submitted papers

1. R. Johnson, Y. Ding, V. Venkateswaran, **A. Bhattacharya**, 15 co-authors of UCLA Precision Health Data Discovery Repository Working Group and 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*. Preprint, *medRxiv*. https://www.medrxiv.org/content/10.1101/2021.09.22.21263987v1.full.pdf

2. **A. Bhattacharya***, J. Hirvo*, W. Zhou, N. Cox, E. Gamazon, B. Pasaniuc for the Global Biobank Meta-Initiative. *Best practices for multi-tissue, trans-ethnic, meta-analytic transcriptome-wide association studies: lessons from the Global Biobank Meta-Initiative*. Draft ready for submission. Co-first author.

3. 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*. Submitted, *Journal of Neurodevelopmental Disorders*.

4. G. Jones, K.A. Hoadley, H. Benefield, L. Olsson, A. Hamilton, **A. Bhattacharya**, E. Kirk, 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*. In review at *Cancer Epidemiology, Biomarkers, and Prevention*, 2021.

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*. In revision at *Nature Communications*, 2021. https://www.medrxiv.org/content/10.1101/2021.04.12.21255170v1.

6. 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.

7. H. Santos, **A. Bhattacharya**, B. Nephew, C. Murgatroyd, X. Tan. *Oxytocin function and emotional regulation in Latina mothers*. *Submitted*, 2021.

Works in preparation

1. V. Lo Faro*, J. Hirvo*, **A. Bhattacharya**, N. Jansonius, H. Snieder, N. Cox for the Global Biobank Meta-Initiative. *A genome-wide association meta-analysis identifies new primary open-angle glaucoma loci*. *In preparation*.
2. **A. Bhattacharya**, B. Neale, S. Lindström, P. Kraft, B. Pasaniuc. *Pan-cancer multi-tissue distal-eQTL-enriched transcriptome-wide association study reveals common pathways for risk of 17 cancers*. *In preparation*.
3. **A. Bhattacharya***, M. Kim*, C. Wen, B. Pasaniuc, M. Gandal. *Isoform-level transcriptome-wide associations of the fetal brain with neurodevelopment*. *In preparation*.
4. Y. Ding, **A. Bhattacharya***, K. Hou, B. Pasaniuc. *A powerful and flexible procedure to fine-map causal genetic variants in admixed populations*. *In preparation*.

Presentations

- **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. *Distal mediator-enriched, placental transcriptome-wide analyses of 40 traits suggest genetic mechanisms supporting the Developmental Origins of Health and Disease hypothesis*.
  - *Society for Epidemiologic Research, June 2021*. Selected for oral presentation in So Much More Than GWAS: How Genetics Can Strengthen Causal Inference session.
  - *UCLA QCBio Research Seminar Series, April 2021*. Invited talk.
  - *Singapore Institute for Clinical Sciences Lecture Series, August 2021*. Invited talk.
  - *World Congress of Psychiatric Genetics, October 2021*. Selected for oral presentation in Genome-wide Approach session.
  - *American Society for Human Genetics Annual Meeting, October 2021*. Platform talk in Mechanisms of Fetal CNS Development session.
  - *US Developmental Origins of Health and Disease Society Annual Meeting, November 2021*. Junior investigator keynote in the Gene, Epigenetics, and Fetal Programming session.
- **A. Bhattacharya**, A.M. Hamilton, M.A. Troester, M.I. Love. *DeCompress: tissue compartment deconvolution for targeted RNA panels using compressed sensing*.
  - *International Conference on Computational Advances in Bio- and medical Sciences, December 2020*. Invited talk at Computational Advances for Next Generation Sequencing Workshop.
- **A. Bhattacharya**, M.I. Love. *Multi-Omic strategies for transcriptome-wide association studies and applications to the DOHaD hypothesis*.
  - *American Society for Human Genetics Annual Meeting, October 2020*. Selected for platform talk in Rare Variants and Complex Disease session.
- **A. Bhattacharya**, M.I. Love. *MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies*.

  - *Society for Epidemiologic Research, December 2020*. Selected for oral presentation in Genetics in Epidemiology session.
  - *International Conference on Intelligent Systems for Molecular Biology, July 2020*. Selected for virtual oral presentation (VarI-COSI).
  - *International Genetic Epidemiology Society Meeting, July 2020*. Selected for virtual poster presentation (due to COVID).
  - *RNA 2020, May 2020*. Selected for virtual poster presentation (due to COVID).

- **A. Bhattacharya**, M. García-Closas, A. Olshan, C. Perou, M. Troester, M. Love. *A framework for transcriptome-wide association studies in breast cancer*.
  - *NCPF Workshop on Applying Big Data to Address the Social Determinants of Health in Oncology, October 2019*. Poster presentation at the National Academies of Science.
  - *American Society of Human Genetics Meeting, October 2019*. Poster presentation.
  - *International Genetic Epidemiology Society Meeting, October 2019*. Talk and highlighted poster presentation. One of 3 best poster awards.
  - *AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved, September 2019*. Talk and poster presentation.

- **A. Bhattacharya**, H. Santos (presenting). *Placental Multi-Omics Prediction of Autism Spectrum Disorder at Age 10. Annual Meeting of the U.S. Developmental Origins of Health and Disease Society, September 2019*. Oral Presentation.

- **A. Bhattacharya**, M. Troester, M. Love. *Examining racial disparities in recurrence in the Carolina Breast Cancer Study: a transcriptome-wide association approach*. Plenary talk for Susan G. Komen. *American Association of Cancer Research, November 2018*

Service

- Referee and Reviewer Experience
  - Referee for *npj Breast Cancer*, *Communications Biology*, *American Journal of Human Genetics*, *Genetics*, *Frontiers in Genetics*, *G3*, *Human Genomics*
  - Abstract reviewer for the Society of Epidemiologic Research Annual Meetings

- Formal Mentorship
  - Mentor - Bruins-In-Genomics (B.I.G.) Summer Undergraduate Research Program 2021

Teaching Experience

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