

Arjun Bhattacharya

Assistant Professor, MD Anderson Cancer Center

bhattacharya-lab.com

abhattacharya3@mdanderson.org

ACADEMIC APPOINTMENTS**University of Texas MD Anderson Cancer Center***Assistant Professor, Department of Epidemiology
Affiliate, Institute for Data Science in Oncology*Houston, TX
September 2023—**UCLA Institute for Quantitative and Computational Biosciences***Fellow*Los Angeles, CA
July 2021—July 2023**Department of Pathology and Laboratory Medicine, UCLA***Postdoctoral Fellow*Los Angeles, CA
August 2020—August 2023**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
- Advisors: Prof. Michael Love (Biostatistics, Genetics) and Prof. Melissa Troester (Epidemiology)

University of North Carolina*BS, Mathematical Decision Sciences; BS, Biology*Chapel Hill, NC
2011—2015

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

AWARDS, GRANTS, AND HONORS

UCLA QCB Collaboratory Service Award	2023
Semifinalist, Epstein Postdoctoral Award, American Society of Human Genetics (top 10%)	2022
James V. Neel Award, International Genetic Epidemiology Society	2022
Most Outstanding Oral Presentation, World Congress of Psychiatric Genetics	2022
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. C. Wen, M. Margolis, R. Dai, P. Zhang, P. Przytycki, D. Vo, **A. Bhattacharya**, N. Matoba, C. Jiao, M. Kim, E. Tsai, C. Hoh, N. Aygün, R. Walker, C. Chatzinakos, D. Clarke, H. Pratt, PsychENCODE Consortium, M. Peters, M. Gerstein, N. Daskalakis, Z. Weng, A. Jaffe, J. Kleinman, T. Hyde, D. Weinberger, N. Bray, N. Sestan, D. Geschwind, K. Roeder, A. Gusev, B. Pasaniuc, J. Stein, M. Love, K. Pollard, C. Liu*, M Gandal*. [Cross-ancestry, cell-type-informed atlas of gene, isoform, and splicing regulation in the developing human brain](#). Preprint, medRxiv, 2023. Provisionally accepted, **Science**, 2024.
2. C. Yap, D. Voi, M. Heffel, **A. Bhattacharya**, C. Wen, K. Keeper, J. Zheng, Z. Zheng, E. Hannon, D. Vellame, A. Franklin, C. Caggiano, J. Mill, N. Zaitlen, A. Gusev, B. Pasaniuc, C. Lou, M. Gandal. *Genetic and methylomic interrogation of cellular vulnerability to autism, schizophrenia, and Alzheimer's disease in the human brain*. Provisionally accepted, **Science Advances**, 2024.
3. V. Venkateswaran, K. Boulier, Y. Ding, R. Johnson, **A. Bhattacharya***, **B. Pasaniuc***. [Polygenic scores for tobacco use provide insights into systemic health risks in a diverse EHR-linked biobank in Los Angeles](#). Accepted, **Translational Psychiatry**, 2023.

4. **A. Bhattacharya**, D. Vo, C. Jops, M. Kim, C. Wen, J. Hervoso, B. Pasaniuc*, M. Gandal*. [Isoform-level transcriptome-wide association uncovers extensive novel genetic risk mechanisms for neuropsychiatric disorders in the human brain](#). **Nature Genetics**, 2023.
5. 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](#). **Nature Genetics**, 2023.
6. E. Petteer, Y. Ding, K. Hou, **A. Bhattacharya**, A. Gusev, N. Zaitlen, B. Pasaniuc. [Genotype error due to low-coverage sequencing induces uncertainty in polygenic scoring](#). **American Journal of Human Genetics**, 2023.
7. R. Mester, K. Hou, Y. Ding, G. Meeks, K. Burch, **A. Bhattacharya**, B. Henn, B. Pasaniuc. [Impact of cross-ancestry genetic architecture on GWAS in admixed populations](#). **American Journal of Human Genetics**, 2023.
8. X. Wang, Z. Lu, **A. Bhattacharya**, B. Pasaniuc, N. Mancuso. [twas_sim, a python-based tool for downstream comparison and power analysis](#). **Bioinformatics**, 2023.
9. 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](#). **Nature Genetics**, 2023.
10. 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](#). Forthcoming, **Cell Genomics**, 2022.
11. M. Gandal*, J. Haney*, B. Wamsley, C. Yap, S. Parhami, P. Emani, N. Chang, G. Chen, G. Hoftman, D. de Alba, G. Ramaswami, C. Hartl, **A. Bhattacharya**, C. Luo, T. Jin, D. Wang, R. Kawaguchi, D. Quintero, J. Ou, Y. Wu, N. Parikshak, V. Swarup, T. Belgard, M. Gerstein, B. Pasaniuc, D. Geschwind. [Broad transcriptomic dysregulation across the cerebral cortex in ASD reflects a loss of cortical regional heterogeneity](#). **Nature**, 2022.
12. **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](#). **Cell Genomics**, 2022.
13. 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](#). **Cell Genomics**, 2022.
14. M. Kanai, R. Elzur, W. Zhou, **the Global Biobank Meta-analysis Initiative**. [Meta-analysis fine-mapping is often miscalibrated at single-variant resolution](#). **Cell Genomics**, 2022. **Consortium author**.
15. Y. Wang, S. Namba, E. Lopera, S. Kerminen, K. Tsuo, K. Läll, M. Kanai, W. Zhou, K. Wu, M. Favé, L. Bhatta, P. Awadalla, B. Brumpton, P. Deelen, K. Hveem, V. Lo Faro, R. Mägi, Y. Murakami, S. Sanna, J. Smoller, J. Uzunovic, B. Wolford, **the Global Biobank Meta-analysis Initiative**, C. Willer, E. Gamazon, N. Cox, I. Srakka, Y. Okada, A. Martin, J. Hirbo. [Global Biobank analyses provide lessons for developing polygenic risk scores across diverse cohorts](#). **Cell Genomics**, 2022. **Consortium author**.
16. J. Partanen, P. Häppölä, W. Zhou, A. Lehisto, M. Ainola, E. Sutinen, R. Allen, A. Stockwell, O. Leavy, J. Oldham, B. Guillen-Guio, N. Cox, J. Hirbo, D. Schwartz, T. Fingerlin, C. Flores, I. Noth, B. Yaspan, R. Jenkins, L. Wain, S. Ripatti, M. Pirinen, International IPF Genetics Consortium, **the Global Biobank Meta-analysis Initiative**, T. Laitinen, Riitta Kaateenaho, M. Myllärniemi, M. Daly, J. Koskela. [Leveraging global multi-ancestry meta-analysis in the study of idiopathic pulmonary fibrosis genetics](#). **Cell Genomics**, 2022. **Consortium author**.
17. S. Namba, T. Konuma, K. Wu, W. Zhou, **the Global Biobank Meta-analysis Initiative**, Y. Okada. [A practical guideline of genomics-driven drug discovery in the era of global biobank meta-analysis](#). **Cell Genomics**, 2022. **Consortium author**.
18. K. Tsuo, W. Zhou, Y. Wang, M. Kanai, S. Namba, R. Gupta, L. Majara, L. Nkambule, T. Morisaki, Y. Okada, B. Neale, **the Global Biobank Meta-analysis Initiative**, M. Daly, A. Martin. [Multi-ancestry meta-](#)

- [analysis of asthma identifies novel associations and highlights the value of increased power and diversity](#). **Cell Genomics**, 2022. **Consortium author**.
19. 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](#). **Genome Medicine**, 2022.
 20. 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](#). **Cell Genomics**, 2022. **Lead TWAS analyst for Global Biobank Meta-analysis Initiative**.
 21. 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.
 22. **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. [Placental genomics mediates genetic associations with complex health traits and disease](#). **Nature Communications**, 2022.
 23. 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.
 24. G. Jones, K.A. Hoadley, H. Benefield, L. Olsson, A. Hamilton, **A. Bhattacharya**, E. Kirk, H. Tiplados, 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.
 25. K. Hou, **A. Bhattacharya**, R. Mester, K. Burch, B. Pasaniuc. [On power GWAS in admixed populations](#). **Nature Genetics**, 2021.
 26. G. Jones, K. Hoadley, L. Olsson, A. Hamilton, **A. Bhattacharya**, E. Kirk, H. Tiplados, 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.
 27. **A. Bhattacharya**, Y. Li, M. Love. [MOSTWAS: Multi-Omic Strategies for Transcriptome-Wise Association Studies](#). **PLOS Genetics**, 2021.
 28. **A. Bhattacharya**, A. Hamilton, M. Troester, M. Love. [DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing](#). **Nucleic Acids Research**, 2021.
 29. 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.
 30. 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.
 31. **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.
 32. **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.
 33. 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.
 34. 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. 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 revision, Cancer Research Communications, 2023.
2. V. Venkateswaran, E. Petter, K. Boulier, Y. Ding, **A. Bhattacharya***, **B. Pasaniuc***. [Interplay of serum bilirubin and tobacco smoking with lung and head and neck cancers in a diverse, EHR-linked Los Angeles biobank](#). Preprint, medRxiv, 2023.
3. M. Kim, D. Vo, C. Jops, C. Wen, A. Patowary, **A. Bhattacharya**, C. Yap, H. Zhou, M. Gandal. [Multivariate variance components analysis uncovers genetic architecture of brain isoform expression and novel psychiatric disease mechanisms](#). Preprint, medRxiv, 2022. In review, Nature Communications
4. A. Patel, M. Garcia-Closas, W. Zheng, B. Pasaniuc, A. Olshan, H. Nichols, K. North, C. Perou, M. Love, **A. Bhattacharya***, M. Troester*. *Evidence of heterogeneity in germline regulation of tumor expression across breast cancer subtypes in gene-level germline investigation of breast cancer mortality*. Manuscript under BCAC review and available upon request, 2022.
5. A. Patel, M. Garcia-Closas, W. Zheng, B. Pasaniuc, A. Olshan, H. Nichols, K. North, C. Perou, M. Love, M. Troester, **A. Bhattacharya**. *Evidence for divergent germline genetic etiology of breast cancer molecular subtypes via distal-mediator enriched transcriptome-wide association studies*. Manuscript under BCAC review and available upon request, 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 revision, Cell Reports Medicine, 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.

SELECTED AND INVITED TALKS

Considerations for computational molecular precision medicine

1. **UT MD Anderson Cancer Center, Division of Cancer Prevention and Control Grand Rounds, March 2024**. Invited talk.

Integrative computational methods to unlock the wealth of information in bulk RNA-sequencing.

2. **UNC-Chapel Hill BIOS Genomics Seminar, January 2024**. Invited talk.
3. **UTHealth Houston School of Public Health Human Genetics Center Seminar Series, January 2024**. Invited talk.
4. **American Statistical Association STATGEN 2024 Conference, May 2024**. Invited talk.

Gene-level germline associations with breast cancer subtype and survival

5. **Breast Ovarian Consortia Meeting, June 2023**. Invited talk.

Leveraging the breadth and depth of transcriptomics to understand the genetic etiology of complex traits

6. **NYU Center of Human Genetics and Genomics Seminar Series, February 2023**. Invited talk.
7. **MD Anderson Department of Cancer Epidemiology Seminar Series, January 2023**. Invited talk.
8. **Emory School of Medicine Human Genetics Seminar Series, January 2023**. Invited talk.
9. **UNC Computational Medicine Seminar Series, January 2023**. Invited talk.
10. **USC Keck Center of Genetic Epidemiology Seminar Series, December 2022**. Invited talk.
11. **Carnegie Mellon Computational Biology Speaker Series, December 2022**. Invited talk.
12. **Lieber Institute for Brain Development Speaker Series, November 2022**. Invited talk.
13. **Regeneron Genetics Center Speaker Series in Statistical Genetics, October 2022**. Invited talk.

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

14. **The American College of Neuropharmacology Annual Meeting, December 2023.** Invited panel talk at Translating Insights from Postmortem Brain Studies into Knowledge of Disease Mechanisms and Novel Treatment Strategies panel.
15. **University of Pennsylvania Symposium, Genetics and Epigenetics of Behavior, May 2023.** Invited talk.
16. **Vanderbilt University Medical Center Division of Epidemiology, December 2022.** Invited talk.
17. **American Society for Human Genetics Annual Meeting, October 2022.** Platform presentation. **Semifinalist for Epstein Postdoctoral Trainee Award.**
18. **Harvard University Program in Genetic Epidemiology and Statistical Genetics Seminar Series, October 2022.** Invited talk.
19. **World Congress of Psychiatric Genetics, September 2022.** Oral presentation in Cross-Disorder and Comorbidity Session. **Most Outstanding Oral Presentation Award, 2022 Early Career Investigator Program.**
20. **International Genetic Epidemiology Society Annual Meeting, September 2022.** Oral presentation. **James V. Neel Award** for Most Outstanding Oral Presentation by a young investigator.

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

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

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

27. **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

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

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

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

SERVICE

Editorial Experience

- Guest Editor for *PLOS Genetics*

Referee and Reviewer Experience

- Referee for *Nature Genetics*, *Nature Biotechnology*, *Nature Communications*, *American Journal of Human Genetics*, *eLife*, *PLOS Genetics*, *PLOS Computational Biology*, *British Journal of Cancer*, *npj Breast Cancer*, *HGG Advances*
- Abstract reviewer for the Society for Epidemiologic Research Annual Meetings
- Abstract reviewer for the American Society of Human Genetics Annual Meeting 2023
- Reviewer for MD Anderson NCI-funded Summer Research Trainee Program in Cancer Prevention, 2024

Formal Mentorship

- Undergraduate students mentored:
 1. Nolan Cole (Mentored through Bruins-In-Genomics Summer Research Program; Current: Biostatistics PhD student at University at Washington)
 2. Paige Lee (Mentored through Bruins-In-Genomics Summer Research Program; Current: MS student in Data Science at Harvard University)
 3. William Wu (Mentoring while an undergraduate at Rice University)
 4. Erika Vasquez (Mentoring while an undergraduate at Rice University)
- Graduate students mentored:
 1. Achal Patel (Mentored while a PhD candidate in Epidemiology at UNC-Chapel Hill; Current: Data Scientist, Genentech)
 2. Vidhya Venkateswaran (Mentored while a PhD student in Oral Biology at UCLA; Current: Senior Research Fellow and NIH DATA Scholar, NIDCR)
 3. Yung-Han Chang (Mentoring while a M.S. student in Biostatistics)

TEACHING EXPERIENCE

UCLA QCB W5, <i>RNA-seq Analysis</i>	Fall 2021 to Summer 2023
BIOS 735, <i>Introduction to Data Science</i>	Spring 2019
BIOS 550, <i>Basic Elements of Probability and Statistical Inference</i>	Spring 2018
BIOS 673, <i>Probability and Statistics</i>	Spring 2017

COMPUTING SKILLS

- Advanced: R (including software development), SAS, LaTeX, HPC environments
- 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.