Himel Mallick, PhD, FASA

CONTACT INFORMATION

Weill Cornell Medicine
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EDUCATION AND TRAINING

Harvard T. H. Chan School of Public Health (HSPH), Boston, MA, USA
Broad Institute of MIT and Harvard, Cambridge, MA, USA

Postdoctoral Fellowship, Computational Biology and Bioinformatics **2015 – 2019**

- Research Topic: Statistical Methods for Microbial Community Multi-omics
- Advisor: Professor Curtis Huttenhower

University of Alabama at Birmingham (UAB), Birmingham, AL, USA

Ph.D., Biostatistics (GPA: 4.0/4.0) **2009 – 2015**

- Thesis: Some Contributions to Bayesian Regularization Methods
- Advisor: Professor Nengjun Yi
- Activities and Societies: Phi Kappa Phi, Delta Iota Epsilon, Golden Key International Honour Society, Sigma Xi, Delta Omega
- Best Student Paper Award, American Statistical Association
- Best Student Paper Award, International Indian Statistical Association
- Best Paper Award, Science Unbound Foundation

Indian Institute of Technology (IIT), Kanpur, India

M.Sc., Statistics (Class Rank: 4) **2007 – 2009**

University of Calcutta, Kolkata, India

B.Sc., Statistics (First Class Honours) **2004 – 2007**

HONORS AND AWARDS

Ritu Banga Impact in Healthcare Research Award, New York, NY, April 2026

The Kidney Precision Medicine Project (KPMP) Fall Travel Grant (Fall 2025, Fall 2026), Washington, DC

The Stan Altan Nonclinical Biostatistics Paper Award, The ASA Biopharmaceutical Nonclinical Biostatistics Working Group, New Brunswick, NJ, June 2023 and June 2025

UAB National Alumni Society Young Alumni Rising Star Award, University of Alabama at Birmingham, September 2024

UAB School of Public Health Alumni Award for Research, University of Alabama at Birmingham, April 2024

Elected Member of the International Statistical Institute, International Statistical Institute, September 2023

Fellow of the American Statistical Association (FASA), American Statistical Association, August 2023

Early Career Award in Statistics and Data Sciences (ECASDS), International Indian Statistical Association (IISA), Bengaluru, India, December 2022

ISME Early Career Scientist Travel Award, National Centre of Microbial Resource

(NCMR) at National Center of Cell Science (NCCS), Pune, India, November 2018

IMS New Researchers Travel Award, IMS, July 2018

IMS New Researchers Conference Travel Award, IMS, July 2017

Program in Quantitative Genomics Travel Fund, HSPH, December 2016

Technical Writing Workshop Travel Grant, National Institute of Statistical Sciences (NISS), August 2016

AMS-Simons Travel Grant, American Mathematical Society (AMS), May 2016

The DV Gokhale International Grants in Statistics Program Award, Institute of International Education, 2013–2015

Featured in Graduate Student Spotlight, UAB, August 2015

Love of Learning Award, Phi Kappa Phi, May 2015

Grants-in-Aid of Research, Sigma Xi: The Scientific Research Society, December 2014

BBVA Compass Mortgage Financial Services Endowed Award in Graduate Education, UAB National Alumni Society, September 2014

'Creativity is A Decision' Award, UAB Nutrition Obesity Research Center, August 2014

Graduate Student Government Travel Scholarship, UAB, April 2014 and July 2012

Naomi Fineberg Distinguished New Researcher Award, UAB, October 2013

Caroline P. Ireland Research Travel Scholarship, UAB, May 2013

Boyd Harshbarger Travel Award, Southern Research Council on Statistics, June 2013

NSF Travel Grant, International Indian Statistical Association, January 2013

NSF Travel Grant, International Society for Bayesian Analysis, June 2012

Best Talk, UAB Graduate Student Research Days, March 2012

Tuition Scholarship and Travel Award, Summer Institute in Statistical Genetics, University of Washington, Seattle, WA, June 2011

UAB Graduate Fellowship in Biostatistics, 2009–10

Scholarship for Academic Excellence, IIT Kanpur, Kanpur, India, 2008–2009

Excellence Award for Graduating with 'First Class Honours' (B.Sc.), 2007

First Place (Top 0.5%) in the Graduating Class of 2004 in High School, 2004

Professional Experience

Cornell University, New York, NY

Tenure-track Faculty of Biostatistics, Population Health Sciences **April 2023** –
Adjunct Faculty, Department of Statistics and Data Science **June 2023** –
Adjunct Faculty, Division of Gastroenterology and Hepatology **Nov 2025** –

- As a tenure-track faculty member at Cornell, I am building a cross-disciplinary team of statisticians, computational biologists, and AI scientists, bringing together powerful techniques from AI/ML, statistics, systems biology, and omics data science to develop reverse translation solutions for target identification and biomarker discovery.
- I hold a joint appointment in the Division of Gastroenterology and Hepatology as well as the Department of Statistics and Data Science, where my primary goal is to mentor and collaborate with Cornell investigators.

University of Turku, Turku, Finland

Visiting Researcher **Summer 2025; Summer 2026**

- Collaborating with the Turku Data Science Group (Department of Computing) on multimodal AI, multi-omics integration, and uncertainty-aware machine learning methodologies.
- Contributing to joint research initiatives focused on microbiome science, foundation models, and translational data science.

Merck Research Laboratories, Rahway, NJ

Associate Principal Scientist, Biostatistics **January 2022 – April 2023**
Senior Scientist, Biostatistics **March 2019 – January 2022**

- Led multiple data science projects providing end-to-end bioinformatics and biostatistics support across all stages of biomarker discovery and development including assay quality control, drafting SAP, and performing statistical analyses
- Supported Merck's internal efforts in the single-cell and spatial transcriptomics initiatives for translational oncology studies
- Liaised with digital pathology scientists and bioinformaticians on crucial statistical analyses for both exploratory and clinical development purposes
- Employed machine learning classification to the discovery of clinically actionable biomarkers from integrated multi-omics profiles to enable better disease outcome prediction and patient stratification
- Secured funding to initiate and execute multiple academic collaborations to conduct research on various 5-year strategic initiatives specified by the organization
- Successfully hired and co-mentored four Ph.D. summer interns towards the development and implementation of sophisticated statistical and AI/ML approaches for enabling personalized medicine
- Published research across several disease areas (infectious diseases, oncology, and microbiology) that utilized innovative statistical methodology and systems biology techniques spanning a wide range of translational applications

Harvard University and **Broad Institute**, Cambridge, MA, USA

Postdoctoral Researcher, Biostatistics **October 2015 – March 2019**

- Lead developer of MaAsLin 2, a R/Bioconductor package for associating microbial multi-omic data with arbitrarily complex clinical metadata
- Lead developer of MelonnPan, a computational method to predict metabolite profiles from metagenomic sequencing data using concepts from machine learning and ecology, implemented in R
- Contributed to grant writing, manuscript preparation, interdisciplinary collaborations, and teaching and mentoring of graduate and undergraduate students and trainees

Mayo Clinic, Rochester, MN

Intern, Biostatistics **May 2015 – August 2015**

- Developed Bayesian adaptive trial designs for clinical trials utilizing surrogate endpoints in the presence of biomarkers

University of Alabama at Birmingham, Birmingham, AL

Research Assistant, Biostatistics **August 2010 – April 2015**

- Developed Bayesian machine learning methods for high-dimensional feature selection in personalized medicine applications

- Developed and validated risk prediction models for assessing short-term mortality in obese adults
- Conducted high-dimensional predictive modeling of zero-inflated count phenotypes to identify genetic susceptibility markers in Rheumatoid Arthritis patients

Novartis Pharmaceuticals Corporation, East Hanover, NJ

Intern, Biostatistics **May 2014 – August 2014**

- Developed novel Bayesian methods to conduct heterogeneity of treatment effect (HTE) analyses in phase III clinical trials

University of Arkansas for Medical Sciences, Little Rock, AR

Intern, Biostatistics **June 2013 – August 2013**

- Developed methods for detecting maternal-fetal gene-gene interactions associated with obstructive heart defects in newborns from mother-offspring paired genetic data

Indian Statistical Institute, Kolkata, India

Intern, Biostatistics **May 2008 – July 2008**

- Performed research on non-linear statistical modeling of cross-sectional growth curve data by the Preece-Baines growth model

PEER-REVIEWED PUBLICATIONS † INDICATES CO-FIRST AND * INDICATES CORRESPONDING AUTHORSHIP (GOOGLE SCHOLAR CITATIONS = 13480, H-INDEX = 26, I-10 INDEX = 38)

76. **Mallick H*** et al. (2027+). IntegratedLearner: A Unified Multimodal Framework for Modeling Multiomics Data. *Nature Methods* (In Submission).

75. Arora N, ..., **Mallick H*** (2027+). TweedSpot: A Scalable Framework for SVG detection using Self-Adaptive Spatial Tweedie Models. *Nature Communications* (In Submission).

74. Arora N, ..., **Mallick H*** (2027+). Zentangler: A Framework for Causal Multimodal Mediation Analysis of Multi-omics Data. *Nature Methods* (In Submission).

73. Liu Z, ..., **Mallick H*** (2027+). Tweedieverse - the Swiss Army Knife of Omics Differential Analysis. *Bioinformatics* (In Submission).

72. **Mallick H*** et al. (2027+). MimeSys - Simulating Synthetic Multimodal Datasets with Arbitrary Association Structure. *Briefings in Bioinformatics* (In Submission).

71. Gao C, ..., **Mallick H*** (2027+). GPTLasso: Multiview Multistudy Transfer Learning using Pretraining and LASSO. *Biometrics* (In Submission).

70. **Mallick H*** et al. (2027+). Attention is All You Need - Smart Pseudobulk Representation of Single-cell Sequencing Data. *Nature Computational Science* (In Submission).

69. Sarkar S, ..., **Mallick H*** (2027+). Multi-study Meta-analysis of Differential Microbiome Networks. *Bioinformatics* (In Submission).

68. Roy S†, Sarkar S†, ..., **Mallick H*** (2027+). Bayesian Cooperative Learning for Multimodal Integration. *Journal of Computational and Graphical Statistics* (In Submission).

67. Gould AL, . . ., **Mallick H*** (2027+). High-dimensional Array Bayesian Screening Based on Distributions with Structural Zeroes. *Statistics in Medicine* (In Submission).

66. Verma S, . . ., **Mallick H***, Ghosh TS* (2027+). HuMMANet: A Harmonized Cross-Study Resource for Integrative Analysis of Human Gut Microbiome Metabolome Associations. *Nature Microbiology* (In Submission).

65. Dey D, Sen T, **Mallick H** (2027+). FedMHAR: Federated Multimodal Human Activity Recognition using Multi-Agent Reinforcement Learning. *IEEE Journal of Biomedical and Health Informatics* (In Submission).

64. Li H, . . ., **Mallick H**, et al. (2027+). Detecting and Quantifying Mediation of Health Outcomes by Microbial Communities. *Genome Biology* (In Submission).

63. Stoffel E, . . ., **Mallick H**, et al. (2027+). Beyond MELD: Organ Failure Markers Improve Prediction of Transplant-Free Survival in Severe Alcohol-Associated Hepatitis. *Clinical Gastroenterology and Hepatology* (In Submission).

62. Sharaiha R, . . ., **Mallick H**, et al. (2027+). Durable Weight Loss and Metabolic Improvement Ten Years After Endoscopic Sleeve Gastroplasty. *Gut* (In Submission).

61. McNatt C, **Mallick H**, Kushner T (2027+). Inadequate HDV screening among patients with HBV in pregnancy and association of HDV with adverse pregnancy outcomes: results from a multicenter retrospective study. *Gut* (In Submission).

60. Blocker O, . . ., **Mallick H**, et al. (2027+). Barriers Beyond Biology: The Impact of Psychosocial Variables on Listing for Early Liver Transplantation in Severe Alcohol-Associated Hepatitis. *Clinical Gastroenterology and Hepatology* (In Submission).

59. Gaur P, . . ., **Mallick H**, et al. (2026). First-Trimester Liver Biochemistries and Adverse Pregnancy Outcomes in Primary Biliary Cholangitis and Primary Sclerosing Cholangitis. *American Journal of Obstetrics and Gynecology MFM* (In Preparation).

58. Nirmalkar S, . . ., **Mallick H**, . . . (2027+). Microbiota Transplant Therapy (MTT) Improves Gastrointestinal Symptoms in Children with Pitt-Hopkins Syndrome: A Randomized Clinical Trial. *Nature Communications* (In Submission).

57. Johnson KE, . . ., **Mallick H**, et al.(2027+). Early Adverse Events are Less Common in PCABs versus PPIs: A Propensity Score–Matched Multicenter Cohort Study. *American College of Gastroenterology* (In Submission).

56. Janardhan S, . . ., **Mallick H**, et al. (2027+). Impact of EHR-Enabled MASLD Care Pathways to Improve Detection of Advanced Fibrosis in Adults with Type 2 Diabetes. *JHep Reports* (In Submission).

55. Chatterjee S$^{\dagger *}$, Fadikar A†, . . ., **Mallick H*** (2026). Group Heteroscedasticity: A Silent Saboteur of Power and False Discovery in RNA-Seq Differential Expression. *Genetic Epidemiology* (In Submission).

54. Gaur P, . . . , **Mallick H**, et al.(2027+). Associations of Primary Biliary Cholangitis and Primary Sclerosing Cholangitis with Adverse Pregnancy Outcomes: A Propensity Score-Matched Analysis of a U.S. Multicenter Cohort. *American Journal of Obstetrics and Gynecology MFM* (In Press).

53. Roy S†, Sarkar S†, . . . , **Mallick H*** (2027+). Conformalized Multiview Learning. *Statistical Applications in Genetics and Molecular Biology* (In Press).

52. Borman T, . . . , **Mallick H**, et al. (2027+). Orchestrating Microbiome Analysis with Bioconductor. *Nature Communications* (In Press).

51. **Mallick H**†, Nirmalkar K†, Adams J, Brown RK (2026). Multi-omics Integration of Microbiota Transfer Therapy in Children with Autism Spectrum Disorder. *npj Biofilms and Microbiomes* (In Press).

50. Liu Z, . . . , **Mallick H*** (2026). Repurposing without Reinventing the Wheel - Ensemble Models for Differential Analysis. *Bioinformatics* (In Press).

49. Lange M, . . ., **Mallick H**, et al. (2026). HBV-Infected Mothers in the United States Have an Increased Risk of Adverse Pregnancy and Neonatal Outcomes: Systematic Review and Meta-Analysis. *Journal of Viral Hepatitis* (In Press).

48. Gaur P, . . . , **Mallick H**, et al.(2027+). Associations of Primary Biliary Cholangitis and Primary Sclerosing Cholangitis with Adverse Pregnancy Outcomes: A Propensity Score-Matched Analysis of a U.S. Multicenter Cohort. *American Journal of Obstetrics and Gynecology MFM* (In Press).

47. Buckholz A, **Mallick H**, . . . , et al. (2026). Sleep Irregularity is Associated with Reduced Wellbeing in Patients with Cirrhosis. *JHep Reports* (In Press).

46. Kushner T, . . . , **Mallick H**, et al. (2026). Steatotic Liver Disease, Clinical Subtypes, and Adverse Perinatal Outcomes: The Prospective Fatty Liver in Pregnancy Study. *Clinical Gastroenterology and Hepatology* (In Press).

45. Anceschi N, Ferrari F, **Dunson D***, **Mallick H*** (2026). Bayesian Joint Additive Factor Models for Multiview Learning. *Biometrics* 82(3): ujag021. (**Runner-up, ISBA Biostats and Pharma Junior Researcher Award, 2024**).

44. Zhang X, **Mallick H***, Rahnavard A* (2026). Meta-analytic Microbiome Target Discovery for Immune Checkpoint Inhibitor Response in Advanced Melanoma. *Communications Medicine* 6:288.

43. Buckholz A, . . ., **Mallick H***, Brown RS* (2026). Sociodemographic Disparities in Hepatitis C Care Utilization and Testing in the United States. *Communications Medicine* 6:155.

42. Nickols WA, . . ., **Mallick H**, et al. (2026). MaAsLin 3: Refining and Extending Generalized Multivariable Linear Models for Meta-omic Association Discovery. *Nature Methods* 23(3):554–564. [Citations: 247]

41. Iqbal A, **Mallick H**, Ogundimu EO (2025). A Commentary on Chatterjee et al. (2018): A Corrected Framework for Group Sparsity in Zero-Inflated Negative Binomial Models. *Statistics in Medicine* 44(28-30):e70356.

40. Paul E, He J, **Mallick H*** (2025). Accelerated Bayesian Reciprocal LASSO. *Communications in Statistics - Simulation and Computation* 54(4):1175-1191.

39. Paul E, **Mallick H*** (2024). Unified Reciprocal LASSO Estimation via Least Squares Approximation. *Communications in Statistics - Simulation and Computation* 53(9):4352–4362.

38. Paul E, . . ., Baumgartner R*, **Mallick H*** (2024). A Survey of Bayesian Statistical Methods in Biomarker Discovery and Early Clinical Development. *Communications in Statistics: Case Studies, Data Analysis and Applications* 10(1):67–93.

37. **Mallick H**$^{\dagger *}$, Porwal A†, . . ., Paul E* (2024). An Integrated Bayesian Framework for Multi-omics Prediction and Classification. *Statistics in Medicine* 43(5):983–1002. (**Winner, ISBA Biostats and Pharma Junior Researcher Award, 2024**). [Citations: 45]

36. Alhamzawi R, Alhamzawi A, **Mallick H*** (2023). The Reciprocal Elastic Net. *Communications in Statistics: Case Studies, Data Analysis and Applications* 9(4):422-436.

35. Alhamzawi R, **Mallick H*** (2022). Bayesian Reciprocal LASSO Quantile Regression. *Communications in Statistics - Simulation and Computation* 51(11):6479-6494.

34. Ma S, Shungin D, **Mallick H**, Schirmer M, Nguyen L, Kolde R, Franzosa EA, Vlamakis H, Xavier RJ, Huttenhower C (2022). Population Structure Discovery in Meta-Analyzed Microbial Communities and Inflammatory Bowel Disease using MMUPHin. *Genome Biology* 23(1):208. [Citations: 226]

33. **Mallick H**$^{\dagger *}$, Chatterjee S†, . . ., Rahnavard A*, Hicks S* (2022). Differential Expression of Single-cell RNA-seq Data using Tweedie Models. *Statistics in Medicine* 41(18):3492-3510. (**Winner, Stan Altan Nonclinical Biostatistics Paper Award, 2025**). [Citations: 48]

32. **Mallick H** et al. (2021). Multivariable Association Discovery in Population-scale Meta-omics Studies. *PLOS Computational Biology* 17(11):e1009442. (**Winner, Stan Altan Nonclinical Biostatistics Paper Award, 2023**). [Citations: 3,193]

31. Rahnavard G*, . . ., **Mallick H*** (2021). Omics Community Detection using Multiresolution Clustering. *Bioinformatics* 37(20):3588–3594.

30. **Mallick H***, Alhamzawi R, Paul E, Svetnik V (2021). The Reciprocal Bayesian LASSO. *Statistics in Medicine* 40(22):4830-4849. [Citations: 31]

29. Ma S, Ren B, **Mallick H**, et al. (2021). A Statistical Model for Describing and Simulating Realistic Microbial Community Profiles. *PLOS Computational Biology*, 17(9):e1008913. [Citations: 105]

28. Nguyen LH, . . ., **Mallick H**, et al. (2020). Association Between Sulfur-Metabolizing Bacterial Communities in Stool and Risk of Distal Colorectal Cancer in Men. *Gastroenterology* 158(5):1313-1325. [Citations: 209]

27. Quinn RA, ..., **Mallick H**, et al. (2020). Global Chemical Effects of the Microbiome Include New Bile-acid Conjugations. *Nature* 579(7797):123-129. [Citations: 725]

26. **Mallick H**, Franzosa EA, McIver LJ, Banerjee S, Sirota-Madi A, Kostic AK, Clish CB, Vlamakis H, Xavier R, Huttenhower C (2019). Predictive Metabolomic Profiling of Microbial Communities Using Amplicon or Metagenomic Sequences. *Nature Communications* 10(1):3136-3146. [Citations: 342]

25. Chowdhury S[†], Chatterjee S[†], **Mallick H**[†*], Banerjee P, Garai B (2019). Group Regularization for Zero-inflated Poisson Regression Models with An Application to Insurance Ratemaking. *Journal of Applied Statistics* 46(9):1567-1581.

24. Lloyd-Price, ..., **Mallick H**, et al. (2019). Multi-omics of the Gut Microbial Ecosystem in Inflammatory Bowel Diseases. *Nature* 569(7758):655–662. [Citations: 3,828]

23. Franzosa EA, ..., **Mallick H**, et al. (2019). Gut Microbiome Structure and Metabolic Activity in Inflammatory Bowel Disease. *Nature Microbiology* 4(2):293-305. [Citations: 2,451]

22. Banerjee P[†], Garai B[†], **Mallick H**[†*], Chowdhury S, Chatterjee S (2018). A Note on the Adaptive LASSO for Zero-inflated Poisson Regression. *Journal of Probability and Statistics*, 2834183.

21. Chatterjee S[†], Chowdhury S[†], **Mallick H**[†*], Banerjee P, Garai B (2018). Group Regularization for Zero-inflated Negative Binomial Regression Models with An Application to German Healthcare. *Statistics in Medicine* 37(20):3012-3026.

20. Borren NZ, Conway G, Garber JJ, Khalili H, Budree S, **Mallick H**, Yajnik V, Xavier RJ, Ananthakrishnan AN (2018). Difference in Clinical Course, Genetics, and the Microbiome between Familial and Sporadic Inflammatory Bowel Diseases. *Journal of Crohn's and Colitis* 12(5):525-531. [Citations: 37]

19. **Mallick H**[*], Yi N (2018). Bayesian Bridge Regression. *Journal of Applied Statistics* 45(6):988-1008. (**Winner, International Indian Statistical Association Student paper Award, 2014**). [Citations: 47]

18. Abu-Ali GS[†], Mehta RS[†], Lloyd-Price J, **Mallick H**, Branck T, Ivey KL, Drew DA, DuLong C, Rimm E, Izard J, Chan AT, Huttenhower C (2018). Metatranscriptome of Human Fecal Microbial Communities in A Cohort of Adult Men. *Nature Microbiology* 3(3):356-366. [Citations: 286]

17. Mehta RS[†], Abu-Ali GS[†], Drew DA, Lloyd-Price J, Subramanian A, Lochhead P, Joshi AD, Ivey KL, Khalili H, Brown GT, DuLong C, Song M, Nguyen LH, **Mallick H**, Rimm E, Izard J, Huttenhower C, Chan AT (2018). Stability of the Human Fecal Microbiome in A Cohort of Adult Men. *Nature Microbiology* 3(3):347-355. [Citations: 353]

16. **Mallick H**[†], Ma S[†], Vatanen T, Franzosa EA, Morgan X, Huttenhower C (2017). Experimental Design and Quantitative Analysis of Microbial Community Multiomics. *Genome Biology* 18(1):228. [Citations: 220]

15. Schwager EH, **Mallick H**, Ventz S, Huttenhower C (2017). A Bayesian Method for Detecting Pairwise Associations in Compositional Data. *PLOS Computational Biology* 13(11):e1005852. (**Winner, American Statistical Association Section on Bayesian Statistical Science (SBSS) Student paper Award, 2017.**) [Citations: 59]

14. **Mallick H***, Yi N (2017). Bayesian Group Bridge for Bi-level Variable Selection. *Computational Statistics and Data Analysis* 110(6):115-133. (**Winner, American Statistical Association Section on Bayesian Statistical Science (SBSS) Student paper Award, 2015.**)

13. Zhang X, **Mallick H**, Tang Z, Zhang L, Cui X, Benson AK, Yi N (2017). Negative Binomial Mixed Models for Analyzing Microbiome Count Data. *BMC Bioinformatics* 18:4. [Citations: 214]

12. Zhang X†, **Mallick H**†, Yi N (2016). Zero-inflated Negative Binomial Regression for Differential Abundance Testing in Microbiome Studies. *Journal of Bioinformatics and Genomics* 2(2). [Citations: 57]

11. **Mallick H**, Tiwari H (2016). EM Adaptive LASSO - A Multilocus Modeling Strategy for Detecting SNPs Associated With Zero-inflated Count Phenotypes. *Frontiers in Genetics* 7:32. (**Winner, Science Unbound Foundation Best paper Award, 2016.**)

10. Renfro LA, **Mallick H**, Ming-Wen An, Sargent D, Mandrekar S (2016). Clinical Trial Designs Incorporating Predictive Biomarkers. *Cancer Treatment Reviews* 43:74–82. [Citations: 99]

9. **Mallick H***, Yi N (2014). A New Bayesian Lasso. *Statistics and Its Interface* 7(4):571–581. [Citations: 91]

8. Li M, Cleves MA, **Mallick H**, Erickson SW, Tang X, Nick TG, Macleod SL, Hobbs CA (2014). A Genetic Association Study Detects Haplotypes Associated with Obstructive Heart Defects. *Human Genetics* 133(9):1127–1138.

7. Weige CC†, Birtwistle MR†, **Mallick H**, Yi N, Berrong Z, Cloessner E, Duff K, Tidwell J, Clendenning M, Wilkerson B, Farrell C, Bunz F, Ji H, Shtutman M, Creek KE, Banister CE, Buckhaults PJ (2014). Transcriptomes and shRNA Suppressors in a TP53 Allele-specific Model of Early-onset Colon Cancer in African Americans. *Molecular Cancer Research* 12:1029 –1041.

6. Lakoski SG, **Mallick H**, McClure LA, Safford M, Kissela B, Howard G, Cushman M (2014). A Risk Algorithm for Assessing Short-term Mortality for Obese Black and White Men and Women. *Obesity* 22(4):1142–1148.

5. Yi N, Xu S, Lou X, **Mallick H** (2014). Multiple Comparisons in Genetic Association Studies: A Hierarchical Modeling Approach. *Statistical Applications in Genetics and Molecular Biology* 13(1):35-48. (**Winner, Science Unbound Foundation Best paper Award, 2014.**)

4. Kelleher J, Bhat R, Salas AA, Addis D, Mills EC, **Mallick H**, Tripathi A, Pruitt EP, Roane C, McNair T, Owen J, Ambalavanan N, Carlo WA (2013). Oronasopha-

ryngeal Suctioning Versus Wiping the Mouth and Nose at Birth: A Randomized Controlled Equivalency Trial. *The Lancet* 382(9889):326-330. [Citations: 98]

3. **Mallick H**, Li M (2013). Penalized Regression Methods in Genetic Research. *OA Genetics* July 1;1(1):7.

2. **Mallick H**, Yi N (2013). Bayesian Methods for High Dimensional Linear Models. *Journal of Biometrics and Biostatistics* S1:005. [Citations: 70]

1. Kelleher J, **Mallick H**, Soltau TD, Harmon CM, Dimmitt RA (2013). Mortality and Intestinal Failure in Surgical Necrotizing Enterocolitis. *Journal of Pediatric Surgery* 48(3):562–572. [Citations: 32]

Book Chapters

5. Liu Y, **Mallick H** (2026). Multimodal Mediation Analysis. In *Orchestrating Microbiome Analysis with Bioconductor*.

4. **Mallick H** et al. (2025). *The Event of Multiomics in Metagenomics*. In J. Izard & M. Rivera (Eds.), *Metagenomics for Microbiology* (2nd ed., pp. 243–270). Elsevier.

3. Liu Y, **Mallick H** (2025). Multi-omics Prediction and Classification. In *Orchestrating Microbiome Analysis with Bioconductor*.

2. Liu Y, **Mallick H** (2025). Microbe Set Enrichment Analysis (MSEA). In *Orchestrating Microbiome Analysis with Bioconductor*.

1. Liu, Y, **Mallick H** (2025). Meta-analyses. In *Orchestrating Microbiome Analysis with Bioconductor*.

Non-peer-reviewed Publications

9. **Mallick H** et al. (2026). Methods for Imaging and Omics Data Science: Advances, Applications, and Spatiotemporal Innovations [Editorial]. *Frontiers in Genetics*, 17:1922890.

8. **Mallick H** et al. (2022). Methods for Single-Cell and Microbiome Sequencing Data [Editorial]. *Frontiers in Genetics*, 13:920191.

7. **Mallick H**, Bucci V, An L (2020). Statistical and Computational Methods for Microbiome Multi-omics Data [Editorial]. *Frontiers in Genetics*, 11:927.

6. Alhamzawi R, Yu K, **Mallick H** (2019). Quantile Regression and Beyond in Statistical Analysis of the Data [Editorial]. *Journal of Probability and Statistics*, 2635306.

5. **Mallick H** (2019). Predicting the Diverse Metabolic Activities in the Microbiome [Community Blog Article]. *Nature Microbiology Community*, July 2019.

4. **Mallick H** (2018). Nontraditional Collaboration - A Success Story at JSM 2016 [Community Blog Article]. *American Statistical Association*, August 2018.

3. **Mallick H** (2018). And They Lived Happily Ever After - A Microbial Fairy Tale of DNA and RNA [Community Blog Article]. *Nature Microbiology Community*, January 2018.

2. **Mallick H** (2015). Some Contributions to Bayesian Regularization Methods with Applications to Genetics and Clinical Trials [Doctoral Dissertation]. *University of Alabama at Birmingham*, August 2015.

1. **Mallick H**, Yi N (2013). Hierarchical Models for Genetic Association Studies [Editorial]. *Journal of Biometrics and Biostatistics* 4:e124.

Funded Grants (PI)

Mallick H (PI, Joint with David Dunson). Scalable Bayesian Biomarker Discovery using Large-scale Multi-omics Data Integration (MRL Academic Collaboration Grant, Period: Two Years, Total Amount: **$300,000**), 2023 (Funded)

Mallick H (PI, Joint with Jeong Hwan Kook, Radha Krishnan, and John Kang). Exploring H&E Images and Molecular Biomarker Data to Delineate Keytruda Response Mechanism of Action (MRL Summer Internship Grant, Period: Three Months), 2022 (Funded)

Mallick H (PI, Joint with Erina Paul and Vladimir Svetnik). Statistical Methods for Multi-omics Data Integration (MRL Summer Internship Grant, Period: Three Months), 2021 (Funded)

Mallick H (PI, Joint with Vladimir Svetnik). Scalable Bayesian Machine Learning for Multi-omics (MRL Summer Internship Grant, Period: Three Months), 2020 (Funded)

Mallick H (PI, Mentor: Nengjun Yi). Advances and Applications in Bayesian Regularization Methods (NSF Doctoral Dissertation Improvement Grant, Period: One Year, Total Amount: **$12,495**), 2015 (Funded, Withdrawn)

Mallick H (PI, Mentor: Nengjun Yi). Effectively Selecting A Target Population for A Future Clinical Trial (Grants–in–Aid of Research by Sigma Xi, Period: One Year, Total Amount: **$400**), 2014 (Funded)

Keynote Presentations

NIELIT Bio-AI Conclave 2026, Gauhati University, Guwahati, India, Dec 2026: From Microbes to Medicine: Foundation Models for Microbial Communities

Bioinformatics Day, Finnish Society for Bioinformatics, Espoo, Finland, May 2026: Foundation Models for Microbial Community Multiomics

Nebraska Microbiome Research Group Fall 2025 Mini Summit, University of Nebraska Medical Center, Omaha, NE, Dec 2025: Multimodal AI for Microbiome Multiomics

2023 International Conference on Technology, Applied Mathematics, and Statistics, University of Al-Qadisiyyah, Al Diwaniyah, Iraq (Virtual), March 2023: Integrated Machine Learning for Multi-omics Prediction and Classification

2021 BVCN Conference (Holistic Bioinformatic Approaches used in Microbiome Research), Bioinformatics Virtual Coordination Network (BVCN), June 2021: Tweedieverse: A Single Home for Microbiome Multi-omics Differential Analysis

2020 International Virtual Conference on Statistics, University of Al-Qadisiyyah, Al Diwaniyah, Iraq, May 2020: The Reciprocal Bayesian LASSO

Invited Talks

Indian Statistical Institute (Statistical Quality Control and Operations Research), Kolkata, India, Jan 2027: Foundation Models for Microbial Communities

Indian Institute of Science (Department of Computational and Data Sciences), Bengaluru, India, Jan 2027: Foundation Models for Microbial Communities

Biostatistics Research Seminar, Virginia Commonwealth University, Richmond, VA, Oct 2026: Bayesian Multimodal AI for Scalable Biomedical Discovery

National Institute of Research and Innovation, Riga, Latvia, Aug 2026: Multimodal AI for Scalable Biomedical Discovery

University of Helsinki, Helsinki, Finland, Aug 2026: Foundation Models for Microbial Community Metabolomics

Bioconductor Africa Seminar Series (Virtual), Aug 2026: Multi-omics data integration with Bioconductor (Invited Tutorial)

Research Spotlight Speaker at the WCM Biostatistics Internship Program, Weill Cornell Medicine, New York, NY, July 2026: Meta-Analytic Microbiome Target Discovery for Immune Checkpoint Inhibitor Response in Advanced Melanoma (Invited Guest Lecture)

Human-Centric Artificial Intelligence for Sustainable Future (HAIF) Program at the University of Turku, Turku, Finland, June 2026: Causal Reasoning for Responsible AI (Invited Guest Lecture)

NCI Virtual Workshop "Emerging Technologies in Cancer Epidemiology", June 2026: Scalable Multimodal AI for Cancer Microbiome Epidemiology

WCM Meyer Cancer Center's Cancer Genetics and Control Research Program Meeting, New York, NY, Jan 2026: Meta-analytic Microbiome Target Discovery for Immune Checkpoint Inhibitor Response in Advanced Melanoma

Biodesign Center for Health Through Microbiomes, Arizona State University, Phoenix, AZ (Virtual), July 2025: Orchestrating Microbiome Multi-omics Integration and Analysis

Turku Data Science group, University of Turku, Turku, Finland, July 2025: Scalable, Uncertainty-aware, Interpretable Multimodal AI

Bayesian BioPharm Meeting, Los Angeles, CA (Virtual), June 2025: An Integrated Bayesian Framework for Multi-omics Prediction and Classification

International Indian Statistical Association Conference, Lincoln, NE, June 2025: Bayesian Joint Additive Factor Models for Multiview Learning

Institute for Mathematical and Statistical Innovation (IMSI) Workshop 'Statistics Meets Tensors - Methodology, Theory, and Applications', Chicago, IL, May 2025: Bayesian Joint Additive Factor Models for Multiview Learning

Eastern North American Region (ENAR) Meeting of the International Biometric Society, New Orleans, LA, March 2025: Metabolite Prediction in the Human Microbiome – A Transfer Learning Approach

Indraprastha Institute of Information Technology, Delhi, India, February 2025: Scalable, Uncertainty-aware, Interpretable Machine Learning for Multimodal AI Agents

Indian Statistical Institute (Center for Artificial Intelligence and Machine Learning), Kolkata, India, February 2025: Scalable, Uncertainty-aware, Interpretable Machine Learning for Multimodal AI Agents

International Indian Statistical Association Conference, Kochi, Kerala, India, December 2024: Repurposing without Reinventing the Wheel - Ensemble Models for Differential Analysis

Department of Quantitative Health Sciences, University of Hawaii John A. Burns School of Medicine (Virtual), September 2024: Scalable Uncertainty Quantification for Multimodal Integration

ASA Connecticut Chapter Mini Conference, Ridgefield, CT, April 2024: Multimodal Integration in the Age of Million Cells and Billion Parameters

Eastern North American Region (ENAR) Meeting of the International Biometric Society, Washington, DC, March 2024: Bayesian Cooperative Learning for Multi-omics Integration

Indian Statistical Institute (Applied Statistics Unit), Kolkata, India, January 2024: Multimodal Integration in the Age of Million Cells and Billion Parameters

Ahmedabad University (School of Arts and Sciences), Ahmedabad, India, January 2024: Multimodal Integration in the Age of Million Cells and Billion Parameters

Indian Institute of Technology Kanpur (Department of Mathematics and Statistics), Kanpur, India, January 2024: Multimodal Integration in the Age of Million Cells and Billion Parameters

Joint Statistical Meetings (Topic-contributed Session), Toronto, ON, August 2023: Methods for Multi-omics Integration

Nonclinical Biostatistics Conference, New Brunswick, NJ, June 2023: Bayesian Cooperative Learning for Multi-omics Data Integration

Joint Statistical Meetings (Invited Session), Washington, DC, August 2022: Biomarker Discovery in Spatial Transcriptomics and Digital Pathology

Cornell University, New York, NY, April 2022: Methods for Multi-omics Data Science and Integration

Arizona State University, Phoenix, AZ, March 2022: Methods for Multi-omics Data Science and Integration

International Indian Statistical Association Conference, Chicago, IL (Virtual), May 2021: Differential Expression of Single-cell RNA-seq Data using Tweedie Models

National Institutes of Health, Bethesda, MD (Virtual), March 2021: Statistical Methods and Software for Multi-omics Data Science with A View Towards Public Health and Precision Medicine

The Ohio State University, Columbus, OH (Virtual), March 2021: A One-Size-Fits-All Statistical Framework for Differential Analysis of Multi-omics Data

Indian Institute of Science, Bengaluru, India (Virtual), July 2020: Bayes Regularization and Microbiome Multi-omics: A Two-tailed Narrative

University of British Columbia, Vancouver, Canada (Virtual), May 2020: Bayes Regularization and Microbiome Multi-omics: A Two-tailed Narrative

National Cancer Institute, Bethesda, MD (Virtual), April 2020: Bayes Regularization and Microbiome Multi-omics: A Two-tailed Narrative

Medical College of Wisconsin, Milwaukee, WI, February 2020: Bayes Regularization and Microbiome Multi-omics: A Two-tailed Narrative

Emory University, Atlanta, GA, February 2020: Bayes Regularization and Microbiome Multi-omics: A Two-tailed Narrative

Joint Statistical Meetings (Topic-contributed Session), Denver, CO, July 2019: Multivariable Association in Population-scale Meta'omic Surveys

New England Statistics Symposium (NESS), Hartford, CT, May 2019: Metabolite Prediction in the Human Microbiome

University of Florida, Gainesville, FL, May 2019: Statistical Methods for Microbiome Multi-omics

MRL Exploratory Science Center (ESC) Workshop, Boston, MA, April 2019: Metabolite Prediction in the Human Microbiome

MD Anderson Cancer Center, Houston, TX, Nov 2018: Multi-omics Population Studies of the Human Microbiome in Health and Disease

Pfizer Innovation Research Laboratory, Cambridge, MA, Oct 2018: Statistical and Computational Methods for Novel Biomarker Discovery in the Human Microbiome

Merck Research Laboratories, Rahway, NJ, August 2018: Multi-omics Population Studies of the Human Microbiome in Health and Disease

Lilly Research Laboratories, Indianapolis, IN, August 2018: Multi-omics Population Studies of the Human Microbiome in Health and Disease

University of Massachusetts, Amherst, MA, May 2018: Microbiome Epidemiology and Public Health - Some Statistical and Computational Considerations

Wake Forest University School of Medicine, Winston-Salem, NC, March 2018: Multi'omic Epidemiological Approaches for the Human Microbiome in Health and Disease

Stanford University School of Medicine, Stanford, CA, March 2018: The Human Microbiome and Public Health

Food and Drug Administration (FDA), CDER, Division of Biometrics, Silver Spring, MD, October 2017: Statistical Methods for Novel Biomarker Discovery in the Human Microbiome

Novartis Pharmaceuticals Corporation, East Hanover, NJ, August 2017: Translating

the Microbiome into Medicine - Some Statistical and Computational Considerations

Joint Statistical Meetings (Topic-contributed Session), Baltimore, MD, August 2017: Metabolite Prediction in the Human Microbiome

Vedanta Biosciences, Cambridge, MA, April 2017: Computational Screens for Novel Microbial Biomarker Discovery in IBD

Joint Statistical Meetings (Topic-contributed Session), Seattle, WA, August 2015: Bayesian Group Bridge for Bi-level Variable Selection

Harvard T. H. Chan School of Public Health (Huttenhower Lab, Department of Biostatistics), Boston, MA, July 2015: Bayesian Penalized Regression - Advances and Applications

Novartis Pharmaceuticals Corporation, East Hanover, NJ, August 2014: On Bayesian Penalized Regression and Its Application to Subgroup Selection in Clinical Trials

Indian Statistical Institute (Applied Statistics Unit), Kolkata, India, January 2013: Some Recent Developments on Bayesian Regularization Methods

Indian Institute of Technology Kanpur (Department of Mathematics and Statistics), Kanpur, India, February 2013: Bayesian Regularization Methods - A Journey

Contributed Talks

MRL Machine Learning Working Group, Rahway, NJ, March 2023: Bayesian Cooperative Learning for Multi-omics Data Integration

MRL Single-cell Working Group, Rahway, NJ, March 2023: Cell type-specific Differential Expression of Spatial Transcriptomics Data using Tweedieverse

MRL Single-cell Working Group, Rahway, NJ, December 2022: TME-aware Differential Expression of Microsatellite Instability in Colorectal Cancer (CRC) Spatial Transcriptomics

Merck Biometrics Research Fall Workshop, Rahway, NJ, November 2022: Meta-analytic Target Discovery for Immune Checkpoint Inhibitor Response in Advanced Melanoma

MRL Branchburg/Princeton Seminar, Princeton, NJ, October 2022: Meta-analytic Target Discovery for Immune Checkpoint Inhibitor Response in Advanced Melanoma

Merck Data Science Symposium, Rahway, NJ, August 2022: Orchestrating Single-cell Data Science with Tweedieverse

Merck Digital Pathology Working Group, Rahway, NJ, July 2022: Biomarker Discovery in Spatial Transcriptomics and Digital Pathology

Merck Image Analytics Working Group, Rahway, NJ, June 2022: Biomarker Discovery in Spatial Transcriptomics and Digital Pathology

Merck Biometrics Research Fall Workshop, Rahway, NJ, May 2022: IntegratedLearner for Patient-level Prediction from Non-patient-level Imaging and Omics Data

MRL Branchburg/Princeton Seminar, Princeton, NJ, May 2022: An Integrated Bayesian Framework for Multi-omics Prediction and Classification

MRL Stat Study Group Series, Rahway, NJ, March 2022: Tweedieverse: A Single Home

for Multi-omics Differential Analysis

SDSU Data Science Symposium, Brookings, SD, February 2022: Tweedie Mixed Models for Spatial Transcriptomics and Digital Pathology

Merck Biometrics Research Fall Workshop, Rahway, NJ, December 2021: Spatial Tweedie Mixed Models for Spatially Resolved Transcriptomics

Merck Data Science Symposium, Rahway, NJ, September 2021: An Integrated Bayesian Framework for Multi-omics Prediction and Classification

MRL Biometrics Research Spring Workshop, Rahway, NJ, May 2021: IntegratedLearner: A Framework for Multi-omics Prediction and Classification

MRL Biometrics Research Fall Workshop, Rahway, NJ, December 2020: Tweedieverse - A Versatile 'One Size Fits All' Approach for Analyzing Multi-omics Data

MRL Single-cell Working Group, Rahway, NJ, November 2020: Flexible and Adaptive Differential Expression Analysis of Single-cell RNA-seq Data

MRL Microbiome Working Group, Rahway, NJ, October 2020: Towards A Gold Standard for Analyzing Microbiome Multi-omics Data

Joint Statistical Meetings (JSM), Philadelphia, PA, August 2020: The Reciprocal Bayesian LASSO

MRL Biometrics Research Spring Workshop, Rahway, NJ, May 2020: Tweedieverse + BayesRecipe: A Two-tailed Narrative

MRL Stat Study Group Series, Rahway, NJ, February 2020: Reciprocal Regularization - Promises and Implications for Merck Applications

MRL Biometrics Research Fall Workshop, Rahway, NJ, December 2019: A Unified Modeling Framework for Multi-omics Data

MRL Machine Learning Working Group, Rahway, NJ, September 2019: Non-identical Twins - Two Tales of Feature Selection

MRL Microbiome Working Group, Rahway, NJ, August 2019: MGXSimulator - Simulating Synthetic Microbiome Datasets with Arbitrary Association Structure

Nonclinical Biostatistics Conference, Rutgers University, New Brunswick, NJ, June 2019: Multivariable Association in Population-scale Meta'omic Surveys

MRL Biometrics Research Spring Workshop, Rahway, NJ, May 2019: Statistical Methods for Microbiome Multi-omics

MRL Branchburg/Princeton Seminar, Princeton, NJ, April 2019: Metabolite Prediction in the Human Microbiome

International Conference on Microbiome Research (ICMR), Pune, India, November 2018: Multivariable Association in Population-scale Meta'omic Surveys

HSPH PDA Interdepartmental Research Symposium, Boston, MA, September 2018: Multivariable Association in Population-scale Meta'omic Surveys

Intelligent Systems for Molecular Biology (ISMB), Chicago, IL, July 2018: Multivariable Association in Population-scale Meta'omic Surveys

Genomics Get Together, Dana-Farber Cancer Institute, Boston, MA, April 2018: Multivariable Association in Population-scale Meta'omic Surveys

STARR CRC Microbiome Meeting, Harvard T. H. Chan School of Public Health, Boston, MA, October 2017: Overview of Statistical Methods for Microbiome Epidemiology

IMS New Researchers Conference (NRC), Baltimore, MD, July 2017: Zero-inflated Models for Genetic Association Studies (Flash Talk)

Computational Systems for Integrative Genomics (CSIG), Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ, June 2017: Metabolite Prediction in the Human Microbiome

Eastern North American Region (ENAR) Meeting of the International Biometric Society, Washington, DC, March 2017: Predictive Metabolomic Profiling of Microbial Communities Using Shotgun Metagenomic Sequences

Genomics Get Together, Dana-Farber Cancer Institute, Boston, MA, September 2016: MelonnPan - A Model-based Genomically Informed High-dimensional Predictor of Microbial Community Metabolic Profiles

Joint Statistical Meetings (JSM), Chicago, IL, August 2016: A Genomically Informed High-dimensional Predictor for Microbial Community Metabolic Profiles

Public Defense of Dissertation, Department of Biostatistics, UAB, Birmingham, AL, May 2015: Some Contributions to Bayesian Regularization Methods with Applications to Genetics and Clinical Trials

Integrated Information Sciences Business Unit, Novartis Pharmaceuticals Corporation, East Hanover, NJ, August 2014: Subgroup Selection by Penalized Regression - A Systematic Comparison of Bayesian and Frequentist Approaches

Joint Statistical Meetings (JSM), Boston, MA, August 2014: Bayesian Bridge Regression for Genetic Association Studies

International Indian Statistical Association (IISA) Conference, Riverside, CA, July 2014: Bayesian Bridge Regression

Naomi Fineberg Distinguished New Researcher Seminar, UAB, Birmingham, AL, Dec 2013: Bayesian Penalized Regression via Scale Mixture of Uniform Distributions

Biostatistics Journal Club Meeting, UAB, Birmingham, AL, Oct 2013: On Bayesian P-values – Does It Make Sense?

PB&J Research Meeting, Division of Biostatistics, Department of Pediatrics, University of Arkansas for Medical Sciences, Little Rock, AR, August 2013: On Bayesian Penalized Regression

International Indian Statistical Association (IISA) Conference, Chennai, India, January 2013: The Bayesian Adaptive Bridge

Biostatistics Journal Club Meeting, UAB, Birmingham, AL, Feb 2011: On Adaptive

Linear Regression - A Compromise Between OLS and LAD

Poster Presentations

The Liver Meeting (AASLD), Denver, CO, November 2026: Metabolomic and Lipidomic Signatures of Steatotic Liver Disease in Pregnancy from the Prospective Fatty Liver in Pregnancy Cohort

The Kidney Precision Medicine Project (KPMP) Fall Meeting, Bethesda, MD, September 2026: Attention is All You Need - Smart Pseudobulk Representation of Single-cell Sequencing Data

The Kidney Precision Medicine Project (KPMP) Fall Meeting, Washington, DC, September 2025: Attention is All You Need - Smart Pseudobulk Representation of Single-cell Sequencing Data

Celebration of Statistics and Data Science, Ithaca, NY, September 2025: Bayesian Cooperative Learning for Multimodal Integration

International Conference on Microbiome Research (ICMR), Pune, India, November 2018: Multivariable Association in Population-scale Meta'omic Surveys

Computational Systems for Integrative Genomics (CSIG), Cambridge, MA, July 2018: Multivariable Association in Population-scale Meta'omic Surveys

Intelligent Systems for Molecular Biology (ISMB), Chicago, IL, July 2018: Multivariable Association in Population-scale Meta'omic Surveys

IMS New Researchers Conference (NRC), Baltimore, MD, July 2017: Zero-inflated Models for Genetic Association Studies

Southern Regional Council on Statistics (SRCOS) Summer Research Conference, Burns, TN, June 2013: A New Bayesian Lasso

UAB Public Health Research Day, Birmingham, AL, April 2013: A Risk Algorithm for Assessing Short-term Mortality Among Obese Black and White Men and Women: The REGARDS Study

Joint Statistical Meetings (JSM), San Diego, CA, July 2012: A New Bayesian Lasso

World Meeting of the International Society for Bayesian Analysis (ISBA), Kyoto, Japan, June 2012: A New Bayesian Lasso

Selected Short Courses, Workshops, and Symposiums

Leadership in Academic Medicine Program (LAMP) Program, Cornell University, New York, NY, September 2024 - August 2025

An Introduction to the Statistical Foundations of Transfer Learning, NESS 2024 (Virtual)

Tutorial on Deep Learning and Generative AI, NESS 2024 (Virtual)

Targeted Learning in the tlverse: Techniques and Tools for Causal Machine Learning, ENAR 2024, Baltimore, MD, March 2024

Faculty Advancement and Research Mentorship (FARM) Program, Cornell University, New York, NY, October 2023 - September 2024

From R Markdown to Quarto, Vanderbilt University, Nashville, TN, October 2023

Preparing to Teach Statistics and Data Science workshop, JSM 2023, Toronto, ON, Canada, August 2023

Julia for Data Science and Statistical Computing, JSM 2022, Washington, DC, August 2022

Diverse Leader Program, Merck Research Laboratories (Virtual), May 2021 - October 2021

Bayesian Regression Trees, Nonclinical Biostatistics Conference (Virtual), June 2021

Stan and Rstanarm for Bayesian Analysis, Nonclinical Biostatistics Conference (Virtual), June 2021

Spatial Statistical Learning, International Statistical Institute (Virtual), June 2021

ENAR Fostering Diversity in Biostatistics Workshop, International Biometric Society, Baltimore MD, March 2021

Causal Mediation Analysis, Columbia University, New York, NY, August 2020

Bootstrap Learning Python With R, JSM 2019, Denver, CO, July 2019

An R Shiny Tutorial with Nonclinical Applications, Nonclinical Biostatistics Conference, Rutgers, NJ, June 2019

ENAR Workshop for Junior Biostatisticians in Health Research, International Biometric Society, Philadelphia, PA, March 2019

Symposium on Careers and Collaboration in Science (B-SoCCS, organized by Boston Postdoctoral Association (BPDA)), Broad Institute of MIT and Harvard, Cambridge, MA, June 2017

eLife Peer Review Workshop, Harvard T. H. Chan School of Public Health, Boston, MA, June 2017

Workshop on Challenges in Microbiome Data Analysis (organized by Simons Center for Data Analysis, Simons Foundation and Center for Microbiome Informatics and Therapeutics, MIT), Cambridge, MA, Feb 2017

Technical Writing Workshop (JSM 2016), National Institute of Statistical Sciences, Chicago, IL, August 2016

Computational Systems for Integrative Genomics (CSIG), Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, April 2016

MCMC in Genetics + Introduction to QTL Mapping, Summer Institute in Statistical Genetics (SISG), University of Washington, Seattle, WA, Summer 2011

Introduction to C++ and Web Programming, Association for Computing Activities Summer School, IIT Kanpur, India, Summer 2009

Teaching Experience

- Course Director and Instructor for Modern Methods for Causal Inference (Elective

course for MS/PhD students at WCM):

  - Fall 2024 – Present
    - A full-semester course on the fundamentals of causal inference.

- Co-Instructor for Big Data in Medicine (Elective course for MS/PhD students at WCM):
  - Spring 2024 – Present
    - Instructor of Module 3 ('Omics Data Science')
    - Prepared and delivered homework, labs, lecture materials for five three-hour teaching sessions and one final exam

- Short Course Instructor for Omics Data Science:
  - June 2026, EuroBioC Conference, Turku, Finland (Joint with Leo Lahti, Thomaz Bastiaanssen, Tuomas Borman, Anna Kaisanlahti and Giulio Benedetti)
  - April 2026, Physalia Courses (Metatranscriptomics), Virtual
  - March 2025, ENAR Spring Meeting, New Orleans, LA (Joint with Ali Rahnavard)
  - December 2024, IISA Conference, Kochi, Kerala, India
  - August 2023, Joint Statistical Meetings, Toronto, ON, Canada (Joint with Ali Rahnavard)
  - February 2022, SDSU Data Science Symposium, Brookings, SD (Joint with Ali Rahnavard)
  - September 2021, ICSA Conference, Virtual (Joint with Ali Rahnavard)
  - March 2021, George Washington University, Virtual (Joint with Ali Rahnavard)
    - Delivered a series of lectures on 'Omics Data Science'
    - Assisted course participants on hands-on data analyses

- Short Course Instructor for Multimodal AI and Multimodal Causal Inference:
  - March 2027, ENAR Spring Meeting, Boston, MA
  - December 2026, Physalia Courses (Bayesian Statistics), Virtual
  - November 2026, Physalia Courses (Causal Inference), Virtual
  - July 2026, ISMB Conference, Virtual (Joint with Saptarshi Roy and Sreya Sarkar)
  - March 2026, Physalia Courses (Multimodal AI for Systems Biology), Virtual (Joint with Saptarshi Roy, Sreya Sarkar and Aditya Shankar Pal)
  - June 2025, IISA Conference, Lincoln, NE
    - Delivered a series of lectures on 'Multimodal AI and Multimodal Causal inference'
    - Assisted course participants on hands-on data analyses

- Teaching Assistant for Introduction to Clinical Statistics, Fall 2019, Biostatistics and Research Decision Sciences (BARDS) Department, Late Development Statistics (LDS), Merck, Rahway, NJ
  - Responsible for leading workshops and assisting course participants in solving assignments and preparing final presentation

- Instructor for Introduction to Biostatistics, Summer Program in Epidemiology, Summer 2018, Department of Epidemiology, Harvard T. H. Chan School of Public Health, Boston, MA
  - Prepared and delivered eleven lectures and graded four homework assignments and one final exam for twenty undergraduate students with very heterogeneous prior experience

- Guest Lecturer for Genomic Data Manipulation (BST 281), Spring 2018, Department of Biostatistics, Harvard T. H. Chan School of Public Health, Boston, MA
  - Delivered two lectures on *Python Modules* and *Command Line Utilities*

- Guest Lecturer for Introduction to Data Structures and Algorithms (BST 234), Spring 2018, Department of Biostatistics, Harvard T. H. Chan School of Public Health, Boston, MA
  - Delivered two lectures on *Concepts of Algorithms, Complexity, and Sorting Algorithms*

- Teaching Assistant for Introduction to SAS Software (EPI 623), Fall 2011, Department of Epidemiology, School of Public Health, University of Alabama at Birmingham, Birmingham, AL
  - Responsible for assisting students in writing codes and grading assignments and exams

Synergistic Activities

- Editorial Board Membership
  - IEEE Journal of Biomedical and Health Informatics, Associate Editor (2026 – Present; handled 20+ manuscripts)
  - Sankhya B (2025 – Present)
  - Statistical Applications in Genetics and Molecular Biology, Associate Editor (2025 – Present)
  - Frontiers in Genetics (2016 – Present)
  - Frontiers in Applied Mathematics and Statistics (2022 – Present)
  - Journal of Probability and Statistics (2018 – 2019)

- Handling Editor (26 papers in 8 Journals):
  - Frontiers in Genetics (16 papers)
  - Journal of Probability and Statistics (3 papers)
  - Frontiers in Immunology (2 papers)
  - Frontiers in Applied Mathematics and Statistics (1 paper)
  - PLOS Computational Biology (1 paper)
  - Sankhya B (1 paper)
  - Frontiers in Pediatrics (1 paper)
  - Frontiers in Microbiology (1 paper)
  - Frontiers in Digital Health (1 paper)

- Peer Reviewer (200+ papers in 50+ Journals):

- Proceedings of the Python in Science Conferences (SciPy 2018, 2020) (16 papers)
- Statistics in Medicine (14 papers)
- BMC Bioinformatics (9 papers)
- The Lancet Psychiatry (7 papers)
- Frontiers in Genetics (9 papers)
- Bioinformatics (6 papers)
- Stat (6 papers)
- Biometrical Journal (5 papers)
- Computational Statistics (5 papers)
- Statistical Methods in Medical Research (5 papers)
- Communications in Statistics - Theory and Methods (4 papers)
- Frontiers in Microbiology (4 papers)
- Genome Biology (4 papers)
- Journal of Applied Statistics (4 papers)
- Biometrics (3 papers)
- Computational Statistics and Data Analysis (3 papers)
- Genetics (3 papers)
- Human Genetics (3 papers)
- International Conference on Artificial Intelligence and Statistics (3 papers)
- Journal of Computational and Graphical Statistics (3 papers)
- Nature Communications (3 papers)
- PLOS One (3 papers)
- Advances in Data Analysis and Classification (2 papers)
- Bioinformatics Advances (2 papers)
- Bioinformatics and Biology Insights (2 papers)
- Cell Reports Methods (2 papers)
- Computational and Structural Biotechnology Journal (2 papers)
- Electronic Journal of Statistics (2 papers)
- Frontiers in Cellular and Infection Microbiology (2 papers)
- iScience (2 papers)
- Microbiome (2 papers)
- Nature Microbiology (2 papers)
- Scientific Reports (2 papers)
- Statistics in Computing (2 papers)
- Annals of Applied Statistics (1 paper)
- BMC Medical Research Methodology (1 paper)
- Briefings in Bioinformatics (1 paper)
- Canadian Journal of Statistics (1 paper)
- Communications in Statistics - Simulation and Computation (1 paper)
- Frontiers in Immunology (1 paper)
- Journal of Big Data (1 paper)

  - Journal of Bioinformatics and Genomics (1 paper)
  - Journal of Crohn's and Colitis (1 paper)
  - Journal of Probability and Statistics (1 paper)
  - IEEE Journal of Biomedical and Health Informatics (1 paper)
  - Liver Transplantation (1 paper)
  - PLOS Biology (1 paper)
  - Statistics in Biopharmaceutical Research (1 paper)
  - The American Statistician (1 paper)
  - eLife (1 paper)

- Guest Editorship (5 special issues in 3 journals):
  - Guest Associate Editor: Special issue on "Computational Methods for Spatial Biomedical Data Analysis", Frontiers in Applied Mathematics and Statistics, 2023 - Present
  - Guest Associate Editor: Special issue on "Methods for Imaging and Omics Data Science: Advances, Applications, and Spatiotemporal Innovations", Frontiers in Genetics, 2022 - Present
  - Guest Associate Editor: Special issue on "Methods for Single Cell and Microbiome Sequencing Data", Frontiers in Genetics, 2020 - 2022
  - Guest Associate Editor: Special issue on "Statistical and Computational Methods for Microbiome Multi-omics Data", Frontiers in Genetics, 2018 - 2020
  - Guest Editor: Special issue on "Quantile Regression and Beyond in Statistical Analysis of the Data", Journal of Probability and Statistics, 2018 - 2019

- Invited Reviewer (Non-journal)
  - Invited Reviewer, ENAR Student paper Competition, 2025
  - Invited Reviewer, American Statistical Association SBSS Student paper Competition, 2016, 2018
  - Invited Abstract Reviewer, American Society for Nutrition (ASN) Annual Meeting, 2019
  - Invited Abstract Reviewer, Applied Public Health Statistics Section, American Public Health Association (APHA) Annual Meeting and Expo, 2019

- Study Sections
  - NSF Division of Integrative Organismal Systems (IOS), 2026
  - NSF Division of Mathematical Sciences (DMS), 2024
  - NSF Information Integration and Informatics (III), 2024
  - NSF Information Integration and Informatics (III), 2024
  - Invited Grant Reviewer, Medical College of Wisconsin, 2023
  - NCI Clinical and Translational Exploratory/Developmental Study Section, 2019
  - Invited Grant Reviewer, University of Missouri, 2016

- Session Organizer
  - Organizer and Chair of Invited Session "Multimodal AI for Systems Biology", ENAR 2027

- Organizer of Invited Session "Statistical Foundations of Foundation Models", ENAR 2027
- Organizer of Invited Session "Advances in Foundation Models and LLMs for Biomedical Data Science", JSM 2025
- Organizer of Invited Session "Recent Advances in Transfer Learning for Biomedical Data", ENAR 2025
- Organizer of Invited Session "Interpretable Models for Omics Data Science and their Diverse Applications", IISA 2024
- Organizer and Chair of Invited Session "Statistical Methods in Health and Related Areas: Opportunities and Challenges", IISA 2024
- Organizer of Invited Panel "Future of Statistics and Data Science in the Era of ChatGPT and LLMs", JSM 2024
- Organizer of Invited Session "Scalable Bayesian Biomarker Discovery using Large-scale Multi-omics Data Integration", ISBA 2024
- Organizer of Invited Session "Diagonal Integration of Multimodal Data", STATGEN 2024
- Co-organizer of Topic-contributed Session "Scalable Bayes for Omics Data Science", STATGEN 2024 (Joint with Arinjita Bhattacharyya)
- Organizer of Topic-Contributed Session "Success Stories in Biomarker Discovery and Validation - Statistical and Computational Aspects", JSM 2023
- Organizer and Chair of Invited Session "Bayesian methods for multimodal data integration", IISA 2023
- Organizer of Invited Session "Omics Data Science: Advances and Applications", IISA 2022
- Organizer of Invited Session (Sponsor: International Chinese Statistical Association) on "Innovations in Digital Pathology and Spatial Transcriptomics: Statistical Challenges and Major Impact", JSM 2022
- Organizer of Invited Session (Sponsor: ASA Section on Bayesian Statistical Science) on "Scalable Bayes for Large Multi-omics Data Integration and Inference", JSM 2021
- Organizer of Invited Session "Methods for Single-cell and Microbiome Sequencing Data", IISA 2021
- Organizer and Chair of Topic-Contributed Session (Sponsor: ASA Biometrics Section) on "Methods for Single-cell and Microbiome Sequencing Data", JSM 2020
- Organizer of Topic-Contributed Session (ASA Biometrics Section) on "Recent Advances in Zero-inflated Regression Models", JSM 2017

- Miscellaneous
  - Invited Panelist, Panel on AI for Drug Discovery, NIELIT Bio-AI Conclave 2026, Gauhati University, Guwahati, India, December 2026
  - Invited Faculty Panelist, Virtual Panel on "Careers in Academia, Research, and PhD Pathways", Master's Project I/Professional Development Course (MS in Biostatistics and Data Science), Weill Cornell Medicine, 2025, 2026
  - Scientific Program Committee Member, IISA 2025
  - Chair of Topic-Contributed Session (Sponsor: ASA Section on Statistics in Epidemiology) on "Advancements in Multi-Omics Integration Techniques", JSM 2022

- Organization Committee Member, Nonclinical Biostatistics Conference 2021
- Moderator, "AI/ML in Pharma" (Virtual Poster Session), Merck Technology Symposium, 2021
- Panelist, "Microbiome Experimental Design", Merck Systems Biology of the Microbiome Symposium, 2019
- Program Committee Member, SciPy 2018, 2020
- Chair of Contributed Session (ASA Mental Health Statistics Section, ASA Section on Statistics in Imaging) on "Utilizing High-dimensional and Complex Data in Personalized Medicine", JSM 2017
- Co-authored MURI Grant Proposal: Human Gut-Brain Axis Model (GuBA) for Analysis of Nutrition and Physical Stress Impact on Cognitive Function (PI: Rebecca Carrier, Northeastern University), 2016
- Co-authored NIH R24 Grant Proposal: A Comprehensive Platform for Novel Therapy Development from the Microbiome (PIs: Curtis Huttenhower, Ramnik Xavier, Broad Institute of MIT and Harvard), 2016
- Chair of Contributed Session (ASA Biometrics Section, ASA Biopharmaceutical Section) on "Methods for Genetics and Genomics Data", JSM 2016

- Outreach
  - Webinar Committee, International Indian Statistical Association, 2024 – 2025
  - Media Subcommittee Lead, Membership Engagement Committee, ASA Section on Statistical Genetics and Genomics, 2024 – 2025
  - Membership Engagement Committee, ASA Section on Statistical Genetics and Genomics, 2023 – 2025
  - Member, DIA-ASA Nonclinical Biostatistics Bayesian Preclinical/Discovery Scientific Working Group, 2019 – 2023
  - Mentored high school students as part of the Meyer Cancer Center Summer Internship Program (MCC SIP), Summer 2024 - Summer 2026
  - Delivered a joint presentation in collaboration with Merck BARDS on 'Careers in Statistics, Mathematics, Data Science, and Computer Science in the Pharmaceutical Industry' to high school students at Franklin High School, Somerset, NJ (January 2021)

Mentoring and Advising

- Internship Mentoring at Merck
  - Gang Qu (Tulane University, 2022, joint with Jia Kang)
  - Joshua Wang (MD/PhD, NYU Grossman School of Medicine, 2022, joint with Jia Kang)
  - Anupreet Porwal (University of Washington, 2021, joint with Erina Paul)
  - Satabdi Saha (Michigan State University, 2020, joint with Vladimir Svetnik)
- PhD Dissertation Committee Service
  - Xinyang Zhang (PhD, George Washington University; Advisor: Ali Rahnavard; Expected Graduation: 2026)
  - Bahar Sayoldin (PhD, George Mason University; Advisor: TBD; Expected Graduation: 2028)
  - Yihan Liu (PhD, Yale University; Advisor: TBD; Expected Graduation: 2029)
- Graduate and Undergraduate Mentoring at Harvard University
  - Siyuan Ma (PhD, 2015–2019)
  - Emma Schwager (PhD, 2015–2017)
  - Boyu Ren (PhD, 2015–2017)
  - John Joshua Miller (BS, 2017)
- Research Assistant and Volunteer Mentoring at WCM
  - Nalin Arora (MS, Cornell University, 2025 – Present)
  - Juncheng Li (MS, Cornell University, 2025 – Present)
  - Chuxuan Gao (MS, Cornell University, 2025 – Present)
  - Ziyu Liu (MS, Cornell University, 2024 – Present)
  - Aditya Shankar Pal (Indian Statistical Institute Kolkata, 2024 – Present)
  - Sreya Sarkar (University of Iowa, 2024 – Present)
  - Yihan Liu (Yale University, 2023 – Present)
  - Saptarshi Roy (Texas A&M University, 2023 – Present)
  - Jie Yang (UT Dallas, 2024 – 2025)
  - Zimo Zhang (MS, Cornell University, 2024 – 2025)
  - Jialin Gao (MS, Cornell University, 2023 – 2025)
  - Yijia Sun (MS, Cornell University, 2023 – 2024)
  - Mainak Bardhan (PhD, University of Miami, 2024)
  - Chaitali Dagli (PhD, University of Alabama at Birmingham, 2024)
  - Christine Kuryla (Columbia University, 2023 – 2024)
  - Anjan Mandal (University of Nevada Las Vegas, 2023 – 2024)
- High School and Outreach Mentoring at WCM
  - Tamim Rashid (Brooklyn Technical High School, 2026)
  - Ekra Malik (Academy Of American Studies, 2026)
  - Catherine Wong (John Bowne High School, 2025)

- Estella Yee (Stuyvesant High School, 2025)
- Alba Vojta (Marymount School of New York, 2024)
- Arden Barnwell (Stuyvesant High School, 2024)

– Undergraduate Mentoring at WCM

- Vivian Myers (Smith College, 2026)
- Shantey Soto (Cornell University, 2026)

– MS BDS Capstone and Portfolio Project Mentoring at WCM

- **Capstone (2026):** *moduLLM: LLM Fine-Tuning for Biological Module Detection.* Group members: Yujun Che, Yousen Lin, Qirui Liu, Meng Wei.
- **Capstone (2025):** *Spatially Constrained Deep Learning for Spatial Multi-Omics Integration.* Group members: Juncheng Li, Xindan Liang, Fanxi Wang, Yihan Xing.
- **Capstone (2025):** *Exploring Determinants of Recognition in Professional Excellence: A Framework for Data-Driven Analysis.* Group members: Mian Jiang, Peihao Song, Yiyan Yang.
- **Capstone (2025):** *High-Dimensional Multi-View Mediation Analysis with Intermediate Fusion.* Group members: Jingxuan Zhang, Mengyang Sheng, Zhixi Liu.
- **Portfolio (2024):** *Flexible Statistical Models for Omics Data Science.* Group members: Ziyu Liu.
- **Capstone (2024):** *Metabolite Prediction in the Human Microbiome Using Transfer Learning.* Group members: Zimo Zhang, Anan Wang, Akash Das.

Co-curricular Activities	VP, External Relations (Academia), Harvard Big Data Club, 2017 – 2018
	Judge at the 13th Annual Broad Institute Scientific Retreat Poster Competition, 2017
	Member, Postdoctoral Association at HSPH, 2015 – 2019
	Member, NextGen Association at the Broad Institute, 2015 – 2019
	Senator, Graduate Student Government at UAB, 2011 – 2015
	Member, Budget Committee of Graduate Student Government at UAB, 2012 – 2014
	Secretary, Association of Indian Students at UAB, 2010 – 2011
	Judge at UAB Expo (Annual Undergraduate Poster Competition), 2013, 2015
	Co-organizer, Science Exhibition at Ramakrishna Mission Residential College, 2006
Notable Software	R Package **Zentangler**: Causal multimodal mediation analysis of multi-omics data
	R Package **IntegratedLearner**: End-to-end multi-omics biomarker discovery
	R Package **Tweedieverse**: Differential analysis of multi-omics data
	R Package **BayesRecipe**: Bayesian reciprocal regularization
	R Package **MelonnPan**: Predict metabolites from microbial gene abundances
	R Package **MaAsLin2**: Association of microbial features with rich metadata
	R Package **AMAZonn**: Variable selection in zero-inflated count models
	R Package **Gooogle**: Group regularization for zero-inflated count models
	R Package **DAssemble**: Ensemble models for differential analysis
	R Package **BayesCOOP**: Bayesian cooperative learning for multimodal integration
	Python Package **Commingle**: Attention-based deep learning for tabular data
	R Package **JAFAR**: Bayesian joint additive factor models
	R Package **UBR**: Unified Bayes regularization for linear models

Professional Memberships (Past and Present)	American Statistical Association
	International Society for Computational Biology
	International Biometric Society
	Institute of Mathematical Statistics
	International Indian Statistical Association
	International Society for Bayesian Analysis
	International Chinese Statistical Association
	American Association for the Advancement of Science

Online Profiles	GitHub:// **himelmallick** ResearchGate:// **Himel_Mallick** Google Scholar:// **Himel Mallick** LinkedIn:// **mallickhimel** Twitter:// **Mallick_Himel** Web of Science:// **himel-mallick**

Computer Skills	Programming Languages:	C, C++, Python, Julia, SQL, PyTorch
	Statistical Software:	SAS, R, MATLAB, SPSS
	Computing Platforms:	Windows, Macintosh, Linux
	Applications:	MS Office, LaTeX, Adobe Illustrator, Shiny, Git

References

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More references are available upon request.