

# Ibrahim Hossain Sajal



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## About Me

I am a statistician with a PhD in Data Science & Statistics, specializing in scalable Bayesian and genetic modeling to drive biomarker discovery and risk prediction in biomedical research.

## Education

### Ph.D. in Data Science & Statistics

University of Texas at Dallas  
Richardson, TX, USA (2019 - 2024)

### Master's. in Applied Statistics

University of Dhaka  
Dhaka, Bangladesh (2017 - 2018)

### Bachelor's in Applied Statistics

University of Dhaka  
Dhaka, Bangladesh (2013 - 2016)

## Skills

### Programming & Computing:

R, Python, SAS, SQL, HPC, Shell scripting

### Statistical Modeling:

Survival Analysis, Conditional & Penalized Regression (LASSO), Variable Selection, Cross-Validation, Multiple Imputation, Bayesian Inference, MCMC, Latent Variable Models

### Machine Learning:

Supervised & Unsupervised Learning, Decision Trees, Bagging, Random Forest, Boosting, SVM, KNN, Variational Inference

### Genomics & Causal Analysis:

GWAS, Mendelian Randomization, Instrumental Variable, Mediation Analysis, Differential Gene Expression

## Awards

- Fellows Award for Research Excellence
- Mei Lein Fellowship
- Boyd Harshburger Travel Award
- ABGOD Conference Travel Award
- PhD Research Small Grant Program
- SISG Scholarship
- Academic Excellence Award

## Experience

### Postdoctoral Fellow

National Cancer Institute, NIH (2025 - Present)

- Identified proteomic biomarkers linking risk factors to cancer using integrative omics (UKB-PPP) and gene expression analyses.
- Developed a scalable, summary-statistics-based multivariate testing framework to improve detection of genetic associations.
- Analyzed pan-cancer phenotypes and protein networks to uncover pathway-level signals relevant to target discovery (KEGG, Hallmark).
- Conducted survival analyses in lung cancer to evaluate prognostic impact of clinical risk factors and polygenic risk scores.

### Graduate Research Assistant

The University of Texas at Dallas (2020 - 2024)

- Developed **CBCRisk-Black** and **CBCRisk-Mastectomy**, two personalized absolute risk prediction tools to support clinical decision-making in contralateral breast cancer.
- Analyzed large-scale population and registry datasets (BCSC, SEER) to identify risk factors and estimate cancer incidence and hazard rates.
- Designed haplotype-based genetic association test, **bivariate Quantitative Bayesian LASSO**, for correlated disease phenotypes.
- Extending Bayesian LASSO models to high-dimensional, multivariate settings using mean-field variational inference to enable scalable genetic discovery.

## Publications

- Sajal, I. H.,** & Biswas, S. (2023). Bivariate quantitative Bayesian LASSO for detecting association of rare haplotypes with two correlated continuous phenotypes. *Frontiers in Genetics*, 14, 1104727.
- Sajal, I. H.,** Chowdhury, M., Wang, T., Euhus, D., Choudhary, P. K., & Biswas, S. (2022). CBCRisk-Black: a personalized contralateral breast cancer risk prediction model for black women. *Breast cancer research and treatment*, 194(1), 179-186.

## Presentations

- Joint Statistical Meetings (2025) — Invited Talk
- NIH Research Festival (2025) — Poster
- Advances in Statistical and Computational Methods for Analysis of Biomedical, Genetic, and Omics Data (2023) — Poster
- Southern Regional Council on Statistics (2022) — Poster

**Work Authorization:** Approved EAD, Permanent Residency Pending