Personal Statement

I am Menna Arafat, a physician and bioinformatician working on computational modeling of biological systems, with a focus on multi-omics integration and machine learning. Over the past five years, I have contributed to projects across genomics, transcriptomics, epigenomics, proteomics, and metabolomics, using both bulk and single-cell datasets. My main interest is in developing frameworks that characterize the molecular architecture of disease and examine pathway communication and regulatory organization and how these structures differ between normal and disease states.

In my recent work, I have applied network-based methods to cancer datasets. In a study published with Springer Nature, I analyzed metabolomic data from colorectal cancer and used weighted network modeling to identify groups of metabolites linked to tumor features. This revealed patterns that were not detected using standard differential analysis. In another study published in Cells, I modeled metabolomic and proteomic profiles to define subtype-specific network modules in rhabdomyosarcoma. The analysis identified subtype-specific molecular networks that reflect differences in underlying regulation. I also developed CrosstalkX, an R package that infers interactions between pathways and transcription factors using protein interaction data and mutual information. The aim was to provide a robust way to study pathway communication in complex biological systems, particularly in cancer-related contexts.

I seek to pursue a PhD in computational biology with focus on disease modeling with probabilistic machine learning. I am interested in graph-based representation learning and diffusion-based frameworks where latent variables summarize molecular profiles while retaining regulatory structure. I want to use these representations to track how biological states evolve from normal to disease and what underlying regulatory networks get rewired to shape this evolutionary path. I completed many courses on machine learning including Stanford's CS224W Machine Learning with Graphs (Professor Jure Leskovec), which strengthened my understanding of graph encoders and message passing. In this program, I plan to apply these methods to multi omics integration, trajectory inference, and graph-based learning.

Additional details on my research projects and software contributions are available at: **https://menna-arafat.github.io/research/**