Department of Statistics
UNIVERSITY OF GEORGIA
Colloquium Series

GEORGIA 1785

"Unraveling Disease Mysteries: Statistical Models Reveal Cellular Conversations using Spatial Transcriptomics data."

Susmita Datta

When and Where:

11/21/2024
4:00 PM — 5:00PM

Room 204 Caldwell Hall

Abstract:

Understanding cell microenvironments from spatially resolved transcriptomics data is a cutting-edge approach in biomedical research. This innovative method enables scientists to investigate the spatial organization of cells near diseased tissues and identify their inter - and intracellular communications through biochemical signaling, crucial for elucidating disease mechanisms and developing targeted treatments. Traditionally, most computational methods provide ad hoc measurements to estimate intercellular communication. While straightforward, these methods often lack the accuracy and reliability that robust statistical models can offer. To address these limitations, our research proposes a novel generalized linear regression model known as Bayesian Tweedie Modeling of Communications (BATCOM) [1]. This model is designed to infer cellular communications from spatially resolved transcriptomics data, particularly spot-based data, by estimating communication scores between cell types while considering their spatial distances. BATCOM offers a nuanced and statistically sound approach to understanding cellular interactions. By incorporating spatial distance into the communication score estimations, BATCOM provides a more accurate representation of how cells interact within their microenvironments, significantly improving upon traditional methods that often overlook the spatial aspect of cellular communications. Additionally, we explore a frequentist approach using the generalized additive model (GAM) framework. Implemented in the associated TWCOM [2] software in R, this approach enhances scalability and integration, making it more user-friendly for researchers. We demonstrate the superiority of our method using single-cell and spatial RNA-seq data for cutaneous squamous cell carcinoma, the second most common skin cancer in the USA. These advancements in statistical modeling are crucial for advancing our understanding of disease mechanisms. Accurate inference of cellular interactions can reveal new insights into how diseases develop and progress at the cellular level, informing the development of more effective treatments and interventions. By integrating BATCOM and TWCOM into user-friendly software, we ensure these advanced statistical methods are accessible to a wide range of researchers, accelerating biomedical discoveries and improving patient outcomes. Our research enhances our understanding of disease mechanisms, paving the way for new discoveries and therapeutic strategies in biomedical research.

About the Speaker:

Dr. Susmita Datta is a tenured Professor in the Department of Biostatistics at the University of Florida (UF). She was recruited as part of UF's Preeminence Initiative, aimed at elevating the university's national standing. She also serves as Co-Director of the Biostatistics, Epidemiology, and Research Design (BERD) Program at the UF Clinical and Translational Science Institute. Prior to joining UF, Dr. Datta was a tenured Professor at the University of Louisville, where she also held the roles of University Distinguished Scholar and Graduate Director of the master's and Ph.D. programs in Bioinformatics and Biostatistics. Dr. Datta's research is widely recognized, with more than 140 publications in peer-reviewed journals. She has also authored several book chapters and published a book, Statistical Analysis of Proteomics, Metabolomics, and Lipidomics Data (Springer Nature, 2026). Her work, supported by continuous funding from the National Science Foundation (NSF) and the National Institutes of Health (NIH), has led to invited lectures around the world. She currently holds five NIH R01 and R37 grants, with two as Principal Investigator. Dr. Datta is a Fellow of the American Statistical Association (ASA) and the American Association for the Advancement of Science (AAAS), as well as an elected member of the International Statistical Institute (ISI). Her research interests span bioinformatics, genomics, proteomics, metabolomics, lipidomics, clustering and classification techniques, infectious disease modeling, population biology, systems biology, survival analysis, multi-state models, and big data analytics. Her disease focus areas include cancer, Alzheimer's disease, cardiovascular disease, Parkinson's disease, sepsis, fetal alcohol syndrome, and nutritional planning for premature babies. In addition to her research, Dr. Datta serves on NIH study sections and is an associate editor for Briefings in Bioinformatics and Bioinformation. She is also one of three editors for the Springer-IISA Series on Statistics and Data Science. Dr. Datta is a passionate advocate for women in STEM. She has served as President of the Caucus for Women in Statistics (CWS) and as a member of the American Statistical Association's Committee of Women in Statistics (COWIS). She was also a founding executive committee member of the Women in Statistics and Data Science (WSDS) conference. Throughout her career, Dr. Datta has received numerous awards, though she particularly treasures the Best Theoretical Student Prize from the Department of Statistics at the University of Georgia. She has served as a RECOM member for ENAR and as a Board of Trustees member for the International Indian Statistical Association (IISA).