

# **16th UMBC Probability and Statistics Conference**

May 9-10, 2025

*All technical events are in the  
Interdisciplinary Life Science Building (ILSB) of UMBC.*

## **May 9, 2025:**

1-1.50PM: Short course part-I

1.50-2PM: short break

2-2.50PM: Short course part-II

2.50-3PM: short break

3-3.50PM: Short course part-III

3.50-4.15PM: Coffee break

4.15-5.30PM: Keynote-I (Amanda Mejia, Indiana University)

*Chair: DoHwan Park*

## **May 10, 2025:**

10AM-5PM: *Poster presentations in the foyer*

*(Coordinators: Thu Nguyen, Yi Huang, Fred Azizi, Jhilam Sur)*

9-9.15AM: Welcome address

9.15-10.30AM: Keynote-II (Tapabrata Maiti, Michigan State University)

*Chair: Thomas Mathew*

10.30-11AM: Break (*Posters are put up by presenters*)

11AM-12.15PM: Keynote-III (Martin Lindquist, Johns Hopkins University)

*Chair: Yehenew Kifle*

12.15-1.30PM: Lunch break

1.30-3PM: Invited talks (Michael Lucagbo, Weixin Wang, Wei Qian)

*Chair: Yaakov Malonovsky*

3-3.30PM: Break

3.30 - 5PM: Invited talks (Sanjay Chaudhuri, Kevin McIlhany, Steve Damelin)

*Chair: Yi Huang*

5 - 5.15PM: Valedictory session (*Posters are taken down*)

6 PM: Banquet at [The Mint Room in Ellicott City](#)

## **16th UMBC Probability and Statistics Day Conference**

**Short course (May 9, 2025):**

***Principles of functional Magnetic Resonance Imaging***

**Presenter: Professor Martin Lindquist, Johns Hopkins University**



**Brief description of the course:**

Functional Magnetic Resonance Imaging (fMRI) is one of the most widely used techniques for studying the human brain in action. With fMRI, we can obtain snapshots roughly every second of signals related to brain activity and metabolism at about 320,000 locations across the brain, sampling the processes that enable us to perform any of the other thousands of mental activities that make us human. This course provides an overview of fMRI and the research community that has grown around it, comparing and contrasting fMRI with other neuroimaging modalities. Further it will discuss the types of inferences researchers have traditionally sought to make about mind, brain, and behavior, providing background and terminology about the MR scanner and the generated signal and how to preprocess and understand fMRI data. Finally, it will cover the analysis needed to create brain maps, discuss how to understand brain networks including studies of functional and effective connectivity, as well as network analysis, and illustrate how fMRI data can be used to predict outcomes, classify participants, and create brain-based biomarkers.

## **Conference Keynote addresses (May 9-10, 2025)**

### **Keynote-I: Professor Amanda Mejia, Indiana University**



**Bio:** Amanda Mejia is an associate professor in the Department of Statistics at Indiana University (IU) and holds a Ph.D. in biostatistics from Johns Hopkins University. Her research centers around the development of statistical techniques for the analysis of functional neuroimaging data. She leads the Statistical Methods for Individualized Neurodiscovery (StatMIND) lab at Indiana University, which aims to advance the use of functional neuroimaging in clinical settings by developing and applying methods to extract accurate measures of individuals' brain function from this noisy data. Dr. Mejia works at the interface of neuroimaging and statistics, and her work has appeared in top journals in both fields. She is an associate editor for the journals *Biostatistics* and *Statistics and Data Science in Imaging* (launched in 2024) and serves on the editorial board of *Imaging Neuroscience*. Her work is funded by the National Institutes of Health and the National Science Foundation. She is the recipient of an IU Outstanding Junior Faculty Award and was selected as the 2023 Math Fellow for the J&J WiSTEM2D Fellowship Program.

**Title:** Leveraging population information in brain connectivity studies via Bayesian ICA

**Abstract:** Functional connectivity (FC)—the temporal synchrony between brain networks—is a widely popular measure of brain functional organization. Typically, FC is estimated using fixed, hard parcellations, which fail to capture the intrinsic overlapping and individualized nature of functional brain topography. Independent component analysis (ICA) offers a more flexible approach, modeling overlapping spatial topography while estimating FC. However, traditional FC estimation via ICA can be sub-optimal due to ad-hoc methods and the need for temporal dimension reduction. Bayesian ICA can address these limitations, avoiding dimension reduction,

yielding more accurate estimates, and facilitating inference via posterior distributions. We have developed a computationally feasible single-subject Bayesian ICA model that leverages population information via priors on both the spatial component maps and their temporal correlation (i.e., their FC). A novel informative prior for correlation matrices integrates population information on FC into the model. Approximate Bayesian estimation and inference are performed via a computationally efficient variational Bayes algorithm. Realistic simulation studies and analyses of data from the Human Connectome Project demonstrate that this algorithm produces more accurate measures of brain function in individuals and facilitates inference on both spatial topography and FC. Because it is designed for single-subject analysis, this Bayesian ICA framework has potential clinical applicability. Finally, we discuss several scientific applications and areas of future work.

**Keynote-II: Professor Tapabrata Maiti, Michigan State University and US National Science Foundation**



**Bio:** Professor Taps Maiti is a Foundation Professor at Michigan State University in the Department of Statistics and Probability. He currently serves as a program director in the Division of Mathematical Sciences at the National Science Foundation (NSF). Professor Maiti is a Fellow of the American Statistical Association (ASA), a Fellow of the Institute of Mathematical Statistics (IMS), and a Fellow of the American Association for the Advancement of Science (AAAS), which is the world's largest scientific organization. He has served on the editorial boards of many prestigious journals. He is currently a co-editor for the Annals of Applied Statistics and the Journal of Statistical Analysis and Data Mining, the American Statistical Association's data science journal. Additionally, he continues to serve as an Associate Editor for the Journal of the American Statistical Association - Theory & Methods. Professor Maiti is a dedicated educator and advocate for modern statistical science. He has lectured internationally,

published numerous papers in a variety of journals, and supervised over 40 Ph.D. students. Additionally, he served as the graduate director of the Department of Statistics and Probability for a decade and was co-director of the Center for Business and Social Analytics at Michigan State University.

**Title:** Statistical Understanding of Deep Learning with Big Data

**Abstract:** Deep learning has profoundly impacted science and society as it has successfully applied data-driven artificial intelligence. One of the key features of deep learning is that its accuracy improves as the size of the model and the amount of training data increases. This property has significantly improved state-of-the-art learning architectures across various fields in the past decade. However, the lack of a mathematical/statistical foundation has limited the development of deep learning to specific applications and has prevented it from being more broadly applied with high confidence. This foundational gap becomes even more apparent when applied to statistical estimation and inference under limited training sample regimes. To address this issue, we aim to develop statistically principled reasoning and theory that can validate the application of deep learning and pave the way for interpretable deep learning. Our approach is based on Bayesian statistical theory and methodology and scalable computation. We demonstrate the methods with a wide range of applications.

**Keynote-III: Professor Martin Lindquist, Johns Hopkins University**



**Bio:** Martin Lindquist is a Professor of Biostatistics at Johns Hopkins University. His research focuses on mathematical and statistical problems relating to functional Magnetic Resonance Imaging (fMRI). Dr. Lindquist is actively involved in developing new analysis methods to enhance our ability to understand brain function using human neuroimaging. He has published over 100 articles, and serves on the editorial boards of several scientific journals both in statistics and neuroimaging. He is a fellow of the American Statistical Association. In 2018 he

was awarded the Organization for Human Brain Mapping's 'Education in Neuroimaging Award' for teaching statistical issues to the neuroimaging community and the development of online classes that have taught fMRI methods to more than 100,000 students world-wide.

**Title:** Individualized spatial topography in functional neuroimaging

**Abstract:** Neuroimaging is poised to take a substantial leap forward in understanding the neurophysiological underpinnings of human behavior, due to a combination of improved analytic techniques and the quality of imaging data. These advances are allowing researchers to develop population-level multivariate models of the functional brain representations underlying behavior, performance, clinical status and prognosis, and other outcomes. Population-based models can identify patterns of brain activity, or 'signatures', that can predict behavior and decode mental states in new individuals, producing generalizable knowledge and highly reproducible maps. These signatures can capture behavior with large effect sizes and can be used and tested across research groups. However, the potential of such signatures is limited by neuroanatomical constraints, in particular individual variation in functional brain anatomy. To circumvent this problem, current models are either applied only to individual participants, severely limiting generalizability, or force participants' data into anatomical reference spaces (atlases) that do not respect individual functional topology and boundaries. Here we seek to overcome this shortcoming by developing new topographical models for inter-subject alignment, which register participants' functional brain maps to one another. This increases effective spatial resolution, and more importantly allows us to explicitly analyze the spatial topology of functional maps and make inferences on differences in activation location and shape across persons and psychological states. In this talk we discuss several approaches towards functional alignment and highlight promises and pitfalls.

## **Banquet Speaker (May 10, 2025)**

**Professor Ji-Hyun Lee, University of Florida**



**Bio:** Dr. Ji-Hyun Lee is Professor of Biostatistics at the University of Florida and Associate Director for Cancer Quantitative Sciences at the UF Health Cancer Center. She provides strategic leadership and promotes collaborative, rigorous research across the center. Dr. Lee holds a master's and doctoral degrees in Biostatistics from UNC Chapel Hill. Her work focuses on clinical trial design, group randomized trials, and best statistical practices. She is a Fellow of the American Statistical Association (ASA) and a certified PStat®. She currently serves the ASA as the 2025 ASA President.

**Title:** A Conversation on Science, the People Who Make It Work, and Leadership

**Abstract:** We often celebrate the exceptional—the standout individuals, the high-profile discoveries, the headline-making science. But real progress usually depends on something quieter: steady, thoughtful work by teams of professionals who rarely make the spotlight. As a biostatistician, collaborator, and team scientist, I've seen how statistical thinking shapes research and improves patient care—not through grand gestures but through consistent, collective effort. In this talk, I'll push back on the idea that only the extraordinary drive change. I'll share stories from my own path and reflect on how science and leadership are built from everyday contributions. Now, as ASA's 2025 President, I hope to help strengthen our community, advance our field, and highlight the power of the people who make it all work.

## **Invited Talks (May 10, 2025)**

### **1. Dr. Michael D. Lucagbo, University of Philippines Diliman**

- a. **Title:** Regression-based Statistical Reference Regions and Multivariate Decision Limits
- b. **Abstract:** Reference ranges and decision limits are invaluable in laboratory medicine, as these are indispensable tools for the interpretation of laboratory test results. When assessing measurements on a single analyte, univariate reference intervals and decision limits are required. In many cases, however, measurements on several analytes are needed by medical practitioners to diagnose more complicated conditions such as kidney function or liver function. In such situations, a multivariate reference region (MRR) or multivariate decision limits are needed. A multivariate region is more desirable than separate univariate reference and decision limits because the latter approach results in less specificity against false positives and disregards the cross-correlations between variables. To incorporate covariate information, we develop regression-based MRRs and multivariate decision limits under a multivariate normal setting. In constructing the MRRs, we use a tolerance region criterion. On the other hand, in constructing the decision limits, we use a criterion related to

Bayesian tolerance intervals. Moreover, to make the reference regions and decision limits amenable for component-wise outlier detection, we use rectangular regions. The accuracies of the proposed procedures are evaluated through coverage probabilities and expected volumes.

## 2. Ms. Weixin Wang, University of Maryland Baltimore County

- a. **Title:** Adaptive Constrained ICA with Mixing Matrix Column Constraints: Application to fMRI Data
- b. **Abstract:** Independent Component Analysis (ICA) is a powerful data-driven method that has been widely applied in functional magnetic resonance imaging (fMRI) data analysis to uncover underlying sources. An attractive way to boost ICA performance is via constraints to guide ICA factors to be similar to user-supplied "references", allowing incorporation of prior-knowledge into the factorization. However, most existing constrained ICA methods typically only impose source constraints and are unable to impose constraints on the mixing matrix. With multi-subject medical imaging datasets, constraining the mixing matrix with subjects' symptom-related measurements, such as clinical scores or cognitive variables, enhances the algorithm's ability to identify brain activities associated with these symptoms. This offers a novel perspective for understanding the pathologies underlying various psychiatric disorders. Therefore, to overcome the limitations of existing constrained ICA algorithms, we introduce a new constrained ICA algorithm: adaptive-reverse constrained matrix entropy bound minimization (arc-M-EBM), which imposes constraints on the mixing matrix and uses adaptive-reverse thresholding to avoid overfitting or underfitting. This approach ensures flexibility and leads to more accurate and interpretable source separation. Simulations demonstrate that arc-M-EBM outperforms traditional ICA methods. Application to resting-state fMRI data from 176 subjects from healthy controls and patients reveals significant relationships between constrained components and clinical measures, enhancing our understanding of brain-behavior relationships.

## 3. Dr. Wei Qian, University of Delaware

- a. **Title:** An Integrative Dimension Reduction Approach for High-dimensional Multi-source Data
- b. **Abstract:** As technological advances significantly expand data availability, integrative analysis of multiple data sources has become increasingly important tools for biomedical studies. In this paper we propose an integrative and nonconvex-regularized dimension reduction method to achieve simultaneous dimension reduction and variable selection for multi-source data analysis in high dimensions. The proposed method aims to extract sufficient information with source-specific latent factors in supervised fashion to enhance both estimation efficiency and interpretability, without imposing either a parametric distribution assumption for the response or a linear regression assumption for the predictors. Our asymptotic results establish consistency properties in both integrative central

subspace estimation and variable selection for the proposed method, where the number of predictors in each data source is allowed to increase exponentially fast with sample size. Promising performance of the integrative estimator and efficient numerical algorithms is demonstrated through extensive simulation and real-world multi-source data analysis.

**4. Dr. Sanjay Chaudhuri, University of Nebraska-Lincoln**

- a. **Title:** Principal Component-based Constraint Reduction with Application to Entropy Estimation
- b. **Abstract:** In many problems in statistics, the task is to minimise a suitable objective function of variables under a set of linear equality constraints that depend on the data and possibly some parameters. In the presence of a large number of such constraints, the problem often becomes ill-conditioned and impossible to solve. Some methods for constraint reduction are thus required. In this article, we consider a principal component-based constraint reduction method. We show that any feasible solution for the optimisation problem under the proposed reduced constraints is also nearly feasible for the original problem. A good approximation of the required optimal solution can thus be obtained by minimising the objective just under the reduced constraints. The principal components-based construction ensures that all specified constraints are used, none of them are fully dropped, thereby allowing a user to include all relevant constraints without any preselection. The proposed procedure can be used in several problems where techniques such as empirical likelihood, exponential tilting, etc., are applied. In this article, we apply it to the problem of non-parametric differential entropy estimation using the k-nearest neighbour method. This is a joint work with Riddhimoy Ghosh, Department of Statistics, University of Nebraska-Lincoln.

**5. Dr. Kevin McIlhany, US Naval Academy**

- a. **Title:** Eulerian Analysis of Velocity Fields of the Chesapeake Bay
- b. **Abstract:** Two views have been held historically for velocity vector fields in fluid dynamics; the Eulerian viewpoint set in an absolute coordinate frame, and the Lagrangian view, set in the moving frame of a fluid particulate. Examples of Eulerian analyses are wind-tunnel experiments, while examples of Lagrangian come from dynamical systems approaches of advecting large sets of fluid parcels bound by equations of motion. The Lagrangian viewpoint has dominated CFD since the dawn of the desktop computer, making accessible the complicated simulations required. This study revisits the Eulerian view from a modern perspective to apply new techniques to the field.

**6. Dr. Steven Damelin, zbMATH Open, Leibniz Mathematical Institute for Information, European Mathematical Society**

- a. **Title:** The Intrinsic Geometry of Representation, Alignment, Manifold and Deep Learning of neural biological data within a neural state space and biological neural manifolds
- b. **Abstract:** Consider the responses of a population of biological neurons to a set of stimuli. Dimensional reduction refers to manipulations used to identify the shape, location and orientation of this biological neural data within this neural state space. This data may live on a lower dimensional neural manifold and to understand the intrinsic geometry of this representation, one needs to develop mathematical and statistical tools to find this manifold and its geometry. We will explain recent mathematical and statistical tools developed by the speaker and his collaborators to help to understand this problem. As it turns out this problem relates interestingly to a mathematical alignment, manifold and deep learning problem between responses of neural net biological neural data and data generated by the underlying biological system. We will discuss this connection. The talk will focus primarily on a new way to understand alignment, deep and manifold learning using Whitney Extensions. The main reference is the authors new book.