Computational Neuroscience Summer School
July 27 – July 31, 2015

SPEAKER TITLES/ABSTRACTS

Mark Kramer
Boston University

"Neural Spike Train Analysis: An Introduction to Computational Models of Individual Neurons:
 biophysics and dynamics"

In this introductory tutorial, we will discuss mathematical models of single neuron action potential or "spiking" activity. We will first introduce basic biophysical ideas to motivate these models, and then examine how these models behave. We will focus on both biophysical models (e.g., integrate and fire, Hodgkin and Huxley) and dynamical models (e.g., FitzHugh-Nagumo). We will use two software packages to implement, simulate and study these models: MATLAB and XPPAUT. All students are encouraged to attend this tutorial with their computers, and participate in guided open-lab exercises.

Hans-Georg Mueller and Jane-Ling Wang
University of California, Davis

"Functional Data Analysis for Medical Imaging Data"

With the advance of modern technology, more and more data are being recorded continuously during a time interval or intermittently at several discrete time points for many units or subjects. These are instances of ``functional data''. Functional Data Analysis (FDA) encompasses the statistical methodology for such data. Broadly interpreted, FDA deals with the analysis and theory of data that are in the form of functions, also including medical imaging data.

In the lectures, we provide an introduction into the most commonly used methods of FDA. The most prevalent approach to represent a sample of random functions is Functional Principal Component Analysis (FPCA) and the related concept of modes of variation. This approach is based on simple statistical notions such as mean and covariance function of a random process that can be inferred from the data. FPCA is an important dimension reduction tool and in sparse data situations can be used to impute functional data that are sparsely observed. Other series expansions with random coefficients, such as expansions into B splines, applying mixed linear models, are also common.

Another core topic of FDA is functional regression, where one pairs functions or scalars as predictors with responses that are also functions or scalars. A classical models is functional linear regression, which can be implemented in various ways, especially when the predictors are functional. A key issue in functional linear regression is the inversion of a covariance operator, which is an ill-posed problem that needs to be handled differently from traditional linear

regression with vector covariates. Such an inverse problem is also present in some forms of functional correlation, a topic that connects to quantifying functional connectivity of the brain. We discuss several functional correlations and their pros and cons for applications to medical imaging.

Beyond the linear modeling approaches, nonlinear methods have found increasing interest. These include polynomial and quadratic regression relations, dimension reduction methods such as additive and single index models, and other nonlinear approaches.

Further topics of interest are warping and manifold learning, and the learning of time dynamics from observed realizations of the underlying stochastic process.

Justin Romberg
Georgia Institute of Technology

"The Mathematics and Applications of Compressed Sensing"

This short course will cover the mathematical fundamentals of compressed sensing and overview some of its applications in signal processing. Here is a rough agenda:

Lecture 1: Introduction and Mathematical Fundamentals I. We will introduce the basic ideas of compressed sensing from a conversational standpoint. Then we will prove one of the foundational results: that random projections provide stable embeddings for sparse vectors. The discussion requires only a basic knowledge of probability.

Lecture 2: Introduction to Mathematical Fundamentals II. We will show how the sparse recovery problem is solved by l1 minimization. We will also discuss other algorithms for sparse recovery (iterative thresholding, orthogonal matching pursuit, etc).

Lecture 3: Low rank recovery in signal processing. We discuss the "matrix completion" problem, where we try to recover a low rank matrix from incomplete observations of that matrix. We will discuss some of the applications in sampling theory, machine learning, and signal processing.

Lecture 4: Quadratic and bilinear problems. We will discuss how progress in low-rank recovery gives us new insights in how to solve quadratic and bilinear systems of equations. In particular, we will talk about recent progress in phase retrieval and blind deconvolution.

Lecture 5: Streaming reconstruction. We discuss streaming reconstruction algorithms from generalized measurements in the contexts of least-squares and L1 minimization.

Yu-Ping Wang
Tulane University

"Big Data Integration and Analysis: Integration of Fmri Imaging, Genomics, Networks and Biological Knowledge"

In this talk, I will present our recent efforts on the development of sparse models for multi-scale and multi-modal genomic and image data integration and analysis. I will show how to use sparse group CCA model to correlate genomic and image data; how to design sparse models (e.g., collaborative low rank regression) for integrating genomic, imaging and protein-protein

interaction networks; and how to develop a scaled L_p based sparse regression model for biomarker detection, leading to improved diagnosis of mental illnesses (e.g., schizophrenia).

Laurent Younes
Johns Hopkins University

"Shape Analysis and Diffeomorphisms for Medical Imaging Data"

Over the last couple of decades, multiple studies have provided evidence of anatomical differences between control groups and cognitively impaired groups at the population level, for a collection of diseases, including schizophrenia, depression, Huntington's or dementia. In the particular case of neuro-degenerative diseases, a repeated objective has been to design anatomical biomarkers, measurable from imaging data, that can describe the evolution of the disease, either at the population or at the patient level. This goal has become even more relevant with the recent emergence of longitudinal studies, involving patients at early stages or ``converters'' which showed that, when the effect is measured at the population level, anatomical changes caused by diseases like Alzheimer's or Huntington's were happening several years before cognitive impairment can be detected on individual subjects.

Shape analysis methods in this framework generally operate in two phases: a normalization step, in which shapes are represented by aligned coordinates, in the sense that coordinates with the same index are directly comparable across subjects. The second step is the statistical study of the transformed coordinates, which generally involves data analysis methods in large dimensions. In this tutorial, we will focus on alignment methods that rely on optimal control formulations, in which registration of one shape to another is based on finding an optimal transformation process between them. The cost that is minimized is a combination of data fidelity and of a smoothness penalty term. This approach has been successful in addressing multiple shape analysis problems in neuro-imaging and other domains, and is versatile enough to allow for reformulations with diverse image/shape modalities, or for database co-registration problems, or for the inclusion of constraints in the deformation process. We will review the theoretical foundations that sustain the approach, and discuss the relevant algorithms with some remarks on their numerical implementation. After discussing the alignment process, we will present a few examples of statistical analyses that have recently been performed on datasets related to neuro-degenerative diseases, namely Huntington and Alzheimer's. Once the problem of multiple comparisons in testing hypotheses is properly addressed, the statistical tools that are used are quite conventional, and lead to interesting results that induce or confirm hypotheses relative to the location and timeline of the diseases' propagation.

Hongtu Zhu
University of North Carolina

"Advanced Statistical Methods for Integrating Imaging and Genetics"

Motivated by recent work on studying massive imaging, genetic, and clinical data invarious biomedical studies, our group proposes three sets of statistical models including imaging on scalar models, image-on-genetic association models, and prediction models for big data integration. Our statistical models explicitly overcome many challenges in big data integration, brain development, and genetic analysis of high-dimensional brain measurements. We develop some fast estimation procedures to simultaneously estimate parameters of interest. We systematically investigate the asymptotic properties (e.g., consistency and asymptotic normality)

of various parameter estimates. Our Monte Carlo simulation and real data analysis have confirmed the excellent performance of our models in different applications. Our novel statistical methods are applicable to a variety of neuroimaging studies and imaging genetic studies of, e.g., neuropsychiatric disorders, major neurodegenerative diseases, substance use disorders, as well as normal brain development.