BIOINFORMATICS SEMINAR
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UNSUPERVISED, SEMI-SUPERVISED AND SUPERVISED LEARNING METHODS FOR LARGE-SCALE BIOLOGICAL DATA ANALYSIS – AN INTEGRATIVE APPROACH

An underlying theme in many modern scientific fields of inquiry is the deluge in the volume of data generated requiring analysis and interpretation in order to extract actionable information that can be used for policy and decision making. Advances in high-throughput "omics" technologies in the past two decades have given rise to large-scale biological data that is measured on a variety of scales. These studies enable the simultaneous measurement of the expression profiles of tens of thousands of "omic" features, from an ever increasing number of individual patient samples that may represent phenotypes, experimental conditions or time points. Examples include genomic, proteomic, metabolomic, transcriptomic, radiomic and high-throughput compound screening studies that are fundamental to molecular pattern discovery. Similarly, studies in biomedical imaging and neuroscience generate tens of thousands of signals from brain or muscle activity under a variety of experimental conditions across the time-frequency domain. For example, identifying muscle synergies helps advance our understanding of motor control in healthy and pathological conditions. When information on patient outcome such as survival or disease recurrence is also available, one of the goals of an investigator is to understand how the expression levels of "omics", clinical, laboratory and demographic features relate to an individual's survival over the course of a disease. These massive data sets offer tremendous potential for growth in our understanding of the pathophysiology of many diseases. Broadly, my research spans unsupervised, semi-supervised and supervised learning methods for analyzing large data sets stemming from genomics, neuroscience, imaging and biomedical informatics. In this talk, I will provide a mildly technical overview of the statistical and computational approaches that have been developed in my laboratory for addressing these problems with a focus on applications.

BIOGRAPHY

Dr. Devarajan is an Associate Research Professor in the Department of Biostatistics & Bioinformatics at Fox Chase Cancer Center (FCCC) and an affiliated faculty member in the Center for High-dimensional Statistics at Temple University's Big Data Institute. His primary research interests encompass statistical machine learning and data science with applications in bioinformatics, neuroscience, medicine and natural language processing. It spans unsupervised and supervised learning, as well as survival analysis, and primarily focuses on the development of statistical and computational approaches to analyze massive data sets generated in these areas. Dr. Devarajan is a member of the Research Review Committee and serves as the Vice Chair of the Data Safety and Monitoring Board at FCCC. Prior to joining FCCC, Dr. Devarajan held research positions at the Bristol-Myers Squibb Pharmaceutical Research Institute in Princeton, New Jersey and in the Cancer Bioinformatics Group at AstraZeneca Pharmaceuticals in Boston. He has worked extensively in cancer genomics on the design and analysis of high-throughput studies and animal model experiments, and provided statistical expertise and support for large-scale biological data analysis in biomarker discovery.

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