For favour of posting

DEPARTMENT OF STATISTICS AND ACTUARIAL SCIENCE
THE UNIVERSITY OF HONG KONG

50th Anniversary Seminar Series

Professor Yuanjia WANG

Department of Biostatistics, Mailman School of Public Health
Columbia University
Division of Biostatistics, New York Psychiatric Institute
USA

will give a talk
entitled

IDENTIFYING BIOMARKER SIGNATURES FOR NEURODEGENERATIVE DISEASES FROM LARGE-SCALE BIOMARKER MEASURES WITH NETWORK STRUCTURE

Abstract

Potential disease-modifying therapies for neurodegenerative disorders need to be introduced prior to the symptomatic stage in order to be effective. However, current diagnosis of neurological disorders mostly rely on measurements of clinical symptoms and thus only identify symptomatic subjects in their late disease course. Thus, it is of interest to select and integrate biomarkers that may reflect early disease-related pathological changes for earlier diagnosis and recruiting pre-sypmtomatic subjects in a prevention clinical trial. In many clinicial studies of neurological disorders, researchers collect measurements of both static and dynamic biomarkers over time (e.g., clinical assessments or neuroimaging biomarkers) to build time-sensitive prognostic model. An emerging challenge is that due to resource-intensive or invasive (e.g., lumbar puncture) data collection process, biomarkers may be measured infrequently and thus not available at every observed event time point. Leveraging all available, infrequently measured dynamic biomarkers to improve prognostic model of event occurrence is an important and challenging problem. In this paper, we propose a kernel-smoothing based approach to borrow information across subjects to remedy infrequent and unbalanced biomarker measurements under a time-varying hazards model. A penalized pseudo-likelihood function is proposed for estimation and accommodate network structure among biomarkers, and an efficient augmented penalization minimization algorithm is adopted for computation. We apply the proposed method to a recently completed natural history study of Huntington's disease (HD) to predict time to disease conversion using structural change at huntingtin gene and longitudinal, whole brain structural magnetic resonance imaging biomarkers. Lastly, we discuss an approach to estimate causal networks using high-dimensional biomarkers with an application to discover protein signaling network from human immune T-cell data and to HD data for constructing brain atrophy network.

on

Tuesday, July 18, 2017

(Refreshments will be served from 10:45 a.m. outside Room 301 Run Run Shaw Building)

11:00 a.m. – 12:00 noon

at

Room 301, Run Run Shaw Building

Visitors Please Note that the University has limited parking space. If you are driving please call the Department at 3917 2466 for parking arrangement.

ALL INTERESTED ARE WELCOME