

AMSS-PolyU Joint Research Institute
Distinguished Lecture by

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Harvard School of Public Health, Harvard University

Statistical Methods for Testing for Rare Variant Effects in Next Generation Sequencing Association Studies



Abstract

An increasing number of large scale sequencing association studies, such as the whole exome sequencing studies, have been conducted to identify rare genetic variants associated with disease phenotypes. Testing for rare variant effects in sequencing association studies presents substantial challenges as the design matrix is very sparse. We first provide an overview of statistical methods for testing for rare variant effects in next generation sequencing association studies. The proposed methods are evaluated using simulation studies and illustrated using data examples.

Biography

Education:

- B.Sc, Tsinghua University 1989
- Ph.D. in Statistics, University of Washington 1994, supervised by Prof. Norman Breslow

Research Areas:

- Analysis of correlated data, such as longitudinal, clustered and spatial data
- Analysis of high-dimensional genomic and 'omics data
- Mixed models, Nonparametric and semiparametric regression
- Statistical genetics and genomics

Fellowships:

- Elected fellow of the American Statistical Association in 2000
- Elected fellow of Institute of Mathematical Statistics in 2007

Main Awards:

- The Spiegelman award of the outstanding health statistician from the American Public Health Association in 2002
- COPSS Presidents' Award in 2006
- MERIT award from the National Cancer Institute, USA (2007-2016)

Main Academic Services:

- Director of the Program in Quantitative Genomics, Harvard School of Public Health, Harvard University founding
- Co-editor of the journal Statistics in BioSciences
- Chairperson of Committee of President of Statistical Societies (COPSS)

Date : 20 December 2012 (Thursday)

Time : 3:00pm - 4:00pm (Tea reception at 4:00pm)

Venue : Room AG710, PolyU

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ALL ARE WELCOME !