Biostatistics - Theory and Methods II

Chair: Mireille Schnitzer (Harvard School of Public Health)

SAYANTEE JANA, McMaster University

A Moderated Trace Test for the Growth Curve Model and Its Application for Gene-Filtering in Time-Course Microarray Data

Traditional tests for analyzing longitudinal data are not applicable in high-dimensional setup (when $n < p$). We propose a moderated test using the Growth Curve Model, which is useful for analyzing high-dimensional longitudinal data. Extensive simulations demonstrated that our moderated test is unbiased, and is monotone with respect to sample size and parameter value, regardless of the covariance. We illustrated the application of our method for gene-filtering in time-course micro-array data using lung cancer data, where measurements were taken from normal and chemically treated human lung tissues. We were able to identify 1053 (4.7%) significant ones out of 22,227 genes.

STEFAN KONIGORSKI, University of Toronto

A Censored Regression Method to Adjust for Medication Effects in Genetic Analysis of a Quantitative Trait When the Treatment Received Depends on the Trait

In some observational studies, receiving a treatment or not is response-dependent. For example, the use of antihypertensive medication to lower blood pressure (BP) depends on the individual's pre-treatment BP measure. In genetic association analysis of BP, adjusting BP for the effect of medication is crucial when the objective is to identify genes associated with high or low BP. A naive analysis based on modeling BP with the treatment as a covariate leads to biased estimates of genetic effects. We propose a new method based on censored regression, assuming that a treated individual's true underlying BP is higher than the observed.

CHEL HEE LEE, University of Saskatchewan

Zero-Truncated Poisson Imprecise Probability Model for Quantifying Prior Ignorance

Prevalence estimates based on the intensity of usage of medical services are biased because zero counts are not observed. Such zero counts can be accommodated using a zero-truncated Poisson model. We quantify our epistemic ignorance by applying the imprecise probability inferential paradigm of Walley to this model. Normal and log-gamma priors are studied by constructing a three parameter exponential family of distributions which includes both priors. Finally, we present a visualization of updating as a translation on the hyperparameter space of this family of posteriors and graphically demonstrate the reduction of imprecision.

ZHIHUI (AMY) LIU, McGill University

Measuring the Yearly Mortality Reductions Due to a Cancer Screening Program: A Round-by-Round Approach

Summary statistics from cancer screening trials are of limited use for projecting the mortality reduction pattern expected from a sustained screening program. Earlier, to project the timing, duration, and magnitude of the reductions under any specified regimen, we had formulated a 3-parameter model, characterizing the impact of each round of screening, that can be fitted to year-by-year mortality data. Now, we extend it to (i) accommodate trials with >1 screening arm, (ii) combine information across trials with different regimens, (iii) account for age-specific regimens. We quantify how precisely the sustained asymptote in the mortality reduction curve can be measured.

MARYAM ZOLGHADR, University of Gothenburg

Optimal Design of Dilution Experiments under Volume Constraints

We develop methods to construct a one-stage design of dilution experiment under the total available volume constraint typical for bio-medical applications. We consider different optimality criteria based on the Fisher information in both non-Bayesian

and Bayesian settings. It turns out that the optimal design is one atomic, meaning that all the dilutions should be of the same size. Our proposed approach to solve such optimization problems is a variational analysis of functionals of a measure. The advantage of the measure optimization approach is that additional requirements like a total cost of experiment can be easily incorporated into the goal function.