

BIostatISTICS SEMINAR

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Bayesian mixed hidden Markov models for categorical outcomes with differential misclassification

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3:30pm - 4:30pm, CHS 33-105A

Refreshments served at 3:00 PM in room 51-254 CHS

ABSTRACT: We discuss a fully Bayesian Mixed Hidden Markov Model (BMHMM) for handling differential misclassification in categorical outcomes in a multi-level setting. Questionnaire-based health status outcomes are often prone to misclassification which, if ignored, may lead to biased effect estimates. Analytical challenges posed by such misclassified outcomes are further complicated when simultaneously exploring factors for both the misclassification and health processes in a multi-level setting. The BMHMM generalizes the traditional Hidden Markov Model (HMM) by introducing random effects into three sets of HMM parameters for joint estimation of the prevalence, transition and misclassification probabilities. This formulation not only allows joint estimation of all three sets of parameters, but also accounts for cluster level heterogeneity based on a multi-level model structure. Using this novel approach, both the true health status prevalence and the transition probabilities between the health states during follow-up are modeled as functions of covariates. The observed, possibly misclassified, health states are related to the true, but unobserved, health states and covariates. Results from simulation studies are presented to validate the estimation procedure, to show the computational efficiency due to the Bayesian approach and also to illustrate the gains from the proposed method compared to existing methods that ignore outcome misclassification and cluster level heterogeneity. We apply the proposed method to examine the risk factors for both asthma transition and misclassification in the Southern California Children's Health Study (CHS).

(Joint Work with Yue Zhang, PhD, Biostatistics Unit, Group Health Research Institute, Seattle, WA)