UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

BIOSTATISTICS SEMINAR

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Semiparametric Regression Analysis of Interval-Censored Competing Risks Data

Interval-censored competing risks data arise when each study subject may experience an event or failure from one of several causes and the failure time is not observed exactly but rather known to lie in an interval between two successive examinations. We formulate the effects of possibly time-varying covariates on the cumulative incidence or sub-distribution function (i.e., the marginal probability of failure from a particular cause) of competing risks through a broad class of semiparametric regression models that captures both proportional and nonproportional hazards structures for the sub-distribution. We allow each subject to have an arbitrary number of examinations and accommodate missing information on the cause of failure. We consider nonparametric maximum likelihood estimation and devise a fast and stable EM-type algorithm for its computation. We then establish the consistency, asymptotic normality, and semiparametric efficiency of the resulting estimators by appealing to modern empirical process theory. In addition, we show through extensive simulation studies that the proposed methods perform well in realistic situations. Finally, we provide an application to a study on HIV-1 infection with different viral subtypes.

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Semiparametric Structural Equation Models with Latent Variables for Right-Censored Data

Structural equation modeling is commonly used to capture complex structures of relationships among multiple variables, both latent and observed. In this presentation, a general class of structural equation models with a semiparametric component for potentially censored survival times is proposed. Nonparametric maximum likelihood estimation and a combined Expectation-Maximization and Newton-Raphson algorithm for its computation are considered. Conditions for model identifiability are proposed, and the consistency, asymptotic normality, and semiparametric efficiency of the estimators are established. Finally, performance of the proposed methods is shown to be satisfactory through simulation studies and an application to a motivating cancer study that contains a variety of genomic variables is provided.

Thursday, March 24, 2016
3:30 pm - 4:30 pm
Blue Cross Blue Shield Auditorium
(0001 Michael Hooker Research Center)