Method of Sieves to Jointly Model Survival and Longitudinal Data

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Abstract

In biomedical studies, longitudinal covariates are often used to monitor the progress of a disease as well as survival time. However, a sparse covariate history, possibly in combination with measurement error, adds complications to the survival analysis. Moreover, marginal analysis of the longitudinal covariates may incur biases due to informative dropout of the longitudinal processes when death is the endpoint for survival time. Joint modeling survival and longitudinal data can gain information from both components and has emerged as an effective way to model their relationship. A prevalent approach is the semiparametric joint likelihood approach by Wulfsohn and Tsiatis (1997). However, it suffers from computational instability due to the large number of parameters involved in the likelihood and difficulties with standard error estimation. In this article, we propose the method of sieves for practical applications and establish asymptotic consistency and the rate of convergence of the proposed sieve maximum-likelihood estimate (SMLE) including the estimate for the baseline hazard function. Results from numerical studies support this approach. Finally the proposed SMLE is applied to a liver cirrhosis study for further illustration.

Keywords: asymptotic theory; EM algorithm; joint likelihood; missing data; Monte Carlo integration; nonparametric maximum likelihood method.