

## **Title:** Joint Modeling of Longitudinal Data and Informative Dropout in the Presence of Multiple Changepoints

**Abstract:** In longitudinal studies of patients with the Human Immunodeficiency Virus (HIV), objectives of interest often include modeling of individual-level trajectories of HIV Ribonucleic Acid (RNA) as a function of time. Empirical evidence suggests that individual trajectories often possess multiple points of rapid change, which may vary from subject to subject --- both in number and in location. Presence of such changepoints make the modeling of individual viral RNA levels difficult, since usual methods become unsuitable.

In this talk, we present a new robust multiple-changepoint model for longitudinal trajectories. The proposed method uses a joint model to incorporate information from the longitudinal data as well as from informative dropouts, which are common in such studies. A Dirichlet process prior is used to model the distribution of the changepoints. The Dirichlet process leads to a natural clustering, and thus, sharing of information among subjects with similar trajectories. A fully Bayesian approach for model fitting and prediction is implemented using the Gibbs sampler on the ACTG 398 clinical trial data.