



JOHNS HOPKINS  
BLOOMBERG  
SCHOOL of PUBLIC HEALTH

*Department of Biostatistics*

# BIOSTATISTICS SEMINAR

## Using Joint Longitudinal-Survival Models for Individual Prediction and Estimation of Treatment Effects.

Jeremy M.G. Taylor  
Department of Biostatistics, University of Michigan

### *Abstract*

For monitoring patients treated for prostate cancer, Prostate Specific Antigen (PSA) is measured periodically after they receive treatment. Increases in PSA are suggestive of recurrence of the cancer and are used in making decisions about possible new treatments. The data from studies of such patients typically consist of longitudinal PSA measurements, censored event times and baseline covariates. Methods for the combined analysis of both longitudinal and survival data have been developed in recent years, with the main emphasis being on modeling and estimation. We analyze data from a prostate cancer study in which the patients are treated with radiation therapy using a joint model.

Here we focus on utilizing the model to make individualized prediction of disease progression for censored and alive patients, based on all their available pre-treatment and follow-up data. In this model the longitudinal PSA data follows a non-linear hierarchical mixed model. The clinical recurrences are modeled using a time-dependent proportional hazards model where the time dependent covariates include both the current value and the slope of post-treatment PSA profile. Estimates of the parameters in the model are obtained by the Markov chain Monte Carlo (MCMC) technique. The model is used to give individual predictions of both future PSA values and the predicted probability of recurrence up to three years in the future. An efficient algorithm is developed to give individual predictions for subjects who were not part of the original data from which the model was developed. Thus the model can be used by others remotely through a website portal, to give individual predictions that can be updated as more follow-up data is obtained. In this talk I will discuss the data, the models, the estimation methods, the statistical issues, the website ([psacalc.sph.umich.edu](http://psacalc.sph.umich.edu)) and using the model to estimate the effect of a salvage treatment.

This is joint work with Menggang Yu, Donna Ankerst, Cecile Proust-Lima, Ning Liu, Yongseok Park and Howard Sandler.

**The Johns Hopkins Bloomberg School of Public Health  
Department of Biostatistics, Wednesday, November 10, 2010  
Room W2030 School of Public Health, 4:00-5:00pm**