Biostatistics Seminars
Winter 2017

Ruth Pfeiffer, PhD

Senior Investigator/Biostatistics Branch, Division of Cancer Epidemiology and Genetics
National Cancer Institute, NIH, HHS

An efficient procedure to combine biomarkers with limits of detection for risk prediction

Tuesday, 28 March 2017
3:30 pm – 4:30 pm - Purvis Hall, 1020 Pine Ave. West, Room 24

ALL ARE WELCOME

Abstract:
Only a few procedures have been proposed so far that address how to combine information from multiple correlated markers that are also left and/or right censored due to lower or upper limits of detection. We extend dimension reduction approaches, specifically likelihood-based sufficient dimension reduction (LDR) to regression or classification with censored predictors. These methods apply generally to any type of outcome, including continuous and categorical outcomes. Using an expectation maximization (EM) algorithm, we find linear combinations that contain all the information contained in correlated markers for modeling and prediction of an outcome variable, while accounting for left and right censoring due to detection limits. We also allow for selection of important variables through penalization. We assess the performance of our methods extensively in simulations and apply them to data from a study conducted to assess associations of 47 inflammatory markers and lung cancer risk and build prediction models. This is joint work with Diego Tomassi, Liliana Forzani and Efstathia Bura E

Bio:
Dr. Pfeiffer received a master's degree in applied mathematics from the Technical University of Vienna, Austria, and a Master's in applied statistics and a Ph.D. in mathematical statistics both from the University of Maryland, College Park, USA. She joined the Biostatistics Branch at the National Cancer Institute, NIH, as a postdoctoral fellow, was appointed as a principal investigator and tenured as a senior investigator. At NCI she is an active collaborator on many research projects and mentors several fellows and junior investigators. Her research focuses on statistical methods for absolute risk prediction, laboratory methods and problems arising in genetic epidemiology. She is the recipient of a Fulbright Fellowship, an elected Member of the International Statistical Institute, and an elected Fellow of the American Statistical Association.
http://dceg.cancer.gov/about/staff-bios/pfeiffer-ruth

www.mcgill.ca/epi-biostat-occh/news-events/seminars/biostatistics