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CONTROL ID: 3338368
PRESENTER: Chao-Kang Jason Liang
PRESENTER (INSTITUTION ONLY): National Institute of Allergy and Infectious Diseases
TITLE: Quantifying the time-varying prognostic performance of survival models
ABSTRACT BODY:
Abstract Body: Many prognostic models are created using survival data. In practice, the development of such models remains fairly ad hoc, and the temporal aspect of survival data is often underused. I will outline a number of existing methods for evaluating prognostic survival models. In particular, the emphasis will be on tools that can quantify how prognostic performance varies with time. I will also present a complementary new tool we have developed, the hazard discrimination summary (HDS; Biometrics 2017). HDS is an interpretable, risk-based measure of how a model's discrimination varies with time. I will also describe a connection between HDS and the Cox model partial likelihood.
AUTHORS/INSTITUTIONS: C.J. Liang, Biostatistics Research Branch, National Institute of Allergy and Infectious Diseases, Rockville, Maryland, UNITED STATES|P. Heagerty, Department of Biostatistics, University of Washington, Seattle, Washington, UNITED STATES|

CONTROL ID: 3347480
PRESENTER: Chul Moon
PRESENTER (INSTITUTION ONLY): Southern Methodist University
TITLE: The Bayesian Elastic Net based on Empirical Likelihood
ABSTRACT BODY:
Abstract Body: The elastic net estimates can be interpreted as Bayesian posterior estimates when the regression parameters have a prior that compromises between Gaussian and independent Laplace (i.e., double-exponential) priors. A significant challenge in the elastic net is that it assumes that data are normally distributed, which makes it not robust to model misspecification. In this article, we propose a Bayesian semiparametric approach for an elastic net model that is based on empirical likelihood. This approach relaxes the normal assumption on data, and hence we avoid problems with model misspecification. Under the Bayesian empirical likelihood approach, the resulting posterior distribution lacks a closed-form and has nonconvex support, which makes the implementation of traditional Markov chain Monte Carlo methods such as Gibbs sampling and Metropolis-Hastings very challenging. To solve the nonconvex optimization and nonconvergence problems, we implement the Hamiltonian Monte Carlo approach.
AUTHORS/INSTITUTIONS: C. Moon, Statistical Science, Southern Methodist University, Dallas, Texas, UNITED STATES|A. Bedoui, Boehringer Ingelheim, Ingelheim, GERMANY|

CONTROL ID: 3349451

PRESENTER: Renato Assuncao

PRESENTER (INSTITUTION ONLY): UFMG

TITLE: Detecting Spatial Clusters of Disease Infection Risk Using Sparsely Sampled Social Media Mobility Patterns

ABSTRACT BODY:

Abstract Body: Standard spatial cluster detection methods used in public health surveillance assign each disease case to a single location (typically, the patient's home address), aggregate locations to small areas, and monitor the number of cases in each area over time. However, such methods cannot detect clusters of disease resulting from visits to non-residential locations, such as a park or a university campus. Thus we develop two new spatial scan methods, the unconditional and conditional spatial logistic models, to search for spatial clusters of increased infection risk. We use mobility data from two sets of individuals, disease cases and healthy individuals, where each individual is represented by a sparse sample of geographical locations (e.g., from geo-tagged social media data). The methods account for the multiple, varying number of spatial locations observed per individual, either by non-parametric estimation of the odds of being a case or by matching case and control individuals with similar numbers of observed locations. Applying our methods to synthetic and real-world scenarios, we demonstrate robust performance on detecting spatial clusters of infection risk from mobility data, outperforming competing baselines.

AUTHORS/INSTITUTIONS: R. Assuncao, R.N. Souza, W. Meira, Computer Science, UFMG, Belo Horizonte, Minas Gerais, BRAZIL|D. Neill, Center for Urban Science and Progress, New York University, New York, New York, UNITED STATES|

CONTROL ID: 3367661
PRESENTER: Misung Yi
PRESENTER (INSTITUTION ONLY): Thomas Jefferson University
TITLE: Spatial index cancer tissue protein biomarkers
ABSTRACT BODY:
Abstract Body: Introduction: Quantitative Immunofluorescence (QIF) is used for immunohistochemistry (IHC) quantification of proteins that serve as cancer biomarkers. A common application of QIF-IHC is analysis of protein expressions in tissue microarrays (TMAs) that incorporate tumor tissues from large cohorts of patients. This technology combined with integrated image analysis allows for high-throughput measurement of proteins in individual cancer cells. However, only the mean signal intensity (MSI) of the protein expression across cancer cells is usually considered for developing protein biomarkers.
Methods: We propose a new approach for developing biomarkers using the information on spatial distribution of cellular signal intensity (CSI) of protein expression in cancer cell population. We view the protein QIF expression levels as marks in marked point process of cancer cells in the tissue and develop new spatial index predictors of clinical outcomes based on conditional mean and conditional variance of the marked point process. These characteristics of the marked point process are estimated using nonparametric kernel density estimates of under the assumption of second-order intensity reweighted stationary processes, which allow accommodating marked point processes with variably inhomogeneous point patterns of cancer cells.
Results: A simulation study demonstrates the ability of the proposed spatial indices to discriminate marked point patterns similar to the ones observed for protein expression in cancer cells. The utility of new spatial index protein biomarkers is investigated and compared to the standard MSI predictors using the protein expressions in tissue microarrays (TMAs) incorporating tumor tissues from over 1,000 breast cancer patients.
Discussion: The new approach provides new insight into standard IHC protein biomarkers and identifies novel biomarkers that do not have a prognostic value if only the mean signal intensity is considered.

Keywords: Nonparametric statistics, Personalized medicine, Risk Prediction; Statistical machine learning; Other-Marked point process, Marked point patterns, Second-order characteristics of marked point processes Microscopic image analysis, Quantitative Pathology
AUTHORS/INSTITUTIONS: I. Chervoneva, M. Yi, Thomas Jefferson University, Philadelphia, Pennsylvania, UNITED STATES|H. Rui, Medical College of Wisconsin Cancer Center, Milwaukee, Wisconsin, UNITED STATES|

CONTROL ID: 3367815

PRESENTER: Dong-Yun Kim

PRESENTER (INSTITUTION ONLY): National Institutes of Health

TITLE: A new sequential monitoring method for event rate in a clinical trial

ABSTRACT BODY:

Abstract Body: In this talk, we introduce a new continuous monitoring method for the event rate of time-to-event data when patients enter the clinical trial in a staggered fashion. Built on a sequential probability ratio test using boundaries derived from the nonlinear renewal theory with stationary perturbations (Kim and Woodroofe 2003), the sequential method uses both the counts of primary events and cumulative time of patients on trial. The monitoring gives an early warning if the target event rate is unlikely to be achieved by the end of the follow-up period. If necessary, this method can be used to suggest an extension of follow-up period to achieve the target rate with specified probability. We illustrate the method using the data from a Phase III clinical trial.

AUTHORS/INSTITUTIONS: D. Kim, National Institutes of Health, Bethesda, Maryland, UNITED STATES|