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PRESENTER: Ashok Krishnamurthy

PRESENTER (INSTITUTION ONLY): Mount Royal University

TITLE: Application of the Spatial SVEIRD model to the Ebola outbreak in Congo

ABSTRACT BODY:

Abstract Body: Over the last two decades, advanced methods have been developed to model the spatio-temporal evolution of real-world epidemics. Tracking and forecasting the full spatio-temporal evolution of an epidemic can help public health officials to plan their emergency response and health care.

We present advanced methods of spatial data assimilation to epidemiology, in this case to the ebb and flow of Ebola across the landscape of northeastern provinces in the Democratic Republic of Congo (DRC).

Data assimilation is a general Bayesian technique for repeatedly and optimally updating an estimate of the current state of a dynamic model. We present a stochastic spatial Susceptible-Vaccinated-Exposed-Infectious-Recovered-Dead (S-V-E-I-R-D) compartmental model to capture the transmission dynamics and the spatial spread of the ongoing Ebola outbreak in the DRC.

In this application the machinery of data assimilation acts to integrate incoming weekly incidence data into a fully spatial population model of Ebola transmission, within a Bayesian framework for the tracking process. For the current outbreak in DRC we use registered data (province-wide weekly counts of total Ebola cases and confirmed dead) from the World Health Organization (WHO) situation reports.

Our simulations show good correspondences between the stochastic model and the available sparse empirical data. A comparison between weekly incidence data set and our SVEIRD model coupled with Bayesian data assimilation highlights the role of a realization conditioned on all prior data and newly arrived data. In general, the SVEIRD model with data assimilation gives a better fit than the model without data assimilation for the same time period.

Our analyses may shed light more broadly on how the disease spreads in a large geographical area with places where no empirical data is recorded or observed.

The analysis presented herein can be applied to a large class of compartmental epidemic models. It is important to remember that the model type is not particularly crucial for data assimilation, the Bayesian framework is the key. Data assimilation neither requires nor presupposes that the model of the infectious disease be in the family of S-I-R compartmental models. The projected number of newly infected and death cases up to March 1, 2020 are estimated and presented. We provide a discussion and interpretation of our results.

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CONTROL ID: 3339525

PRESENTER: Yeongjin Gwon

PRESENTER (INSTITUTION ONLY): University of Nebraska Medical Center

TITLE: Network Meta-Regression for Ordinal Outcomes with Uncertain Categories: Applications in Comparing Crohn's Disease Treatments

ABSTRACT BODY:

Abstract Body: We often face a huge challenge in properly analyzing aggregate ordinal outcome data when there is no information to separate certain two subcategories exactly. In this talk, we propose a network meta-regression approach for modeling ordinal outcomes with uncertain categories in order to evaluate efficacy of treatments for Crohn's Disease. Specifically, we develop regression models based on aggregate trial-level covariates for the underlying cut points of the ordinal outcomes as well as for the variances of the random effects to capture population heterogeneity across trials. Our proposed models are particularly useful for indirect comparisons of multiple treatments that have not compared head-to-head within the network meta-analysis framework. Moreover, we introduce Pearson residuals and construct an invariant test statistic to evaluate goodness-of-fit in the setting of ordinal outcome meta-data. A case study demonstrating the usefulness of the proposed methodology is carried out with creating three different allocations of counts in those uncertain categories. We also conduct a full Bayesian analysis via the latent count approach.

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CONTROL ID: 3358890

PRESENTER: Myeonggyun Lee

PRESENTER (INSTITUTION ONLY): New York University School of Medicine

TITLE: Partially Linear Single Index Hazards Regression with Time-Dependent Covariates

ABSTRACT BODY:

Abstract Body: In studies with time-to-event outcomes, covariates of interest may also change over time. The classical Cox regression model can handle time-dependent covariates and assumes a constant effect on the log hazard function, which can be a limiting assumption in practice. In addition, when multiple time-dependent covariates are under study, it is also of great interest to model their joint effects by allowing a flexible functional form and to delineate their relative contributions to survival risk. Motivated by a cohort study investigating the effects of metabolic syndrome (MetSyn) on the risk of developing lung disease after a particulate exposure, we propose a partial single index hazards regression model with time-dependent covariates. We consider five components of MetSyn [body mass index, triglycerides, high density lipoproteins, glucose, and blood pressure]. The proposed method not only reduces the dimensionality of the covariates but also provides efficient estimates of the covariate effects. The flexible link function also allows nonlinear effects and interactions from the time-dependent variables on the log hazard function. We develop a two-stage iterative algorithm, in which a B-spline smoothing method is used to model the structured nonparametric single index component for the nonlinear covariate effects, followed by maximum partial likelihood estimation. We derive the asymptotic properties of the estimators for statistical inference. The proposed methods are illustrated using Monte Carlo simulation studies and applied to our cohort study.

Keywords: B-spline; nonparametric regression; partially linear single index model; time-dependent Cox regression model; metabolic syndrome; environmental exposures

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CONTROL ID: 3361051

PRESENTER: Seungyong Hwang

PRESENTER (INSTITUTION ONLY): University of California, Davis

TITLE: Estimating fiber orientation distribution through blockwise adaptive thresholding with application to HCP young adults data

ABSTRACT BODY:

Abstract Body: Recent technological advancements in neuroimaging make large amounts of brain imaging data available. However, extraction of meaningful information remains challenging due to the sheer volume and complexity of the data. Hence, there is a pressing need for statistical procedures that are computationally scalable and can accurately capture the neuronal structures from brain imaging data. We propose a fast algorithm for estimating the fiber orientation distribution (FOD) based on diffusion MRI data. This procedure treats the observed diffusion MRI signal at each voxel as a convolved and noisy version of the underlying FOD, and utilizes the spherical harmonics basis for representing FOD. The proposed method efficiently resolves the noise-amplification issue associated with this ill-posed inverse problem through appropriate regularization. Specifically, the coefficients at each level of spherical harmonics are shrunk by using a James-Stein type nonlinear shrinkage function adapted to this block of coefficients. This procedure significantly suppresses the noise and yields an estimator with low L2 risk. To further improve the estimation accuracy, a post estimation one-step super-resolution sharpening process is employed to enhance the localized peaks of the estimated FOD. The estimated FODs are used as input to a peak detection algorithm and the derived directions are then fed into a fiber tracking algorithm for reconstruction of the white matter fiber tracts. Subsequently, various brain structural related features (e.g., number of fibers) are derived. We illustrate the proposed method using both synthetic data and data from the Human Connectome Project (HCP). Moreover, we investigate the relationships between gender and handedness with brain structural connectivity features based on the HCP young adults data. We find significant gender main effects on the number of fibers within five subcortical regions. We also find significant gender-handedness interaction effects in two sub-cortical regions (Hippocampus and Amygdala).

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CONTROL ID: 3367655

PRESENTER: Mark J Meyer

PRESENTER (INSTITUTION ONLY): Georgetown University

TITLE: Bayesian Wavelet-packet Historical Functional Linear Models

ABSTRACT BODY:

Abstract Body: Historical Functional Linear Models (HFLM) quantify associations between a functional predictor and functional outcome where the predictor is an exposure variable that occurs before, or at least concurrently with, the outcome. Prior work on the HFLM has largely focused on estimation of a surface that represents a time-varying association between the functional outcome and the functional exposure. This existing work has employed frequentist estimation methods, with little attention paid to formal inference or adjustment for multiple testing. In this work, we propose a new functional regression model that estimates the time-varying, lagged association between a functional outcome and a functional exposure. Building off of recently developed function-on-function regression methods, the model employs a novel wavelet packet decomposition of the exposure and outcome functions that allows the user to strictly enforce the temporal ordering of exposure and outcome, which is not possible with existing wavelet-based functional models. We take a fully Bayesian approach, which allows us to conduct formal inference on the time-varying lagged association, while adjusting for multiple testing. We investigate the operating characteristics of our wavelet-packet HFLM, as well as the resulting inference procedures, in simulation and use the model to analyze data on the impact of lagged exposure to particulate matter finer than 2.5 μ g on heart rate variability in a cohort of journeyman boilermakers over the course of a day's shift.

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CONTROL ID: 3367728

PRESENTER: Rocío Joo

PRESENTER (INSTITUTION ONLY): University of Florida

TITLE: Mining the literature of movement ecology

ABSTRACT BODY:

Abstract Body: The field of movement ecology has experienced unprecedented growth in the last decade, due to technological advances that have brought large volumes of tracking data from various devices (e.g. GPS, accelerometers, video cameras), and analytical and programming tools that aid data processing and analysis. We identified >8000 scientific publications from the last decade, and used a text mining procedure to review the research done in movement ecology in several dimensions (research topics, species studied and methodological tools). A “dictionary” approach was used for aspects like software or biologgging device used, a list of possible software/devices was known a priori. Dictionaries are list of terms (e.g. “R Software”, “R Development Core”), grouped at a higher level under a set of categories (e.g. the category “R”). When a term in the dictionary was found in the text of a manuscript (e.g. in Material and Methods or the abstract), the manuscript was associated to the category the term corresponded to. Research topics, however, were not defined a priori. To identify the unknown and hidden topics in the publications, we fitted Latent Dirichlet Allocation models to the abstracts, which are three-level (topic, words, abstract) hierarchical Bayesian models for documents. Topics were defined by the model as a mixture of words, and as each abstract could be composed of one or more topics, the choice of words in the abstract would reflect the topics behind it; the probability of a given word appearing in an abstract would depend on the topic the abstract is addressing. In this presentation, we describe the methodology used to analyze the state of the field of movement ecology and present results based on the dictionary and topic modeling approaches.

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CONTROL ID: 3367765

PRESENTER: Joshua Keller

PRESENTER (INSTITUTION ONLY): Colorado State University, Colorado School of Public Health

TITLE: Error in Estimating Area-Level Air Pollution Exposures for Epidemiology

ABSTRACT BODY:

Abstract Body: In air pollution epidemiology, measurements of relevant exposure concentrations are typically made at point locations, resulting in spatial misalignment between the exposure data and health outcomes aggregated at the area level. To obtain values that match the spatial units of the health data, observations can be averaged directly or prediction models developed. We present a framework for evaluating the error in aggregating exposure concentrations to the area unit. We present estimators of mean squared error that can be used for model selection. We find that exposure prediction models, even when misspecified, outperform monitor averages in settings with realistic numbers of monitors and that important reductions in error of the health effect estimate can be obtained when restricting to areas with a monitor. In an analysis of long-term particulate matter concentrations across the United States, we estimated the error of the prediction model approach to be less than that of the monitor averaging approach on average across counties. We present health effect estimates about particulate matter exposure and pediatric asthma morbidity in the Medicaid population using each approach. Our findings support the use of a prediction model for estimating area-wide averages, even when restricting to areas that contain a monitor.

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CONTROL ID: 3367804

PRESENTER: Clarice Garcia Borges Demétrio

PRESENTER (INSTITUTION ONLY): ESALQ/USP

TITLE: COM-Poisson models with varying dispersion

ABSTRACT BODY:

Abstract Body: We propose an extension of the COM-Poisson model to jointly model the mean and the dispersion as functions of covariates taking into account, possibly, under- and overdispersion in the same count data set. Estimation and inference are based on the likelihood paradigm. Results from a simulation study show that the maximum likelihood estimators are consistent and unbiased for both mean and dispersion parameters. The methodology is illustrated with the analysis of a data set. The R codes and data set are available online.

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CONTROL ID: 3367823

PRESENTER: Saonli Basu

PRESENTER (INSTITUTION ONLY): University of Minnesota

TITLE: Estimation of SNP-based Heritability in Multi-Ethnic Studies

ABSTRACT BODY:

Abstract Body: SNP-based heritability of a trait is measured by the proportion of variance explained by additive effects of the observed single nucleotide polymorphisms (SNPs) over the entire genome. The Genome-wide complex trait analysis (GCTA) approach is now being routinely used to estimate SNP-based heritability for many complex traits. The basic concept behind this approach is to fit the effects of all the SNPs as random effects in a mixed linear model, where the variance of these genetic effects attributes to the heritability of the trait. The approach models the genotypic covariances among individuals in the sample: these covariances are captured by estimating a genetic relationship matrix (GRM). Heritability is estimated by the restricted maximum likelihood (REML) approach and the estimation relies heavily on the GRM estimated from the SNPs. Presence of subtle population substructures in the data could significantly impact the GRM estimation and may introduce bias in the heritability estimation. The common practice of accounting for such population substructure is to adjust for the top few principal components of the GRM as fixed effects in the mixed linear model. However, such adjustments often fail to correct for the bias due to population substructure. Here we propose an alternative way of estimating heritability in multi-ethnic studies through an estimating equation approach. Our proposed approach introduces adjustments for the population stratification in the estimating equation and allows for the additive genetic variance and residual variance to vary by ethnicity. We study the performance of our approach and the GCTA-REML approach with or without PC adjustments in presence of population stratification through extensive simulation studies. We estimate the heritability of height, BMI and other anthropometric traits in the UK Biobank cohort to investigate the impact of subtle population substructure on SNP-based heritability estimation for moderately and highly heritable traits.

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