Found 9 Records

CONTROL ID: 3340636

PRESENTER: Lawrence Lubyayi

PRESENTER (INSTITUTION ONLY): University of the Witwatersrand, Medical Research Council / Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine Uganda Research Unit

TITLE: Analysis of multivariate longitudinal immuno-epidemiological data using a pairwise joint modelling approach

ABSTRACT BODY:

Abstract Body: Background: Immuno-epidemiologists are often faced with multivariate outcomes, measured repeatedly over time. Such data are characterised by complex inter- and intra-outcome relationships which should be accounted for during analysis. Scientific questions of interest might include determining the joint effect of a treatment on the evolution of all outcomes together, or grouping outcomes that change in the same way. Modelling different outcomes separately may not be appropriate because it ignores the underlying relationships between them. In such situations, a joint modelling strategy is necessary. This work describes a pairwise modelling approach and discusses its benefits over more simple analytic approaches, with application to data from a study of the response to BCG vaccination in the first year of life, conducted in Entebbe, Uganda.

Methods: The study aimed to determine the effect of maternal latent Mycobacterium tuberculosis infection (LTBI) on infant immune response (TNF, IFN-g, IL-13, IL-10, IL-5, IL-17A and IL-2 responses to PPD), following immunisation with BCG. A simple analysis ignoring the correlation structure of multivariate longitudinal data is first shown. Univariate linear mixed models are then used to describe longitudinal profiles of each outcome, and are then combined into a multivariate mixed model, specifying a joint distribution for the random effects to account for correlations between multiple outcomes. Due to model fitting complexity because of the high number of outcomes, a pairwise joint modelling approach, where all possible pairs of bivariate mixed models are fitted, is used to obtain parameter estimates.

Results: Both univariate and pairwise longitudinal analysis approaches are consistent in finding that LTBI had no impact on the evolution of cytokine responses to PPD. Estimates from the pairwise joint modelling approach were more precise. Advantages of the pairwise approach include the opportunity to test for the effect of LTBI on the joint evolution of all outcomes and the ability to estimate association structures of the outcomes.

Conclusions: The pairwise joint modelling approach reduces the complexity of analysis of high-dimensional multivariate repeated measures, allows for proper accounting for association structures and can improve our understanding and interpretation of longitudinal immuno-epidemiological data.

AUTHORS/INSTITUTIONS: L. Lubyayi, J. Levin, Department of Epidemiology and Biostatistics, School of Public Health, University of the Witwatersrand, Johannesburg, SOUTH AFRICA|L. Lubyayi, P.A. Mawa, S. Cose, A.M. Elliott, Immunomodulation and Vaccines Programme, Medical Research Council / Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine Uganda Research Unit, Entebbe, UGANDA|P.A. Mawa, Uganda Virus Research Institute, Entebbe, UGANDA|S. Cose, A.M. Elliott, Department of Clinical Research, London School of Hygiene and Tropical Medicine, London, UNITED KINGDOM|E.L. Webb, MRC Tropical Epidemiology Group, Department of Infectious Disease Epidemiology, London School of Hygiene and Tropical Medicine, London, UNITED KINGDOM|

CONTROL ID: 3342321
PRESENTER: Fatima Jaouimaa
PRESENTER (INSTITUTION ONLY): University of Limerick
TITLE: Hierarchical Multi-Parameter Regression Survival Models
ABSTRACT BODY:
Abstract Body: Standard survival models introduce covariates through a single (scale) parameter, and we refer to this standard practice as Single-Parameter Regression (SPR). In contrast Multi-Parameter Regression (MPR) allows covariates to enter the model through multiple distributional parameters, i.e., scale and shape, and Burke and MacKenzie (2017) highlighted its flexibility in the context of survival data. We extend their work to handle multivariate survival data by introducing random effects in both the scale and the shape regression components. We consider a variety of possible dependence structures for these random effects (independent, shared, and correlated), and estimation proceeds using a h-likelihood approach. As the shape parameter may be viewed as a dispersion parameter for log-time, our proposal bears similarities to Double Hierarchical Generalized Linear Modelling (DHGLM). We investigate the performance of our estimation procedure using simulated data, and also consider a real data example
AUTHORS/INSTITUTIONS: K. Burke, F. Jaouimaa, University of Limerick, Limerick, IRELAND|

CONTROL ID: 3342497

PRESENTER: Yu Jin Kim

PRESENTER (INSTITUTION ONLY): The University of Auckland

TITLE: Analysis of Correlated Data from Two-phase Designs

ABSTRACT BODY:

Abstract Body: In resource-limited settings, a cost-efficient approach is to implement a two-phase design. Most statistical methods for the analysis of two-phase designs focus on settings where individual observations are independent. However, it is often the case that study participants are naturally correlated. For instance, patients are treated by clinics and they are correlated within a clinic or observations can be correlated when study participants have repeated measures. Ignoring correlation among observations may underestimate the true variance and may produce test statistics that are wrongly read as significant or not-significant, which results into invalid inferences or conclusions. Therefore, it is important to consider dependencies among the observations for estimation and inference. A recent method for the analysis of marginal models when the data exhibits correlation and arises from a two-phase design is weighted generalized estimating equations (WGEE). In this work, we consider the case of longitudinal data with missing information.

We compare two approaches to estimating the sampling weights: 1. A logistic model; 2. Calibrated weights. We illustrate the methods using longitudinal data from New Zealand on knee replacements performed between 2010 and 2015.

AUTHORS/INSTITUTIONS: Y. Kim, Statistics, The University of Auckland, Auckland CBD, NEW ZEALAND|

CONTROL ID: 3356133

PRESENTER: Ryo Tajiri

PRESENTER (INSTITUTION ONLY): Saga university

TITLE: Sparse Nested Component Analysis of Multimodal Brain Images

ABSTRACT BODY:

Abstract Body: Multimodal analysis combines and analyzes various types of brain images, and it has been widely applied in recent studies on brain diseases (Emine et al. 2019). In such analyses, dimension reduction is effective. One of the methods is the Supervised Multiblock Sparse Component Analysis (Kawaguchi et al. 2017). In this study, we propose the Sparse Nested Component Analysis developed from this conventional method.

Both methods consider two weights “within” and “between” images, and each brain image is compressed into each one-dimensional score by "within" weights, and the scores obtained from each brain image are combined as a total score by "between" weights. Therefore, "between" weights represent the contribution of each brain image in the total score. As in normal principal component analysis, multiple components of "within" weights are calculated in order, from the first component in the conventional method. Thus, complex high-dimensional data such as brain images are converted into one-dimensional scores that can be easily processed. These scores can serve as helpful biomarkers for disease diagnosis. We developed the proposed method based on an algorithm that can calculate multiple components of “between” weights for each “within” weight. Thus, it is expected that the more useful components for disease diagnosis can be extracted using the proposed method.

The proposed method was applied to real data from the Alzheimer's Disease Neuroimaging Initiative (ADNI), which consists of a collection of datasets for all subjects with both of the two modalities; structural Magnetic Resonance Imaging (sMRI) and Diffusion Tensor Imaging (DTI) data. We implemented this method using the R software and calculated the scores. The proposed method provides useful scores for disease diagnosis that could not be obtained using the conventional method. In addition, it can be used for classification with reasonable prediction accuracy based on the receiver operating characteristic (ROC) analysis.

Reference

Emine E.T. et al. (2019). Multimodal Neuroimaging: Basic Concepts and Classification of Neuropsychiatric Disease, Clinical EEG and Neuroscience, 50(1) 20-33.

Kawaguchi A, Yamashita F (2017). Supervised Multiblock Sparse Multivariable Analysis with Application to Multimodal Brain Imaging Genetics. Biostatistics, 18(4) 651-665.

AUTHORS/INSTITUTIONS: R. Tajiri, A. Kawaguchi, Saga university, Saga, Saga, JAPAN|

CONTROL ID: 3356283

PRESENTER: Freedom Nkululeko Gumedze

PRESENTER (INSTITUTION ONLY): University of Cape Town

TITLE: Case-deletion diagnostics for mixed-effects location scale models

ABSTRACT BODY:

Abstract Body: Mixed-effects location scale models allow simultanbeous modelling of between-subject and within-subject variability. These models include log-linear models for the between-subject and withi-subject variability. The log-linear models could potentially include covariates. We explore Cook-type influence diagnostics for the mixed-effects location scale model. We also extend these diagnostics to the multivariate longitudinal data case of the mixed-effects location scale model. A real dataset is analyzed to illustrate the influence diagnostgics.

AUTHORS/INSTITUTIONS: F.N. Gumedze, Statistical Sciences, University of Cape Town, Rondebosch, Western Cape, SOUTH AFRICA|

CONTROL ID: 3367614
PRESENTER: Hae-Won Uh
PRESENTER (INSTITUTION ONLY): University Medical Center Utrecht (UMCU)
TITLE: Identification of well performing bio-markers in smartphone acquired PPG signals
ABSTRACT BODY:
Abstract Body:
Our dataset consists of around 4500 photoplethysmographic (PPG) signals acquired with smartphone cameras. Data pre-processing was performed by subtracting a moving average and dividing by the envelope (the absolute value of the Hilbert transform of the signal) in order to detrend and demodulate each signal. Then a peak detection algorithm was constructed, and poor signals with a low quality score representing incorrect demodulation and noise with low quality indexes were filtered out.

From the filtered data ca 100 features were extracted: the signal, the peak sequence, the difference between consecutive peaks sequence and the second derivative of the signal (SDPPG), etc. Our aim was to predict health ageing from these features. As outcome, we considered chronological age as well as dichotomized one (young vs old). For feature selection and to avoid overfitting, we repeatedly applied linear and logistic ridge regression 100 times over 100 different subsamples of the training dataset, and averaged the ranking of two regression results using absolute value of coefficients. This procedure resulted in selecting two features: Turning Point Ratio (basically a counter of local extrema) and 1 feature from the SDPPG group (the “a” wave - since it is the easiest to acquire and to interpret). These two features performed well for classification of young/old on the external test set (AUC=0.86), and by adding other covariates (smoking, gender, weight, etc) we achieved AUC=0.91.

Alternatively, we also considered a convolutional neural network (CNN) approach. Using chunks of 15 consecutive peaks of pre-processed signals as dataset we compared various types of CNN and topologies. The best results were achieved from a 12 layers ResNet (residual neural network) with comparable prediction performance of young/old classification, AUC=0.90.

Our results highlight that 2 properly selected features combined with the covariates can perform as well as using computer intensive CNNs, which may lead to a possibly faster analysis of wearables with few or no disadvantages.
AUTHORS/INSTITUTIONS: H. Uh, Biostatistics and Research Support, University Medical Center Utrecht (UMCU), Utrecht, NETHERLANDS|G. Castellani, Experimental, Diagnostic and Specialty Medicine, Almar Mater Studiorum – Universita Di Bologna, Bologna, ITALY|N. Curti, L. Dall'Olio, Department of Physics and Astronomy, Almar Mater Studiorum – Universita Di Bologna, Bologna, ITALY|

CONTROL ID: 3367827

PRESENTER: Ellis Patrick

PRESENTER (INSTITUTION ONLY): The University of Sydney, Westmead Institute for Medical Research

TITLE: Identification of spatial ordering and distinct tissue microenvironments in high-parameter imaging cytometry datasets.

ABSTRACT BODY:

Abstract Body: Understanding the interplay between different types of cells and their immediate environment is critical for understanding the mechanisms of cells themselves and their function in the context of human diseases. Recent advances in high-parameter imaging cytometry technologies have fundamentally revolutionized our ability to observe these complex cellular relationships providing an unprecedented characterisation of cellular heterogeneity in a tissue environment.

Imaging cytometry data facilitates the identification of spatial organization of cell-types. That is, imaging cytometry data can be used to identify evidence that cell-types are aggregating or colocalising with each other. Established immunohistochemistry protocols only enable the visualization of a few cell-types concurrently and as such, analytical methods have been developed to identify the presence of pairwise spatial relationships between cell-types. However, high-parameter imaging cytometry technologies have now made it possible to simultaneously quantify hundreds or thousands of pairwise interactions between cell subsets. This has produced an urgent and exciting need to develop analytical frameworks that are necessary to tease apart and prioritise these high-dimensional interactions for further investigation.

In this presentation, I will introduce a novel methodology for identifying consistent spatial organisation of multiple cell-types in an unsupervised way. In short, our method clusters local indicators of spatial association (LISA) functions to enable the characterization of interactions between cell-types in contrast to traditional pairwise analysis. LISA curves are a localised summary of an L-function derived from a Poisson point process model and have been used in varied contexts to identify landmines or denoise images for text recognition. I will demonstrate the effectiveness of this framework on data generated from multiple high-parameter imaging cytometry assays including CODEX, CycIF and IMC. These illustrations showcase the utility of these new technologies and demonstrate that analysing cell-type interactions as a complex system, as opposed to a battery of pairwise tests, provides clear interpretational advantages.

AUTHORS/INSTITUTIONS: E. Patrick, School of Mathematics and Statistics, The University of Sydney, The University of Sydney, New South Wales, AUSTRALIA|E. Patrick, Westmead Institute for Medical Research, Westmead, New South Wales, AUSTRALIA|

CONTROL ID: 3374222

PRESENTER: Simon Bussy

PRESENTER (INSTITUTION ONLY): INSERM, UMRS 1138, Centre de Recherche des Cordeliers, Paris, France

TITLE: Lights: a generalized joint model for high-dimensional multivariate longitudinal data and censored durations

ABSTRACT BODY:

Abstract Body: In many clinical studies, it has become increasingly common to record the values of longitudinal outcomes until the occurrence of an event of interest.

With the development of electronic health records and an increased focus on personalized medicine, the need to implement multivariate models that account for a large number of longitudinal outcomes simultaneously is critical. Despite this, the state-of-the-art methods in this context have predominantly focused on univariate data, or on problems where the number of longitudinal outcomes are very low.

Our paper introduces a prognostic method called lights (generaLized joInt hiGH-dimensional longiTudinal Survival) to deal with the problem of joint modeling of longitudinal data and censored durations, in a high-dimensional context. The later introduces a latent variable modeling the heterogeneity within the patient population, with subgroups at different risks, and supposes a group-specific marker trajectory with a generalized linear mixed model for each longitudinal marker given the subgroup. Furthermore, a group-specific Cox risk of event includes multiple shared associations defined through a known functional family.

Inference is achieved using a novel fast stochastic approximation of a quasi-newton EM algorithm, by minimizing the negative log-likelihood penalized with elastic-net or group lasso regularization on the different parameter vectors of the model, depending on the desired interpretability power.

The estimated latent class membership posterior probabilities are used as discriminative marker rule in the cross-validation procedure for selecting the best regularization hyper-parameters.

The statistical performance of the method is examined on an extensive Monte Carlo simulation study, and finally illustrated on a publicly available dataset.

On this high-dimensional dataset, our proposed method is compared to the state-of-the-art models regarding risk prediction in terms of C-index, and regarding computing times. It provides powerful interpretability by automatically pinpointing significant covariates being relevant from a clinical perspective. Thus, we propose a powerfull tool for personalized medicine, with the ability of automatically determining significant prognostic longitudinal biomarkers, which is of increasing importance in many areas of medicine.

AUTHORS/INSTITUTIONS: S. Bussy, S. Zohar, A. Jannot, INSERM, UMRS 1138, Centre de Recherche des Cordeliers, Paris, France, Paris, FRANCE|A. Barbieri, INSERM, UMR 1219, Bordeaux Population Health Research Center, Univ. Bordeaux, Bordeaux, FRANCE|A. Jannot, Biomedical Informatics and Public Health Department, EGPH, APHP, Paris, FRANCE|

CONTROL ID: 3387232
PRESENTER: Zahra Aminifarsani
PRESENTER (INSTITUTION ONLY): Lorestan University
TITLE: Quantification Analysing of the Fluorescence Microscopy Images
ABSTRACT BODY:
Abstract Body: Colocalization analysis is a popular method for
the quantitative analysis in fluorescence microscopy imaging. The localization
of marked proteins in the cell nucleus allows a deep insight into biological processes in the nucleus. Several metrics have been developed for measuring the
co-localization of two markers, however, they depend on subjective thresholding
of background and the assumption of linearity.
We propose a robust method in order to
estimate the bivariate distribution function of two color channels. From this, we
can quantify their co- or anti-colocalization. The proposed method is a combination of the Maximum Entropy Method (MEM) and a Gaussian Copula, which
we call the Maximum Entropy Copula (MEC). This new method can measure
the spatial and nonlinear correlation of signals to determine the marker colocalization in fluorescence microscopy images.
RESULTS The proposed method is compared with MEM for bivariate probability distributions.
The new colocalization metric is validated on simulated and
real data. The results show that MEC can determine co- and anti-colocalization
even in high background settings. MEC can, therefore, be used as a robust tool
for colocalization analysis.
AUTHORS/INSTITUTIONS: Z. Aminifarsani, statistics, Lorestan University, Khorramabad, IRAN (THE ISLAMIC REPUBLIC OF)|