LIST OF POSTER ABSTRACTS – SAM2026 - Bordeaux

POSTER 1

- Caterina Gregorio caterina.gregorio@ki.se

Title: Hidden multistate models to study multimorbidity trajectories

Authors: Valentina Manzoni, Francesca Ieva, Amaia Calderon Larrañaga, Davide Liborio Vetrano, Caterina Gregorio

Institution: Karolinska Institutet, Solna, Sweden

Abstract :

Background

Multimorbidity among older adults is common, heterogeneous, and highly dynamic. It is also strongly linked to disability and increased healthcare utilization. However, current methods for studying multimorbidity trajectories are either descriptive or based on discrete-time models, which struggle to handle irregular observation intervals and right-censoring effectively

Methods

We developed a continuous-time hidden multistate modeling framework to study transitions among latent multimorbidity patterns, accounting for interval censoring and misclassification. A simulation study compared different model specifications under varying sample sizes and follow-up schemes. The best-performing specification was applied to longitudinal data from the Swedish National Study on Aging and Care - Kungsholmen (SNAC-K), including 2,716 multimorbid participants followed for up to 18 years.

Results

Simulation results showed that hidden multistate models substantially reduced bias in estimating transition hazard compared to non-hidden models. Fully time-inhomogeneous models outperformed piecewise approximations. Analysis of SNAC-K confirmed the feasibility and practical utility of this framework: it enabled identification of risk factors for accelerated progression toward complex multimorbidity and revealed a gradient of mortality risk across patterns.

Discussion

Continuous-time hidden multistate models provide a robust alternative to traditional approaches, while enabling individualized predictions. Such methodological advances are critical for identifying risk factors and designing targeted interventions and secondary preventive strategies for multimorbidity in aging populations.

POSTER 2

- Thomas Spain T.Spain@liverpool.ac.uk

Title: Prediction models for repeated medical events: joint modelling approaches and current practice

Authors: Thomas Spain, Laura J. Bonnett, Maria Sudell

Institution: Department of Health Data Science, Institute of Population Health, University of Liverpool

Abstract :

Many chronic conditions are characterised by recurrent events alongside longitudinally evolving patient information. Despite this, prognostic models in applied research commonly simplify the data structure by analysing time to first event or modelling event counts using predictors measured at baseline. These approaches fail to fully exploit available longitudinal information and obscure important differences between recurrent event modelling frameworks.
This work focuses on prediction modelling for repeated medical events using joint modelling methodologies that link longitudinal predictors with recurrent event processes. We are conducting a systematic review to identify and categorise existing applications of joint recurrent event models in chronic condition research. Models are classified according to their recurrent event framework (e.g. Andersen-Gill; Prentice, Williams & Peterson; marginal; and frailty-based models), the specification of longitudinal components, the association structure linking longitudinal and event processes, estimation strategies, and available software. Attention is paid to how models are formulated for prediction, including the use of dynamic risk updating and the reporting of validation or performance measures.
Based on gaps identified in the review, we are undertaking an empirical comparison of commonly used recurrent event and joint modelling frameworks fitted to the same dataset. This comparison is designed to assess predictive performance under a unified validation strategy and the latest results will be presented at the conference.
This work aims to clarify the current methodological landscape for recurrent event prediction and provide practical guidance for statisticians developing and evaluating prediction models that incorporate longitudinal information.

POSTER 3

- Teun B Petersen Teun.Petersen@mrc-bsu.cam.ac.uk

Title: Decomposing the Uncertainty of Dynamic Risk Predictions using Value of Information

Authors : Teun B Petersen, Sida Chena, Angela M Woodb, Christopher H Jacksona, Jessica K Barretta
Institution: MRC Biostatistics Unit, University of Cambridge, Cambridge, UK ; Department of Public Health and Primary Care, University of Cambridge, Cambridge, UK

Abstract :
Quantifying the uncertainty of clinical risk predictions is essential for determining a model's reliability and showing the strength of evidence. In dynamic risk prediction, longitudinal trajectories are used to make risk predictions as new data becomes available. These are often estimated using joint models (JMs) for longitudinal and time-to-event data. JMs consist of two sub-models: a mixed-effects model to describe the repeated measurements (e.g. of a patient's biomarkers), and a Cox proportional hazards model, which are interlinked by shared random effects. The uncertainty in risk predictions from JMs stems therefore from multiple sources which could be disentangled for more effective clinical interpretation.
We propose a framework to decompose the uncertainty of dynamic risk estimates into two key components: 1) patient-specific uncertainty, which arises from estimating an individual's trajectory from a limited number of longitudinal measurements, and 2) model-specific uncertainty, which is inherent to the underlying prediction model fitted

on a finite dataset. To this end, we borrow the concept of the expected value of partial perfect information from value-of-information literature and apply it to the reduction in uncertainty as a consequence of knowing a patient's random effects. We apply this method to predicting hospital readmission for heart failure patients, using electronic health record data from 32,471 patients admitted for heart failure in the East of England region. Given that early heart failure rehospitalisation is frequent and might often be preventable, a clearer understanding of individual readmission risk and its sources of uncertainty could aid decisions on post-discharge care and monitoring strategies.
High patient-specific uncertainty may indicate that collecting additional longitudinal measurements for a patient could improve the precision of their risk estimate. While high model-specific uncertainty highlights the limitations of the sample size of the JM. Illustrating this distinction allows clinicians to better assess the reliability of individual predictions, supports more informed, shared decision-making, and could improve sample size calculations for future dynamic risk models.

POSTER 4

- Maria Sudell mesudell@liverpool.ac.uk

Title: Network meta-analysis of joint longitudinal and time-to-event data using Stan

Authors *Maria Sudell, Catrin Tudur Smith, Ruwanthi Kolamunnage-Dona*
Institution: University of Liverpool

Abstract: In healthcare, it is common that there are many possible treatments for a given condition. Commonly, no clinical trials exist that compare all possible treatment simultaneously. As such, methods such as Network Meta-Analysis (NMA) exist to combine information supplied by multiple studies across a connected network of treatments, to allow comparison of different treatments even if they have never been compared head-to-head in a clinical trial.
Modern healthcare often involves tracking biomarkers over time, and using these repeated measures to predict clinical events of interest. Joint models for longitudinal and time-to-event data provide an approach to simultaneously analyze such outcomes and estimate the relationship between them. However, methods to analyze related longitudinal and time-to-event data across a network of treatment options, where contributing studies investigate different combinations of treatments, are lacking.
This research defines a novel joint modelling approach that encompasses network meta-analytic techniques, to allow investigation of the relationship between longitudinal and time-to-event outcomes in the presence of a connected network of treatments. Consistency equations are demonstrated to hold across the association structure in current value shared parameter joint models. The developed methodology is implemented in the Stan statistical software, and demonstrated in the INDANA cardiovascular dataset.

POSTER 5

- Lisa Crépin lisa.crepin@u-bordeaux.fr

Title: Regularized estimation in high-dimensional mechanistic models

Authors Lisa CRÉPIN[1], Morgan CRAIG[2], Cécile PROUST-LIMA[3], Mélanie PRAGUE[1]
Institution:[1] Université de Bordeaux, Inria, Inserm, Bordeaux Population Health Research Center, Vaccine Research Institute, Créteil, France [2] Université de Montréal, Centre de recherche Azrieli du CHU Sainte-Justine, Montréal, Canada

[3] Université de Bordeaux, Inserm, Bordeaux Population Health Research Center
Abstract: Mechanistic models are widely used to describe and explain biological processes over time. However, they typically rely on a limited number of observable compartments and sparse longitudinal data. As a result, these models are often either too simple to capture complex bio logical phenomena, such as immune response dynamics following vaccination, or they face identifiability issues, particularly when considering interindividual variability in the form of nonlinear mixed-effects models based on systems of differential equations. In parallel, with ongoing technological advances, longitudinal high-throughput data (e.g., -omics, including transcriptomics and proteomics data) are increasingly available in various contexts and could bring valuable information into mechanistic models to better capture underlying biological processes. However, when considering complex models with multiple unobserved compartments, integrating such high-dimensional data to inform the dynamics of unobserved biological compartments remains a major challenge, both mathematically and for broader public health applications. We hypothesize that observed -omics biomarkers can be used to infer and explain the dynamics of unobserved immune compartments. Our goal is therefore to find biomarkers that can accurately translate the dynamics of these compartments.

Here, we propose an estimation and regularization method for mechanistic models that involve multiple unobserved compartments, measured by high-dimensional longitudinal biomarker data. We aim to identify relevant biomarkers by regularizing the parameters linking them to the la tent unobserved compartments while simultaneously estimating the population parameters from the structural mechanistic model. To do so, we are developing an iterative algorithm able to estimate and regularize all the parameters of the model. The algorithm iterates between a regularization step and a mechanistic inference step. The first step updates coefficients linking latent compartments to biomarkers by computing penalized log-likelihood derivatives, approximated via second-order Taylor development. The mechanistic inference step focuses on estimating the mechanistic parameters using the Stochastic Approximation Expectation-Maximization (SAEM) algorithm, implemented through the Monolix software, considering the updated regularized coefficients from the first step. This approach allows us to find which biomarker's dynamics can accurately describe the dynamics of the unobserved compartments of our model.

To demonstrate our methodology, we investigated the robustness of the proposed approach in simulation and used it in an application on immune responses to the Pfizer/BioNTech COVID-19 mRNA vaccine (BNT162b2). Rinchai et al. (*Science Advances*, 2022) examined daily collected blood samples of 15 infection-naïve individuals for 9 days following each one of the two vaccine injections. The dataset contains 8172 gene expression measurements, regrouped in 34 pathways defined by Biomart (Durinck et al. 2005). We also used the serological samples obtained at baseline, day 7 and day 14 to inform on the observed compartment of antibodies.

To find which gene accurately translates the dynamics of unobserved compartments in our post vaccination immune response model, in particular the short-lived antibody secreting cells compartment, we therefore apply our developed method implemented in the REMixed R package. Here, we will discuss this particular application and show how REMixed performs when integrating gene expression measurements into a mechanistic model of immune response post-vaccination.

POSTER 6

- Ziyuan Wang ziyuan.wang-4@postgrad.manchester.ac.uk

Title: Dynamic Prediction of Acute Kidney Injury in Heart Failure Patients: Joint Modelling of Serum Creatinine and Time-to-AKI

Authors: Ziyuan Wang, University of Manchester

Abstracts: We developed a dynamic prediction model for time to acute kidney injury (AKI) among patients diagnosed with heart failure (HF) in England, using data from the Clinical Practice Research Datalink (CPRD).

We employed a shared-parameter joint model linking the longitudinal serum creatinine process with time to AKI to account for the association between the two processes. The model was estimated using Markov chain Monte Carlo (MCMC). Due to the computational burden of model estimation, we adopted a consensus approach.

We assessed the model's predictive performance using leave-one-region-out internal–external validation. Predictive performance over time was evaluated in terms of discrimination and calibration, and we examined how different choices of observation and prediction windows influenced performance.

POSTER 7

- Jih-Chang Yu jcyu@gm.ntpu.edu.tw

Title: Semiparametric Transformation Models for Interventional Path-Specific Effects with Multiple Time-to-Event Mediators

Authors: Jih-Chang Yu

Institution: National Taipei University, Taiwan

Abstract:

Disease progression is often characterized by a sequence of time-to-event milestones subject to right censoring and structural dependence, where the occurrence of later events may preclude earlier ones. For instance, in the progression from hepatitis B infection to death, patients may experience intermediate events such as liver cirrhosis and hepatocellular carcinoma. Quantifying causal effects along specific pathways is scientifically critical yet methodologically challenging, because multiple time-to-event mediators are correlated and constrained by an event-ordering structure. While recent nonparametric approaches have addressed interventional path-specific effects (iPSE) in this context, they often rely on stratification to adjust for confounding, which can lead to substantial efficiency loss—particularly when confounders are continuous or high dimensional. To balance robustness and efficiency, we adopt a semiparametric transformation model family that enables data-adaptive specification selection within the family while adjusting for confounders by including them as covariates. Simulation studies show that this approach achieves substantially smaller variance than the nonparametric estimator and accurately recovers the target iPSE when the selected model is correctly specified. In an analysis of the motivating clinical dataset, our conclusions are consistent with prior nonparametric results but with stronger statistical significance, demonstrating practical gains from transformation-family model selection.

POSTER 8

- Alexander Brown abrown94@qub.ac.uk

Title : Robust Mixed-Effects Models With Component-Specific Degrees of Freedom: Independent and Nested Approaches

Authors: Alexander Brown, Lisa McFetridge, Charles Gillan, Karen Cairns, Murali Shyamsundar,
Institution: Queen's University Belfast

Abstract: In longitudinal data, outliers are common in random effects (b-outliers) and random error terms (e-outliers), violating the Gaussian assumption of mixed-effects models, reducing efficiency (Pinheiro 2001). A common approach is to assume multivariate t-distributed data to accommodate heavy tails. However, this imposes identical marginal distributions across all random effects. Random intercepts and random slopes, while often correlated, may also have varying tail weights, a scenario current approaches cannot flexibly accommodate.

This study considers two distributions to allow for independent degrees of freedom. The first, T-IC, is a multivariate t-distribution with independent chi-squared terms introduced by Ogasawara (2022), enabling component-specific marginals. The second, T-NC, is a novel distribution that extends T-IC through nested chi-squared scaling, producing tail dependence while preserving separate degrees of freedom. Yu et al. (2014) proposed a robust model for T-IC distributions (RMT-IC); as T-IC and T-NC distributions were not previously available, the model can now be evaluated using these formulations.

A simulation study was performed that compares (i) the Gaussian mixed-effects model, (ii) the standard robust t-model with a shared degree of freedom (RMT), (iii) the RMT-IC, and (iv) a novel model for T-NC random effects. Results show that the Gaussian and RMT models perform poorly under both T-IC and T-NC data. For the RMT, when the degrees of freedom for the slope and intercept had good separation (5 and 30, respectively), coverage for variance components fell to 48–64%, intercept variance was overestimated by 21.95%, slope variance was underestimated by 12.86%, and MSE increased substantially. A shared degree of freedom in the RMT model is therefore too restrictive when the b-outliers have differing degrees of freedom.

For T-NC data, the RMT-IC performed well overall, but overestimated covariance (10.30%), which increased with correlation between the random effects and occurred primarily with heavy outliers. In contrast, the RMT-NC improved covariance estimation under tail dependence regardless of correlation.

To illustrate real-world impacts, RMT-IC and RMT-NC were applied in the analysis of ICU patients' biomarkers in the ICU at Royal Victoria Hospital Belfast from April 2020 to January 2024. Longitudinal urea measurements were analyzed, as urea has been seen to be a predictor of patient mortality in ICU patients. With extreme patient responses, this enhanced coverage and accuracy boost confidence in the identification and interpretation of treatment effects and biomarker associations, aiding clinical decision-making.

This work highlights the impacts on bias and precision that restrictive assumptions on the marginal distributions of the random effects can produce, where the commonly used RMT introduces substantial bias under such conditions where heterogeneity exists.

POSTER 9

- Daniel Phillips daniel.phillips@st-hughs.ox.ac.uk

Title: Multiple imputation for joint modelling applied to correlates of protection after vaccination
Authors: Daniel Phillips
Institution: University of Oxford
Abstract: We developed a two-stage multiple imputation approach to fit joint models of longitudinal and time-to-event data. The method is a useful alternative when a Bayesian joint model will not converge. We use multiple imputation to propagate the uncertainty in the longitudinal component through to the time-to-event component. To account for informative censoring, we include the event indicator and Nelson-Aalen estimate of cumulative hazard as predictors in the longitudinal component. Since the resulting posterior is not Gaussian, Rubin's rules do not apply, so we use an approximate Bayesian sampling method to pool the results. We apply this method to estimate vaccine-induced immune correlates of protection for COVID-19, that is, the relationship between antibody levels and vaccine-induced protection against infection. We model decaying log antibodies in a Bayesian linear hierarchical model. We exponentiate the current value of the longitudinal trajectory to include time-changing antibody levels in the time-to-infection model. This allows us to estimate the relationship between antibody levels at the time of exposure and subsequent infection. We apply our method to data from the Oxford-AstraZeneca COVID-19 vaccine trials (COV002, NCT04400838).

POSTER 10

- Lise Gamboa lise.gamboa@u-bordeaux.fr

Title: Interpreting Random Survival Forests with Longitudinal Predictors Using Partial
Dependence Plots
Authors : Lise Gamboa, Robin Genuer, Cécile Proust-Lima
Institution: Univ. Bordeaux, Inserm Bordeaux Population Health Research Center, France
Abstract: Random Survival Forests (RSF) are an extension of Random Forests designed for time to-event data. The main advantage of this method is that they provide a flexible alternative to traditional survival models such as the Cox model. In particular, they can capture non-linear relationships and interactions between variables without requiring strong modeling assumptions. More recently, the DynForest methodology (Devaux et al. 2023) extended RSF to the case of longitudinal predictors, allowing the repeated predictor measures collected over time to be incorporated into RSF. Although these models often achieve good predictive performance, they remain difficult to interpret. As with many machine learning methods, it is not clear how the predictors influence the prediction, and the issue is even more complicated with time-varying predictors. This work aimed to propose an interpretation tool to quantify and better understand how exposure trajectories influence a time-to-event in DynForest. We focused on Partial Dependence Plots (PDP), an interpretability tool in machine learning that had been studied in the context of survival analysis from time-independent predictors (Langbein et al 2024). We adapted PDP to the context of longitudinal predictors and investigated the quantification of the associated uncertainty. The proposed approach is evaluated through simulation studies and illustrated on real data.