Wednesday 10th July

0830-0900	Short Course Registration		
0900 - 1230	Course 1: Extended Mixed Effects Regression Modelling	Course 2: Design of Complex Experiments in Biological Research	Course 3: Investigating Spatial Heterogeneity with Geographically Weighted Models
1230 - 1330	Lunch		
1130-1330	Registration		
1330 - 1400	Opening Ceremony		
1400 - 1500	Keynote Presentation: Professor Per Andersen		
1500 - 1530	Tea/Coffee Break		
1530 - 1630	Contributed Session 1: Joint Models	Contributed Session 2: Statistics for Omics	Contributed Session 3: Time series and Spatial data
1630 - 1700	Poster Lightning Presentations		
1700 - 1830	Poster and Drinks Reception		

Thursday 11th July

0900 - 1030	Invited Session 1: Complex Survival Data		
1030 - 1100	Tea/Coffee		
1100 - 1230	Contributed Session 4: Survival Analysis	Contributed Session 5: Bioinformatics and Statistical Genetics	Contributed Session 6: Design of Experiment
1230 - 1330	Lunch		
1330 - 1500	Contributed Session 7: Statistics for Agriculture	Contributed Session 8: Multivariate and High-dimensional Data	Contributed Session 9: Bayesian Methods
1500 - 1530	Tea/Coffee Break		
1530 - 1700	Invited Session 2: Intensive Longitudinal Data		
1700 - 1800	Contributed Session 10: Mixture Models	Contributed Session 11: Causality	Contributed Session 12: Longitudinal Data
1800 - 1930	Tours		
2000 - 2300	Conference Dinner and Awards		

Friday 12th July

0900 - 1030	Invited Session 3: Post-selection Inference
1030 - 1100	Tea/Coffee Break
1100 - 1230	Special Session: The Past, Present and Future of Agricultural Statistics
1230 - 1330	Fisher Memorial Lecture: Professor Brian Cullis and Dr Alison Smith
1330 - 1345	Closing Ceremony
1345 - 1430	Lunch

Keynote Presentation

Multi-State Models in Medical Research

Per Kragh Andersen

In longitudinal studies of patients, a number of ***disease states*** can often be identified. Thus, patients who have undergone bone marrow transplantation may experience a relapse or die in remission; patients with affective disorders may be in psychiatric hospital, out of hospital, or have died, and patients with liver cirrhosis and esophageal varices may experience a variceal bleeding or they may die with or without a bleeding. A suitable mathematical framework for modeling data from such longitudinal studies is that of ***multi-state models***. In such models, the basic parameters are the ***intensities of transition*** between the states from which other ('marginal') parameters of interest – such as state occupation probabilities, average time spent in a given state, and expected number of recurrent events - may, in principle, be derived. We will briefly review classical methods for analyzing transition intensities, including the Cox regression model and other hazard models. However, we will also discuss methods by which such marginal parameters may be directly targeted, i.e. without going via the intensities. In particular, we will discuss how marginal parameters may be analyzed using *pseudo-observations*. The methods will be illustrated via examples from hematology, psychiatry, and other medical fields.

39th Fisher Memorial Lecture

The Fisher Memorial Trust was set up to promote interest in the life and work of the great statistician, evolutionary biologist and geneticist, Sir Ronald Aylmer Fisher (1890-1962) and to maintain his scientific legacy by encouraging discussion of the scientific fields in which he was active. As such, the Fisher Memorial Lecture is organised and sponsored by the trust, which in 2019 takes place at the Channel Network Conference.

Design Tableau

Alison Smith and Brian Cullis

One of our main research interests over the past 30 or more years has been the use of linear mixed models (LMM) for the analysis of data from crop improvement programmes. These data arise from comparative experiments in which the aim, typically, is to select the “best” varieties. In order to maximise the accuracy of selection we have developed analytic procedures that involve LMM with complex variance and correlation structures. For example, we use separable auto-regressive models to mitigate the impact of spatial trend within experiments conducted in the field, and factor analytic models to extract key information about variety by environment interaction in the analysis of multi-environment trial data.

We were fortunate enough to have trained and worked as young biometricians when analysis

of variance (ANOVA) techniques were the primary method of analysis for comparative experiments.

Our tool of trade was the GENSTAT package, so that the elegant notation of Wilkinson and Rogers and the framework of Block and Treatment structures became ingrained in our statistical thinking. So, despite the complexity of the LMM we now use, we appreciate the importance of maintaining these fundamental concepts, in particular the link between the analysis and the experimental design. We are concerned that this view is shared by only a few, as is evidenced by what we regard as a widespread mis-use of LMM for comparative experiments. This may either be due to an unintentional lapse in transitioning from ANOVA to LMM or a complete lack of exposure to traditional methods of analysis for comparative experiments.

Over recent years, we have made it a priority to fill in this gap for our young statistical colleagues at the University of Wollongong. In particular we have attempted to provide a link between ANOVA and LMM and to explain how to derive LMM that reflect the randomisation employed in the design of the experiment, no matter how complex. We found this to be a non-trivial task and tried numerous educational tools but without great success. A turning point was Brian's introduction of an Honours Statistics course on experimental design at the University of Wollongong. He based this course on Rosemary Bailey's book and found words of wisdom that have inspired us to develop an approach that we have termed "Design Tableau" (DT). The main aim of DT is to provide a simple, but general series of steps for specifying the LMM for a comparative experiment. It is founded on the seminal work of Sir Ronald Fisher, John Nelder, Rosemary Bailey and Robin Thompson. The motivation and concepts underlying Design Tableau will form the basis of our presentation. We will discuss the formal link between ANOVA and LMM, describe the steps that constitute DT, illustrate DT for simple cases in which the LMM may be used to re-produce an ANOVA and finally demonstrate how DT can be applied in a wide range of complex comparative experiments.

Invited Session 1: Complex Survival Data

To make the most of the wealth of data from recent longitudinal studies, new models for survival data analysis have been recently developed. They allow to model simultaneously several events and/or recurrent events and/or model jointly the evolution of longitudinal markers accounting for complex observation designs and correlation structures. This session will present some of these recent developments in the field of survival models, multi-state models and joint models.

Non-standard bootstrap for non-standard time-to-event outcomes

Jan Beyersman, Institute of Statistics, Ulm University

The motivation behind this talk are outcomes in randomized clinical time-to-event trials where neither Kaplan-Meier-type methodology nor competing risks suffice. In a study on stem cell transplanted leukemia patients, we will aim at demonstrating superiority w.r.t the outcome probability "alive w/o immunosuppressive therapy". In a treatment trial for severe infectious diseases, we will aim at demonstrating non-inferiority w.r.t the outcome probability "cured and alive" on the entire follow-up period. Both of these outcome probabilities are non-monotone, and the first outcome is complicated by immunosuppressive therapy being switched on and off a random number of times. To this end, we will suggest ("wild" or "weird") bootstrapping on the multivariate hazard scale which will be subsequently translated onto probabilities. Comparison of treatment groups will be based on time-simultaneous confidence bands. Unlike the standard bootstrap which draws with replacement from the data, we will not require an i.i.d. data structure, but only general martingale properties. Examples of deviations from an i.i.d. setting are event driven trials in oncology or nested case-control studies. We will also outline how a third bootstrap approach can be used for planning, e.g., of sample size based on published data only.

The use of joint modelling to evaluate failure-times surrogate endpoints

Virginie Rondeau, Biostatistics Team, Bordeaux Population Health Inserm Research Center

Casimir Sofeu-Ledoux and Takeshi Emura

A surrogate endpoint can be used instead of the most relevant clinical endpoint to assess the efficiency of a new treatment. Before being used, a surrogate endpoint must be validated based on appropriate methods. Numerous validation approaches have been proposed with the most popular used in a context of meta-analysis, based on a two-step analysis strategy. For two failure-time endpoints, two association measurements are usually used, Kendall's tau at the individual-level and the adjusted coefficient of determination (R2adj) at the trial-level. However, this adjusted coefficient is not always available due to model estimation constraints. We propose a one-step validation approach based on a joint frailty model, including both individual-level and trial-level random effects. Parameters have been estimated using a semi-parametric penalized marginal log-likelihood method, and various numerical integration approaches were considered. Both individual and trial-level surrogacy was evaluated using a new definition of Kendall's tau and the coefficient of determination. Estimators' performances were evaluated using simulation studies and satisfactory results were found. The model was applied to individual patient data meta-analyses in gastric cancer to assess disease-free survival as a surrogate for overall survival, as part of the evaluation of adjuvant therapy. The proposed joint surrogate model showed satisfactory results compare to the existing two-step copula and one-step Poisson approaches. We proposed a tool to predict the effect of treatment on

the true endpoint, based on the observed effect of treatment on the surrogate endpoint. A user-friendly R package associated to this new surrogate endpoints validation approach will be exposed.

Expanded correlated mover-stayer multi-state models for characterising joint activity and damage in the hands of patients with psoriatic arthritis

Brian Tom, MRC Biostatistics Unit, University of Cambridge

In psoriatic arthritis, manifestations of the disease typically result in joints becoming swollen and/or painful (i.e. active joints), which are reversible through treatment or management strategies or spontaneously, and may lead to permanent joint damage. Understanding the interplay between disease activity (as measured by activity in the joints) and damage is of clinical importance as both processes are related to functional impairment. In this talk, we present an expanded multi-state model for the disease activity and damage processes at the individual hand joint level, which accounts for many important features of our cohort of psoriatic arthritis patients from the University of Toronto Psoriatic Arthritis clinic. Firstly, as there are 28 hand joints in a patient and there are extensive lengths of patients' follow-up, we use observation-level multivariate random effects to account for correlation between joints and time-varying unobserved heterogeneity. Secondly, we introduce dynamic covariates which capture the serial correlation due to the disease activity and damage processes' history and relax the Markov assumption. As there is some empirical evidence to suggest that a subset of patients will not progress to damage in the hands, we additionally introduce a mover-stayer component to our model. The models are fitted using maximum likelihood estimation and through both standard and novel parameterisations that provide interpretability, allow us to address important clinical questions regarding pattern of disease, whether damage begets damage, the relationship between disease activity and damage before and after the occurrence of damage and the existence and prevalence of a stayer subpopulation.

Invited Session 2: Intensive Longitudinal Data

The future in many scientific domains lies in devices recording in real-time and at high temporal frequency environmental, biological, physical and behavioral information. Such intensive longitudinal data require the development of new statistical methods that can for instance handle their functional nature. They also offer the possibility of exploring the dynamic of temporal changes by investigating for instance the heterogeneity both at the mean and variability levels. The speakers will illustrate such issues and developments in environmental studies with climate change effects on forests and in biomedical studies with the study of heart rate variability.

Shared parameter mixed-effects location scale models for intensive longitudinal data

Donald Hedeker, University of Chicago, hedeker@uchicago.edu

Intensive longitudinal data are increasingly encountered in many research areas. For example, ecological momentary assessment (EMA) and/or mobile health (mHealth) methods are often used to study subjective experiences within changing environmental contexts. In these studies, up to 30 or 40 observations are usually obtained for each subject over a period of a week or so, allowing one to characterize a subject's mean and variance and specify models for both. In this presentation, we focus on an adolescent smoking study using EMA where interest is on characterizing changes in mood

variation. We describe how covariates can influence the mood variances and also extend the statistical model by adding a subject-level random effect to the within-subject variance specification. This permits subjects to have influence on the mean, or location, and variability, or (square of the) scale, of their mood responses. The random effects are then shared in a modeling of future smoking levels. These mixed-effects location scale models have useful applications in many research areas where interest centers on the joint modeling of the mean and variance structure.

Modelling tree health and mortality for mitigation of climate change effects on forests

Nicole Augustin, University of Bath

Forest health is monitored in Europe by The International Co-operative Programme on Assessment and Monitoring of Air Pollution Effects (ICP Forests) in cooperation with the European Union. More recently climate change has contributed to the decline in forest health and monitoring data are increasingly being used to investigate the effects of climate change on forests in order to decide on forest management strategies for mitigation.

We present two applications on modelling extensive yearly monitoring forest health survey data from Germany.

The first application is for official reporting of forest health. We use a Generalised additive mixed model to model defoliation, an indicator for tree health, of 5 different tree species in Germany. The temporal trend of defoliation differs between areas because of site characteristics, climate and pollution levels, making it necessary to allow for space-time interaction in the model.

In the second application we combine forest health data on mortality and crown defoliation. On a changing grid, defoliation, mortality and other tree and site specific variables are recorded. We are interested in the process leading to tree mortality and this requires the inclusion of all potential drivers of tree mortality in the model. We use a smooth additive Cox model which allows for random effects taking care of dependence between neighbouring trees and non-linear smooth functions of time varying predictors.

This is joint work with Axel Albrecht, Stefan Meining, Heike Puhlmann (Forest Research Institute, Freiburg, Germany), Karim Anaya-Azquierdo, Alice Davis (University of Bath), Nadine Eickenscheidt, Nicole Wellbrock (Thuenen Institute, Germany) and Simon Wood (University of Bristol).

From the bottom of my heart. Models for pseudo-cardiograms obtained with mobile phones.

Paul Eilers, Erasmus University Medical Center, Rotterdam, The Netherlands

The blood flow in our skin fluctuates with the beating of our heart, and light reflection of the skin fluctuates with it. This makes it possible to measure heart rate with the camera of a modern mobile phone. This is called photoplethysmography (PPG). On Google Play or in Apple's App Store many applications can be found that can do this.

A step further is to record the (spatially averaged) camera signal over a longer time, say 60 seconds, roughly equivalent to 60 heart beats. It is a proxy for a true electrocardiogram (ECG) and can, in principle, provide important information on the condition and the functioning of the heart. A typical goal is the detection of arrhythmia, such as arterial fibrillation.

The PPG signal does not show sharp peaks like a true electrocardiogram (ECG). It looks more like a sine wave, with a small amplitude, on a strongly drifting baseline. Almost exclusively, researchers try to locate local peak maxima and use the distances between peaks to determine (aberrations in) the heart rate. Because of the low quality of the signal, the precision of this procedure is poor. I will present two statistical models as an improvement.

After trend removal, the signal looks like a sine wave with varying frequency and amplitude. Its logarithm can be modeled as a smooth series of complex numbers. The real part represents the amplitude and the imaginary part the phase. Both series are modeled with P-splines. The derivative of the phase gives the momentary frequency. This model is highly nonlinear, but it is possible to find good starting values for a fast, linearized, fitting procedure.

The second model assumes that sharp spikes are distorted by an impulse response function and that we measure a superposition of those strongly smeared out spikes. The goal is then to estimate the input spikes and the impulse response from a data series. This can be done, using regression with a so-called L0 penalty.

I will present theory and implementation of both models and apply them to real data. This is joint work with Hae-Won Uh (UMC Utrecht).

Invited Session 3: Post-selection inference in regression

In regression researchers often prefer simple models. They also want to do inference on the parameters of their model. If the same data are naively used for model selection and for inference, huge biases may occur. Post-selection inference addresses the question how to do proper inference in a selected model, taking into account the fact that the same data were used twice in the analysis.

Post-selection inference for genetic association studies

Ruth Heller, Department of Statistics and Operations Research, Tel-Aviv University

In genetic association studies, there is a natural grouping of the genome into regions of interests (ROIs, e.g., genes), which are comprised of single variants. For powerful identification of association with the phenotype at the region level, the test statistics of single variants within an ROI can be aggregated into a test statistic for the global null hypothesis that none of the single variants are associated with the phenotype. Following ROI discovery, the focus turns to identification of the single variants that drive the association, within the ROI. Failure to account for ROI discovery (e.g., few dozen genes out of the original 20,000) can lead to biased inference. We provide post-selection inference for the family of single variants within a discovered ROI. Our inference is exact for the normal model, and asymptotically justified otherwise. We adapt our post-selection inference to the setting in which only summary level data is available from the study of interest. Analyses that only use summary level data are very attractive since they can thus avoid privacy concerns and logistics of sharing individual level data. These analyses need information about the linkage disequilibrium (LD) between the variants, which can be obtained from reference panels. We shall discuss the interesting connection between the size of the study and the reference panel used, for valid and powerful post-selection inference.

Joint work with Nilanjan Chatterjee, Tzviel Frostig, and Amit Meir

Quantifying model uncertainty by model confidence sets

Aldo Solari, Department of Economics, Management and Statistics, University of Milano-Bicocca

A researcher often has at her disposal a collection of candidate models which could be fitted to data, and has to decide which ones are good models and which ones are bad models. Statistical inference can be used to conclude whether a model is good or bad but sometimes it leaves us with uncertainty: there is not enough evidence to reach a decision. Therefore the application of an inferential procedure provides a model confidence set, i.e. a partition of candidate models into good models, bad models and uncertain models.

On the one hand, the idea of quantifying model uncertainty by a model confidence set is interesting per se, because it provides an assessment of the power coming from the data to discriminate the models. On the other hand, a model confidence set can be used in combination with the application to the same data of model selection algorithms that deliver one or more "best" models. If the selected "best" model belongs to the set of bad models, then this selection is not admissible from the model confidence set perspective.

Two questions now arise: 1. What is the precise definition of good and bad models? 2. How to construct model confidence sets with strong inferential guarantees? We will look at these questions within the classical framework of Gaussian linear models, both with fixed and random designs.

With regard to the first question, what a good model is good for? We will first distinguish between the use of modelling for explanation and for prediction. Next, what are good and bad relative to? We will argue that from a variable selection perspective, i.e. of reducing the complexity of the full model, good and bad should be understood as relative to the full model, i.e. better than the full model and worse than the full model.

Typically model selection is not the final purpose of the analysis: for the selected models we are usually interested in e.g. estimation of their parameters or in prediction of future values. A particularly challenging task is to perform post selection inference, i.e. to perform model selection followed by statistical inference on the parameters of the selected models, all with the same data. We will discuss the relationship of the proposed approach with this challenging goal.

Statistical inference with F-statistics when fitting simple models to high-dimensional data

Hannes Leeb, University of Vienna and DataScience@UniVienna
Lukas Steinberger, University of Freiburg

We study linear subset regression in the context of the high-dimensional overall model $y = \Theta + \Theta' z + \varepsilon$ with univariate response y and a d-vector of random regressors z, independent of ε. Here, 'high-dimensional' means that the number d of available explanatory variables is much larger than the number n of observations. We consider simple linear sub-models where y is regressed on a set of p regressors given by $x = M'z$, for some $d \times p$ matrix M of full rank $p < n$. The corresponding simple model, i.e., $y = \alpha + \beta' x + \varepsilon$, can be justified by imposing appropriate restrictions on the unknown parameter Θ in the overall model; otherwise, this simple model can be grossly mis-specified. In this paper, we establish asymptotic validity of the standard F-test on the surrogate parameter β, in an appropriate sense, even when the simple model is mis-specified.

Special Session: The past, present and future of agricultural statistics

To mark 100 years of applied statistics at Rothamsted Research, there will be a special session celebrating the past, present and future of statistics in agriculture.

The invited speakers will be

Eileen Magnello, University College London
John Fenlon, University of Warwick
Fred van Eeuwijk, Wageningen University and Research

Contributed Session 1: Joint Modelling

Atanu Bhattacharjee

Joint Modeling of Longitudinal and Time-to-Event Data with Missing Time-Varying Covariates in Targeted Therapy of Oncology

Jessica Barrett

Joint mixed-effects location scale and time-to-event models: Blood pressure variability as a risk factor for cardiovascular disease

Cécile Proust-Lima

Dynamic modelling of Multivariate Latent Processes and Their Temporal Relationships: Application to Alzheimer's Disease

Freedom Gumedze

Variable selection for joint models of multivariate longitudinal and survival data

Contributed Session 2: Statistics for Omics

Magnus Münch

Empirical Bayes for drug efficacy prediction in cell lines

Mitra Ebrahimpoor

Analyzing Time-course Metabolite data in terms of Pathways

Mirrelijn van Nee

Improving clinical prediction for high-dimensional data: an Empirical Bayes approach to co-data learning

Hendriek Boshuizen

Count regression for microbiome data: use with permutation testing

Contributed Session 3: Time Series and Spatial Data

Gabrielle Kelly

Towards reliable spatial prediction

Felix Cheysson

Parametric estimation of locally stationary Hawkes time series

Hideyasu Shimadzu

Modelling growth and reproduction strategy of Daphnia under varying temperature conditions

Jens Hartung

Regional recommendations from cultivar evaluation trials

Contributed Session 4: Survival Analysis

Munir Hiabu

Smooth backfitting of proportional survival hazards

Kamaryn Tanner

Dynamic Predictions of Survival Outcomes: A Comparison of a Machine Learning Ensemble, Landmarking and Joint Modelling

Anja Rueten-Budde

Predictive accuracy for the interval-censored illness-death model

Alex Isakson

Superefficient estimation of future conditional hazards based on high quality marker information

Stephan Bischofberger

Smooth backfitting of additively structured hazard rates

Camille Sabathé

A regression model to evaluate the effect of covariates on complex quantities in **an** *illness-death model dealing with left-truncation and interval-censoring*

Contributed Session 5: Bioinformatics and Statistical Genetics

Mark van de Wiel

Statistical deconvolution of tumor gene expression data

Elizabeth Thompson

Effects of mis-specification of genotypic covariance matrices

Robert Curnow

Mate choice as a factor in speciation

Simone Tiberi

BANDITS: a Bayesian hierarchical model for differential splicing accounting for sample-to-sample variability and mapping uncertainty

Paulo Rodrigues

A complex trait with unstable QTLs can follow from component traits with stable QTLs: An illustration by a simulation study in pepper

David Causeur

Handling dependence in significance tests of high-dimensional parameter

Contributed Session 6: Design of Experiment

Steven Gilmour

Probability-based optimal designs to minimise separation

Peter Godolphin

Universally Balanced Repeated Measurement designs which remain perpetually connected after the loss of complete subjects

Francesco Innocenti

Relative efficiencies of two-stage sampling schemes for mean estimation in multilevel populations when cluster size is informative

Bairu Zhang

Functional analysis of variance (ANOVA) for orthogonal designs

Ahmed Abdullah

Evaluating the Aligned Rank Transform approach for the analysis of factorial associations with differential replication

Hans Hockey

Hockey sticks and broken sticks – part 2 – enhancing the gold standard placebo-controlled, randomized clinical trial for chronic diseases

Contributed Session 7: Statistics for Agriculture

Rosemary Bailey

The Design of Blocked Experiments when the Average Replication is Very Low

Stelian Curceac

Improved characterisation of extreme water flow events in a grassland context using a combined mechanistic and probabilistic modelling framework

Theo Pepler

Combining Cattle Movement Data with Stochastic Epidemiological Models to Identify Key Premises for Disease Spread

Baerbel Kroschewski

Analysis of a long-term nitrogen fertilization experiment on fen grassland

Johannes Forkman

Hypothesis Tests for Principal Component Analysis When Variables are Standardized

Contributed Session 8: Multivariate and High-dimensional Data

Jesse Hemerik

Robust testing in generalized linear models by sign-flipping score contributions

Jelle Goeman

All-Resolutions Inference: interactive inference for neuroimaging

Wessel van Wieringen

The generalized ridge estimator of the inverse covariance matrix

Emeka Uzochukwu

A Sparse Partial Least Squares Regression

Carel Peeters

Stable prediction with radiomics data

Matthieu Pluntz

A Simulation-Based Significance Test for the Lasso

Contributed Session 9: Bayesian Methods

Sophie Vanbelle

Modeling agreement for binary intensive longitudinal data

Jack Euesden

Application of Bayesian Methods to enhance the interpretability of insights from Genome-wide and Phenome-wide association studies in population-scale Biobanks

Kevin Dawson

Bayesian tumour sub-clone phylogeny reconstruction using a Dirichlet process mixture model and new post-processing methods

Gajendra Vishwakarma

A Bayesian Approach for Dynamic Treatment Regimes in Presence of Competing Risk Analysis

Erik van Zwet

A default prior for regression coefficients

Iva Budimir

A stochastic neutral model for the gene lengths distribution

Contributed Session 10: Mixture Models

Sara Wade

Enriched Mixtures of Generalised Gaussian Process Experts: Predicting Uncertainty in Cognitive Decline

Anaïs Rouanet

Nonparametric clustering approach for longitudinal cognitive measurements, baseline imaging and genetic data in precision medicine

Jan Schepers

A New Two-Mode Clustering Method For Binary Outcome Data

Alya Alzahrani

Multivariate Mixture Gaussian Model-based Classification of Hydrogen-Deuterium Exchange Rate

Contributed Session 11: Causality

Jacob Cancino-Romero

Causal joint models for the relationship between frailty, recurrent falls and mortality in the elderly

Ruth Keogh

Using sequential trials to estimate treatment effects in longitudinal observational data: Insights and application

Mia Klinten

Grand A weighted quantile approach to correct for dropout in randomised clinical trials

Sean Yiu

Calibrated Estimation of Inverse Probability of Treatment Weights for Marginal Structural Models

Contributed Session 12: Longitudinal Data

Emilie Leveque

A latent class Zero-Inflated Poisson mixed model for the identification of heterogeneous lifetime exposure intensity trajectories

Richard Parker

Using mixed-effects location scale models to investigate within-individual variability in cognitive function in later life

Corentin Segalas

Curvilinear bivariate mixed model with random changepoint to compare times of change between cognitive markers in Alzheimer's disease

David Hughes

Streamlined Models for Multiple Longitudinal Outcomes

Posters

Sarah Perryman, Nathalie Castells-Brooke, Richard Ostler, and Margaret Glendining

e-RA: the electronic Rothamsted Archive. Long-term data for modern day agroecological research.

Helen Metcalfe

Using nested sampling and residual maximum-likelihood to quantify scale-dependent relations between weeds and soil properties

Simone Tiberi

A flexible permutation approach to detect cell state transitions from high-throughput single-cell data

Jennifer Nicholas

Accounting for measurement error in longitudinal estimation of the effect of a mediator in clinical trials: a case study in multiple sclerosis

Oluwaseun Wale-Orojo

Modelling Categorical Data in Frequency Domain via Mutual Information Approach

Kirsty Hassall

A Bayesian Belief Network for Soil Quality and Health

Ian Nevison

Improving statistical literacy - Lessons from participating in Ethical Review Process committees.

Jess Evans

Modelling the diurnality of N2O emissions on the North Wyke Farm Platform

Mizanur Khondoker

Item Selection Using Penalised Item Response Theory (IRT) Models

Ajibola Taiwo Soyinka

Mutual Information Approach to Analysis of Entropy in Discrete Statistical Designs

Solimun

Consistency Of Bootstrap Resampling In Path Analysis Model With Various Resampling Size

Andrew Mead

An application of covariate-based constrained randomization in livestock research

Kirsty Hassall

Accounting for data sparsity when forming spatially coherent zones

Andrew Mead

A new long-term experiment for exploring the sustainability of arable cropping systems

Satyabrata Pal

In Search of Optimum Randomised Block Designs under Complex Heterogeneity (Within and Between Blocks) Situations

Ajibola Taiwo Soyinka

Order statistics approach to modeling and prediction of early mood swing

Harimurti Buntaran

Cross-validation of Stage-wise Mixed Model Analysis of Swedish Variety Trials with Winter Wheat and Spring Barley

Nseobong Uto

Semi-Latin Rectangles

Dennis te Beest

Possible pitfall of using log-ratio analysis on metagenomics data with many zeroes

Andy Lynch

Low-cost copy number profiling using repeat DNA, with implications for experimental design

Adji Achmad Rinaldo Fernandes

PLS and PWLS Based Comparison Of Nonparametric Smoothing Spline Path Function's Curves Estimation On Several Levels Of Heteroskedasticity

Mei Sum Chan

Biological ageing based on physical and biochemical biomarkers in 0.5 million UK Biobank participants

Hannah Worthington

Capture-Recapture-Recovery Models with Semi-Markov Survival

Christopher Jackson

Focused model comparison in practice: the "fic" package

Danilo Hottis Lyra

Functional QTL mapping and genomic prediction of 3d height in wheat measured using a robotic field phenotyping platform

Elisavet Syriopoulou

Partitioning of excess mortality of Hodgkin Lymphoma patients into treatment and cancer related mortality

John Addy

Identifying cub-populations of children based on their clinical immunological response to malaria

Christine Hackett

QTL mapping of hyperspectral imaging data on a population of raspberry

Maarten van Schaik

Modelling high dimensional count data using random effects