PROGRAMME AND ABSTRACTS

10th International Conference on

Computational and Financial Econometrics (CFE 2016)

`http://www.cfenetwork.org/CFE2016`

and

9th International Conference of the
ERCIM (European Research Consortium for Informatics and Mathematics) Working Group on

Computational and Methodological Statistics (CMStatistics 2016)

`http://www.cmstatistics.org/CMStatistics2016`

Higher Technical School of Engineering, University of Seville, Spain

9 – 11 December 2016

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CMStatistics: ERCIM Working Group on
COMPUTATIONAL AND METHODOLOGICAL STATISTICS

http://www.cmstatistics.org

The working group (WG) CMStatistics comprises a number of specialized teams in various research areas of computational and methodological statistics. The teams act autonomously within the framework of the WG in order to promote their own research agenda. Their activities are endorsed by the WG. They submit research proposals, organize sessions, tracks and tutorials during the annual WG meetings and edit journal special issues. The Econometrics and Statistics (EcoSta) and Computational Statistics & Data Analysis (CSDA) are the official journals of the CMStatistics.

Specialized teams

Currently the ERCIM WG has over 1650 members and the following specialized teams

BM: Bayesian Methodology

CODA: Complex data structures and Object Data Analysis

CPEP: Component-based methods for Predictive and Exploratory Path modeling

DMC: Dependence Models and Copulas

DOE: Design Of Experiments

EF: Econometrics and Finance

GCS: General Computational Statistics WG CMStatistics

GMS: General Methodological Statistics WG CMStatistics

GOF: Goodness-of-Fit and Change-Point Problems

HDS: High-Dimensional Statistics

ISDA: Imprecision in Statistical Data Analysis

LVSEM: Latent Variable and Structural Equation Models

MCS: Matrix Computations and Statistics

MM: Mixture Models

MSW: Multi-Set and multi-Way models

NPS: Non-Parametric Statistics

OHEM: Optimization Heuristics in Estimation and Modelling

RACDS: Robust Analysis of Complex Data Sets

SAE: Small Area Estimation

SAET: Statistical Analysis of Event Times

SAS: Statistical Algorithms and Software

SEA: Statistics of Extremes and Applications

SFD: Statistics for Functional Data

SL: Statistical Learning

SSEF: Statistical Signal Extraction and Filtering

TSMC: Times Series Modelling and Computation

You are encouraged to become a member of the WG. For further information please contact the Chairs of the specialized groups (see the WG's website), or by email at info@cmstatistics.org.

CFEnetwork
COMPUTATIONAL AND FINANCIAL ECONOMETRICS

http://www.CFEnetwork.org

The Computational and Financial Econometrics (CFEnetwork) comprises a number of specialized teams in various research areas of theoretical and applied econometrics, financial econometrics and computation, and empirical finance. The teams contribute to the activities of the network by organizing sessions, tracks and tutorials during the annual CFEnetwork meetings, and by submitting research proposals. Furthermore the teams edit special issues currently published under the Annals of CFE. The Econometrics and Statistics (EcoSta) is the official journal of the CFEnetwork.

Specialized teams

Currently the CFEnetwork has over 1000 members and the following specialized teams

AE: Applied Econometrics

BE: Bayesian Econometrics

BM: Bootstrap Methods

CE: Computational Econometrics

ET: Econometric Theory

FA: Financial Applications

FE: Financial Econometrics

TSE: Time Series Econometrics

You are encouraged to become a member of the CFEnetwork. For further information please see the website or contact by email at info@cfenetwork.org.

of the distribution of interest. Asymptotic properties are described and finite sample results are presented. We motivate the need for robust AIPW estimators with a follow up study on BMI combining data from an intervention study and population wide record linked data.

EO1313:   Robust estimation of mixture models with skew components via trimming and constraints
Presenter: **Agustin Mayo-Iscar**, Universidad de Valladolid, Spain
Co-authors: Luis Angel Garcia-Escudero, Francesca Greselin

Impartial trimming procedures are commonly applied in many statistical settings for getting robust estimators in the presence of contamination. In order to get this robust behavior, when estimating mixture models, it is necessary to apply jointly trimming and constraints. Robust estimators based in these tools are available for estimating the model parameters in mixtures of multivariate distributions, of linear regression models, and of factor analyzers, under normal components. We attempt to extend these benefits to the case of skew-normal components. We will show robust methodology based on the joint application of trimming and constraints for different mixture models settings. A drawback of this kind of approaches is related with choosing the input parameters values that this modelling required. We have available different tools for assisting to the users in getting these values.

EO033   Room 214   OPTIMAL AND EFFICIENT DESIGNS   **Chair: Po Yang**

EO1162:   Mismeasured response adaptive design: Theory and implementation
Presenter: **Xuan Li**, University of Minnesota Duluth, United States

Response adaptive design represents a major advance in clinical trial methodology that helps balance the benefits of the collective and the benefits of the individual and improves efficiency without undermining the validity and integrity of the clinical research. Response adaptive designs use information so far accumulated from the trial to modify the randomization procedure and deliberately skews treatment allocation in order to assign more patients to the potentially better treatment. Little attention has been paid to incorporating the problem of errors-in-variables in adaptive clinical trials. Some important issues of response adaptive clinical design with imperfectly measured outcomes are considered. Optimal allocations under various objectives and asymptotically best response adaptive randomization procedures are investigated in the presence of measurement error. Mismeasurement effects on treatment allocation are discussed for both discrete and continuous responses. The related simulation results are also presented.

EO1507:   Minimum contamination and beta-aberration criteria for screening quantitative factors
Presenter: **Chang-Yun Lin**, National Chung Hsing University, Taiwan

For quantitative factors, the minimum beta-aberration criterion is commonly used for examining the geometric isomorphism and searching for optimal designs. We investigate the connection between the minimum beta-aberration criterion and the minimum contamination criterion. Results reveal that ranking designs by the two criteria can be extremely inconsistent and hence the optimal designs selected by them are likely to be different. We provide statistical justifications showing that the minimum contamination criterion well controls the expected total mean square error of the estimation and demonstrate that it is more powerful than the minimum-aberration criterion on identifying geometrically non-isomophic designs.

EO089   Room 003   ANALYSIS OF MICROBIOME DATA   **Chair: Michele Guindani**

EO1237:   A Bayesian Dirichlet-multinomial regression model for the analysis of taxonomic abundances in microbiome data
Presenter: **Raffaele Argiento**, University of Kent, United Kingdom
Co-authors: Michele Guindani, Marina Vannucci, Duncan Wadsworth, Jessica Galloway-Pena, Samuel Shelburne

A Bayesian Dirichlet-Multinomial regression model is proposed which uses spike-and-slab priors for the selection of significant associations between a set of available covariates and taxa from a microbiome abundance table. The approach allows straightforward incorporation of the covariates through a log-linear regression parametrization of the parameters of the Dirichlet-Multinomial likelihood. Inference is conducted through a Markov Chain Monte Carlo algorithm, and selection of the significant covariates is based upon the assessment of posterior probabilities of inclusions and the thresholding of the Bayesian false discovery rate. We design a simulation study to evaluate the performance of the proposed method, and then apply our model on a publicly available dataset obtained from the Human Microbiome.

EO1239:   A Bayesian nonparametric analysis of heterogeneous data on microbial communities
Presenter: **Sergio Bacallado**, Cambridge University, United States
Co-authors: Lorenzo Trippa, Boyu Ren, Stefano Favaro, Susan Holmes

Human microbiome studies aim to characterise the microbial communities in the body and the effect of environmental factors on them. A range of experimental techniques have been developed in recent years to catalogue the species composition of a biological sample through ribosomal DNA sequencing, to measure the transcription level of microbial genes, and the synthesis of proteins and metabolites. Modelling such heterogeneous data with a coherent assessment of uncertainty from exploratory analysis, through model selection and inference presents a significant challenge. We propose a Bayesian approach based on latent factors, which is capable of combining insights from various experiments in a parsimonious and interpretable way. We discuss how to scale up computations to massive datasets and evaluate the robustness to prior parameters.

EO0983:   Longitudinal microbiome data
Presenter: **Snehalata Huzurbazar**, University of Wyoming, United States
Co-authors: Eugenie Jackson

As longitudinal microbiome studies become more common, it is important that we assess how to analyze such data. Methods for large, sparse multivariate count data collected over time are not common in traditional longitudinal data analysis. The first steps in most microbiome data analysis is often the use of ordination methods to explore the data and visually assess existence of patterns, especially of taxa composition with respect to covariate classes. We first consider options for such visualization for data collected over more than one time period on the same subjects. We then present a review of the literature for longitudinal inference for microbiome data, and consider other alternatives.