# 17TH ANNUAL MEETING OF THE BELGIAN STATISTICAL SOCIETY

## Lommel, (14) 15-16 October 2009

The preliminary program of the next meeting of the Belgian Statistical Society (BSS 2009) is now available on the conference web-site: http://www.sbs-bvs.be/

**Wednesday 14th October** (Young Statisticians Afternoon)

13h30 Registration and welcome

14h00 Contributed talks young statisticians

- Gordon Gudendorf (U.C.Louvain) *Nonparametric estimation of multivariate extreme value copulas*
- Koen Mahieu (K.U.Leuven) *Maxbias Curves for Multivariate Regression Estimators*
- Girma Minalu (U.Hasselt*) Estimating the impact of school closure on social mixing behavior and the transmission of close contact infections in eight European countries*

15h00 Presentations Quetelet price winners

- Bernard Francq (U.C. Louvain) *TBA*
- Dan Lin (U. Hasselt) *Testing Procedures on Comparisons of Several Treatments with one Control in a Microarray Setting*
- Andrea Kvitkovičová (Charles University in Prague) *Changepoint fractional polynomials in modelling the seroprevalence data*
- Elke Moons (U. Hasselt) *TBA*

- Veronique Storme (U.Gent) *Integration of Transcriptomics and Metabolomics for understanding Lignin Biosynthesis*

16h00 Break

16h20 Contributed talks young statisticians

- Jonathan Jaeger (U.C.Louvain) *Functional estimation in systems defined by differential equation using Bayesian smoothing methods*
- Christel Ruwet (U.Liège) *Detection of influential observations on the error rate based on the generalized k-means clustering procedure*

17h00 Quiz

18h00 Dinner

**Thursday, 15th October**

8h30 Registration

9h30 Welcome and Opening of the meeting.

9h40 Invited talk by Prof. Anthony Davison (EPFL, Lausanne)
*Modelling spatial extreme values.*

10h30 Break and Posters

10h50 Contributed talks

Quetelet

- Jan de Neve (U.Gent) *A semiparametric unified approach for the detection of differential gene expression in microarrays.*

- Emanuele Del Fava (U.Hasselt) *The co-infection between HCV and HIV: A joint modelling approach.*

- Tatsiana Khamiakova (U.Hasselt) *Gene filtering of microarray experiments with a complex design.*

- Forcheh Chiara Anyiawung (K.U.L.) *A novel approach for exploring functional relationships in gene expression data.*

Methodology

- Herbert Thijs (U.Hasselt) *The future of missing data.*

- Roula Tsonaka (K.U.L.) *A goodness-of-fit test for the random effects distribution in mixed models.*

- Olga Reznikova (U.C.L.) *On the estimation of the dynamic conditional correlation models.*

- Teh Amouh (F.U.N.D.P.Namur) *Stratified aggregation rule for multiple classifier systems.*

12h10 Lunch and Posters

14h00 Quetelet invited talk by Prof. Dimitris Rizopoulos (Erasmus University Rotterdam)
*Challenges in joint modelling of longitudinal and time-to-event data.*

14h50 Contributed talks

Biostatistics

- Réjane Rousseau (U.C.L.) *Combination of Independent Component Analysis and statistical modelling for the identification of metabonomic biomarkers in 1H-NMR spectroscopy.*

- Qi Zhu (U.Hasselt) *A Bayesian approach to modeling of the enzymatically 18O-labeled mass spectra.*

- Lixin Zhang (U.Liège) *Revisiting the multivariate coefficient of variation for comparing electrophoretic techniques in External Quality Assessment (EQA) schemes.*

Methodology

- Ilaria Prosdocimi (K.U.L.) *Analyzing Italian induced abortion data with extended generalized additive models.*

- Géraldine Laurent (U.Liège) *Estimation of the error distribution in right censored and selection biased regression models.*

- Jan Johannes (U.C.L.) *Global and local minimax-optimal estimation in functional linear model.*

15h50 Break and Posters

16h20 Contributed talks

Biostatistics

- Geert Molenberghs (U.Hasselt) *On the identifiability of the incomplete-data models and random-effects.*

- Teshome Birhanu (U.Hasselt) *Pseudo-likelihood estimation for incomplete data.*

Methodology

- Michiel Debruyne (U.Antwerpen) *An outlier map for support vector machine classification.*

- Arnout Van Messem (V.U.B.) *Consistency and robustness properties of SVMs for heavy-tailed distributions.*

17h00 Invited talk by Prof. Marc Hallin (U.L.B.)
*Multivariate quantiles and statistical depth: from L1 optimization to halfspace contours.*

17h50 Break

18h00 General assembly of the Belgian Statistical Society

19h00 Dinner

**Friday, 16th October**

9h00 IAP invited talk by Prof. Alois Kneip (University of Bonn)
*Functional linear regression.*

9h50 Contributed talks

Biostatistics

- Aysun Çetinyürek Yavuz (U.Liège) *A flexible Cox proportional hazards model for interval-censored data using Bayesian P-splines with an extension to frailty model.*
- Bart Van Rompaye (U.Gent) *Analyzing competing risks survival data faced with misclassified causes-of-death.*
- Jan Ramon (K.U.L.) *Handling missing values and censored data in PCA of pharmacological matrices.*

B-ENBIS

- Vishva M. Danthurebandara (K.U.L.) *Effect of choice complexity on design efficiency in conjoint choice experiments.*

- Bagus Sartono (U.Antwerpen) *A new method for the orthogonal blocking of strength-three orthogonal arrays.*

- Christian Ritter (U.C.L.) *Introducing R2wd and R2PPT, two R packages to create Word documents and Powerpoint presentations from R.*

10h50 Break and Posters

11h20 Contributed talks

Quetelet

- Kristof De Beuf (U.Gent) *Analysis of tiling array data using wavelet-based functional mixed models.*

- Amparo Yovanna Castro (U.Hasselt) *The estimation of the force of infection for HCV among injecting drug users (IDU's) using interval censored data.*

Methodology

- Tim Verdonck (U.Antwerpen) *A deterministic algorithm for the MCD estimator.*

- Stephan Van der Veeken (K.U.L) *Robust transformation to symmetry: a maximum trimmed likelihood approach.*

12h00Biostatistics invited talk by Prof. Marta Fiocco (Leiden University Medical Center)
*A new multivariate gamma distribution and its implication for the Poisson correlated gamma frailty model.*

12h50Closing

13h00 Lunch

Posters

Abdelkamel Alj (U.L.B.) *The exact quasi-likelihood of time dependent VARMA Models*

Tom Cattaert (U. Liège) *Selecting multiple epistatic models using MB-MDR*

Lieven De Clercq (K.U.L.) *TBA*

Auguste Gaddah (U. Hasselt) *A flexible Koziol-Green model*

Arthur Gitome (U. Hasselt) *Resampling based multiple testing in microarray experiments: permutations or bootstrap?*

Nele Goeyvaerts (U. Hasselt) *Statistical Inference on Parvovirus B19 immunology using data on social contacts and serological status*

Maarten Jansen (K.U.L.) *Multiscale kernel smoothing using a lifting scheme*

Christophe Ley (U.L.B.) *On the singularity of Fisher information in skew-symmetric density estimation*

Harrison Machiaria (U. Antwerpen) *Equivalent-estimation versus D-optimal second-order split-plot designs*

Setia Pramana (U. Hasselt) *Order restricted semi-parametric inference for testing dose-response relationship in pre-clinical microarray experiments*

Maik Schwarz (U.C.L.) *Consistent density deconvolution under partially known error distribution*

Christelle Senterre (U.L.B.) *The contribution of biostatistics to the epidemiologic study of injuries*

Leen Slaets (K.U.L.) *Clustering based on multiresolution time warping*

Kukatharmini Tharmaratnam (KUL) *A model selection strategy for regression models based on robust estimators*

Pushpike Thilakarathne (KUL) *The use of mixed models to identify differentially expressed genes when a single replicate per biological condition is present*

Catherine Timmermans (U.C.L.) *Measuring dissimilarities between time series using their unbalanced Haar wavelets expansion*

Dina Vanpaemel (K.U.L.) *Detecting influential data points in extreme value statistics*