

B-Stat News

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EDITORIAL

Membership is important !

Another year over! Time has come again to send all members of the SBS-BVS my personal wishes for a happy and successful New Year 2007.

Another year over! Time passes by rapidly. Emails and electronic transactions change our daily life ever more, not only in depth but also in pace. On Saturday morning, when browsing through my infinite list of weekly emails, those received on Monday or Tuesday seem to me ages ago. By contrast, long time received emails can be retrieved in a second, giving me the impression that I got them yesterday. I remember the time when a scientific paper published in one of the best journals was a matter of discussion and appreciation for many years, while today nobody would talk about it a month later. The same applies to daily life events and persons. Evanescence is probably a good word to term the 21st century information society.

Another year over! Time has been plain, however. The SBS-BVS and its members have been active not only in Belgium but also worldwide in many ways. I would like to specially commend on the UCL statistical team which organised the BSS2006 annual meeting in Houffalize on a short notice but with a remarkable success. The afternoon for young statisticians, sponsored in part by the society, gathered over 60 participants and was highly appraised. I wish the group in Antwerp in charge of BSS2007 the same successful outcome.

Another year over! Time has also come to renew your annual dues. Everyone in the society should contribute to its financial health and stability. One way to do this is to promptly pay the membership fee. Delays cause costly reminders, unnecessary paperwork and headaches to the treasury office. Today, there are also legal reasons for doing so. According to the new law on “asbl/vzw”, the official list of members has to be established and deposited every year. Members leaving the society for any reason should always notify the secretarial office about their resignation. Likewise address changes should be rapidly reported to the secretary. I hope that all members will recognise these elementary rules which apply to all societies.

Members can live without the society but the society can not live without its members! Like cells in the human body, members are the cellular components of the society, making it alive, active, and moving forward. Membership is really important!

Adelin Albert
President of the SBS-BVS

**14TH ANNUAL MEETING OF THE BELGIAN STATISTICAL
SOCIETY, HOUFFALIZE**

12 - 13 OCTOBER 2006

The BSS 2006 meeting was organized by the Institute of Statistics of UCL and took place in the Ol Fosse d'Outh seminar center at Houffalize in the province of Luxembourg. This meeting was organized jointly with the biostatistical section of the society and with three statistical groups linked to SBS-BVS: b-ENBIS (the Belgian branch of the European Network for Business and Industrial statistics), RSS-3CC (the Three Country Corner local group of the Royal Statistical Society) and the Quetelet Society.

In addition to the traditional activities, this 2006 edition was marked by two special events: it was preceded by a special afternoon for young statisticians and was followed by a workshop and a hike on Friday afternoon. In total 141 persons registered: 63 students, 48 participants from academics and 31 from private companies or other organisations.

The afternoon for young statisticians started the day before the official meeting on 11 October. During this stimulating and pleasant event, three young Belgian PhDs in statistics presented their career path and the asset of having a PhD when working in private companies or public organisations. Each of the 60 participants had also the opportunity to discover the work of the others in a quiz-based poster-session.

On October 11 and 12, a varied and rich scientific program was proposed to the participants of the “official” SBS-BVS meeting. Each of them could find presentations in his own specialisation and open his mind to various other subjects. The five plenary sessions given by the invited speakers were especially appreciated for their scientific quality and the clarity of the presentations adapted to the variety of the public. They covered a very broad range of topics such as: data mining (Bart Baesens – KULeuven), statistical problems in organ donation and transplantation (Dave Collett -UK Transplant), sampling methodology in the Pisa study (Erich Neuwirth - University of Vienna), nonparametric regression in survey estimation (Jean Opsomer - Iowa State University) and statistical and mathematical models in epidemiology (Ziv Shkedy, Hasselt University).

These plenary sessions were completed by six thematic sessions organised jointly with our partners b-ENBIS, RSS-3CC, Quetelet society and the Biostatistical session of SBS-BVS. Within the 30 presentations, many PhD

students had the opportunity to present their work. This stimulating oral scientific program was completed by a poster session (coupled with a cocktail) where 34 young statisticians presented their work and which showed how diverse and rich the work of the young generation in Belgium can be. In the workshop on Friday afternoon, Christian Ritter (UCL and Monnet Center) offered to 25 participants an introduction to the “deployment of statistics in an office environment”.

As usual, the atmosphere of the conference was friendly and pleased. The winners of the quiz of the poster session opened the bar on Wednesday afternoon with the bottles of Chouffe they gained in the competition. This local Belgian beer set the tone to the two relaxed and happy evenings of the conference. The hike on Friday afternoon was also a success: 15 participants could discover the beautiful neighbourhood of the conference centre and finish their afternoon on the terrace with the workshop participants around cakes and ... some more beer.

The organising and the scientific committees want to thank all the participants for their contribution to the success of this meeting! We are looking forward to meet you again next year in Antwerp!

**GENERAL ASSEMBLY OF THE BELGIAN
STATISTICAL SOCIETY**

University of Namur, 14 February 2007

The SBS-BVS annual General Assembly will take place at the “Facultés Universitaires Notre-Dame de la Paix” in Namur (Auditorium MA1, second floor in the Economics Building), on Wednesday 14 February 2007 at 17:00.

It will be preceded, in auditorium E1 (first floor in the same building), by two scientific talks according to the following program:

14:30 – 15:30 *Probabilistic models in cluster analysis*

Hans-Hermann BOCK
RWTH Aachen University, Germany

15:30 – 16:00 Coffee break

16:00 – 17:00 *Clustering in the presence of outliers*

Günter RITTER
University of Passau, Germany

You are all cordially invited.

15TH ANNUAL MEETING OF THE BELGIAN STATISTICAL SOCIETY

Antwerp, 19-20 October 2007



The 15th annual meeting of the Belgian Statistical Society will be held on Friday 19 and Saturday 20 October 2007 in the Crowne Plaza Hotel in Antwerp. The meeting will be preceded by a Young Statistician Day in the same location on Thursday 18 October.

StatUa, the forum for statistics and applied statistics at the University of Antwerp, will take care of the practical organisation of the 15th edition of the annual meeting, which will feature sessions organized by the Biostatistical Section of the Belgian Statistical Society, the Three Country Corner local group of the Royal Statistical Society, the Quetelet Society and the Belgian branch of the European Network for Business and Industrial Statistics in addition to the contributed sessions. Workshops will be scheduled on Saturday afternoon.

More details will soon be posted at www.sbs-bvs.be !

FIRST IBS CHANNEL NETWORK MEETING

ROLDUC, THE NETHERLANDS

The first IBS Channel Network meeting will be held at the conference centre Rolduc (12th century former abbey, The Netherlands) May 8-11, 2007. The scientific programme committee has selected the following three broad themes as the invited programme:

High-dimensional data

Opening Keynote lecture: Ulrich Mansmann
Invited lectures: Age Smilde, Cajo Ter Braak

Methods in epidemiology

Invited lectures: Daniel Commenges, Miguel Hernan

Adaptive designs in clinical trials

Invited lectures: Chris Jennison, Fabian Tibaldi
Closing Keynote lecture: Marc Buyse

You are invited to submit an abstract for a contributed oral/poster presentation. Contributions may cover a wide range of topics, but contributions devoted to one of the topics of the invited sessions are particularly encouraged. Deadline for abstracts is: January 30, 2007. More information is available on the conference website:

www.bms-aned.nl/Rolduc2007

For your information, the Channel Network is a loose confederation of IBS Regions, founded at the end of 2005, comprising the Belgian Region, the British and Irish Region, the French Region and the Netherlands Region. It is managed by a Steering Group with members drawn from each of constituent regions, and currently coordinated by Andrew Mead from the British and Irish Region. The Channel Network Conference is intended to be the major activity of the Channel Network, and will be held every two years, with the venue rotated around the constituent regions.

FORTHCOMING STATISTICAL EVENTS

February 16, 2007 – Diepenbeek (University of Hasselt) room C110
A latent class mixture model for incomplete longitudinal Gaussian data
Lien Beukens (Universiteit Hasselt)

February 23, 2007 – Diepenbeek (University of Hasselt) room C105
Flexible estimation of serial correlation in linear mixed models
Jan Serroyen (Universiteit Hasselt)

February 23, 2007 – Louvain-la-Neuve (Institut de statistique, UCL)
Special afternoon on "*Nonparametric estimation under constraints*"
Jérémie Bigot, Université Toulouse III, France
Geurt Jongbloed, Vrije Universiteit Amsterdam, The Netherlands

March 2, 2007 – Diepenbeek (University of Hasselt) room C105
Predictive modeling of failure time data: a recast of the c-index
Kristiaan Pelckmans (ESAT,K.U.Leuven)

April 26–27, 2007 – Diepenbeek (University of Hasselt)
Statistical inference for dependent data.

NEWS FROM OUR MEMBERS*

Cedric Heuchenne, formerly at the Institute of Statistics UCL, is now teaching at the School of Business ULg.

Frans Desmedt, National Institute of Statistics, retired in 2006.

Philippe Lambert, formerly professor of biostatistics at UCL, has been appointed professor of statistics at the Institute of Human and Social Sciences, University of Liège.

Didier Renard, formerly at the Eli Lilly Development Centre, Mont-Saint-Guibert, moved to Novartis in Basel, Switzerland.

Peter Slock, formerly at the National Institute of Statistics, is now working at the “Belgian national office for pensions”, Brussels.

*Members are invited to notify the B-Stat news editors about professional or position changes.

RECENT PHD THESES

Katholieke Universiteit Leuven (KULeuven)

Roselinde Kessels. *Optimal Designs for the Measurement of Consumer Preferences.* (23/10/2006) – Promotors: Prof. Martina Vandebroek and Prof. Peter Goos (UA).

This thesis focuses on the design of conjoint experiments for measuring the trade-offs people make in choosing between alternative products and service providers. Marketing consultants and researchers frequently use these experiments to predict people's choices for prospective goods. In this way, they assist companies in launching innovative products or services. The entire process from collecting consumer preference data to analyzing them and simulating the marketplace is generally known as conjoint analysis.

Conjoint analysis assumes that a product or service can be decomposed into its component attributes and levels. A good is thereby described by levels for each of the attributes. For example, a car is characterized by the attributes price, transmission, airbags, door lock and audio system. A possible profile or alternative of a car is then a car with a price of 18,000€, manual transmission, front and dual side airbags, an auto lock function and a radio and CD player. By presenting a series of profiles to a number of test persons and finding out which are most preferred, conjoint analysis allows the determination of the relative importance of each attribute and level in the purchasing decision. The relative values or utilities respondents derive from the attribute levels are also called part-worths. Conjoint analysis is based on the fact that the part-worths can better be measured when the attributes are *considered jointly* rather than in isolation.

Respondents usually evaluate profiles in one of the following two ways. They either choose their preferred profile from a set of profiles, also called a choice set, and they repeat this task for several other choice sets presented to them. Such a conjoint experiment is a choice-based conjoint experiment, also referred to as a conjoint choice or discrete choice experiment, or more succinctly, a choice experiment. Or, the respondents rate a number of profiles on a scale, for example a 10-point scale. This type of conjoint experiment is a rating-based conjoint experiment. In the thesis we deal with the question of how to properly design choice-based and rating-based conjoint experiments. This means that we search for profiles that, when administered to respondents, yield maximum information on the part-worths. To find the best possible design in each case, we make use of design criteria or optimality criteria resulting in optimal designs. The thesis is split into two parts each involving the design of one type of conjoint experiment.

Katholieke Universiteit Leuven (KULeuven)

Rembert De Blander. *Essays on Endogeneity and Parameter Heterogeneity in Cross-Section and Panel Data.* (28/04/2006) - Promotor: Prof. Marinus Verbeek (Erasmus University Rotterdam), Co-promotor: Prof. Geert Dhaene (K.U.Leuven)

In this thesis, both the Correlated Random Coefficient (*CRC*) model as well as a dynamic panel data model are considered.

The CRC model is a random coefficient model the crucial characteristic of which is the possible correlation between regressors and coefficients. Assuming that the constant term is also associated with a random and correlated coefficient, the CRC model encompasses standard models that allow for endogenous regressors. A first paper presents an estimator for the linear CRC model which is an extension of Garen's (1984) Selectivity Bias Method, but the outcome equation is augmented with more terms compared to Garen. In a second Paper, I discuss semiparametric estimation of a linear correlated random coefficient model (Heckman and Vytlacil (1998)). I include two unknown functions of the residuals in the equation of interest, one of which is multiplied by the treatment variable. I propose to estimate these unknown functions by series regression, resulting in root N-consistent estimation of the parameters of interest. By making use of the unified treatment of models for truncation, sample selection and limited dependent variables (Heckman (1976)), and of generalized residuals (Gouriéroux et al. (1987)), this approach is valid as well for discrete treatments. A third paper, finally, considers estimation methods for the CRC model when panel data are available, which allows for estimation of the average treatment effect by IV as described by Wooldridge (2003), using Hausman and Taylor (1981) style instruments. The part concerning dynamic panel data focusses on the derivation of unit root tests for fixed time dimension, which extends Harris and Tzavalis' (1998) tests to panel data models with AR(1) errors. The limiting distributions of the test statistics (for increasing N and fixed T) are shown to be normal. Closed-form expressions for the first and second moments of the test statistics are derived. Heterogenous initial conditions and drift in the data generating process are taken into account by including fixed effects and individual-specific linear time trends in the regression. This inclusion makes the least squares estimators of the autoregressive parameters inconsistent for fixed T, and appropriate bias-corrections are proposed.

Electronic access:

<http://www.kuleuven.ac.be/doctoraatsverdediging/cm/3H05/3H050156.htm>

Universiteit Gent (UGent)

Beatrijs Moerkerke. *To be or not to be significant: on more powerful methods for multiple testing* (17/11/2006) - Promotor: Prof. dr. E. Goetghebeur.

Recent advances in technology are leading to the production of enormous amounts of data. To turn these data into information, statisticians are equipped with statistical models and techniques for estimation and hypothesis testing. They traditionally draw inference with well understood error margins. The dimension of today's datasets however has led to a multiplicity of analyses and tests that are leading to the present new and fundamental challenges to hypothesis testing. If no adjustments are made to account for this multiplicity, the number of false positive results can grow unacceptably large. This is at the heart of the multiple testing problem, which forms the topic of this thesis.

The multiple testing problem has received particular attention in the field of statistical genetics where a huge number of candidate genes may be tested for an association with phenotype, based on relatively small samples. This has led to a whole range of new (ad hoc) statistical developments. These procedures mainly aim to avoid a flood of false positives, i.e. to protect against false findings that put researchers on the wrong track. They thus focus on the null of no association. Unfortunately, by reducing the number of selected genes, one also loses some ability to detect interesting findings. The strategy that is developed in this thesis also quantifies evidence against an important alternative to gain power.

In chapter 1, we introduce the multiple testing problem and a range of error measures through which repeated tests are being evaluated. We present popular procedures designed to control these different error measures.

In chapter 2, we borrow from lessons learned in the field of statistical genetics to confront multiplicity questions in the study of high dimensional Quality of Life (QOL) outcomes. Specifically, we investigate the impact of treatment on symptoms and functionality in several aspects of daily life of breast cancer patients. Unlike classical analysis of QOL-questionnaires, we extend existing techniques to compare treatments in terms of all individual items as they reflect different symptoms that matter to the patients. More in particular, we develop permutation based procedures to detect items of the QOL-questionnaire that differ significantly over observed treatments even in the face of multiple testing.

While in chapter 1 and 2, existing methods are studied and extended, a new powerful methodology to deal with the multiple testing problem is developed from chapter 3 onwards.

To avoid a flood of false positives and to avoid losing too much power, we strive for a better balance between the magnitude of a genetic effect and its precision in chapter 3 and 4. We complement the traditional p-value (p_0) with an alternative p-value (p_1), a measure of impotence, which summarizes evidence against a target alternative. We build a formal decision criterion by balancing gene-specific type I and type II errors to optimize an expected gain. This criterion turns out to be cast in terms of p_0 and p_1 and leads to an intuitive measure of relative evidence based on which genes are ranked and selected. We call this procedure the balanced test. The technique is applied and developed in the context of statistical selection of genetic markers for plant breeding and for detecting differentially expressed genes in hereditary breast cancer.

In chapter 5, we take this testing procedure one step further and develop two-stage designs for screening genetic markers when the cost of measurements is high. Based on a first sample, a genetic marker is selected if it shows enough evidence against the null and in favor of a specified worthwhile alternative, while a sufficiently convincing lack of effect results in acceptance of the null. Otherwise the genetic marker is situated in a grey zone and more data are gathered at the second stage after which a binary decision is made on all available data. We develop designs and decision rules which optimize an expected gain.

We return to the original multiple testing framework in chapter 6 and study experimentwise properties of our procedure. The balanced test achieves a higher power to detect specified alternatives than methods based on classical p-values. This is a consequence of considering evidence against both the null and alternative hypothesis and handling gene-specific decision criteria. It appears to also provide a more stable solution than standard techniques.

In this thesis, the multiple testing problem is approached in a more specific way to provide a solution for the lack of power of classical tests. The development of new techniques that rethink the ultimate goals of hypothesis testing in a context where many tests are performed is important. This process involves a reflection on existing methods and the recognition of some of their shortcomings when keeping the original (biological) question in mind. Some important steps towards this goal are taken here and smoothen the path for further work on this topic such as the detection of gene-gene interactions.

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Next issue:
Results of the survey about B-Stat News.

We would like to publish in this *Newsletter* any statistical matter such as :

- information about universities, institutes (1 to 3 pages);
- lists of recent publications and technical reports;
- abstracts of recent PhD theses;
- news of members;
- forthcoming statistical events and announcements;
- short papers about teaching methods in statistics, statistics in the industry, official statistics, etc.

Suggestions are welcome: please, contact us.

Suitable information for the next issue, prepared as **(LA)TEX or WORD FILES**, should reach the editors of the Newsletter **BEFORE March 15, 2007**, preferable by e-mail to:

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