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Næste nummer af "MEDDELELSER" udkommer 1. September 2006.
Bidrag skal være redaktøren i hænde senest

Den 21. august kl. 12.00.

Bidrag bedes sendt til:

Meddelelser, v/ Marc Andersen
Genmab A/S
Toldbodgade 59B
1253 København K
eller med e-mail til: red@dsts.dk

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MEDDELELSER

Dansk Selskab for Teoretisk Statistik

Indhold

31. årgang nr. 5

Juni 2006

Selskabets bestyrelse:

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Selskabets www-adresse: Http://www.dsts.dk

Generiske e-mail-adresser i selskabet:
Formand: fmd, formand, chair, chairman **Kasserer:** kass, kasserer, treas, treasurer
Redaktor: red, redaktoer, edit, editor **Sekretær:** sekr, sekretaer, secr, secretary
Webmaster: web, webmaster, www
Meddelelser: medd, meddelelser, newsl, newsletter
Bestyrelsen: best, bestyr, bestyrelse, board

Medlinfo er **nedlagt**!
http://www.dsts.dk/da/ **skal** benyttes til **indmeldelse** og **adresseændring** i DSTS.

Forskerskolen i Biostatistik: Kursusprogram efterår 2006

Compliance and causal analysis
København, 3.-5. oktober
Tilmeldingsfrist: 1. september

Design of Experiments
Århus, 23.-27. oktober
Tilmeldingsfrist: 15. september

Missing data, particularly in Longitudinal Studies
København, 9.-10. november
Tilmeldingsfrist: 8. oktober

Kurserne var omtalt mere detaljeret i majnummeret af Meddelelser. Der henvises desuden til Forskerskolens hjemmeside, www.phdbiostat.dk

DEPARTMENT OF APPLIED MATHEMATICS AND STATISTICS
UNIVERSITY OF COPENHAGEN

Onsdag den 7. juni 2006:
Speaker: Alexey Sorokin, Department of Mathematical Statistics, Moscow State University.
Title: "Weighted Residual Empirical Process, Estimation and Testing in Heteroscedastic Models. "

Abstract:

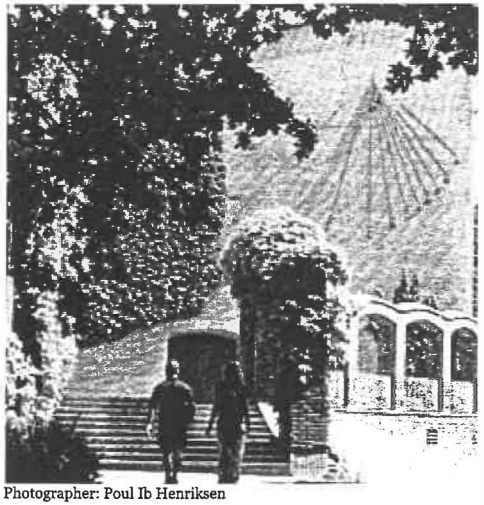
The topic of the report is the analysis of estimates and tests in heteroscedastic time series, based on weighted empirical residual process (w.r.e.p.). We consider the case when model parameters may depend on the number of observations n. Our first result is asymptotic normality for two types of estimates: minimum distance and generalized M. The second one deals with the tests of hypothesis about actual dimension of the model equations. We'll compare their asymptotic efficiency against local alternatives to those of tests based on (Q)ML estimates. Due to time limits, we may also briefly discuss the construction of finite sample confidence intervals for parameter values.

Fredag den 23. juni 2006:
Speaker: Piet de Jong, Macquarie University, Sydney, Australia.
Title: "Extending Lee–Carter demographic forecasting. "

Abstract:

This seminar discusses different approaches to long term demographic forecasting. Demographic forecasts are immensely important to society. Yet existing methods are simplistic and often suffer from shortcomings. One established method is the "Lee–Carter" method. The seminar considers this method, and points out its shortcomings. The method is cast into "state-space" form and is used as a springboard to more sophisticated approaches based on modern time series methods. These approaches include building in smoothness via regression, "functional" methods, double spline methods, methods based on the Wang transform and "joint" mortality modelling across countries and different groups. An attempt is made to evaluate the different approaches, and arrive at some consensus regarding the advantages and disadvantages of different methods. Approaches are illustrated using different mortality data sets.

Scandinavian Institute in Statistical Genetics



Photographer: Poul Ib Henriksen

University of Aarhus
Aarhus, Denmark

July 24 - 28, 2006

UNIVERSITY OF WASHINGTON
DEPARTMENT OF BIOSTATISTICS

University of Aarhus
Danish Graduate School in Biostatistics
Bioinformatics Research Center (BiRC),
University of Aarhus

Scandinavian Institute in Statistical Genetics

University of Aarhus, Aarhus, Denmark

July 24 - 28, 2006

General Information

The Institute in Statistical Genetics offers a series of two- and one-half-day workshops that introduce participants to modern methods of interpreting genomic data. The workshops being offered at the University of Aarhus are a subset of those offered at the Summer Institute in Statistical Genetics, now held at the University of Washington after 10 years at North Carolina State University.

The Scandinavian Institute in Statistical Genetics is sponsored by the University of Aarhus and the Danish Graduate School in Biostatistics. It is being organized locally by the Bioinformatics Research Center (BiRC) at the University of Aarhus.

Registration Deadline and Fees

The early registration and payment deadline is Friday, June 16, 2006. The early registration tuition fee is US $550. A reduced fee of US $400 is offered to academic and government participants. After June 16, 2006, add US $100 per participant. Tuition covers course materials and four refreshment breaks a day. Hotel rooms and meals are not included in the tuition fee.

Hotels

Accommodations are available at hotels in Aarhus. Reservations should be made with Kongres-Kompagniet, using the reservation form at www.kongreskompagniet.dk/sisg2006. To obtain the room rates stated below, reservations must be made with KongresKompagniet before June 1, 2006. After that date, rooms may still be booked, but availability and rates are not guaranteed.

Diakonhoejskolen: Lyseng Allé 15, 8270 Hoejbjerg, 80 rooms (1 or 2 beds per room), private toilet/bath. Telephone, TV, and internet are available in common areas. Room rate per person per night: € 40 for a 2-bed room and € 47 for a single bedroom, including breakfast. Diakonhoejskolen is about 8 km from the university campus. The university will arrange fares for public buses, which operate every 20 minutes between Diakonhoejskolen and the university.

Hotel Cab Inn: Kannikegade 14, 8000 Aarhus C, 30 rooms, private toilet/bath, telephone and TV. Internet connections are available in some rooms and in the reception and lounge areas. Room rates: € 77 - € 113 depending on type; rate includes breakfast. Cab Inn is in the city center 15 minutes walk from university campus. Public buses connect the hotel with the university campus.

Hotel Scandic Plaza: Banegaardspladsen 14, 8000 Aarhus C, 50 rooms, private toilet/bath, telephone, TV and internet connection (ask for user name and password at reception). Room rates: single € 94, double € 120, including breakfast. The Scandic Plaza is in the city center 20 minutes walk from university campus. Public buses connect the hotel with the university.

Other Hotels: If you wish to book rooms at another hotel (special prices not negotiated), see http://www.visitaarhus.dk.

Daily Schedule

8:30 am	Registration
9:00 - 10:30	Class Session
10:30 - 11:00	Break
11:00 - 12:30	Class Session
12:30 - 1:30 pm	Lunch (and registration on Wednesday)
1:30 - 3:00	Class Session
3:00 - 3:30	Break
3:30 - 5:00	Class Session
5:00 - 6:00	Refreshments (except Friday)

Scandinavian Institute in Statistical Genetics

University of Aarhus, Aarhus, Denmark

July 24 - 28, 2006

Registration Procedure

You may register on-line via secure server at http://www.biostat.washington.edu. Space in each module is limited and will be filled on a first-come, first-served basis.

Registration Deadline and Late Fee: The early registration and payment deadline is Friday, June 16, 2006. The early registration fee is $550 per module, with a reduction to $400 for academic and government participants. After June 16, 2006, add $100 per participant.

Cancellation: A $100 processing fee will be deducted from refunds requested after June 1, 2006. No refunds will be processed after June 16, 2006.

Payment Method: Payment can be made by credit card (VISA, MasterCard, or American Express), purchase order (U.S. companies and organizations only), or by check or money order in U.S. dollars drawn on a U.S. bank. Checks should be made payable to the University of Washington.

How to Register: Visit the conference web site at http://www.biostat.washington.edu where you may register and make payment on-line using VISA, MasterCard, or American Express. If you wish to pay by check, you can print the registration form and submit it by mail as directed. You will receive your registration confirmation by email.

Registration Questions: Direct registration inquiries to:

Summer Institute in Statistical Genetics
c/o UW Engineering Professional Programs
10303 Meridian Ave. N., Suite 301
Seattle, WA 98109 USA
Email: uw-epp@engr.washington.edu
Phone: 866-791-1275 (toll free) or 206-543-5539
Fax: 206-543-2352

Conference Inquiries: Inquiries about the conference may be sent to:

Summer Institute in Statistical Genetics
University of Washington
Department of Biostatistics Box 357232
Seattle, WA 98195-7232 USA
Email: sisg06@u.washington.edu
Phone: 206 543-1044; fax: 206-543-3286

Course Schedule

Module 1 July 24 - 26 **Population Genetic Data Analysis** (B. Weir and K. Holsinger)
Module 2 July 24 - 26 **Principles of Quantitative Genetics** (B. Walsh and W. Muir)
Module 3 July 24 - 26 **Microarray Analysis** (G. Gibson and J. Storey)
Module 4 July 26 - 28 **Interpreting DNA Evidence** (B. Weir and J. Buckleton)
Module 5 July 26 - 28 **Quantitative Trait Locus Mapping** (Z-B Zeng and R. Doerge)
Module 6 July 26 - 28 **Association Mapping** (D. Nielsen and J. Lunceford)
Module 7 July 26 - 28 **Coalescent Theory** (C. Wiuf and M. Schierup)

Fee Calculation

Academic or government participant: $400 per module x ____ modules = $_____

Industry or other participant: $550 per module x ____ modules = $_____

Late fee (after June 16, 2006): $100 $_____

Total payment $_____

Instructional Program

Module 1: Population Genetic Data Analysis

Instructors: B. Weir and K. Holsinger
Dates: 9:00 am July 24 - 12:30 pm July 26

This module covers estimation of allele and haplotype frequencies, inferences about Hardy-Weinberg and linkage disequilibrium, characterization of population structure, linkage estimation, joint genotype probabilities, and relationship estimation. Includes using public domain software packages, including GDA and PowerMarker.

Module 2: Principles of Quantitative Genetics

Instructors: B. Walsh and W. Muir
Dates: 9:00 am July 24 - 12:30 pm July 26

This module covers quantitative trait models, variances and covariances of relatives, estimation of variance components, response to selection, and the effects of mutation.

Module 3: Microarray Analysis

Instructors: G. Gibson and J. Storey
Dates: 9:00 am July 24 - 12:30 pm July 26

This module provides an overview of array technologies, image analysis and normalization, experimental design, statistical modeling and inference (e.g., detecting differential gene expression, ANOVA, multiple testing, false discovery rate, clustering, and classification), and expression QTL. Applications to molecular and evolutionary biology are covered. The module includes software demonstrations.

Module 4: Interpreting DNA Evidence

Instructors: B. Weir and J. Buckleton
Dates: 1:30 pm July 26 - 5:00 pm July 28

This module covers statistical and population genetic topics for the interpretation of forensic DNA profiles. Topics addressed include allelic independence, Bayes' theorem and likelihood ratios, genotype probabilities for one and two individuals, effects of relatives and population structure, interpretation of mixtures, low copy number profiles, and paternity index and missing person calculations. Includes using GDA and DNAMix-3 public domain software.

Module 5: Quantitative Trait Locus Mapping

Instructors: Z.-B. Zeng and R. Doerge
Dates: 1:30 pm July 26 - 5:00 pm July 28

This module covers linkage map construction, single-marker analyses, multiple and partial regression methods, and interval, composite-interval, and multiple-interval mapping. Model selection and determining significance levels are addressed. Includes using the Windows QTL-Cartographer software package.

Module 6: Association Mapping and Clinical Trials

Instructors: D. Nielsen and J. Lunceford
Dates: 1:30 pm July 26 - 5:00 pm July 28

Topics for this module include an introduction to the theory of linkage disequilibrium and mapping, population and family-based association techniques for discrete and quantitative traits, detecting and accounting for population structure, estimating haplotypes from population data, haplotype blocks, and multiple testing issues.

Module 7: Coalescent Theory

Instructors: C. Wiuf and M. Schierup
Dates: 1:30 pm July 26 - 5:00 pm July 28

Sequence variation within populations is important to medical genetics and to the study of evolutionary history. Coalescent models that describe genealogical histories underlying sampled chromosomes in natural populations are central to the analysis of such data. The module covers the derivation and properties of the basic model and its extension to include factors such as recombination, geographical structure, and natural selection; use of the coalescent in analyzing data, considering different statistical approaches to inference in the settings of disease mapping, estimating recombination rates, and detecting recent adaptive evolution; and use of coalescent methodologies in large-scale surveys of genetic variation, such as the HapMap project. Computer programs that can analyze real data and simulate genealogies will be demonstrated and used in computer sessions.

Faculty

John Buckleton, Principal Scientist, ESR Forensic, New Zealand

Rebecca Doerge, Professor of Statistics, Purdue University, USA

Greg Gibson, William Neal Reynolds Distinguished Professor of Genetics, North Carolina State University, USA

Kent Holsinger, Professor of Ecology and Evolutionary Biology, University of Connecticut, USA

Jared Lunceford, Senior Biometrician, Merck and Co.

William Muir, Professor of Genetics, Purdue University

Dahlia Nielsen, Research Assistant Professor of Statistics, North Carolina State University, USA

Mikkel Schierup, Associate Professor of Ecology and Genetics, University of Aarhus, DK

John Storey, Assistant Professor of Biostatistics, University of Washington, USA

Bruce Walsh, Professor of Ecology and Evolutionary Biology, University of Arizona, USA

Bruce S. Weir, Director, Scandinavian Institute in Statistical Genetics and Professor and Chair of Biostatistics, University of Washington, USA

Carsten Wiuf, Professor, Bioinformatics Research Center (BiRC) and Aarhus University Hospital, DK

Zhao-Bang Zeng, William Neal Reynolds Professor of Statistics and Genetics, North Carolina State University, USA

larix

Statistiker søges

Da Larix har for mange opgaver til de hoveder vi er, søger vi nu en erfaren statistiker. Larix er et mindre konsulentfirma med fokus på statistik og data management. Vores kunder kommer især fra farma- og biotekbranchen. Det drejer sig både om store firmaer hvor vi arbejder for deres statistik og/eller data management afdelinger, og små firmaer hvor vi dækker deres statistikbehov og data management behov. Vi er nu 2 statistikere, 3 data managere og en IT person.

Vi har brug for at du

* har en matematisk statistisk uddannelse som cand. stat., ingeniør eller lignende.
* er god til mundtlig og skriftlig kommunikation – også på engelsk
* er god til at samarbejde, er nem at omgås og er serviceminded
* kan bevare overblikket i pressede situationer
* har relevant erfaring med klinisk statistik og ICH-GCP
* er god til at programmere i SAS

Vi tilbyder et spændende og udfordrende job, hvor du vil komme til at arbejde med en række forskellige typer af statistiske opgaver, primært ifm. kliniske studier. Eksempelvis vil du komme til at lave de statistiske analyser og afrapporteringer fra kliniske studier, skrive statistiske analyseplaner, og give input til forsøgsprotokoller inklusive sample size beregninger. Nogle opgaver løses hos Larix, men de fleste løses som konsulent udstationeret hos kunden. Derudover tilbyder vi en konkurrencedygtig løn med bonus og pension, efteruddannelse, fleksibel planlægning af arbejdet og ikke mindst nogle gode kolleger.

Hvis du er interesseret i at høre mere så check vores hjemmeside www.larix.dk, eller ring til Klaus Juel Olsen, Head of Statistics på 61 61 80 11. Send en ansøgning med CV på e-mail til kjo@larix.dk eller med snail mail til Larix Aps, Bymidten 78, 3500 Værløse.

Kalender 2006

(arrangementer annonceret i MEDDELELSER)

Dato	Medd.	Aktivitet
7/6	4/06	Seminar, Afd. Anv. Mat og Stat.: Alexey Sorokin: Weighted Residual Empirical Process, Estimation and Testing in Heteroscedastic Models
10/6	2/06	PhD and Post Doc course on Inference and Simulation for Spatial Point Processes. Dept. Of Mathematical Sciences, Aalborg University, Denmark.
11-15/6	1/06	Nordstat 2006 conference: Rebild, Danmark.
23/6	5/06	Seminar, Afd. Anv. Mat og Stat.: Piet de Jong, Macquarie University, Sydney, Australia: Extending Lee-Carter demographic forecasting.
24-28/6	5/06	Summer School in Statistical Genetics, Aarhus 2006
18-20/9	2/06	Sixth Annual Meeting on Business and Industrial Statistics (ENBIS-6), Wroclaw, Poland.
3-5/10	4/06	Forskerskolen i Biostatistik, København: Compliance and causal analysis
23-27/10	4/06	Forskerskolen i Biostatistik, Århus: Design of Experiments
9-10/11	4/06	Forskerskolen i Biostatistik, København: Missing data, particularly in Longitudinal Studies

For kurser og seminarer, i Lund, se: http://www.maths.lth.se/matstat/seminar/
BiRC seminars, se: http://www.birc.au.dk/Aktivities/BiRCSeminar
Forskerskolen i Biostatistik: Forskerskolens hjemmeside, http://www.phdbiostat.dk

NYT om Navne

I anledning af at Senior statistiker Judith L. Jacobsen fylder 50 år d. 9 august i år, inviteres venner og forretningsforbindelser til reception hos Statcon ApS på adressen: Karlebovej 39, 2980 Kokkedal onsdag d. 9 august kl. 15:30 - 19:30.

Deadlines i år 2006

MEDDELELSER udkommer		Frist for indlevering af bidrag:
6:	1. september	21. august
7:	2. oktober	22. september
8:	1. november	20. oktober
9:	4. december	24. november