Næste nummer af "MEDDELELSER" udkommer 3. december 2007.
Bidrag skal være redaktøren i hænde senest **den 23. november kl. 12.00.**

Deadlines i år 2007

MEDDELELSER udkommer	Frist for indlevering af bid
8:	5. november	26. oktober
9:	3. december	23. november

Deadlines i år 2008

MEDDELELSER udkommer	Frist for indlevering af bid
1:	4. februar	25. januar
2:	3. marts	22. februar
3:	7. april	28. marts
4:	5. maj	25. april
5:	2. juni	23. maj
6:	1. september	22. august
7:	6. oktober	26. september
8:	3. november	24. oktober
9:	1. december	21. november

MEDDELELSER
Dansk Selskab for Teoretisk Statistik

Julemøde i selskabet
Tirsdag 4. december 2007 kl. 17.15
Auditorium 18.01.11, Center for Sundhed og Samfund, KU*

Kan den hierarkiske faktormodel frikendes?

Jens Ledet Jensen, Afdeling for Teoretisk Statistik, Århus Universitet

I medierne blev afgørelsen fra UVVU i juli udlagt som en "frikendelse" af Helmuth Nyborg. Da UVVU jo har et snævert kommissorium, er der stadig rum for os andre til at diskutere de modeller Nyborg bruger, og de konklusioner han kommer frem til, ud fra en matematisk-statistisk synsvinkel. Jeg vil fokusere på den hierarkiske faktormodel. Hvorfor er denne model indført og hvordan estimerer vi denne? Er modellen biologisk rimelig? Dette vil udgøre første halvdel af foredraget. I den anden del vil jeg diskutere modellen i forbindelse med at studere gruppeforskelle, specielt forskel mellem de to køn. Kan vi estimere forskel i en eventuel "generel faktor", hvad er det som Nyborgs metode estimerer, og er der bias problemer? De berørte emner vil blive illustreret med data.

Af oplagte grunde vil synspunkterne der fremføres være en lægmands synspunkter.

Officiel diskutant vil være Svend Kreiner, Biostatistik Afdeling, Københavns Universitet

Efter foredraget vil der være middag på "en restaurant i nærheden". Tilmelding til næstformanden (nfmd@dsts.dk), senest tirsdag den 27. november 2007.

*: Øster Farimagsgade 5, 1014 København K (det gamle Kommunehospital, trappe K, se http://www.publhealth.ku.dk/ifw/omos/oversigtskort_KH/?print=1)

Leif Brøndum 1935 – 2007

Før han blev kemiingeniør i 1959 var Leif Brøndum blevet interesseret i statistik. På det tidspunkt var der kun en håndfuld akademiske statistikere i Danmark, og Universitetets Statistiske Institut var det eneste sted, hvor der var undervisning i statistik beregnet for aktuar og cand. polit. studerende, idet cand. stat. studiet var under etablering. Det lykkedes imidlertid for Leif Brøndum at få arrangeret et lic. techn. studium i industriel statistik formelt på Afdelingen for Mekanisk Teknologi på Danmarks Tekniske Højskole men reelt på Universitetets Statistiske Institut. Efter afslutning blev han ansat som undervisningsassistent på Danmarks Tekniske Højskole. For at supplere sin teoretiske uddannelse med erfaring i praktisk anvendelse af statistiske metoder fik Leif Brøndum i 1962 ansættelse som statistiker på Tuborg, hvor han etablerede en statistisk afdeling. Samtidig deltog han som underviser på de meget eftertragtede kurser i statistisk kvalitetskontrol og forsøgsplanlægning, som afholdtes i Dansk Ingeniørforenings regi. Denne aktivitet fortsatte Leif Brøndum gennem alle årene, og der må være mange hundrede ingeniører, som han har givet en grundig indføring i statistik.

Interessen for undervisning medførte, at Leif Brøndum kom til Danmarks Ingeniørakademi i 1969, hvor han blev primus motor i opbygning af en omfattende undervisning i statistisk metoder for kemiingeniører. Afbrudt af et sabbatår på Stanford Universitet i 1972-3 fortsatte Leif Brøndum sammen med Jørgen Monrad at udbygge undervisningen i statistik for ingeniørstuderende og udarbejdede en imponerende serie lærebøger. I en periode i 1980erne var Leif Brøndum også ekstern lektor i statistik på Danmarks Farmaceutiske Højskole. Indtil han af helbredsmæssige årsager måtte stoppe som ingeniørdocent på Danmarks Ingeniørakademi i 1998 havde Leif Brøndum sikkert undervist flere studerende og kandidater på efteruddannelse end nogen anden statistiker her i landet. Han vil derfor blive husket af mange som en inspirerende og dygtig underviser, der kunne formidle de statistiske principper og metoder også for ikke-matematisk orienterede personer.

Aage Vølund

Afskedsreception
torsdag d. 29. november 2007, kl. 14.30 for

Lektor Jørgen Hilden

Institut for Folkesundhedsvidenskab og Biostatistisk Afdeling ved Københavns Universitet afholder en reception i anledning af Jørgen Hildens fratræden torsdag den 29. november 2007, kl. 14.30 på Det gamle Kommunehospital (CSS), Øster Farimagsgade 5A, København K, trappe B, 2. sal, lokale 5.2.46. Alle er velkomne.

Jørgen Hilden, 70 år d. 9. november 2007, har været ansat siden 1965 ved de biostatistiske enheder ved Københavns Universitet først i Arvebiologisk Institut og senest i Institut for Folkesundhedsvidenskab. Ud over studenterundervisningen i statistik, har han ydet rådgivning til utallige sundhedsvidenskabelige forsknings-projekter. Hans egen forskning har i senere år væsentligt været inden for medicinsk statistisk beslutningsteori og meta-analyse. Han er eks-bestyrelsesmedlem / -formand i Dansk Selskab: for Datalogi, for Medicinsk Informatik, og for Medicinsk Filosofi, Etik og Metode.

Mette Madsen

Institutleder

Niels Keiding

Afdelingsleder

Seminarer i anvendt statistik

Seminaret afholdes kl. 15.15 på det gamle Kommunehospital, Øster Farimagsgade 5, opgang B. Der serveres te i Biostatistisk Afdelings bibliotek (opgang B, 2. sal) en halv time før.

Mandag d. 19. november 2007, lokale 5.1.16.

Agathe Le Lay [1,2] & Gérard Duru[1]

[1]Université Lyon 1, LIRIS MA2D, Villeurbanne, France

[2]Global Health Economics and Outcome Research Department, Novo Nordisk A/S, Denmark

Can Discrete Event Simulation be of use when modelling major depressive disorders?

Depression is among the major contributors to worldwide disease burden and adequate modelling requires a framework designed to depict real world disease progression as well as its economic implications as closely as possible. In light of the specific risk factors associated with depression (multiple episodes at varying intervals, impact of disease history on course of illness, socio-demographic characteristics), we will clarify to what extent "Discrete Event Simulation" (DES) techniques provide methodological benefits in depicting disease evolution compared with standard methods, e.g. Markov modelling techniques. Importantly, we will show that DES flexibility allow patients with differing attributes to move from one event to another in sequential order while simultaneously taking into account important risk factors such as age, gender, disease history and patients attitude towards treatment, together with any disease-related events (adverse events, suicide attempt etc.). We will hence demonstrate that these methodological characteristics make discrete event simulation particularly suitable in analysing recurrent and chronic diseases.

Per Kragh Andersen

THIELE CENTRE
FOR APPLIED MATHEMATICS IN NATURAL SCIENCE

Department of Mathematical Sciences
University of Aarhus

Activities at the Thiele Centre

Seminars:

Thursday 8 November 2007, 14:15, building no. 1531, Koll.D
Andrew du Plessis, University of Aarhus:
Topology and digital images

Thursday 22 November 2007, 14:15, building no. 1531, Koll.D
Seiji Hiraba, University of Aarhus:
Markov particle systems associated with multi-dimensional absorbing stable motion
ABSTRACT:
In 1998, we considered infinite independent Markov particle systems with jumps in more general setting as possible, and gave the sample path properties and martingale characterizations. As examples of motion processes, we gave multi-dimensional Brownian motion, absorbing Brownian motion on a half space, multi-dimensional stable motion and, in particular, absorbing stable motion on a positive half line, i.e., subordinated absorbing Brownian motion on a positive half line by the increasing strictly stable Lévy process starting from 0.

In this talk, we shall extend the motion process to the multi-dimensional absorbing stable motion on a half space. In this case it is not easy comparing with the case of absorbing Brownian motion on a half space, because components are not independent. Moreover we consider the Markov particle system with singular immigration. We can also give similar results to the above.

Thursday 6 December 2007, 14:15, building no. 1531, Koll.D
Lars N. Andersen, University of Aarhus:
Parallel computing, failure recovery, and extreme values

Thursday 13 December 2007, 14:15, building no. 1531, Koll.D
Mogens Bladt, Technical University of Denmark:
Title to be announced.

DSTS 2-day Meeting 20-21 November 2007, DTU, Lyngby.

20/11 9.00-13.30: Mini Workshop
20/11 14.00 – 21/11 13.00: Main 2 Day Meeting

Mini Workshop on Point process modelling and statistical inference.

Tuesday 20. November, 9.00-13.30: Everyone interested are welcome to participate.
Registration: see below.
Venue: Aud 31, Building 306, DTU Campus, Lyngby (Matematiktorvet, 2800 Kgs. Lyngby)

Mini Workshop Programme:
9.00-9:30: **Niels Richard Hansen**, Dep. of Mathematical Sciences, Copenhagen University:
Point process models of motifs in biological sequences.

9:30-10:00 **Maja Pohar Perme**, Inštitut za biomedicinsko informatiko, Univerza v Ljubljani:
Checking hazard regression models using pseudo-observations

10:00-10:15 Pause

10:15-10:45 **Thomas Scheike**, Dep. of Biostatistics, Copenhagen University:
Flexible regression models for the cumulative incidence function

10:45:11:15 **Jakob Gulddahl Rasmussen**, Dep. of Mathematical Sciences, Aalborg University:
Connectivity in one-dimensional ad hoc networks

11:15-11:30 Pause

11:30-12:00 **Carlos Diaz Avalos**, Departamento de Probabilidad y Estadistica, Universidad Nacional Autonoma de Mexico:
Space-time modeling of forest fires in Oregon. An application of point process models

12:00-12:30 **Rasmus Plenge Waagepetersen**, Dep. of Mathematical Sciences, Aalborg University:
Estimation of clustering parameters for inhomogeneous spatial point processes

12:30-13:30: Free lunch for registered mini workshop participants

Jesper Møller, Institut for Matematiske Fag, Aalborg Universitet.

2 Day Meeting Programme:

Tuesday 20. November

14.00-14.45 **Hans-Peter Piepho**, Professor and leader of the Bioinformatics Unit, University of
Hohenheim:
Issues in the design and analysis of plant breeding and variety trials.
14.45-15.15 Coffee
15.15-16.00 **Lars Kai Hansen,** Professor in Intelligent Signal Processing, IMM, DTU:
Learning to detect signals from labeled and unlabeled data
16.00-16.45 **Per Chr. Hansen**, Professor in Scientific Computing, IMM, DTU:
Large-Scale Ill-Posed Problems and Applications
16.45-18.15 Beer/water outside the auditorium.
19.00- Dinner, Restaurent Akropolis, H C Ørsteds Vej 70, 1879 Frederiksberg C.

Wednesday 21. November

09.00-09.45 **Mogens Bladt,** Guest Professor **& Bo Friis Nielsen,** Assoc. Professor, IMM, DTU:
Distributions with rational Laplace transform
09.45-10.30 **Thomas Gerds,** Assoc. Professor, Dep. of Biostatistics, Copenhagen University: The
VAML game [Validation and Assessment of Machine Learning]
10.30-11.00 Coffee
11.00-11.45 **Julie Lyng Forman,** Dep. of Biostatistics, Copenhagen University:
Inference from Diffusion Driven Models.
11.45-12.30 **Uffe Høgsbro Thygesen,** Senior Researcher, Danish Institute for Fisheries Research,
DTU:
Markov models of animals moving in the sea
12.30-13.00 Sandwiches

Venue:
Aud 31, Building 306, DTU Campus, Lyngby (Matematiktorvet, 2800 Kgs. Lyngby)

Registration:
You register by sending an email to Ellen Borup (emb@imm.dtu.dk), IMM no later than 2. Nov.
2007. Please indicate clearly whether you want to participate in the mini workshop. The fee is DKK
225 for students (excl. Ph.D. students) and DKK 450 for all others. The fee is to be paid to: DSTS,
Jyske Bank, Reg. no. 7853, Account no 1117188. Please indicate clearly the person(s) for which the
payment is intended.

Abstracts:

Hans-Peter Piepho: Issues in the design and analysis of plant breeding and variety trials.

Plant breeding and variety testing relies heavily on field experiment conducted in multiple
environments. This talk will cover both the analysis of individual trials and the joint analysis of
series of trials.

Most agricultural field trials involve a layout of plots in rows and columns. Resolvable row-column
designs have proven effective in obtaining efficient estimates of treatment effects. Further
improvement may be possible by post-blocking or by inclusion of spatial model components. This
paper reviews options for augmenting a baseline row-column model for individual trials by the
addition of spatial components having a linear variance structure (Lee and Piepho, 2007; Piepho
and Williams, 2007). The main focus will be on spatial variance-covariance structures that have a
linear form, including separable linear variance models and simple state-space models such as
random walks (Pieho and Ogutu, 2007). Relationship to nearest-neighbour methods based on first
and second differences will be discussed. The usefulness of these options is assessed by analysing a
number of field trials, most of which are uniformity trials.

When integrating results from a series of field experiments, modelling of genotype-by-environment
interaction becomes the prime issue. This paper will review mixed models for this purpose,
focussing on factor-analytic variance-covariance structures (Piepho, 1997), which have a fixed
effects counterpart known as the "Additive Main Effects Multiplicative Interaction" (AMMI)
model. Such models may be used to exploit similarities among different agro-ecological regions
(Piepho and Möhring, 2005), and tey are now being implemented in the German variety testing
system as will be exemplified in the talk. I will also discuss the validity of standard mixed model
analysis as dependent on the missing data pattern (Piepho and Möhring, 2006) as well as the merits
and demerits of a two-stage analysis, where in the first step adjusted genotype means from
individual trials are computed, which are then summarized by a joint analysis across the series in
the second step (Piepho and Möhring, 2007).

References

Piepho, H.P. (1997): Analyzing genotype-environment data by mixed models with multiplicative
effects. *Biometrics* **53**, 761-766.
Piepho, H.P., Möhring, J. (2005): Best linear unbiased prediction for subdivided target regions.
Crop Science **45**, 1151-1159.
Piepho, H.P., Möhring, J. (2006): Selection in cultivar trials – is it ignorable? *Crop Science* **146**,
193-202.
Piepho, H.P., Möhring, J. (2007): On weighting in two-stage analysis of series of experiments.
Biuletyn Oceny Odmian **32**, 109-121.
Piepho, H.P., Ogutu, J.O. (2007): Simple state-space models in a mixed model framework. *The
American Statistician* **61**, 224-232.
Piepho, H.P., Williams, E.R. (2007): Two-dimensional linear variance structures for field trials.
submitted.
Lee, Y., Piepho, H.P. (2007): Ambiguity in random walks and implications for the analysis of field
trials. *submitted*

Lars Kai Hansen: Learning to detect signals from labeled and unlabeled data

Labeled examples are "expensive" in many real world signal detection applications, hence, it is of interest to formulate algorithms that can learn to classify from mixtures of labeled and unlabeled data. I will present a theoretical analysis of the labeled-unlabeled problem, an algorithm than can learn from unlabeled data, and an application to email classification.

Per Chr. Hansen: Large-Scale Ill-Posed Problems and Applications

Inverse problems arise in geophysics, tomography, image deblurring and many other areas where the goal is to compute interior or hidden information from exterior data. A common feature of these ill-posed problems is that the solution is extremely sensitive to perturbations, and hence some form of stabilization or regularization is need in order to compute a meaningful solution. In this talk we present some state-of-the-art Krylov subspace method for large-scale inverse problems. The key feature of these methods is that they provide a good "signal subspace" for the desired solution. This, in turn, allows us to compute regularized solutions via a projection onto this lower-dimensional subspace - a feature which is extremely important when we do not know a good a priori value of the regularization parameter.

Mogens Bladt & Bo Friis Nielsen: Distributions with rational Laplace transform

We review what is currently known about one-dimensional distributions on the non-negative reals with rational Laplace transform, also known as matrix-exponential distributions. In particular we discuss a flow interpretation which enables one to mimic certain probabilistically inspired arguments which are known from theory of phase-type distributions. We then move on to present ongoing research for higher dimensions. We discuss a characterization result, some closure properties, and a number of examples. Finally we present open problems and future perspectives.

Thomas Gerds, Anders Albrektstein, Tune Pers, Svend Kreiner, Thorkild Sørensen, Claus Holst: The VAML game [Validation and Assessment of Machine Learning]

In this talk I describe a game where the players build a risk prediction model. Each model predicts the conditional probability distribution of a response variable given a vector of covariates. To build the model, each player chooses a statistical tool, and gets an input matrix with the covariate values of independent subjects and also the true values of the response variable for the same subjects. The predictive performance of the models is evaluated with a strictly proper scoring rule [1] and the 632+ bootstrap method [2]. The game will be illustrated with data from 99 subjects that took part in a NUGENOB trial [3]. The response is the continuous measurement of a respiratory quotient and the covariate vector includes the high-dimensional information from the metabolic platforms 1-H NMR and LC-MS and the subjects age, BMI, blood values, etc. For this game, the players (Anders, Tune, Svend, Thomas) use tools like Random Forests, LASSO, PRIM, Logic Regression, Item Response Theory, Graphical Models, Support Vector Machines and BAMSE. In the talk I will explain how to assess and compare the performances of prediction models obtained with these rather different statistical tools.

[1] Leonard J Savage (1971). Elicitation of personal probabilities and expectations. *Journal of the American Statistical Association*, 66:783-801.
[2] Bradley Efron and Robert Tibshirani (1997). Improvements on cross-validation: The .632+ bootstrap method. *Journal of the American Statistical Association*, 92:548-560.
[3] http://www.nugenob.com/

Julie Lyng Forman: Inference from Diffusion Driven Models.

Diffusion-type models provide a natural and flexible framework for modeling phenomena that evolve continuously and randomly with time. However their statistical analysis is complicated. Only rarely the functional form of the likelihood function of a diffusion is explicitly known. Inference from diffusion driven models such as summed diffusions, integrated diffusions, and stochastic volatility models of course is no less involved. General estimating equations often present a simple alternative means for fitting these models. I will illustrate the use of estimating equations for diffusion-type models driven by diffusions having linear drift and quadratic squared diffusion coefficient. These I term *the Pearson diffusions* as their invariant distributions belong to the Pearson system. The Pearson diffusions have polynomial eigenfunctions which in turn yield explicit recursive formula for their conditional moments.
Further I will present a new goodness of fit test based on estimating equations for varying sampling frequencies. The basic idea is to compare the parameter estimates based on the full data to those obtained from downsamples. The test can be used to distinguish different kinds of diffusion driven models.

Uffe Høgsbro Thygesen:
Markov models of animals moving in the sea

Markov processes are often used as models for the movements of animals. Examples from the marine environment are bacteria moving to locate food, plankton being advected with a turbulent flow, and fish swimming. In this talk I will give examples of questions we aim to answer using such models, and the analysis of the models we undertake. A common issue in our work is the range of spatial and temporal scales, and therefore I will give and example of diffusion approximations that are useful approximations on a larger scale. I will also discuss deriving optimal behaviour. Finally, I will give an example of geolocation of fish based on date storage tags, i.e. state and parameter estimation in a diffusion model for the movements of a fish.

Per Bruun Brockhoff, IMM, DTU.

Statistical evaluation of diagnostic and predictive models
Course No: 2008-3-12

Aim and content: The course deals with criteria for evaluating models for the current status (diagnosis) and the future status (prediction) of subjects in a population. For example, the aim of such a model could be to decide if a subject has cancer or if a subject will develop cancer in the future. In medical applications the basis for these models are covariates such as age, gender, smoking status, and also bioinformation such as blood values, microarrays and single nucleotide polymorphisms. Various statistical tools can be used to build a diagnostic or prognostic model. A very simple diagnostic model is a medical test. Given a marker variable which can be measured for each subject, the medical test diagnoses the disease if the marker value exceeds a certain threshold. The logistic regression model is more complex as it adjusts for confounding factors. Thereby it can often achieve better diagnostic and predictive results. A rather different approach is a classification tree which allows for simple interactions between the covariates. Very good predictive performances can be achieved with a random forest that combines many classification trees in a majority vote. The diversity of possible modelling approaches requires objective and flexible criteria for evaluation and comparison. The course will introduce the receiver operating characteristic (ROC) and the Brier score. The ROC curve is a graphical tool for evaluating single biomarkers and complex risk prediction models. For varying threshold values in the range of a biomarker the ROC curve plots the sensitivity versus (1 - specificity). It can equivalently be represented by the fraction of the true positive rate versus the false positive rate. The Brier score is the squared difference of a subjects true status and the predicted probability for this status obtained with a model. The prediction error is defined as the expected Brier score for all kinds of models. In particular, it can be used to compare the predictions of different statistical models also with experts guess. Traditionally these tools are used in areas like signal detection, weather forecasting, medical diagnostics, medical prediction making, econometrics, and during the last two decades also in machine learning and data mining. The course will introduce ROC analysis and the prediction error based on the Brier score on an elementary mathematical level. We will explain these tools and the statistical models referred to above, and then illustrate the use with data from a clinical trial and from a Danish cohort study. We will also talk about suitable resampling techniques and thereby detect potential overfitting and make models comparable. Finally we address extensions of the criteria to survival analysis.

Participants: Ph.D.-students in medicine, epidemiology or biostatistics, and other interested scientists.

Language: English.   **Form:** Lectures.   **ECTS-credits: 2.5**

Course director(s): Associate professor Thomas Gerds.
Teacher(s): Tianxi Cai (Harvard University, Boston, USA), Thomas A. Gerds.

Date: 15 – 17 January 2008.   **Place:** Kommunehospitalet
Fee: DKK 3.000,- of which the operating costs amount to DKK 500,-.
Course secretary: Susanne Kragskov Laupstad, Department of Biostatistics, University of Copenhagen. Tel. +4535327901.
Registration: Before 1 January 2008.
No admission after deadline. Admission for Ph.D. students will be allocated on a first-come, first-served basis. Applications from external participants will be considered after the closing date. The application must be sent to: Ph.D. Administration, Blegdamsvej 3B, DK-2200 Copenhagen N.

Kursus om forskervejledning
d. 21. og 22. januar 2008
Hindsgavl Slot, Middelfart

Målgruppe
Kurset henvender sig til undervisere på Danmarks Forskerskole i Folkesundhedsvidenskab og Forskerskolen i Biostatistik, som vejleder (eller skal til at vejlede) ph.d. studerende.

Kursets omfang
Kurset omfatter to internatdage, samt en mindre skriftlig opgave inden kursets start

Kursets overordnede formål
Kursets formål er at give deltagerne mulighed for at reflektere over og udvikle sin rolle som forskervejleder.

Kursusmål
Målet er at deltagerne efter endt kursus har fået:

- Større bevidsthed omkring ansvar og krav til rollen som forskervejleder
- Kendskab til grundlæggende vejledningsprincipper og strategier i forskellige faser af forskningsforløbet
- Trænet færdigheder i spørgeteknik, der fremmer selvstændig tænkning hos den ph.d. studerende
- Skrivepædagogiske redskaber til at give feedback på studerendes tekster
- Diskuteret betydningen af forskningsmiljø, personligt lederskab og netværksdannelse
- Styrket sin viden om identificering og håndtering af konflikter og problemer under vejledningsforløbet

Kursusform
Kurset gennemføres som en blanding af kortere forelæsninger, tematiserede gruppediskussioner, øvelser og opgaver.

Kursusledere
Gitte Wichmann-Hansen, adjunkt, og Berit Eika, professor, Enhed for Medicinsk Uddannelse

Antal deltagere
Max. 25 deltagere pr. kursus

Tilmelding og frist:
Send e-mail til Lisbeth Lyng Hansen, L.L.Hansen@pubhealth.ku.dk med oplysning om navn, titel, institution og afdeling, og med angivelse af, om overnatning ønskes senest **fredag d. 16. november 2007**.

Statistician for Coloplast

The Biometrics department in Coloplast is looking for a statistician.

The Biometrics department is part of Clinical Development and manages data entry, data management and statistics for all clinical studies.

The statistician will contribute to the entire clinical development phase from idea to the final launch of product.

Your primary tasks
- Participate in planning of clinical studies in cooperation with clinical colleagues, e.g. sample size estimation
- Conduct statistical analyses and discuss the results with internal and external partners
- Prepare statistical reports
- Develop statistical methods and IT solutions within the area
- Statistical planning and analysis within other areas, e.g. health economics

Your professional and personal qualifications
- You have a master degree in statistics, mathematics, engineering, economics or similar
- You have a solid overview of and interest in applied statistics
- You have some experience of programming in SAS
- You are able to communicate statistical results for non-statisticians
- You are fluent in English and have a global mindset
- You are good at building relationships with colleagues in Denmark and abroad
- You may be a new candidate or have some years of experience with statistical analysis of e.g. health related data

We are
The statistician will be part of Biometrics, which is headed by a senior statistician and furthermore consists of 2 data managers, one full-time assistant for data entry, and one part-time student for SAS programming.

Clinical Development works with clinical studies within all business areas: smaller early development studies with a few patients, larger studies for documenting efficacy and safety of the products as well as large post-marketing studies.

Clinical Development is part of Global R&D, but has important interfaces with Global Marketing, e.g. within health economics. Clinical Development is physically placed in Humlebæk with departments in France and US as well.

Coloplast is a global company with main business areas Ostomy Care, Urology & Continence Care and Wound & Skin Care. We have more than 2000 employees in Denmark and more than 7000 worldwide.

We offer
- A job with a high impact in the organisation
- A large influence on the job content
- Good opportunity for further development of professional and personal competences
- A salary that meets your qualifications
- A working week of 37 hours (excl. lunch) with flex time and a possibility to work at home

Contact
If you have questions or want to know more about the position, please contact senior manager Birger Stjernholm Madsen at +45 30 85 24 75.

Please send your application by e-mail to dkbsm@coloplast.com, by November 19'th the latest. Indicate "Statistician" in the subject field.

Kalender 2007

Dato	No.	Aktivitet
5-9/11	3	Department of Mathematical Sciences, University of Copenhagen. Ph.D.-course: *Statistical Analysis of Microarray Expression Data with R and Bioconductor*
8/11	8	Thiele Centre, University of Aarhus. Andrew du Plessis, University of Aarhus: *Topology and digital images*
19/11	8	Biostatistisk Afdeling, Københavns Uiversitet. Agathe Le Lay (Université Lyon 1, Global Health Economics and Outcome Research Department, Novo Nordisk A/S), Gérard Duru (Université Lyon 1): *Can Discrete Event Simulation be of use when modeling major depressive disorders?*
20-21/11	6	DSTS, DTU, Lyngby *DSTS 2-day Meeting*
22/11	8	Thiele Centre, University of Aarhus. Seiji Hiraba, University of Aarhus: *Markov particle systems associated with multi-dimensional absorbing stable motion*
29/11	8	Institut for Folkesundhedsvidenskab og Biostatistisk Afdeling ved Københavns Universitet: *Afskedsreception for Lektor Jørgen Hilden.*
4/12	8	DSTS, Julemøde, Center for Sundhed og Samfund, Københavns Universitet Jens Ledet Jensen, Afdeling for Teoretisk Statistik, Århus Universitet: *Kan den hierarkiske faktormodel frikendes?*
6/12	8	Thiele Centre, University of Aarhus. Lars N. Andersen, University of Aarhus: *Parallel computing, failure recovery, and extreme values*
13/12	8	Thiele Centre, University of Aarhus. Mogens Bladt, Technical University of Denmark: *Title to be announced*

No.: Nummer af meddelelser hvor arrangement er annonceret.

Kalender 2008

Dato	No.	Aktivitet
15-17/1	8 / 07	Ph.D course, Biostatistisk Afdeling, Københavns Universitet Tianxi Cai (Harvard University, Boston, USA), Thomas A. Gerds: *Statistical evaluation of diagnostic and predictive models*
21-22/1	8 / 07	Danmarks Forskerskole i Folkesundhedsvidenskab/ Forskerskolen i Biostatistik, Hindsgavl Slot, Middelfart: *Kursus om forskervejledning*

No.: Nummer af meddelelser hvor arrangement er annonceret.