7. Research Centers

MaPhySto

The Danish National Research Foundation has recently established a Centre for Mathematical Physics and Stochastics (MaPhySto) with start April 1, 1998. Its Scientific Director is Ole E. Barndorff-Nielsen. The objective of the Centre is to strengthen the areas Mathematical Physics and Stochastics (and the interplay between these), by organizing conferences, summer schools and other activities in these areas.

More information can be found at the Centre's web page at

`http://www.maphysto.dk`

or by writing to the MaPhySto address:

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Workshop on Computational Stochastics (MaPhySto) January 17–22, 2000, University of Aarhus (Denmark)

Computational stochastics is a new and expanding area of stochastics, dealing with computational methods of analyzing complex mathematical and statistical models. The workshop intends to reveal and discuss the potential strength and impact of this new discipline in a variety of applications. It is held at the Department of Mathematical Sciences, University of Aarhus, and organized by StocLab (Laboratory for Computational Stochastics) and MaPhySto, University of Aarhus.

The organizing committee consists of Søren Asmussen (Lund) and Eva B. Vedel Jensen (Aarhus).

More Information

From the web-page

`www.maphysto.dk/events/CompStoc2000/.`

Here you also can register and find travel information. The registration fee is DKK 500 (approx. $ 75).

Concentrated Advanced Course on Lévy Processes January 24–28, 2000, University of Aarhus (Denmark)

The course will take place at the Department of Mathematical Sciences, University of Aarhus. Each day there will be 2–4 hours of lectures plus exercise sessions. The lectures will be given by Ken-iti Sato (Nagoya University). The following forthcoming book will be a reference: K. Sato, *Lévy Processes and Infinitely Divisible Distributions*, Cambridge University Press, 1999.

Content of Main Course

Lévy processes are stochastic processes on the Euclidean space, stochastically continuous and with stationary independent increments. Examples are Brownian motion, Poisson processes, stable processes (such as Cauchy processes), and subordinators (such as Gamma-processes). They form a basic class in stochastic analysis. This course aims at giving an introduction to elementary properties of Lévy process and to transformations between Lévy processes. Familiarity with the method of characteristic functions and some knowledge of Brownian motion, Poisson processes, and infinitely divisible distributions are expected. The following are the main contents of the lectures.

- Characterization of Lévy processes by the Lévy-Khintchine representation of infinitely divisible distributions. Probabilistic meaning of the characterization.
- Transformations of Lévy processes to Lévy processes. Especially, the subordination invented by Bochner and the density transformation (mutual absolute continuity in the path space in finite time) of Skorohod, Newman, and Kunita-S. Watanabe will be discussed in detail.
- Large time behaviors of Lévy processes. Especially recurrence, transience, and oscillation are characterized. (Chung-Fuchs, Spitzer, Port-Stone, Shepp, Kesten, Erickson)
- Time evolution of unimodality and multimodality of the distributions of Lévy processes on the line. (Wolfe, Yamazato, Sato, Toshiro Watanabe)

Additional lectures

In addition to the main lectures there there will be a mini-course (4 hours) with lectures by Francesco Mainardi (University of Bologna) on *Fractional Calculus in the Theory of Probability and Stochastic Processes*. Furthermore there will be a couple of one-hour guest lectures.

Further Information and Registration

From the web page

`www.maphysto.dk/events/LevyCAC2000/`

you may find more information on this event. From there it is also possible to register for the course, there is no registration fee. The deadline for registration is *December 20, 1999*.

Summer School on Stereology and Geometric Tomography May 20–25, Sandbjerg Manor (Denmark)

The summer school is addressed to PhDs, PostDocs and other researchers in mathematics. Scientists from the natural sciences with a strong background and interest in mathematics are also welcome. The number of participants is limited to 50. Participation will therefore be by application only.

The aim of the summer school is to give an overview of modern stereology and its relation to geometric tomography, including both the mathematical and statistical theory and the practical applications.

Stereology is the area of stochastics dealing with statistical inference about spatial structures from geometric samples of the structure such as two-dimensional sections and one-dimensional probes. The development of stereological methods involve the use of advanced mathematical tools, especially from geometric measure theory and integral geometry.

Geometric tomography is closely related to stereology, as is apparent from its definition: "geometric tomography is the area of mathematics dealing with the retrieval of information about a geometric object from data about its sections, or projections, or both". Geometric tomography has connections with convex geometry, geometric probing in robotics, computerized tomography, and other areas.

The teaching team includes

- Adrian Baddeley (Univ. of West. Australia)
- Richard Gardner (W. Washington University)
- Hans Jørgen G. Gundersen (Univ. of Aarhus)
- Eva B. Vedel Jensen (University of Aarhus)
- Kiên Kiêu (Institut National de la Recherche Agronomique, Versailles)

Registration

To apply for participation please fill out the registration form located at

`www.maphysto.dk/events/S-and-GT2000/register.html`

The deadline for application is *March 1, 2000*. The registration fee is DKK 750.

Further Information

From the web-page

`www.maphysto.dk/events/S-and-GT2000/`

you may find regularly updated information on this and other events. You are also welcome to contact the organizer Eva B. Vedel Jensen (e-mail: stoclab@imf.au.dk).

Wilfrid Kendall at the Pinetree Town and Country Club Singapore

EURANDOM

Statistics and probability in computational biology

Molecular biology will be a vitally important area of scientific research during the next decade. The genomes of a number of micro-organisms have been sequenced and completing the sequence of the human genome will take another 3 or 4 years. Then most of the relevant genetic information about the human species will in principle be available in a gigantic sequence database of 3.4x109 base pairs. Molecular biology will be a vitally important area of scientific research during the next decade. The available information has to be extracted from the database. Genes have to be identified and expression data analysed. Better and faster methods are needed to search extremely large databases for specific patterns and for comparison with similar databases. Mathematical models for the relevant biological processes have to be improved and tested and this will lead to new methods of analysis. Ultimately, this will open up possibilities for e.g. understanding evolution, pinpointing the genetic causes for certain diseases and starting the development of new drugs. Mathematics and computer science can provide the tools to achieve these goals.

Program Objectives

The research will go in a number of different but related directions.

- Probabilistic methods for sequence analysis
- Understanding evolutionary forces on a molecular level
- Analysis of extremely large datasets

Collective Expertise

The collective expertise of the partners in this network covers the areas of computational biology, probability theory and mathematical statistics, which is the subject of the research and the training programme of the network. All partners have an excellent international reputation in their respective subjects. The different partners have complementary tasks, but there are also common interests.

Team 1 is based on EURANDOM, the European institute for statistics, probability and operations research and their applications, and these are the areas of its expertise. Key persons: R. D. Gill, M. C. M. de Gunst, M. S. Keane, W. R. van Zwet.

Team 2 is based on the Gothenburg Stochastic Centre, the Swedish national centre for statistics and probability. Key persons: O. Nerman, M. Rudemo, P. Jagers, Z. Taib.

Team 3 is based on the Department of Electronics and Informatics of the University of Padova. It brings to the network its expertise in the analysis of extremely large datasets. Key persons: A. Apostolico, L. Colussi, G. Lancia.

Team 4 is based on the Centre for Biological Sequence Analysis at the Technical University of Denmark at Lyngby. This team brings to the network its expertise on gene structure with a recent emphasis on statistical gene finding using an integrated model estimated on the basis of a conditional maximum likelihood method. Key persons: S. Brunak, A. Krogh.

Team 5 is based on the Institut National de la Recherche Agronomique, Centre de Recherches de Jouy-en-Josas (INRA-CRJJ). It contributes expertise in computer science, statistics and artificial intelligence applied to biological fields such as genetics (building genetic maps, identifying and locating QTL) and sequence analysis (alignment of sequences, prediction and visualisation of RNA secondary structure, location of small RNA, identification of protein domains. Key person: E. de Turckheim.

Team 6 is based on the theoretical bioinformatics unit at the Deutsche Krebsforschungszentrum at Heidelberg. This team provides expertise on statistical aspects of sequence alignment and the analysis of gene transcript levels in cells. Key person: M. Vingron.

Team 7 is based on the Max-Planck-Institut für evolutionäre Anthropologie at Leipzig. It brings to the network expertise on a broad front of the mathematical theory of evolution. Key persons: A. von Haeseler, G. Weiss, D. Metzler.

Team 8 is based on the mathematical genetics group of the Department of Statistics in the University of Oxford. This team adds to the programme its expertise in stochastic modelling and statistical analysis of data documenting DNA sequence and related molecular variation within and between populations. Key persons: P. Donnelly, A. Etheridge, R. C. Griffiths, N. Laws.

Team 9 is based on the Applied Mathematics Department at the ETH in Zürich. This team provides considerable probabilistic expertise applied to macromolecular systematics, in particular to detecting distant relationships between proteins. Another area of expertise is methods for finding "useful" genes in libraries of genomic sequences, for instance those relevant to the infection of host cells by organisms such as malaria. Key person: A. Barbour.

Team 10 is based on the bioinformatics group at The Sanger Centre at Cambridge, which is Europe's leading genome sequencing centre where most of the sequencing of the human genome was done so far. The team contributes its unique expertise in probabilistic modelling for sequence analysis. Key person: R. Durbin.

Training

It is generally agreed that there is a shortage of research workers in computational biology and that the situation in Europe is worse than in the US in this respect. The rapid progress in molecular biology has produced a growing need for experts in this multidisciplinary field. Because of the increasing complexity of the mathematical problems involved, it is no longer enough to have some limited mathematical knowledge. Many of the methods employed in computational biology are statistical or probabilistic, and up-to-date knowledge in these areas is needed to be effective.

In principle, training will be provided for post-docs in probability and statistics. The training program envisages providing a two-year training period. The post-docs will be trained in computational biology, or more specifically in the application of statistics and probability theory to molecular biology. The objective of the training programme is to educate highly qualified and much needed experts who are at the forefront of research in computational biology as well as in statistics and probability. Contacts with potential users and possible future employers will be encouraged.

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Further information

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