

# ESMTB Infoletter

## January 2008



[www.esmtb.org](http://www.esmtb.org)

Dear colleague

with this ESMTB Infoletter you receive information about conferences, workshops, schools and open positions. Please send relevant information to be included in the next ESMTB infoletter to [info@esmtb.org](mailto:info@esmtb.org).

Best regards, Andreas Deutsch  
Dresden, 15th of January 2008

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## Conferences

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**Genomic Disorders 2008 - studying the Genome to Understand Human Development and Disease at Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, UK**

**Date: 2008-03-17 to 2008-03-20**

This meeting aims to present and discuss the latest findings relating to the genomic basis of human variation, congenital disorders and acquired diseases.

We aim to facilitate interaction between scientists and physicians investigating the genomic bases of disease and to further foster links among genomic scientists and clinicians. It has been recognized for some time that genomic rearrangements are a cause of some genetic syndromes e.g. Smith-Magenis syndrome and Williams syndrome. More recently, it is becoming clear that genomic rearrangements make a significant contribution to the wider burden of human disease and are the cause of some types of diabetes, neuropathy, haemoglobinopathy and dementia.

Topics to be discussed will include copy number variation and assays, structural variation predisposing to genomic rearrangement, mechanisms underlying genomic disorders, genomic rearrangements in common diseases and genetic syndromes, model organisms in the study of genomic disorders and potential therapeutic approaches.

[http://firstcontact.hinxton.wellcome.ac.uk/display\\_info.asp?id=94](http://firstcontact.hinxton.wellcome.ac.uk/display_info.asp?id=94)  
<mailto:l.criddle@wtconference.org.uk>

**Computational Cell Biology at Wellcome Trust Genome Campus, Hinxton, UK**

**Date: 2008-03-26 to 2008-03-30**

Following the success of the first Cold Spring Harbor Laboratory meeting on Computational Cell Biology in March 2007, a second conference on Computational Cell Biology will be held at the Wellcome Trust Conference Centre on the Wellcome Trust Genome Campus in Hinxton, UK. The meeting will begin in the afternoon of Wednesday March 26 (3pm), and end with a banquet on Saturday evening March 29, with normal departure on Sunday morning March 30.

The specific goal for this meeting is to foster fruitful and creative dialogs between experimental cell biologists and mathematical - computational modelers with common interests in the regulation of cell physiology. Emphasis will be placed on areas of greatest current interest and importance, such as cell signaling, motility, cell proliferation and death, calcium dynamics, microbial physiology, and development. Sessions will also be devoted to new experimental technologies and software developments.

The format of the meeting will consist of oral sessions including a combination of invited talks and talks selected from the abstracts, plus sessions devoted to posters and new software development.

Abstracts should contain only new and unpublished material and must be submitted electronically by the abstract deadline. Selection of material for oral and poster presentation will be made by the organizers and individual session chairs. Status (talk/poster) of abstracts will be posted on our web site as soon as decisions have been made by the organizers.

We are eager to have as many young people as possible attend since they are likely to benefit most from this meeting. We have some funds to partially support graduate students and postdocs. Apply in writing to [meetings@cshl.edu](mailto:meetings@cshl.edu) stating need for financial support - preference is given to those submitting abstracts.

<http://meetings.cshl.edu/meetings/compuk08.shtml>

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### **International Conference on Systems Biology of Mammalian Cells (SBMC 2008) at Dresden, Germany**

**Date: 2008-05-22 to 2008-05-24**

The competence network HepatoSys would like to draw your attention to the SBMC 2008 (May 22th - 24th) in Dresden, Germany. This conference will provide an overview of latest developments in cell signaling, proteomics, live cell imaging and dynamic pathway modeling that merge in the interdisciplinary field of Systems Biology in Mammalian Cells. The approach offers challenges and perspectives for life scientists, mathematicians, physicists, chemists, engineers and computer scientists.

In the sessions New theoretical approaches and cutting edge technologies, Signaling Networks, Self-organization and collective phenomena, Developmental Pattern Formation and Biomedicine, internationally renowned speakers will provide an overview and insights into the latest developments.

Junior scientists with a strong interest in quantitative biology, mathematical modeling and Systems Biology are invited to register and submit their abstracts until February 29th. Per session we will select at least one of the most exciting abstracts for oral presentations.

The social program will include activities such as a scenic boat trip on the Elbe river, an outdoor barbecue dinner and will leave plenty of opportunities for intensive and stimulating discussion.

<http://www.sbmc08.de>  
<mailto:ute.heisner@fdm.uni-freiburg.de>

### **4th International Conference on Analysis of Microbial Cells at the Single-Cell Level at Bad Schandau, Dresden, Germany**

**Date: 2008-05-22 to 2008-05-25**

In microbiology cells are often considered to be uniform populations which can be adequately described by average values. Consequently, measurement of the physiology and biochemistry of these cells often relies upon analysing either the culture supernatant or a lysate of all the cells in the population. The availability of tools such as flow cytometry and image analysis which allow measurements to be made on individual cells has changed our perception of microbes within the laboratory and natural environments. It has become increasingly clear that even pure populations derived from a single cell are far from homogeneous.

In recent years new methods have improved analysis of what occurs at the single cell level allowing us to begin to understand why cells and cultures behave in the way that they do. Monitoring expression of genes at the single-cell level via the use of reporters such as GFP and observing the presence and dynamics of sub-populations have added to our understanding of microbial physiology. The commercialisation of smaller, easy-to-use and cheaper instruments has widened access to these techniques. The fourth meeting will include a variety of oral and poster sessions including the following themes:

- New instrumental developments and new fluorescent techniques
- Biotechnological applications
- Human health
- Screening and sorting
- Single cell approaches to cytomics, transcriptomics and proteomics
- Cell biology
- Multicellular organization
- Environmental applications
- Mathematical modelling of microbial life

Early bird registration deadline: January 31st, 2008

Abstract submission deadline: January 31st, 2008

<http://qbab.dbs.aber.ac.uk/sc2008/>

**Computational Developmental Biology - 6th BGRS Conference at Akademgorodok, Novosibirsk, Russia****Date: 2008-06-22 to 2008-06-28**

We kindly invite you to consider the participation in the Computational Developmental Biology section of the next BGRS conference. BGRS is a bi-annual conference on bioinformatics organized by the Institute of Cytology and Genetics of the SB RAS.

The aim of the Computational Developmental Biology section is to foster fruitful and creative dialogs between experimental developmental biologists, mathematicians, computer scientists and scientists working in the field of systems biology of development. Special emphasis will be made on areas of greatest current interest and importance, such as pattern formation, cell fate determination, transcriptional and signaling networks, cell movements, morphomechanics, cell-cell communication, proliferation and death. The session will also be devoted to new experimental technologies and software design.

The participants will be offered a social program for recreation and sightseeing. Those interested in the cultural traditions and wild-life of Siberia will be offered a post-conference tour to Altai mountains.

Abstract submission deadline: March 1st  
Registration deadline: May 1st

<http://www.bionet.nsc.ru/meeting/bgrs2008/index.html>  
<mailto:samson@spbcas.ru>

**Eighth Annual International Gatherings in Biosemiotics at University of the Aegean, Syros, Greece****Date: 2008-06-23 to 2008-06-28**

The Conference Organizing Committee welcomes paper proposals from theorists and researchers in any academic discipline who are investigating the existence of signs and codes in living systems as well as their role in the origin and evolution of life. Biologists, philosophers and researchers from

both the natural sciences and the social sciences are invited to contribute to this interdisciplinary event.

To submit a proposal, interested parties should e-mail to the address below: (1) an abstract of between 250-500 words and (2) an extremely abbreviated one-page CV.

These proposals should be sent to [2008abs@biosemiotics.org](mailto:2008abs@biosemiotics.org) by January 31, 2008 and early submissions are highly encouraged.

The Eighth Annual Gatherings in Biosemiotics is being held under the auspices of the the International Society for Biosemiotic Studies, in cooperation with Dr. John Darzentas and Arnellos Argyris of the University of the Aegean.

<http://www.biosemiotics.org>

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**The European Conference on Mathematical and Theoretical Biology 2008 at George Square complex of Edinburgh University, Edinburgh, Scotland****Date: 2008-06-30 to 2008-07-04**

The European Society for Mathematical and Theoretical Biology (ESMTB) hosts a major international conference every three years and the next and 7th such conference will be held from 30th June - 4th July, 2008 in Edinburgh, in the George Square complex of Edinburgh University.

**CALL FOR MINISYMPOSIA:**

A minisymposium will consist of a 2 hour session dedicated to a single area of research. Each minisymposium may be composed of four 30-minute talks or three 40-minute talks. Applications to organise a minisymposium should be made via the conference web-site: <http://www.maths.dundee.ac.uk/ecmtb08> 2007 onwards.

The deadline for applications is 31st December 2007.

All proposals will be refereed by members of the Scientific Committee and notification of acceptance for minisymposia applications will be made by 1st February 2008.

**REGISTRATION, CONTRIBUTED PAPERS, POSTERS:**

Registration for the meeting will be open on Monday 26th November 2007 and the call for abstracts of Contributed Papers and Posters will be made at this time also.

<http://www.maths.dundee.ac.uk/ecmtb08>  
<mailto:ecmtb08@maths.dundee.ac.uk>

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**German Conference on Bioinformatics 2008 at Biotechnologisches Zentrum, Technische Universität Dresden, Dresden, Germany**

**Date: 2008-09-09 to 2008-09-12**

The German Conference on Bioinformatics is an annual, international conference devoted to all topics in bioinformatics. Its tradition reaches back to 1985, and recent conferences have attracted up to 200 participants from all over the world.

The 2008 conference is organized by the Technische Universität Dresden.

Areas of interest at the German Conference on Bioinformatics 2008 are:

- Sequence Analysis and Comparative Genomics
- Analysis of Functional Genomics Data
- Structural Bioinformatics
- RNA/DNA Structure
- Molecular Interactions and Drug Design
- Systems Biology
- Biochemical and Genetic Networks
- Textmining and Ontologies
- Image Analysis

<http://www.gcb2008.de>  
<mailto:info@gcb2008.de>

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## Schools

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**Biological Networks: Evolution, Interaction and Computation at Lipari Island, Italy**

**Date: 2008-06-14 to 2008-06-21**

The theme of the school, Biological Networks: Evolution, Interaction and Computation, falls within the areas of Bioinformatics & Systems Biology,

and deals specifically with bioinformatics aspects of systems biology. There are four lecture series, each of three hours, and six tutorials, each of one hour. The lectures will cover fundamental aspects relating to the evolution of biomolecular systems and their various levels of interaction. Two series of lectures are devoted to molecular evolution in viruses and more complex genomes, while the other two are devoted to mathematical and computational methods needed to infer networks both for evolutionary and functional studies. We note that detection of similarity and comparison of biological sequences and structures remains a fundamental task; in particular, although methods based on sequence alignments alone seem no longer adequate. Moreover, the comparison of biological networks, in order to infer common features, is a particularly important, yet largely unexplored, computational topic. The tutorials will cover the most recent advances in computational methods to establish similarity among biological structures: sequences, protein structures, networks and graphs. Moreover, they will also highlight recent additional results on protein-protein and protein-DNA interactions. Thus they nicely complement the main lectures. As is clear from the enclosed bibliography, the selected themes have received attention in the scholarly literature that ranges from Nature to BMC Bioinformatics and Bioinformatics. In its entirety the planned summer school will allow young researchers interested in bioinformatics and systems biology to be exposed to cutting edge results in the increasingly important area of network inference and analysis in biology.

Deadline for application is March 31, 2008.

<http://lipari.cs.unict.it/LipariSchool/Bio/index.php>  
<mailto:school@dmf.unict.it>

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## Open Positions

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**Post-doc position in mathematical epidemiology of emerging diseases at Department of Mathematical Sciences, Göteborg, Sweden**

**Deadline for applications: 2008-01-21**

A post-doc position on the mathematical epidemiology of emerging diseases is available within the Center for theoretical biology at GU. The job in-

cludes development of mathematical models for disease spread and propagation at different scales.

The candidate should have a strong background in epidemiological mathematics, stochastic and deterministic mathematical modelling and an interest in theoretical evolutionary biology. The work will be done in close collaboration with theoreticians and evolutionary ecologists within the Center for theoretical biology (<http://tfk.fy.chalmers.se/centrum/index.html>). An interest to collaborate across disciplines is essential.

Dead line for applications: 21 January 2008.

The position is open from May 2008 and is for one year, with the possibility for extension up to one additional year depending on funding and performance. The post doc will be based at the Department of Mathematical Sciences/Mathematical Statistics in Gothenburg. The Department has a stimulating research environment and hosts for example the Stochastic Centre with rich possibilities for interactions. The candidate will be encouraged to participate in joint workshops, seminars and meetings at CTBio.

For further information contact the main host, Bernt Wennberg [wennberg@math.chalmers.se](mailto:wennberg@math.chalmers.se) or co-hosts Karin Harding ([karin.harding@swipnet.se](mailto:karin.harding@swipnet.se)), Peter Jagers ([jagers@math.chalmers.se](mailto:jagers@math.chalmers.se)) or Bernhard Mehlig ([ftrbm@fy.chalmers.se](mailto:ftrbm@fy.chalmers.se)).

#### Applicationy

Send CV, two reprints, a one page statement of research interests and three references directly to: The Registrar, Göteborgs University, Box 100, SE-405 30 Göteborg, Sweden. Please write the reference code on your application ref. nr E36 1744/07. Trade union representatives: SACO Martin Björkman tel. +46 31-7863608, SEKO Lennart Olsson tel +46 31-7861173, OFR-S Eva Sjögren tel +46 31-7861169.

Please contact: [Bernt Wennberg](mailto:wennberg@math.chalmers.se)

**Postdoctoral fellow: mathematical models in spatial ecology at Department of Mathematics and Statistics, University of Ottawa, Canada**

**Deadline for applications: 2008-01-31**

Applications are invited for a postdoctoral fellowship in mathematical ecology at the University of Ottawa in the Department of Mathematics and Statistics. The goal of this interdisciplinary project, which is funded by the Ontario Ministry of Research and Innovation, is to construct and analyze mathematical models for food-webs in river ecosystems. The research will address questions of how different natural and human disturbances and climate change affect population persistence, non-native species invasion, and the composition of existing food-webs on several temporal and spatial scales.

The position is based in Ottawa, Canadas capital, but research collaborations exist with several other research groups in North America (e.g., Calgary, Edmonton, Santa Barbara). It is expected that the successful candidate will spend time visiting these groups for collaboration and exchange.

Applicants should hold a PhD in Applied Mathematics or a related field with strong background in modeling, analysis (ODEs, PDEs), and computation. Previous exposure to ecological models or previous collaborations with experimentalists (biologists, ecologists) are an asset. The position is for one year with a possibility of renewal for a second year. The position includes teaching duties of one one-semester course per year. Salary is approximately \$42,000 per year plus benefits. A small budget for conference travel is also available.

The application should include a detailed CV together with a cover letter stating research interests, as well as three names of potential references. Electronic applications are strongly encouraged. Review of applications will start immediately and will continue until the position has been filled. For further information or to apply please contact Prof. Frithjof Lutscher ([flutsche@uottawa.ca](mailto:flutsche@uottawa.ca)).

Employment equity is University policy and the University strongly encourages applications from women, minorities and other underrepresented groups.

Please contact: [Prof. Frithjof Lutscher](mailto:flutsche@uottawa.ca)

**PhD position on simulating evolutionary dynamics Simula Research Laboratory at Simula Research Laboratory, Lysaker, Norway**

**Deadline for applications: 2008-02-15**

Simula Research Laboratory conducts basic research in the fields of communication technology, software engineering and scientific computing. The research in the Scientific Computing (SC) department is focused on the development of numerical methods, algorithms and software, and large-scale biomedical and systems biology oriented simulation studies applying these methods.

Currently, we plan to extend our biologically inspired research to simulation studies of evolutionary dynamics of genetic networks and their role in species adaptation, formation and development. For this project we seek a candidate for an available PhD position (3 years). The position will be supervised by a new member of our research group; Dr Kirsten ten Tusscher. In the current, post-genomic era, it has become increasingly clear that to understand the functioning of biological cells, tissues, organisms and populations it is not enough to know which genes or proteins they possess. In addition, one also needs to understand how these genes and proteins interact dynamically in complex networks and how these interactions have arisen during evolution. As an illustration, after the human genome was sequenced, people were surprised by the relatively small number of genes found in humans. Based on gene numbers in simpler organisms a much larger number was expected. It is now becoming clear that our larger complexity relative to single celled and simple multicellular organisms resides not so much in the number of genes we have but in the way these genes interact in complex networks. In the current research we will study the role of genetic networks in several key biological evolutionary processes: the adaptation of species to their (changing) environment, the splitting of a species into multiple species, and the development of multicellular organisms.

Simula offers excellent opportunities for doing high quality research, generous support for travels and equipment, and competitive salary (around 47.000,- Euro/69.000,- USD for a Ph.D. position and 58.000,- Euro/84.500,- USD for a Postdoc position).

We are looking for candidates with a strong interest in biological and evolutionary oriented research and a University degree in physics, applied mathematics, computer science, artificial intelligence, biomedical engineering, or computational biology. The position requires excellent English writing skills and high marks from the BSc and MSc degree. Women are encouraged to apply. For more information visit <http://www.simula.no/jobs>, or contact Kirsten ten Tusscher ([tentusse@simula.no](mailto:tentusse@simula.no)) or Joakim Sundnes ([sundnes@simula.no](mailto:sundnes@simula.no)). To apply for these positions, email a short application letter and curriculum vitae with publication list to [jobs@simula.no](mailto:jobs@simula.no). The subject of the email must contain 0820 Scientific Computing.

Application deadline: February 15, 2008

Please contact: [Kirsten ten Tusscher](mailto:tentusse@simula.no)

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**PhD/Postdoc position on simulating cardiac arrhythmias Simula Research Laboratory at Simula Research Laboratory, Lysaker, Norway**

**Deadline for applications: 2008-02-15**

Simula Research Laboratory conducts basic research in the fields of communication technology, software engineering and scientific computing. The research in the Scientific Computing (SC) department is focused on the development of numerical methods, algorithms and software, and large-scale biomedical and systems biology oriented simulation studies applying these methods. To further strengthen our research in the area of cardiac modeling we seek a candidate for an available PhD or Postdoc position. The research will be focused on simulating cardiac arrhythmias using a biophysically detailed model of the human heart, and will be supervised by a new member of our research group; Dr Kirsten ten Tusscher. Despite the large socio-economic costs of people suffering from cardiac arrhythmias and sudden cardiac death and despite decades of research the causes and mechanisms of cardiac arrhythmias are still poorly understood. The goal of the current research project is to contribute to a better understanding of the anatomical structures and biological processes important in causing arrhythmias. More specifically, in the project we will look at the role of anatomical heterogeneities present in cardiac muscle (capillar-

ies, connective tissue, intricate anatomical structures such as Purkinje system, and the papillary and trabecular muscles of the heart) in arrhythmia dynamics. In addition, we will study the complex role of intracellular calcium (involved in excitation, contraction and metabolism) in arrhythmia dynamics.

Simula offers excellent opportunities for doing high quality research, generous support for travels and equipment, and competitive salary (around 47.000,- Euro/69.000,- USD for a Ph.D. position and 58.000,- Euro/84.500,- USD for a Postdoc position).

We are looking for candidates with a strong interest in biological and biomedical research and a University degree in physics, applied mathematics,

computer science, artificial intelligence, biomedical engineering, or computational biology. The position requires excellent English writing skills and high marks from the BSc and MSc degree. Women are encouraged to apply.

For more information visit [www.simula.no/jobs](http://www.simula.no/jobs) or contact Kirsten ten Tusscher ([tentussc@simula.no](mailto:tentussc@simula.no)) or Joakim Sundnes ([sundnes@simula.no](mailto:sundnes@simula.no)). To apply for these positions, email a short application letter, curriculum vitae, copies of transcripts and grades, and a publication list to [jobs@simula.no](mailto:jobs@simula.no). The subject of the email must contain 0810 Scientific Computing.

Application deadline: February 15, 2008

Please contact: [Kirsten ten Tusscher](mailto:tentussc@simula.no)