

ESMTB Infoletter

May 2010



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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.

Best regards, Andreas Deutsch
Dresden, 17th of May 2010

Conferences

EMBO Conference Series: From Functional Genomics to Systems Biology at EMBL Advanced Training Centre, Heidelberg (Germany)

Date: 2010-11-13 to 2010-11-16

The past decade has seen an exponential growth in genome-wide data measuring diverse cellular parameters, such as TF binding, gene expression, translation, protein abundance, protein-protein interactions, and genetic phenotypic interaction. In order to gain a systems level understanding of a given process, cell or organism, the current challenge is to convert these static qualitative maps into dynamic quantitative models of cellular processes. This rather daunting task can only be achieved through a multidisciplinary approach, which requires intensive integration of technology and thinking from many diverse fields, including basic biology, genomics, computational biology, mathematics, engineering and physics.

The main objective of this conference is to bring people together from these diverse disciplines to exchange ideas, promote cross-disciplinary collaborations and to form a synthesis of appropriate systems-level approaches. The meeting will cover all aspects of functional genomic approaches to systems biology, going from the genome to phenotype. These include transcriptional networks, protein interaction networks, functional interaction networks (synthetic lethal screens, genetics, RNAi), synthetic biology, multi-dimensional data integration and qualitative and quantitative modelling. This broad scope has been the format of this meeting every since it was initiated in 2002.

The meeting has since been held every two-years, with the 2010 meeting being the fifth biennial meeting.

Registration and abstract deadline: 15 August 2010

<http://www.embl.de/events/2010/OMX10-01>

Workshops

Plant Systems Biology UK Workshop 2010 at University of Nottingham, Nottingham (UK)

Date: 2010-06-01 to 2010-06-03

This workshop brings together participants from the UK plant systems biology community. As well as progress updates from CISB and SABR projects, it provides a great opportunity for post-docs and postgraduate students to present their work, network with colleagues and hear about available tools and resources.

The workshop will start with project overviews from CSBE, CPIB, PRESTA, ROBUST and ONDEX. Contributed talks from PDRAs and postgraduate students will comprise the majority of the programme. Sessions 2-8 will be multidisciplinary, and themed by physical scale, through networks, cells, tissues and multiscale approaches. The final distribution of these themes across the sessions will be dependent on the abstracts received. Joint talks combining experimental and modelling work are encouraged. Talks which describe tools and resources are also encouraged and will be incorporated into the themed sessions. Talks by a single presenter will be allocated a 20 minute slot integrated talks by two speakers will be given 40

minute slots. Please indicate clearly on your submitted abstract if your talk is to have two presenters and requires a double slot.

<http://www.cpib.ac.uk/2010/psb-uk-workshop-2010/>
<mailto:susie@cpib.ac.uk>

Schools

Jena Life Science Forum 2010 - The Molecular Language of Life at University of Jena (Jena, Germany)

Date: 2010-08-23 to 2010-08-27

Please see attached pdf (in German) for details.

<http://www.frege.uni-jena.de>
<mailto:stefan.artmann@uni-jena.de>

Open Positions

Postdoctoral Computational Biologist at NKI-AVL and the VU University, Amsterdam (The Netherlands)

Deadline for applications: 2010-07-01

Computational Modeling of Signaling and Regulatory Pathways in Th17 Differentiation

Lymphocytes are central in the regulation of immune response. T-lymphocytes differentiate into functionally distinct subsets. Proper regulation of the balance between various subsets is crucial for an optimal immune system and for host defense against pathogens and cancer. Recently, a new T-cell subset, Th17, which plays a central role in host defense, was discovered. In this project, our aim is to identify the underlying regulatory mechanisms and molecular networks that govern the formation of Th17 cells.

We will achieve this by generating comprehensive datasets and performing state-of-the-art computational modeling based on these data. The data sets will include time series RNA and miRNA expression data, siRNA perturbation experiments based on kinome and phosphatome libraries, (phospho)protein expression and Chip-Seq data. To

construct the computational models, we will build both data-driven machine learning models and knowledge-driven (logical and Petri-net) models of the regulatory networks. Our aim is to fuse the results of these two approaches to obtain a single, hybrid model. Computational predictions of key control mechanisms will be tested experimentally and the resulting data will be employed to refine the models.

The successful candidate will be primarily responsible for constructing models of the regulatory Th17 developmental networks, developing new computational methodologies where required and liaising with the computational and biological partners in this project.

The vacancy is a research position within the field of bioinformatics/computational biology and the research will be carried out in close collaboration with the involved partners. The ideal candidate has a background in bioinformatics, computer science, statistics, physics, or biology, strong algorithmic and/or machine learning skills, and experience with the analysis of high-throughput data.

The temporary employment will be for a period of three years. The gross monthly salary for a Post-doc will range from 3140,- to 3.495,- and depends on previous experience. We can help you find housing. The NKI-AVL has been listed in the top 25 of Best Employers in 2009 offering a specialized cancer research institute and hospital with good working conditions and an excellent atmosphere.

To apply, and for further information please contact Lodewyk Wessels, tel.: +31-20-5127987, e-mail: l.wessels@nki.nl or Jaap Heringa, tel.: heringa@few.vu.nl +31 20 59 87649 (direct) or +31 20 59 87483 (secr.)

Please contact: [Lodewyk Wessels](#)

PhD position at University Medical Centre Utrecht (The Netherlands)

Deadline for applications: 2010-05-31

Project: Modelling the spread of multi-resistant Gram-negative enteric bacteria: the interaction between animal and human reservoirs.

Research project Gram-negative bacteria producing extended-spectrum β -lactamases (ESBL) are rapidly emerging in Dutch hospitals and worldwide. Nosocomial infections caused by these bacteria are associated with increased morbidity, mortality and health care costs. Although ESBL are also frequently found in agricultural industry, where their prevalence probably results from extensive antibiotic use. Yet, the interaction between the animal reservoir and the human reservoir is not well understood. Curtailing spread of ESBL in health care settings will be a challenging task, and the most (cost)-effective strategy to do so is unknown. Intervention studies to fill this knowledge gap require long periods of follow-up, and are unlikely to provide answers in due course. This study will combine longitudinal prevalence and incidence ESBL surveillance data from ongoing (inter-)national studies in different human and patient populations, as well as to-be-collected data from missing epidemiological niches (i.e., veterinary reservoirs) with mathematical modelling to quantify the interaction between both reservoirs. The results of this study will also guide infection prevention strategies for controlling ESBL.

The PhD candidate should have successfully completed a masters degree in theoretical biology, mathematics, biostatistics, or social sciences with a strong quantitative background. Experience with mathematical modelling and advanced statistical techniques is an advantage. The candidate should have a broad interest in the application of mathematical methods to epidemiological and public health questions. He/she should be able to communicate well with researchers from other disciplines and should be eager to learn to solve problems on the interface of theoretical epidemiology and public health. With support of the research team, the applicant is expected to write scientific papers on the results of the project and give presentations at national and international meetings.

Please contact: [Prof.dr. M.J.M. Bonten](#)
[Download PDF here](#)

PhD position at University Medical Centre Utrecht (The Netherlands)

Deadline for applications: 2010-05-31

Project: Respondent driven detection and control

strategies for emerging infectious diseases

In recent years syndromic surveillance was explored as a means for detecting outbreaks of infectious diseases as timely as possible based on data other than routine surveillance data. However, it has proven difficult to implement syndromic surveillance in real time. Reasons are the difficulties in interpreting aspecific syndromes in terms of specific pathogens, the efforts involved in providing morbidity and mortality data on a population level in a timely manner, and the simple fact that only larger outbreaks will have a detectable impact on the population level. These factors preclude the effectiveness of syndromic surveillance for newly emerging pathogens that per definition occur in small localized clusters. The aim of this project is to develop and investigate webbased, respondent driven methods for investigating the transmission of infectious diseases and explore them as alternative methods for detection of small outbreaks of possibly unknown pathogens. We want to investigate whether a signal can be amplified by making use of localized information that is available to individual respondents only. To do this, a combination of social sciences tools and mathematical modelling will be used. One part of the project will be the development of a webbased questionnaire to explore social networks, the other part will be a theoretical analysis of the effectiveness of intervention in outbreaks using information obtained or spread via social networks.

The PhD candidate should have successfully completed a masters degree in theoretical biology, mathematics, biostatistics, or social sciences with a strong quantitative background. Experience with mathematical modelling and advanced statistical techniques is an advantage. The candidate should have a broad interest in the application of mathematical methods to epidemiological and public health questions. He/she should be able to communicate well with researchers from other disciplines and should be eager to learn to solve problems on the interface of theoretical epidemiology and public health. With support of the research team, the applicant is expected to write scientific papers on the results of the project and give presentations at national and international meetings.

Please contact: [Dr. Mirjam Kretzschmar](#)
[Download PDF here](#)

PhD-researcher Mathematics at University Medical Centre Utrecht (The Netherlands)**Deadline for applications: 2010-06-04**

The Utrecht University Focus Area Epidemiology has provided funding for the project: Combining within host models for immune response and waning immunity with population level transmission models, supervised by Odo Diekmann (Department of Mathematics) and Mirjam Kretzschmar (Julius Centre for Health Sciences and Primary Care, UMCU, as well as RIVM)

The interaction between various strains of a pathogen is mediated by the immune system of the host. The level of immunity of an individual determines its susceptibility, but also its infectiousness, duration of the infectious period and severity of symptoms. In order to unravel the mechanisms behind shifts in (relative) incidence/prevalence of strains, e.g. as a result of a mass vaccination program, we therefore need nested models, i.e., models at the population level that have models for within host processes as building blocks. The aim of this project is to develop an efficient mathematical framework for the formulation and analysis of such nested models, building on established methodology for Physiologically Structured Population Models. The link to actual data will concentrate on *Campylobacter*, in close interaction with Prof. A. Havelaar and Dr. A. Swart of the RIVM.

The candidate will also participate in the education program of the department of Mathematics

(max 15% of the time).

The position will start at approximately 1 September 2010.

We are looking for excellent and enthusiastic researchers who have a MSc in Mathematics. Also researchers with a MSc in Theoretical Biology or Physics with a strong mathematical background are invited to reflect.

The candidate is offered a full-time position for 4 years. The gross salary is in the range between 2,042.- and 2,612.- gross per month. The salary is supplemented with a holiday bonus of 8% and an end-of-year bonus of 8,3% per year. In addition we offer: a pension scheme, a partially paid parental leave, flexible employment conditions in which you may trade salary for vacation days or vice versa. Conditions are based on the Collective Employment Agreement of the Dutch Universities. The research group will provide the candidate with necessary support on all aspects of the project.

Please send your application (including a letter of motivation, curriculum vitae and contact details of at least one reference) before 4 June to Faculty of Science, Personnel department, PO Box 80010, 3508 TA Utrecht, The Netherlands or e-mail: Science.PenO@uu.nl. Please mention vacancy number 62002

Please contact: Prof. Odo Diekmann
<http://www.math.uu.nl/Positions/62002.pdf>
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