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, 21st of January 2015

JMB Table Of Contents

Current table of contents (Volume 70 Nr. 1-2 January 2015):

- Macroscopic equations for bacterial chemotaxis: integration of detailed biochemistry of cell signaling
  Chuan Xue

- Coding sequence density estimation via topological pressure
  David Koslicki, Daniel J. Thompson

- The role of spatial organization of cells in erythropoiesis
  N. Eymard, N. Bessonov, O. Gandrillon, M. J. Koury

- Stochastic modelling of T-cell activation
  Hannah Mayer, Anton Bovier

- On a poroviscoelastic model for cell crawling
  L. S. Kimpton, J. P. Whiteley, S. L. Waters

- RNA folding pathways and kinetics using 2D energy landscapes
  Evan Senter, Ivan Dotu, Peter Clote

- Mathematical modeling in biological populations through branching processes. Application to salmonid populations
  Manuel Molina, Manuel Mota, Alfonso Ramos

- The impact of self-protective measures in the optimal interventions for controlling infectious diseases of human population
  Semu Mitiku Kassa, Aziz Ouhinou

- Modelling in vivo action potential propagation along a giant axon
  Stuart George, Jamie M. Foster, Giles Richardson

- Success, failure, and spreading speeds for invasions on spatial gradients
  Bingtuan Li, William F. Fagan, Kimberly I. Meyer

- Optimization of an amplification protocol for misfolded proteins by using relaxed control
  Jean-Michel Coron, Pierre Gabriel, Peipei Shang

- Implications of the spatial dynamics of fire spread for the bistability of savanna and forest
  E. Schertzer, A. C. Staver, S. A. Levin

- An immuno-epidemiological model with threshold delay: a study of the effects of multiple exposures to a pathogen
  Redouane Qesmi, Jane M. Heffernan, Jianhong Wu

- The reconstructed tree in the lineage-based model of protracted speciation
  Amaury Lambert, Hélène Morlon, Rampal S. Etienne
Workshops

DSABNS 2015 at Centro de Matematica e Aplicacoes Fundamentais (CMAF), Lisbon University, Portugal

Date: 2015-02-04 to 2015-02-06

The workshop has both theoretical methods and practical applications and the abstracts included in the program will cover research topics in population dynamics, eco-epidemiology, epidemiology of infectious diseases, molecular and antigenic evolution and methodical topics in the natural sciences and mathematics.

The program includes lectures by the invited speakers, contributed talks and poster session by the participants. The workshop does not charge registration fee.

Participants are kindly requested to register at http://dsabns2015.fc.ul.pt/inscricao by January 31 2015


Cellular Heterogeneity: Role of Variability and Noise in Biological Decision-Making at EMBL Heidelberg, Germany

Date: 2015-04-15 to 2015-04-18

The purpose of this symposium is to bring together researchers across different disciplines with a shared interest in studying the origins and consequences of variability in biological systems, ranging from stochastic molecular fluctuations to emerging cell population-level phenomena. The symposium will highlight the important role that single-cell approaches now have across the whole life sciences, be it in studying the dynamics of a molecular system in tissue culture cells or developing organisms, in understanding cell fate decisions during stem cell differentiation, in interpreting results from large-scale perturbations, or in mapping the cellular heterogeneity underlying drug resistance in cancer.

Topics

Cell population phenomena
Noise, variability, and heterogeneity in development
Quantitative cell biology at the single-cell level
Single-cell technologies
Theoretical aspects/modelling

Open Positions

PhD in Topological methods to explore novel biological information in omics data at University of Glasgow, UK

Deadline for applications: 2015-01-31

A funded PhD position is available with Dr Liam Watson (Mathematics) and Dr Kathryn Elmer (Evolutionary Biology), in the School of Mathematics and Statistics at the University of Glasgow.

As part of the Lord Kelvin Adam Smith scheme, a fully-funded 4 year interdisciplinary PhD project is available on Convergence, connectivity, and continuity - Topological perspectives for mining novel biological information from omics data.

The project, housed in Mathematics, will interact closely with biology, exploring molecular evolutionary patterns through topological methods in data analysis.

Applications should be sent before 31 January 2015, potential applicants are encouraged to contact Liam Watson (Liam.Watson@glasgow.ac.uk) and/or Kathryn Elmer (Kathryn.Elmer@glasgow.ac.uk) directly for more information.

Please contact: Liam Watson
http://www.gla.ac.uk/services/postgraduateresearch/scholarships/kelvinsmith/shortlistedscholarship/

PhD in Mathematical Biology at University of Glasgow, UK

Deadline for applications: 2015-02-28

PhD opportunity to study: Why host-immunity is sub-optimal: an evolutionary game theory approach

We are seeking applications from mathematicians and other graduates of quantitative disciplines for this PhD position in mathematical biology, jointly supervised by Christina Cobbold, School of Mathematics and Statistics, and Louise Matthews and Mike Stear from the Institute of Biodiversity, Animal Health and Comparative Medicine, College of Medical, Veterinary and Life Sciences.

This project will develop new mathematics in evolutionary game theory (adaptive dynamics) to tackle the evolution of host immune responses and improve the control of a livestock disease with major welfare and economic impacts. Game theory is the conceptual framework for examining the strategic interactions that underpin behaviours in diverse social, economic and biological systems: weapons arms races, pricing strategies among competing firms, contests between males seeking mates, and the uptake of vaccination. Game theory tells us, for example, that if vaccination is voluntary, some individuals will choose to free-ride on the protection provided by others. Consequently there will be insufficient coverage to eradicate disease. Thus, individually optimal strategies do not necessarily produce the optimal outcome for the population.

We propose a similar free-riding mechanism for evolution of sub-optimal immune responses by livestock to parasite infection, with the consequence that selective breeding of resistant animals could be used to optimise livestock health. This also provides a mechanism to explain the extraordinary variation in immune responsiveness observed in natural infections. New mathematics will be developed to allow adaptive dynamics models to capture genetic as well as phenotypic variation between individuals. This project will offer an evolutionary mechanism for the genetic diversity in resistance to infection and use the results to develop selective breeding strategies for parasite control.

The project will take place within the Boyd Orr Centre for Population and Ecosystem Health - http://www.gla.ac.uk/boydorr - which is an interdisciplinary, cross-institutional research grouping based in the University of Glasgow. Potential applicants are welcome to contact us directly at louise.matthews@glasgow.ac.uk and christina.cobbold@glasgow.ac.uk for further details.

Louise Matthews - http://www.gla.ac.uk/boydorr/people/byname/louisematthews
Christina Cobbold - http://www.maths.gla.ac.uk/~cc
Mike Stear - http://www.gla.ac.uk/researchinstitutes/bahcm/staff/michaelstear/

Application details
Interested individuals should apply to the 4 year BB-SRC DTP program advertised on “Find a PhD” http://www.findaphd.com/search/PhdDetails.aspx?CAID=816

Please contact: louise.matthews@glasgow.ac.uk