



Reporting from the 9th European Conference on Mathematical and Theoretical Biology, Gothenburg, Sweden¹

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The 9th European Conference on Mathematical and Theoretical Biology took place in the Swedish port city of Gothenburg between June 15th and 19th, 2014. The busy conference was hosted by the Chalmers University of Technology where biomathematicians, biologists, biophysicists and bioinformaticians gathered to exchange ideas, experience and build bridges between the different sciences.

Plenary talks were given by researchers in mathematical biology from across Europe and covered a broad range of topics. Mathisca de Gunst (Amsterdam) reported on the growing importance of network modeling in neuroscience. David Rand (Warwick) discussed new experimental and theoretical results about cell cycles, circadian clocks and signals, and touched upon the importance of studying the interactions and coupling between these highly dynamical regulatory and signalling systems. Johannes Birkner (Mainz) talked about multiple merger coalescents in population genetics and challenges in explaining genetic variability in species from a statistical perspective. Marie Doumic (INRIA-Paris) presented theoretical and simulation results and parameter estimation methods in a model for the kinetics of protein polymerisation in amyloid diseases. The study of this polymerisation is of importance in understanding the aggregation and deposition of

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misfolded (amyloid) proteins, in diseases such as Prion or Alzheimer's. The talk of Tom Britton (Stockholm) pointed out some statistical mismatches in the estimation of key epidemiological parameters (basic reproduction number R_0 , critical vaccination coverage) of new emerging infectious diseases. When homogeneous mixing is assumed and (unknown) community structures – neglected, slightly conservative estimates for population parameters can be derived. Trevor A. Graham's (London) presentation was about quantifying clonal evolution in the human colon by means of a novel "lineage tracing" strategy and a reductionist mathematical analysis for parameter estimation. Last but not least, there was a rare plenary on paleobiology. Mikael Fortelius (Helsinki) reviewed recent progress in analyzing and simulating the complex, biased and incomplete fossil record and some of its underlying processes, including the gain and loss of biodiversity in relation to environmental change using mathematical and computational methods.

Hot topics in the scientific programme were: evolution and population genetics, population dynamics, regulatory networks, cancer, diabetes and epidemics models, physiology, neuroscience, immunology, ecology, as well as novel numerical methods and simulation tools.

Numerical methods and software products for simulation of biological processes were presented at several minisymposia. Position-jump models of biological processes on irregular lattices were presented by the group from Wolfson Centre of Mathematical Biology in Oxford, UK. There was a conference tutorial by Maciej Swat on simulations of biomedical virtual tissue and multi-cell development using CompuCell3D. Other novel software environments for spatial stochastic simulations of intracellular pathways presented at the conference were URDME and PyURDME. PyURDME is a Python module for spatial stochastic simulation, developed by a Swedish-American team.

Springer prizes for best talk and best poster were awarded at the closing ceremony of the conference.

The weather during the busy week was wonderful so the conference participants could experience the beautiful nature of Gothenburg's Dutch-style canals, coast, islands and lakes, gather for a drink with new friends and collaborators in Gothenburg's beergardens in the long white nights, or simply cheer for their favourite football teams at the World Cup.

Peter Rashkov obtained his Ph.D. in Mathematics in 2010 from Jacobs University in Bremen, Germany. He is currently a post-doc at the Centre for Synthetic Microbiology in Marburg, Germany. His current research interests are mathematical modelling in biology with focus on dynamical systems applications to regulatory networks in cells.