# Mini-symposium in biomathematics

# Thursday, October 22, 2015

**All are welcome, no sign-up.**

## Program

15:15-15:35 *Barbara Boldin*: Evolution to self-extinction in epidemic models with frequency-dependent incidence

15:40-16:00 *Reinhard Bürger*: When does sexual selection drive divergence of a peripheral population?

16:00-16:30 **Coffee Break**

16:30-16:50 *Elisenda Feliu*: Identifying parameter regions for multistationarity in biochemical reaction networks

16:55-17:15 *Ryszard Rudnicki*: Stochastic semigroups and their applications in biological models

**Venue**
HC Ørsted Institutet, Auditorium 4
University of Copenhagen
Universitetsparken 5
2100 Copenhagen Ø

**How to get there**
Information on how to reach the institute from hotels/metro stations/railway stations can be found **here**.

**Organizer**
Dynamical Systems Interdisciplinary Network, University of Copenhagen
`www.dsin.ku.dk`
Susanne Ditlevsen, Department of Mathematical Sciences, University of Copenhagen

# Abstracts

## Evolution to self-extinction in epidemic models with frequency-dependent incidence

**Barbara Boldin** *Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska, Slovenia*, barbara.boldin@upr.si

Evolutionary suicide, or evolution to self-extinction, is an intriguing phenomenon in which adaptive evolution drives a viable population to extinction. In 2001, Gyllenberg and Parvinen (Bull. Math. Biol. 63: 981-993, 2001) showed that, in a wide class of deterministic population models, a discontinuous transition to extinction is a necessary condition for evolutionary suicide. An implicit assumption of their work is that the invasion fitness of a rare strategy is defined also in the extinction state of the population. Epidemic models with frequency-dependent incidence, which are often used to model the spread of sexually transmitted infections or the dynamics of infectious diseases within herds, violate this assumption. We show that in these models, evolutionary suicide can occur through a non-catastrophic bifurcation whereby pathogen adaptation leads to a continuous decline of host (and consequently pathogen) population size to zero.

## When does sexual selection drive divergence of a peripheral population?

**Reinhard Bürger** *Department of Mathematics, University of Vienna, Austria*, reinhard.buerger@univie.ac.at

Speciation and divergence in peripheral populations have long sparked much research. Unidirectional migration, received by some peripheral populations, can hinder the evolution of distinct differences from their founding populations. In this talk, I give a brief account of some of the results obtained recently in collaboration with Maria Servedio (The effects of sexual selection on trait divergence in a peripheral population with gene flow. Evolution, in press). In this paper we explore the effects that sexual selection, long hypothesized to drive the divergence of distinct traits used in mate choice, can play in the evolution of such traits in a partially isolated peripheral population. Using a population genetic continent-island model, we show that with phenotype matching, sexual selection increases the frequency of an island-specific mating trait only when female preferences are of intermediate strength. We identify regions of preference strength for which sexual selection can instead cause an island-specific trait to be lost, even when it would have otherwise been maintained at migration-selection balance. We also show that novel preference strengths almost universally cannot increase, precluding the evolution of premating isolation in peripheral populations at the early stages of species divergence.

## Identifying parameter regions for multistationarity in biochemical reaction networks

**Elisenda Feliu** *Department of Mathematical Sciences, University of Copenhagen, Denmark*, efeliu@math.ku.dk

The number of states in which a cell can be at any given time is linked to the flexibility in its decision making and to cell-to-cell variability. Particularly, bi- and multistable cellular systems provide mechanisms for rapidly switching between different responses. Identifying whether a system exhibits multistationary behavior or not is, however, challenging. Even more complex is to identify regions in the parameter space where multistationarity occurs.

In this talk I will focus on biochemical reaction networks modelled by means of ordinary differential equations. I will present a method to identify constraints on reaction rate constants that ensure that multistationarity arises. The method is based on topological degree theory. This work is joint work with Carsten Conradi, Maya Mincheva and Carsten Wiuf.

## Stochastic semigroups and their applications in biological models

**Ryszard Rudnicki** *Institute of Mathematics, Polish Academy of Science, Poland*, rudnicki@us.edu.pl

Stochastic semigroups have been intensively studied because they play a special role in applications. They are generated by partial differential equations of different types and describe the behaviour of the distributions of Markov processes like diffusion processes, piece-wise deterministic processes and hybrid stochastic processes. We present some results concerning their long-time behaviour: asymptotic stability and sweeping. We present some applications to piecewise deterministic stochastic processes appearing in gene expression models and in the Stein's neural activity model.