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MATHEMATISCHES INSTITUT



# Kick-Off Workshop

## Quantitative and Computational Systems Science Center

July 17, 2014

Organisers:

Francesca Biagini  
Peter Pfaffelhuber  
Constanze Schmaling

## Program

09:00–09:15	Registration
09:15–09:30	Opening
09:30–10:30	PETER PFAFFELHUBER Efficiency in spatial multi-scale biochemical reaction networks
10:30–11:30	TANJA STADLER A unified framework for phylodynamic inference of epidemic spread
11:30–12:00	Coffee
12:00–13:00	ARNE TRAUlsen Stochastic evolutionary game dynamics of cooperation and punishment
13:00–14:00	Lunch snacks

## Efficiency in spatial multi-scale biochemical reaction networks

PETER PFAFFELHUBER (University of Freiburg)

Spatial heterogeneity in cells can be described using models with homogeneous compartments with molecular diffusion between them. Changes in the amount of molecules within compartments are also due to biochemical reactions, and are often such that some molecular types fluctuate on a slower time scale than others, leading to a multi-scale reaction network. We ask here: How sensitive is the dynamics of slower molecular types to the heterogeneous distribution of molecules amongst compartments? What kind of spatial distribution gives the fastest turnover of molecules? Using stochastic averaging, we derive rigorous results for the long term behaviour of spatially heterogeneous multi-scale biochemical reactions, and illustrate them on examples of Michaelis-Menten enzymatic kinetics. We present simple analytic results that significantly reduce the complexity and expedite simulation of stochastic compartment models of chemical reactions. This is joint work with Lea Popovic (Concordia).

## A unified framework for phylodynamic inference of epidemic spread

TANJA STADLER (ETH Zurich)

Epidemiological processes leave a fingerprint in the pattern of genetic structure of pathogen populations. I present a unified framework to infer these epidemiological processes directly from pathogen sequence data. The framework is based on phylogenetic analysis using common epidemiological models, such as SIR models. Our method is flexible as it allows for epidemic dynamics changing through time, or for heterogeneous host and pathogen populations. The method is intended as a powerful alternative to the commonly used coalescent skyline plot, as it overcomes the limitations of the coalescent approaches. Finally I discuss novel insights into the HIV-1 epidemic revealed by our method. The new methodology is available within the BEAST v2.0 software package.

# Stochastic evolutionary game dynamics of cooperation and punishment

ARNE TRAUlsen (MPI Plön)

Evolutionary game theory is a framework to study evolving populations when the fitness of individuals depends on the interaction with others in the population. The most popular example is the evolution of cooperation, which studies behaviors that reduce the own fitness and instead increase the fitness of others. Such behaviors seem to contradict the idea of natural selection at first sight. Problems on the evolution of cooperation appear on all levels of biological and social organization, from selfish genetic elements such as meiotic drive to the maintenance of human social systems and the prevention of climate change. In humans, a thoroughly discussed mechanism to maintain cooperation is punishment, which implies that those who do not cooperate are punished. However, to explain the emergence of such behaviors is a challenge for conventional deterministic models. Moreover, such systems often experience multiple stable equilibria, necessitating agent based approaches or stochastic mathematical models to decide which of these will be relevant in the long run.