

# MATHEMATICAL BIOLOGY II

*Place and time:* In M100 on Thursday, Jan 4, at 16:00–17:30  
*Organizers:* Mats Gyllenberg (University of Helsinki)  
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## Intercity influenza - how does gravity work?

JULIA GOG (*University of Cambridge*), [jrg20@cam.ac.uk](mailto:jrg20@cam.ac.uk)

**Abstract.** We will focus on recent work to understand how pandemic influenza spread in the US. Here, we traditionally model the population as being in a series of patches – effectively a metapopulation. Disease transmission between patches is often represented by a gravity model. In this talk, we will see what this tells us about the spread of pandemic influenza, and also some current theoretical challenges in this area.

## Nested dynamics and parasite evolution

MIRCEA T. SOFONEA (*CEFE (CNRS), Montpellier*),  
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**Abstract.** In nature, species face a diversity of parasite types. While some evolutionary epidemiology models already incorporate parasite polymorphism, few make the connection between epidemiology and within-host parasite growth. As parasite polymorphism can even occur within the same host, distinct parasite types can interact in various ways and thus interfere with their transmission and therefore their evolution. The combinatorial and dynamical complexity explains why we still lack general predictions regarding parasite evolution in such multiple infection contexts. Seeking for a general trend in virulence evolution, we model each dynamical level on which parasite evolution relies by nonlinear coupled ODEs and random mutations. We notably use fixed point stability analysis to draw a typology of infection patterns that allows us to address virulence evolution under a general framework. As a result, we observe an unavoidable selection bias towards higher virulence when phenotypic mutations are small, which is confirmed by further stochastic simulations.

*Joint work with Samuel Alizon and Yannis Michalakis.*

## Mathematics of biodiversity

GÉZA MESZÉNA (*Eötvös University*), [geza.meszena@elte.hu](mailto:geza.meszena@elte.hu)

**Abstract.** Application of mathematics in ecology & evolution is often restricted to specific modelling of specific biological situations. Instead, we should use deep mathematics to understand deep biological issues, as biodiversity.

Species are adapted to the ways and circumstances of their life, i.e. to their ecological niches. Therefore, it is parsimonious to assume that origin and maintenance of species diversity rest on the diversity of niches. However, the details of this proposition are far from settled in the biological discourse not independently from the limited use of mathematical theory.

The correct mathematical treatment identifies ecological niches with the dimensions of the feedback loop regulating community. Coexistence is robust, when species are sufficiently niche-segregated in this sense. The very same regulating feedback, when multidimensional, makes selection frequency-dependent. In turn, frequency-dependence leads to branching evolution, as described by adaptive dynamics theory. Therefore, the regulation approach unifies the ecology and evolution of diversity.

This overall mathematical picture can be specialized to any particular ecological/evolutionary situations in an exact way. The lecture touches on three particular issues: (1) description of local interactions in the framework, (2) role of spatial segregation in speciation and (3) multilocus population genetics of speciation.