Project #3: Epidemic models

Deadline: 06.07.2026, 12:00h

In this project we consider epidemic models, and in particular SIRS-type models, a classic real-world application of the theory dynamical systems. SIRS models are compartmental models. Each individual in the modeled population is in one of three compartments: Individuals that could get infected are in the S compartment (susceptible), after infection an individual moves to the I compartment (infected), after recovering from the infection, individuals stay immune for a while, residing in the R compartment (recovered). Immunity is lost over time moving them back to the S compartment and the cycle restarts.
In the standard formulation, a mean-field model of the form

$$\dot{S} = -\beta\, S\, I + \gamma\, R\,, \qquad \dot{I} = \beta\, S\, I - \mu\, I\,, \qquad \dot{R} = \mu\, I - \gamma\, R\,, \tag{1}$$

is considered, where β, μ and γ are the rates of infection, recovery and immunity wane, respectively. Usually, one defines by $\mathcal{R}_0 = \beta/\mu$ the *basic reproduction number*, indicating the average number of infections per infected individual as a useful metric for the potency of the disease.
The goal of this project is to consider a SIRS model on a network. For all the important basics on network theory, refer to chapter 1 of the lecture notes. Before starting, study the mean-field equations (1) briefly.

SIRS model as a cellular automaton As a first step, simulate a SIRS model on a grid of N cells. Each cell represents an individual and each individual is in one of the three SIRS states. Initialize the grid with one or more patient(s) zero. Design a set of rules by which individuals spread the disease according to the SIRS cycle. A classic choice would be that contagion is possible between next neighbor cells or, to resemble the mean-field case and study finite-size effects, a model where each cell can infect every other cell, but you can get creative here. Create a visualization, play around with different parameter settings and grid sizes, and compare to the mean-field model (1). If you need inspiration, check out this neat 'Complexity Explorable' by physicist Dirk Brockmann:

`https://www.complexity-explorables.org/explorables/critical-hexsirsize/`.

Network simulation Now consider a network structure. The network perspective opens new questions, primarily about the network topology. A randomly connected network (Erdős–Rényi network) can be a starting point, but social networks tend to be scale-free, i.e. have a power-law degree distribution. Further, networks can have clusters resembling communities of individuals (such as après-ski parties in Ischgl ☺). Study different network topologies, compare between them, with the cellular automaton, and the mean-field theory. Make some plots that present your results.

Hint:

- You are free to choose the programming language. Python is a solid choice, but you could also mimic the Complexity Explorable and create a website.
- Of course, use AI to simplify coding, though make sure to understand what is going on.

Extensions Enrich the model! You might, for example, make the infection rate seasonal, $\beta(t) = \beta_0 (1 + \varepsilon \cos \omega t)$. Other natural extensions include vital dynamics (births and deaths), an incubation compartment (SEIRS), or vaccination. Get creative.

Minimum requirements and format

As always, the project is deliberately open – you choose the format and the details of your project. Here are some minimum requirements:

- Hand in the project by the deadline (08.07.26, 12:00h) via email to `nevermann@itp.uni-frankfurt.de`
- Present your project in the tutorial session on 08.07.26 and be prepared to answer questions.
- Do all the requirements on the sheet. As usual, the format is up to you, though feel encouraged to make an interactive website (not mandatory).