handed out: June 16, 2020
handing in: June 25, 2020
presentation/discussion: June 26, 2020

Explore aspects of the **contagious disease model** using Utopia's `ContDisease` implementation.
As base for all your simulations in this exercise choose

- a value for f, say $f = 10^{-7}$
- either a uniform or a heterogeneous domain, the latter with rocky patches, and
- include immunity or not.

As domain choose a square with periodic boundaries and side length as a power of 2, say 1024 (more if you have a more powerful computer). As always, implement everything for a sufficiently small grid until the workflow all the way to the analysis is established and only then increase the size to the desired value.

Refer to Fig. 6.36 from the lecture notes for a representation of the macroscopic system, possibly also to the time series Fig. 6.32.
The abbreviations $\rho_s = \rho_{\text{susc}}$ and $\rho_a = \rho_{\text{active}}$ are used in the following.

As always, make sure that you are using the latest version of the Utopia docker image by invoking `docker pull ccees/utopia:latest`.

For these exercises, it is best to work interactively with Utopia using a Jupyter Notebook, as you will have more direct and convenient access to the data of individual simulations. The Utopia docker image provides such a capability out of the box; the main idea is to use the *container* to run the Jupyter Notebook server and then log on to it via your *host* machine's web browser. For a guide on setting this up, refer to the docker hub page.[1] For information regarding the interface, consult the Utopia documentation.[2]

A note regarding working with large amounts of data: It is advisable to monitor the memory usage of the docker container, e.g. by running the `docker stats` command in a terminal of your host machine. In cases where the data you want to analyse will exceed your host machine's physical memory limits, you can configure the `DataManager` to load data in a delayed fashion.[3] As this comes with a performance penalty, you will only want to do this as a last resort.

1. **Contagious Disease Model (CDM)** present ☐

   Explore the propagation of contagious diseases in heterogeneous environments and the role of immunizations. Look at the following cases:

   - Let the environment consist of randomly distributed rocky patches (cells) with density ρ_r.
   - Study the role of (random) immunity g.

   For understanding and analysis, do as for the FFM:

   - Look at the dynamics by plotting the spatial distribution over time. A movie may be helpful.[4]
   - Compare time series of the density $\rho(t)$ with that for the uniform base situation. Specifically, plot the asymptotic mean density and its variance as a function of the pertinent parameter(s).

   Discuss differences to the forest fire model.

[1] `https://hub.docker.com/r/ccees/utopia`, section Working Interactively
[2] `https://hermes.iup.uni-heidelberg.de/utopia_doc/latest/html/frontend/interactive.html`, sections on Basic Concepts and Examples. Skip the API references (the blue boxes that document the interface) on first reading; it only makes sense to dive into those once you have more specific questions.
[3] See `https://hermes.iup.uni-heidelberg.de/utopia_doc/latest/html/frontend/data.html`
[4] For high grid resolutions, you might have to increase the pixel density of the plot or movie using the `animation.writer_kwargs.ffmpeg.saving.dpi` parameter in the plot configuration.

2. **Threshold of a Contagious Disease** present ☐

A contagious disease is eventually self-maintaining, hence needs no further external infections. Study this in a square domain with side length n, e.g., with $n = 1024$, by inserting N infections and observe their possible dying out or propagation.

As initial state choose a uniform domain with density ρ_0. What is the impact of ρ_0, i.e., how to choose the value?

To introduce infections in the `ContDisease` model, use the `infection_control` option. Think of the different modes for inserting these infections:

- initial condition: infect N randomly selected occupied sites,
- deterministic sequence: infect N randomly selected occupied sites at time intervals Δt,
- fully probabilistic: choose a rate f of infection and a duration Δt of infectious time such that $N = \rho_0 n^2 f \Delta t$, and think about the role of f.

To do:

(a) What do you expect for the possible asymptotic values of $\overline{\rho}$? (No simulation needed.)

(b) Plot $\rho(t)$ for at least one of the infection modes and for different choices of parameters.

3. **Spatial Structures** present ☐

The density ρ_s is not necessarily a good indicator for the spatial structure (e.g., Fig. 6.29). As first steps towards more powerful characterizations explore

(a) a one-dimensional power spectrum and covariance function along a transect of the domain and

(b) the corresponding two-dimensional fields.

Do this for a few characteristic phases on the trajectory towards the fixpoint and discuss your observations.

You can use the `numpy.fft` library for the discrete Fourier transformation. Take care to correctly label the frequency space.