Assignment 3

Fredrik Mattisson

May 10, 2020

1 A firing brain

I have implemented the boundary conditions in this model as if the grid were folded into a torus. That is, cells interact horizontally and vertically across the left-right and top-bottom boundaries, and the corner cells also interact with their diagonally opposite counterparts.

To illustrate typical states at various time steps, I have plotted the average of corresponding states from a sample of five randomly selected simulations, shown in fig. 1. This gives a rough idea of what typical distributions of firing neurons might look like at these time steps. Corresponding examples of states are shown in fig 2. The average number of firing neurons across all simulations is shown as a function of time in fig. 3.

Out of the 100 simulations, only 8 converged to a fixed state. Two converged to orbits of period 80, six to orbits of period 160, and the other 84 converged to orbits of period 40. The typical equilibrium behavior is small clusters of firing neurons where two horizontally or vertically adjacent neurons cause the firing to propagate, moving the cluster. A few of these clusters moving horizontally and/or vertically in such a way such that they do not collide produce orbits of period $N = 40$ in this case, which is what we see in the vast majority of these simulations.
The simplest such cluster consists of only two neurons, shown in fig. 4, a. Examples of other shapes exhibiting the behaviors described in the question are shown in fig. 4, b and c respectively. However, I was not able to find a stationary oscillating shape.

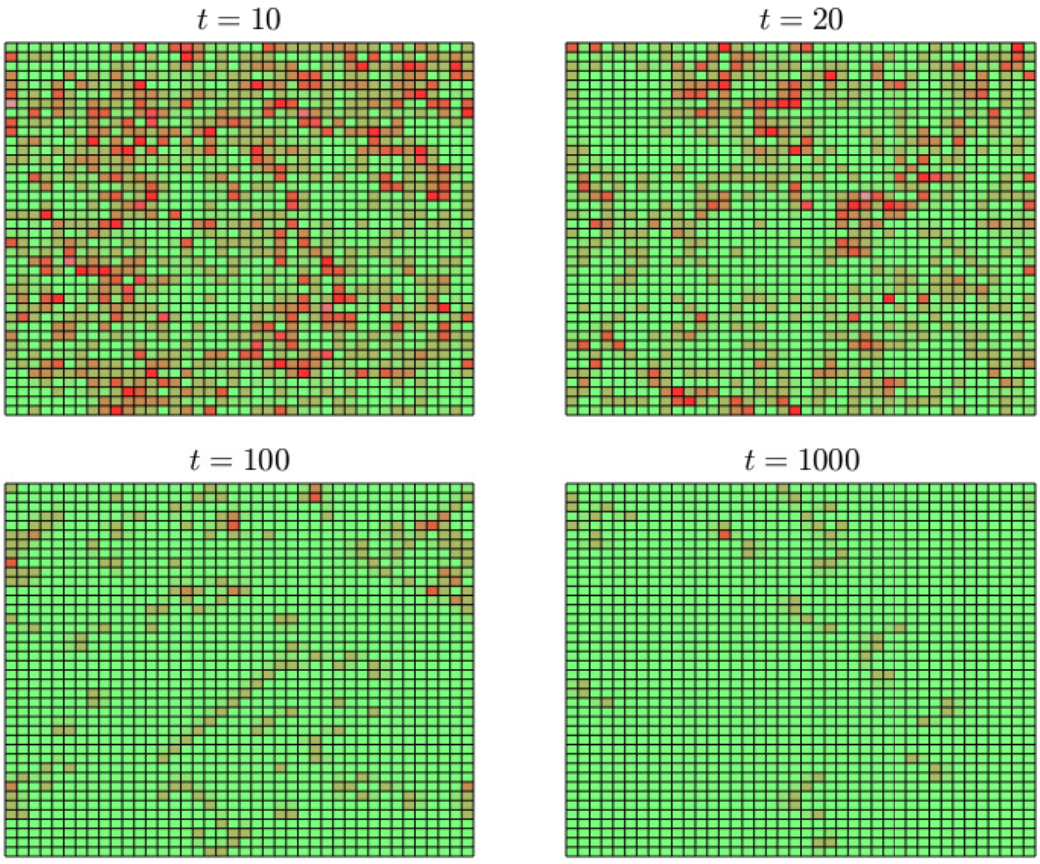


Figure 1: Averages of states from a random sample of five simulations with $p = 0.3$

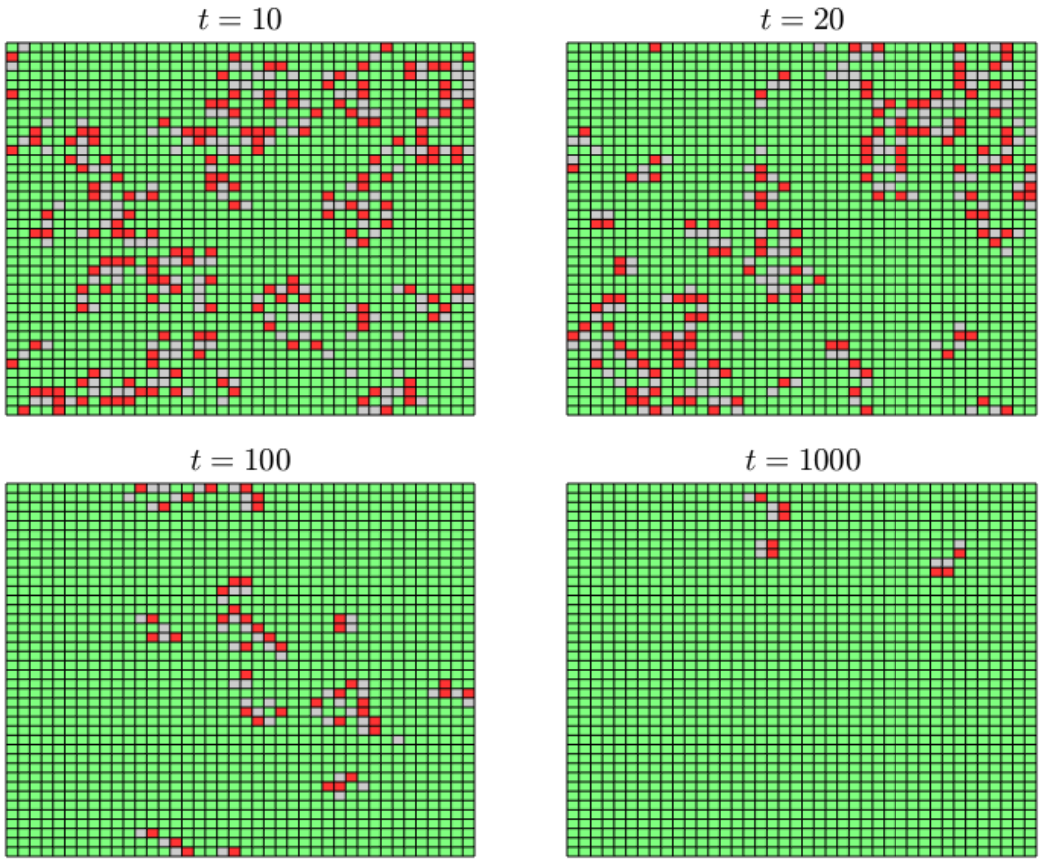


Figure 2: Examples of states from a random sample of five simulations with $p = 0.3$ Green cells are ready, red are firing and gray are resting.

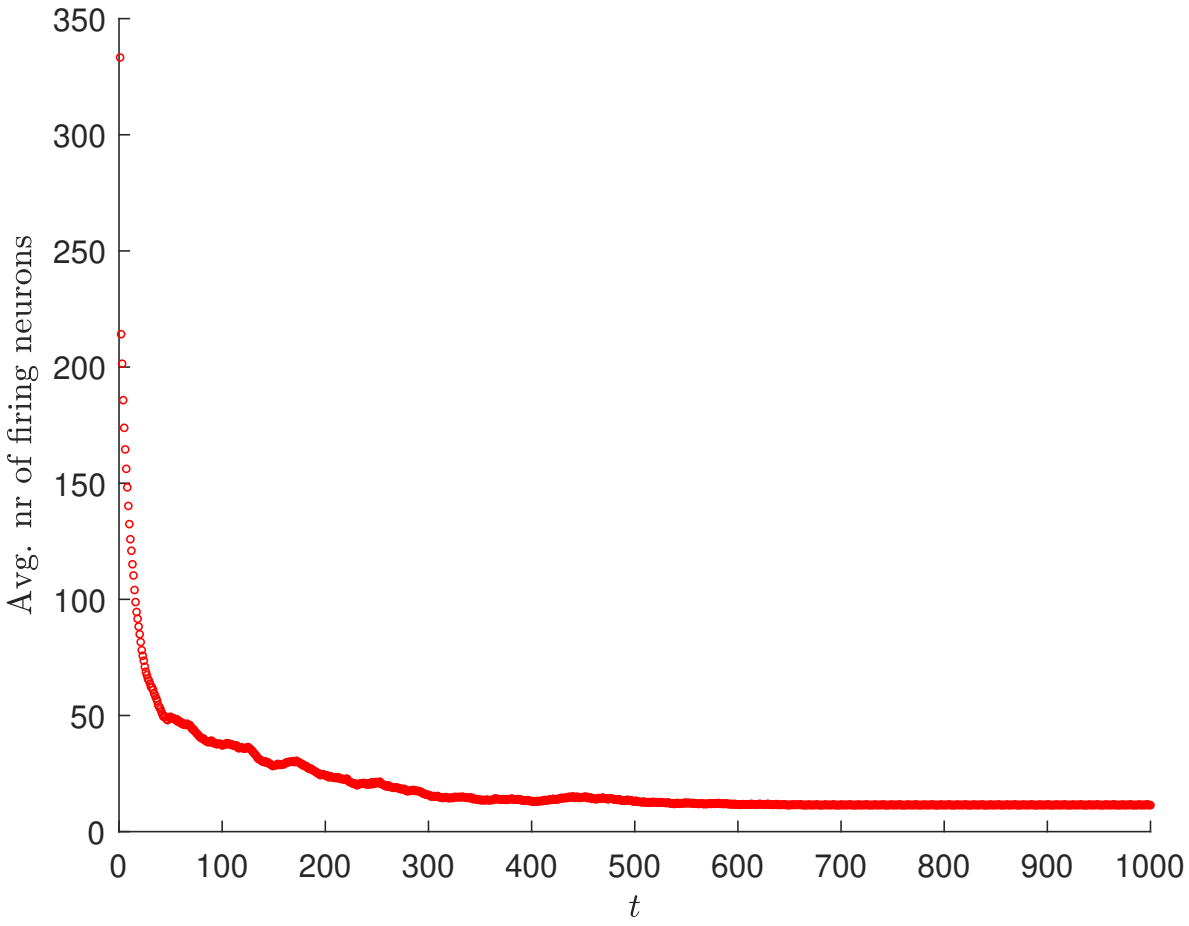


Figure 3: Average nr of firing neurons across 100 simulations $p = 0.3$

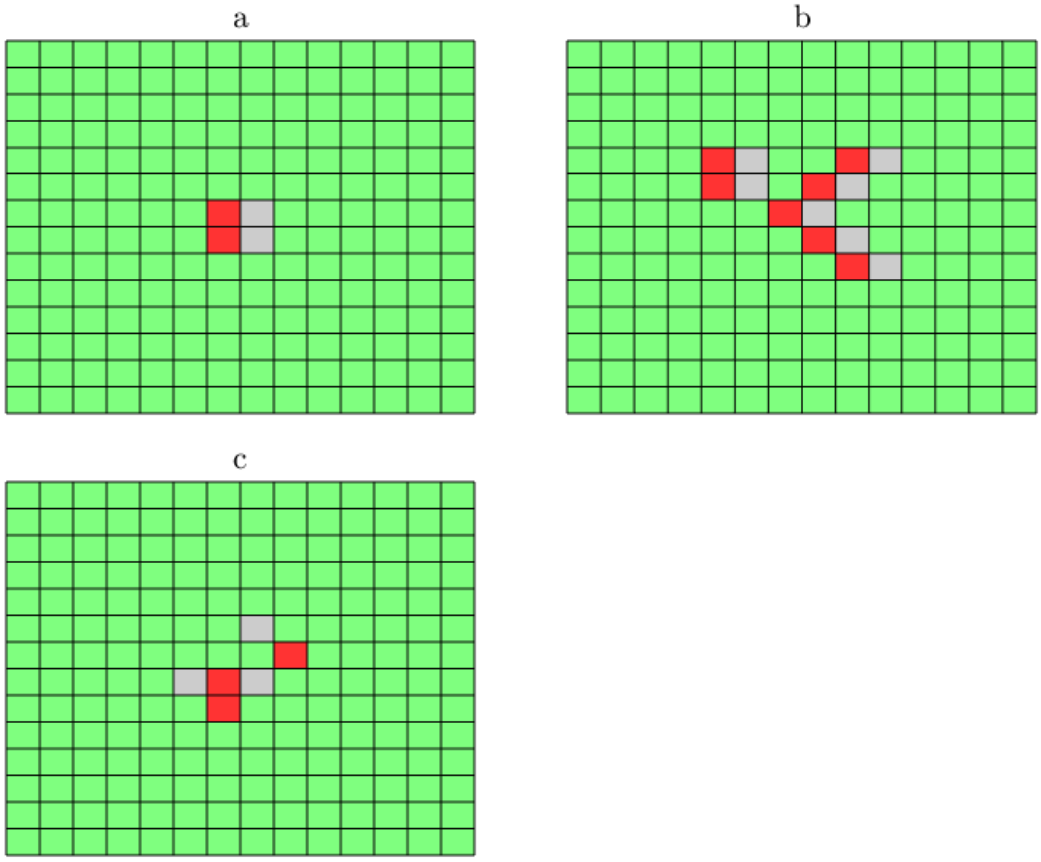


Figure 4: Examples of shapes that
a : moves horizontally one cell per time step, preserving its shape
b : moves horizontally one cell per time step, launching other shapes behind it
c : moves diagonally, changing its shape and returning to its original shape with period 4

2 Spatial epidemics

To be clear, I have interpreted the given rules as follows:
In each time step, infected individuals may first recover with probability γ. After that, those individuals who are susceptible and adjacent to an infected individual become infected. This means that an infected individual may recover only to be immediately infected again, if its infected neighbors did not also recover. Also, I have implemented the linear domain of this first model without periodic boundary conditions. Note: This was implemented before the document was updated with some changes to the rules. I'm not sure if you intended to change the semantics of the rules.

To approximate the probability of an epidemic $P(E;\,\gamma)$, I run M trials of K simulations each, where each simulation S_k runs for T time steps. If $S_k(T) > 0$, then S_k is considered an epidemic. Then $P_m(E;\,\gamma)$ is approximated as the number of epidemic simulations divided by K. Finally, $P(E;\,\gamma)$ is approximated as the mean of the sequence $P = \big(P_i(E;\,\gamma)\big)_{i\,\in\,[1,\,M]}$. This produces a 95% confidence interval $[\hat{P} - \epsilon,\ \hat{P} + \epsilon]$, where $\epsilon = 1.96\,\sigma\sqrt{M}^{-1}$ and σ is the standard deviation of P. The result is shown in fig. 5, with $M = 20$, $K = 100$ and $T = 50$.

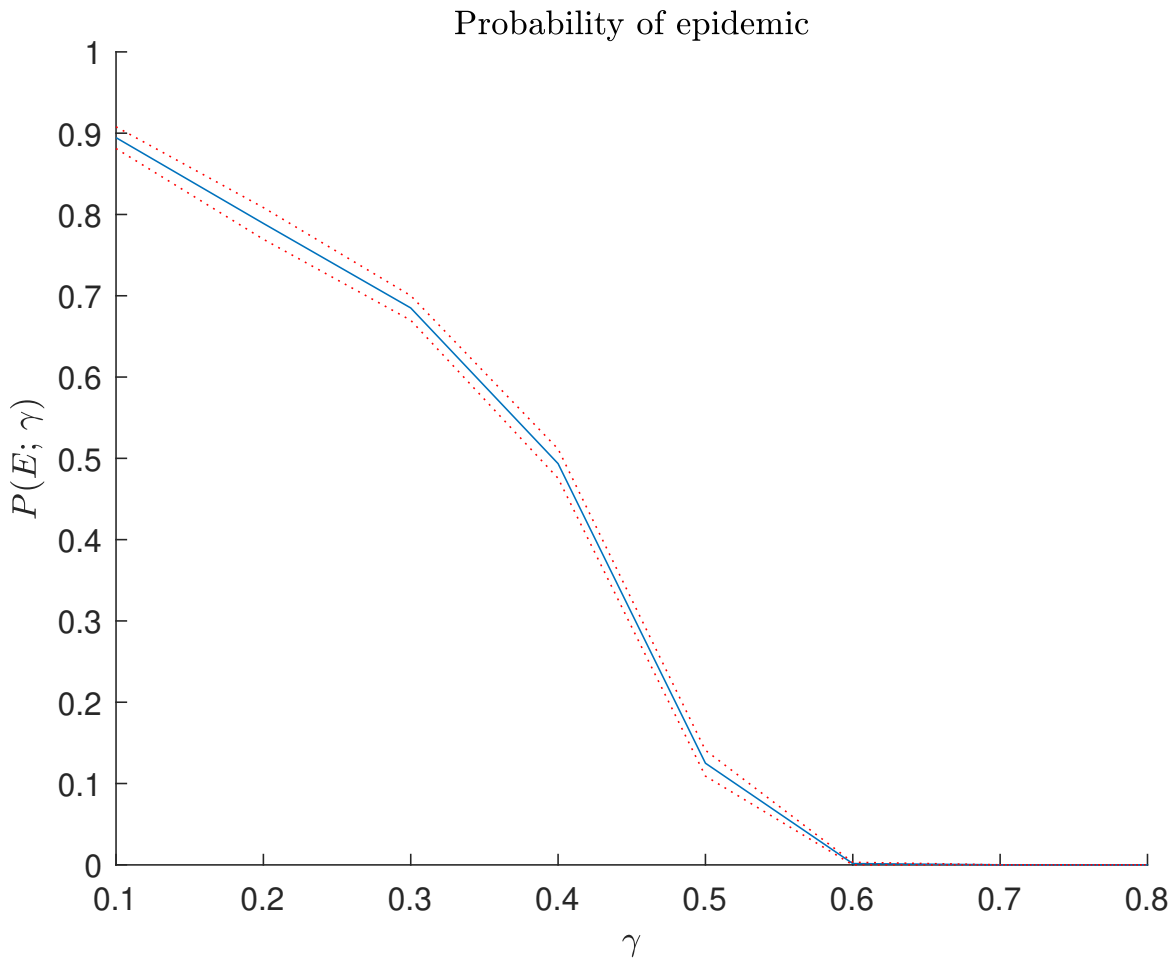


Figure 5: Approximation based on 20 trials of 100 simulations with 50 time steps. Confidence interval in dotted red.

For consistency, I plot the corresponding metric $P(E;\, \gamma, p_0)$ in fig. 6, where p_0 is the probability that an individual starts in the infected state. The initial state is randomized for each simulation, and always includes at least one infected individual.

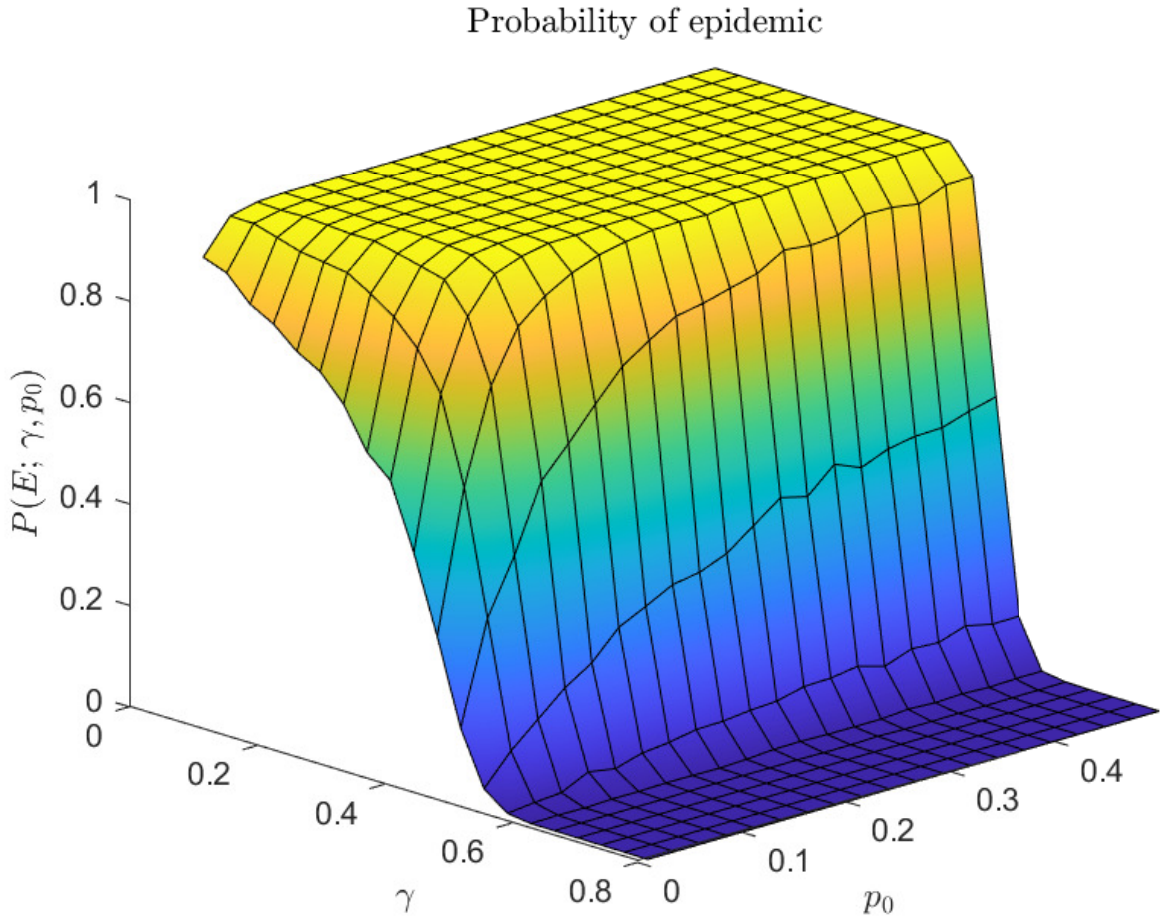
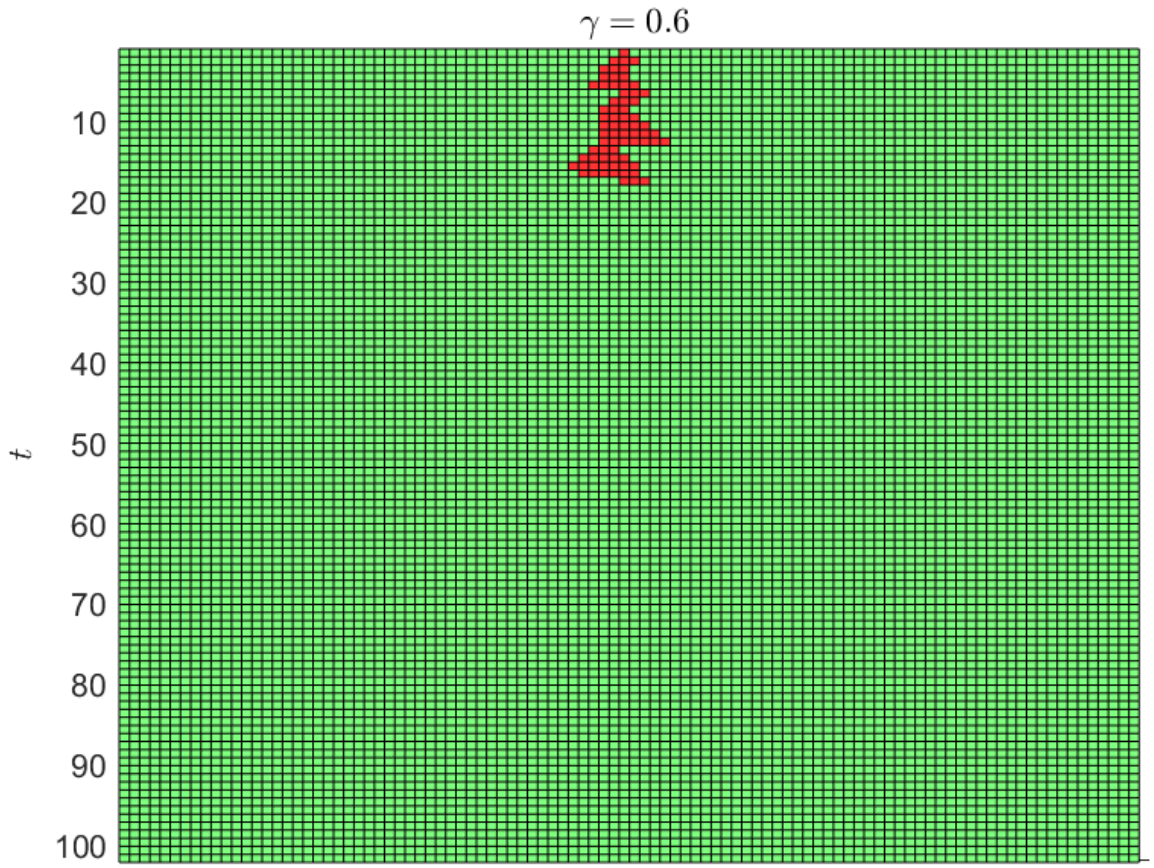
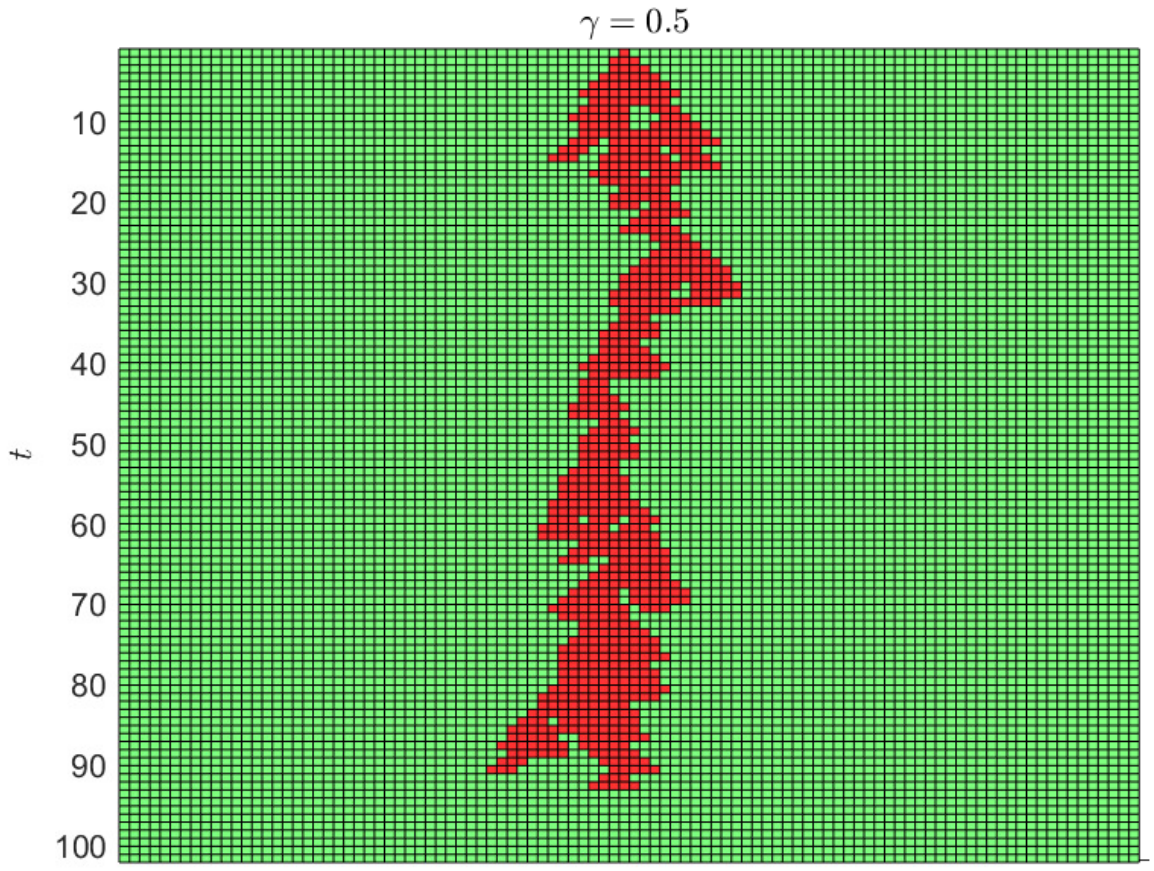
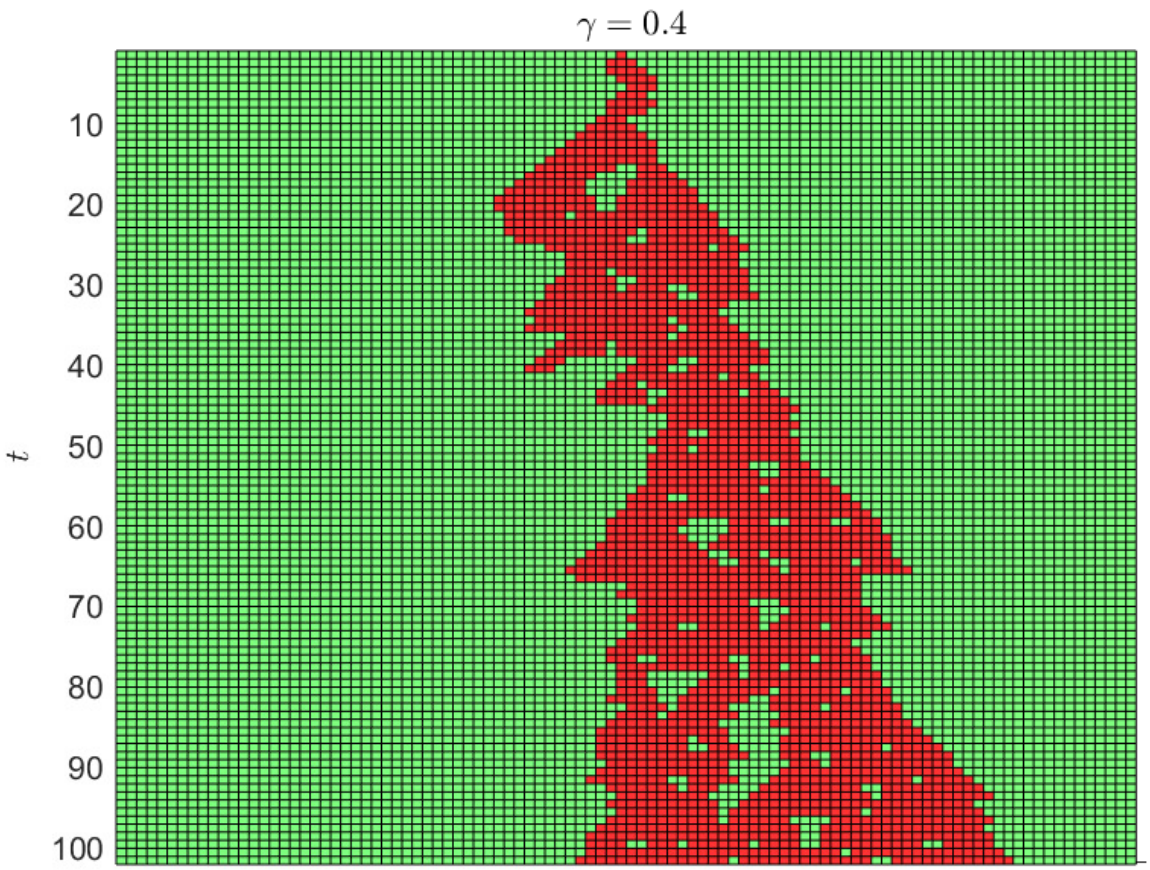


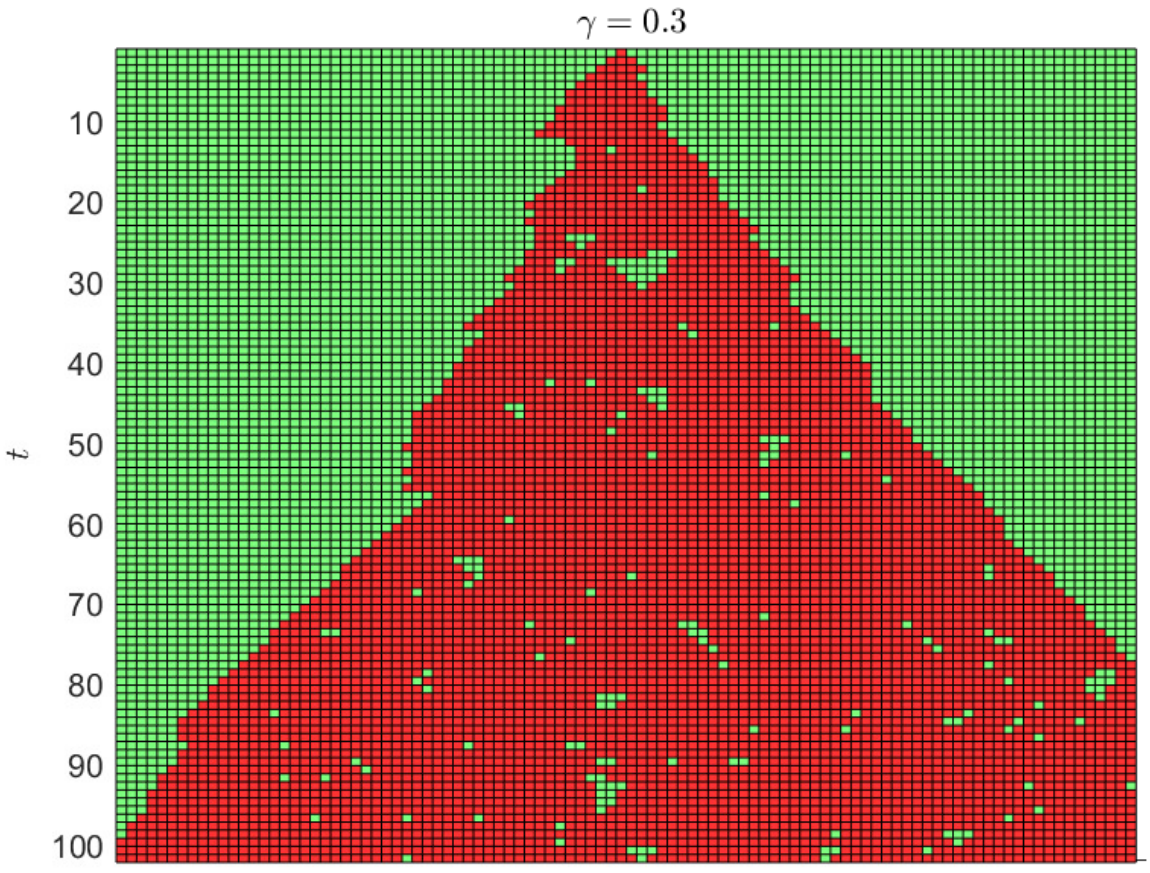
Figure 6: Approximation based on 20 trials of 100 simulations with 50 time steps.
$\gamma \in [0.1, 0.8]$ and $p_0 \in [0.01, 0.5]$

Selected examples of the evolution over 100 time steps for values of $\gamma \in \{0.6, 0.5, 0.4, 0.3\}$ are shown in the figures on pages 8 and 9.


$\gamma = 0.6$
10
20
30
40
50
60
70
80
90
100
t


$\gamma = 0.5$
10
20
30
40
50
60
70
80
90
100
t


$\gamma = 0.4$
10
20
30
40
50
60
70
80
90
100
t


$\gamma = 0.3$
10
20
30
40
50
60
70
80
90
100
t

3 Spatial epidemics – SIRS model

For the grid version, I have chosen to implement a compartmental model based on SIRS. The motivation is that a basic SIR model without vital dynamics will always converge to a fixed state where the epidemic dies out as the infectious population goes to zero. Including a transition from recovered back to susceptible makes for a more interesting system, that can exhibit unstable equilibrium states. It also serves to model that the antibodies present in a recovered individual may not give perfect immunity, or the virus may mutate in such a way as to render them ineffective. The automata rules are as follows:

1. A cell makes at most one state transition per time step.
2. An infectious cell recovers with probability γ.
3. An infectious cell (that did not recover) transmits the virus to each of its susceptible neighboring cells with probability β.
4. A recovered cell becomes susceptible again with probability κ.

Note that rule 3. implies that, at any given time step, the probability for a susceptible cell with n infectious neighbors to contract the virus is

$$P(S \to I;\, n) = \sum_{i=1}^{n} \binom{n}{i} \beta^i (1-\beta)^{n-i} \implies P(S \to S;\, n) = (1-\beta)^n \,,$$

and rule 1. implies that $P(R \to I) = 0$. In the initial state, each cell has probability p_0 of being infectious, and at least one cell is always starts out as infectious. For a first simulation, I set $N = 50$, $p_0 = 0.005$, $\beta = 0.4$, $\gamma = 0.2$ and $\kappa = 0.02$. This produced a very fast moving epidemic followed by an unstable equilibrium where the virus would remain endemic in the population, leading to recurring outbreaks as the herd immunity decays over time. fig. 7 shows how the infectious and recovered populations evolve over time in one such simulation, and fig. 8 shows examples of what the state looks like at selected time steps. Green cells are susceptible, red infectious and gray recovered.

This model is quite sensitive to changes in the parameter κ. Reducing it from 0.02 to 0.015 caused the typical equilibrium to instead be the fixed state in which $I = 0$. Increasing κ causes I to oscillate about some value with oscillations having smaller amplitude and higher frequency as κ increases.

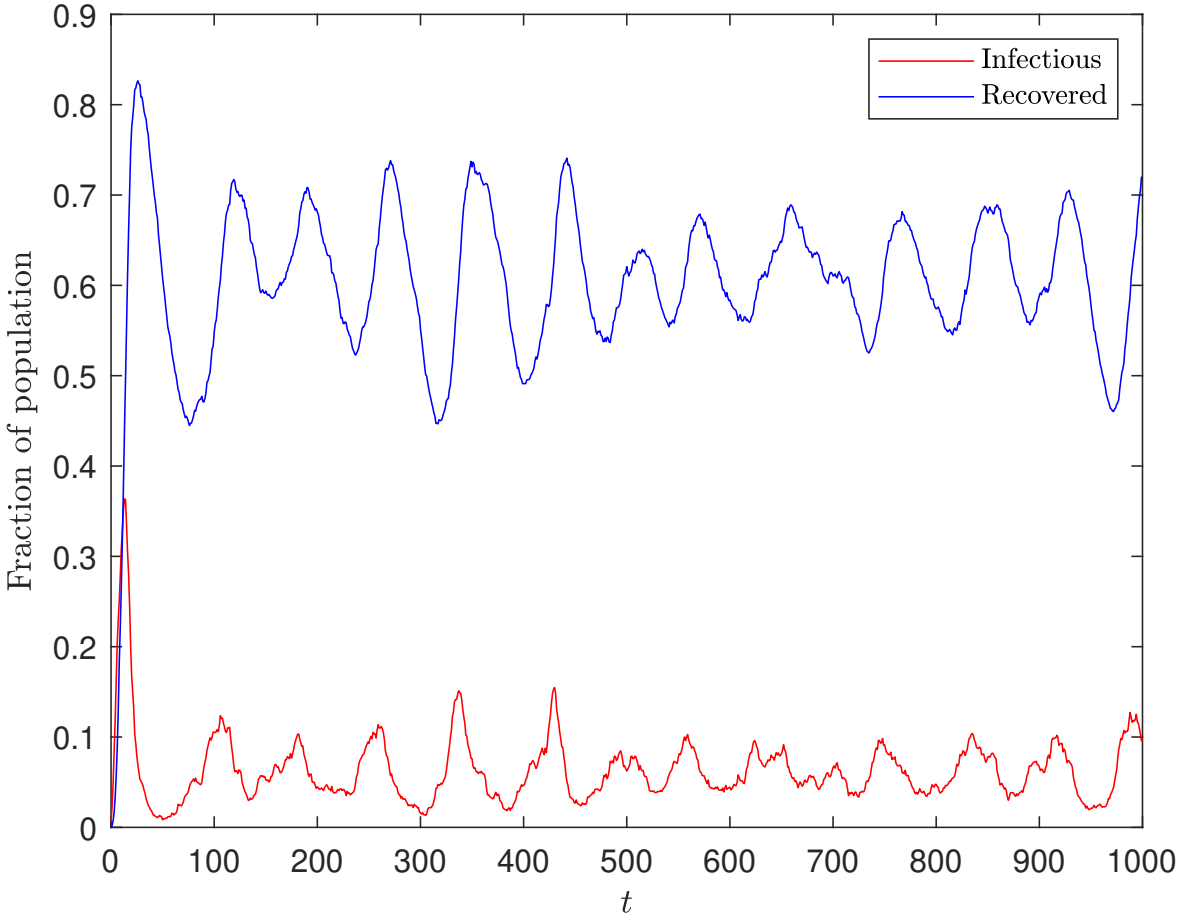


Figure 7: Example of infectious and recovered population over 1000 time steps with $p_0 = 0.005$, $\beta = 0.4$, $\gamma = 0.2$, $\kappa = 0.02$

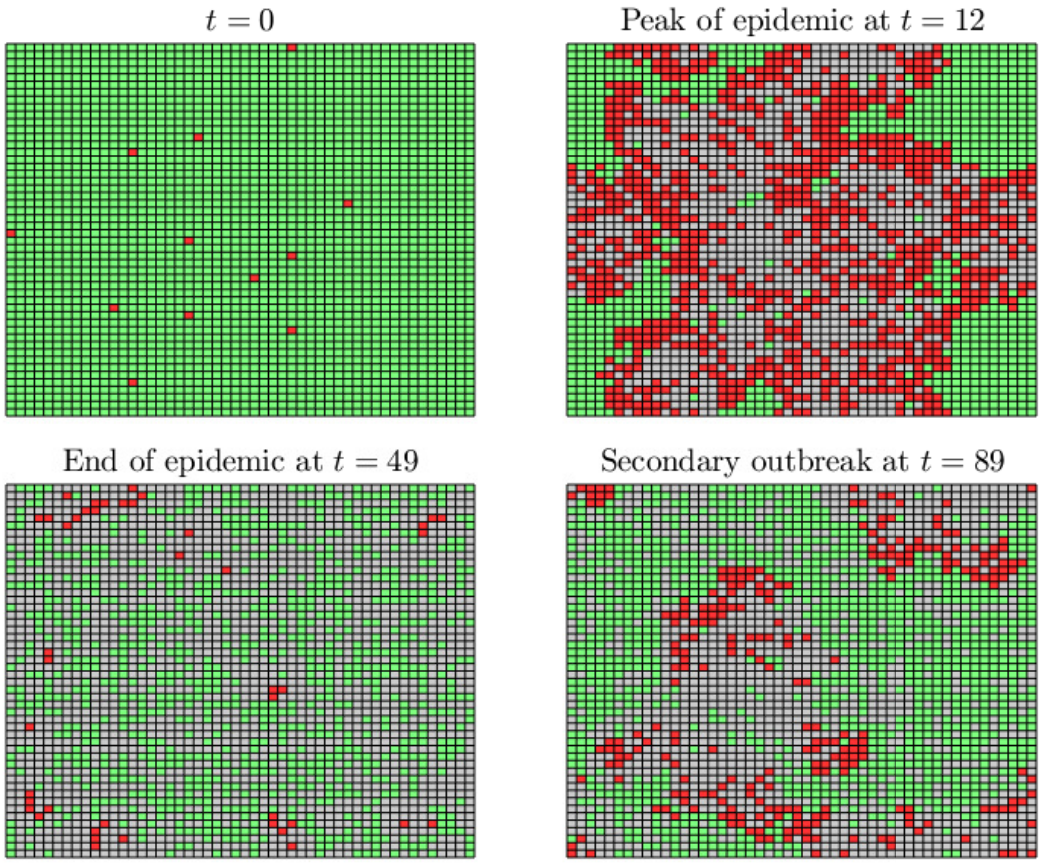


Figure 8: Examples of various states with $p_0 = 0.005$, $\beta = 0.4$, $\gamma = 0.2$, $\kappa = 0.02$

A Code

All the code for this lab can be checket out at
https://github.com/Fredrik-M/BERV-MCS/tree/master/MCS/lab_3

The implementations of the models are found in
https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab_3/brain/step.m,
https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab_3/epi/step_lin.m
and https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab_3/epi/step.m

The scripts
https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab_3/brain/sim.m
and https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab_3/epi/sim.m
can be used to run interactive simulations from an initial state.