

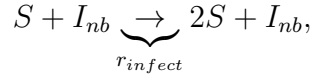
ESAM 448 Random Processes Homework 3

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Problem 1: SIR Model

The SIR model is characterized by two transitions that the individuals undergo: the infection of an individual by its neighbors:



where I_{nb} indicates infected neighbors, and the recovery (or death) of the infected individuals:



Consider a square $L \times L$ lattice of individuals who become infected by their neighbors with a rate

$$r_{infect} = r_i I_{nb},$$

where I_{nb} is the number of adjacent individuals that are infected. For a site (i, j) , consider all 8 sites $(i + \Delta i, j + \Delta j)$ with $\Delta i, \Delta j \in \{-1, 0, +1\}$ as neighbors. Use periodic boundary conditions (employing the Matlab function `cirshift`). To implement this model of three $L \times L$ matrices $\mathbf{S}, \mathbf{I}, \mathbf{R}$, which indicates which state the individual on each site is at given time. Thus, an infected individual (i, j) corresponds to $S_{ij} = 0, I_{ij} = 1, R_{ij} = 0$, etc. Use the Gillespie algorithm to advance the state of the system. In each step, keep track of the numbers of susceptible, infected, and removed individuals (N_S, N_I, N_R). Stop simulation when no transition occur any more. To get an idea of whether your code is making the right steps it is useful to plot the matrices $\mathbf{S}, \mathbf{I}, \mathbf{R}$ (using `imagesc`) for successive time steps.

(a) For the initial condition where only a single individual in the center of the system is infected ($I_{10,10} = 1$, and $I_{ij} = 0$ for $i, j \neq 10$, $S_{10,10} = 0$, and $S_{ij} = 1$ for $i, j \neq 10$, $\mathbf{R} = 0$) determine the time t_{exit} it takes until no transition occurs any more.

1. Plot the histogram of t_{exit} for $L = 20$ using $N_{trial} = 1000$ runs. Use $r_{infect} = 0.5$ and $r_{remove} = 1.1$. What is the mean of t_{exit} ?
2. Write your code as a function that is called according to `[texit] = YourNameHW3.m(ntrial,L)`.

(a) The histogram of t_{exit} is plotted in Figure 1. The mean of t_{exit} is 10.082.

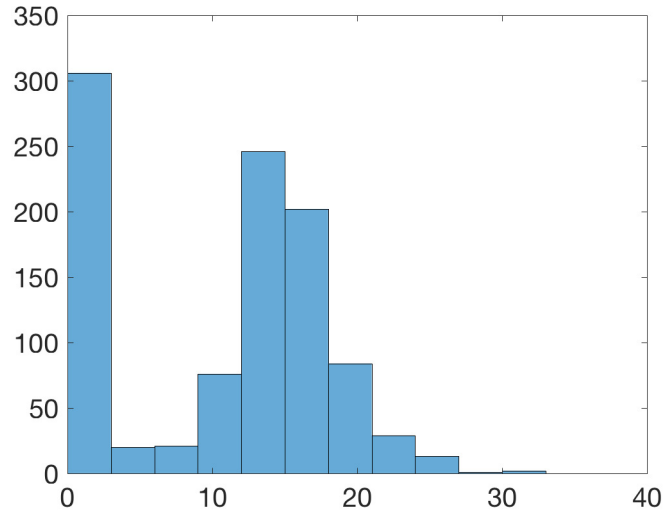


Figure 1: The histogram of t_{exit} for $L = 20$ using $N_{trial} = 1000$ runs ($r_i = 0.5, r_{rem} = 1.1$). The mean of t_{exit} is 10.082.

(b) To get a feeling for the system, investigate the dependence of its dynamics on r_{remove} . For a system of size $L = 100$, use as initial condition a state in which only the individuals ($i = 50, j = 47 : 53$) are infected. Describe qualitatively the behavior of the system for $0 \leq r_{remove} \leq 1.5$ with $r_i = 0.5$ fixed. Plot a few representative snapshots of the resulting states and comment on them.

(b) In Figure 2, we plot the snapshots of the states when $r_{rem} = 1$. It means people will not die after getting infected with the disease. The snapshots show that the disease spreads from the infected individual and eventually the entire population.

In Figure 3, we plot the snapshots when $r_{rem} = 0.5$. We can see that the infection spreads to almost the entire population and eventually almost everybody is removed.

In Figure 4, the removal rate $r_{rem} = 1$. Since the rate of infected individuals dying is higher than the previous case, we can see that the disease spreads at a slower rate because the disease kills some of the infected individuals before they can transmit it to their neighbors. But still, given long enough time, almost the entire population is removed (with more gaps of susceptible groups among them).

Finally, we set $r_{rem} = 1.5$. The removal rate is so high that it kills infected individuals before they can spread the disease. So eventually, only a small group of people gets infected in the first place.

In Figure 6, we plot the total number of susceptible, infected, and removed people as time progresses with different removal rate r_{rem} . The plots are consistent with our observations of the snapshots.

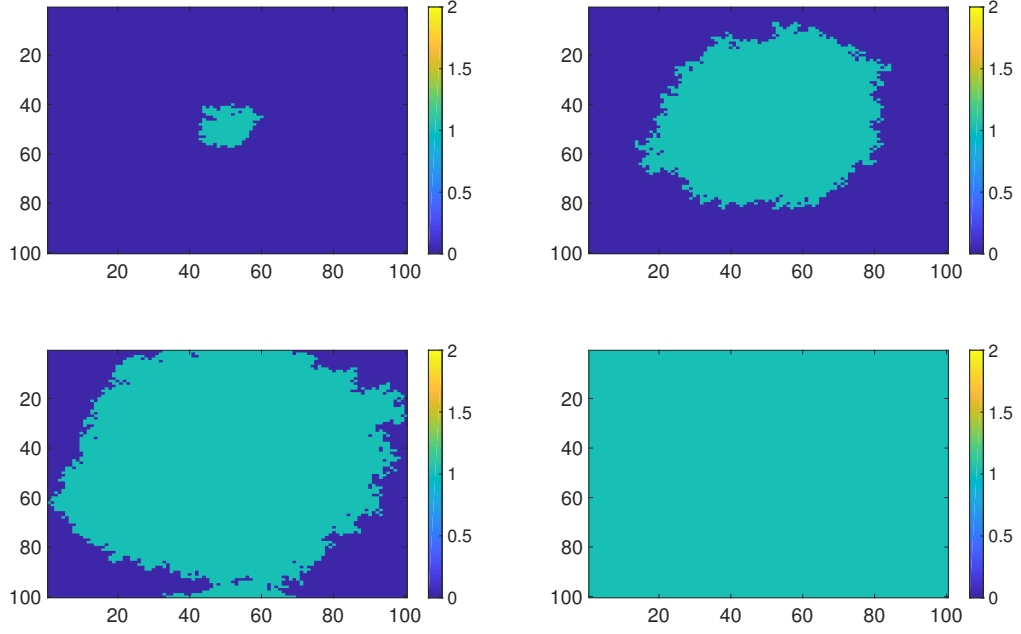


Figure 2: $r_{rem} = 0$

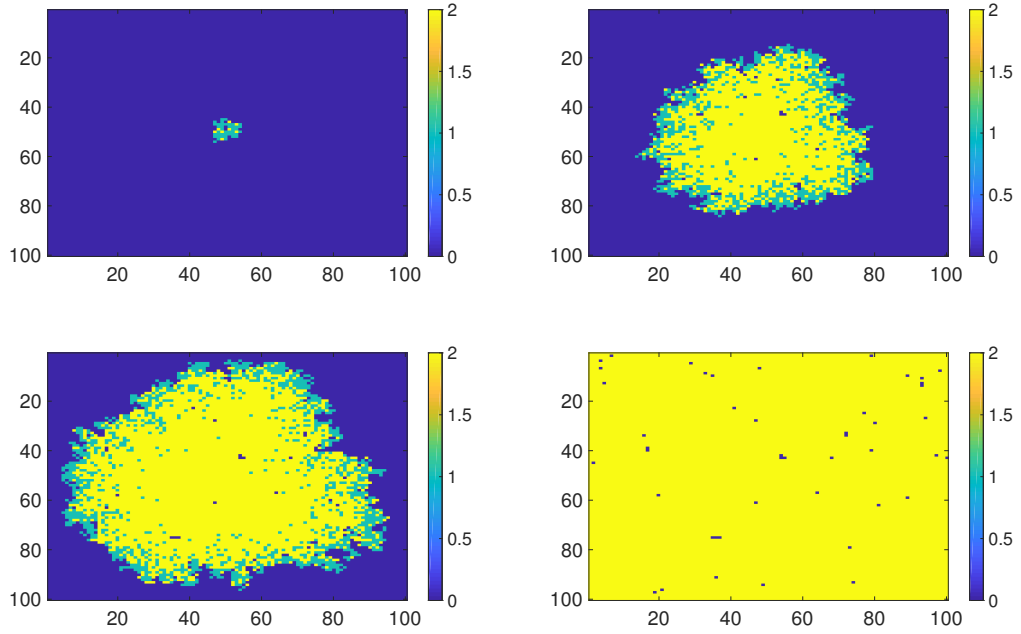


Figure 3: $r_{rem} = 0.5$

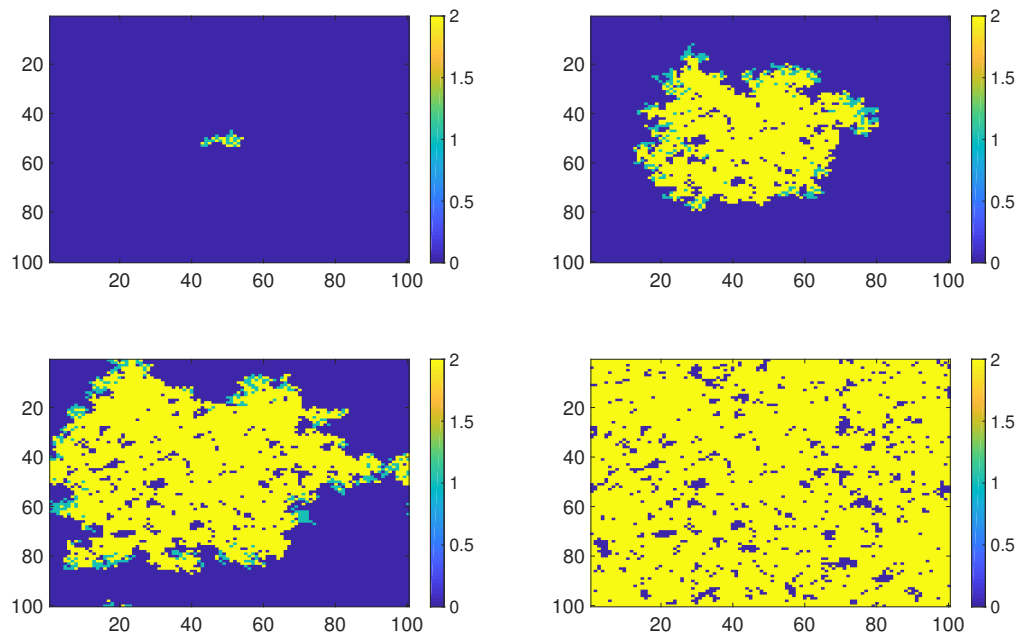


Figure 4: $r_{rem} = 1$

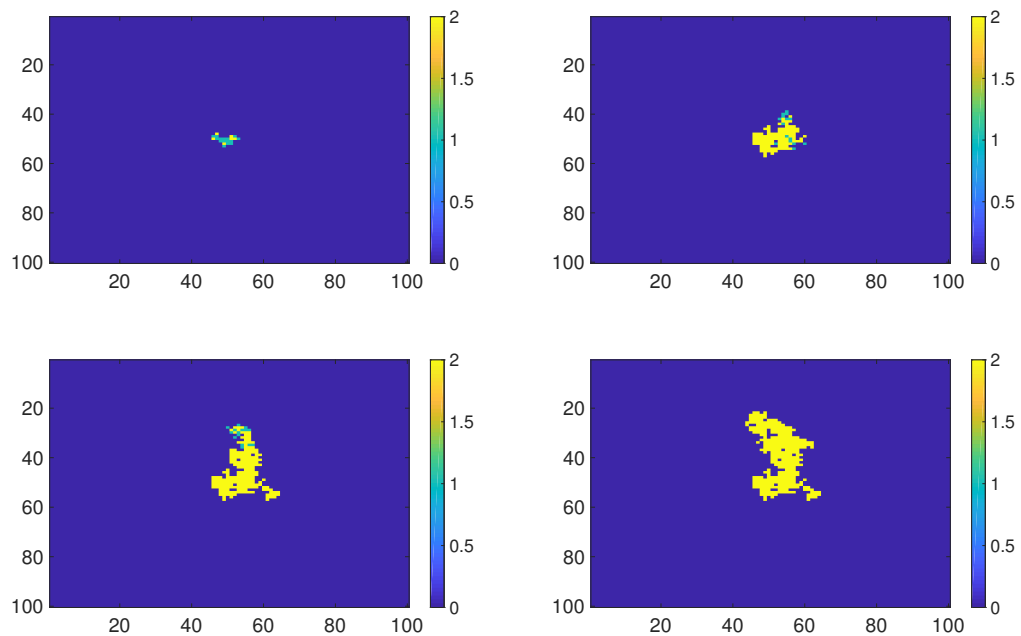


Figure 5: $r_{rem} = 1.5$

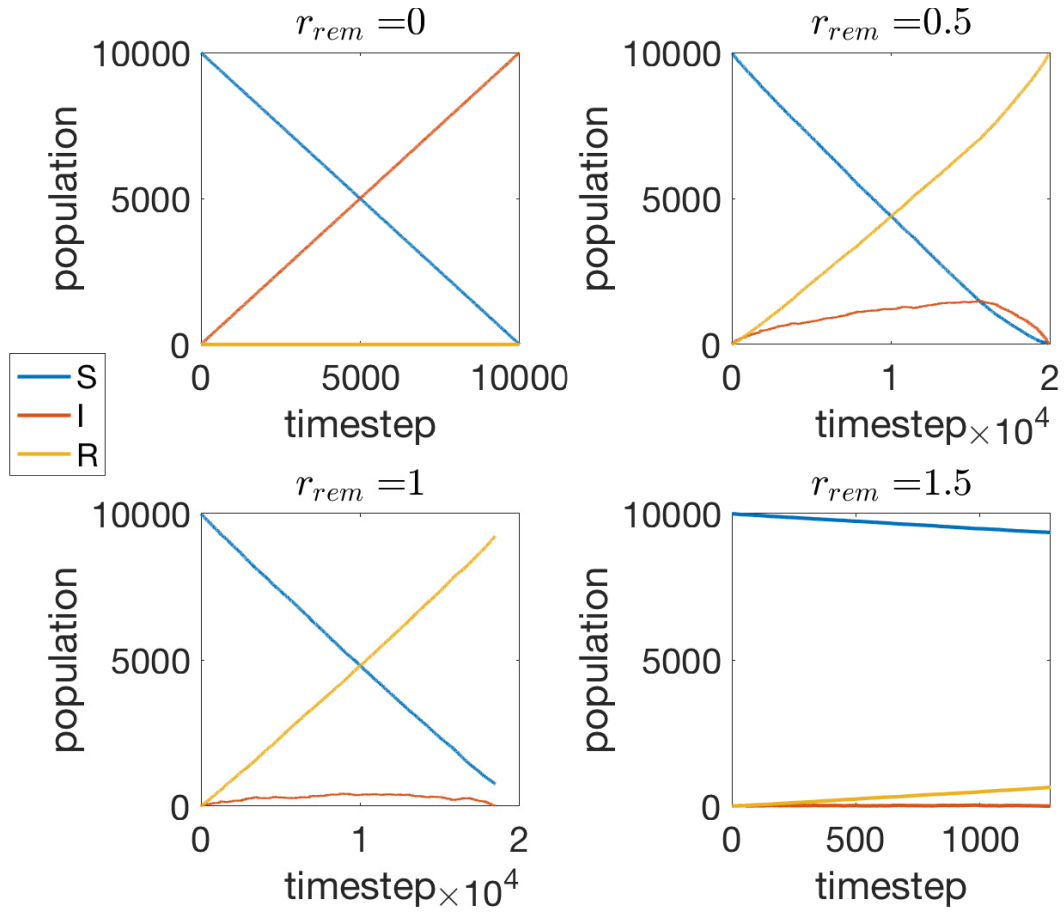


Figure 6: $L = 50$

(c) Consider now the evolution of the disease outbreak in a population in which a random fraction p_{immune} of individuals has been vaccinated, which makes them immune to the disease, i.e. they are already in state R at time $t = 0$. Start again with a localized infection of a single individual at $(50, 50)$ in a system of size $L = 100$. For 100 realizations determine the time t_{exit} as a function of $p_{immune} \in [0, 0.4]$ and the number N_D of individuals dying in the disease outbreak (i.e. $N_D = N_R(t_{exit}) - N_R(0)$). Plot the mean and standard deviation (as error bars) of t_{exit} and N_D as a function of p_{immune} . Comment on the ability of the immunizations to save lives within the framework of this simple model.

In Figure 7, we plot the mean and standard deviation of t_{exit} and N_D against p_{immune} . We can tell that as the ratio of vaccinated people increases, the length of the disease outbreak decreases and the number of removed individuals also decreases. This suggests that immunization can reduce the number of people dying in an outbreak of a contagious disease.

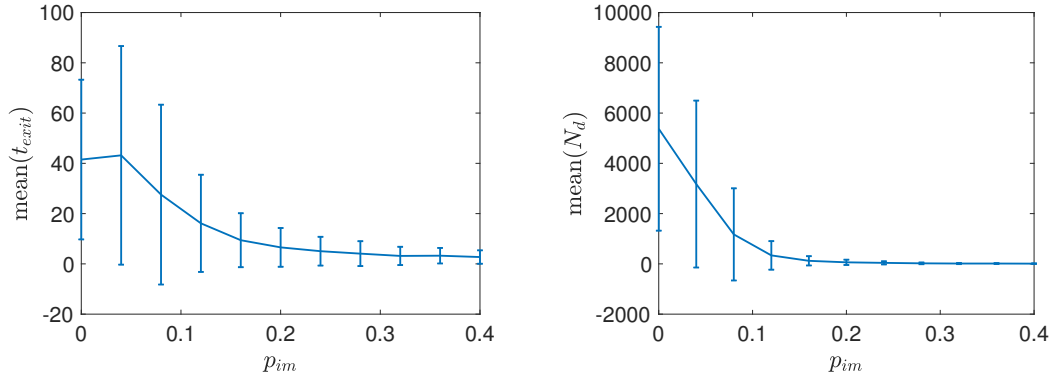


Figure 7: $L = 100, N_{trial} = 100, r_{rem} = 1.1, r_i = 0.5, p_{immune} \in [0, 0.4]$