

# Stochastic SEIR Model

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## 1 Introduction

Infectious diseases are significant and often bring drastic changes to human civilization. In order to project how infectious diseases progress and enhance disease prevention and containment, different epidemic models have been proposed. Some well-known deterministic models like SIR are foundations of more complex prediction models. However, there is always uncertainty in the nature of epidemic growth and spread. Probabilities are incorporated to formulate stochastic models. This project will use methodology proposed in [1] to simulate stochastic SEIR model and investigate how basic reproduction number  $R_0$  affect possibility of extinction. Dynamics of different compartments in deterministic and stochastic SEIR will also be compared and visualized.

## 2 Original Deterministic Model

[1] assumes the total population remains constant over time, as long as there is no death due to the epidemic.

$$\begin{aligned}\dot{S} &= \mu(S + I + R) - \mu S - \frac{\beta SI}{N} \\ \dot{I} &= \frac{\beta SI}{N} - (\mu + \gamma + \alpha)I \\ \dot{R} &= \gamma I - \mu R\end{aligned}\tag{1}$$

Meaning of symbols and parameters are as follows.

$S$ : number of susceptible individuals

$I$ : number of infectious individuals

$R$ : number of recovered individuals

$N$ : sum of  $SIR$

$\beta$ : Transmission rate

$\mu$ : Natural mortality rate

$\gamma$ : Recovery rate

$\alpha$ : Mortality rate caused by infection

## 3 Modified Deterministic Model

In addition to the three compartments, susceptible, infectious, and recovered that are in the SIR model, an extra compartment  $E$  which stands for exposed is added. Individuals in this compartment are already infected but are not infectious, thus they are unable to transmit the disease. Let  $N = S + E + I + R$  and new parameter  $\sigma$  be inverse of the latent period. All other parameters remain the same.

$$\begin{aligned}
\dot{S} &= \mu N - \mu S - \frac{\beta SI}{N} \\
\dot{E} &= \frac{\beta SI}{N} - (\mu + \sigma)E \\
\dot{I} &= \sigma E - (\mu + \gamma + \alpha)I \\
\dot{R} &= \gamma I - \mu R
\end{aligned} \tag{2}$$

## 4 Method

In the stochastic SEIR model, the continuous variables are replaced by discrete numbers. Waiting time between consecutive occurrence in each process  $i$  follows exponential distribution with rate  $\lambda_i$ . For example,  $E$ , the number of the exposed, transits to  $E - 1$  at a rate of  $\mu E$ , and the coupled transition  $I$  to  $I + 1$  follows the same rate. There are 9 such processes in the proposed stochastic SEIR model, which are listed in Table 1.

Gillespie's direct method is used to simulate stochastic models. The direct method exploits the superposition theorem of Poisson process to directly generate the waiting times between successive events in the full system of coupled Poisson processes. In this stochastic SEIR model, we consider a set of 9 independent Poisson processes with rates  $\lambda_i (1 \leq i \leq 9)$ . The superposition of 9 Poisson processes is a single Poisson process with rate  $\Lambda = \sum_{i=1}^9 \lambda_i$ . Therefore, the time to the next event,  $\tau$ , in the entire population follows the exponential distribution with rate  $\Lambda$ . After time  $\tau$ , the  $i$ th process produces the next event with probability  $\frac{\lambda_i}{\Lambda}$ . Exact algorithm is provided in [2].

Table 1: Processes in stochastic SEIR model

Process	Probability
birth	$a_1 = \mu N$
natural death of susceptible	$a_2 = \mu S$
natural death of infectious	$a_3 = \mu I$
natural death of exposed	$a_4 = \mu E$
natural death of recovered	$a_5 = \mu R$
exposure	$a_6 = \beta SI/N$
infection	$a_7 = \sigma E$
recovery	$a_8 = \gamma I$
death of infected due to infection	$a_9 = \alpha I$

## 5 Result

All numerical simulations in this section use following parameters.

$$\begin{aligned}
\beta &= 0.2 \\
\sigma &= 0.2 \\
\gamma &= 0.03 \\
\alpha &= 0.01 \\
\mu &= 0.005 \\
N(0) &= 100 \\
S(0) &= 99 \\
E(0) &= R(0) = 0 \\
I(0) &= 1
\end{aligned}$$

## 5.1 SIR Model

Let the end time of simulation be 300 and only run one simulation of stochastic SIR model using different seeds. Deterministic solutions are obtained by solving the system of differential equations using ode45, and stochastic solutions are obtained by running Gillespie's direct method introduced above. Both are plotted in the same graph. Results are shown in Figure 1.

In the stochastic model,  $I = 0$  means the epidemic goes to extinction, thus the solution trajectories stop for all compartments in the model shown in subfigure a, b, d. Otherwise the epidemic keeps progressing until the end time of simulation shown in subfigure c. Because the fluctuation is great when only one simulation is ran per time, Figure 2 shows accumulation of 100 runs with 100 time steps rolling average for clearer visualization. Similarly deterministic solutions are also plotted for easy comparison. In all 4 subfigures, it is noticeable that although the peak of  $I$  arrives roughly at the same for both models, it is lower for the stochastic one than the deterministic one. It is reasonable because epidemic may go to extinction before the end time in one run of simulation in the stochastic model, as shown in Figure 1, whereas epidemic always exists at the end time in the deterministic model.

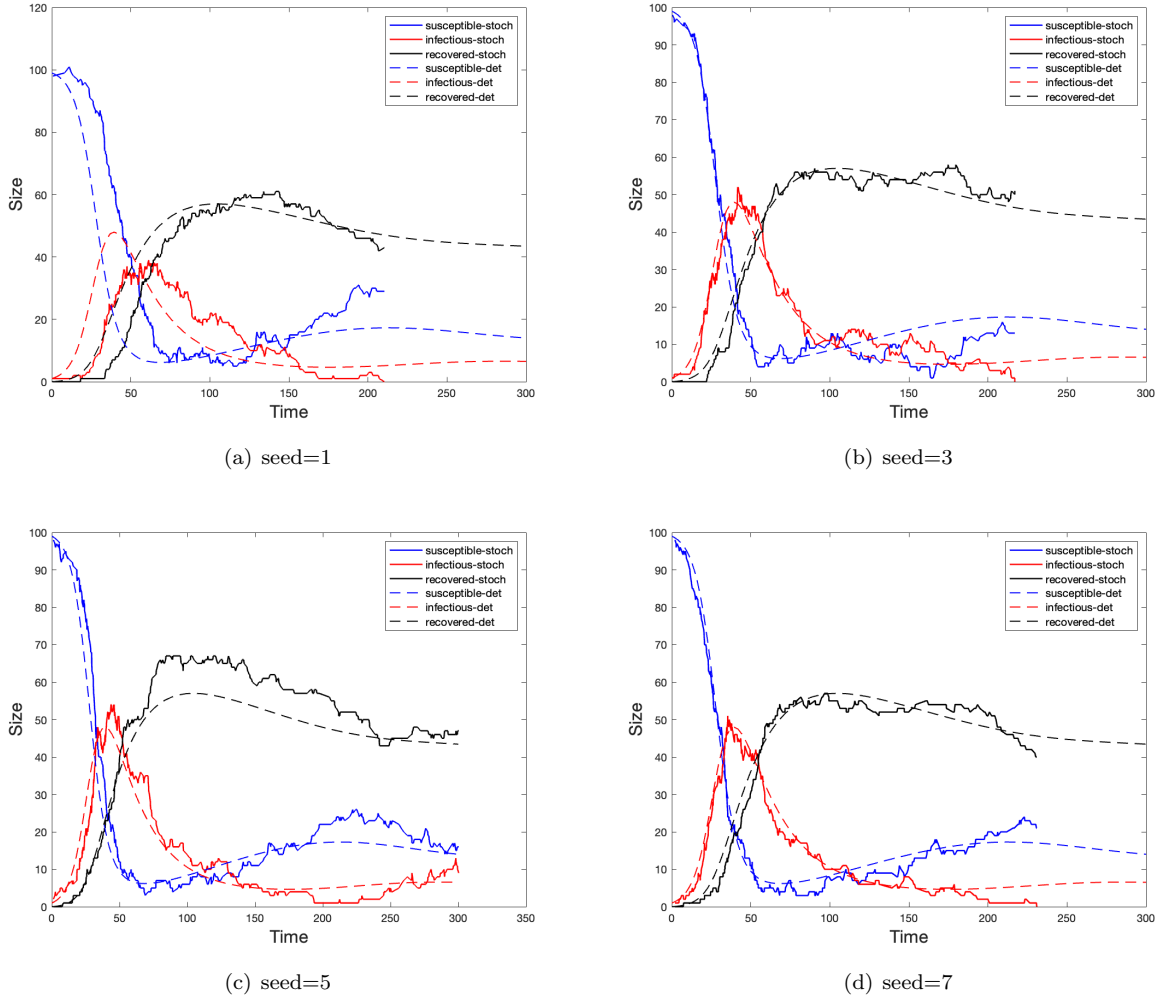
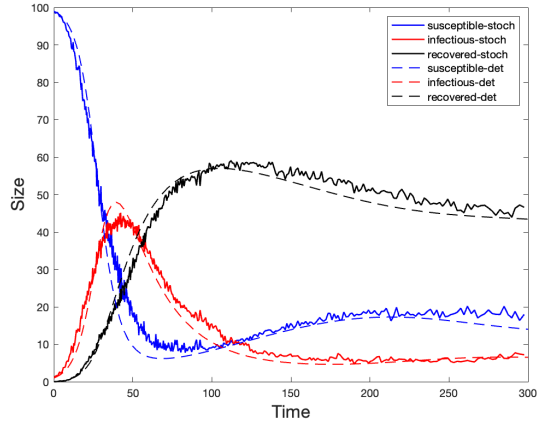
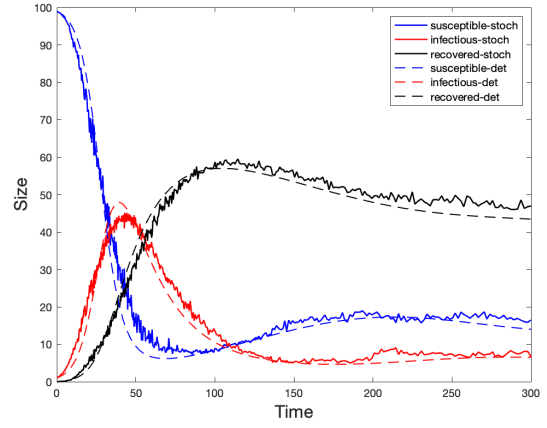


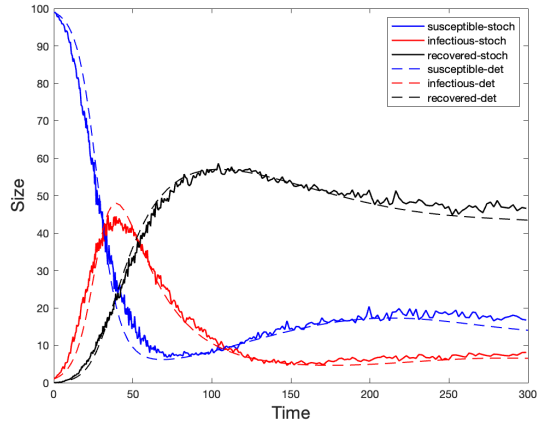
Figure 1: stochastic and deterministic solution trajectories of SIR model using different seeds



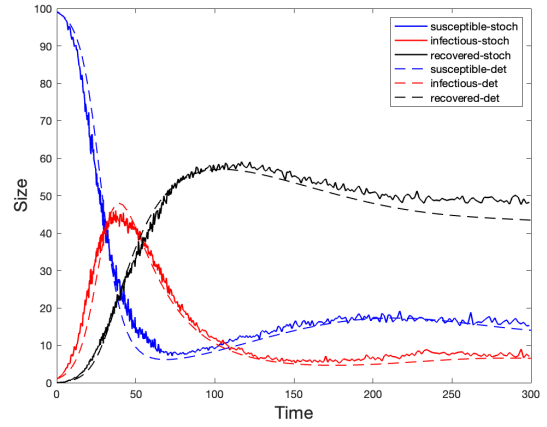
(a) seed=1



(b) seed=3



(c) seed=5



(d) seed=7

Figure 2: 100 time steps rolling average stochastic and deterministic solution trajectories of SIR model

## 5.2 SEIR Model

Using the same parameters and end time, perform simulations on proposed SEIR model. Adding a new compartment  $E$  does not change the fact that epidemic may go to extinction before end time is reached in one run of simulation, as shown in Figure 3. Lower peak of rolling average of  $I$  in the stochastic model in Figure 4 also demonstrates possibility of extinction. Comparing to SIR model, SEIR model has later arrival time of peak of  $I$  in both stochastic case and deterministic case. In addition, the peak is also lower for SEIR model, as shown in Figure 5. Regardless of type of model, it takes time for individuals in compartment  $E$  to become infectious to increase value of  $I$ . In the deterministic case, the entire population always decreases due to death of infection. Splitting original  $I$  into  $E$  and  $I$  naturally decreases number of individuals in  $I$ . In the stochastic case, because the time between consecutive occurrence follows exponential distribution, by adding some waiting time for an individual to become infectious, the expected occurrence of infection decrease.

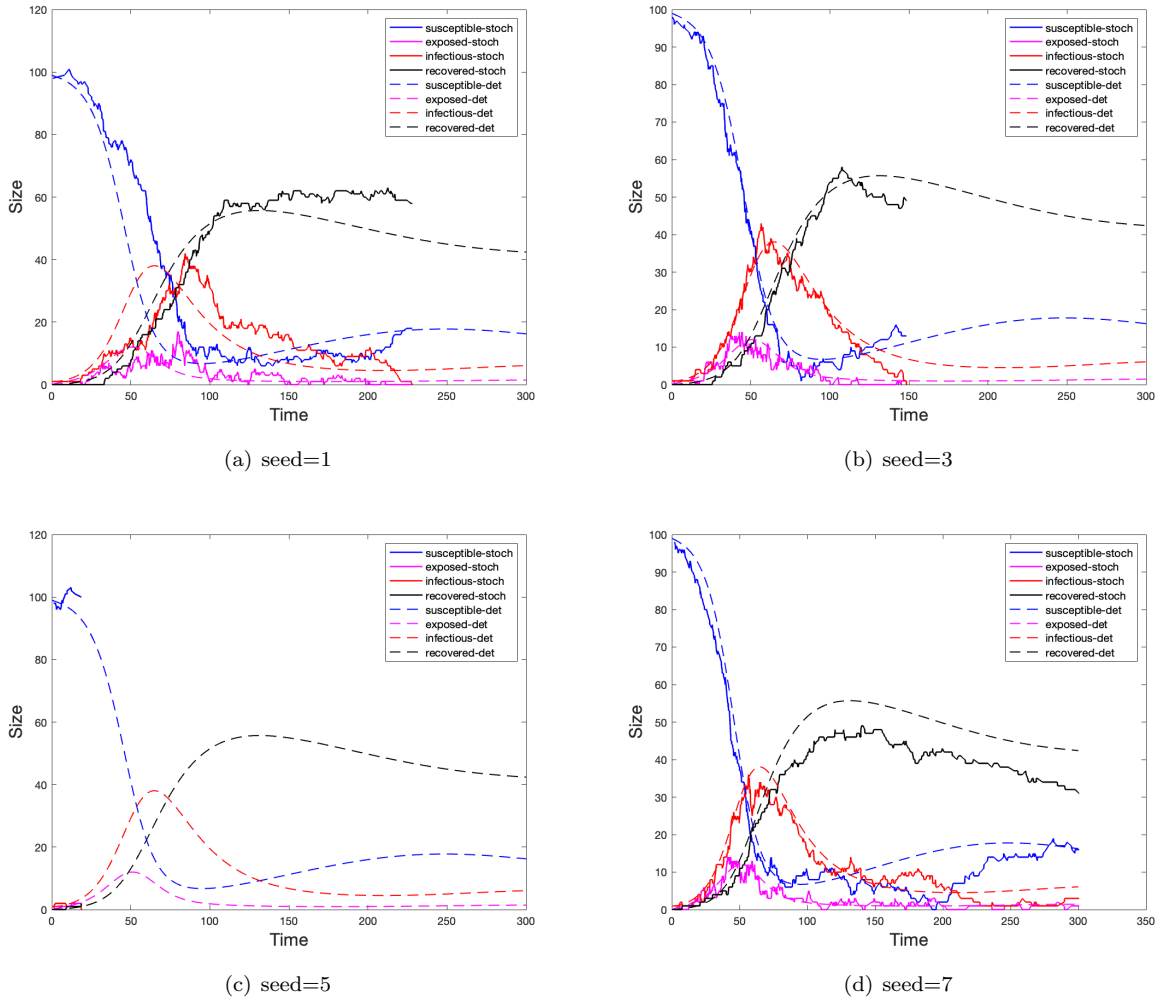


Figure 3: stochastic and deterministic solution trajectories of SEIR model using different seeds

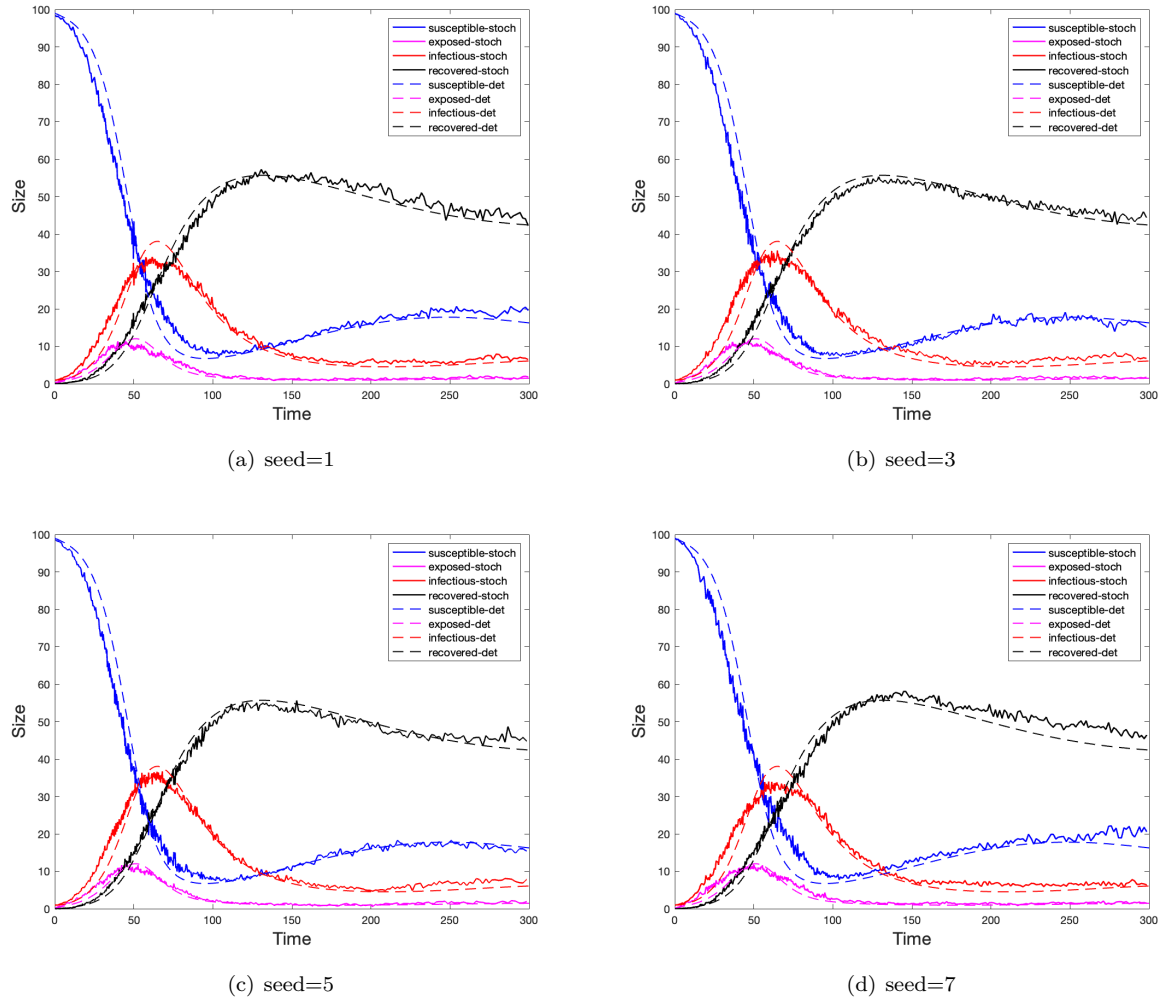


Figure 4: 100 time steps rolling average stochastic and deterministic solution trajectories of SEIR model

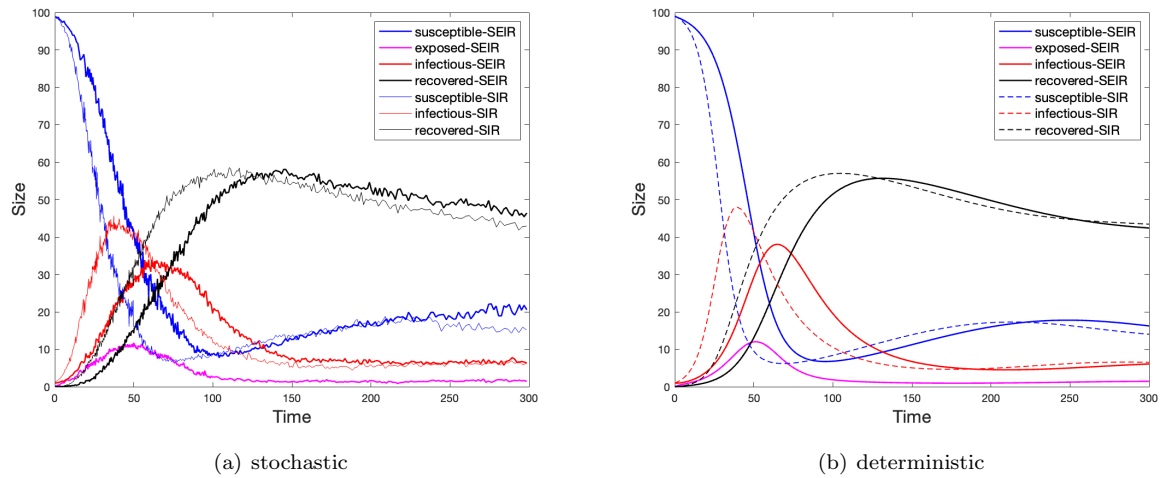


Figure 5: Compare SEIR and SIR in both stochastic and deterministic cases

### 5.3 Extinction of Epidemic

The basic reproductive rate  $R_0$  of SIR and SEIR is  $\frac{\beta}{\mu+\gamma+\alpha}$ ,  $\frac{\sigma\beta}{(\mu+\sigma)(\mu+\gamma+\alpha)}$  respectively. In the deterministic models,  $R_0 < 1$  means the epidemic will eventually go to extinction. However, it is not the case in stochastic models. By changing the value of  $\beta$ , transmission rate, different  $R_0$  can be obtained. For each  $R_0$ , run two stochastic models 1000 times. Corresponding probability that extinction occurs is shown in Figure 6. Both SEIR and SIR have roughly the same curve that indicates possibility of extinction when  $R_0$  exceeds 1. The possibility is still greater than 0.5 when  $R_0 = 6$ . Therefore,  $R_0$  alone cannot explain the progress of an stochastic epidemic.

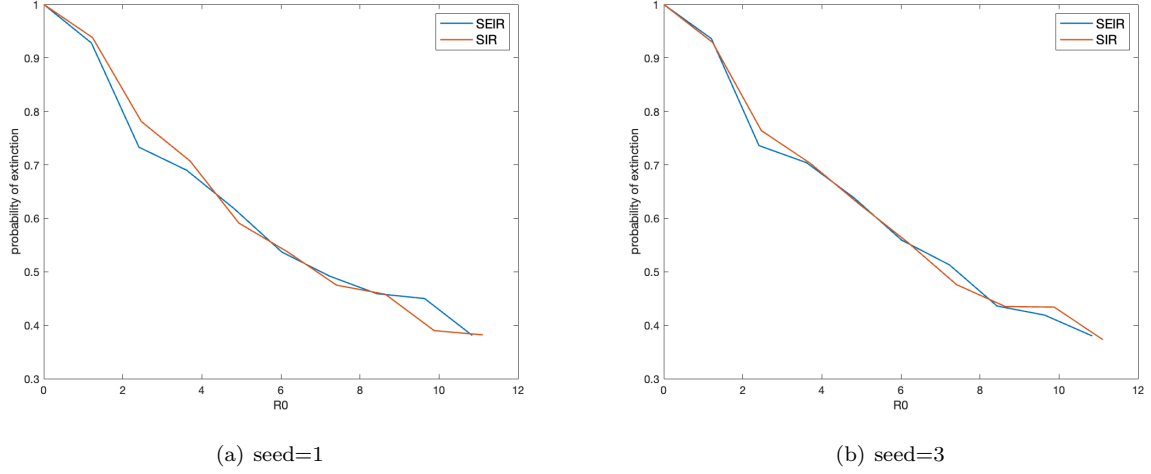


Figure 6: probability of extinction vs.  $R_0$

## 6 Reference

- [1] Regoes, R. (n.d.). Stochastic simulation of epidemics . Retrieved May 12, 2022, from <https://ethz.ch/content/dam/ethz/special-interest/usys/ibz/theoreticalbiology/education/learningmaterials/701-1424-00L/stochSIR.pdf>
- [2] Masuda, Naoki, and Christian L. Vestergaard. “Gillespie Algorithms for Stochastic Multiagent Dynamics in Populations and Network.” ArXiv.org, 10 Dec. 2021, <https://arxiv.org/abs/2112.05293v1>.