MS4217: Lab 1

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Frost-Reed model

How it works?

Models for the spread of infectious diseases and the development of epidemics are of interest to health scientists, epidemiologists, biologists, and public health officials. Stochastic models are relevant because of the randomness inherent in person-to-person contacts and population fluctuations.

The SIR (Susceptible–Infected–Removed) model is a basic framework, which has been applied to the spread of measles and other childhood diseases. At time t, let St represent the number of people susceptible to a disease, It the number infected, and R_t the number recovered and henceforth immune from infection. Individuals in the population transition from being susceptible to possibly infected to recovered

$(S \rightarrow I \rightarrow R)$. The deterministic SIR model is derived by a system of three nonlinear differential equations, which model interactions and the rate of change in each subgroup. A stochastic SIR model in discrete time was introduced in the 1920s by medical researchers Lowell Reed and Wade Frost from Johns Hopkins University.

In the Reed-Frost model, when a susceptible individual comes in contact with someone who is infected there is a fixed probability z that they will be infected. Assume that each susceptible person is in contact with all those who are infected. Let p be the probability that a susceptible individual is infected at time t. This is equal to 1 minus the probability that the person is not infected at time t, which occurs if they are not infected by any of the already infected persons, of which there are I_t.

This gives,

$$p = 1 - (1 - z)^{I_t}.$$

Disease evolution is modelled in discrete time, where one time unit is the incubation period—also the recovery time-of the disease.

The model can be described with a coin-flipping analogy. To find I_{t+1}, the number of individuals infected at time $t + 1$, flip S_t coins (one for each susceptible), where the probability of heads for each coin is the infection probability p. Then, the number of newly infected individuals is the number of coins that land heads. The number of heads in n independent coin flips with heads probability p has a binomial distribution with parameters n and p. In other words, I_{t+1} has a binomial distribution with $n = S_t$ and $p = 1 - (1 - z)^{I_t}$. Having found the number of infected individuals at time $t + 1$, the number of susceptible persons decreases by the number of those infected. That is, $S_{t+1} = S_t - I_{t+1}$. Although the Reed-Frost model is not easy to analyze exactly, it is straightforward to simulate on a computer.