Mathematical modelling of a classroom disease epidemic simulation, via the handshake game

Zetian (Jacky) Lyu

School of Mathematics & Statistics, University of Melbourne

Introduction

Whether it's a seasonal cold or the COVID-19, studying the outbreak of a disease has always been a big subject of scientists and mathematicians. Those studies are essential for predicting the progress of epidemics and how to best control them.

The Handshake Game

The handshake game is a classroom activity designed to simulate the outbreak of a disease. One participant plays the initial carrier, and the virus will spread through "handshakes". Read more: https://go.unimelb.edu.au/gj3i.

This project aims to model a disease epidemic through this game. Data has been collected from a simulated population of 100 participants, each engaged in 5 handshakes and the infectious period is set to 5.

The SIR Model

The Susceptible, Infected and Removed (SIR) model is a well-known model in mathematical epidemiology. It is based on three assumptions that:
1) The population is constant and homogenous mixing.
2) The rate of transmission, β, is constant
3) The rate of recovery, γ, is also constant

Let $S(t)$, $I(t)$, $R(t)$ be the respective number of people in the corresponding group at time t. Under continuous and discrete timelines, the model can be written as follows:

Continuous time (using derivatves):
$$\frac{dS}{dt} = -\beta IS$$
$$\frac{dI}{dt} = \beta IS - \gamma I$$
$$\frac{dS}{dt} = \gamma I, t \in \mathbb{R}$$

Discrete time:
$$S(n+1) = S(n) - \beta I(n)S(n)$$
$$I(n+1) = I(n) + \beta I(n)S(n) - \gamma I(n)$$
$$R(n+1) = R(n) - \gamma I(n), n \in \mathbb{N}$$

Where $S(0) = 99, I(0) = 1, R(0) = 0$

The discrete time, deterministic model

As a starting point, the discrete time SIR model was fitted to the data. Using the method of gradient descent, the values of β=0.0155, γ=1 were found to minimise the residual sum of squares (RSS). The calculated values of S, I, R are plotted together with observed data in diagram 1.
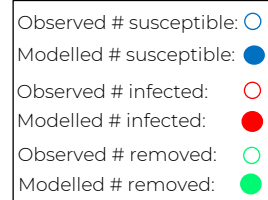
Observed # susceptible: ○
Modelled # susceptible: ● (blue)
Observed # infected: ○ (red)
Modelled # infected: ● (red)
Observed # removed: ○ (green)
Modelled # removed: ● (green)

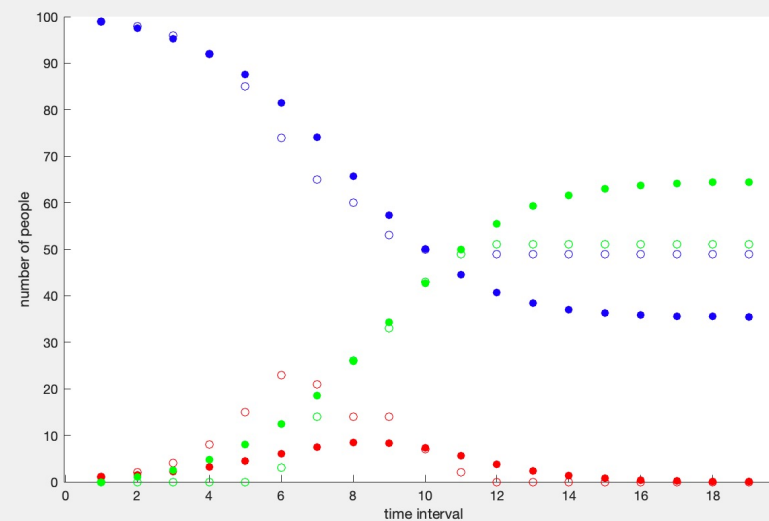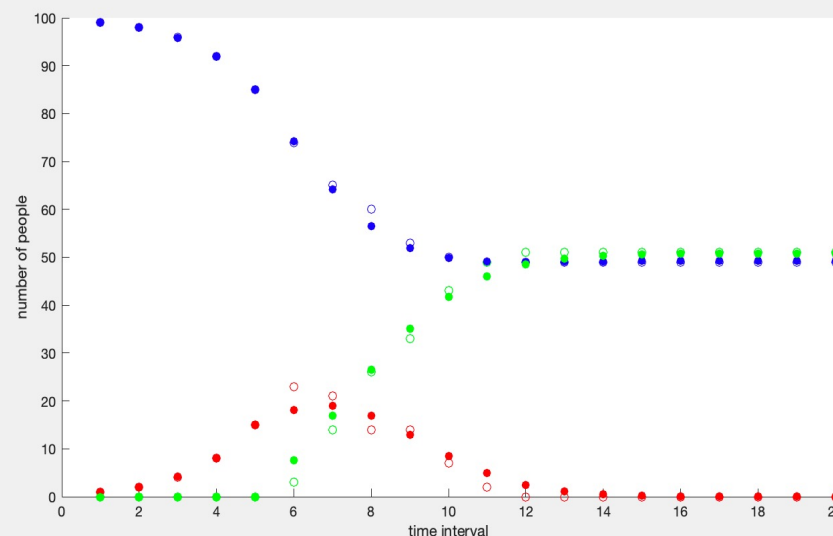### Diagram 1. Fitting using constant β and γ

The model did fit the data to a certain degree, yet not to a reliable extent. Some notable observations are:
1) During the first five days there are no recovered patients (due to the infectious period) yet recovered patients has been modelled.
2) There is a difference between the peak/parabolic behavior of the early infectious population.
3) The asymptotic behavior of S and R varies significantly from the observed data.

Based on those observations, the following conclusions are made:
a) The parameter γ is required to be a step function, remaining as 0 for the first infectious period.
b) The parameter β needs to be larger at the initial time intervals (i.e. peaking at t=6), but then decreases and eventually approaches a smaller value as t increases (to counter difference in asymptotic behaviors).

One of the functions which follows the behavior of the described β is a transformed arctan. For example, the graph below plots y = arctan(-x+2)+1.5:

Now, let β = a*arctan(b*t+c)+d, where a,b,c,d are parameters. Let γ be a step function s.t. γ=0 for t ∈ [0,5]. Using the same method of minimizing RSS, the following values are calculated:
$$\beta = 0.0064 \times \arctan(-0.2582t + 2.3872) + 0.0038$$
$$\gamma = \begin{cases} 0, & t \in [0,5] \\ 0.5087, & t > 5 \end{cases}$$

The new calculated values of S, I, R are plotted together with observed data in diagram 2. Evidently, the updated model has a much-improved fit with the observed data, seemingly more reliable and consistent. Implementing the alterations based on the SIR are shown to be essential to fit data from the handshake game.

Diagram 2. Improved fitting using arctan function β and step function γ

Conclusion

It is observed that the handshake game can be modelled via the SIR model, with the transmission rate, β, modelled by an arctan function against time, and the recovery rate, γ, modelled by a step function.

The varying transmission rate overtime corresponds to the nature of the game: The participants who are moved to the I group at an earlier stage were more likely to be infected within their first few handshakes, thus infecting all other participants they shook hands with afterwards; whereas for the participants who were later moved to the I group, they were more likely to be infected in their last few handshakes, thus not infecting many others. This explains the decrease in the transmission rate overtime.

A stochastic modelling approach were also taken at the later stages of the project, but the results are not presented on this poster.

Implications

o Assisting the teaching process: Helping teachers to better understand the handshake game so they can set reasonable expectations when using it in student activities.
o Reflecting upon the SIR model: Understanding the limitations and strengths of this popular model will assist scientists to design more effective models.

Acknowledgments