Mathematical Modelling of a Classroom Disease Epidemic Simulation

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Introduction:

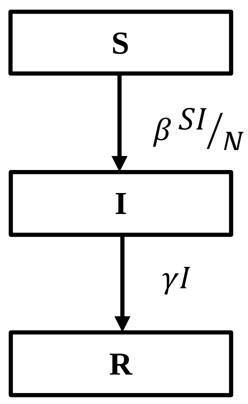
SIR Models (S = Susceptible, I = Infected, R = Recovered) can be utilized to describe the scenario where an acute infectious disease takes place. This project fits an SIR model (and its variations) to a classroom simulation of an infectious disease outbreak (The 'Handshake' Disease), which can be used in teaching infectious disease modelling to high-school and university level students.

SIR Model: Theoretical Background

Define: At time t:

$$\begin{cases} S\text{: the number of susceptible people} \\ I\text{: the number of infected people} \\ R\text{: the number of recovered people} \end{cases}$$

Schematic Diagram:



Where

$$\begin{cases} \beta = \text{transmission rate} \\ \gamma = \text{recovery rate} = \dfrac{1}{\text{ave. infectious period}} \\ N = \text{total population} \end{cases}$$

are assumed to be constants.

SIR Equations:

- **Continuous Model:**

$$\begin{cases} \dfrac{dS}{dt} = -\beta\dfrac{SI}{N} \\ \dfrac{dI}{dt} = \beta\dfrac{SI}{N} - \gamma I \\ \dfrac{dR}{dt} = \gamma I \end{cases}$$

- **Discrete Model:**

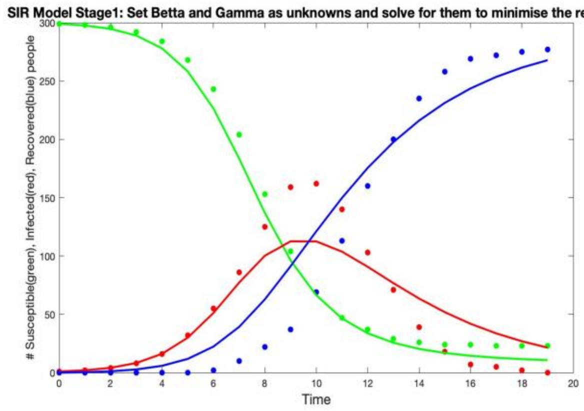
$$\begin{cases} S_{n+1} = S_n - \dfrac{\beta S_n I_n}{N} \\ I_{n+1} = I_n + \dfrac{\beta S_n I_n}{N} - \gamma I_n \\ R_{n+1} = R_n + \gamma I_n \end{cases}$$

Classroom Disease Simulation: The 'Handshake' Disease

The 'handshake' disease is a simulated disease where the disease is transmitted by handshakes. For detailed information about the classroom activity, see reference [2].

Analysis: (Software Used: MATLAB_2019a)

PART 1: Fit the Standard SIR Model to One Typical Result from the 'Handshake' Game



Parameter Used:

handshakes = 10;

Infectious period = 5;

Total number of people = 300;

Initial # infected people = 1.

Result:

$\beta = 0.9836$;

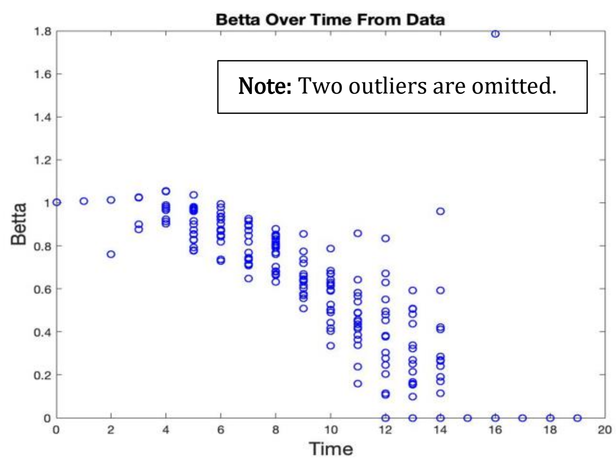
$\gamma = 0.2639$;

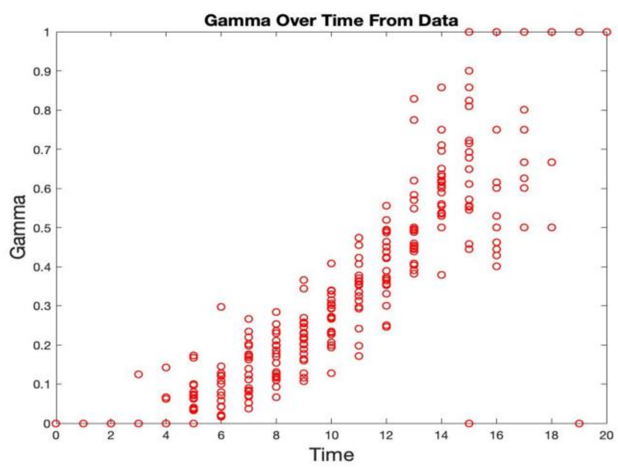
residual = 13432.

Conclusion: Setting β and γ as constants does not give a good fit quantitatively.

PART 2: The Behavior of β and γ Over Time Obtained from Discrete SIR Model

Based on the same parameter configuration as in Part 1 and 20 data sets, I got:



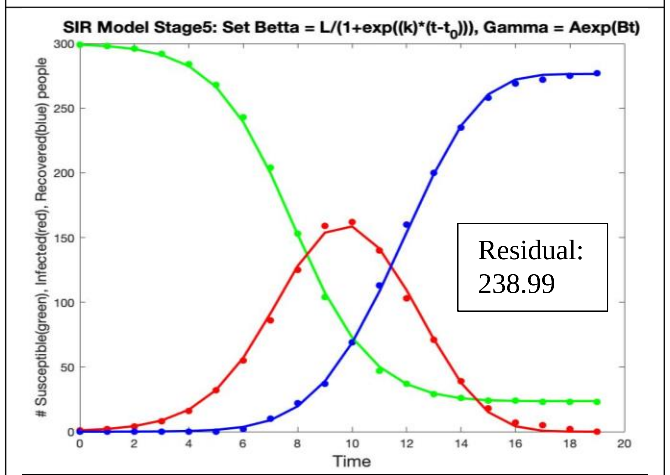


Conclusion: It can be seen that neither β nor γ keeps constant in the 'Handshake' disease. This is the reason why the standard SIR model could not give a good fit.

PART 3: Fit Some Variations of SIR Model to the 'Handshake' Disease Data

After trying a sequence of models of different forms with time-varying β and γ based on the information in Part 2, I figured out: $\beta(t) = \frac{L}{1+e^{k(t-t_0)}}$ (logistic function) and $\gamma(t) = Ae^{Bt}$ provides the best fit. For example, for the same set of data in Part 1:

$$\beta(t) = \frac{0.7375}{1+e^{1.1816(t-21.1466)}}$$
$$\gamma(t) = 0.0082e^{0.3294t}$$



Discussion:

However, note that $\beta(t) = \frac{0.7375}{1+e^{1.1816(t-21.1466)}}$ remains almost constant throughout the valid time span, $0 \le t \le 19$. Therefore, one can argue that setting $\beta = 0.7375$ also gives a relatively accurate result.

In fact, I have verified this idea using MATLAB and a more general conclusion is: β = const. and $\gamma(t) = Ae^{Bt}$ also gives a good fit. This model is simpler and much more efficient compared to the one setting β as a logistic function. Hence, for educational purposes, setting β = const. and $\gamma(t) = Ae^{Bt}$ can be seen as an optimum choice.

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REFERENCES:

[1]. Keeling, M. J., & Rohani, P. (2011). *Modelling infectious diseases in humans and animals.* Princeton University Press.

[2]. http://go.unimelb.edu.au/267r