**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:

**Schematic Diagram:**

Where

are assumed to be constants.

**SIR Equations:**

* **Continuous Model:**

* **Discrete Model:**

**S**

**I**

**R**

### **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**

A close up of a map

Description automatically generated

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

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

A close up of a map

Description automatically generated A close up of a map

Description automatically generated

**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 and based on the information in Part 2, I figured out: (logistic function) and provides the best fit. For example, for the same set of data in Part 1:

|  |
| --- |
|  |
| **A close up of a map  Description automatically generated** |

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

**Note:** Two outliers are omitted.

Residual: 238.99

Parameter Used:

# handshakes = 10;

Infectious period = 5;

Total number of people = 300;

Initial # infected people = 1.

Result:

;

;

.

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

**Discussion:**

However, note that remains almost constant throughout the valid time span, . Therefore, one can argue that setting also gives a relatively accurate result.

In fact, I have verified this idea using MATLAB and a more general conclusion is: and also gives a good fit. This model is simpler and much more efficient compared to the one setting as a logistic function. Hence, for educational purposes, setting and can be seen as an optimum choice.

### **Acknowledgements:**

The Vacation Scholarship Program offered me valuable experience and rewarding insights into what it is like when conducting mathematical research.

I would like to thank Dr. Anthony Morphett for his patient guidance, expert advice, and inspiring encouragement throughout this project.

**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>