

PROJECT REPORT

SIMULATING THE SPREAD OF INFECTIOUS DISEASE

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1.0 AIM

Using mathematics and computer to simulate the spread of infectious diseases based on the given data.

2.0 INTRODUCTION

Infectious diseases constitute a significant burden to global health and will continue to be that for the foreseeable future. Infectious diseases are a leading cause of death globally.

To better understand the spread of disease, we need to make approximations and be ready for the worst-case scenario. For that, we use mathematics to solve some equations and can find the possible outcomes.

Modelling is a very efficient way to show the outbreak of an epidemic and the effects of control measures taken. Many models have been developed in the past, but the most common is the "SIR Model", named after the categories – "susceptible, infectious, recovered" developed by Kermack and McKendrick.

3.0 SIR MODEL

The SIR model is a representation that divides a population with respect to a disease's impact on an individual over time. An individual can be categorised as:

SUSCEPTIBLE (S): These are the group of people who are not affected but in danger.

INFECTED (I): These are the group of people who are suffering from the disease.

RECOVERED (R): These are the people who have recovered from the disease.

3.1 ASSUMPTIONS

These are some assumptions :

1. The total population remains constant, i.e., no birth or death during that period.
2. This model also does not consider the age (a far higher portion of older people die from the disease than young people), the patients' pre-existing conditions, and the healthcare quality.
3. After getting infected, the patients will soon recover and not get infected again. The disease confers immunity. This means that once an individual has recovered, they cannot contract the illness again during the same outbreak. Diseases with very short-term (or no) immunity are commonly modelled with SI models. Herd immunity is also not considered.
4. The transmission and recovery rate is also constant.

3.2 VARIABLES

Following are the variables:

1. Total population (N): The people that are susceptible to the disease might or might not get the disease.
2. Initially infected population: The people initially affected by the disease come into this category.
3. Transmission rate (γ): Number of people getting infected due to its transmission in one day or the probability of someone getting infected.
4. Recovery rate (β): Number of people recovering each day or the probability of someone to get recover.
5. Basic reproduction number (R_0): Ratio of recovery rate over transmission rate.

3.3 EQUATIONS

$$\frac{dS}{dt} = -\frac{\beta IS}{N},$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I,$$

$$\frac{dR}{dt} = \gamma I,$$

$$\Rightarrow \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

So,

$$S + I + R = N$$

Also,

$$R_0 = \frac{\beta}{\gamma}$$

4.0 TECHNOLOGIES REQUIRED

Python needs to be installed.

Some extra modules are required :

- Numpy
- Matplotlib
- Scipy
- Tkinter

5.0 PSEUDO CODE

// This code will take input and integrate using equations

function sir_equ:

$ds_dt = -(\beta) * (\text{infected}) * (\text{susceptible}) / (\text{total-population})$

$di_dt = (\beta) * (\text{infected}) * (\text{susceptible}) / (\text{total-population}) - (\gamma) * (\text{infected})$

$dr_dt = (\gamma) * (\text{infected})$

return integrate (ds_dt, di_dt, dr_dt)

6.0 SIMULATION

A user interface was developed for the ease of the user and to facilitate widespread use of the model. Figure 1 shows an example of user data and application output. We have developed this Graphical User Interface (GUI), which will take input from the user, solve the data using equations and plot the graph.

SIR Model

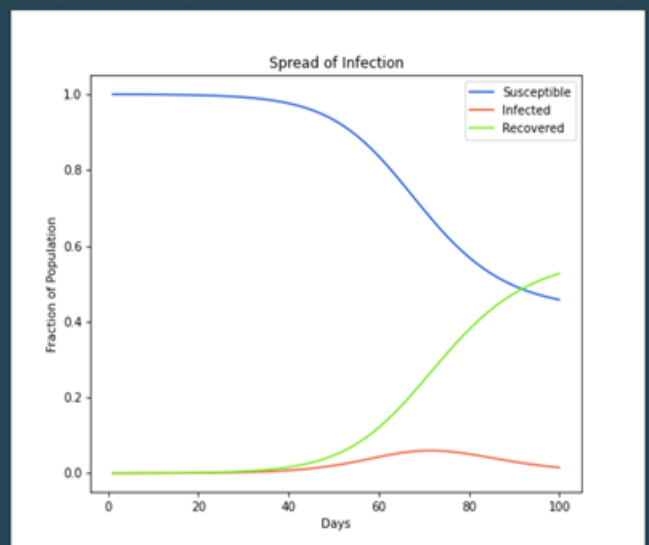
Total Population	<input type="text" value="0"/>
Initially Infected	<input type="text" value="0"/>
Transmission Rate (β)	<input type="text" value="0.0"/>
Recovery Rate (γ)	<input type="text" value="0.0"/>
Days of Simulation	<input type="text" value="0"/>

Simulate

SIR Model

Total Population	<input type="text" value="100000"/>
Initially Infected	<input type="text" value="10"/>
Transmission Rate (β)	<input type="text" value="0.347678"/>
Recovery Rate (γ)	<input type="text" value="0.234576"/>
Days of Simulation	<input type="text" value="100"/>

Simulate



Analysis :

Basic reproduction number is 1.482 and it will cause an epidemic.

After 71 day the number of infected will start decreasing.

7.0 ANALYSIS

It provides information about:

- 1) Will the infection cause an epidemic or not.
- 2) When will the infected population will be at its peak.

8.0 ACCURACY OF THE MODEL

This is a fundamental model with too many assumptions, making it unrealistically. This model can work for a small area, but as the area increases, so will the rate of birth and death.

9.0 CONCLUSION

We have attempted to give the audience a simple overview of how the epidemic proceeds through this project. Also, we have tried our best to make it user-interactive so that the user can see and predict the epidemic's growth.

Also, this model is not that perfect but can give basic approximations about the infection.

This can help us better understand how we can decrease the spread rate and improve the recovery rate.

10.0 REMARKS

Through this model, we learned how to use a machine's computation power and solve problems. This has given us a new perspective on programming and its uses.

11.0 APPENDIX

1. To download and install python, go to <https://www.python.org/>
2. To install additional modules, use “pip install <module_name>” in CMD in Windows and in Terminal in Mac.

12.0 REFERENCES

https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology

<https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model>

<https://www.nature.com/articles/s41598-021-84055-6>

<https://www.nature.com/articles/srep46076>