

# Analysis - Simulating disease spread through Cellular Automata and the SIR model DRAFT

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# 1 Introduction

Since 1999, there have been 11 major disease outbreaks (Daily Sundial, 2020) across the globe, eight of which involved thousands of cases. To effectively control an outbreak and ultimately stop it in its tracks, it's current and past states must be analysed so it's spread can be predicted, which is essential in influencing how governments should deal with such a threat.

This is currently being seen in how the UK government is dealing with COVID-19, where a balance between a total lockdown and total freedom needs to be struck to control how the virus spreads. This balance is essential in allowing businesses to continue operating, keeping the economy afloat and allowing people their freedoms to do what they want.

My project aims to provide a starting point for where a disease outbreak can be modelled either by cellular automata or the SIR model, which can be used in an educational environment to teach people about the spread of diseases. A user will be able to input custom parameters according to the disease they are trying to simulate and be able to introduce special events such as a partial or permanent lockdown, to be able to see how the disease spread could change. A user should also be able to compare the two different ways of simulating a disease.

Source: <https://sundial.csun.edu/156361/news/a-timeline-of-outbreaks-from-2000-to-present/>

## 2 Initial objectives

These objects represent my initial aims of what this project should be able to do. These may change later on throughout this project.

- Simulate the spread of a disease using the SIR model
- Simulate the spread of a disease using the Cellular Automata model
- Input custom parameters or use default values (from a previous disease) including infection rate, incubation period and death rate for the SIR model
- Input custom parameters or use default values (from a previous disease) relating to the number and infectivity of cells for the CA model
- Set a quarantine period or introduce a vaccine (therefore limiting disease transmission)
- Click on a graph and show statistics from that point in time
- Export graphs produced as png
- Upload past simulation results into the program to generate a graph from that previous simulation
- Be able to compare graphs of two different diseases

## 3 Potential user

Mr Bliss - Biology teacher at Abingdon School As this model provides a starting point for modelling disease outbreak, it's most effective use would be in an education environment, where it is used to teach people about how disease can spread and how changes in parameters such as the infection rate, recovery rate, time of infection and immunity can affect how effectively a disease is transmitted throughout a cohort.

## 4 How the problem was researched

To first understand how I could make this project, I had to research the two main methods of modelling disease spread, the SIR model and Cellular Automata. Once I got the basic idea of how each model worked, I further researched how I could implement these in Python, as well as looking at how to use some Python libraries to help me.

- Find out how SIR and Cellular Automata work
- Research how to implement SIR and Cellular Automata in code
- Learn how to use the Matplotlib library to draw graphs for my disease models
- Learn how to use Pandas to export data to an external file
- Learn how to use Tkinter to create a GUI interface and multiple pages
- Learn how to create, use and modify an SQL database using Sqlite3

### 4.1 The SIR model

The SIR model is a simple disease spread model which uses differential equations to determine the number of people in three categories, the susceptible, the infected and the recovered. The susceptible population represent those who can become infected a disease, the infected population represent those currently infected with the disease who are able to spread it to other people and the recovered population represent those who are no longer infected. In some models, people in the recovered population can be infected again.

#### 4.1.1 Equations for the SIR model

##### People in each group

$S = S(t)$  - number of susceptible individuals

$I = I(t)$  - number of infected individuals

$R = R(t)$  - number of recovered individuals

##### The Susceptible equation

$$\frac{dS}{dt} = \frac{-\beta S(t)I(t)}{N}$$

where  $\beta$  is the rate at which infections occur (a positive constant)

##### The Infected equation

$$\frac{dI}{dt} = \frac{\beta S(t)I(t)}{N} - \gamma I(t)$$

where  $\gamma$  is the rate at which people recover

##### The Recovered equation

$$\frac{dR}{dt} = \gamma I(t)$$

##### Model without vital dynamics

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

As this model doesn't take into account vital dynamics ie. people aren't added through birth or removed through death, the sum of all the changes is constant and equal to 0

## 4.2 The CA model TBD

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## 5 Research of existing solutions TDB

TBD

## 6 Interview with target user

### **Q1. How could such a tool like this be used in the classroom?**

A1. As a comparator of diseases; To be able to decide the best method to restrict a disease; To possibly predict the start of a second spike

E1. I will try to implement a feature where the parameters of two diseases could be entered, and a graph could be calculated and shown for both, which would allow a user to compare the spread of the two diseases. I will also add features that a government may try and implement to restrict a disease. This could include a lockdown feature or a vaccine introduction which would allow a user to see how the spread of a disease could change.

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## 7 Prototyping of code TDB

TBD

## 8 Documented design COMMENTED OUT

## 9 The code COMMENTED OUT