Executive Summary: SIR System Modeling

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Abstract

In the next project, we will consider the phenomenon of disease transmission within a closed population system, where individuals' positions and movements are random. These types of models, called SIRs, can be used to forecast disease transmission curves and implement measures to correct the evolution of the disease, ensuring appropriate conditions. It is precisely during times of pandemics or epidemics that the usefulness of these models becomes globally relevant.

Description

The scenario to be considered involves a population group of a species affected by an infectious disease, whose dynamic movement patterns cannot be predicted since each individual can only move according to certain basic rules of possible movements.

Given these unknown dynamics, it will be necessary to formulate and solve a system of differential equations to describe the infected individuals, those susceptible to contracting the disease, and those who have recovered or are no longer contagious.

Main Assumptions

Core assumptions of the model:

- The probability of infection is equal for all individuals in the population.
- The population is homogeneous, meaning that the risk of infection is the same for all susceptible individuals and that the recovery time is the same for all infected individuals.

1 Constant Population Model

The model manages the different sets S, I, and R as if they were well-separated compartments and considers that individuals can move from one to another if they get sick (change $S \to I$) or once sick, recover (change $I \to R$). Furthermore, it is assumed that an individual cannot move from the susceptible set directly to the recovered set.

With these assumptions and considerations, the differential equations for the SIR model are:

$$\begin{aligned} \frac{dS}{dt} &= -\beta \frac{I}{N} S \\ \frac{dI}{dt} &= \beta \frac{I}{N} S - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned} \tag{1}$$

Where:

- $N = S + R + I$
- the quantity $\beta \frac{I}{N}$ represents the rate at which people leave the S compartment (they get infected);
- in the first equation dS represents the change due to people leaving the S compartment (the negative sign is because people are leaving);
- in the second equation dI represents the change due to people leaving the I compartment (one part is due to people moving from the S compartment to the I compartment, and another part is due to people leaving the I compartment because they recover);
- the quantity γ represents the rate at which people recover.

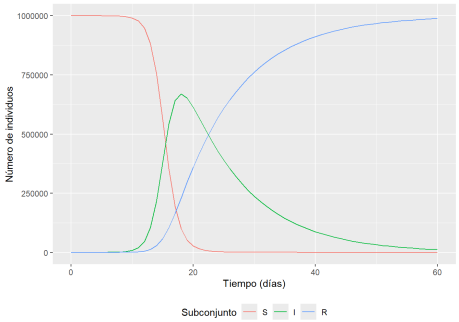

Figure 1: Basic SIR Model

In the SIR model, R_0 is defined

$$R_0 = \frac{\beta}{\gamma} \tag{2}$$

This represents a population rate of infection. It defines whether an epidemic is or is not to happen given an initial condition. It can be thought of as the people each infected person infects at t_0. An epidemic is to arise given that $R_0 > 1$.

Also defined is

$$R_{eff} = R_0 \frac{S}{N} \tag{3}$$

This corresponds to the average number of people each infected person infects at a particular time. Thus it is a function of time.

For the next two sections, we shall consider $\gamma = 0.1$ and $\beta = 1$

1.1 Maximum Number of Infected

The time at which the I is maximized is given by the following expression:

$$\int_{\gamma \frac{N}{\beta}}^{N-1} \frac{N}{\beta S \left[N - S + \frac{\gamma N}{\beta} [ln(N-1) - ln(S)] \right]} dS = t_{I=max} \tag{4}$$

That arraises after analytically solving for S in terms of R $S = (N-1)e^{-\frac{\beta}{N\gamma}R}$ and substituting in the $\frac{dR}{dt}$ forcing the condition $S = \frac{N}{2}$ into the resulting integral's upper limit. Complete procedure here.

$$\begin{aligned} t_{S=max} &= 18.0028\ days \text{ analytically} \\ t_{S=max} &= 18\ days \text{ numerically} \end{aligned} \tag{5}$$

1.2 Susceptibles when equal to $\frac{N}{2}$

The time at which S is half the population is given by:

$$\int_0^{\frac{N\gamma[ln(2N-2)-ln(N)]}{\beta}} \frac{1}{\gamma(N-R-(N-1)e^{-\frac{\beta}{N\gamma}}}dR = t_{s=\frac{N}{2}} \tag{6}$$

That arraises after analytically solving for S in terms of R $S = (N-1)e^{-\frac{\beta}{N\gamma}R}$ and substituting in the $\frac{dI}{dt}$ equation, then forcing the $S(R) = \frac{N}{2}$ to get the upper integral's limit. available at Complete procedure here. From this, we get that.

$$\begin{aligned} t_{S=\frac{N}{2}} &= 15.2886\ days \text{ analytically} \\ t_{S=\frac{N}{2}} &= 15\ days \text{ numerically} \end{aligned} \tag{7}$$

1.3 Simulation as β varies

As β increases, the day in which I is maximized is brought forward, as well as the equilibrium points. This happens since β is proportional to R_0, so it will fasten the pandemic as long as $R_0 > 1$, otherwise, the pandemic won't occur.

1.4 Simulation as γ varies

As γ increases, the day in which I is maximized is delayed, as well as the equilibrium points. This happens since γ is inversely proportional to R_0, so it will slow down the pandemic as long as $R_0 > 1$, otherwise, the pandemic won't occur.

2 Variable Population Model

We can include variations in the modeled populations, such as births and deaths, and vaccination campaigns.

2.1 Births and Deaths Model

If we consider b as the rate of births and μ as the rate of deaths, then we have the following system:

$$\begin{aligned} \frac{dS}{dt} &= bN - \beta\frac{I}{N}S - \mu S \\ \frac{dI}{dt} &= \beta\frac{I}{N}S - \gamma I - \mu I \\ \frac{dR}{dt} &= \gamma I - \mu R \end{aligned} \tag{8}$$

Let's consider $\beta = 0.4\frac{1}{days}$ and $\gamma = 0.2\frac{1}{days}$

In the case where $b = \mu$, the population is kept constant.

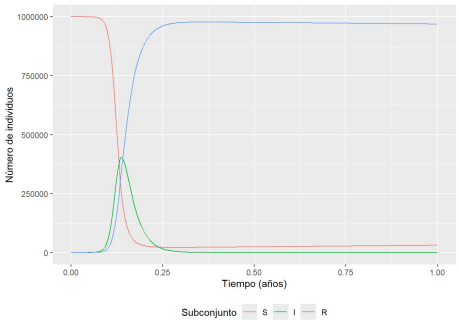

Figure 2: SIR model with births and deaths and constant population

In the case where $b \neq \mu$, the population varies. If we consider $\mu = \frac{1}{10}$ and $b = \frac{1}{70}$, then:

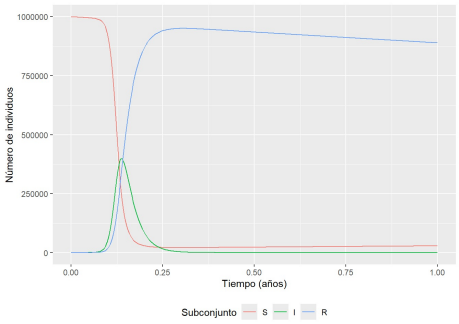

Figure 3: SIR model with births and deaths and non-constant population. ($\mu = \frac{1}{10}$ and $b = \frac{1}{70}$)

As we can appreciate, both graphs behave similarly, with the difference in the final steepness of the recovered group. If $b < \mu$, the steepness is negative, while if $b > \mu$, the steepness is positive.

2.2 Vaccines Model

Let's consider a constant population without births and deaths again, but implementing a vaccination program in which an initial fraction (v) of S is vaccinated into R.

We wish to reach a v big enough such that the epidemic is avoided. This removes the need for full vaccination. Said phenomenon is known as *herd immunity*. This happens after R_{eff} has decayed below 1. Then v has to satisfy:

$$v_{herd\ inmunity} > \frac{\frac{\gamma}{\beta} - 1 + \frac{1}{N}}{-1 + \frac{1}{N}} \tag{9}$$

We can exemplify both situations of the inequality. First, let's assume $\beta = 0.6$ and $\gamma = 0.1$. For a $v = \frac{2}{3}$, which is below herd immunity, then the epidemic occurs:

In the case where $v = \frac{5}{6}$, which is the critical point, the epidemic is avoided.

Complete report available here.

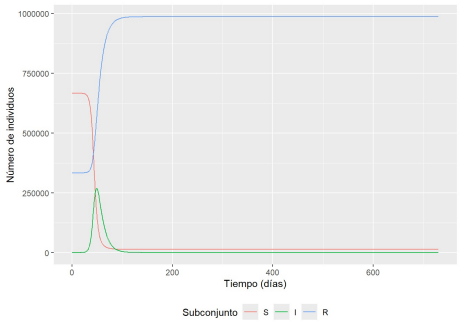

Figure 4: Simulation with vaccination and without herd immunity

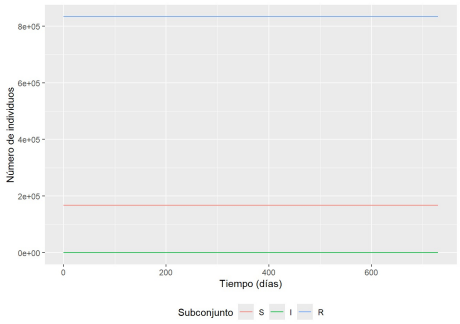

Figure 5: Simulation with vaccination and herd immunity

3 Geometric City Simulations

8 different configurations of SIR systems were simulated in Python. The repository is available at Repo Link. Said experiments confirmed the previously plotted SIR systems experimentally.

See animation at Video here

You can run it yourself with code provided at File Link

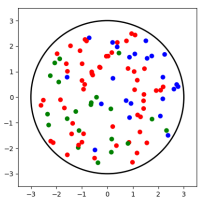

Figure 6: S: Susceptible; I: Infected; R: Recovered

3.1 Square City

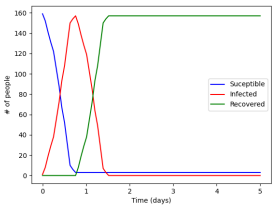

Figure 7: S: Susceptible; I: Infected; R: Recovered

3.2 Circular City

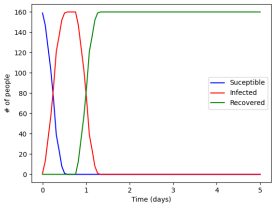

Figure 8: S: Susceptible; I: Infected; R: Recovered

3.3 Clustered Square City

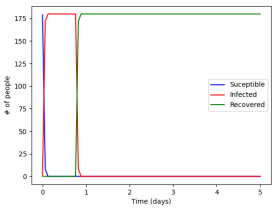

Figure 9: S: Susceptible; I: Infected; R: Recovered

3.4 Clustered Circular City

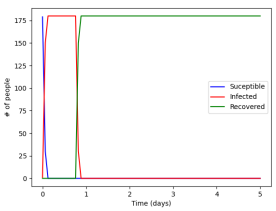

Figure 10: S: Susceptible; I: Infected; R: Recovered

4 Movement Simulations

4.1 Square City

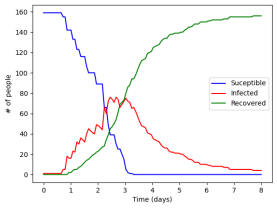

Figure 11: S: Susceptible; I: Infected; R: Recovered

4.2 Circular City

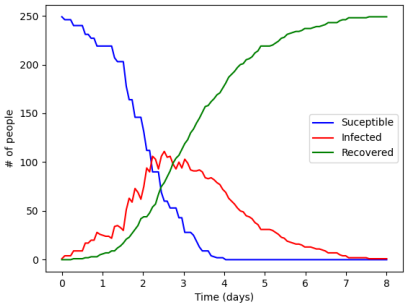

Figure 12: S: Susceptible; I: Infected; R: Recovered

4.3 Clustered Square City

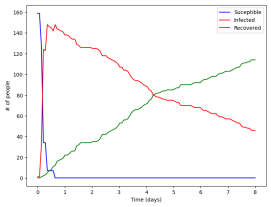

Figure 13: S: Susceptible; I: Infected; R: Recovered

4.4 Clustered Circular City

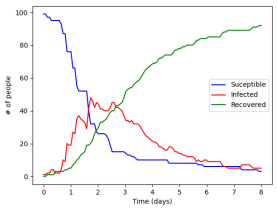

Figure 14: S: Suceptible; I: Infected; R: Recovered

Plot interpretations

We can clearly see four different types of behavior. The simulations without movement are not really interesting; it is just spike alternations between states, and don't result in much interesting behavior, even though one can see that it resembles rather vaguely the SIR tendency. The clustered ones resemble their unclustered homologous with the particularity of being faster in terms of maximums and points of equilibrium.

The movement animations result in a really SIR-looking behavior. In the same fashion that their non-moving counterparts, the clustered ones reflect much more rapid versions of the unclustered variants.

Conclusions

The SIR model provides valuable insight into how infectious diseases spread over time. Our results show that a higher infection rate (β) leads to a faster and larger outbreak, while a higher recovery rate (γ) helps reduce the number of infected individuals. In our simulations, the maximum number of infections occurs around 18 days with approximately 670,000 infected individuals. Effective control of the disease requires maintaining the effective reproductive number below 1. Additionally, incorporating births, deaths, and vaccinations makes the model more realistic, demonstrating that herd immunity can be achieved when a sufficiently large portion of the population is vaccinated. Finally, population movement and clustering significantly accelerate the spread of the infection, highlighting the importance of public health interventions in limiting transmission.

Main Resources Used

The project was developed using **Windows** as the operating system, with **Python** libraries such as `numpy`, `matplotlib`, `pandas`, and `random` for numerical computation, visualization, data handling, and stochastic simulations. Additionally, **RStudio** was employed with the packages `deSolve` (for solving differential equations), `reshape2` (for data reshaping), and `ggplot2` (for advanced plotting and visualization).

References and Resources

- Matplotlib Documentation: https://matplotlib.org/stable/contents.html
- Python Random Module: https://docs.python.org/3/library/random.html
- deSolve Package (CRAN): https://cran.r-project.org/package=deSolve
- ggplot2 Package (CRAN): https://cran.r-project.org/package=ggplot2
- GitHub Repository (Python simulations, R plots, analytic development (Rmd)): https://github.com/AxTulti/SIR_epidemic_ODE_System_Simulations
- Video of Simulations (Google Drive): https://drive.google.com/file/d/1LuTyB34fJdno6j2cBShnVwiP8teuee3J/view?usp=sharing