NUMERICAL SIMULATION OF THE SIR MODEL AND ITS PROPERTIES

Introduction

Compartmental models are a technique used to simplify the mathematical modelling of infectious disease. The population is divided into compartments, with the assumption that every individual in the same compartment has the same characteristics. The models are usually investigated through ordinary differential equations.

Compartmental models may be used to predict properties of how a disease spreads, for example the prevalence (total number of infected) or the duration of n epidemic. Also, the model allows for understanding how different situations may affect the outcome of the epidemic (for instance, what the most efficient technique is for issuing a limited number of vaccines in a given population).

The SIR model is comprised of *susceptible*, *infected* and *recovered* individuals. It is a simplified model for measles, for example.

$$\boldsymbol{S \xrightarrow{\beta} I \xrightarrow{\mu} R}$$

The equations are:

$$\boldsymbol{\frac{dS}{dt} = -\beta SI}$$

$$\boldsymbol{\frac{dI}{dt} = \beta SI - \mu I}$$

$$\boldsymbol{\frac{dR}{dt} = \mu I}$$

If the infection is very powerful, the equilibrium will be reached when $I = S = 0, R = N$. Otherwise, the equilibrium will be reached when $I = 0,\ S + R = N$ (depends on the initial conditions).

The first fixed point transforms from stable to unstable when $\frac{\beta N}{\mu} = 1$. $\frac{\beta N}{\mu}$ is also referred to as *R0*, the basic reproduction ratio (a dynamical value which only makes sense at initial conditions; afterwards, it is the number of secondary infections divided by the number of infected individuals).

Plotting population distributions

To start this exercise, I've recycled the code from http://rstudio-pubs-static.s3.amazonaws.com/6852_c59c5a2e8ea3456abbeb017185de603e.html to plot different population distributions according to the initial parameters we give it. On *Figure 1* is shown the plot for the following parameters (taken from https://towardsdatascience.com/infection-modeling-part-1-87e74645568a):

- $S_0 = 1 - 1 * 10^{-6}, I_0 = 10^{-6}, R_0 = 0$: the disease starts with almost all individuals healthy, and a very small fraction ill. Since the total population is 1, our basic reproduction ratio can be calculated as $\frac{\beta}{\mu}$.
- $\beta = 0'23$
- $\gamma = 0'17$
- Number of days: 350

The results are shown on *Figure 1*. The *R0* value is greater than one, which means that the infection rate is greater than the recovery rate, and thus the infection will grow throughout the population.

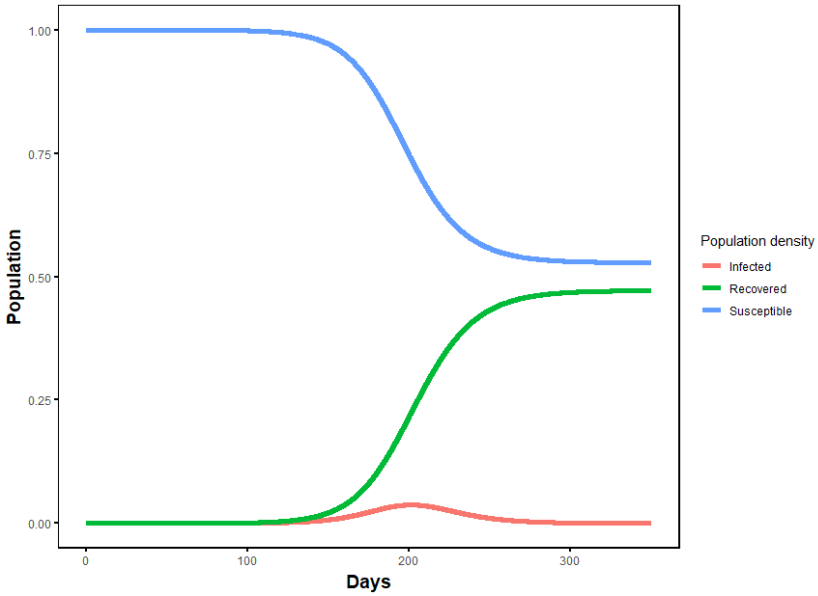

Figure 1

Under these conditions, we can see that the disease is not powerful enough to infect the whole population. The next step, thus, is increasing the infection rate to $\beta = 0'6$ (*Figure 2*) and $\beta = 0'9$ (*Figure 3*). As we can see, with an initial value of susceptibles so low, it is really hard for the infection to infect everyone. As β increases, the fraction of the population that becomes infected is higher.

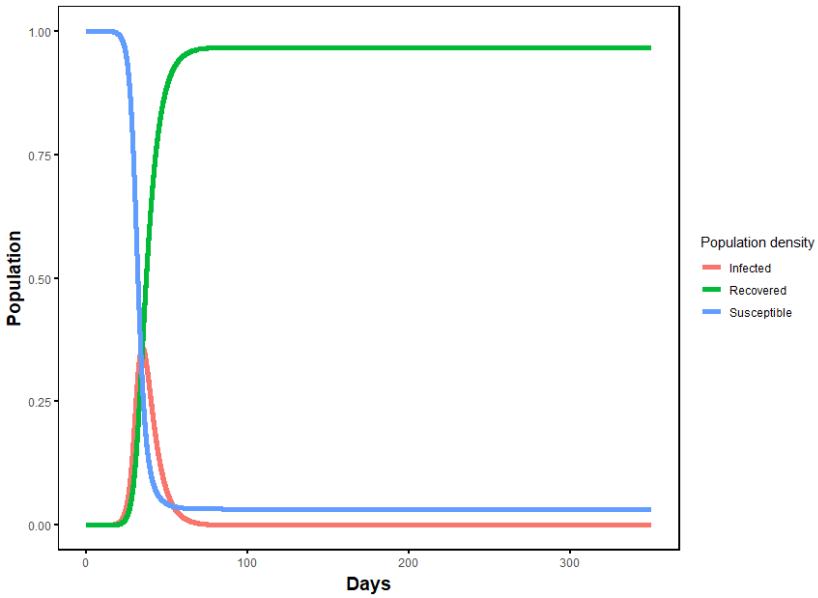

Figure 2

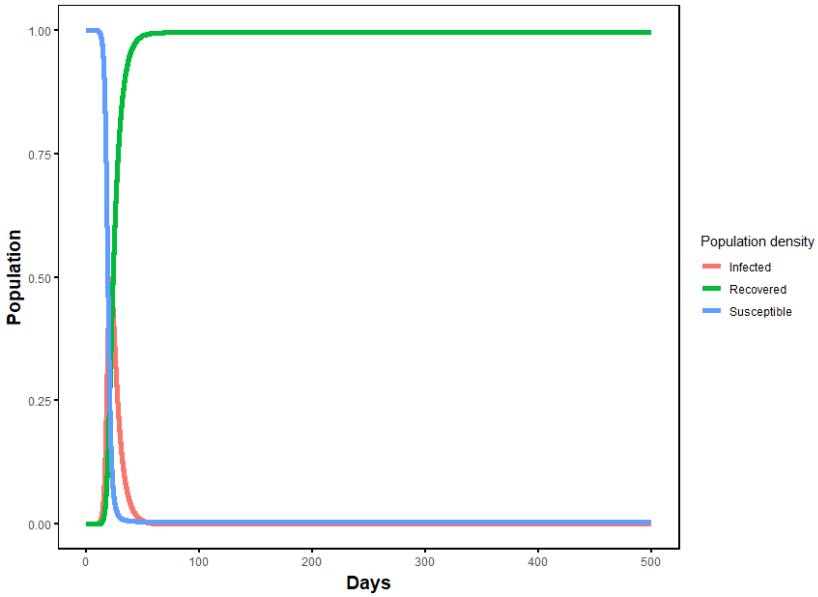

Figure 3

We can also set $\beta = 0'23$ again and change the recovery rate, to $\gamma = 0'05$ *(Figure 4*) and $\gamma = 0'01$ *(Figure 5*). This results in a greater total number of infected, since the infected individuals remain ill more time, having more chances to infect others. If we set the value of the recovery rate above the infection rate, the disease just dies out.

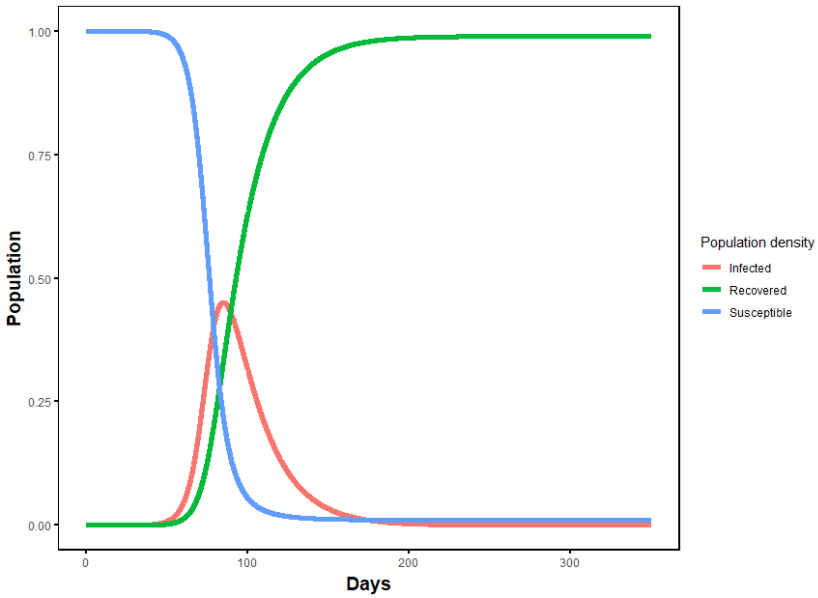

Figure 4

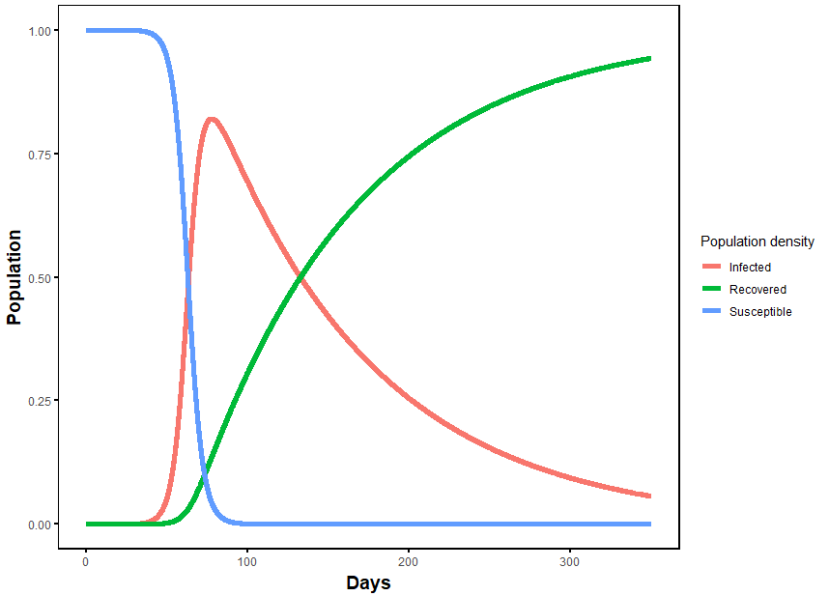

Figure 5

We have seen what happens when we increase β or γ. But what happens when we change both? If we plot the same conditions than in *Figure 5*, but dividing the infection and recovery rates, we get the result on *Figure 6*: the dynamics are exactly the same, but they double the time.

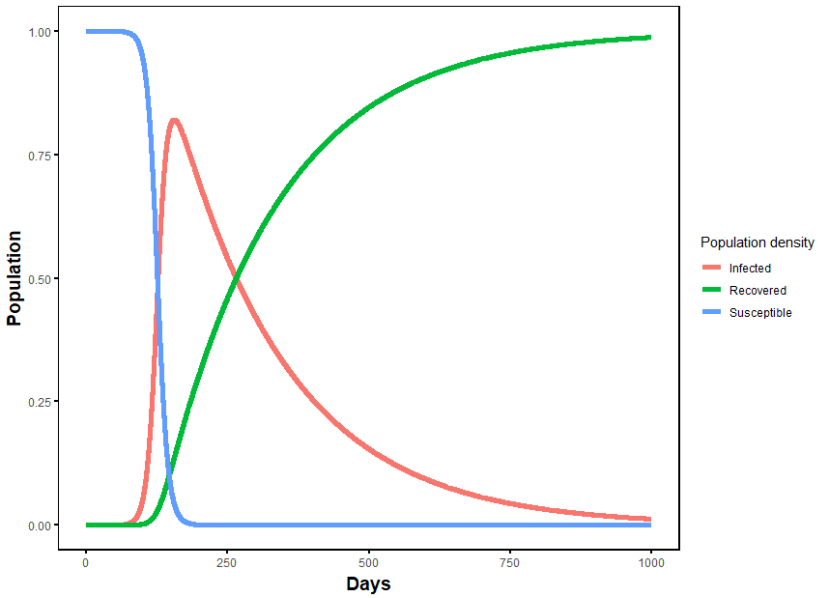

Figure 6

Now that we have checked how the rates affect the dynamics, we can change the initial conditions. For example, if we plot the dynamics of the same rates than in *Figure 5*, but set $S_0 = 0'5, I_0 = 0'5$, we get the results shown on *Figure 7*.

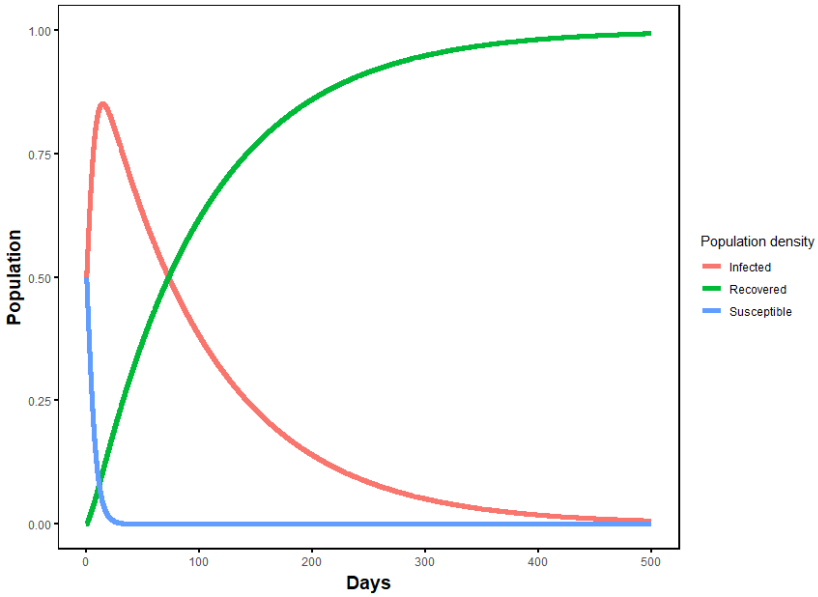

Figure 7

The result is really similar: all the population is infected and recovered. We can also try these initial conditions with the rates of *Figure 1*, which tends to the other stable solution (*Figure 8*). In this case, we do see changes in the dynamics of the population due to the different initial conditions.

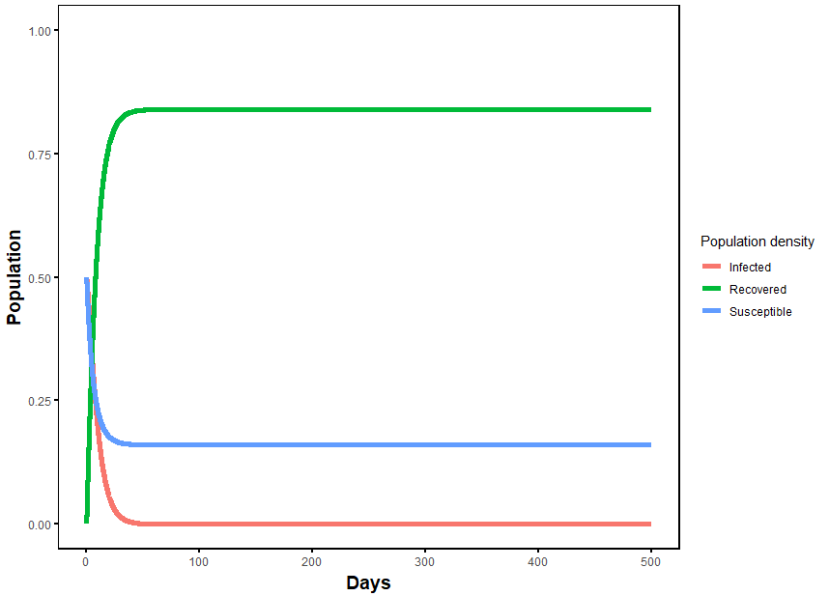

Figure 8

On *Figures 9, 10* and *11* are compared the different solutions depending on the initial conditions (S_0 ranges from 0'1 to 0'9) for the parameters $\beta = 0'23$, $\gamma = 0'17$ and $\beta = 0'23$, $\gamma = 0'01$. Under the first conditions, as we previously saw, the result depends on the initial conditions: the lowest the initial number of infected, the highest the final number of susceptibles. On the other side, under the second conditions, the result is always the same, with all individuals ending up recovered.

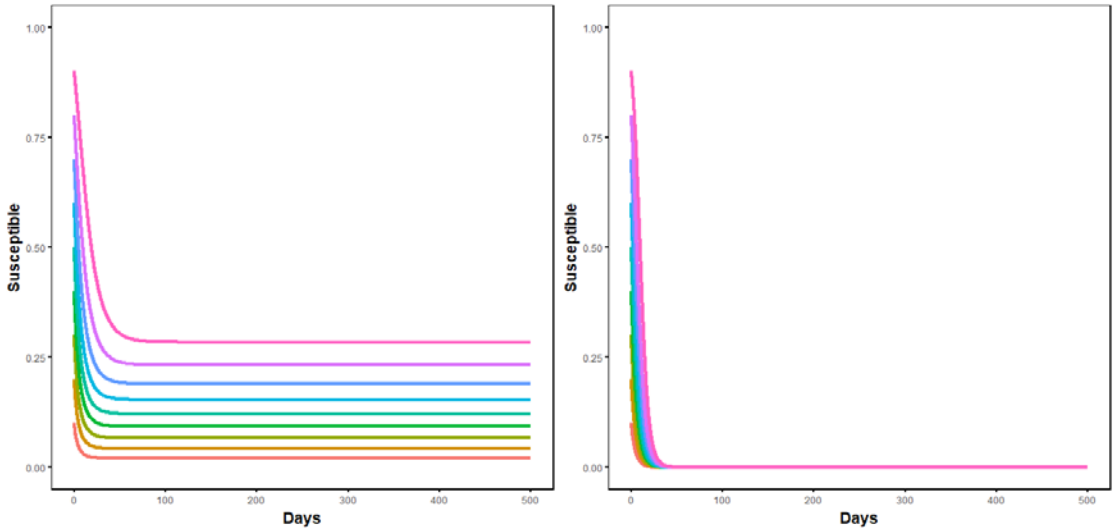

Figure 9

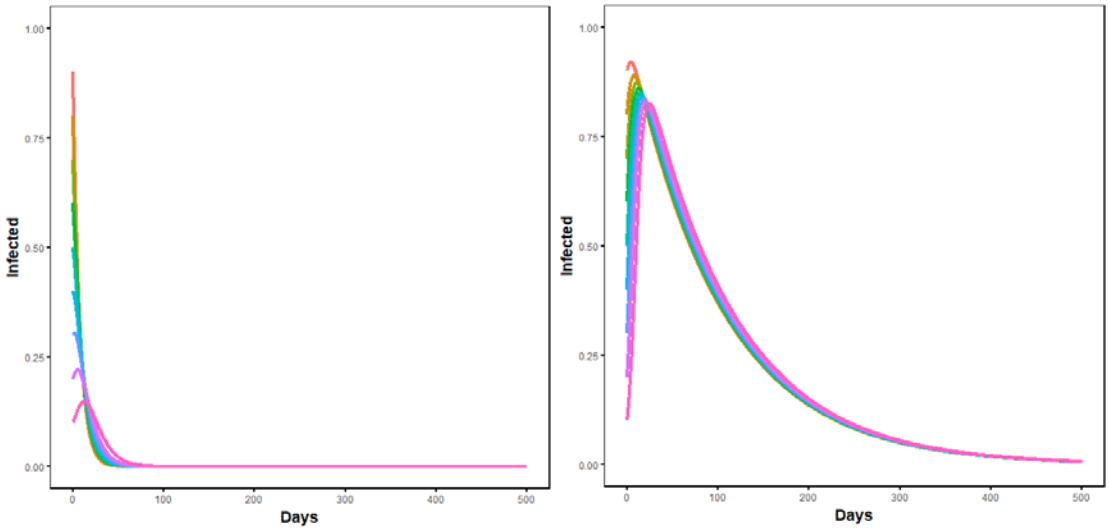

Figure 10

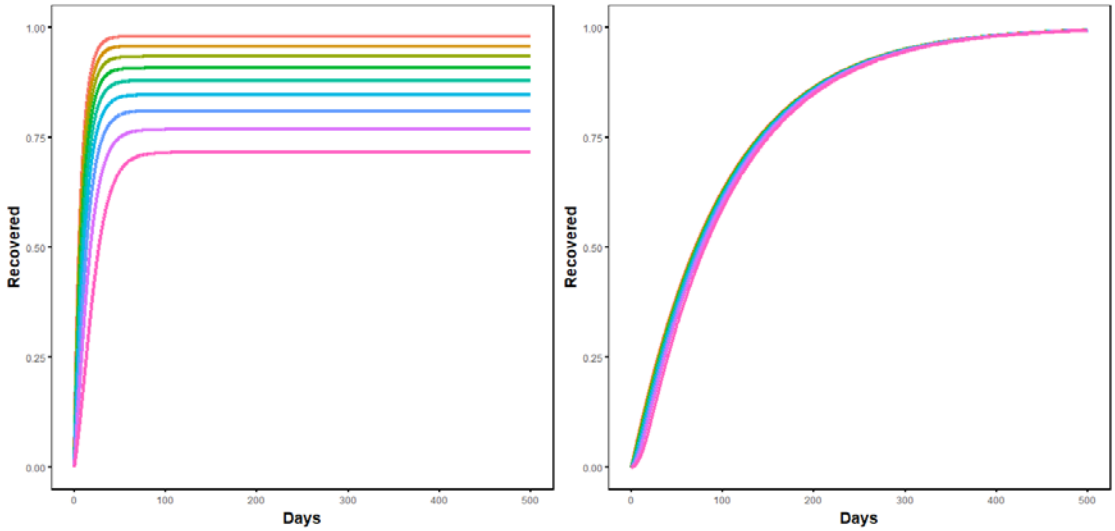

Figure 11