Final Project

Disease Spreading Simulations

SI1336: Simulations & Modeling

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1 Introduction and Background

Compartmental models in epidemiology are the mathematical frameworks for understanding the spread of infectious diseases from pathogens, infectious agents such as a virus or bacterium, onto healthy hosts. Such dynamic models are represented by sets of ordinary differential equations and constants corresponding to transition rates from one state to another. A population is classified into different states such as susceptible and infected groups. One of the most commonly known models is known as the SIR (**S**usceptible/**I**nfected/**R**ecovered with immunity) model.[1]

In this project, two variations of the SIR model will be studied: the epidemic and the endemic model. The epidemic version is used to model the rapid spread of disease. In reality, this model would be used to study outbreaks of diseases such as Ebola, Cholera etc. which spread in a short amount of time (less than one year). The endemic model is used for longer time periods in which vital dynamics, i.e. birth and death rates, needs to be taken into consideration.

1.1 Epidemic SIR

The epidemic SIR model takes into account three different population group states, which are susceptible, infected and recovered. The time derivatives, similar to the SIS equations, are given by the following equations [2]:

$$\frac{dS}{dt} = -\frac{\beta IS}{N} \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I \tag{2}$$

$$\frac{dR}{dT} = \gamma I \tag{3}$$

where β is the infective ratio and γ is the recovery ratio ($\beta, \gamma > 0$). Since the population in this model is static, the time-dependent quantities satisfy the relation:

$$S(t) + I(t) + R(t) = N$$

1.2 Endemic SIR

The endemic model, as stated before, takes into account a dynamic population with birth and death rates. It has the same differential equations however with an extra term given by:

$$\frac{dS}{dt} = \mu N - \mu S - \frac{\beta IS}{N} \tag{4}$$

$$\frac{dE}{dt} = \frac{\beta IS}{N} - \gamma I - \mu I \tag{5}$$

$$\frac{dI}{dt} = \gamma I - \mu R \tag{6}$$

where the constant μ is a life constant ($\mu > 0$). Based on the equations, the total population N has an birth rate of μN which is balanced by a death rate of μS, μI and μR. Therefore, the model satisfies the property that:

$$S(t) + E(t) + I(t) + R(t) = N$$

The deaths balance the amount of births and therefore the total population remains constant.

1.3 Recovery with Immunity/Vaccination

The R population group constantly grows. This means, that it will over time reach N as time progresses ($R \to N$ as $T \to \infty$.) Therefore, the recovery term can be thought of as also representing vaccination of susceptible individuals and the recovery of infected individuals through treatment. This is done for simplicity. It is also assumed that such an outbreak is rapidly controlled.

2 Method

There are several models which can be used for discretisation to solve the model numerically. However, the fourth-order Runge-Kutta method can provide a greater accuracy at the expense of very little extra computational power by calculating new iterations by taking averages over 4 data points. The model is dependent on three differential equations, so the Runge-Kutta routine will be applied for each equation. The fourth order Runge-Kutta method looks the following[3]:

$$k_1 = \mathbf{f}(t_n, y_n)h$$
$$k_2 = \mathbf{f}(t_n + \frac{h}{2}, y_n + \frac{k_1}{2})$$
$$k_3 = \mathbf{f}(t_n + \frac{h}{2}, y_n + \frac{k_2}{2})$$
$$k_4 = \mathbf{f}(t_n + \frac{h}{2}, y_n + k_3)$$
$$y_{n+1} = \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k4) + O(h^5)$$

The term h is known as the step size, which was kept to 1 because otherwise, the contributions per time step t, would be too small and a huge amount of iterations would have to be used in order to observe any good result. The Runge-Kutta method has an error term of $O(h^5)$ which makes it an attractive integrator to use [3].

2.1 SIR Initial Conditions

The rate of change of the susceptible population group is directly dependent on the number of infected individuals already present. Therefore, the infected population is non-zero. The initial recovery rate can also be non-zero, which means that there are already individuals in the total population immune to the disease. This will henceforth be known as the contact rate, denoted σ. Henceforth: $R_0 = R(t = 0) = \sigma$. The total population N used for the simulations was 1000.

3 Results

3.1 Epidemic SIR

This section illustrates the results obtained from various simulations of the epidemic SIR model in Figure 1, 2, 3 and 4. It can be seen that there is a sharp decrease in the Susceptible population group balanced by a sharp increase in the number of infected individuals. As discussed previously, the Recovered population group becomes equal to the total population as the whole population is treated for immunity to the disease ($R \to N$ as $T \to \infty$).

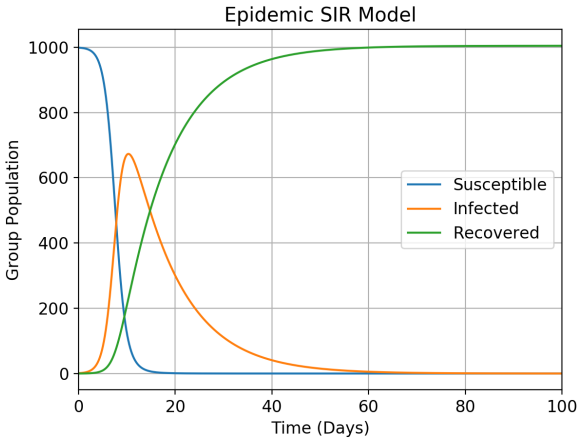

Figure 1: Epidemic SIR: $\beta = 0.01$, $\gamma = 0.001$.

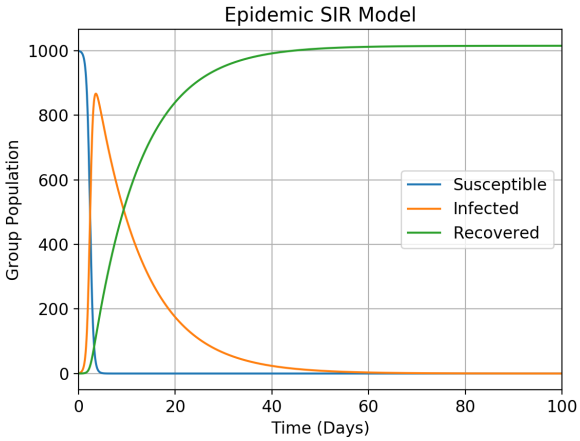

Figure 2: Epidemic SIR: $\beta = 0.03$, $\gamma = 0.001$.

Several tests have been performed with different values of the infective ration β and the recovery ratio γ. Figure 1 and 2 show that an increase in β results in a sharper rate of infection. After varying β, simulations were repeated for different values of γ and these are shown in Figure 3 and 4.

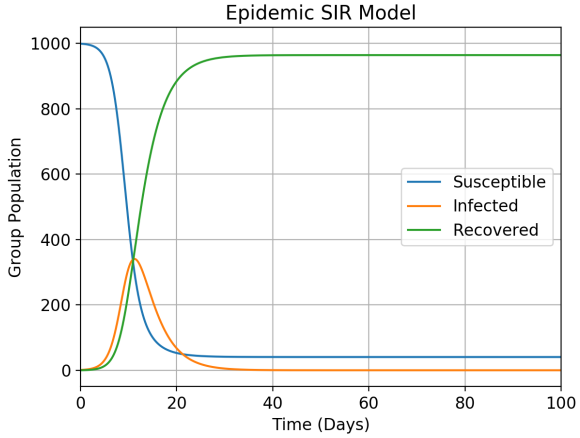

Figure 3: Epidemic SIR: $\beta = 0.01$, $\gamma = 0.003$.

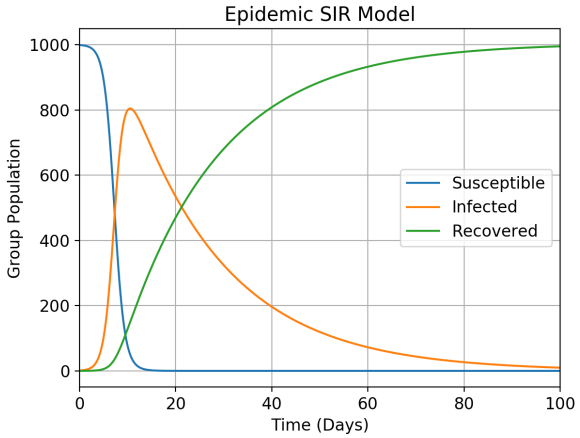

Figure 4: Epidemic SIR: $\beta = 0.01$, $\gamma = 0.0005$.

By increasing the recovery ratio from γ (from 0.001 to 0.003), the amount of infected individuals gains less prominence and an outbreak is more controlled. In figure 4, decreasing γ (from 0.001 to 0.0005), a larger fraction of the population N becomes infected and the recovery time is substantially longer.

3.1.1 Epidemic Phase Space

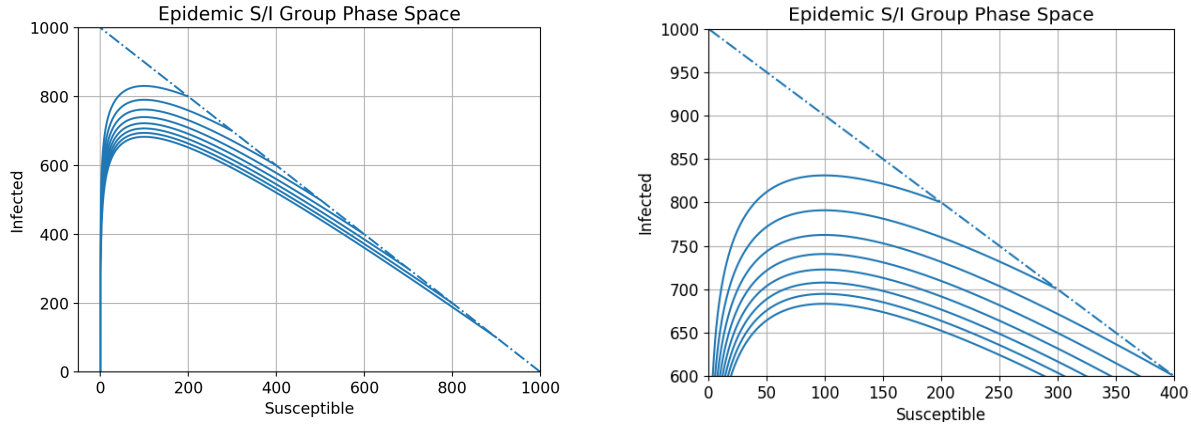

Figure 5: Phase space diagrams for the Epidemic SIR model. Model parameters: $\beta = 0.01$, $\gamma = 0.001$.

The phase space diagrams illustrates phase trajectories of different initial configurations for S and I population groups. The total population N was kept constant at 1000 and combinations such as $I_0 = 800$ and $S_0 = 800$ were used. The dotted line indicates the total population from which the trajectories originate. As time passes, the number of infected individuals increases and then the population rapidly recovers from the disease.

3.2 Endemic SIR

As discussed previously, the Endemic SIR model takes into account a dynamic population and a longer time span. An increase in population by newborns is balanced by an equal number of deaths in each population group. Therefore, a population variation is expected before the entire population becomes immune to the disease ($R \to N$ as $T \to \infty$). Two results are shown in Figure 5 and 6.

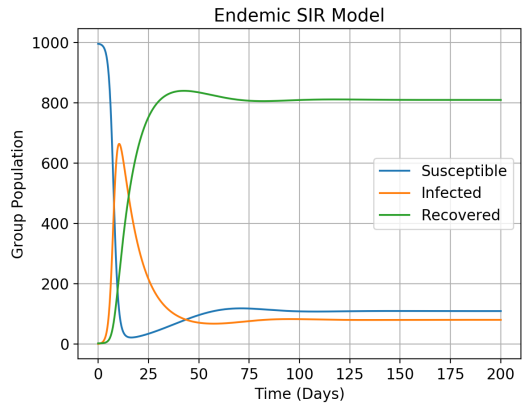

Figure 6: Endemic SIR: $\beta = 0.01$, $\gamma = 0.001$, $\mu = 0.0001$.

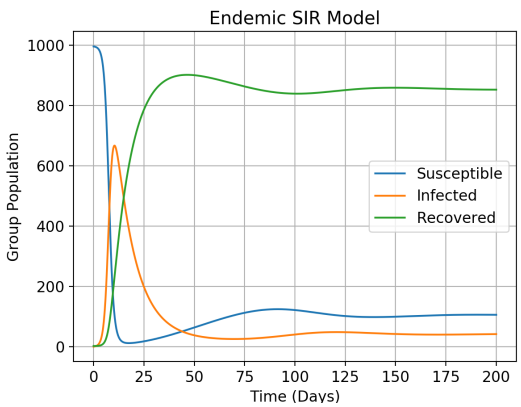

Figure 7: Endemic SIR: $\beta = 0.01$, $\gamma = 0.001$, $\mu = 0.00005$.

In Figure 5 and 6, the life constant μ was 0.0001 and 0.00005 respectively. In Figure 5, the effect of the birth/death is damped after only a short amount of time. Whereas in

Figure 6, where the life constant is half of that in Figure 5, the effect is more prominent. This can be explained by the fact that compared to the other constants β and γ, the μ in Figure 5 is much larger in comparison than the one in Figure 6.

3.2.1 Endemic Phase Space

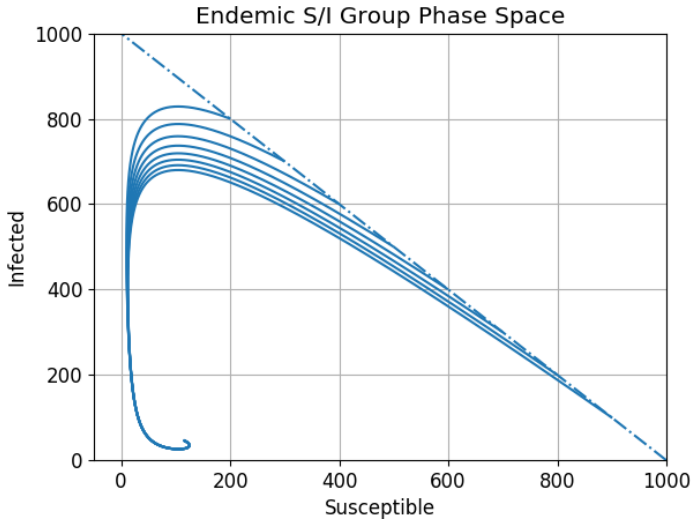

Figure 8: Phase Space Diagram for the Endemic SIR model. Model parameters: $\beta = 0.01$, $\gamma = 0.001$ and $\mu = 0.00005$.

Similarly as for the epidemic model, the phase initial conditions for S_0 and I_0 are shown in the phase plane. However, due to the birth and death rates in the population groups have a different effect as time progresses. The trajectories produce the shape of a curl.

4 Discussion

4.1 Phase Space Trajectories

The phase trajectories for the SIR model illustrate the evolution of the susceptible and infected population groups as the system evolves. The curve represents all the possible states that the system is in throughout its progression. The phase trajectories are determined by the initial conditions I_0 and S_0. An initial condition for the simulations shown have that $R_0 = 0$. The linear plot gives the total population N.

4.1.1 Epidemic SIR

The phase trajectory for the epidemic SIR model is shown that the infected and susceptible population groups tend towards zero, as the total population involved recovers with full immunity, thereby eradicating the disease. Hence, the results reflect the nature of the model: an epidemic outbreak of disease and a quick control and recovery.

4.1.2 Endemic SIR

The phase trajectory for the endemic variation of the SIR model is slightly different to that in the epidemic SIR model. It can be seen that the trajectories curl into a state in which neither of the populations tend towards zero as already observed in the epidemic model. This is known as the endemic equilibrium: a state in which there is no change in any population group. This is the direct result of the population dynamics. The birth rates into the susceptible group and the deaths from the infected and recovered groups lead to a continuous variation in each group.

4.2 Simulation Accuracy

In order to enforce the Runge-Kutta method's accuracy, it can be compared to an analytical solution. The analytical solution is a variation of the SIR model, known as the SIS model, lacking the R or recovered population group. The time derivatives are given by:

$$\frac{dS}{dt} = -\beta SI - \gamma S + \gamma \tag{7}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{8}$$

with the initial conditions $I(0) = I_0$, $S(0) = S_0$. The analytical solution is given by the equations [4]:

$$S(t) = 1 + (S_0 + I_0 - 1)(1 - \mu t) - \frac{\lambda}{\beta + \lambda \left(\frac{\lambda - i_0 \beta}{\lambda i_0 e^{\frac{\beta(s_0+i_0-1)}{\gamma}}} \right) e^{-\lambda t + \frac{\beta(s_0+i_0-1)}{\gamma}}} \tag{9}$$

$$I(t) = \frac{\lambda}{\beta + \lambda \left(\frac{\lambda - i_0 \beta}{\lambda i_0 e^{\frac{\beta(s_0+i_0-1)}{\gamma}}} \right) e^{-\lambda t + \frac{\beta(s_0+i_0-1)}{\gamma}}} \tag{10}$$

where $\lambda = \beta(s_0 + i_0) - \gamma$. The direct comparison between the analytic solution and the Runge-Kutta routine are shown below in Figure 9.

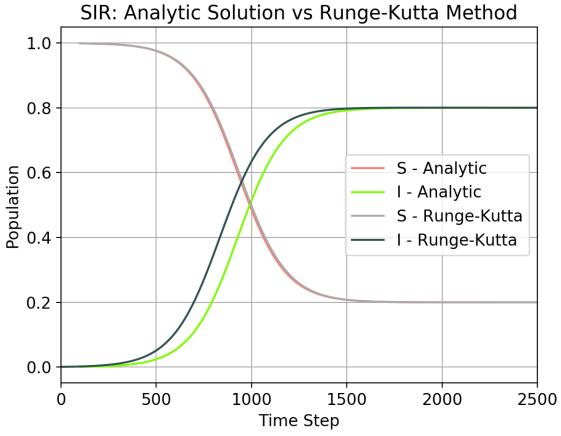

Figure 9: Analytic SIR solution vs. Runge-Kutta result with parameters $\beta = 0.01$ and $\gamma = 0.002$. *Note: No recovery term for this analytic solution.*

As time progresses, it can be seen that the Runge-Kutta method converges towards the analytic solution. Therefore it achieves the same result. However, the comparison for the Infected populations is different to the comparison of Susceptible populations. The Susceptible population curves are almost identical, so the Runge-Kutta method has proved useful. For the Infected population curves, the Runge-Kutta method prematurely starts increasing compared to the analytic solution. Since it converges to the analytic solution, it is a useful method, except for the premature increase.

The use of the recovery ratio γ may be the reason why this occurs. The analytic solution is found by using the variation of the SIR model in section 4.2 (equations 7 and 8) different to the one shown in section 1.1 (equations 1, 2 and 3). It can be seen that $\frac{dS}{dt}$ in eq. 7 has an extra contribution of the recovery factor γ, where there is no extra contribution in the $\frac{dI}{dt}$ derivative. This difference may cause the Runge-Kutta method to increase before the analytic solution.

4.3 Chaotic Behaviour

It can be argued that there is a degree of chaotic behaviour to the SIR model. As it could be seen in Figures 1, 2, 3 and 4, the change in the β and γ factors which was used was fairly large in comparison to the previous values used had a substantial effect on the S and I populations. However, a fractionally small increase/decrease in the factors does not have a substantial noticeable effect. Taking this into account, it can be said that the model does not have a chaotic nature.

5 Conclusion

It can be argued that the SIR model solved using the Runge-Kutta iteration routine is a method which yields good results, although there is a slight anomaly found compared to the analytic solution of the SIR model.

6 Bibliography

[1] https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology

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[3] Gould, Harvey, et al. "An introduction to computer simulation methods: applications to physical systems." Computers in Physics 10.4 (1996): 349-349.

[4] Shabbir, G., H. Khan, and M. A. Sadiq. "A note on Exact solution of SIR and SIS epidemic models." arXiv preprint arXiv:1012.5035 (2010). [5]