uOttawa General Engineering (GNG)

GNG1106 - Lab 10

Objectives

1. Understand differential equations and difference equations
2. Programmatically solve differential equations using Euler's method (i.e., difference equations)
3. Programmatically solve complex equations by bisection search for the solution
4. Practise ASCII file I/O and data plotting, and integrate all learned knowledge in a programming task
5. Learn to break down a programming task into sub-tasks and modules and learn to design code with well structured modules and clean interfaces between the modules.
6. Investigate and learn the spread dynamics of infectious diseases and the role of social distancing

Introduction

The spread of infectious diseases, such as Covid 19, is usually described by a set of differential equations, known as epidemiology models. In this lab, we will investigate, via programming, the dynamics of infectious diseases under a basic epidemiology model, called the SIR model. Although this model is rather simplified, it should give you a good idea how Covid 19 had spread.

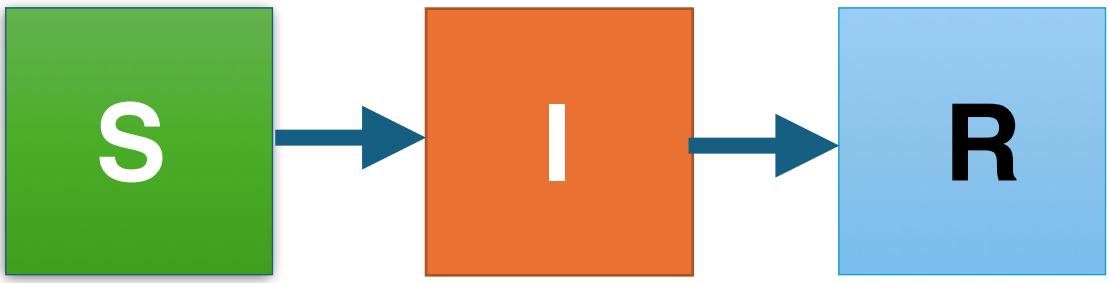

Figure 1

In the SIR model, a population of N people at each time instant is divided into three groups, Group S (Susceptible Group), Group I (Infected Group) and Group R (Recovered Group). The people in Group S are those who are susceptible to the disease and may potentially get infected. The people in Group I are those who are currently infected. The people in Group R are those who were infected and have recovered or died. Note that such a division is not geographic; in fact, on the contrary, a key assumption in this model is that the population is mixed homogeneously (or "uniformly"), namely, every two persons in the population, say A and B, has the same probability to get in contact as any other two persons, say C and D. Further under this model, people in Group S can leave their group and join Group I (namely, getting infected), and people in Group I can leave their group and join Group R (namely, having recovered or died), but people in Group R will stay in Group R forever (that is, these people are no longer susceptible and won't get infected again). Figure 1 shows the possible transitions between the three groups. No other transitions are allowed in the SIR model.

We now give the differential equations of the SIR model, describing the transition dynamics between the three groups. At each time instant t, we will denote by S_t, I_t, and R_t the number of people in Group S, the number of people in Group I, and the number of people in Group R respectively. The SIR model is parameterized by two positive parameters β and γ and is described by the following differential equations:

$$\frac{dS_t}{dt} = -\beta I_t S_t / N \qquad (1)$$

$$\frac{dI_t}{dt} = \beta I_t S_t / N - \gamma I_t \qquad (2)$$

$$\frac{dR_t}{dt} = \gamma I_t \qquad (3)$$

Now if we consider time t to be discrete, in unit of days, the differential equations become the following "difference equations" (in a way similar to the Euler's method):

$$S_{t+1} - S_t = -\beta I_t S_t / N \qquad (4)$$

$$I_{t+1} - I_t = \beta I_t S_t / N - \gamma I_t \qquad (5)$$

$$R_{t+1} - R_t = \gamma I_t \qquad (6)$$

where $t = 0,1,2,...$

In this lab, we will work with Equations (4), (5), and (6) and investigate the dynamics of disease spread under the SIR model. Now we explain the meaning of the parameters β and γ (when time t is in unit of days) and Equations (4), (5), and (6).

The parameter β is the average number of people that every infected person meets (with adequate contact so that the disease will be transmitted by the next day if the person met is susceptible) each day. Since on Day t there are S_t suspected people, the probability that a person he meets is susceptible is S_t/N. Thus each infected person will turn $\beta S_t/N$ people from susceptible to infected by the next day. Because there are I_t infected people on Day t, in total they will turn $\beta I_t S_t/N$ people from susceptible to infected by the next day. Thus the number of susceptible people on Day $t+1$ will be reduced by $\beta I_t S_t/N$, giving rise to Equation (4).

The parameter γ represents the probability that an infected person recovers or dies on each day. Since there are I_t infected people on Day t, on average γI_t people will leave Group I and join Group R. This gives Equation (6).

Based on Equation (4) and (6), by Day $t+1$, $\beta I_t S_t/N$ people join Group I (from Group S) and γI_t people leave Group I and join Group R. Then the net increase of the number of people in Group I on Day $t+1$ is $\beta I_t S_t/N - \gamma I_t$. This gives Equation (5).

Clearly, using Equations (4), (5) and (6) and given the values of β and γ, we will be able to compute the number of people in each group on Day $t+1$ from those numbers on the previous day, Day t.

Note that the parameter γ is related to the nature of the disease and the current art or standard practice of its treatment. As such, γ is difficult to control. On the other hand, the parameter β can be controlled more easily by social distancing or similar measures.

References

Herbert W. Hethcote, *The mathematics of infectious diseases*, SIAM Reviews, Vol 42, No. 4, pp 599-653, Dec, 2000.

Instructions

Consider a city with population $N = 1000000$ (this is about the population of Ottawa). Consider that an infectious disease is about to spread in the city, and on Day 0, there are 200 people infected and all other people are susceptible. Assuming there are in total 2500 beds in all hospitals across the city (25 beds per 10,000 population closely reflects the situation in Canada; see https://www.who.int/data/gho/data/indicators/indicator-details/GHO/hospital-beds-(per-10-000-population)) Assume that there is another parameter θ associated with the disease, which indicates the fraction of people infected by the disease will need to stay in a hospital (and each occupy one bed). For example, if $\theta = 0.1$, then 10% of the infected people will need to be hospitalized. In this lab, you will need to investigate the dynamics of the disease in relation to β and γ over an adequate period of time, and determine how it may impact the hospital systems for a given hospitalization rate θ.

You need to write a program that interacts with the user and performs three tasks. Thus your program has three modes.

1. **Mode 1**: generate disease spread data for plotting. In this mode, the program

    1. asks the user to enter values for β, and γ, and a file name,

    2. computes the values for S_t, I_t, and R_t, for $t = 1,2,....$ Although these values are integers, you should use **`float`** or **`double`** type for them. You need to compute the S, I, R values for an adequate period of time until each of the three values becomes stable, namely, no longer changing with time. Here you may define "no longer changing with time" as that the absolute difference between two consecutive values (e.g., I_t and I_{t+1}) is less than 0.1.

    3. save the computed data as a CSV file with the entered file name so that it can be plotted. (After running this mode, you should plot the data outside the program; see Figure 2 for an example plot).

2. **Mode 2**: determine the impact of the disease on hospitals. In this mode, the program

    1. asks the user to enter values for β, γ, and θ, and

    2. prints a message concerning if the spread of the disease will exceed the capacity of the hospitals (namely, if the number of people requiring hospitalization on any day is higher than the total number of beds in the hospitals until the spread dynamics becomes stable).

3. **Mode 3**: obtain information for social distancing plans. In this mode, the program

    1. asks the user to enter values for γ and θ, and

    2. prints the value β^*, which is largest value of β for which the spread of the disease will not exceed the capacity of the hospitals (for the entered value of γ and θ). Note that solving for β^* boils down to solving an equation equating the peak value of the I_t plot to $\frac{2500}{\theta}$. You must implement a bi-section search algorithm to find β^*. Your estimate $\widehat{\beta}$ of β^* must satisfy $0 \leq \beta^* - \widehat{\beta} \leq 0.005$.

When the program runs, it shows a main menu allowing the user to select any one of the three modes or to exit the program. After the user selects one of the three modes, the program prompts the user to enter the required information and performs the corresponding task as described above. Upon finishing the task, the program returns to the main menu. The program will only exit when the user selects the exit option from the main menu.

Your code needs to be well modularized and you are free to create and implement any function. Your code must be easily readable. Functions and variables should be carefully named for readability. Adequate comments should be provided to explain your design and logic.

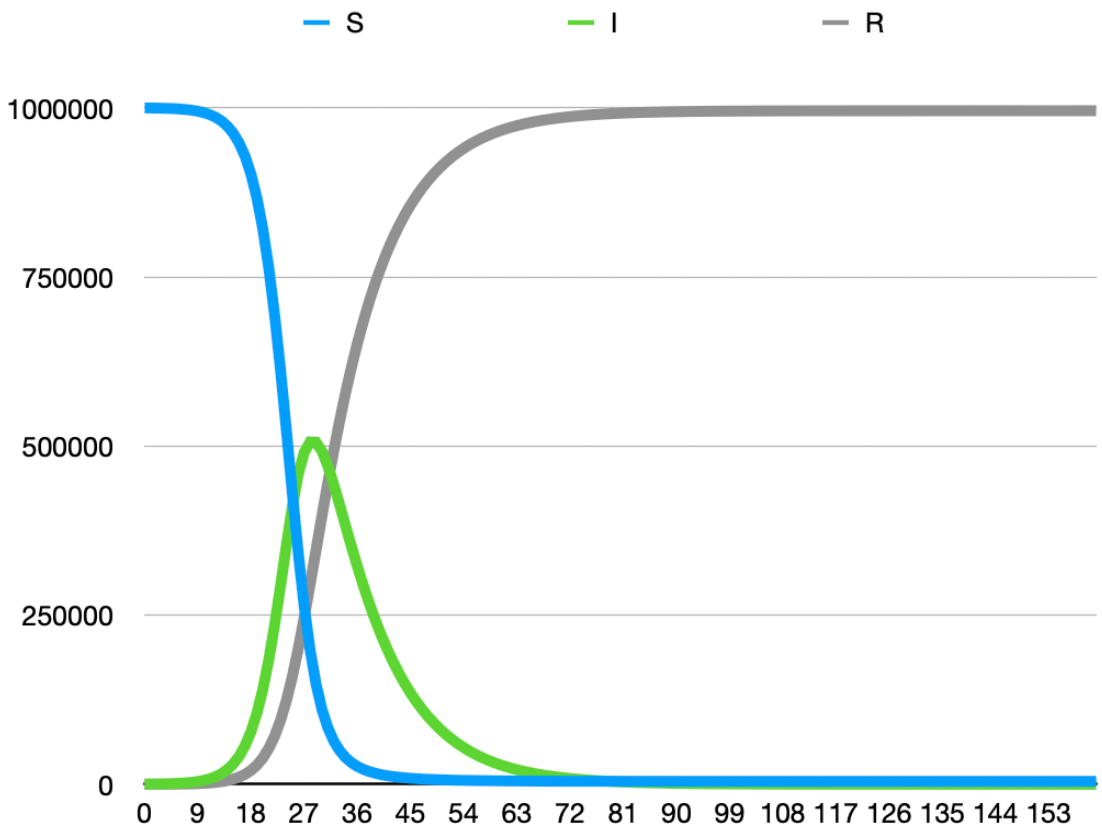

Figure 2

Deliverables

Pre-Lab Submission (20%): Ensure you have submitted your pre-lab before attending the lab session.

In-Lab Deliverable 1 (80%):

- (10%) Correct execution of main menu.
- (30%) Correct plots for 6 test cases of Mode 1, three of which are given below.
    - $\beta = 0.3, \gamma = 0.1$
    - $\beta = 0.7, \gamma = 0.1$
    - $\beta = 0.15, \gamma = 0.1$
- (10%) Correct results for 5 test cases of Mode 2, three of which are given below.
    - $\beta = 0.7, \gamma = 0.1, \theta = 0.1$

    - $\beta = 0.4, \gamma = 0.1, \theta = 0.1$
    - $\beta = 0.12, \gamma = 0.1, \theta = 0.1$
- (25%) Correct results for 5 test cases of Mode 3, two of which are given below.
    - $\gamma = 0.3, \theta = 0.1$
    - $\gamma = 0.2, \theta = 0.05$
- (5%) Understanding
    - the dynamics of disease spread in the SIR model, particularly how it depends on β and γ,
    - the impact of infectious disease on hospital systems and the role of social distancing, and
    - the role of programming in this investigation

Submit the completed code. When you check out, you need to show your TA the running of your program and execution results of the test cases the TA asks for. You will need to answer the questions the TA asks to demonstrated your understanding.

Check out and Submission

You must check out with your TA before submitting the deliverables. During the check out, your TA may inspect your work and to-be-submitted deliverables, and ask you questions to further check your understanding. At the end of the check out, your TA will give you an initial mark for the in-lab component of this lab and let you know. You must then submit the deliverables before the due time of this lab. While this initial mark is likely to be the final, your TA reserves the right to reduce this initial mark after checking more carefully the deliverables you submit

Code Grading Criterion

- **Correctness (80%):** Correct syntax, logic and execution. Decent efficiency (in terms of running time and memory consumption).
- **Style (20%):** Proper structure and modularization of the code, descriptive naming of functions and variables, properly designed prototype, appropriate indentation, adequate comments, and ease of reading.