EE386 Digital Signal Processing Lab **Jul-Dec 2021**

Lab Report - 5

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Note:
The value of α used in this document is given by: $\alpha = 1 + \text{mod}(160; 3) = 2$

Problem 1. (First-Order Model)

The propagation mechanism of an epidemic, such as the one caused by the SARS-CoV-2 virus, can be modelled, at least in its initial phase, as a process in which each infected individual will eventually transmit the disease to an average of R0 healthy people; these newly infected patients will, in turn, infect R0 healthy individuals each, and so on, creating a pernicious positive feedback in the system. The constant R0 is called the basic reproduction number for a virus. In signal processing terms, the infection mechanism is equivalent to a first-order recursive filter. Assume that each infected person spreads the virus over a single day and then recovers and assume that an initial patient zero appears at day n = 0. The number of newly infected people per day is described by the difference equation

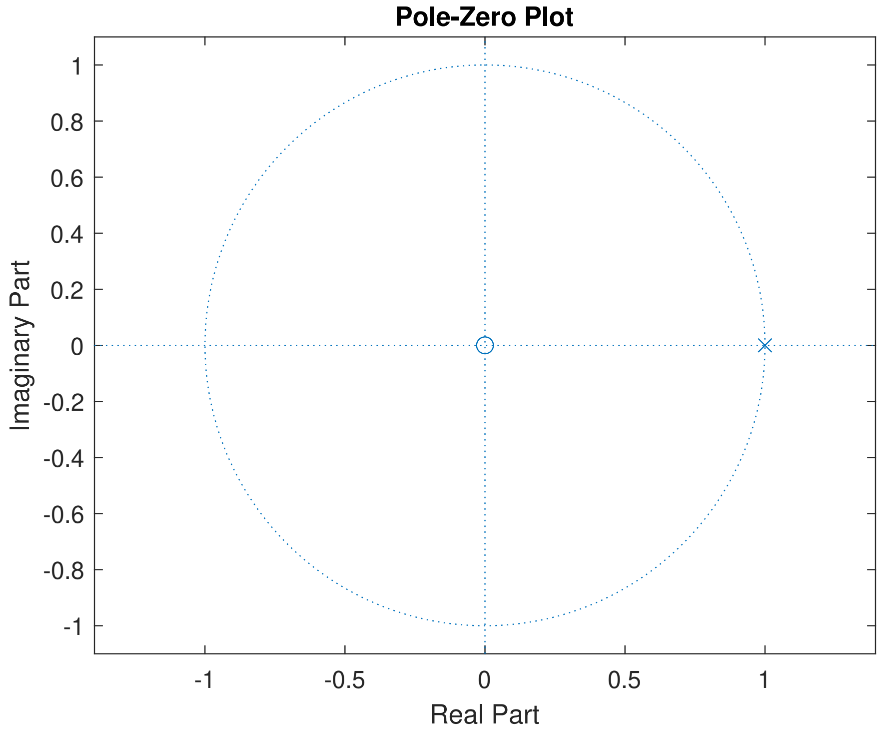
$$y[n] = \delta[n] + R_0\, y[n - 1]$$

(1. What is the transfer function H1(z) of the above system? Plot the pole-zero plot of the system.)

(Solution) The transfer function of the model is as follows,

$$H(z) = \frac{z}{z - R_0} \tag{0.1}$$

The pole-zero plot for $R_0 = 1$ is as follows,



(2. Solve the difference equation and give the time-domain equation for the number of newly infected people. Note that this depends on the parameter R0. Comment on the effect of the parameter R0. Can this be inferred from the pole-zero plot?.)
(Solution) After solving the difference equation we get the solution as -

$$y(n) = \delta(n) \tag{0.2}$$

When $\mathrm{R}_0 = 0$

$$y(n) = R_0^n \tag{0.3}$$

When $\mathrm{R}_0 \neq 0$

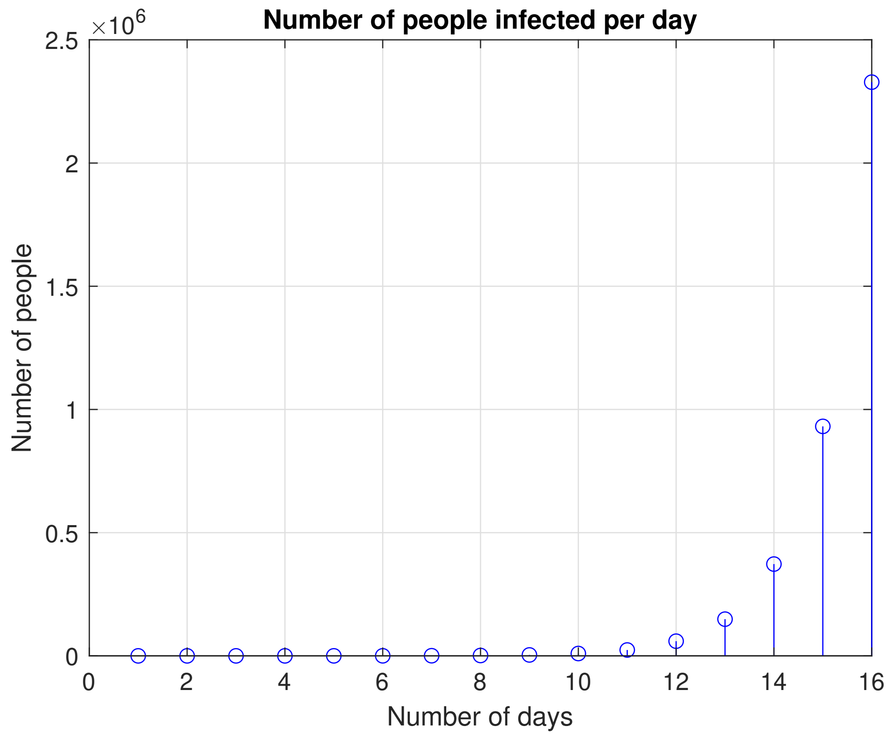
The stability of the system is influenced by R_0, which can be readily deduced from the pole-zero diagram. Since R_0 functions as a pole, it must reside within the unit circle in the Pole-Zero plot for the system to maintain stability.

(3.Suppose R_0 = 2.5, how many days will it take to reach 1 million new daily

infections?) When $R_0 = 2.5$, the solution for this equation is,

$$y(n) = (5/2)^n \tag{0.4}$$

For the number of infections to reach 1 million, y(n) $\geq 10^6$.
Therefore, n = 16 This is verified from the graph plotted for value $R_0 = 2.5$,



(4 :Using a similar one-point trick, and the data available from Covid-19 in India, estimate the value of R_0 in the initial phase of the first wave of infections in India)

This is the data on the newly infected individuals in India during the initial fifty days of the COVID-19 outbreak using the website https://www.covid19india.org/.

Y = [2, 4, 5, 6, 10, 19, 65, 78, 114, 137, 140, 144, 173, 204, 225, 245, 254, 287, 307, 341, 368, 373, 387, 404, 423, 460, 506, 571, 596, 614, 658, 688, 755, 807, 835, 855, 1007, 1143, 1245, 1391, 1607, 1806, 1907, 2111, 2191, 2340, 2528, 2710, 2772, 2865]

To find $R_0(n)$,

$$R_0(n) = \frac{y(n) - \delta(n)}{y(n-1)} \tag{0.5}$$

The average value of R_0 calculated from the above data is,
R_0= 1.17

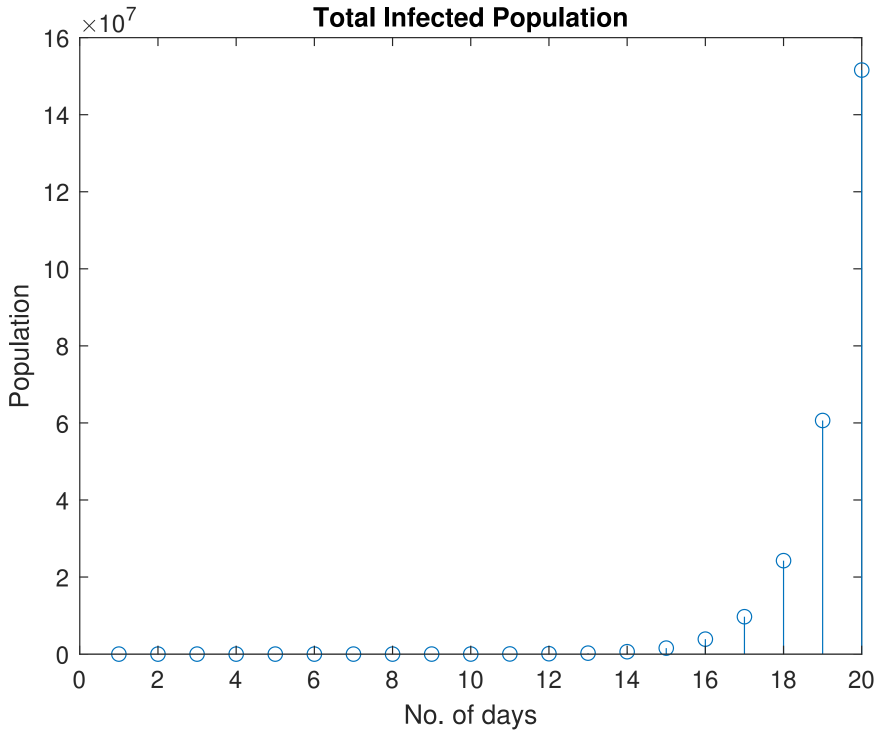
(5.With R_0 = 2.5, plot the new daily infections for the first n = 20 days. Design an integrator filter. Use this filter to obtain the total number of infections for the

first n = 20 days)

(Solution) Transfer function of an integrator filter is as follows,

$$H(z) = \frac{1}{1 - (1/z)} \tag{0.6}$$

By using this filter, we get the following plot for total number of people infected after n=20 days,



2. Increasing the Complexity

The transfer function for the model is as follows,

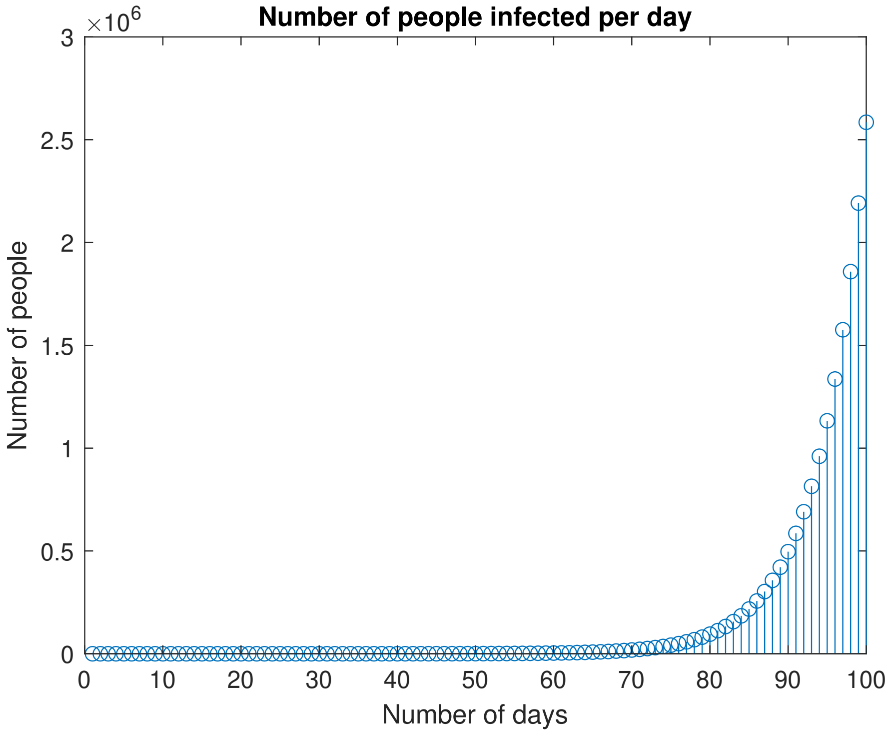
$$H(z) = \frac{1}{1 - \sum_{k=1}^{M} a_k z^{-n}}, M = 12 \tag{0.7}$$

$$a_k = [.1, .15, .25, .26, .34, .42, .25, .2, .15, .1, .1, .1.] \tag{0.8}$$

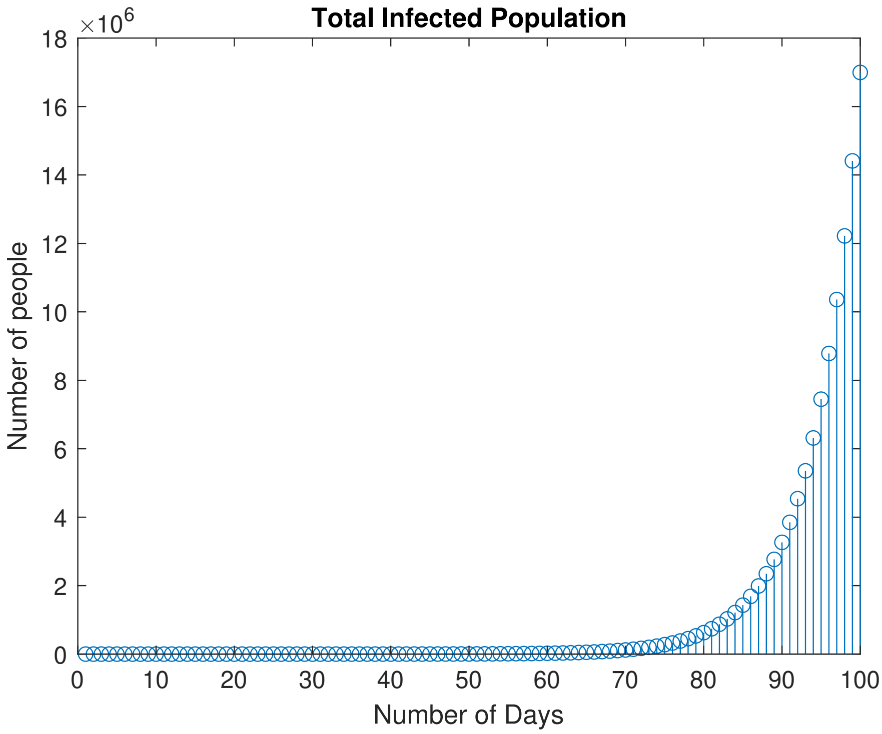
(1.Plot the new daily infections for the first n = 100 days by implementing the filter given in Equation 1.8 with the Kronecker delta as the input. Use an integrator filter to obtain the total number of infections for n = 100 days.)

(Solution)

After graphing the new daily infections for the initial n = 100 days by applying the mentioned filter and using the Kronecker delta as input, the obtained results were -



After using an integrator filter, we get the total infection as the follows,



(2.Comment on the differences between the trends that are obtained with the first-order model. How many days will it take to reach 1 million new daily infections?)
(Solution)

To figure out how long it would take to hit 1 million new daily infections, I looked at a graph and did some math. Both methods gave me the same answer: 95 days. On day 94, we had about 960,580 infections, and by day 95, it reached 1,132,900. So, I concluded it takes 95 days to get to 1 million new daily infections.

Comparing it to the First-Order method, this method's slope isn't as steep, showing a slower increase in infections. Also, it takes a bit longer to hit 1 million infections per day compared to the First-Order method.

(3.Bonus: Comment on a reliable technique to estimate the coefficients $(a_k)_{(k=1)}^{M}$)

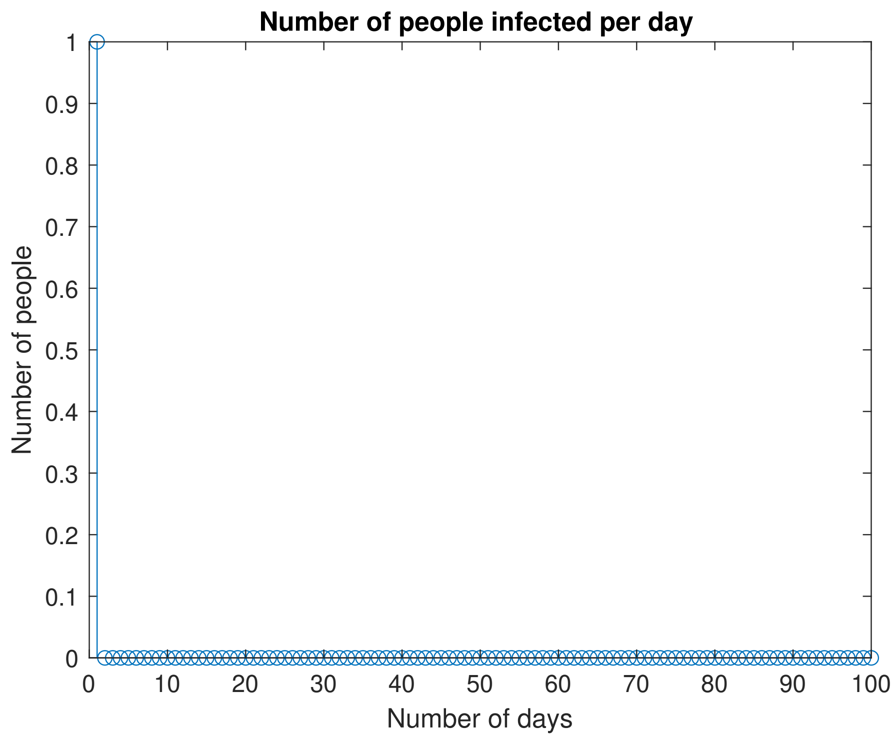
(Solution) In the provided figure in the question, the values of $(a_k)_{(k=1)}^{M}$ represent the number of contagions per day on a specific day, where k indicates the day number, and M equals 12.

Social Distancing The transfer function for the model is as follows,

$$H(z) = \frac{1}{1 - (1-\rho)\sum_{k=1}^{M} a_k z^{-n}}, M = 12 \tag{0.9}$$

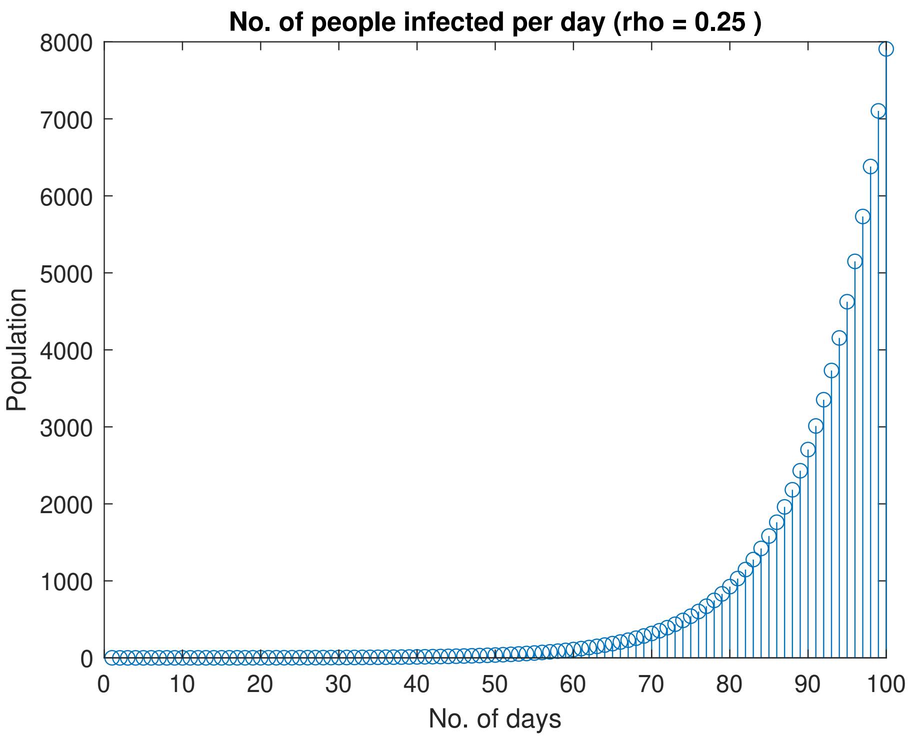
(1.Comment on the role of ρ. What does $\rho = 1$ indicate?)
(Solution) Here, ρ is like a measure showing how social distancing impacts the number of people affected by the coronavirus. When ρ is high, it indicates good social distancing, and if it's low, it means poor social distancing. For instance, when $\rho = 1$, it signifies 100 percent effective social distancing, resulting in only one case on Day 1. This aligns with the outcome obtained from plotting the data.

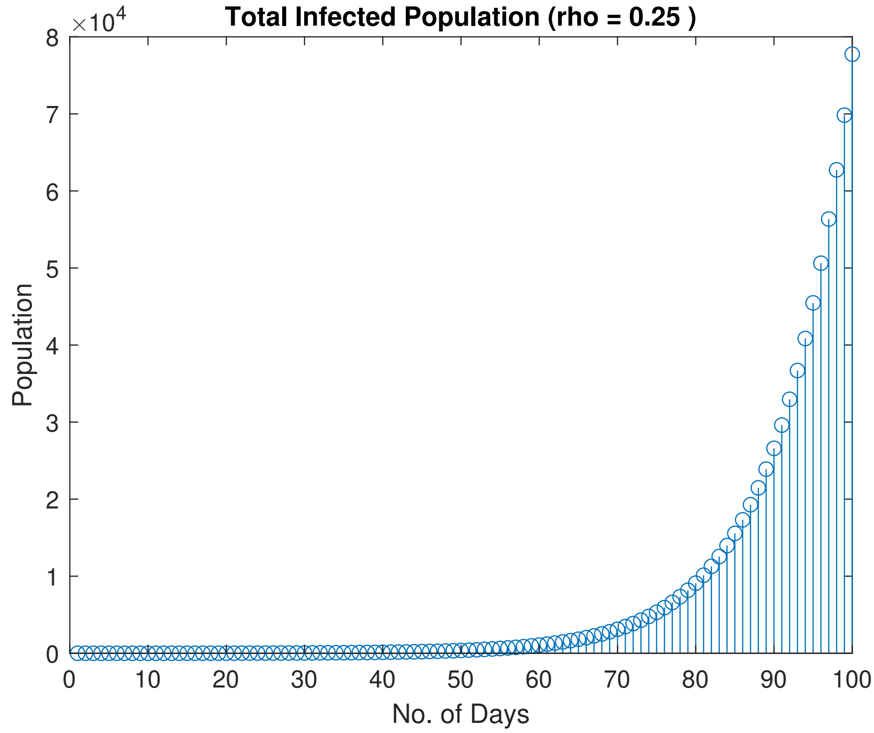
Now, if we consider $\rho = 1$, here's what the graph looks like:

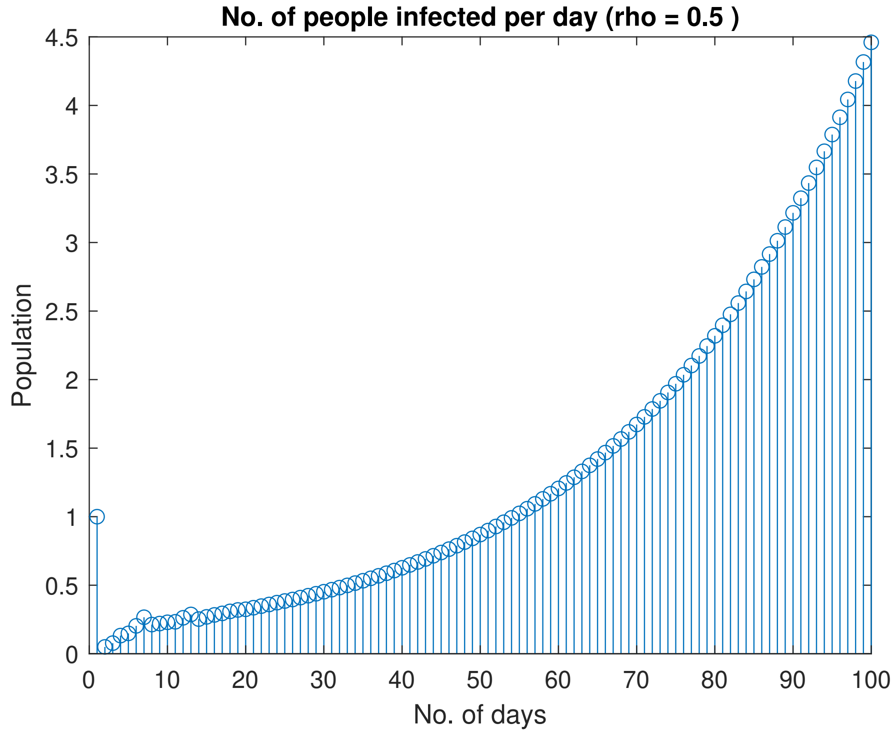


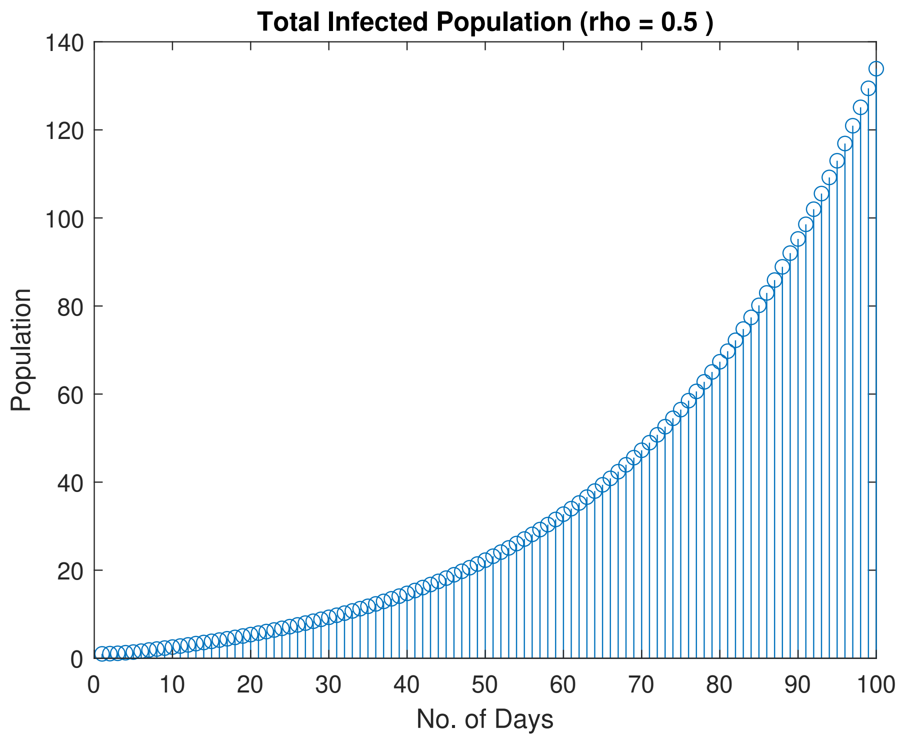
(2.Plot the new daily infections for the first n = 100 days by implementing the filter given in Equation 3.1 with the Kronecker delta as the input for ρ = 0.25, 0.50, 0.75 Use an integrator filter to obtain the total number of infections for n = 100 days)

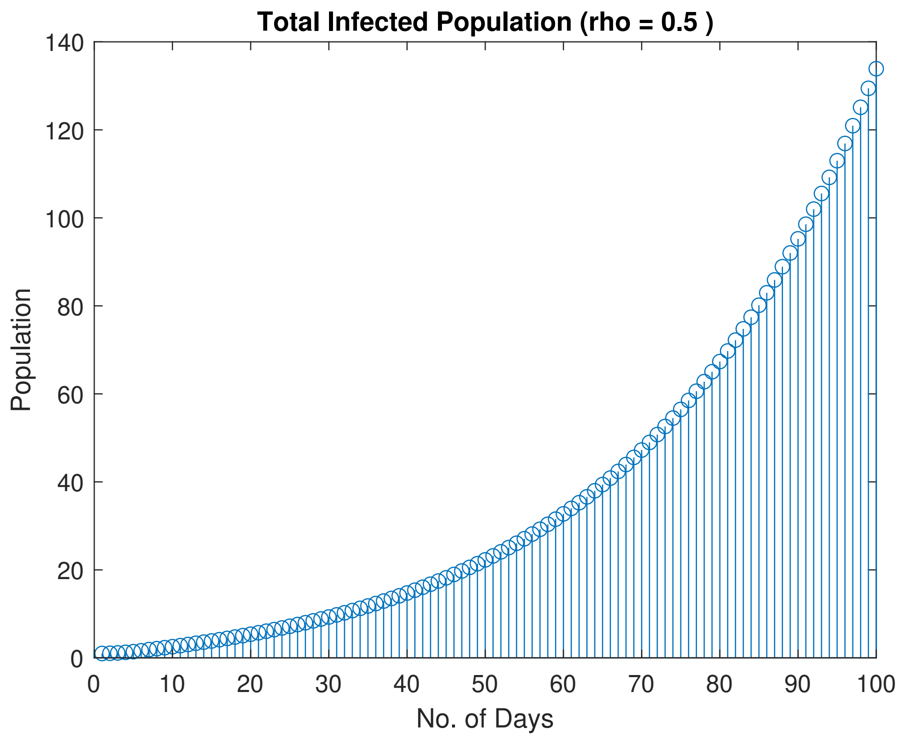
(Solution) For $\rho = 0.25$,$\rho = 0.5$ and $\rho = 0.75$, we get the following plot for number of people infected per day and cumulative infections

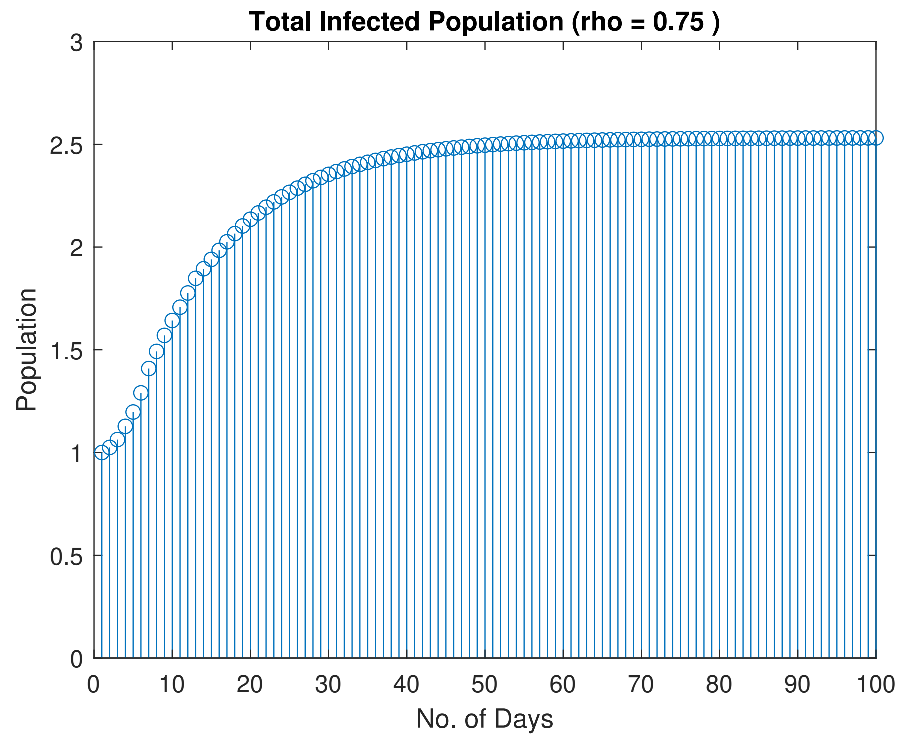

No. of people infected per day (rho = 0.25)
Population
No. of days
0
1000
2000
3000
4000
5000
6000
7000
8000
0
10
20
30
40
50
60
70
80
90
100


Total Infected Population (rho = 0.25)
×10^4
Population
No. of Days
0
1
2
3
4
5
6
7
8
0
10
20
30
40
50
60
70
80
90
100


No. of people infected per day (rho = 0.5)
Population
No. of days
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
0
10
20
30
40
50
60
70
80
90
100


Total Infected Population (rho = 0.5)
Population
No. of Days
0
20
40
60
80
100
120
140
0
10
20
30
40
50
60
70
80
90
100



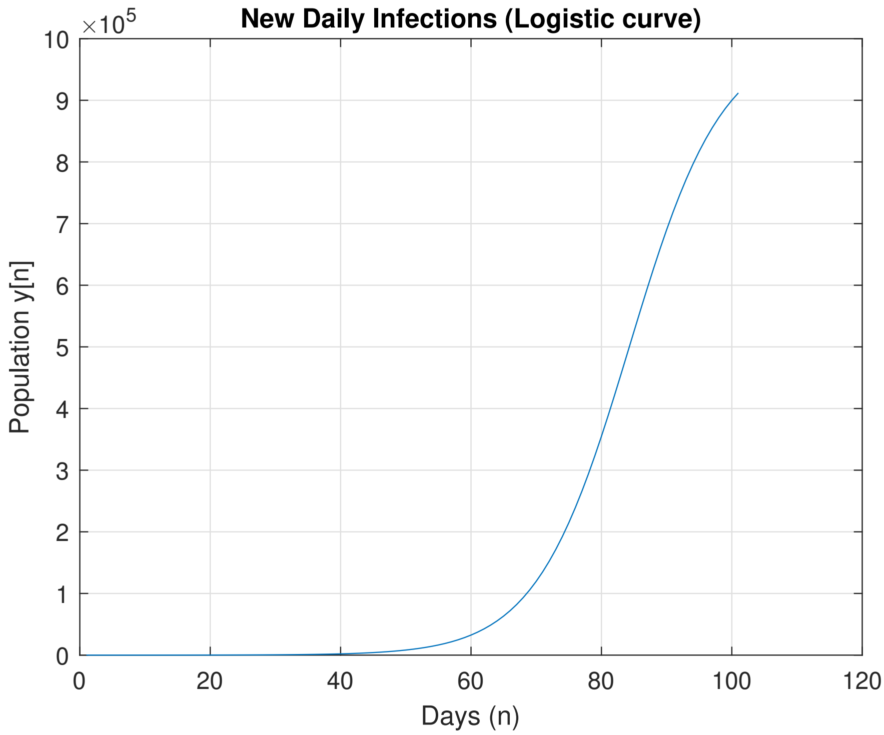


The total number of infected people for $\rho = 0.25$,$\rho = 0.5$ and $\rho = 0.75$ after of 100 days is 7.7745e+04, 133.8987 and 2.5310 respectively.

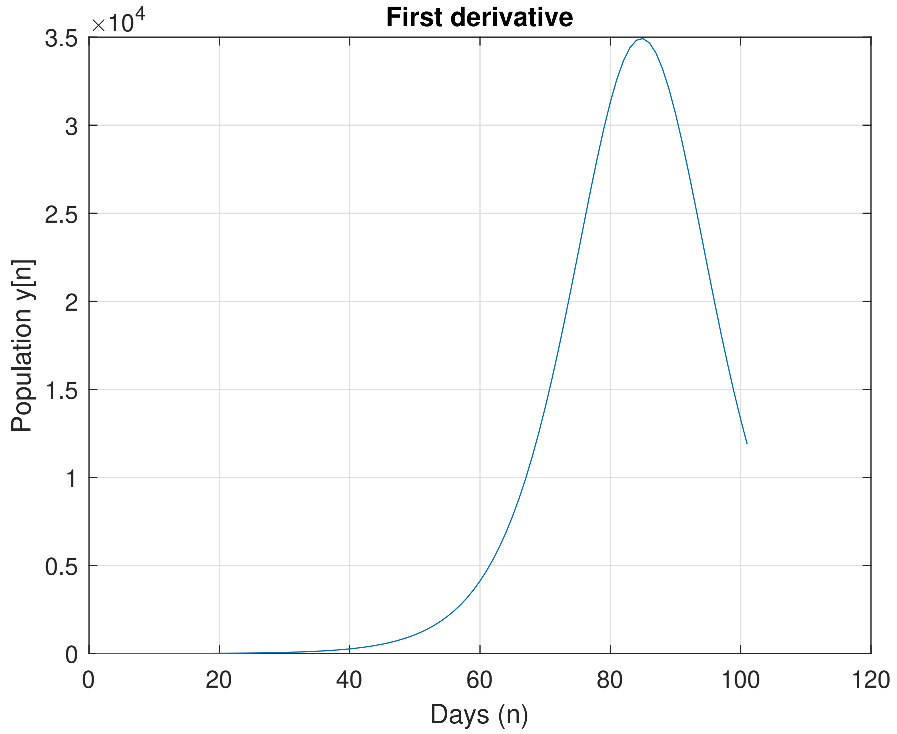
Saturation and Towards Normality The cumulative number of infections, x(n),

$$x(n) = \frac{K}{1 + [K(R_0 - 1) + R_0]R_0^{-(n+1}} - \frac{1}{R_0 - 1} \tag{0.10}$$

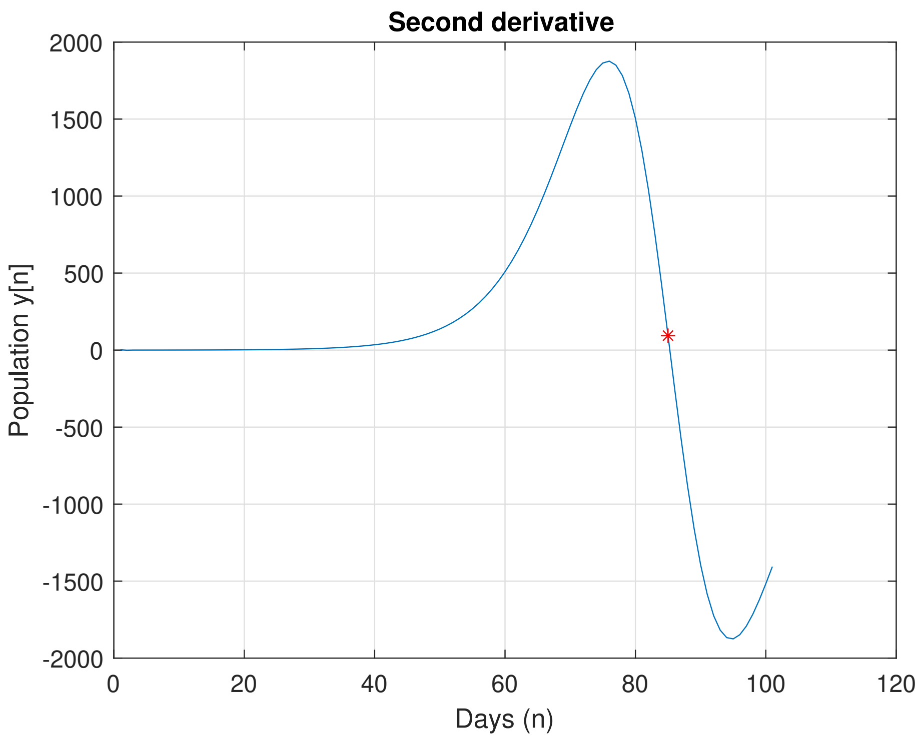
(1.With R_0 = 1.15 and K = 106 , plot the total number of infections in the first-order model versus the logistic evolution for a population of one million for n = 100 days. Does the first order model follow the logistic hypothesis?)
(Solution) Applying logistic evolution to the parameters mentioned earlier, the outcomes are as follows:



(2. Find the point of inflection using the global maximum of the first derivative and the zero-crossing of the second derivative) The first order derivative is plotted as follows,



The second order derivative when plotted is as follows



By analyzing the results obtained from these calculations, I determined that the global maximum is 3.4918e+04, and it occurs at n = 85. Additionally, the zero-crossing point is also equal to this value.

A Code Repositories

`https://github.com/VenugopalRadhakrishnan/DSP-Lab`.