

SIR/SIER MODEL - DATA SCI PROJECT 2022 (Vasu Sukhija)

Introduction:

Within our society today, we are yet to recover from one of the most significant pandemics to hit the world in the time of this generation's existence. Due to this, I decided to model my project around the relation of factors in population rise and fall. My project is largely based on the SIR model which is commonly used to study the spread of the disease. In the model, there is one dependent variable, the time, and along with it are three variables known as S, the susceptible number of people, I, the infected number of people, and R, the recovered number of people. The following are equations that are used to calculate each aspect that would be required.

Method:

It should be first noticed that the fraction of the total population in each of the three categories must also be accounted for in terms of finding the prevalence, which is done thru these equations:

$s(t) = S(t)/N$, the susceptible fraction of the population,

$i(t) = I(t)/N$, the infected fraction of the population, and

$r(t) = R(t)/N$, the recovered fraction of the population.

Thus, in order to find the three dependant variables, we would use the following equations:

The Susceptible Equation:

$$\frac{ds}{dt} = - (b) s(t)i(t),$$

where b is the contacts per day that are sufficient to spread the disease

The Infected Equation:

$$\frac{di}{dt} = (b) s(t)i(t) - (k) i(t),$$

where k is the amount of the infected group that will recover during any given day

The Recovered Equation:

$$\frac{dr}{dt} = (k) i(t)$$

The equation tha can be used to calculate the overall total population

$s(t) + i(t) + r(t) = 1$, which each dependent being a fraction of its precedence

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The above model is based on a few assumptions as well, where we assume that we are ignoring births and immigration so the only way the S values do change is if an individual leaves the susceptible group by becoming infected. We also assume that a fixed fraction k represents a fraction of the infected group that will recover in a single day.

In order to solve the system, I could have used either Runge-Kutta or leap-frog integration, however, I found that to challenge myself, I would use leap-frog as it wasn't the recommended route, however, I felt that a solution could be created for the following model. The leap-frog implementation was used in the instances below for my base model.

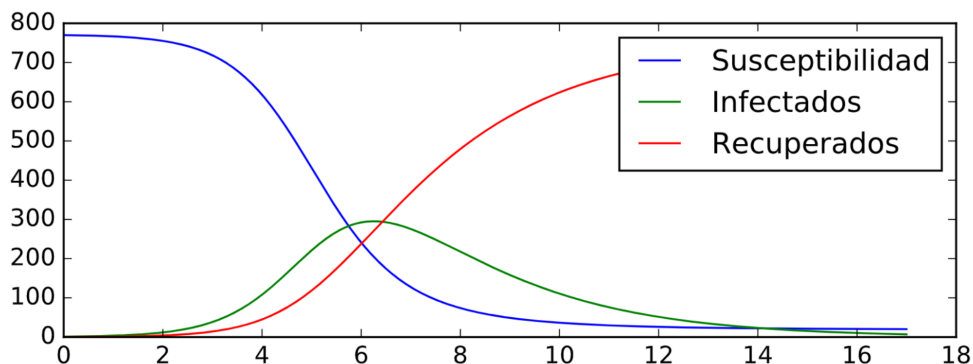
```
S1[1] = S1[0] + h*S(S1[0], I1[0], betha_1);
I1[1] = I1[0] + h*I(S1[0], I1[0], betha_1, gamma_1);
R1[1] = R1[0] + h*R(I1[0], gamma_1);

for(int i = 2; i < total_pts; i++){
    t[i] = t[i-1] + h;
    S1[i] = S1[i-2] + 2*h*S(S1[i-1], I1[i-1], betha_1);
    I1[i] = I1[i-2] + 2*h*I(S1[i-1], I1[i-1], betha_1, gamma_1);
    R1[i] = R1[i-2] + 2*h*R(I1[i-1], gamma_1);
}
```

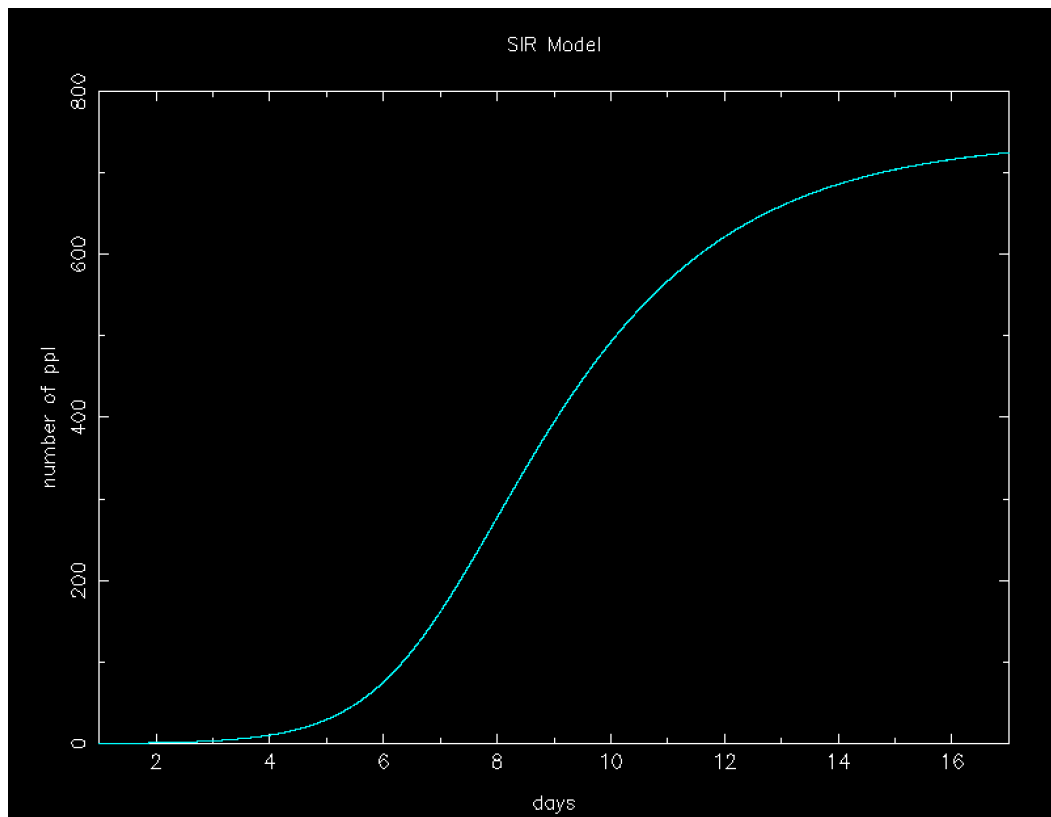
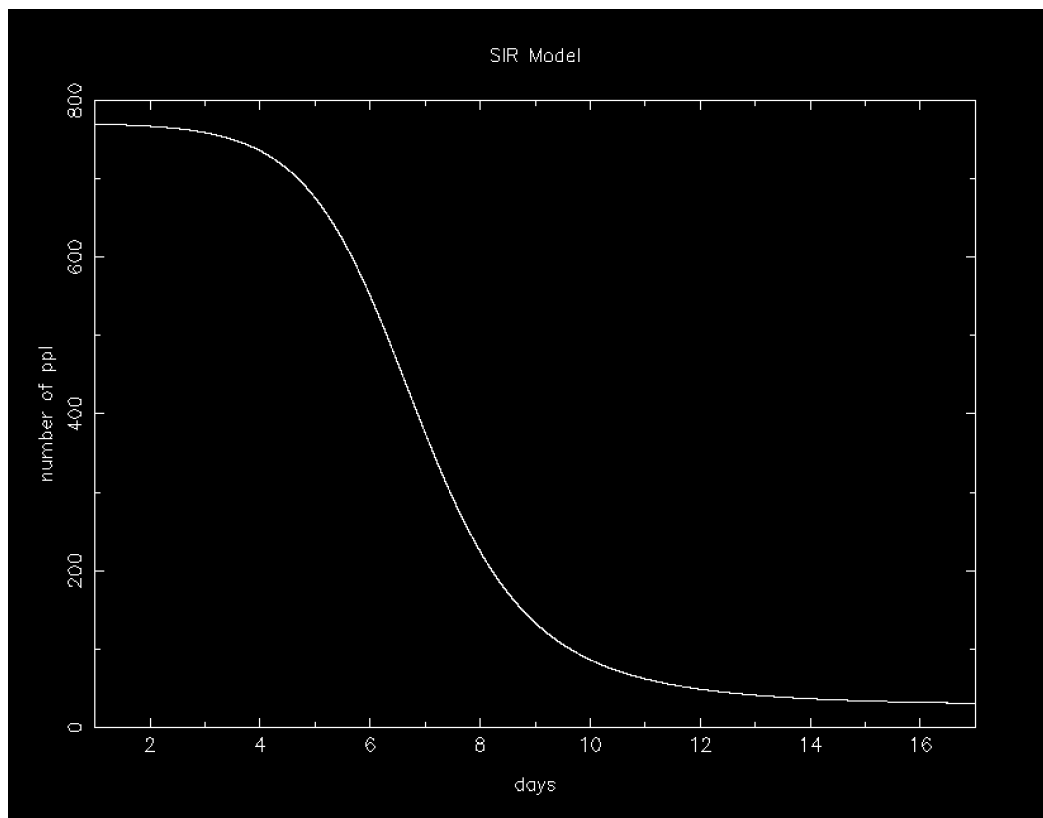
The leap-frog integrator is implementing the values at each stage, where h is the change in time multiplied by 2, and the previous index value of $S(t)$, $I(t)$, and $R(t)$ are sent over into the function and multiplied with the time change and are added onto two previous index values to compute the needed index value.

Testing:

In order to test every aspect of the demo, I used a model that arise from a small Spanish community with a population that's approximated to be around 800 people. The chart below shows the suspected number of people, which would be the entire population and assumes that there is only one infected case with no people recovered. As stated in the explanation of the model above, k and b , which are represented by β and γ , are assumed values that can be adjusted to predict models if a disease was to occur to the people of the community.

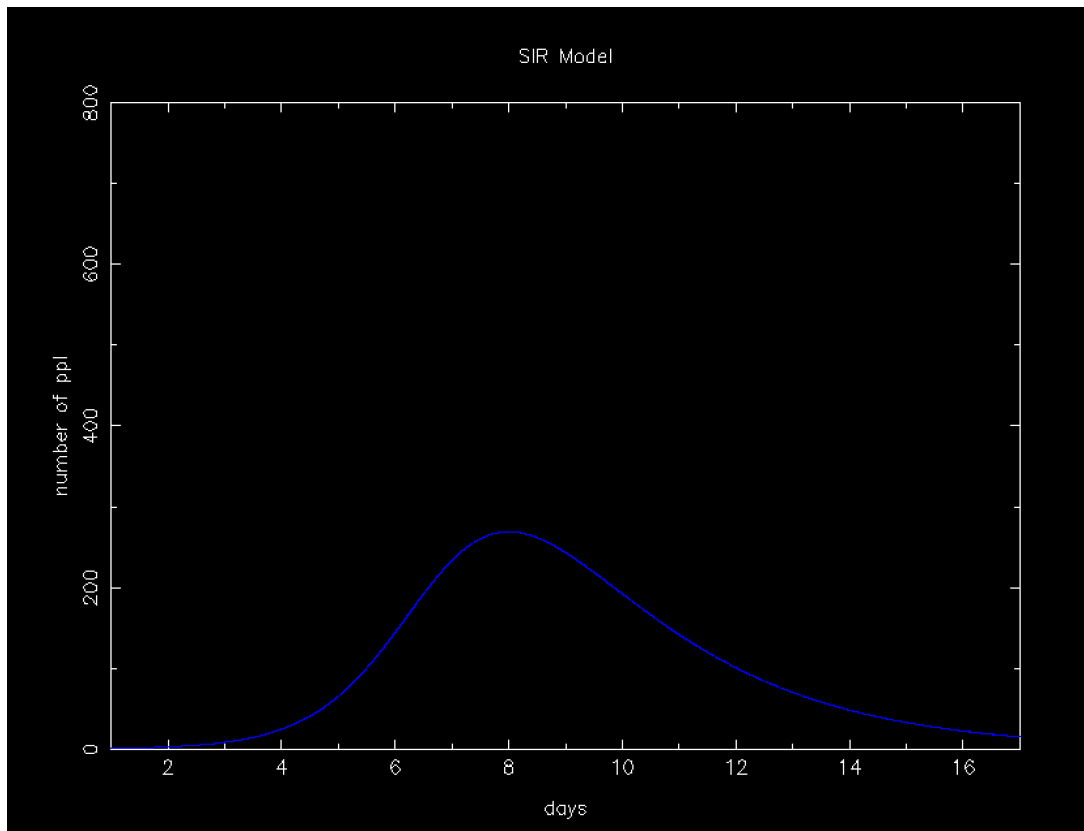


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The above replicates the Suspected number of cases and provides a clear pattern of how the Recovered number of people will also rise. This is due to their dependency on the beta value, which will produce very similar results however the point at which $R(t)$ and $S(t)$ will meet will shift. This meets our test because if we notice the equations at hand $I(t)$ is a combination of $R(t)$ and $S(t)$. Therefore, If there is an infected person in a community, the only way a susceptible person can become infected is if they come into contact (S & I). The likelihood of the susceptible contracting the infection increases with the degree of interaction between the susceptible and the infected. In simplest terms, the degree of the interaction between two factors determines how quickly the susceptibility changes (S & I). Due to this, the susceptibles are becoming fewer with time; as a result, the equation's negative sign denotes a decline.



It needs to be stated that the number of infected people who recover, using gamma as the proportionality constant, adds to the recovered state, determining the rate of recovery. As can be seen, the dark blue line indicates the number of people that are infected per day, and around the 8th day, it can be seen that the largest amount of individuals was infected. If both recovered and suspected individuals are to be looked at, it would be noted that at around the 8th day, the inflection point of the cubic function occurs, showing the largest amount of decline in the suspected number of people and the largest rise in the amount of recovered number of people.

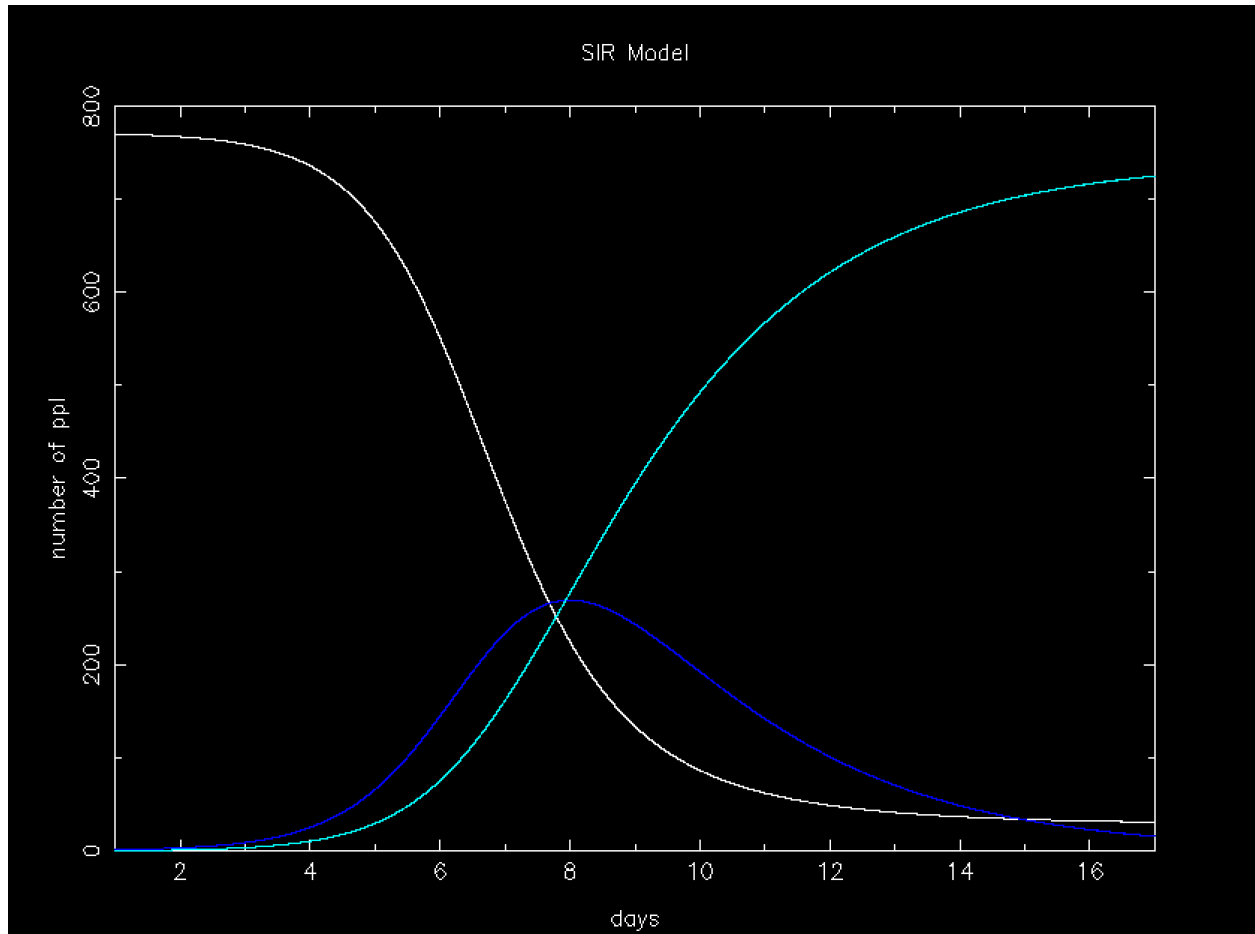
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The h-variable:

In my code, you can find a variable by the name of h, which indicates the amount of change that occurs in the time, and the smaller that value is, the more precise results will be, so choosing too small of a value will result in floating point exceptions since the values are precise to too many decimals, but a high value on the other end will skew the results and lead to issues with the beta value as it will fluctuate from negative to positive.

Verification: Is the equation solved correctly by the program?

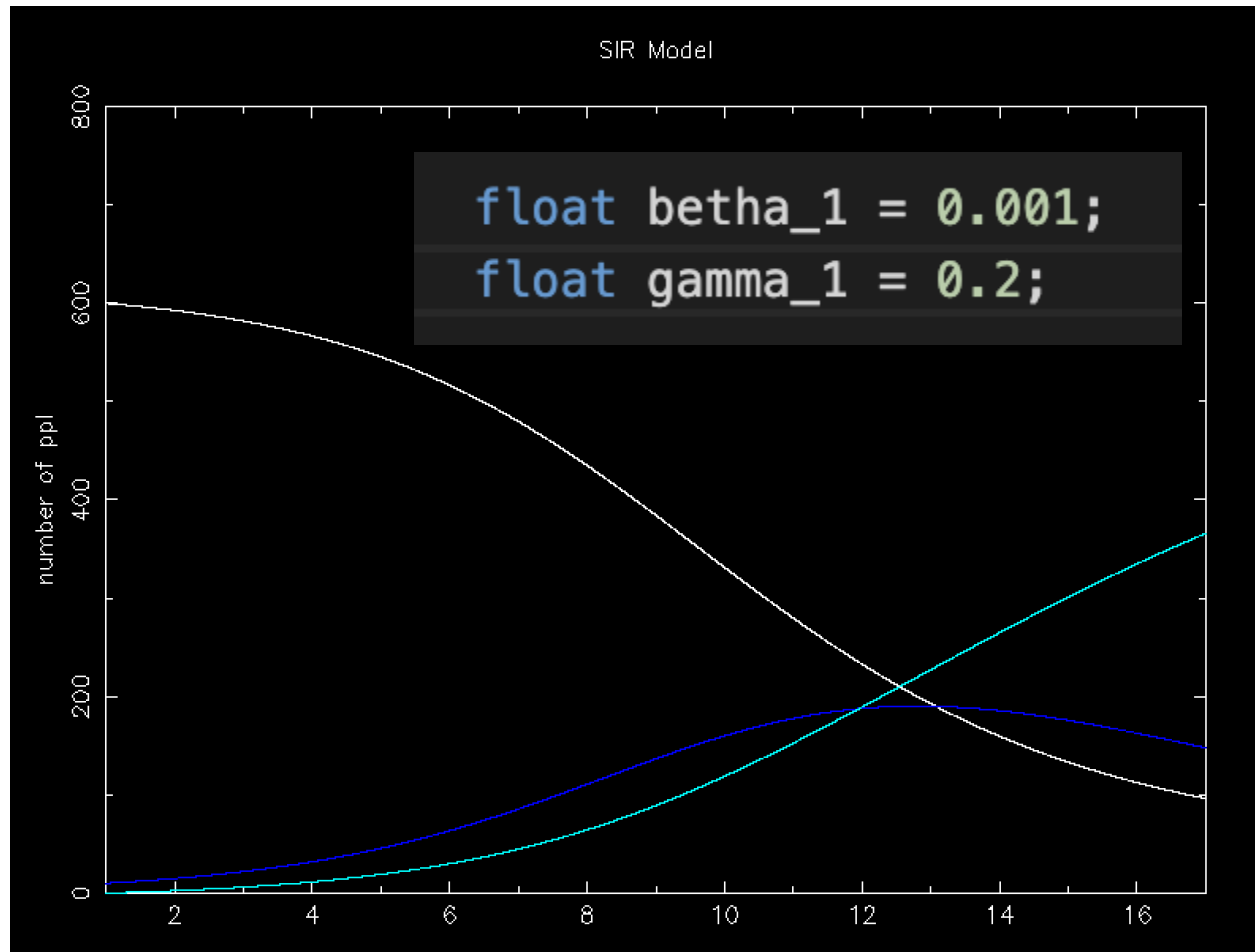
The above models put together provide the image below with no compilation error.



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Validation: Does the population increase/decrease in the model increase/decrease when a real population would increase?

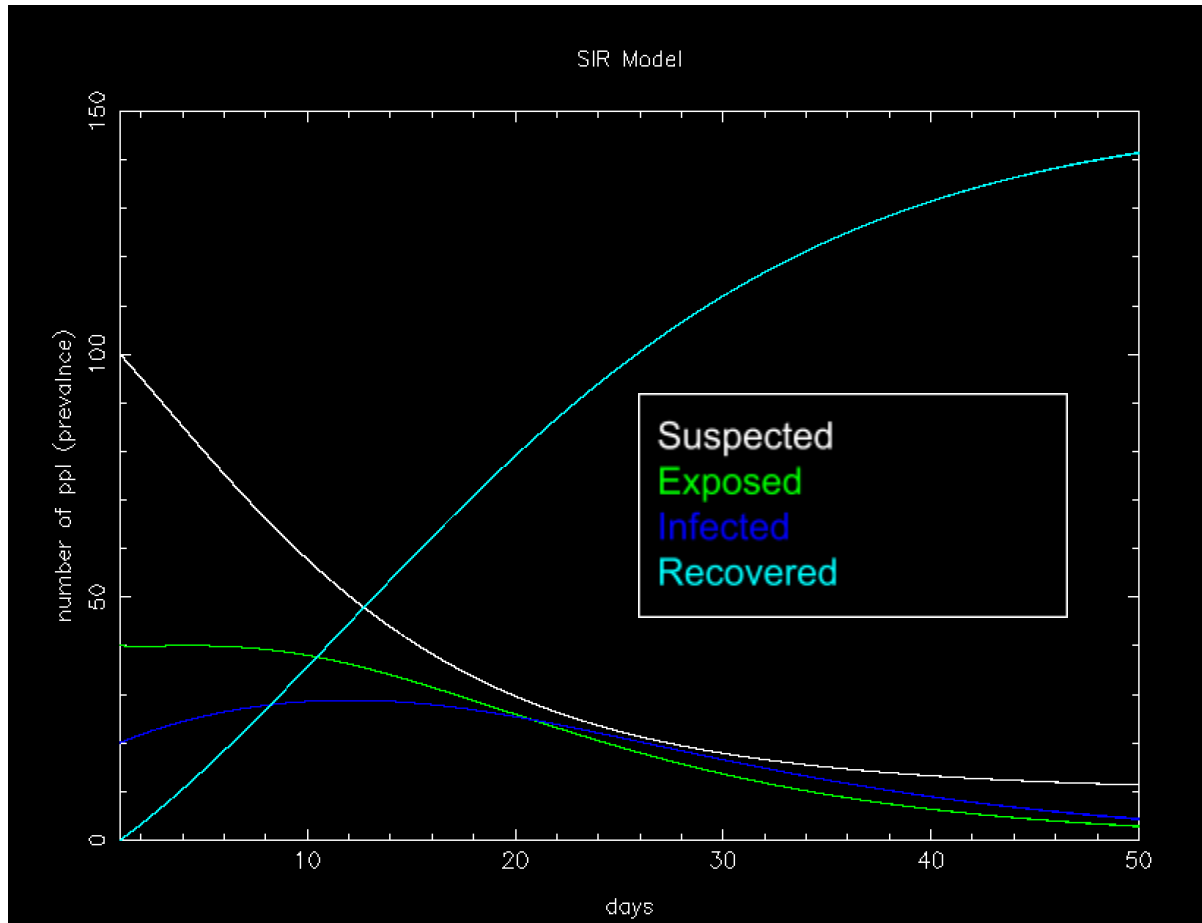
Let the model below be a model of a city that has a lower population amount along with a change in the recovery speed and infection speed of the disease.



The above model is created with an initial population of 600 people and an initial infected number of people being set to 10. Within the model, we are also changing the values of beta and gamma to the ones in the image above ultimately showing that this model is verified under the aforementioned conditions and values.

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Results:



The above model represents my extension which is an SEIR model, where E = Exposed (infected, not yet infectious). The exposed variable in my case is initialized to be double the infected number of people, to which there is a relation since notice that as the number of individual infected rise, the number of exposed individuals rise, and vice versa where a decline in infected people doubles the decline in the number of exposed individuals. As mentioned in the SIR model, the amount of suspected and recovered individuals has a direct relationship as they have the opposite effect of each other. This can be said to be somewhat realistic to the real world, as multiple variables continue to control, as we are introduced to alpha, which represents the disease-induced average fatality rate. However, in the real world, although having the correct formulas and results, it would be reasonable to look at a large-scale model for a larger population, which could be done with better methods and integration methods.

Conclusion:

To conclude the project, it should be mentioned that the everlasting impact of disease goes quite unnoticed when a large amount of the population is explored, however, when brought into light how one infected individual could affect almost all of a population under 1000 people in 17 days brings a greater understanding of the disease. With that being said, if I had the time and facilities to grow my project, I would like to create a model that is accurate for larger data handling methods, along with a method to portray this information for real-life developing diseases for the betterment in the field of science's future.