SIR Modeling

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Final Report – SIR Modeling

Objective

To know exactly what makes a SIR model and to see if there can be other variations of this. The understanding the importance of using the SIR modeling. To discover the benefits we achieve when reviewing the SIR model.

Introduction

Epidemiology has grown to be major in todays modern society. AS we dive into the studies of epidemiology, the relationship with mathematics is steadily increasing as we know it. Both fields get there own personal use of information. For instance the mathematicians are provided with new and exciting branches to test, meanwhile the epidemiologist, use the mathematics to model which proves to be an important research tool in the study of diseases. The SIR model, was first developed by Ronald Ross, William Hamer, and others in the early twentieth century, this system was consisting of three nonlinear differential equations that can still be used to model. Kermack and McKendrinck made theoretical papers, between 1927 and 1933 about infectious disease models, this was also proven to give some advancements to the development of the use of mathematics in epidemiology models. Around the similar time the most basic theory have been developed but the theoretical progress still was continuing. As these advances are being developed, the results of the models are being increasingly used to explain the transmission of several diseases. The way the models explain the affects of these diseases, are by their compartments, they do seem as basic knowledge at first glance, but studying them can prove to learn crucial information of the underlying aspects of the infectious diseases spreading. They can actually evaluate the potential impacts in certain areas such as morbidity

and mortality. In the most recent events the SIR model has been focused and became an increasing trend, the reasoning for this was the outbreak and current pandemic of Covid-19. Scientist and mathematicians were studying the different factors that were affecting these compartments of the model and could be a solution to flatten the curve of infectious people and mortality rates. SIR model is a beginning point to understand what happens rapidly; then, with more understanding and complexity is possible to enrich the model and put more details in the formulation.

What is a SIR Model?

A SIR model is also known as a compartmental model, so certain specific populations are all separated into groups to represent the compartments, based how the disease has affected the individual. Each person is considered to be in 1 compartment at a given time, but this can change and be moved to a different compartment based on the conditions met to be moved within the model. The SIR model is one of the most basic compartmental models, named for its 3 compartments, susceptible, infected, and recovered.

- Susceptible (S): are the individuals who are susceptible to infection, this can include the passively immune once they lose their immunity or, more commonly, any newborn infant whose mother has never been infected and therefore has not passed on any immunity;
- Infected (I): The number of **i**nfectious individuals. Capable of infecting susceptible individuals.
- Recovered or Resistant (R): includes all individuals who have either recovered from the disease and entered removed compartment or died.

When modeling these epidemics, they mostly start with the whole population being susceptible. The rate at which susceptible individuals become infected is dependent on the number of individuals in each of the susceptible and infected compartments. In the beginning of the outbreak, as there are a few infected people, the disease would take some time to spread. As the infected individuals start piling in, rate of infection starts to increase. Now we have an additional factor for calculating rate of spread within the model, the effective contact rate(β). This parameter will represent the transmissibility of the disease as well as the mean number of contacts per individual. There are methods of reducing the spread of the infection rate, such as quarantining infected individuals, social distancing, and closing schools, the effects will appear in the charts in this report. Although these interventions can alter the movement of individuals from the susceptible compartment to the infected compartment, the transition from the infected to the recovered compartment is solely dependent on the amount of time that an individual is contagious, captured in the rate of recovery (γ).

For parameters for the SIR model, we should have only 2, but with little alterations, other parameters can be added such as population and the days an individual contains a disease. Now with the two focused parameters, if the situation arises of the rate of individuals exceeds the rate of which infectious people recover, there would a over abundance in the infectious compartment. The basic reproduction number R_0, the mean number of new infections caused by a single infected individual over the course of their illness, is the ratio between β and γ. As we stated before a decrease in the effective contact rate β through the methods such as quarantining will decrease R_0, essentially lowering the peak infection rate and also known as flattening the curve. However, to maintain the decrease in total infections, the decrease in R_0 generally must be sustained.

Brief History

John Graunt (1620-1674) was the one who started the study of infectious diseases, even making a book about it. The Bills of Mortality are a focus point in his book and they were weekly records of numbers and causes of death in London parishes. The data provide the information from the year of 1603 and onwards. He would then investigate the different causes of death among the list and created a method to estimate the comparative risk of dying from various diseases. This would be the first approach to a theory of competing risk.

In 1906 W.H. Hamer was one of the to discuss the topic of compartmental models with diseases, so he proposes that the spread of infection should depend on the number of susceptible individuals and the number of infective individuals. He suggested a mass action law for the rate of new infections, and this idea is continued to be used, such as our example in this same report. I should mention that the foundations of the entire approach to epidemiology based on compartmental models were laid, surprisingly not the mathematicians, but by public health physicians such as Sir R.A. Ross, W.H. Hamer, A.G. McKendrick, and W.O. Kermack between 1900 and 1935.

Equations to the SIR Model

We want to model infectious diseases. These diseases can spread from one member of a population to another; we try to gain insights into how quickly they spread, what proportion of a population they infect, what proportion dies, etc. One of the easiest ways to model them is with a *compartmental model* and the equations that are used in this model.

First lets start with the variables that will help us develop these equations that will calculate the susceptible, infected and recovered. Lets say we have disease and the probability of

an infected person to infect another individual is about 20%. It happens to be the average number of people an individual is in contact with others per day is about 5. So we have so far is, at each day, an infected individual could up to 5 people and 20% of them can fall ill to the disease. Therefore, we calculate the individual will infect 1 person per day. We can call this beta (**β),** the expected amount of people an infected person infects per day. Since we can see that the number of days that an infected person has and can spread the disease is extremely important, this is **D**. If D=7, so an infected individual would walk around for seven days spreading the disease, and would infect 1 person per day. So we expect an infected person to infect 1 per day times 7 days which totals up to 7 people. This is the basic reproduction number $\mathbf{R_0}$, this would equal to the total number people an infected person is capable infecting: $\mathbf{R_0} = \beta \cdot D$. We actually don't need anything else, just one small notation: **γ** ("gamma") will be 1/D, so to keep track what the value of gamma is then think of D as the number of days an infected person has the disease, and gamma would be the opposite. Gamma is the rate of recovery, or the proportion of infected recovering per day. Now we can move to deriving the final equations for the compartment model.

We are going to set on day t, 60 people are infected(I(t)=60), we have a total population of N = 100, and 30 people have remained susceptible (S(t)=30 and R(t)=100–60–30=10). Now, how do S(t) and I(t) and R(t) take effect in the following days to come? As established we have 60 infected people. Each of them infects 1 person per day (that's β). However, only 30% of people they meet in that day are still susceptible and can be infected (S(t) / N). So, they infect $60 \cdot 1 \cdot 30/100 = 18$ people. So, the 18 people of the compartment of susceptible get infected, so S(t) changes by minus 18. Plugging in the variables, we just derived the first formula:

$$\frac{dS}{dt} = -\beta \cdot I(t) \cdot \frac{S(t)}{N}$$

Now we are going to find out the changes that had occurred within the infected compartment. From the last equation we have received new infected people. So the amount of people that leaves S(t) would then arrive at I(t). So, we have 18 new infected and we already know that the formula would a similar format to the previous: I'(t) = + β · I(t) · S(t) / N. We are adding the β to show we have gained the similar amount that susceptible compartment has lost. The people that have recovered is what we are missing. Remember, we have γ for that, it's the proportion of infected recovering per day. Back to the calculations, we have 60 infected and γ=1/3, so one third of the 60 recovers. That's 1/3 · 60 = 20. Finally, we obtain the formula:

$$\frac{dI}{dt} = \beta \cdot I(t) \cdot \frac{S(t)}{N} - \gamma \cdot I(t)$$

Lets recap really fast, the first part is the people that are recently infected from the susceptible section. The second part is the recoveries from the infection. Finally, we have reached the last equation in SIR, the changes that occur in the recoveries. So the newly recovered are exactly the 20 we just calculated; there are no people leaving the recovered compartment. Once recovered, they are now considered immune:

$$\frac{dR}{dt} = \gamma \cdot I(t)$$

The equations we have attained are called ordinary differential equations *(ODEs)*. These equations will also allow us to see the changes in the number of people susceptible, infected, and recovered. The formulas will let us calculate the values we are looking for in: S(t), I(t) and R(t), the number of people susceptible, infected, and recovered for each day t. The great things about programming in python, the tools will be used to solve the differential equations.

Now we will move on to a SEIR model, this model provides additional compartments from the basic SIR model. For instance, we will be observing a dead state, for individuals that

passed away from the disease. An exposed state, this will be for the individuals that have contracted the disease but are not entirely yet infectious. This is one of the key elements to the SEIR model. Time dependent Ro-values that will allow us to model certain aspects to a pandemic as in quarantine and lockdowns. Lastly, age dependent fatality rates that will assist us in modeling the affects of the disease to a certain age group such as the young people and older individuals.

Every disease comes with value known as the incubation period, the time before the individual becomes infectious and cannot spread the disease to anyone. This will the exposed state to our new model. Intuitively, we'll have the new transitions of the form S → E → I → R: Susceptible people can contract the virus and thus become exposed, then infected, then recovered. Most of the equations will still hold the same value, as the probability is the same all of the susceptible people can be exposed, the rate is the same ("exposition" happens immediately) and as for the people who are infectious that are able to spread the disease and each exposes **β** new individuals per day, the population remains the same. The transition from the infectious to recovered should remain exactly the same. Now we have E to I, the only new transition: the probability will be 1 because its clear when everyone that's exposed becomes infected, the population is E (all exposed will become infected), and this rate will receive a new variable named delta, **δ**. From this new additional transition, we can derive the equations.

$$\frac{dS}{dt} = -\beta \cdot I(t) \cdot \frac{S(t)}{N} \qquad \frac{dE}{dt} = \beta \cdot I(t) \cdot \frac{S(t)}{N} - \delta \cdot E(t)$$

$$\frac{dI}{dt} = \delta \cdot E(t) - \gamma \cdot I(t) \qquad \frac{dR}{dt} = \gamma \cdot I(t)$$

As we have the exposed compartment, we will need the dead state for the SEIR model. If we are dealing with a deadly disease, this will be needed. If we analyze our current compartments, only the individuals that are infected can transition to the state. These people will not die

immediately to the disease so we will have to create a new variable to hold this rate of people dying, ρ (rho). If the person takes up to 6 days until death, then the rate would be 1/6. But there is still something missing for our newest version of this model, the probabilities that would go from infected to recovered and infected to the dead state. So, once again we are adding another variable, the death rate, **α**. For an example to see this in use, lets say we have α=5%, ρ = 1 and γ = 1 (so people die or recover in 1 day) and 100 people are infected, then 5% · 100 = 5 people will die. That leaves 95% · 100 = 95 people recovering. So all in all, the probability for I → D is α and thus the probability for I → R is 1-α.

$$\frac{dS}{dt} = -\beta \cdot I(t) \cdot \frac{S(t)}{N} \qquad \frac{dE}{dt} = \beta \cdot I(t) \cdot \frac{S(t)}{N} - \delta \cdot E(t)$$

$$\frac{dI}{dt} = \delta \cdot E(t) - (1-\alpha) \cdot \gamma \cdot I(t) - \alpha \cdot \rho \cdot I \qquad \frac{dR}{dt} = (1-\alpha) \cdot \gamma \cdot I(t)$$

$$\frac{dD}{dt} = \alpha \cdot \rho \cdot I(t)$$

We have now covered the new compartments and their equations for the SEIR model. Now we are going to tackle the lockdown aspect to out model. The way we are able to model real world developments, the variables have to change over time. First, we implement a simple change: on day L, a strict "lockdown" is enforced, pushing R_0 to 0.9. In the equations, we use β and not R_0, but we know that $R_0 = \beta / \gamma$, so $\beta = R_0 \cdot \gamma$. That means that we define the functions

```
def R_0(t):
    return 5.0 if t < L else 0.9
```

```
def beta(t):
    return R_0(t) * gamma
```

The function (adopted for our purposes) looks like this:

$$R_0(t) = \frac{R_{0start} - R_{0end}}{1 + e^{-k(-x+x0)}} + R_{0end}$$

And here's what the parameters actually do:

- R_{0start} and R_{0end} are the values of R_0 on the first and the last day
- X_0 is the x-value of the inflection point (i.e. the date of the steepest decline in R_0, this could be thought of as the main "lockdown" date)
- k lets us vary how quickly R_0 declines

Lastly. We have finally reached the last compartment being added to our SEIR model, the age dependent fatality rates. We are going to want the fatality rate to be higher when the population of infected is at a higher value. Next is to visualize how can this placed in an equation: we probably need a "base" or "optimal" fatality rate for the case that only few people are infected and another factor that would take the proportion of the current population that is currently infected.

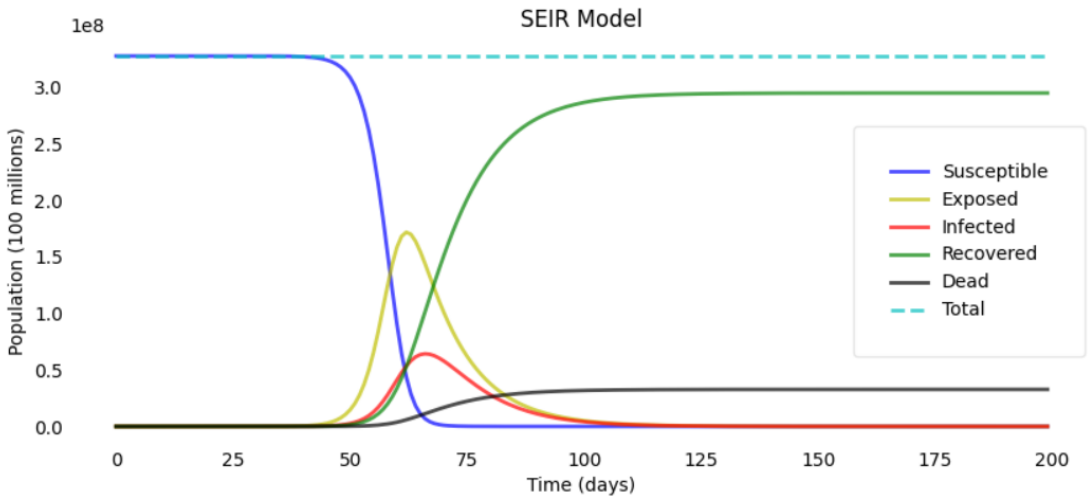
$$\alpha(t) = s \cdot \frac{I(t)}{N} + \alpha_{OPT}$$

Here we have *s* is some arbitrary but fixed (that means we choose it freely once for a model and then it stays constant over time) scaling factor that controls how big of an influence the proportion of infected should have; α_OPT is the optimal fatality rate. For example, if s=1 and half the population is infected on one day, then s · I(t) / N = 1/2, so the fatality rate α(t) on that day is 50% + α_OPT.

Testing Models in Python

I have implemented the SIR and SEIR model into python and see how it impacts the population of the United States. The different functions are placed for different model as we placed new compartments. In total there should be at least 4 charts. There will additional ones that will provide extra information on the mortality rates that are dependent on the age group. I

will provide the basic SIR model so we can see how the chart and different values effect the chart. The rest of the charts will be provided in the appendix of this report. There you can examine the different models and see how the different compartments affect the model as it develops.



Input:

```
N = 328,000,000 # population
D = 4.0 # infections lasts
gamma = 1.0 / D # proportion of infected recovering per day
delta = 1.0 / 4 # incubation period
R_0 = 10.0 # total number of people an infected person can infect
beta = R_0 * gamma # infected person infects per day
alpha = 0.2 # 20% death rate
rho = 1/9 # days from infection until death
```

Applications of the SIR Model

One of the major applications of the SIR model is regards to health. The SIR model can determine values that can help people deal with the diseases. But where do we get our information? We can receive them through reports of being sick in a general area. An example is at a school, 763 boys in the school had contact with a certain infection. Two weeks have past and the infection has been extinguished. The parameters we can estimate of this disease is the

infectious period of $1/\gamma = 2.2$ days and a mean transmission rate $\beta = 1.66$ per day. Therefore, the estimated R0 is 3.652. This has been applied to many different types if influenzas. One great example is SARS, the first epidemic for the 21st century. Researches have used the SIR model, as a first approach to explain this disease. For this model they have added superspreading individuals, infected individuals that infect more than the average number of secondary cases. The effect of superspreaders can be used in cases where there is a higher transmission rate.

Another application can be applied is networking/marketing. We have now social networks and it encourages people to share information and campaigns with others, through email or some other means. We can see the impact by this communication will be on the customer because they are receiving information from others and friends that know their interest; this kind of communication have more impact because is directly targeted. When a marketing message goes viral, it is analogous to an epidemic, since involves a person-to-person transmission, spreading within a population. There are researchers that have set simulations to experiments the influence of several controlled and external factors that could influence viral campaigns.

The last application I would like to discuss is a fun one, this SIR model can be applied also within science fiction. There simulations and charts showing how a zombie outbreak can affect a population. According to mathematical investigation community in 2009, their model, "a zombie outbreak is likely to lead to the collapse of civilization, unless it is dealt with quickly. While aggressive quarantine may contain the epidemic, or a cure may lead to coexistence of humans and zombies, the most effective way to contain the rise of the undead is to hit hard and hit often." The model ended up showing two balances to this zombie outbreak: the disease-free equilibrium that contains no zombies and the doomsday equilibrium, where everyone is a

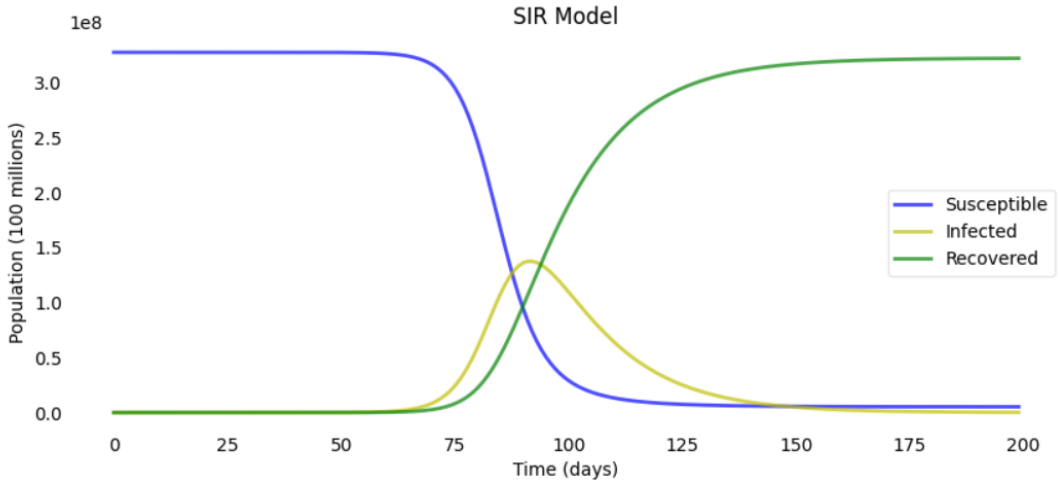
zombie. The application of a linear stability analysis showed that - in the absence of further interventions - the disease-free equilibrium was unstable and the doomsday equilibrium was stable.

Conclusion

I have discovered the effectiveness of a SIR model and how exactly it functions with its differential equations. Throughout the report, I have realized the importance of this model to determine the values that could help fight back against diseases. I have discussed how to achieve the different equations needed for the SIR model, and that would not have been possible if was not for research and scholar articles that I found. I will provide their reference so you can check it out. It is very interesting how much you can change the SIR model and the different compartments to see how it can affect populations and certain areas. This Model became very interesting to explore and would not mind continuing my research for this topic.

Appendix

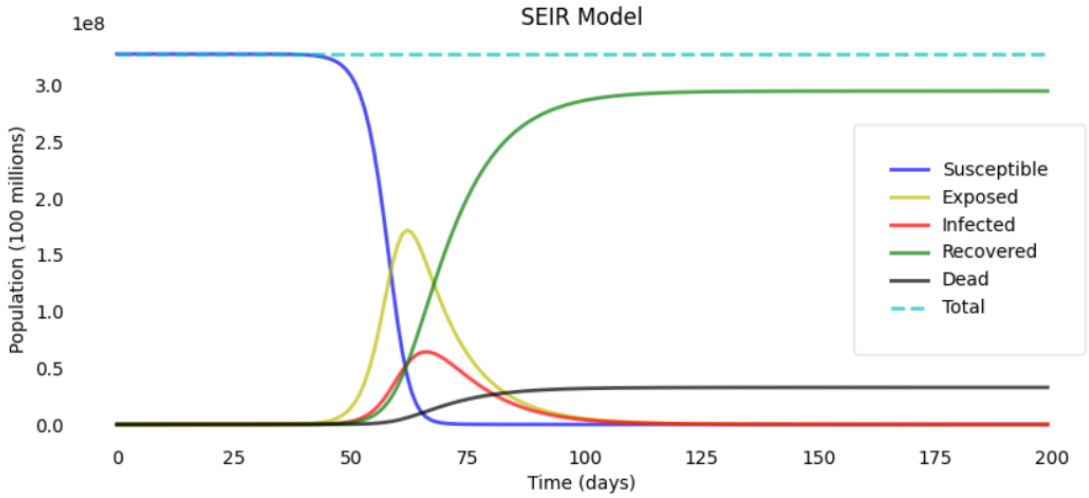
Figure 1 SIR Model



Input:

```
N = 328,000,000 # population
beta = 0.3  # infected person infects
D = 14.0 # infections lasts
gamma = 1.0 / D # proportion of infected recovering per day
```

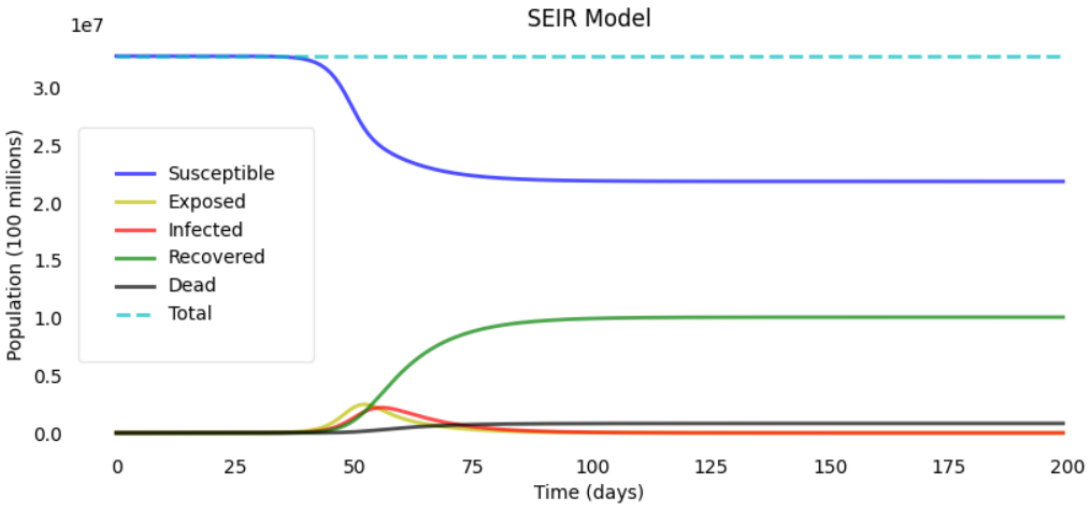
Figure 2 SEIR Model



Input:

```
N = 328,000,000 # population
D = 4.0 # infections lasts
gamma = 1.0 / D # proportion of infected recovering per day
delta = 1.0 / 4 # incubation period
R_0 = 10.0 # total number of people an infected person can infect
beta = R_0 * gamma # infected person infects per day
alpha = 0.2 # 20% death rate
rho = 1/9 # days from infection until death
```

Figure 3 SEIR Model Mortality Rates (Older)

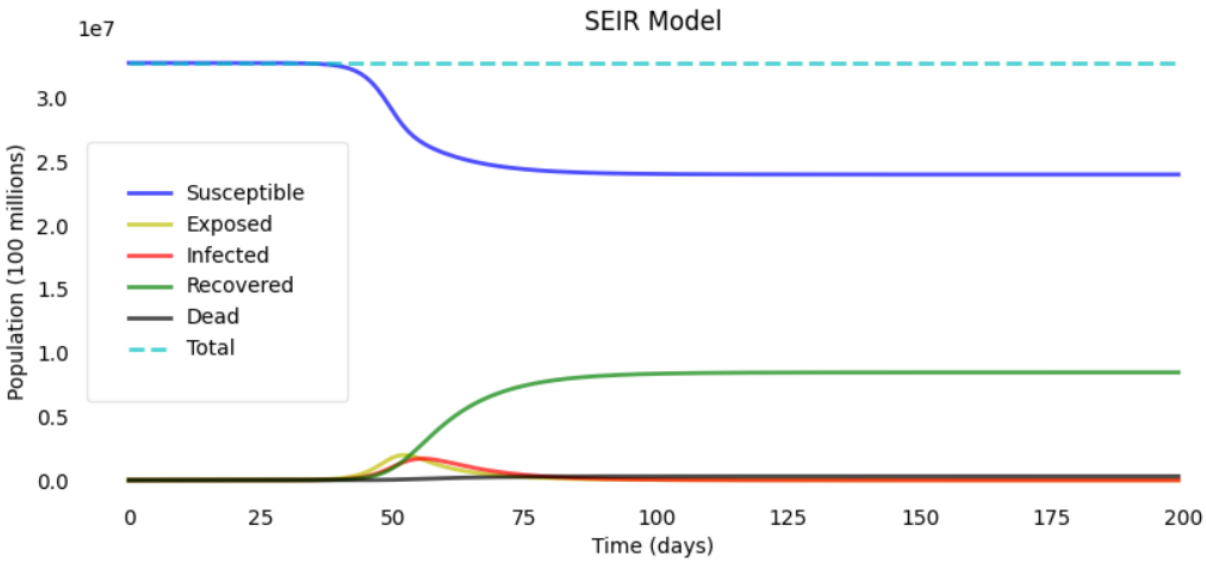


Input:

```
N = 328,000,000 # population
D = 14.0 # infections lasts
gamma = 1.0 / D # proportion of infected recovering per day
delta = 1.0/14.0# incubation period
rho = 1/20 # days from infection  until death


proportion_of_
agegroup = {
"0-29": 0.1,
"30-59": 0.2,
"60-89": 0.3,
"89+": 0.4}
```

Figure 5 SEIR Model Mortality Rates (Young)

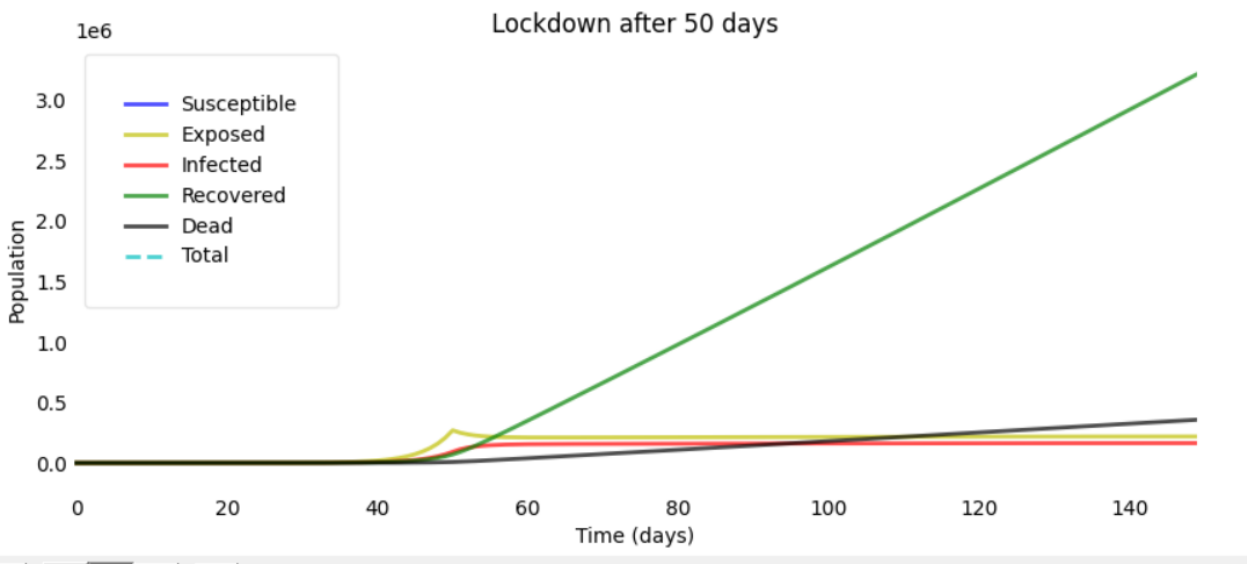


Input:

```
N = 328,000,000 # population
D = 14.0  # infections lasts
gamma = 1.0 / D # proportion of infected recovering per day
delta = 1.0/14.0 # incubation period
rho = 1/20 # days from infection     until death

proportion_of_
agegroup = {
"0-29": 0.4,
"30-59": 0.4,
"60-89": 0.1,
"89+": 0.1}
```

Figure 6 SEIR Model with Lockdowns



Input:

```
L = 50 # days
N = 328,000,000 # population
D = 14.0  # infections lasts
gamma = 1.0 / D # proportion of infected recovering per day
delta = 1.0/14.0 # incubation period

alpha = 0.2  # 20% death rate
rho = 1/20 # days from infection until death
```

References

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