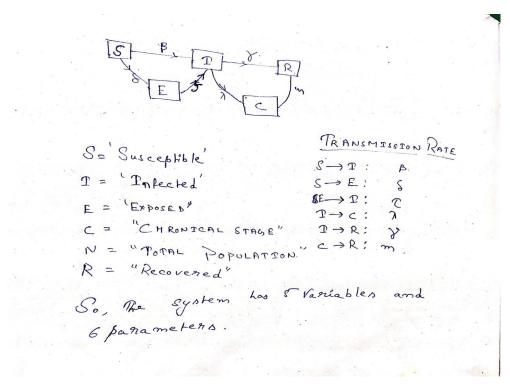
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ROLL NO.: 20CE8062

Subject:- QUANTITATIVE BIOLOGY

A) Compartmental Schematic Diagram of the Model:



B) Table for Variables , Parameters name and Physical significance of Parameters

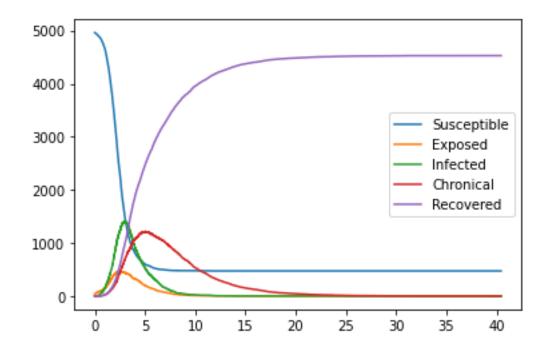
Variables	Parameters	Physical significance of parameters		
Susceptible	Disease spreading rate (β) S I	From the sick and infected people the diseases get spread to the susceptible people who do not have any infection but can be infected if the remain in contact with a infected person. To stof the shift from susceptible to infected the process of lockdown is followed.		

Exposed	Exposure rate (δ) S E	From the susceptible people to the exposed people the transition occurs when a person (susceptible) remains in contact with a infected person and is exposed to the disease. the process occur unconsiously as the infected people don't show symptoms immidiately
Infected	Testing rate (τ) E I	The exposed people carry the disease but don't show any symptoms they can be found out only by testing and rapid testing can only solve this problem. Testing rate has an important role here and helps us to controll the disease.
Chronical	Chronical Recovery rate (γ) Depending on the proper facilities like beds at hospitals a units the rate of repeople who passed considered recover longer be infected their disease and seconsidered recovered by the considered recovered to the consider	
Recovered	Chronical rate(λ) I C	This parameter may depend upon various factors like surroundings or environment hygene condition, climate, Age of infected people ,Condition of health, having any other disease before got infected (high blood
		pressure, asthma , high glucose level) or any genetical influence and also unavailability of proper medicine, space can make the infected person go through this chronical stage rather than got recovered.
	Chronical Recovery rate(m) C R	It is similar to the recovery rate but some extra care and medications are required here. Space availability is a constraint here.

```
import networkx as nx
from collections import defaultdict
import matplotlib.pyplot as plt
import random
N = 5000
G = nx.fast_gnp_random_graph(N, 6./(N-1))
#We have defined our network ( which is a random graph) with N number o
f nodes
#5 is the number that decides how densely the nodes are connected
#We show how node and edge attributes in the contact network 'G' can be
#to scale the transmission rates.
#Let us define H for the spotaneous transitions
H = nx.DiGraph()
H.add node('S')
H.add edge('I', 'R', rate = 0.5)
H.add_edge('I', 'C', rate = 0.5)
H.add edge('C', 'R', rate = 0.25)
H.add edge('E', 'I', rate = 0.65)
# The line above states that the I to 'R' transition occurs with rate
0.5
#Let us define J for the induced transitions
J = nx.DiGraph()
J.add edge(('I', 'S'), ('I', 'I'), rate = 0.6)
J.add edge(('E', 'S'), ('E', 'E'), rate = 0.35)
# The line above states that an 'I' individual will cause an 'S' indiv
idual
# to transition to 'I' with rate equal to 0.6
#Defining initial conditions
IC = defaultdict(lambda: 'S')
for node in range(10):
 IC[node] = 'I'
for node in range (40):
IC[node] = 'E'
return statuses = ('S', 'E', 'I', 'C', 'R')
t, S,E, I,C, R = EoN.Gillespie simple contagion(G, H, J, IC, return sta
tuses,tmax = float('Inf'))
plt.plot(t, S, label = 'Susceptible')
plt.plot(t, E, label = 'Exposed')
plt.plot(t, I, label = 'Infected')
plt.plot(t, C, label = 'Chronical')
plt.plot(t, R, label = 'Recovered')
plt.legend()
```

```
plt.savefig('SEICR.png')
```

#FOR TRYING OUT SIS MODEL, THE SAME CODE WOULD WORK IF YOU MODFLY ACCOR DINGLY. THE ONLY CHANGE YOU NEED IS SET tmax=20 INSTEAD OF tmax = float ('Inf'). THIS DICTATES THE FINISHING TIME AND DOES NOT LOOK FOR AN AUTO MATIC SATURATION. THINK ABOUT WHY THIS IS NEEDED IN SIS.



Spontaneous Process

('I', 'R', rate = 0.5)

```
('I', 'C', rate = 0.5)
('C', 'R', rate = 0.25)
('E', 'I', rate = 0.65)
Induced Process

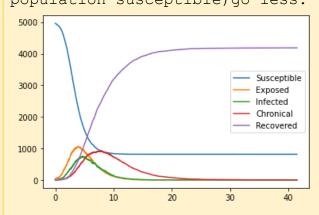
(('I', 'S'), ('I', 'I'), rate = 0.6)
(('E', 'S'), ('E', 'E'), rate = 0.35)
No. of Initially infected people = 10
No. of Initially exposed people = 40
Total population, N = 5000
Average Degree = 6
```

SL	Parameters	Different	Effect of	the	parameter	on
No.		Values of	epidemic			
		Parameters				

Disease			
spreading rate			
(β)			
SI			

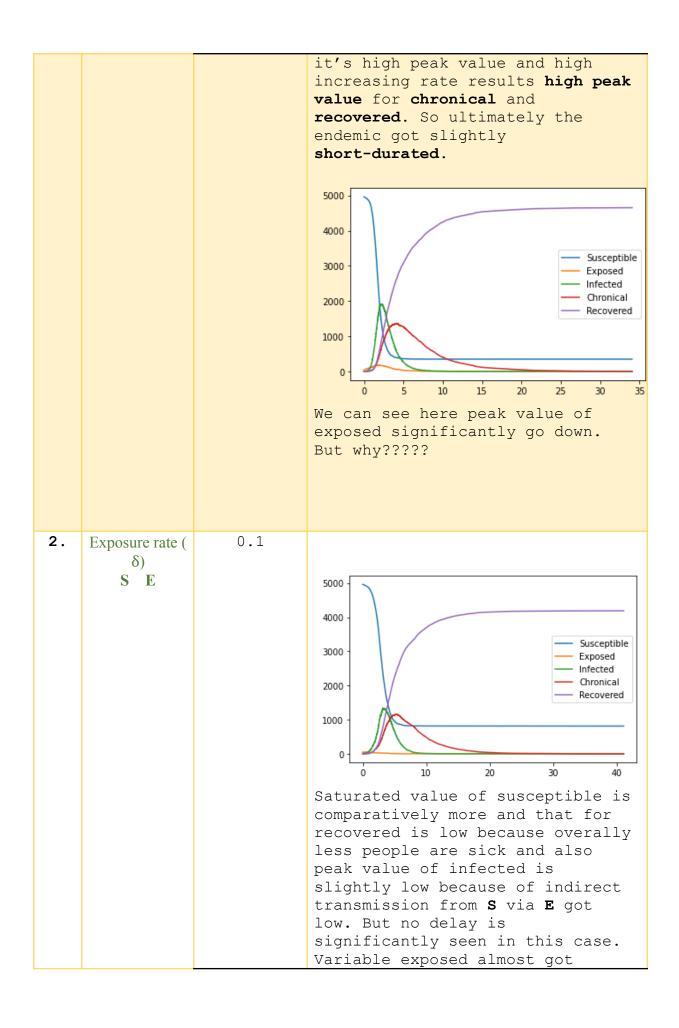
0.1

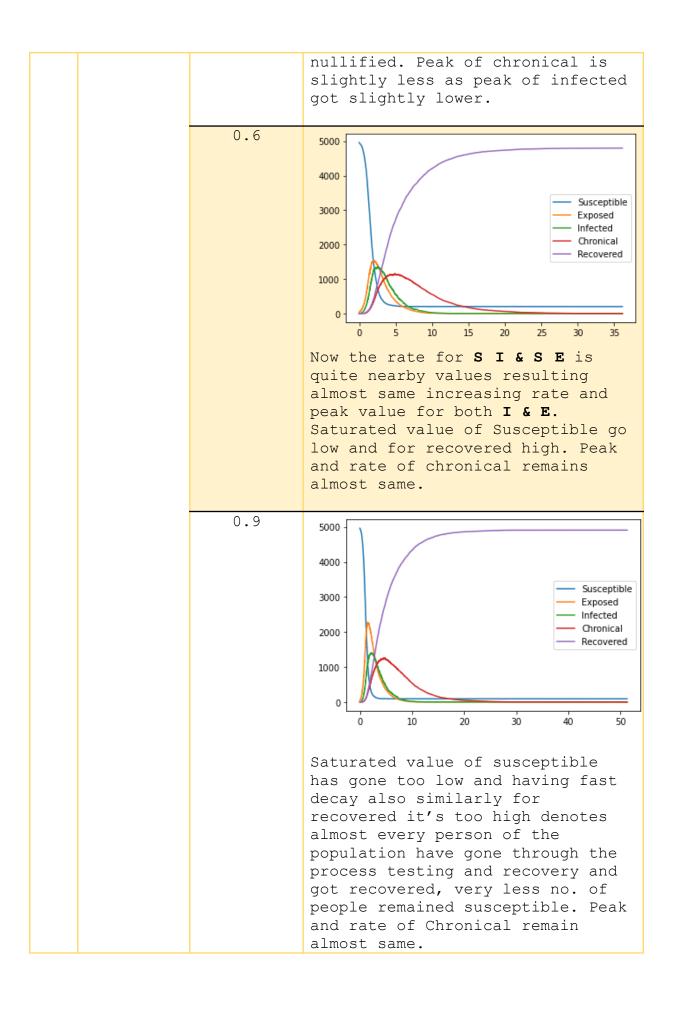
Compared to the previous one (where $\beta=0.6$) here saturated value of susceptible is more and for recovered it is low, as comparatively less people got sick overally so after end of epidemic more people remain susceptible and as then rest three variables become 0 so naturally no. of recovered people (total population-susceptible) go less.

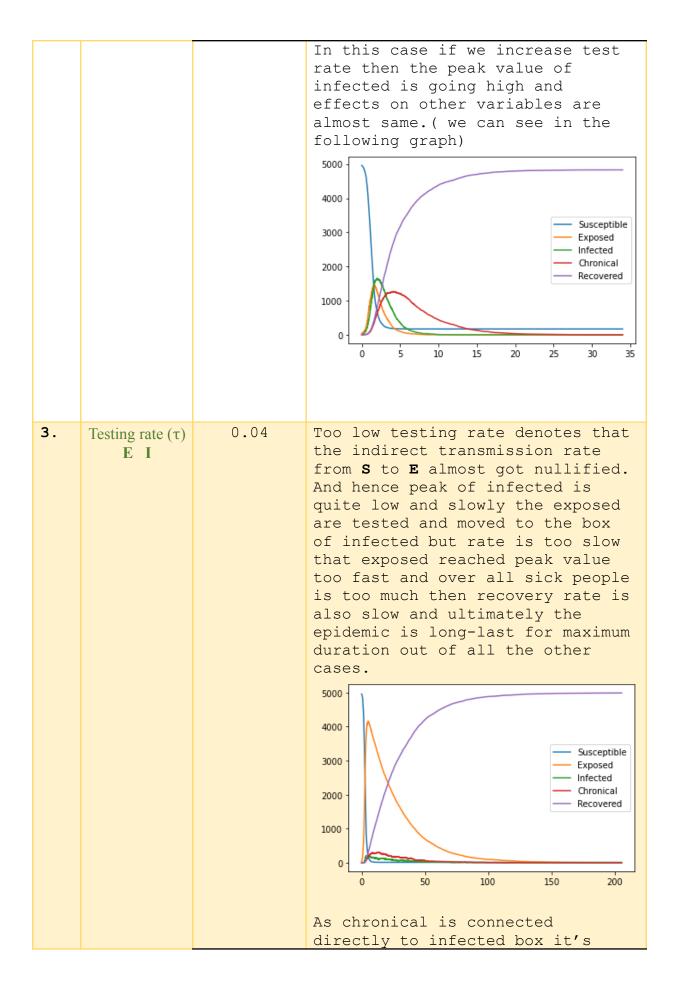


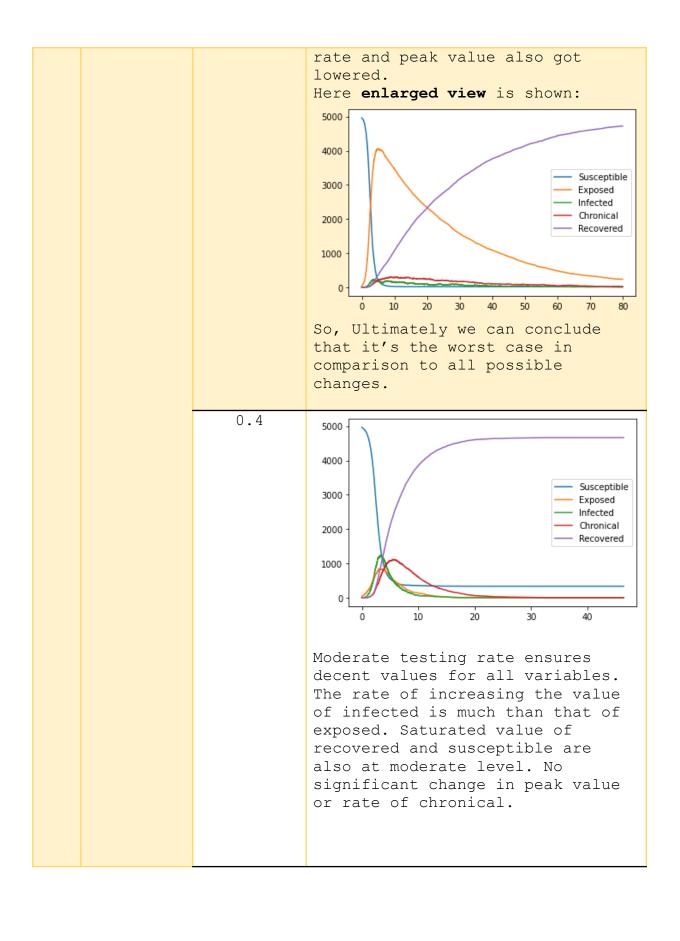
As **S** I transition is low so the variable infected is taking more time to reach at peak however keeping S E and E I transition rate fixed denotes that S I direct transition rate is too low and is going on indirectly via E variable , introducing a delay so ultimately recovery would take much time and we can see in graph variable R is taking slightly more time (5 units time) to reach it's saturated value. Similarly for susceptible also. And as all four variables are connected to I so it's low peak value and low increasing rate results low peak value for chronical and recovered .So ultimately the delay is propagated resulting long-last duration.

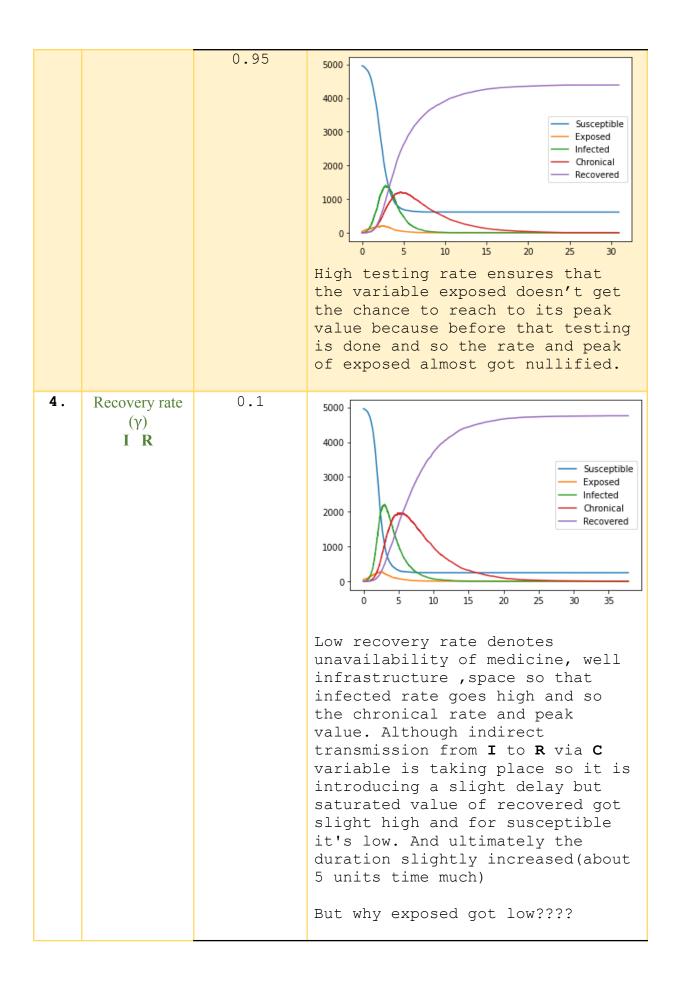
	?? why exposed got high whyyyy???
0.25	Now the rate for S I & S E is quite nearby values resulting almost same increasing rate and peak value for both I & E. Effect on other variables' values remain similar as discussed in previous. Susceptible Exposed Infected Chronical Recovered
0.9	Compared to the previous one (where $\beta=0.6$) here saturated value of susceptible is low and for recovered it is more, as comparatively more people got sick overally so after end of epidemic more people have gone through the process and got recovered and less remained susceptible. As S I transition is high so the variable infected reaches at peak too fast however keeping S E and E I transition rate fixed denotes that S I direct transition rate is too fast and is going on indirectly via E variable ,introducing a delay but direct transition dominates here so ultimately recovery would take less time and we can see in graph variable R quickly reaches it's saturated value. Similarly for susceptible also. And as all four variables are connected to I so

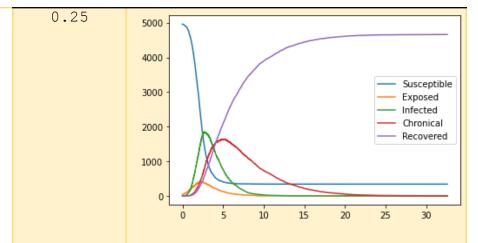




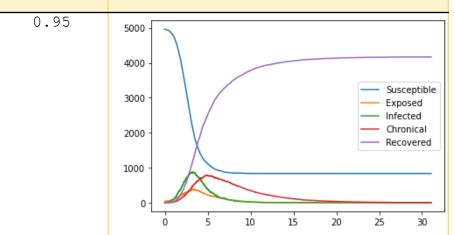






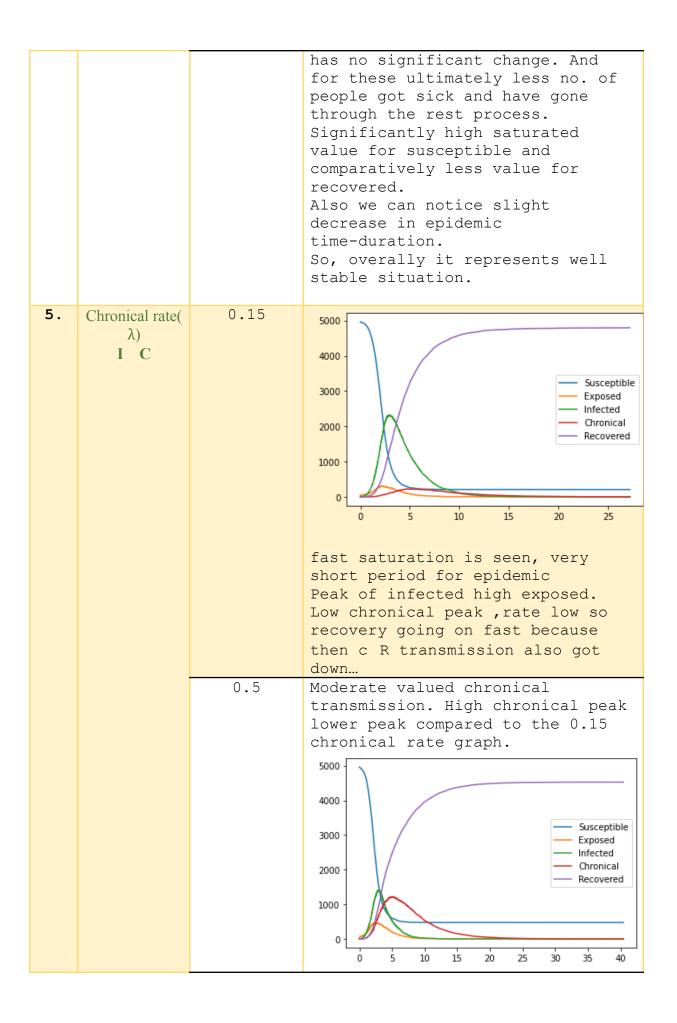


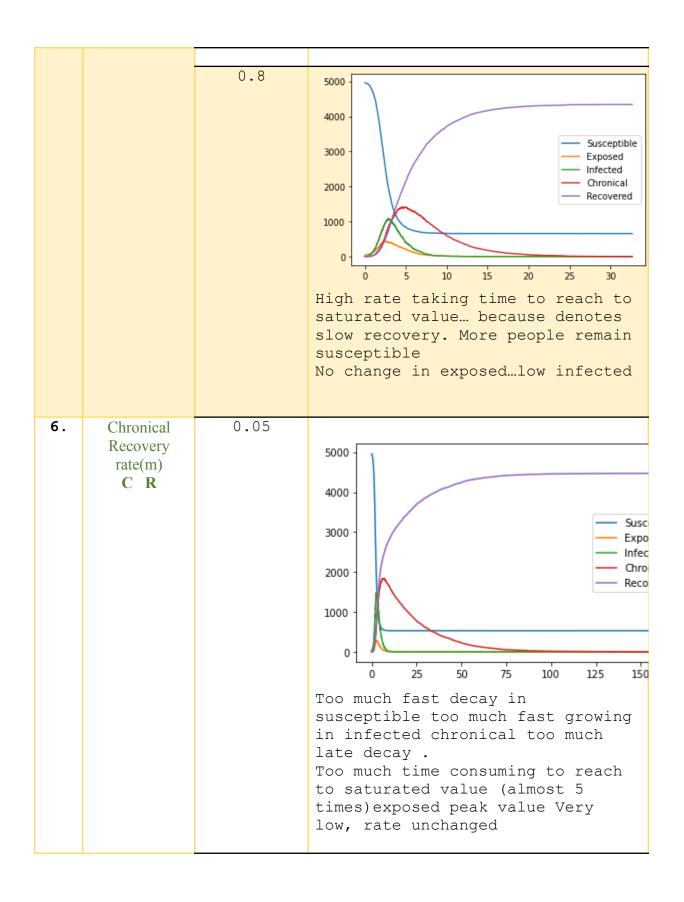
No significant change in Exposed rate and peak value.
Comparatively high value for peak of infected and the rate also.
And so the chronical (similar changes). And slight less rate of recovery results increased duration period. Saturated value of susceptible and recovered remain unchanged.

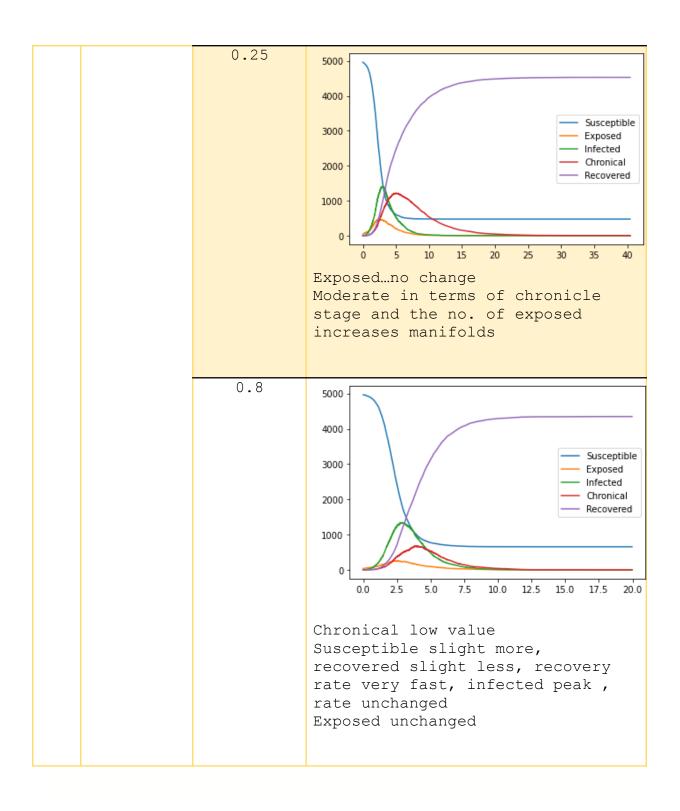


Well recovery rate means good infrastructure ,availability of space, medicine which dominates over S E and other transmissions of the spreading of the disease which indicates Variable I doesn't get much time to reach its peak value. Beforehand the spreading recovery is done. (people got 100% immune here: assumption)
So the infected peak value is quite low and so the chronical

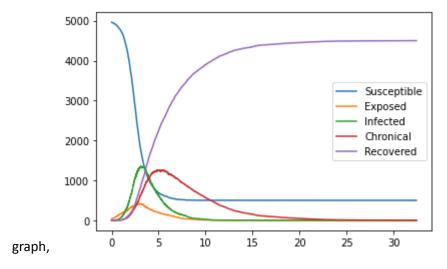
also and peak value of exposed





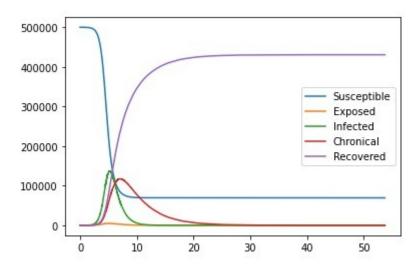


E.) While studying about the model of an epidemic . We come across some interesting facts. Firstly for experimentation we take a control experiment with no. of nodes =5000, degrees per node(avg)=6 and the initial no. of infection = 10 and initial no. of exposed people =40. In the results we see the

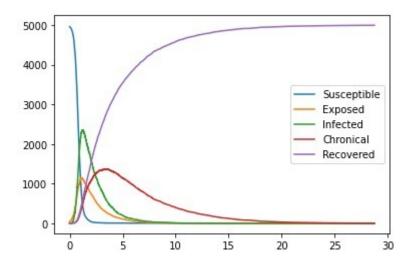


Now to study the various aspects of the graph we first take the nodes.

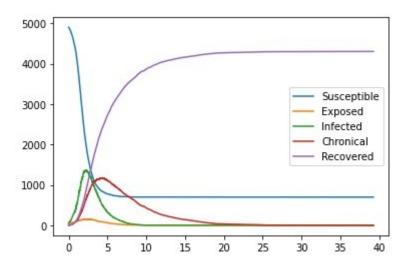
We increase the no. of nodes to 500000 and keeping all other parameters constant we get the following graph



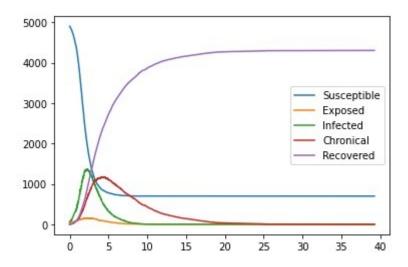
After this we increase the degrees from 6 to 15 and keeping the rest of the parameters at the control level we get the following graph



Again keeping the rest of the parameters at the control value we change the no. of initial infection to 100 from 10 and we get the following graph.



Again keeping all other parameters at the control level we change the value of the initial exposed to 200 from 40.



According to the graphs we received as the results we see that in the first case we can observe that the rate of change of slope of the graph with no. of nodes 500000 is much higer when compared with the control experiment.

When we look at the second graph and compare it with the control we see the infection is much higher and the peak is touched very fast. So we can say that in a well connected society where the people are more connected to each other an epidemic reaches the fast and creates the maximum damage and gests flattened the fastest due to herd immunity.

When we look at the third graph and compare it with the control experiment we see that the graph shifts toward the left hand side if we increase the no. of initial infections the graph shifts towards the left (the infection graph only)

Again we see if we increase the no. of initial exposed and compare it with the control we get the fourth curve which shows us that the exposed graph shifts towards the left. And vice versa now,

When we study mode about the epidemic from the graphs we see that the more the no. of people and more the connected they are the higher id the slope resulting the disease will spread faster in that area. So those areas with a higher population density and a higher percentage of inter connected communities we see that there will be a greater spread of the disease and in those areas there will be a very less reaction time in those areas and may lead to the shortage of medicines and health care facilities in the locality leading to a higher no. of deaths and higher economic imbalance in the area .

When it comes to the future of the disease we see the curve if flattened faster in a well connected locality and as a result herd immunity is developed faster in these areas and there also remains a very less scope of viral genome getting mutated to a new variant and probably more dangerous but in all the other cases the virus sits in the society for an ample amount of time and has more chances of forming a variant and again returning back to the society .

We must also take into view the factors we neglected wile forming the above graphs such as a lockdown or use of masks, or drinking of filtered water and avoidation of raw food . also we neglected the probable use of vaccinations against the microbial genome and also the health care of the area where the epidemic had spread. From the above graphs we can see the above features about the bacteria/ virus and the outcome of the epidemic and the future of the epidemic.

The	End