Final Project

Pandemic Simulator

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Section I

Introduction

In this notebook, we'll develop a model of a pandemic as it directly spreads in a susceptible population, and explore the effectiveness of interventions such as vaccination and quarantining . Epidemiologic modeling is important for understanding disease spread and developing plans to control the spread. In Section II, we establish a strong foundation by building the simpliest SI model to discover the underlying ordinary differential equations that dictate the rules for the system and an inuitive sense for how to extend the model to capture more nuances which correspond to a more realistic model.

According to 2022 census records, the city of Banner Elk in North Carolina has a population of approximately 1,000 people. Banner Elk will be the center of our attention as we simulate the spread of an infection in the city. To simplify our study we assume the town will have a fixed population, i.e., no vital processes. We introduce well-known models of infectious disease, the SI model, the SIR (Kermack-McKendrick) model, SIS model, SIRS model, SIRV model and use them to explain the progression of the disease over the course of 2,000 days.

Section II

Implementation

The following models were produced with the Epidemics on Networks (EoN) package for python

Citations:

Journal of Open Source Software publication

EoN documentation

The following packages are necessary for this notebook:

In [ ]:
```
import EoN
import networkx as nx
from collections import defaultdict
import matplotlib.pyplot as plt
import matplotlib.animation as animation
import numpy as np
from PIL import Image
from IPython.display import HTML
```

SI Model

Initially, we consider a model with no recovery rate, a person is considered to be either susceptible or infected. A real life example of a SI disease is the herpesvirus family of viruses which characteristically establishes latent infection within specific tissues [1]. The interaction between the two classes of population results in a flow from susceptible to infected over time. We can write this as the following rates of change for S and I respectively:

$\frac{dS}{dt} = -\beta SI$

$\frac{dI}{dt} = \beta SI$

This nonlinear system of differential equation can be solved assuming the population remains constant by adding the two equations. We arrive at $\frac{dS}{dt} + \frac{dI}{dt} = 0$ which can be integrated giving us $S(t) + I(t) = S(0) + I(0)$. The initial population is N so we write $S(t) + I(t) = N$ to allow us to replace S in the rates above with $N - I$. Our new equation is as follows

$\frac{dI}{dt} = \beta(N - I)I.$

If $I(0) > 0$, then the equilibrium N will be approached as t approaches infinity. Simply put the SI model predicts that everyone will become infected as long as there is an initial infected population.

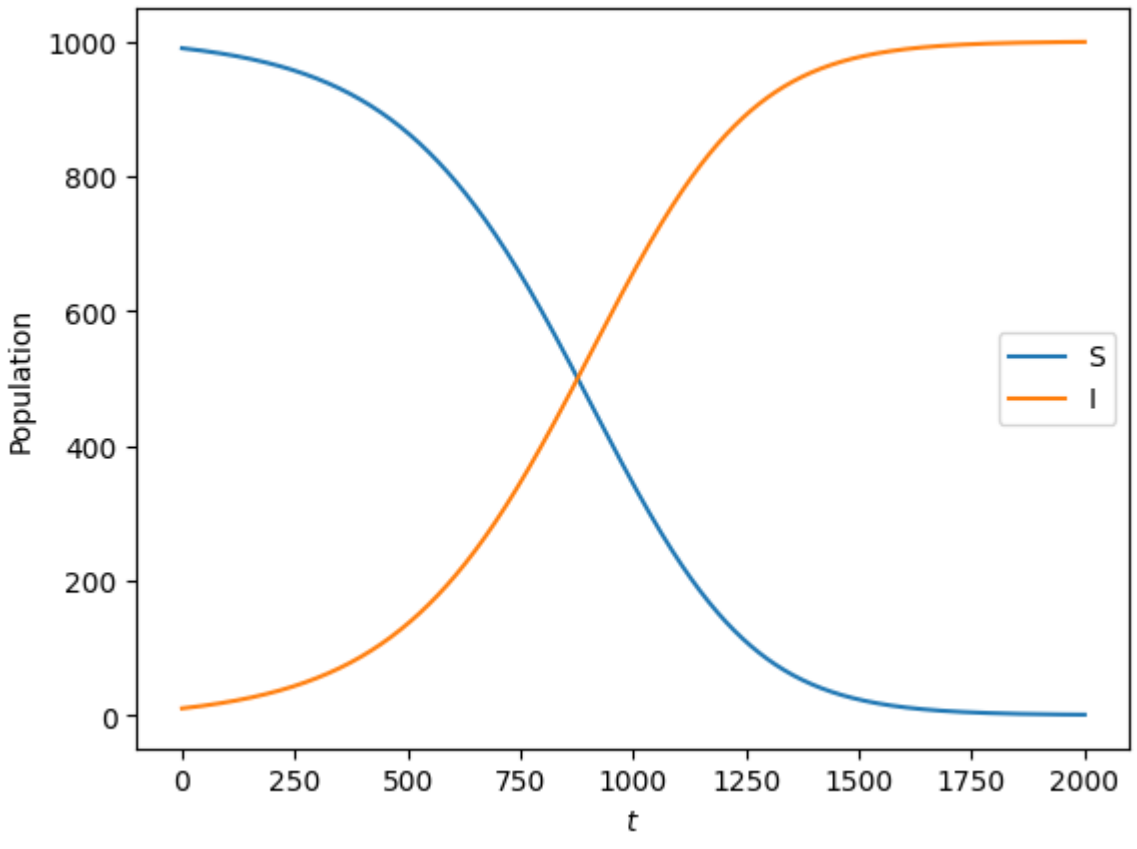
Furthermore, we choose to investigate the value R_0 which is defined as the total number of new infected caused by each infected individual, on average.

$R_0 = \beta \cdot \langle k \rangle \cdot d = 0.0015 \cdot 5 \cdot 2000 = 15$

For a population of 1000 we expect an infected person to cause 15 new infections on average [2].

The graph produced below illustrates how fast an outbreak can occur once enough fuel is provided. There are ~10% infected 400 days in to the simulation, then the infection skyrockets to 50% in another 400 days. We observe in the span of 1600 days from the start a total infection of the population.

In [ ]:
```
N=1000
rho = 0.01      #intial infected
kave = 5
gamma = 0       #recovery rate
beta = 0.0015    #transmision rate

S0 = (1-rho)*N
I0 = rho*N
SI0 = (1-rho)*kave*rho*N
SS0 = (1-rho)*kave*(1-rho)*N
t, S, I = EoN.SIS_homogeneous_pairwise(S0, I0, SI0, SS0, kave, beta, gamma, tmax=2000)

plt.plot(t, S, label = 'S')
plt.plot(t, I, label = 'I')
plt.xlabel('$t$')
plt.ylabel('Population')
plt.legend()
plt.show()
```



SIR Model

The SIR model introduces another compartment for the population to be partitioned into after recovering from an infection. It should be noted that individuals recover with permanent immunity. This type of model is relevant for studying diseases such as measles, mumps, and smallpox.

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

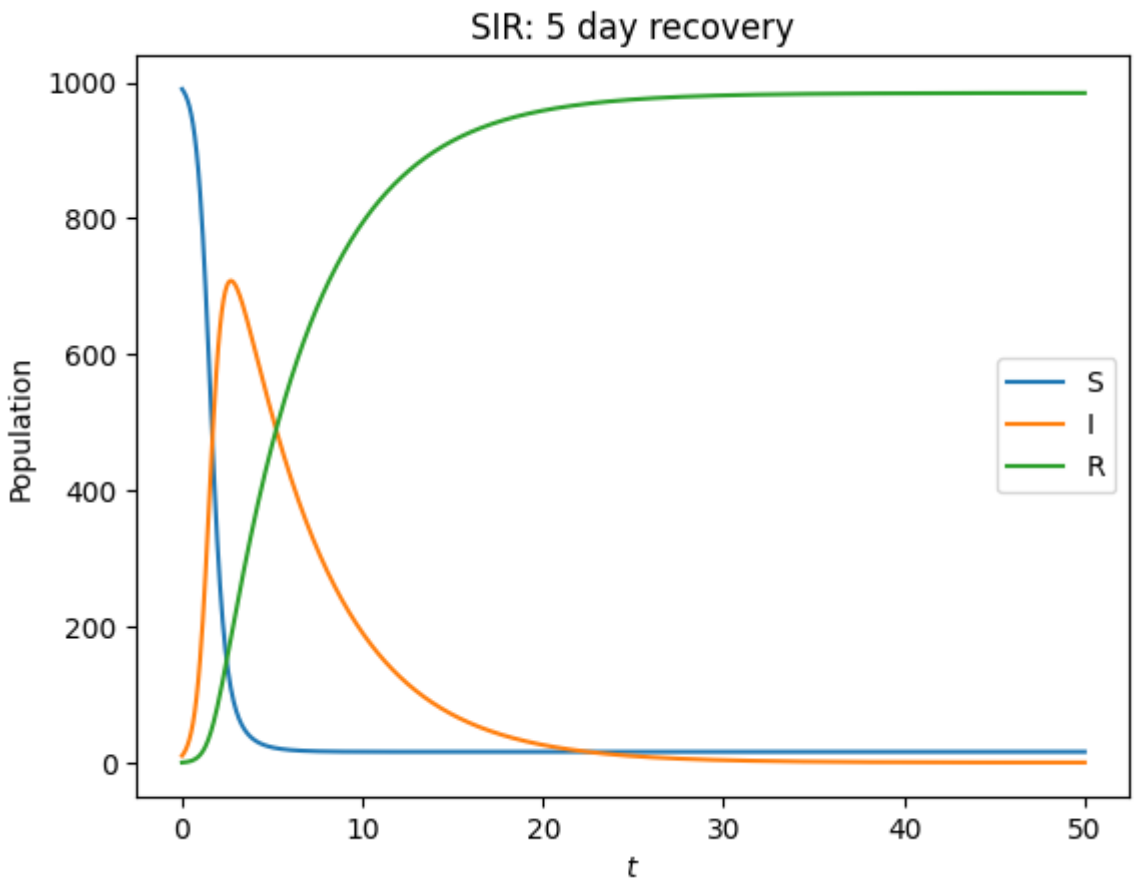
$$\frac{dR}{dt} = \gamma I$$

Initially, $S \approx N$ and $I < N$ we can rewrite the rate of infection as $\frac{dI}{dt} = I(\beta N - \gamma)$. Solving the differential equation gives us $I(t) = I(0)e^{\beta N - \gamma}$. We are interested in a growing exponential, an epidemic, which occurs when $\beta - \gamma > 0$ or equivalently $\beta/\gamma > 1$.

The basic reproductive ratio can now be solved as follows $R_0 = \beta/\gamma = \frac{0.65}{0.2} = 3.25$.

In this closed system, an epidemic will die out because there is not enough susceptible individuals to sustain the disease after the exponential outbreak. In about 4 days the epidemic infects 70% of the population but rapidly drops to 0 by day 30.

In [ ]:
```
N = 1000             #population
rho = 0.01           #initial infected
kave = 5.5             #average degree
gamma = 0.2         #recovery rate
beta = 0.65          #transmission rate

phiS0 = 1-rho
def psi(x):
    return (1-rho)* np.exp(-kave*(1-x))
def psiPrime(x):
    return (1-rho)*kave*np.exp(-kave*(1-x))

t, S, I, R = EoN.EBCM(N, psi, psiPrime, beta, gamma, phiS0, tmax = 50)
plt.plot(t, S, label = 'S')
plt.plot(t, I, label = 'I')
plt.plot(t, R, label = 'R')
plt.xlabel('$t$')
plt.ylabel('Population')
plt.title("SIR: 5 day recovery")
plt.legend()
plt.show()
```



SIS Model

In the SIS model, recovery does not give immunity to the disease since individuals move from the susceptible class to the infective class and then back to the susceptible class upon recovery. This type of model is most appropriate for bacterial agent diseases such as streptococcal sore throat, meningitis and venereal diseases, and for protozoan agent diseases such as malaria and sleeping sickness [3]. As a natural extension from the SI model, the SIS model simply needs the addition of a rate of change from infected to susceptible as follows

$$\frac{dS}{dt} = \gamma I - \beta SI$$

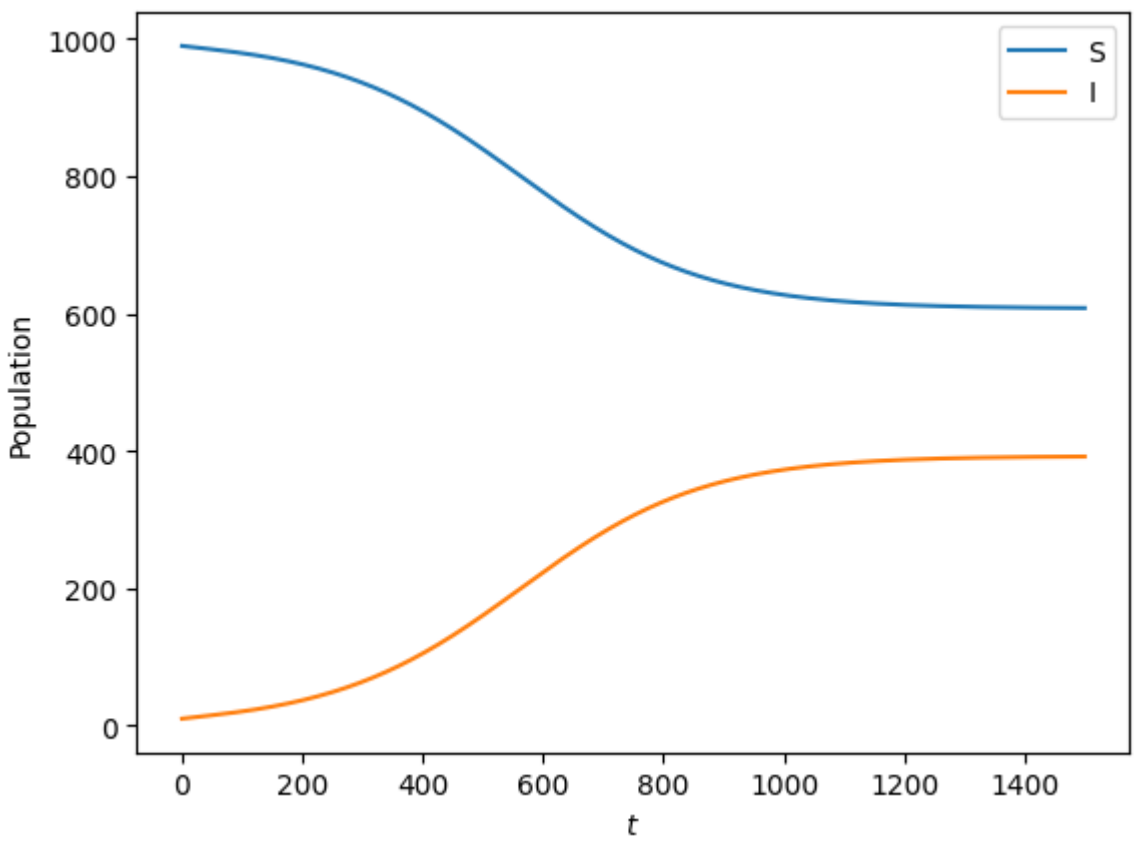
$$\frac{dI}{dt} = \beta SI - \gamma I$$

Using the same substitution in the SI model above, we arrive at the equation

$$\frac{dI}{dt} = I(\beta N - \gamma) - \beta I^2.$$

Assuming there is an positive initial infective fraction, when $\beta/\gamma > 1$, it stands to reason, that ratio approaches a constant endemic value; otherwise, the disease will die out. The graph below shows an outbreak approaching 40% infected population and 60% susceptible population at steady state. For $R_0 = 2.5$, the infected fraction at equilibrium is $\zeta = 1 - (\frac{1}{2.5}) = 40\%$ as expected.

In [ ]:
```
N = 1000
rho = 0.01
kave = 6

gamma = 0.013
beta = 0.004

S0 = 990
I0 = 10
SI0 = (1-rho)*kave*rho*N
SS0 = (1-rho)*kave*(1-rho)*N
t, S, I = EoN.SIS_homogeneous_pairwise(S0, I0, SI0, SS0, kave, beta, gamma, tmax=1500)
plt.plot(t, S, label = 'S')
plt.plot(t, I, label = 'I')
plt.xlabel('$t$')
plt.ylabel('Population')
plt.legend()
plt.show()
```



SIRS Model

The SIRS model is a natural extention of the SIR model, like the SI to SIS transformation, by allowing a recovered individual to become once again infected. Airborne diseases like seasonal influenza and COVID-19 are the most apparent examples of disease accurately modeled by SIRS. We encourage exploration of an intermediary exposed state (SEIR, SEIRS models), but the additional effort is beyond the scope of our investigation. The following equations define the rates in our SIRS model:

$$\frac{dS}{dt} = -\beta SI + \xi R$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

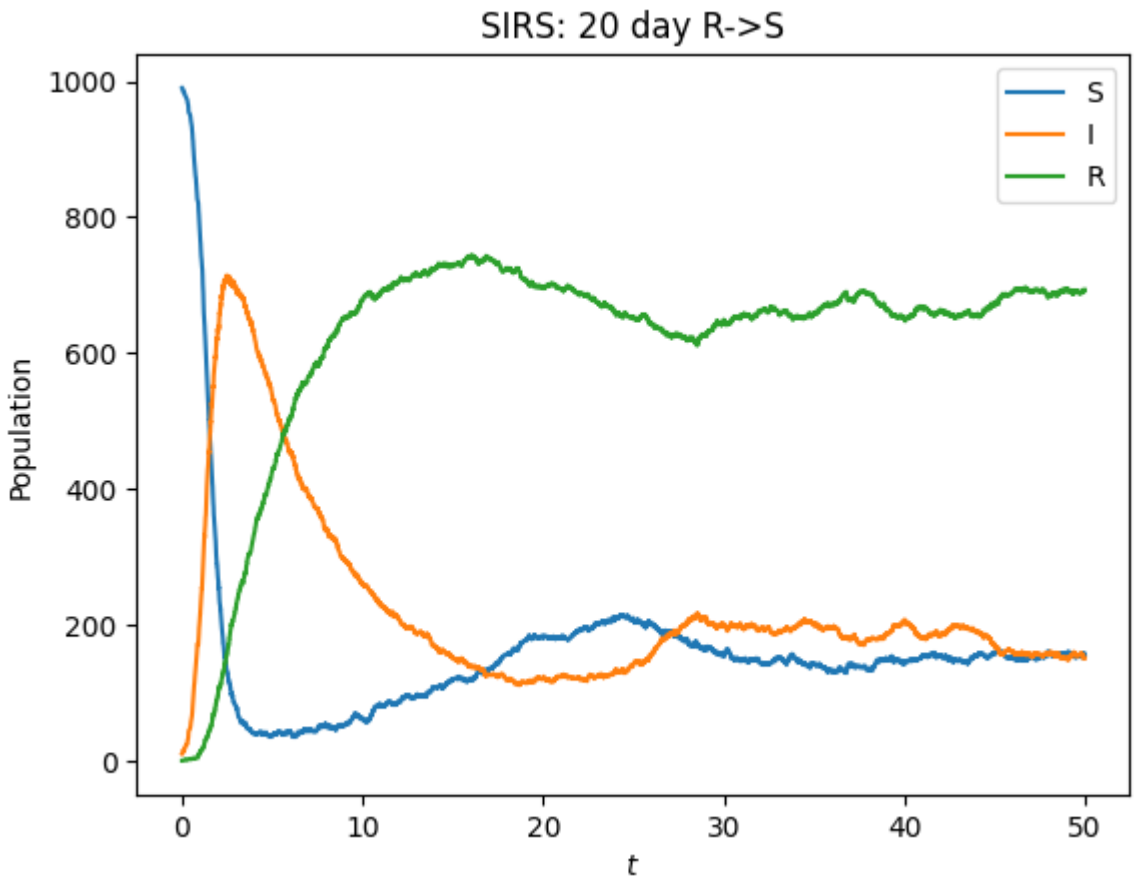
$$\frac{dR}{dt} = \gamma I - \xi R$$

To convert a 20 day turn around, recovery to susceptible, into an applicable rate we invert the number giving us $\xi = 0.05$.

$$R_0 = \beta/(\gamma + \xi) = 0.7/(0.2 + 0.05) = 2.8$$

In [ ]:
```
N = 1000
kave = 5    #expected number of partners
G = nx.fast_gnp_random_graph(N, kave/(N-1))

H = nx.DiGraph()  #DiGraph showing possible transitions that don't require an interaction
H.add_edge('I', 'R', rate = 0.2)   #Recovery rate
H.add_edge('R', 'S', rate = 0.05)   #Recovered -> Susceptible

J = nx.DiGraph()    #DiGraph showing transition that does require an interaction.
J.add_edge(('I', 'S'), ('I', 'I'), rate = 0.7)  #Infect rate

IC = defaultdict(lambda: 'S')
for node in range(10):
    IC[node] = 'I'

return_statuses = ('S', 'I', 'R')

t, S, I, R = EoN.Gillespie_simple_contagion(G, H, J, IC, return_statuses, tmax = 50)

plt.plot(t, S, label = 'S')
plt.plot(t, I, label = 'I')
plt.plot(t, R, label = 'R')
plt.xlabel('$t$')
plt.ylabel('Population')
plt.title("SIRS: 20 day R->S")
plt.legend()
```

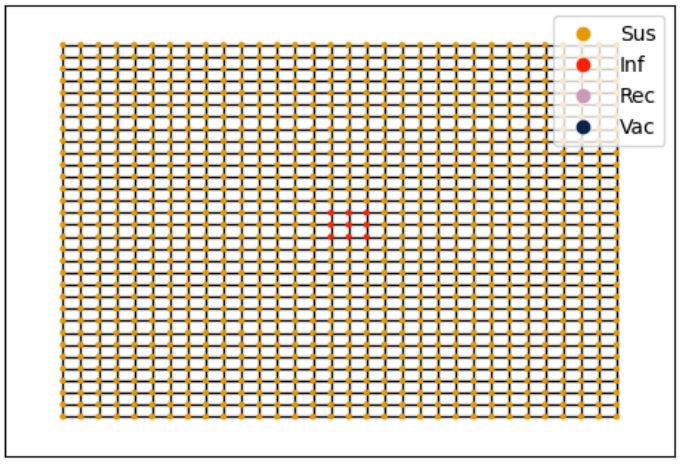
Out[ ]:
```
<matplotlib.legend.Legend at 0x2247289c280>
```

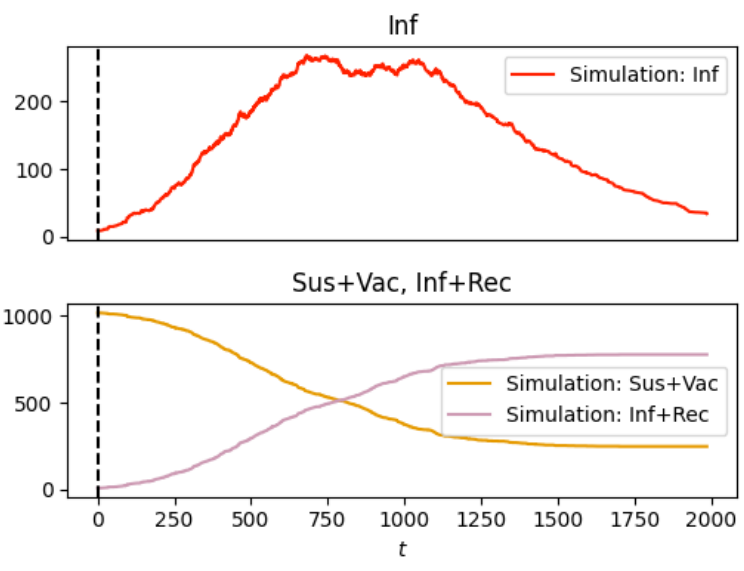


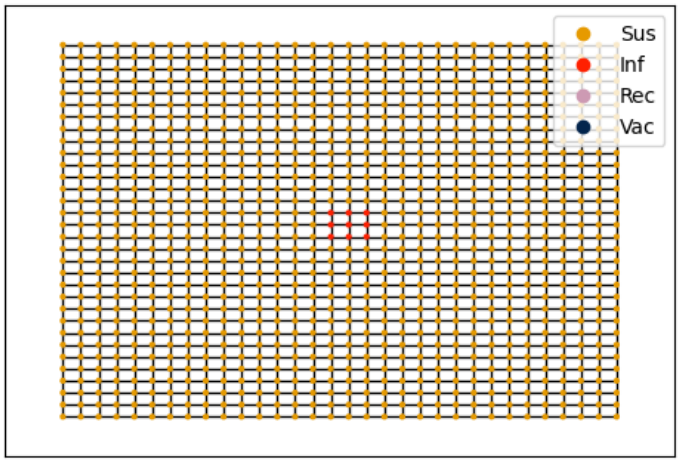
SIRV Model

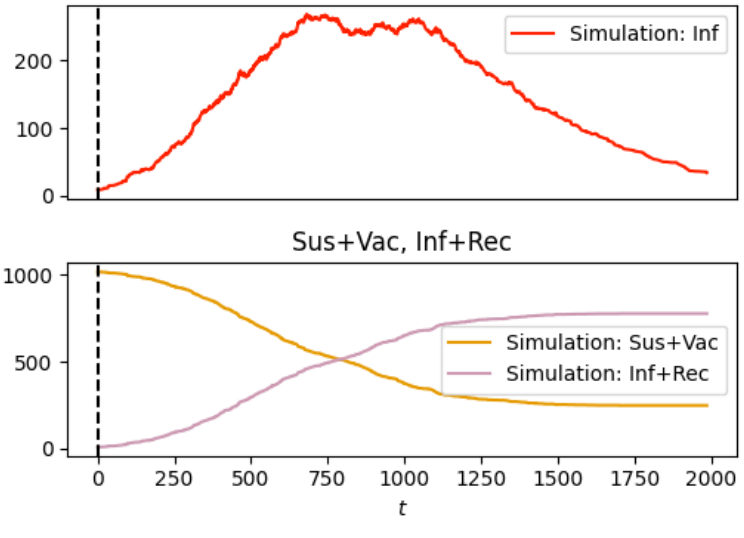
The SIRV model includes the addition of a vaccination, that is an SIR disease where a vaccine prevents infection. Each person has a chance to become vaccinated randomly, without regard for the status of their neighbors, but they must be susceptible. Modeling a vaccine can also give us insight into the herd immunity threshold, which depends on the R_0, where the population as a whole has protection against the disease. A population with herd immunity will see a drop in infection rate where the disease eventually trails off. We have had success overcoming the polio disease in the United States due to the efforts of virologist and medical researcher Jonas Salk. [4]

In [ ]:
```
G = nx.grid_2d_graph(32,32) #each node is (u,v) where 0<=u,v<=32    32x32 = 1024 population
#we'll initially infect those near the middle
initial_infections = [(u,v) for (u,v) in G if 14<u<18 and 14<v<18] # 3x3 = 9 initial infected
H = nx.DiGraph() #the spontaneous transitions
H.add_edge('Sus', 'Vac', rate = 0.0003)
H.add_edge('Inf', 'Rec', rate = 0.0025)
J = nx.DiGraph() #the induced transitions
J.add_edge(('Inf', 'Sus'), ('Inf', 'Inf'), rate = 0.01)

IC = defaultdict(lambda:'Sus')
for node in initial_infections:
    IC[node] = 'Inf'

return_statuses = ['Sus', 'Inf', 'Rec', 'Vac']

color_dict = {'Sus': '#E69A00','Inf':'#ff2000', 'Rec':'#CD9AB3','Vac': '#03254c'}
pos = {node:node for node in G}
tex = False
sim_kwargs = {'color_dict':color_dict, 'pos':pos, 'tex':tex}

sim = EoN.Gillespie_simple_contagion(G, H, J, IC, return_statuses, tmax=2000, return_full_data=True,

times, D = sim.summary()

newD = {'Sus+Vac':D['Sus']+D['Vac'], 'Inf+Rec' : D['Inf'] + D['Rec']}

new_timeseries = (times, newD)
sim.add_timeseries(new_timeseries, label = 'Simulation', color_dict={'Sus+Vac':'#E69A00', 'Inf+Rec':'

sim.display(time=1, node_size = 4, ts_plots=[['Inf'], ['Sus+Vac', 'Inf+Rec']])

ani=sim.animate(ts_plots=[['Inf'], ['Sus+Vac', 'Inf+Rec']], node_size = 4)
ani.save('SIRV_animate.gif', writer="pillow", dpi=100)
```



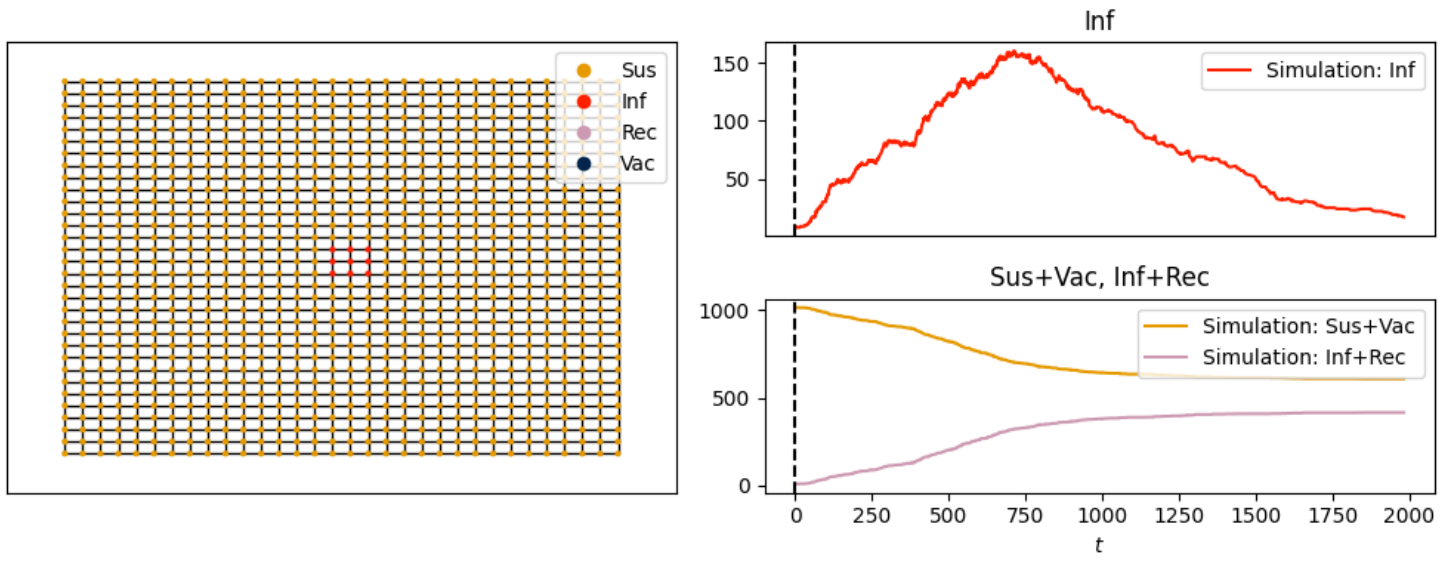


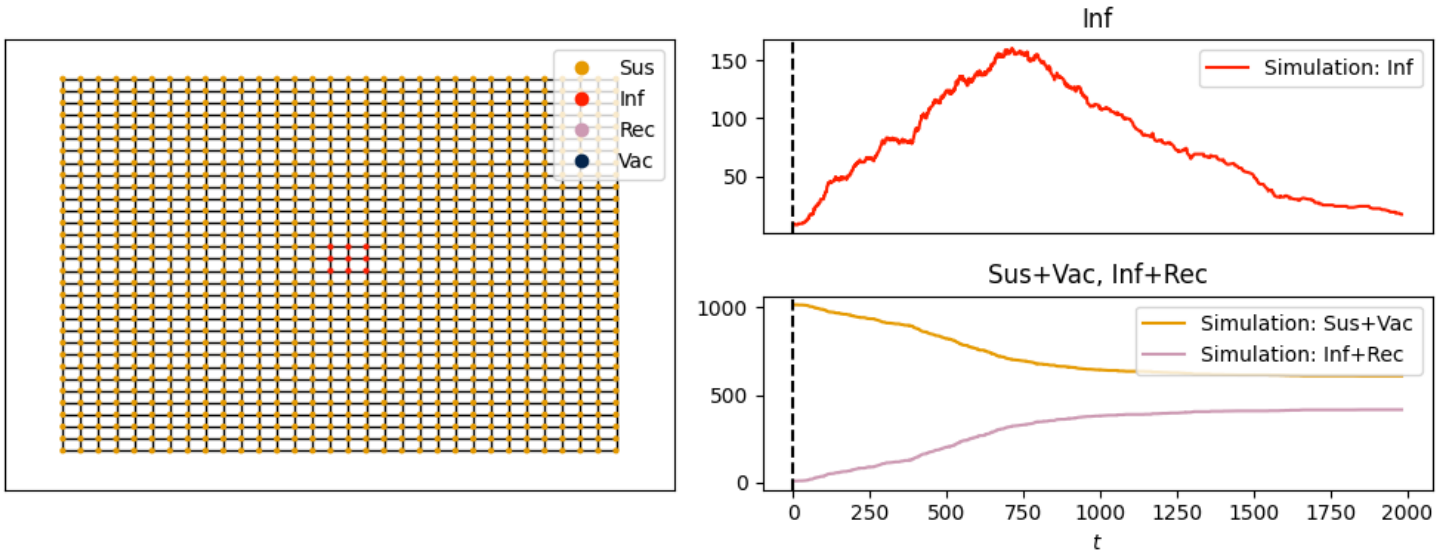




Below we demonstrate the effect of a higher vaccination rate using an identical model as above. We are interested in the effects of the infected population over the time period. It is remarkable that the height of the infection peak is lowered by ~50%, the peak infection duration is shortened by ~20%, and the equilibrium level for infection is lowered by ~65%. There is significant alleviation of infection with an increase of vaccination rates for a population dealing with a pandemic.

In [ ]:
```
G = nx.grid_2d_graph(32,32) #each node is (u,v) where 0<=u,v<=32
#we'll initially infect those near the middle
initial_infections = [(u,v) for (u,v) in G if 14<u<18 and 14<v<18]
H = nx.DiGraph() #the spontaneous transitions
H.add_edge('Sus', 'Vac', rate = 0.0005)
H.add_edge('Inf', 'Rec', rate = 0.0025)
J = nx.DiGraph() #the induced transitions
J.add_edge(('Inf', 'Sus'), ('Inf', 'Inf'), rate = 0.01)

IC = defaultdict(lambda:'Sus')
for node in initial_infections:
    IC[node] = 'Inf'

return_statuses = ['Sus', 'Inf', 'Rec', 'Vac']

color_dict = {'Sus': '#E69A00','Inf':'#ff2000', 'Rec':'#CD9AB3','Vac': '#03254c'}
pos = {node:node for node in G}
tex = False
sim_kwargs = {'color_dict':color_dict, 'pos':pos, 'tex':tex}

sim = EoN.Gillespie_simple_contagion(G, H, J, IC, return_statuses, tmax=2000, return_full_data=True,

times, D = sim.summary()

newD = {'Sus+Vac':D['Sus']+D['Vac'], 'Inf+Rec' : D['Inf'] + D['Rec']}

new_timeseries = (times, newD)
sim.add_timeseries(new_timeseries, label = 'Simulation', color_dict={'Sus+Vac':'#E69A00', 'Inf+Rec':'

sim.display(time=1, node_size = 4, ts_plots=[['Inf'], ['Sus+Vac', 'Inf+Rec']])

ani2=sim.animate(ts_plots=[['Inf'], ['Sus+Vac', 'Inf+Rec']], node_size = 4)
ani2.save('SIRV_animate.gif', writer="pillow", dpi=100)
```



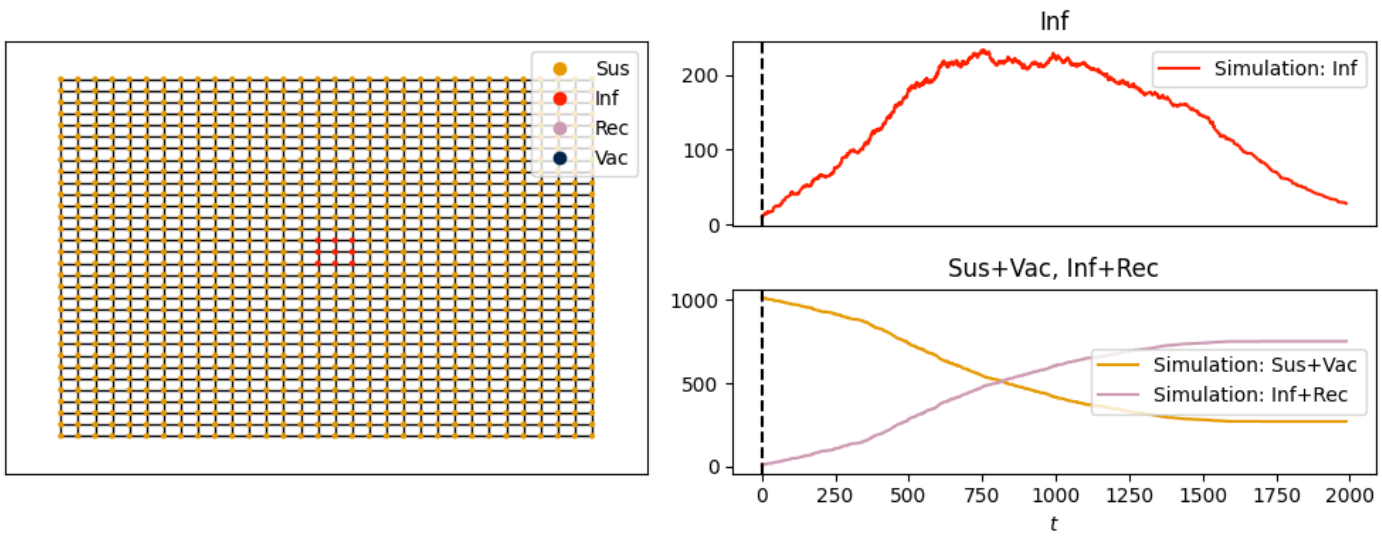


Animating the effects of vaccine

Below we have the animations of the previously discussed simulations of vaccinations in a SIR model. We seek to gain better visual clarity for the spread of infections by exploring different dimensionalities.

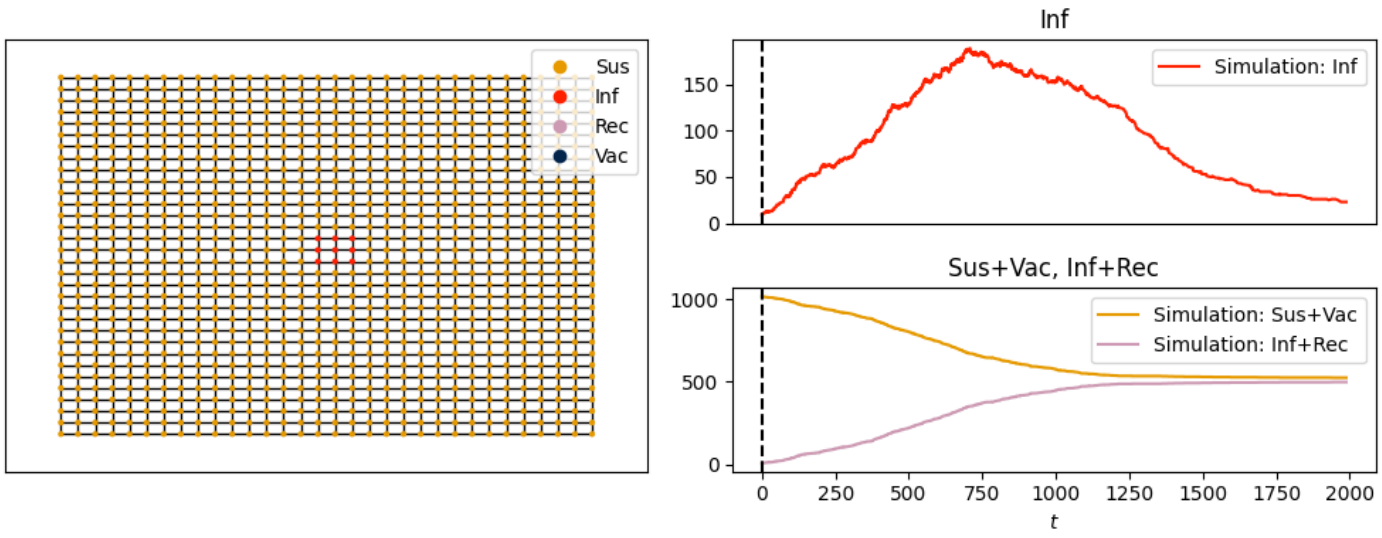
In [ ]:
```
HTML(ani.to_jshtml())
```

Out[ ]:



In [ ]:
```
HTML(ani2.to_jshtml())
```

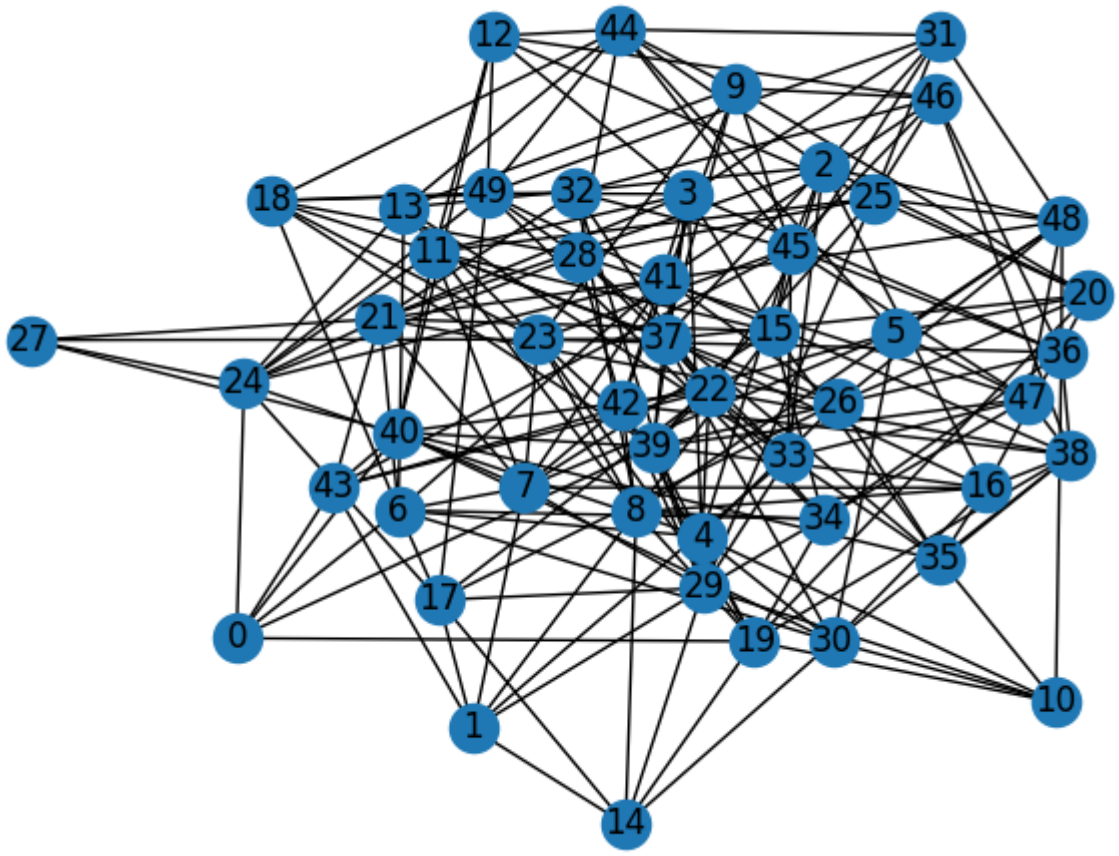
Out[ ]:



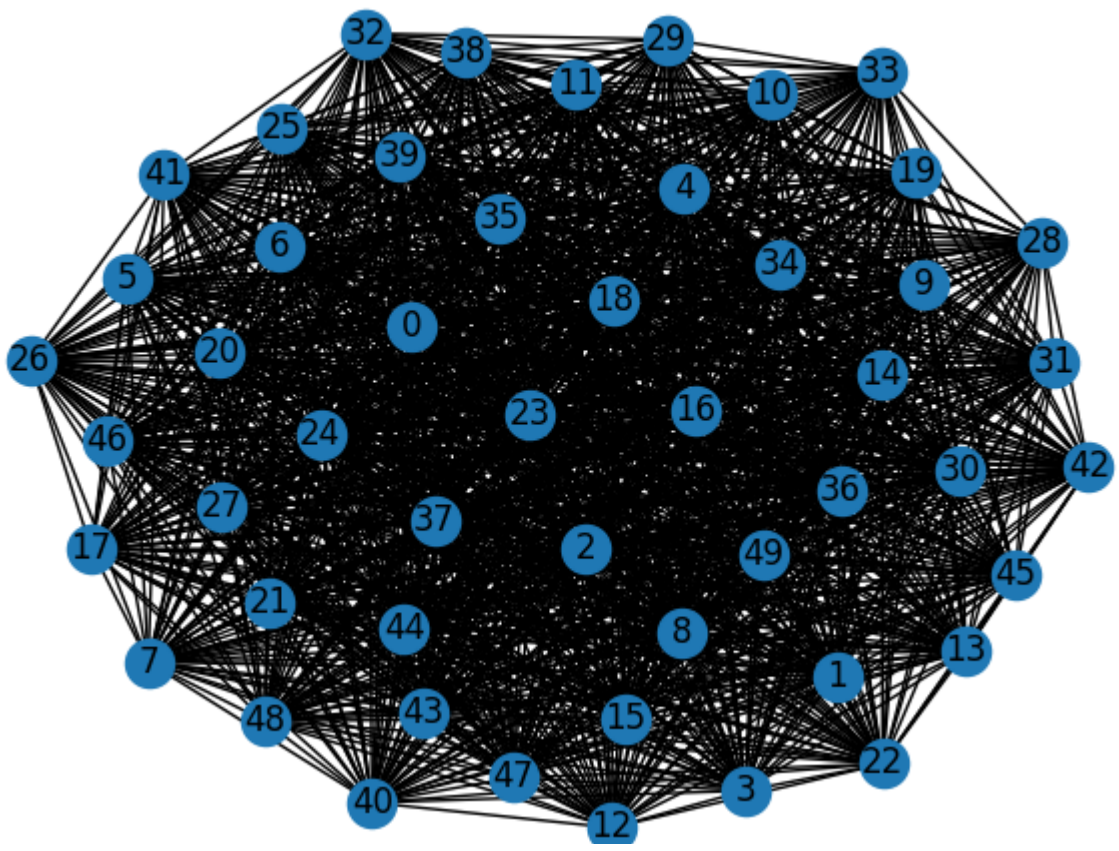
Once Loop Reflect

Node Implementation G(n,p)

Each person in these models are connected to each other via edges. Edges are a representation of how they different nodes(persons) know or interact with one another.



If an $I(t)$ node is connected to a $S(t)$ this does not mean the $S(t)$ node will become infected. There are rules in place that dictate this. For example, a $I(t)$ node has a choice on whether to "go out" or quarantine. If they decide to go out, then they risk infecting on of their friends and family. Further, each node, when infected has a $infection.prob$, if the $infection.prob$ is greater than a random generated number, they will infect that node. It is important to note that on average, each node has one to five connections. This can increase dramatically, if a node decides to go to a party or a big event, with other nodes. To model this, we implemented an increase of connections between nodes, based on friends/families in the community.



Mask vs Maskless

In this scenario, we utilize the node implementation described above to abstract the usage of masks, specifically in the SIR model, in order to demonstrate how effective they can be in curtailing a pandemic.

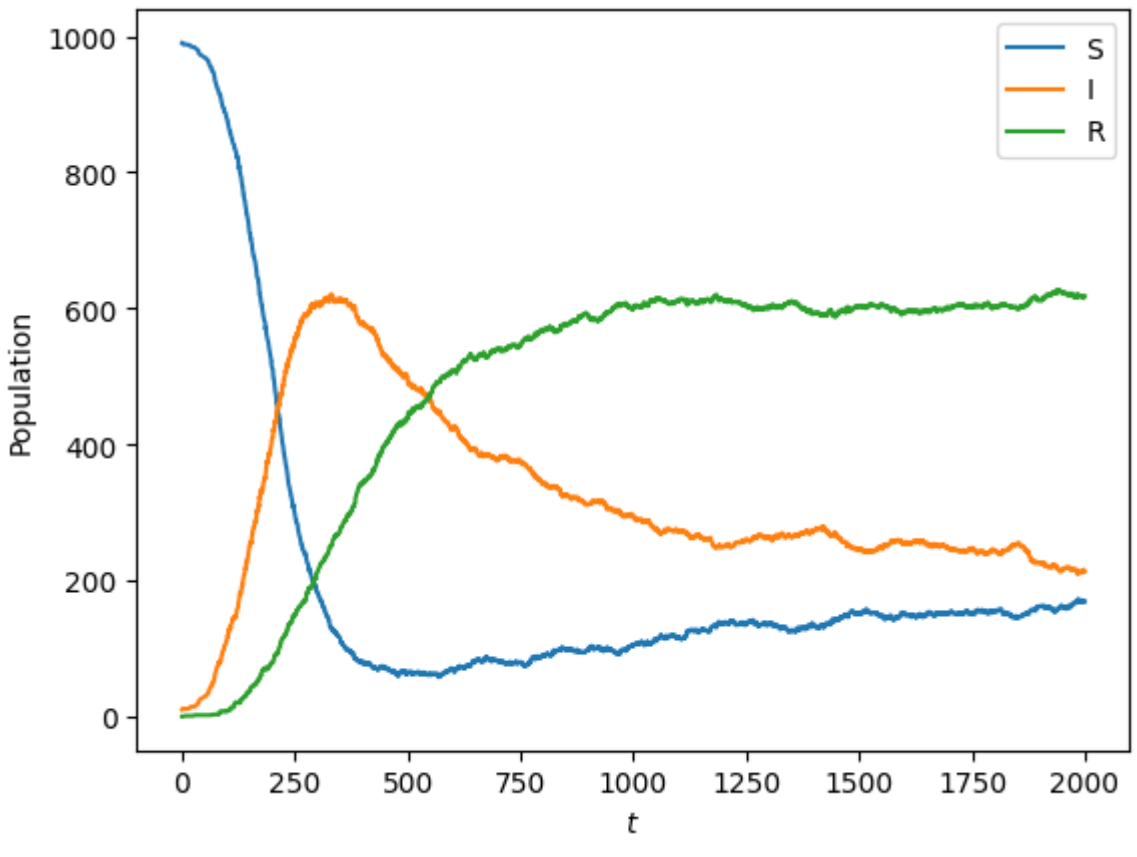
Modeling Maskless

First we run the simulation with the rate of infection without the mask factor applied to account for a maskless population. Overall, we want a baseline epidemic event to act as a control before we model the usage of masks on the same population.

In [ ]:
```
N = 1000
kave = 5    #expected number of friends/family
G = nx.fast_gnp_random_graph(N, kave/(N-1))

H = nx.DiGraph()
H.add_edge('I', 'R', rate = 0.0025)   #Recovery rate
H.add_edge('R', 'S', rate = 0.001)   #Recovered -> Susceptible

J = nx.DiGraph()
J.add_edge(('I', 'S'), ('I', 'I'), rate = 0.0065)  #IS->II, Maskless infection rate

IC = defaultdict(lambda: 'S')
for node in range(10):
    IC[node] = 'I'

return_statuses = ('S', 'I', 'R')
```

```
t, S, I, R = EoN.Gillespie_simple_contagion(G, H, J, IC, return_statuses, tmax = 2000)

plt.plot(t, S, label = 'S')
plt.plot(t, I, label = 'I')
plt.plot(t, R, label = 'R')
plt.ylabel('Population')
plt.xlabel('$t$')
plt.legend()
```

Out[ ]: <matplotlib.legend.Legend at 0x22472851e70>



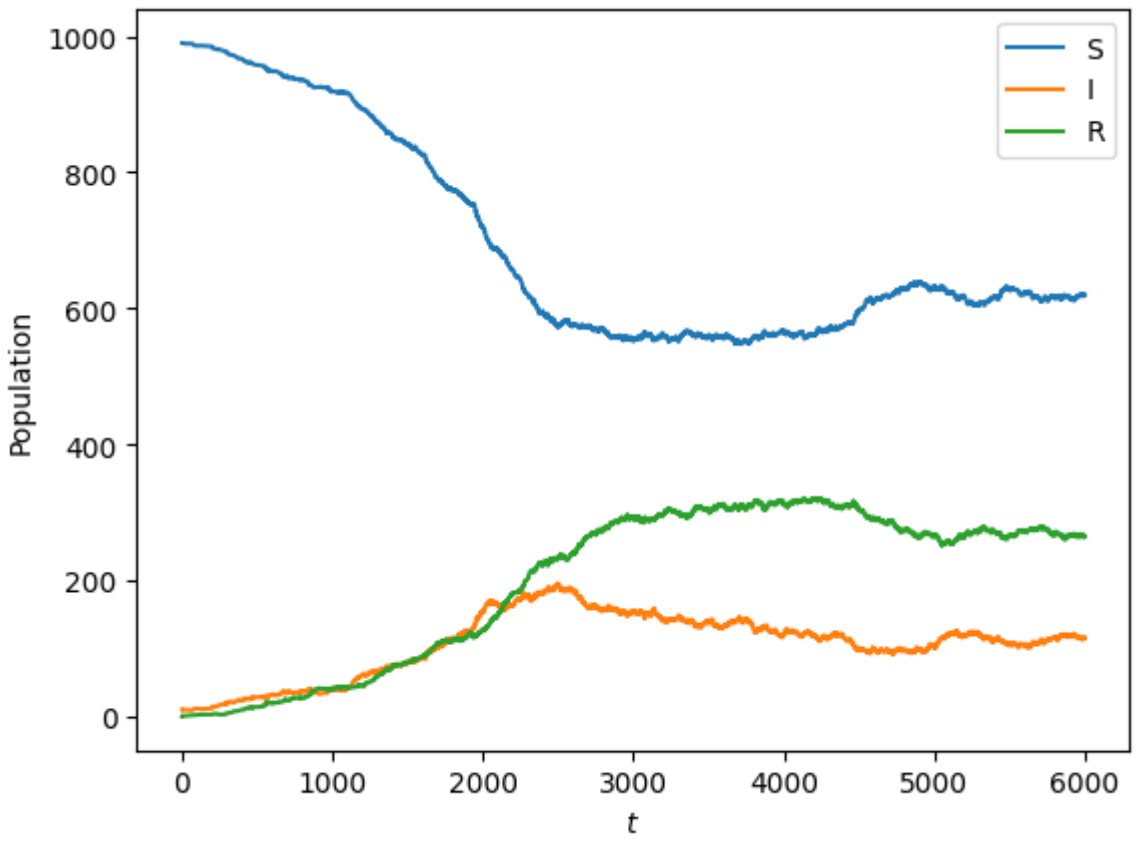
Modeling Masks

Reports indicate that 83% of masks assist with prevention of the COVID-19 virus. This is not a representation of how COVID-19 affects the population, but it is a starting point for how effective masks can be in a generalized pandemic scenario. Without masks, we start an infection rate of 0.0065. Taking 83% of 0.0065, we get 0.001105. As such this is the representation of how masks can affect a pandemic, if the population were to wear them at time [4].

Comparing the graph below to the the Mask simulation from above we see a stark difference in the infection peak height, peak duration, and steady state level. With a mask stopping 83% of an infection actually occuring for susceptible people, we had a significant decrease in many significant aspects of a pandemic. Based on our strong evidence, masks are an effective option for mitigating the negative effects of an epidemic event; however, we must note that different types of masks and their grades are not included, only the nonsurgical N95 is considered.

In [ ]:
```
N = 1000
kave = 5    #expected number of friends/family
G = nx.fast_gnp_random_graph(N, kave/(N-1))

H = nx.DiGraph()
H.add_edge('I', 'R', rate = 0.0025)   #Recovery rate
H.add_edge('R', 'S', rate = 0.001)   #Recovered -> Susceptible

J = nx.DiGraph()
J.add_edge(('I', 'S'), ('I', 'I'), rate = 0.001105)  #IS->II 83% of 0.0065

IC = defaultdict(lambda: 'S')
for node in range(10):
    IC[node] = 'I'

return_statuses = ('S', 'I', 'R')

t, S, I, R = EoN.Gillespie_simple_contagion(G, H, J, IC, return_statuses, tmax = 6000)

plt.plot(t, S, label = 'S')
plt.plot(t, I, label = 'I')
plt.plot(t, R, label = 'R')
plt.ylabel('Population')
plt.xlabel('$t$')
plt.legend()
```

Out[ ]:
```
<matplotlib.legend.Legend at 0x2240229db40>
```



Section III

Conclusion

To conclude we have started with a simplistic SI model and have worked to extend the model to simulate realistic aspects of epidemology. By establishing our models with rigor and maintaining that accuracy we demonstrate our credibility. The models of varying vaccination rates have yielded significant results that give credence to their efficacy in diminishing the severity of a pandemic disease. We can similiarly attribute the utilization of masks as another valuable intervention for disease control. Our instincts as researchers not only guide us to understand the world, but to also impact it positively with the knowledge gleaned from our efforts.