



Complex Network

Home work5

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Question :

- Simulate two epidemic models on two network models
- Four simulation scenarios

1.Epidemic model SIR

The so-called SIR model describes the spread of a disease in a population fixed to N individuals over time T

- Problem description

The population of N individuals is divided into three categories (compartments) :

- individuals S susceptible to be infected;
- individuals I infected;
- recovered from the disease individuals R (and now have acquired immunity to it);

where S , I and R are functions of t

The SIR model, like many others compartmental models in epidemiology depends on particular parameters that we introduce now :

- $\beta > 0$ the rate of contraction of the disease (transmission parameter)
- $\gamma > 0$: mean recovery rate

Individual S becomes infected after positive contact with an I individual. However, he develops immunity to the disease : he leaves I compartment at a γ cure rate.

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from scipy import integrate

%matplotlib notebook

[5] Python

Model functioning

The model is based on the following assumptions :

1. On average, an individual S in the population encounters β individuals per unit time
2. The rate of infected individuals leaving compartment I is γI per unit time (once an individual has been infected, he develops immunity to the disease).
3. The population size $N = S + I + R$ is constant.

This is the system of equations of the model :

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta S}{N} I, \\ \frac{dI}{dt} = \frac{\beta S}{N} I - \gamma I, \\ \frac{dR}{dt} = \gamma I. \end{cases}$$

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Some remarks on the model :

- The average infection period (i.e. the mean period during which an infected individual can pass it on) is equal to $\frac{1}{\gamma}$.
- It's a deterministic model
- The assumption of a constant average number of contacts β is a strong and constraining assumption : it cannot be applied to all diseases.
- We can imagine improving this model by taking into account for example :
 - newborns that would correspond to S susceptible individuals. We would introduce a birth rate b .
 - the deceased who would leave the compartments S or I with the same rate b : this allows to consider a constant population N .

Model diagram

The diagram below sums up the model SIR that we studied.

```

graph LR
    S[Susceptible] -- "βSI/N" --> I[Infectious]
    I -- "γI" --> R[Recovered]
  
```

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Source: Wikipedia

Problem formulation

We pose

$$X = \begin{pmatrix} S \\ I \\ R \end{pmatrix}$$

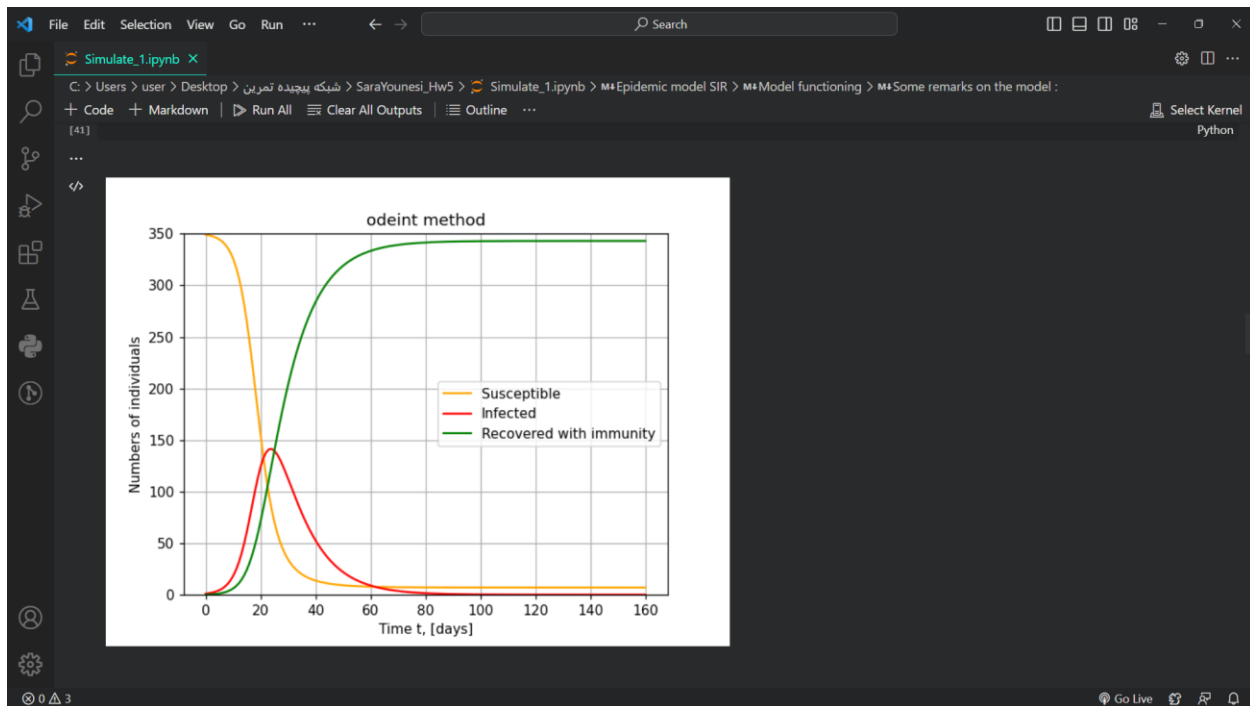
And we write our differential system so:

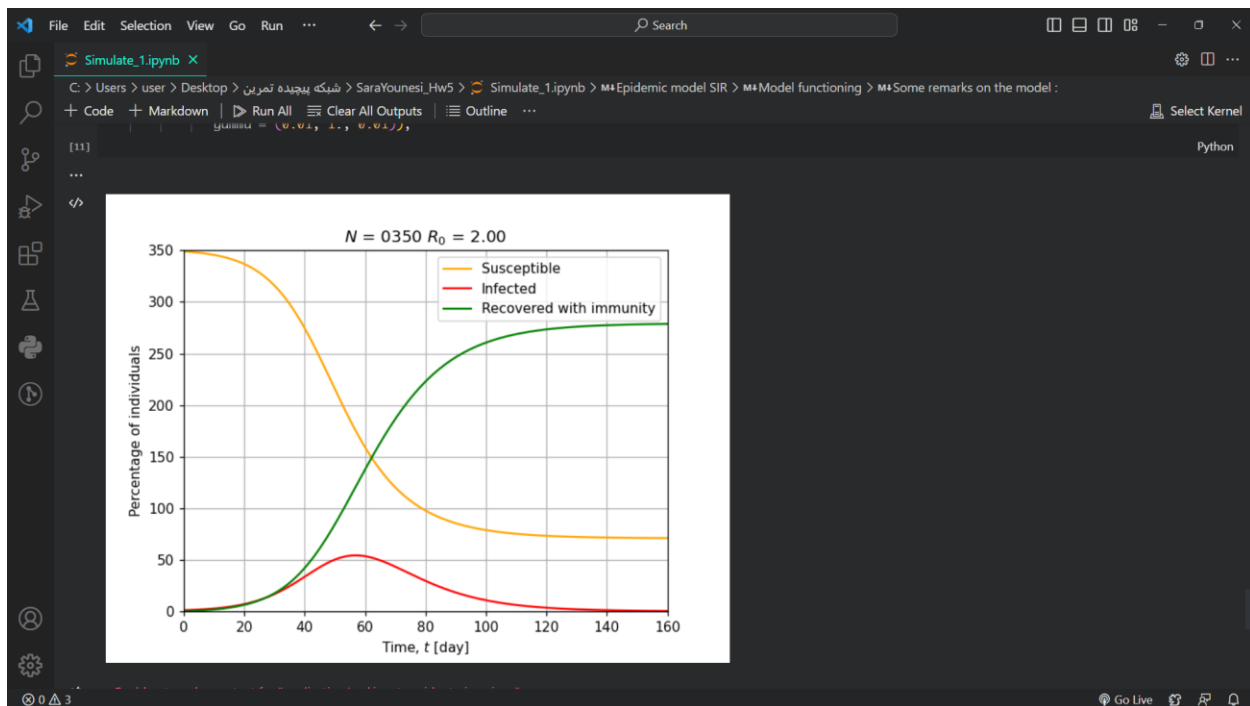
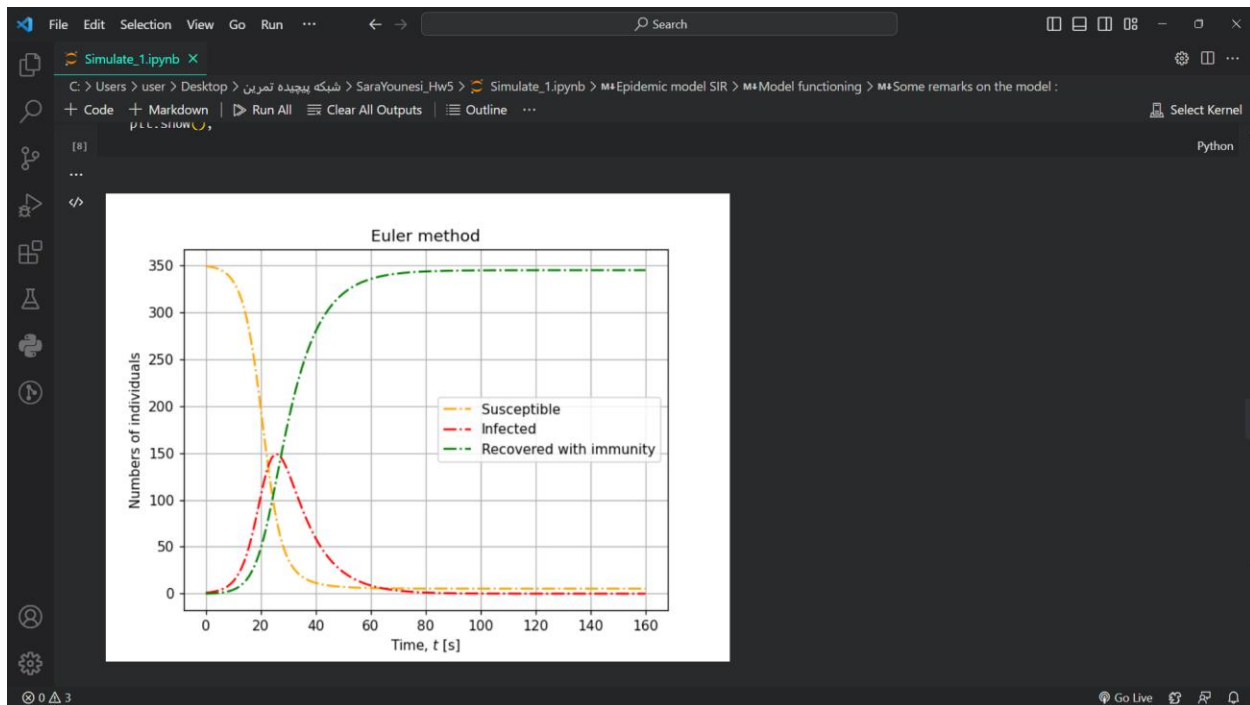
$$\dot{X} = \begin{pmatrix} -\frac{\beta S}{N} I \\ \frac{\beta S}{N} I - \gamma I \\ \gamma I \end{pmatrix} = f(X)$$

Settings

N = 350. #Total number of individuals, N

Go Live





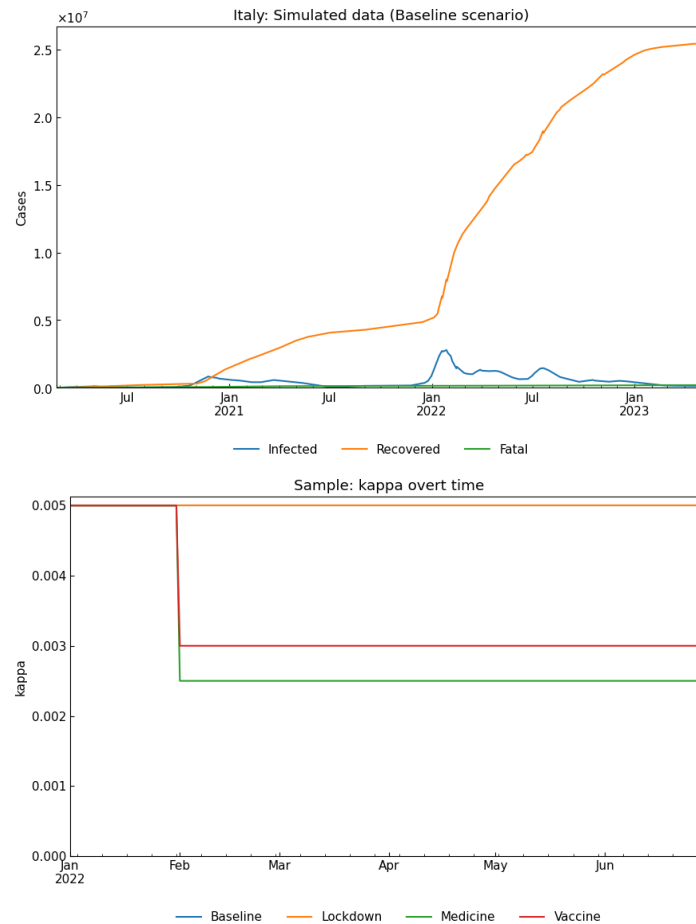
2.Covid 19-SIR

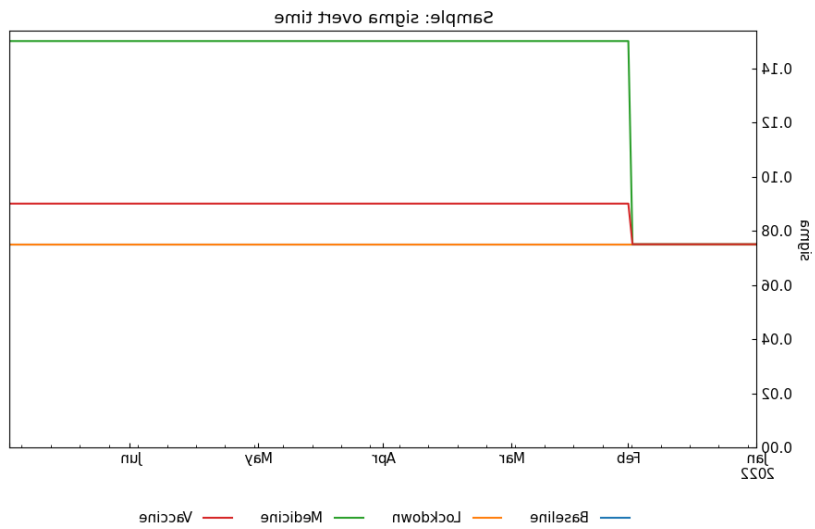
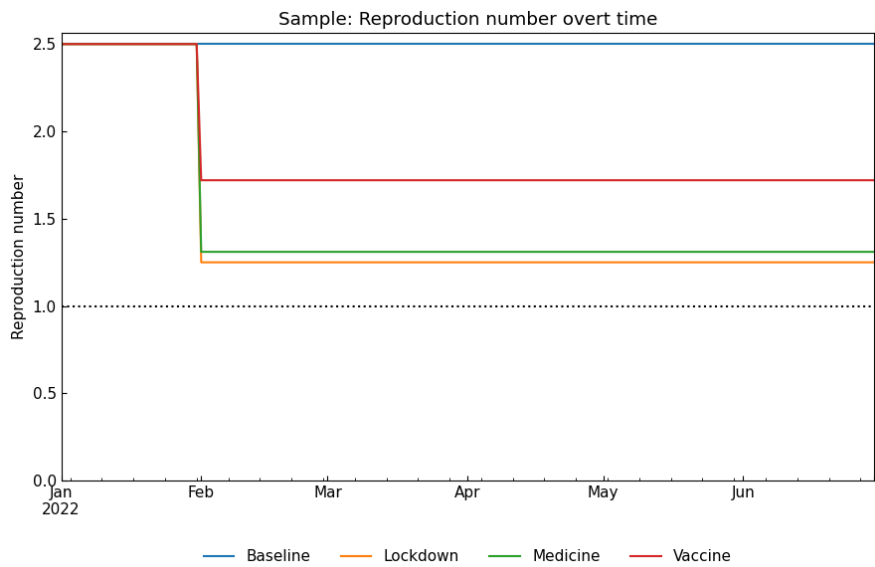
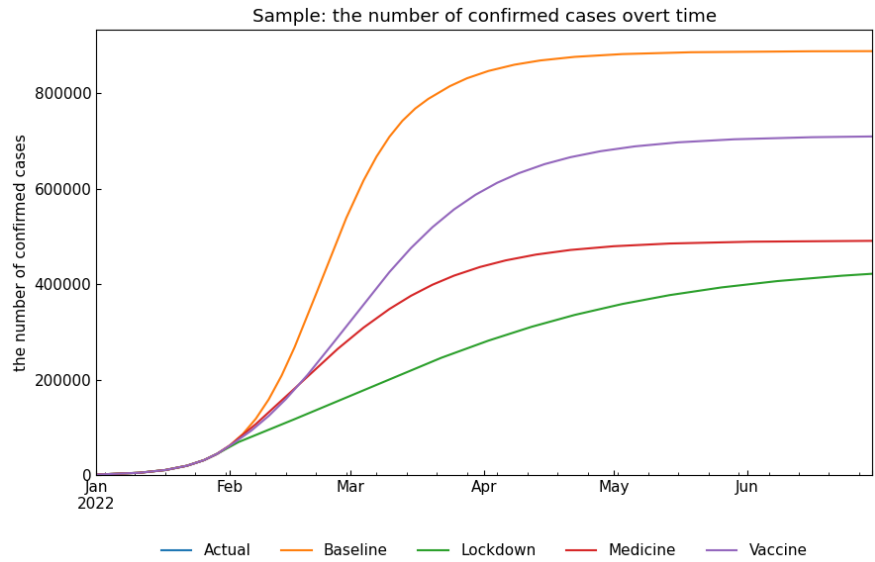
Monitor the spread of COVID-19/Monkeypox with SIR-derived ODE models

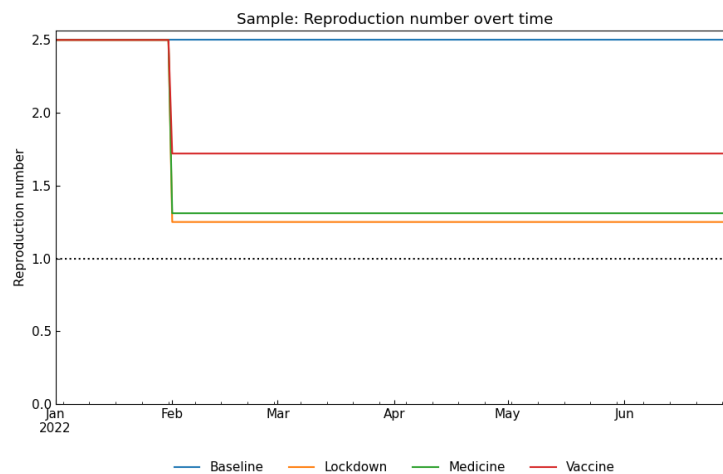
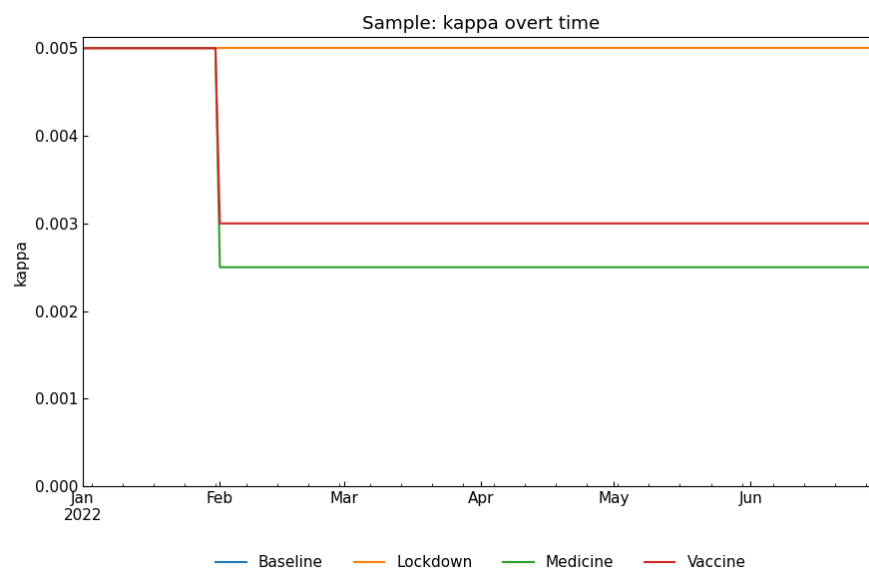
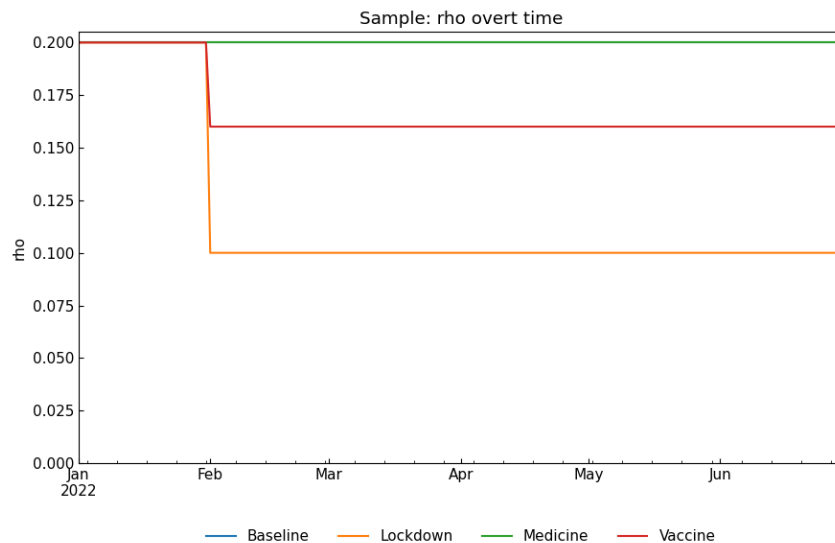
Predict the number of cases in each country/province

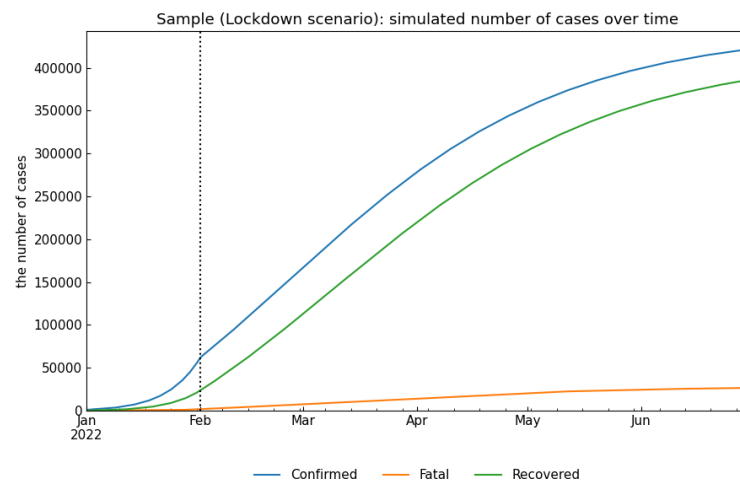
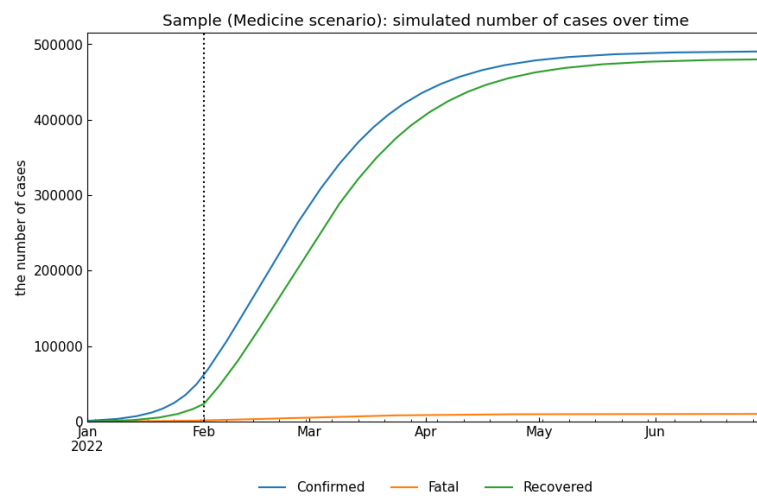
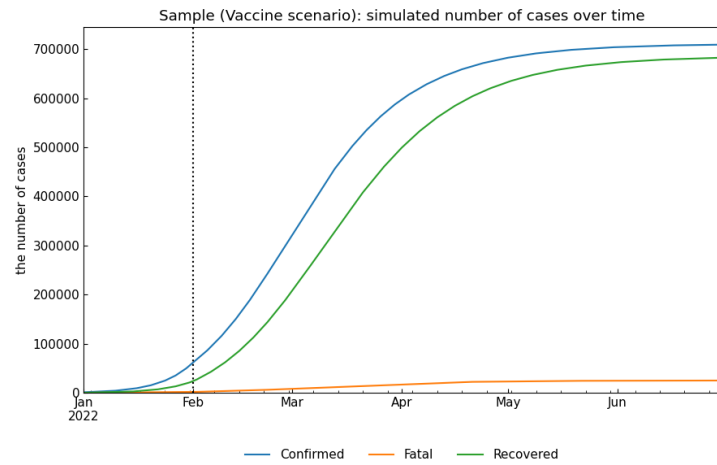
Find the relationship of reproductive number and measures taken by each country

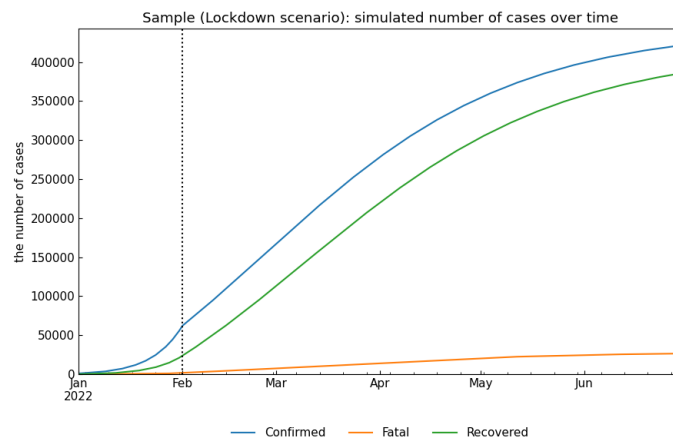
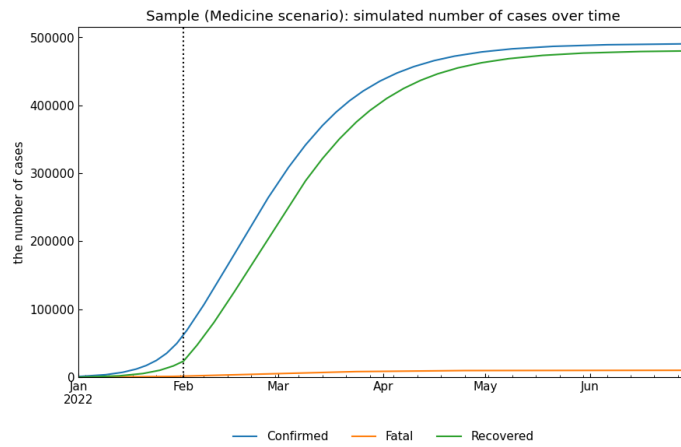
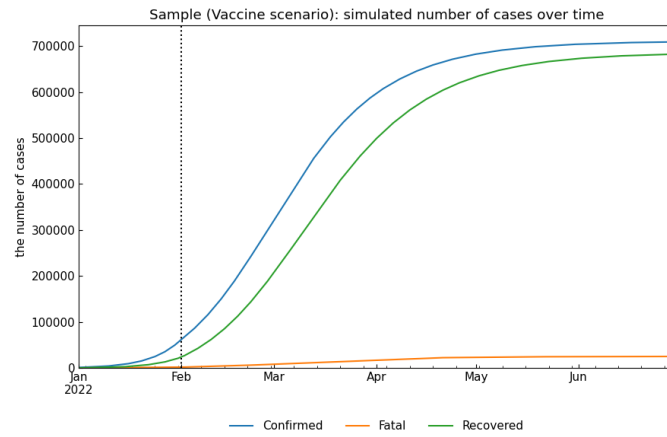
- Problem description

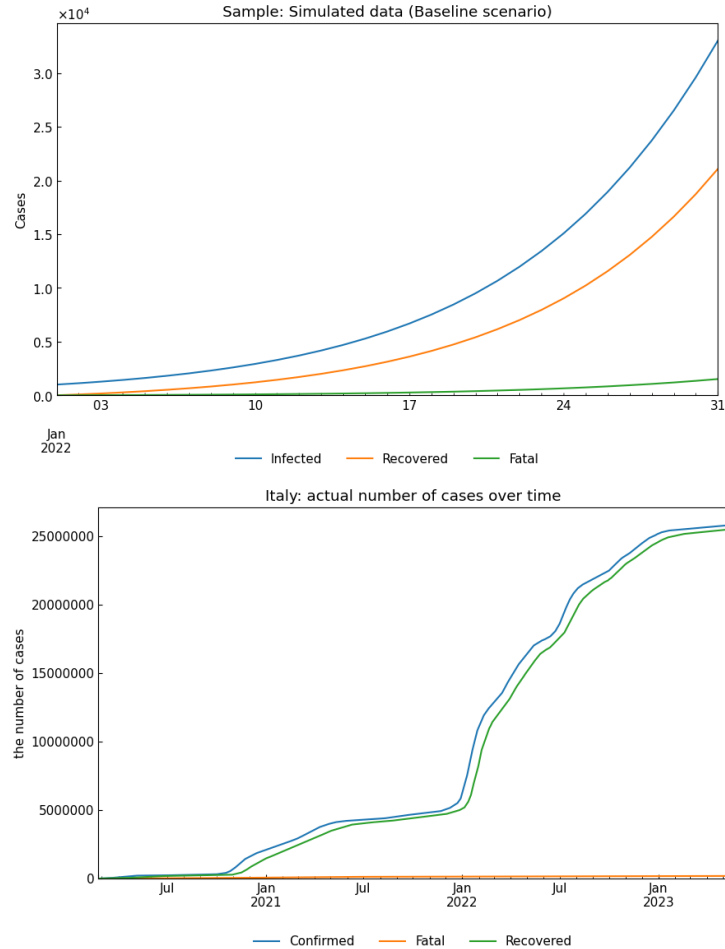










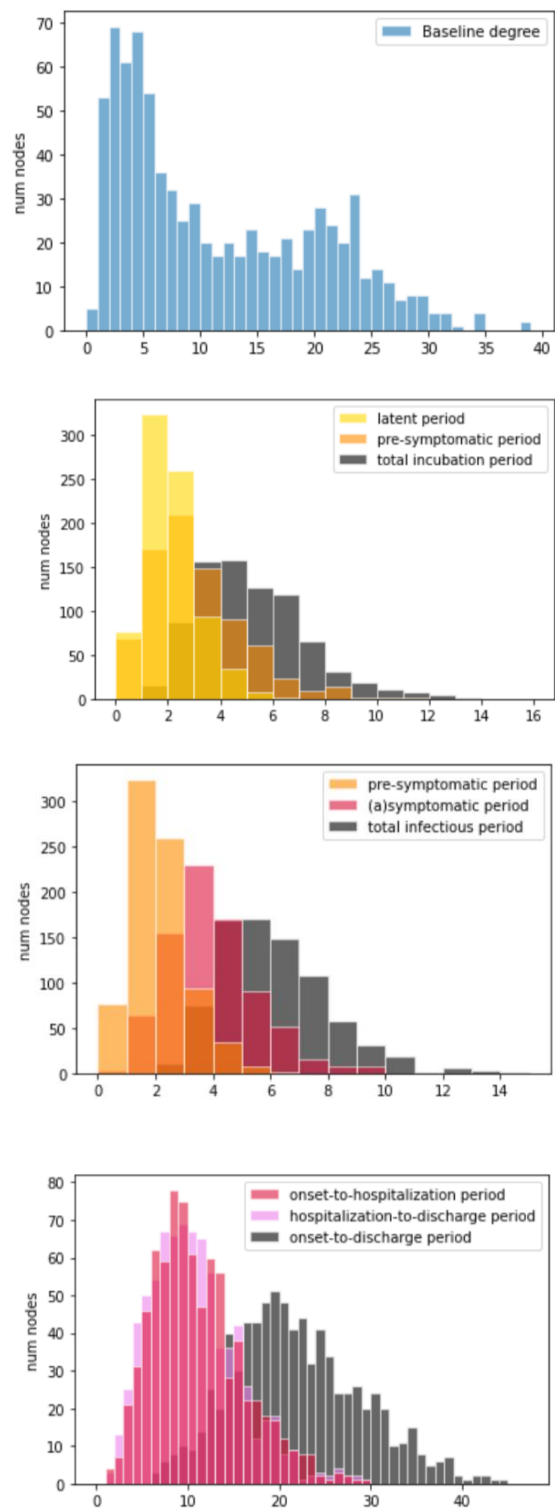


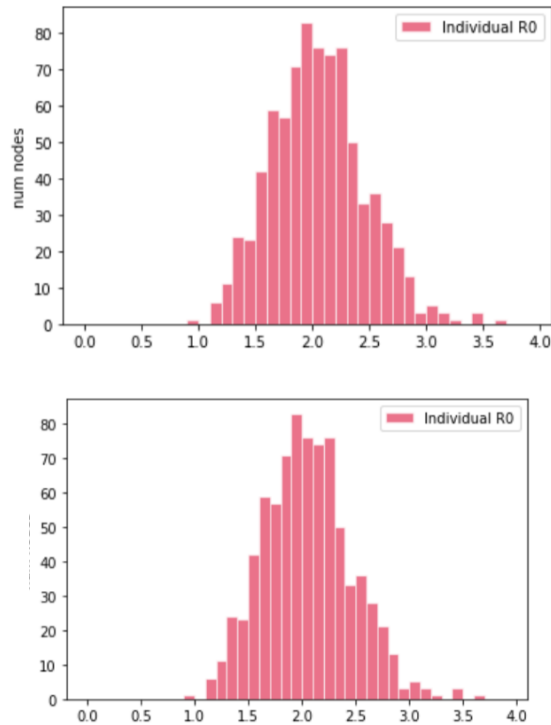
3. Extended SEIRS Community TTI Demo

In this demonstration we will explore the effect of testing, tracing, and isolation interventions on disease transmission in the setting of an age-stratified population with a realistic contact network structured by households and work/school communities.

This notebook provides a demonstration of the functionality of the [Extended SEIRS Network Model](<https://github.com/ryansmcgee/seirsplus/wiki/Extended-SEIRS-Model-Description>) and the [TTI Simulation Loop](<https://github.com/ryansmcgee/seirsplus/wiki/TTI-Simulation-Loop>). This notebook also offers a sandbox for starting to explore TTI scenarios of your own.

Results :

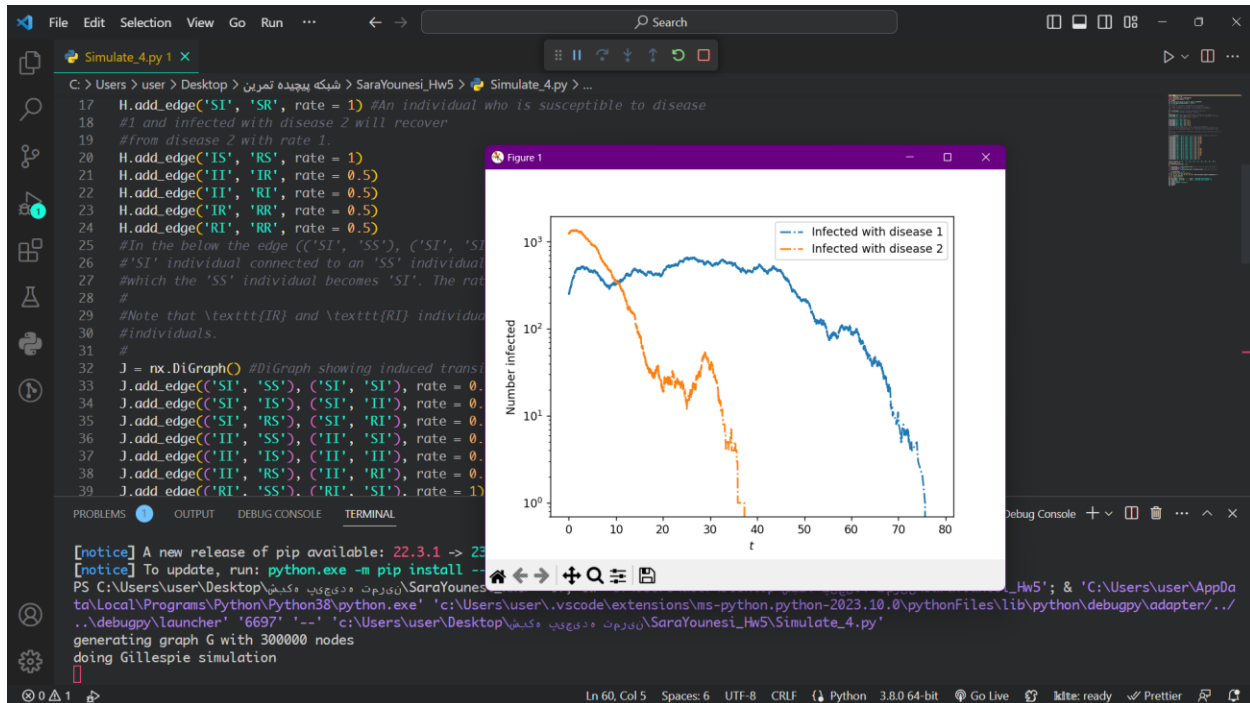




4. Exte cooperative SIR diseases

Interaction between diseases can lead to interesting effects [6, 3, 11, 13]. Now we show two cooperative SIR diseases. In isolation, each of these diseases would fail to start an epidemic. However, together they can, and sometimes they exhibit interesting oscillatory behavior. To help stimulate the oscillations, we start with an asymmetric initial condition, though oscillations can be induced purely by stochastic effects for smaller initial conditions. To the best of our knowledge, this oscillatory behavior has not been studied previously.

Results :



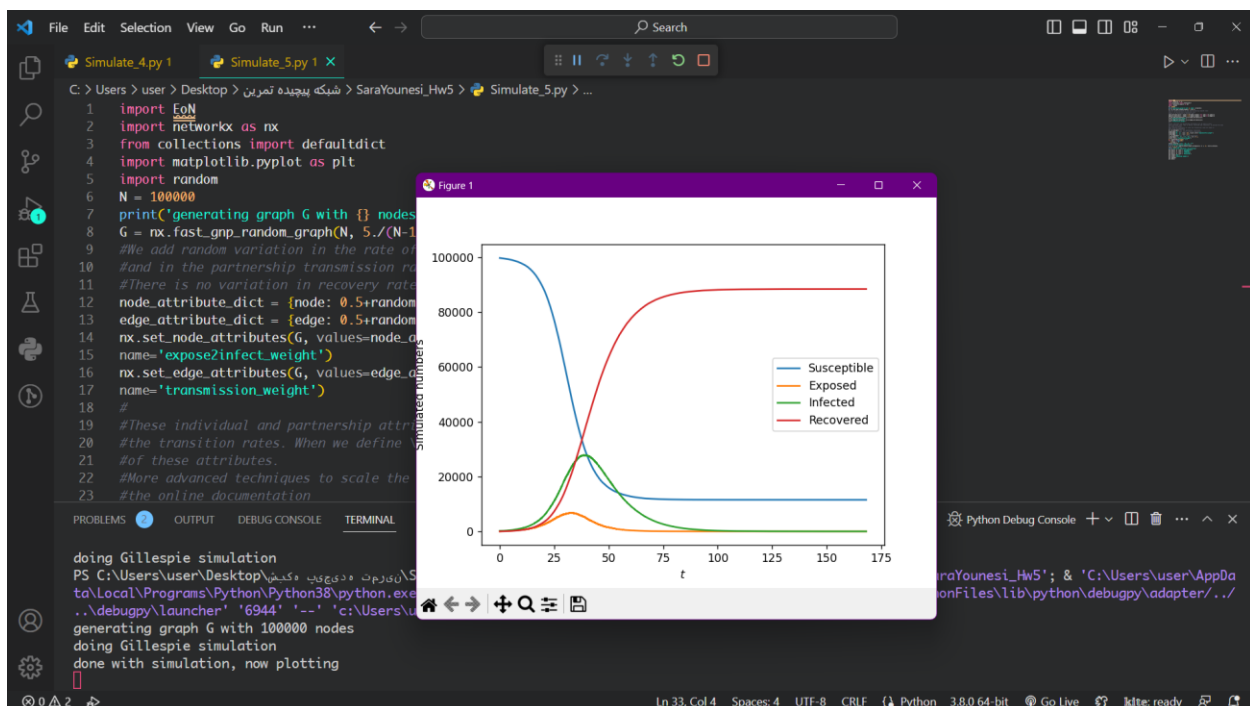
5.Final simulate and Conclusion

Simple contagions EoN provides a function Gillespie simple contagion which allows a user to specify the rules governing an arbitrary simple contagion. Examples are provided in the online documentation, including

- SEIR disease (there is an exposed state before becoming infectious)
- SIRS disease (recovered individuals eventually become susceptible again)
- SIRV disease (individuals may get vaccinated)
- Competing SIR diseases (there is cross immunity)
- Cooperative SIR diseases (infection with one disease helps spread the other) The implementation requires the user to separate out two distinct ways that transitions occur: those that are intrinsic to an individual's current state and those that are induced by a partner. To help demonstrate, consider an "SEIR" epidemic, where individuals begin susceptible, but when they interact with infectious partners they may enter an exposed state. They remain in that exposed state for some period of time before transitioning into the infectious state independently of the status of any partner. They remain infectious and eventually transition into the recovered state, again independently of the status of any partner. Here the "E" to "I" and "I" to "R" transitions are intrinsic to the individual's state, while the "S" to "E" transition is induced by a partner. To formalize this, we identify two broad types of transitions:
 - Spontaneous Transitions: Sometimes individuals change status without influence from any other individual. For example, an infected individual may recover, or an exposed individual may move into the infectious class. These transitions between statuses can be represented by a directed graph H where the nodes are not the original individuals of the contact network G, but rather the potential statuses

individuals can take. The edges represent transitions that can occur, and we weight the edges by the rate. In the SEIR case we would need the graph H to have edges $E' \rightarrow I'$ and $I' \rightarrow R'$. The edges would be weighted by the transition rates. Note H need not have a node ' S ' because susceptible nodes do not change status on their own.

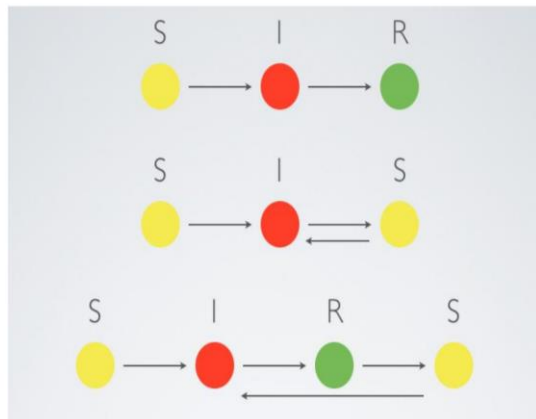
- Induced Transitions: Sometimes individuals change status due to the influence of a single partner. For example in an SEIR model an infected individual may transmit to a susceptible partner. So an (I', S') pair may become (I', E') . We can represent these transitions with a directed graph J . Here the nodes of J are pairs (tuples) of statuses, representing potential statuses of individuals in a partnership. An 11 edge represents a possible partner-induced transition. In the SEIR case, there is only a single such transition, represented by the edge $(I', S') \rightarrow (I', E')$ with a weight representing the transmission rate. No other nodes are required in J . An edge always represents the possibility that a node in the first state can cause the other node to change state. So the first state in the pair remains the same. The current version does not allow for both nodes to simultaneously change states. Examples We first demonstrate a stochastic simulation of a simple contagion with an SEIR example. To demonstrate additional flexibility we allow some individuals to have a higher rate of transitioning from ' E ' to ' I ' and some partnerships to have a higher transmission rate. This is done by adding weights to the contact network G which scale the rates for those individuals or partnerships. The documentation discusses other ways we can allow for heterogeneity in transition rates. Note that this process is guaranteed to terminate, so we can set t_{\max} to be infinite. Processes which may not terminate will require a finite value. The default is 100.



– E.g., SIRS epidemic model on BA network model

Answer

SIRS Model



SIRS Model

- Individuals recover from infection and gain immunity as in the SIR model
- but that immunity is only temporary, and after a certain period of time individuals lose it and become susceptible again

1- Contagion can depend on the link (e.g., link weight) – p is defined for each edge 2- To model the infectious period as random in length – an infected node has a probability q of recovering in each step 3- Separating the I state into a sequence of several states – e.g. early, middle, and late periods of the infection – allowing the contagion probabilities to vary across these states

[SIRS model](#)

The SIR model assumes people carry lifelong immunity to a disease upon recovery; this is the case for a variety of diseases. For another class of airborne diseases, for example seasonal influenza, an individual's immunity may wane over time. In this case, the SIRS model is used allow recovered individuals return to a susceptible state.

[SIRS without vital dynamics](#)

If there is sufficient influx to the susceptible population, at equilibrium the dynamics will be in an endemic state with damped oscillation. The ODE then becomes:

EMOD simulates waning immunity by a delayed exponential distribution. Individuals stay immune for a certain period of time then immunity wanes following an exponential distribution. For more information, see [Immunity](#) parameters.

The graphs below show damped oscillation due to people losing immunity and becoming susceptible again.

The SIRS epidemic model is a mathematical model that describes the dynamics of an infectious disease in a population.https://www.wku.edu/da/covid-19-research/intro_sir_model.php The model divides the population into three compartments: susceptible (S), infected (I) and recovered (R).https://www.wku.edu/da/covid-19-research/intro_sir_model.php The model assumes that infected individuals recover at a constant rate and move to the R compartment, and that recovered individuals lose immunity at a constant rate and move back to the S compartment.https://www.wku.edu/da/covid-19-research/intro_sir_model.php

The BA network model is a mathematical model that generates artificial graphs with scale-free properties. The model starts with a small number of nodes and grows by adding new nodes with a preferential attachment mechanism, meaning that new nodes are more likely to connect to nodes with higher degrees.

To combine the SIRS epidemic model with the BA network model, one can assume that the population is structured as a BA network, where each node represents an individual and each edge represents a contact that can transmit the infection. Then, one can use a stochastic process to simulate the transitions between the S, I and R compartments on the network, taking into account the degree distribution and the network topology. This way, one can study how the epidemic spreads on a scale-free network and how it depends on the network parameters and the disease parameters.

CODE

he code from for simulating the SIRS epidemic model on the BA network model is as follows:

```
import networkx as nx
import matplotlib.pyplot as plt
import EoN
```

```

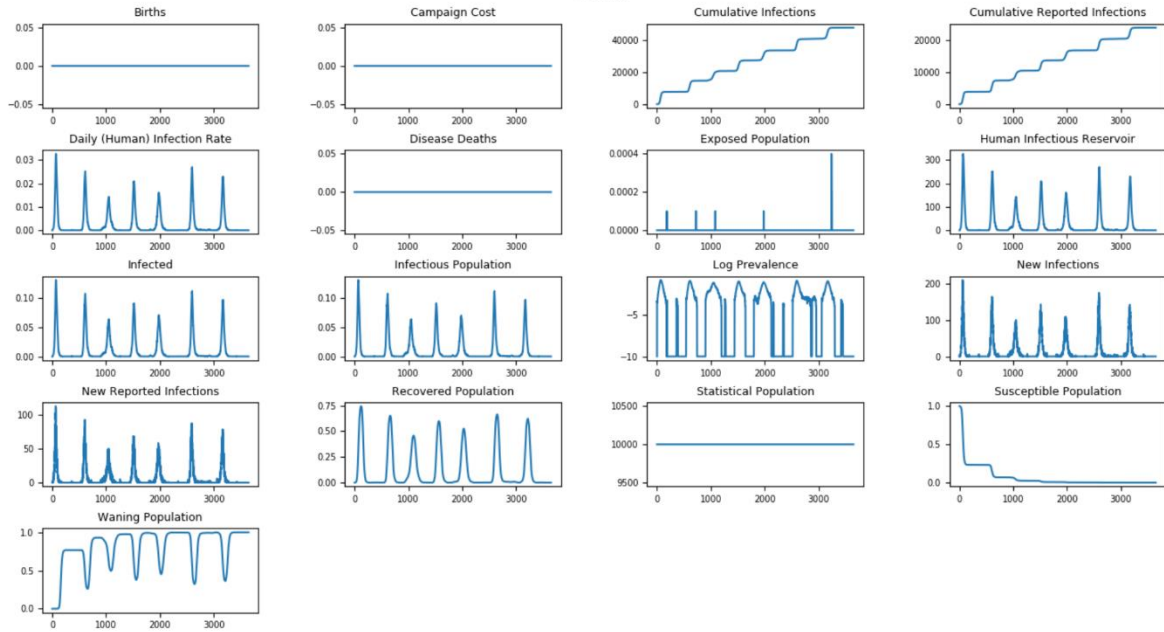
N = 10**5 # number of nodes
G = nx.barabasi_albert_graph(N, 5) # create a BA network
tmax = 20 # maximum time
iterations = 5 # number of simulations
tau = 0.1 # transmission rate
gamma = 1.0 # recovery rate
omega = 0.01 # loss of immunity rate
rho = 0.005 # initial fraction of infected nodes

for counter in range(iterations): # run simulations
    t, S, I, R = EoN.fast_SIR(G, tau, gamma, omega=omega, rho=rho, tmax=tmax)
    if counter == 0:
        plt.plot(t, I, color='k', alpha=0.3, label='Simulation')
    else:
        plt.plot(t, I, color='k', alpha=0.3)

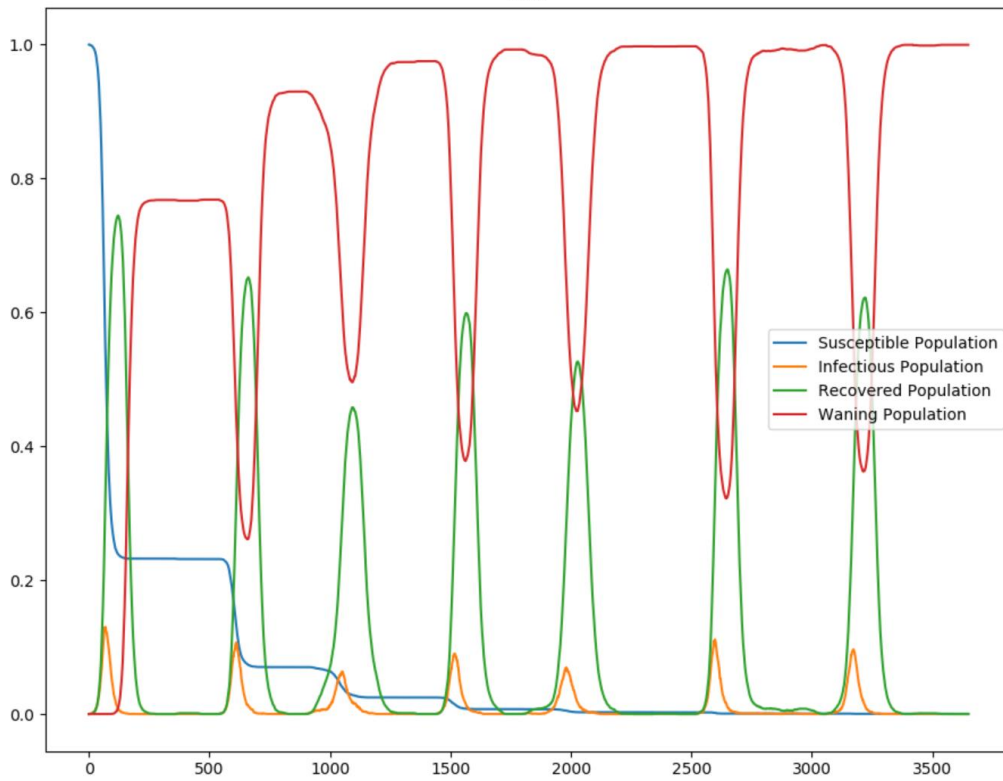
plt.xlabel('$t$')
plt.ylabel('Number infected')
plt.legend()
plt.show()

```

SIRS



SIRS



We focus on the node-based epidemic modeling for networks, introduce the propagation medium, and propose a node-based Susceptible-Infected-Recovered-Susceptible (SIRS) epidemic model with infective media. Theoretical investigations show that the endemic equilibrium is globally asymptotically stable. Numerical examples of three typical network structures also verify the theoretical results. Furthermore, comparison between network node degree and its infected percents implies that there is a strong positive correlation between both; namely, the node with bigger degree is infected with more percents. Finally, we discuss the impact of the epidemic spreading rate of media as well as the effective recovered rate on the network average infected state. Theoretical and numerical results show that (1) network average infected percents go up (down) with the increase of the infected rate of media (the effective recovered rate); (2) the infected rate of media has almost no influence on network average infected percents for the fully connected network and NW small-world network; (3) network average infected percents decrease exponentially with the increase of the effective recovered rate, implying that the percents can be controlled at low level by an appropriate large effective recovered rate.

Source

[Epidemic model SIR — Scientific Python: a collection of science oriented python examples documentation \(scientific-python.readthedocs.io\)](https://scientific-python.readthedocs.io/en/latest/epidemic_model_sir.html)

<https://arxiv.org/pdf/1810.08498.pdf>

<https://cs.stanford.edu/people/jure/pubs/kronecker-jmlr10.pdf>

https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology#The_SIR_model

<https://www.hindawi.com/journals/complexity/2019/2849196/>