Modelling the UKs reponse to coronavirus

ID: 660030047

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import networkx as nx

%config InlineBackend.figure_format = 'svg'
```

```
/usr/local/lib/python3.6/dist-packages/statsmodels/tools/_testing.py:19: FutureWarning:
  import pandas.util.testing as tm
```

Importing Data

The following cell imports and creates the graph that will be used in the simulation.

```
G = nx.read_edgelist('data/facebook_combined.txt')
print('Graph loaded succesfully.')
print('Nodes:', len(G.nodes))
print('Edges:', len(G.edges))
```

```
Graph loaded succesfully.
Nodes: 4039
Edges: 88234
```

The Model

The cells below provide the functions for the simulation. This includes the simulation iteslf, processing data a

```
def simulation(G, days, rI, rS, rQ, rR, rD, lockdownStart, lockdownEnd, reducedRI):
  '''
  This is a simulation of the spread of COVID-19
  over a graph, with slowdown measures that have
  been implemented by the UK government.

  States are recorded in the state array. They
  are categorised as follows:

  Index : State
  0 : Susceptible
  1 : Infected - Symptomatic
  2 : Infected - Asymptomatic
  3 : Infected - Quarantined
  4 : Recovered
  5 : Dead

  Arguments:
    G: Input Graph
    days: Number of days simulation runs for

    rI: Probability of infection
    rS: Probability of having symptoms
    rQ: Probability of being quarantined
    rR: Probability of recovering
    rD: Probability of dying
```

```
    lockdownStart: Day to start lockdown.
    lockdownEnd: Day to end lockdown.
    reducedRI: Value for rI to be changed to.

  Returns:
    Numpy array containing records of how many
    people in each state for every time iteration.
  '''

  # Random seed to replicate results.
  np.random.seed(0)

  # Generate adjacency matrix of graph to optimise code.
  adj = nx.to_numpy_matrix(G)
  N = len(adj)

  # Array to store state of each person.
  state = np.zeros(N)
  nStates = 6

  # Infect certain number of population to start simulation.
  initialInfections = 3
  infect = np.random.randint(N, size=initialInfections)
  state[infect] = 1

  # Array to store results.
  output = []
  statusCount = [np.count_nonzero(state == i) for i in range(nStates)]
  output.append([0] + statusCount)

  for t in range(1, days):

    # Lockdown feature
    if lockdownStart == t:
      rIOriginal = rI
      rI = reducedRI

    if lockdownEnd == t:
      rI = rIOriginal

    # Susceptible.
    for n in np.where(state == 0)[0]:
      incomingIdxs = adj[n].nonzero()[1]
      incomingInfected = np.count_nonzero((state[incomingIdxs] == 1) | (state[incomingIdxs] =
      infection = np.random.rand(incomingInfected) < rI
      infected = np.any(infection)
      symptoms = np.random.rand() < rS

      if infected:
        state[n] = 1 if symptoms else 2

    # Infected - Symptomatic.
    infected = np.where(state == 1)[0]
    quarantine = np.random.rand(len(infected)) < rQ
    quarantineIdxs = infected[quarantine]
    state[quarantineIdxs] = 3

    # Infected - Symptomatic, Asymptomatic and Quanantined.
    infected = np.where((state == 1) | (state == 2) | (state == 3))[0]
    recovery = np.random.rand(len(infected)) < rR
    recovered = infected[recovery]
```

```
      state[recovered] = 4

      # Recovered.
      death = np.random.rand(len(recovered)) < rD
      dying = recovered[death]
      state[dying] = 5

      # Record values of each state.
      statusCount = [np.count_nonzero(state == i) for i in range(nStates)]
      output.append([t] + statusCount)

    return np.array(output)



  def processResults(results):
    '''
    Input results and groups based on state.
    Returns domain, susceptible, infected, recovered, deaths.
    '''

    X = results[:,0]

    S = results[:,1]
    I = results[:,2] + results[:,3] + results[:,4]
    R = results[:,5]
    D = results[:,6]

    return X, S, I, R, D

  def printResults(results):
    '''
    Ouputs key features from the results.
    '''

    X, S, I, R, D = results

    # Find number of nodes.
    n = sum([x[0] for x in results])

    print('Final values:')
    print()
    print('Remaining Susceptible: {:.2f}%'.format(S[-1] * 100 / n))
    print('Total Infected: {:.2f}%'.format((D[-1] + R[-1] + I[-1]) * 100 / n))
    print('Peak Infected: {:.2f}%'.format(max(I) * 100 / n))
    print('Total Deaths: {:.2f}%'.format(D[-1] * 100 / n))
    print()



  def plotResults(results):
    '''
    Takes results from a simulation and outputs
    general states plot and seperate deaths plot.
    '''

    X, S, I, R, D = results

    # Figure size for two graphs.
    plt.figure(figsize=(8, 4))
```

```
  # Graph 1
  plt.subplot(1, 2, 1)
  plt.plot(X, S)
  plt.plot(X, I)
  plt.plot(X, R)
  plt.plot(X, D)

  plt.title('Infection Model over Time')
  plt.xlabel('Time')
  plt.ylabel('People')
  plt.legend(['Susceptible', 'Infected', 'Recovered', 'Dead'])

  # Graph 2
  plt.subplot(1, 2, 2)
  plt.plot(X, D)

  plt.title('Deaths over Time')
  plt.xlabel('Time')
  plt.ylabel('People')

  plt.show()
```

```
def experiment(G=G, days = 100, rI = 0.02, rS = 1, rQ = 0, rR = 0.05, rD = 0.01,
               lockdownStart=None, lockdownEnd=None, reducedRI=0):
  '''
  Calls required functions to simulate model then display data.
  '''

  results = simulation(G, days, rI, rS, rQ, rR, rD, lockdownStart, lockdownEnd, reducedRI)
  results = processResults(results)
  printResults(results)
  plotResults(results)
```

Results

The following cells show the results from the experiments using different parameter values. Explanation of the the report.

The meaning of some parameters is listed below.

- rI: Probability of infection
- rS: Probability of having symptoms
- rQ: Probability of being quarantined
- rR: Probability of recovering
- rD: Probability of dying

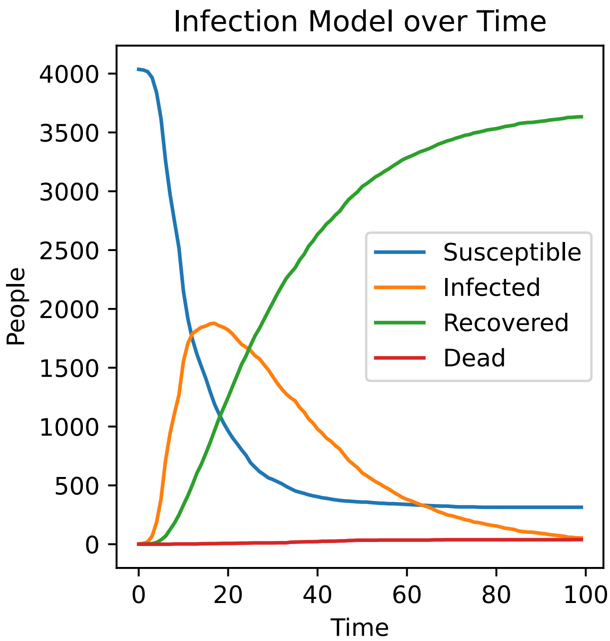
1. SIR Model

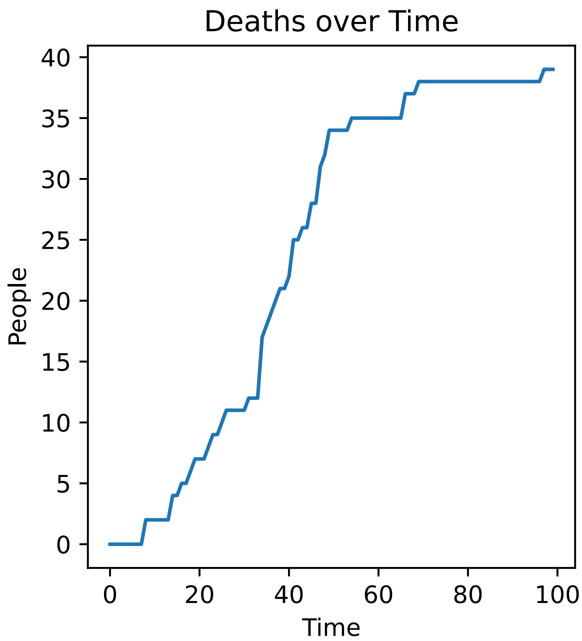
The following simulation has used parameters that represent the basic SIR model. That is all people show syn quarantine. The one difference is that I have include the chance to die instead of recovering. The results are co expect using the regular SIR model. This is a good test for the algorithm as it provides confidence that it is wo

```
experiment()
```

```
Final values:

Remaining Susceptible: 7.77%
Total Infected: 92.23%
Peak Infected: 46.47%
Total Deaths: 0.97%
```





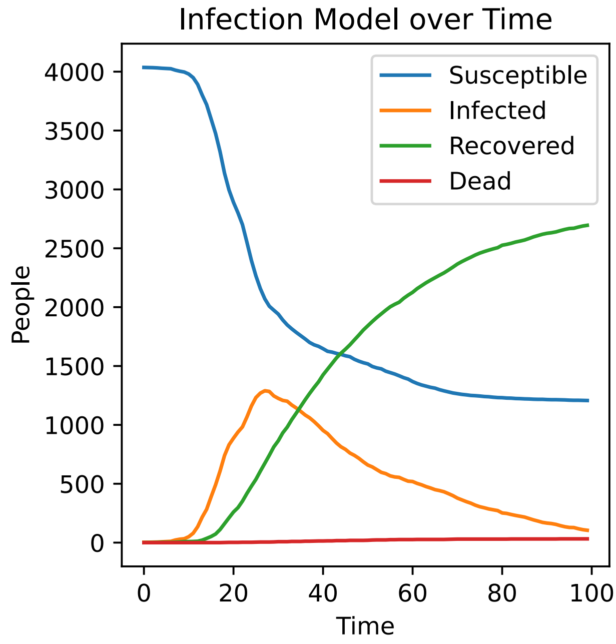
2. Social Distancing

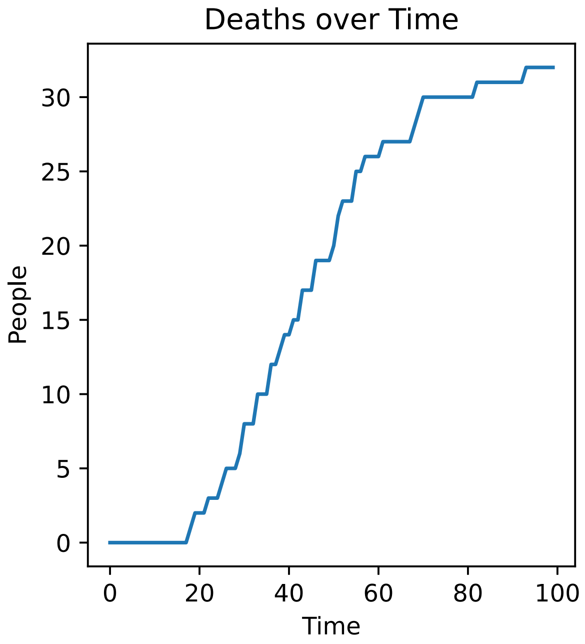
- Simple social distancing measures will reduce the infection rate.
- rI reduced by half from 0.02 to 0.01

```
experiment(rI=0.01)
```

```
Final values:

Remaining Susceptible: 29.88%
Total Infected: 70.12%
Peak Infected: 31.94%
Total Deaths: 0.79%
```





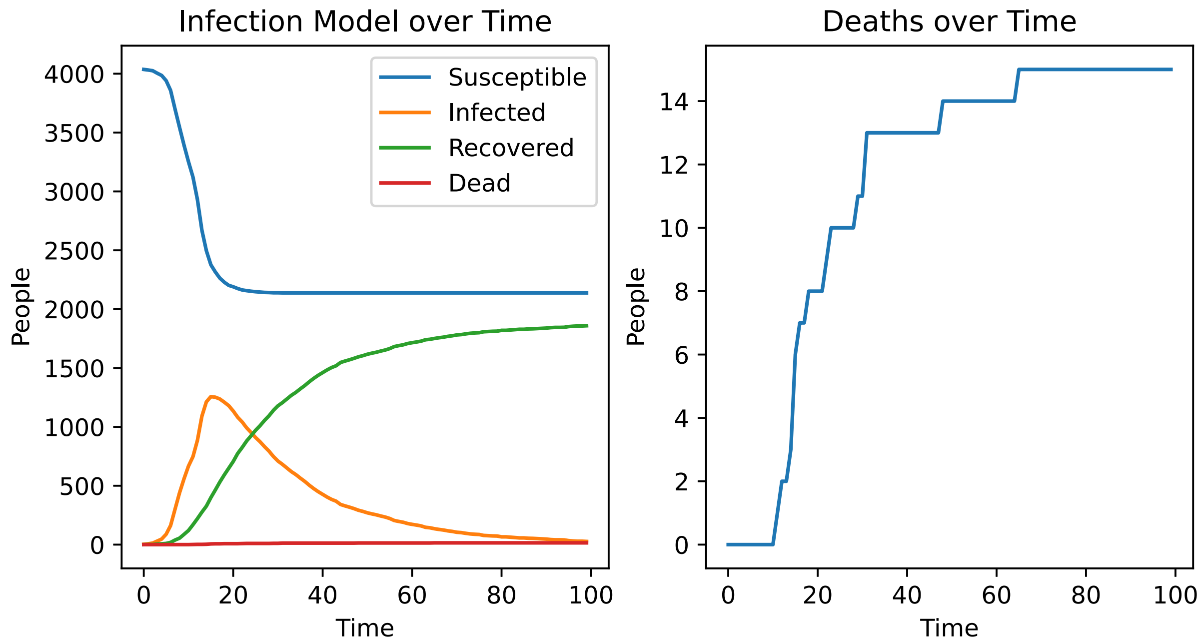
3. Self-Isolation

- Government advised people who experience symptoms to self isolate.
- This model assumes all people experience symptoms.
- rQ set to 0.2

```
experiment(rS = 1, rQ = 0.3)
```

```
Final values:

Remaining Susceptible: 52.93%
Total Infected: 47.07%
Peak Infected: 31.12%
Total Deaths: 0.37%
```



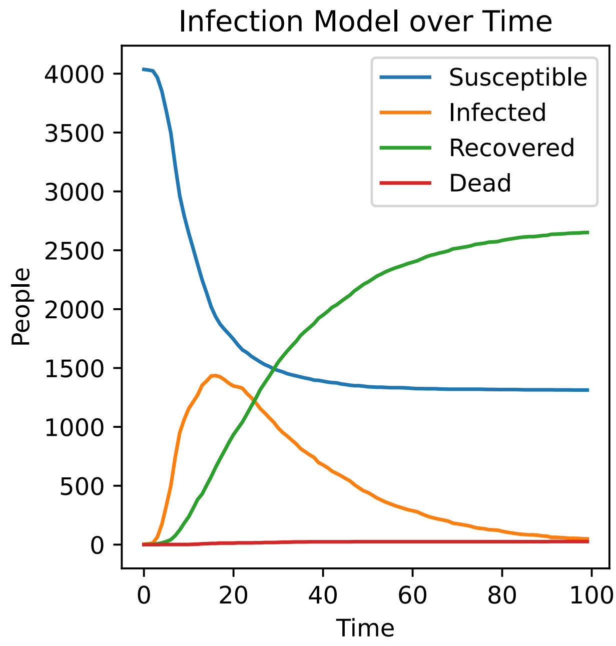
4. Testing

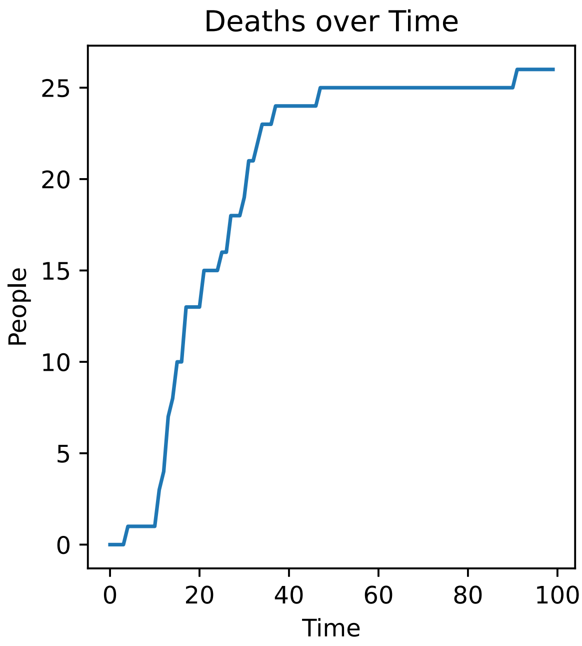
- Data is unclear however CDC estimated 25% of infected are asymptomatic. [Link.]
- rS set to 0.75, cocntinuing with rQ of 0.3.

```
experiment(rS = 0.75, rQ = 0.3)
```

```
Final values:

Remaining Susceptible: 32.51%
Total Infected: 67.49%
Peak Infected: 35.55%
Total Deaths: 0.64%
```





5. Lockdown

- Government imposed nationwide lockdown.

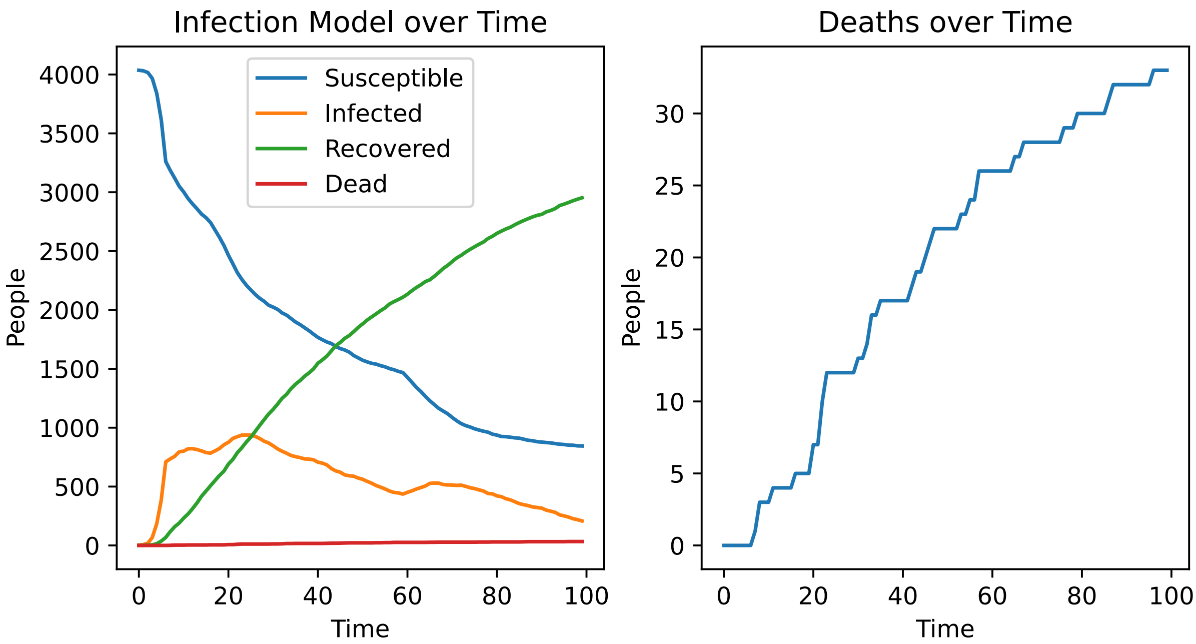
```
experiment(lockdownStart=7, lockdownEnd=30, reducedRI=0.005)
```

```
Final values:
```

```
experiment(lockdownStart=7, lockdownEnd=60, reducedRI=0.005)
```

```
Final values:

Remaining Susceptible: 20.92%
Total Infected: 79.08%
Peak Infected: 23.22%
Total Deaths: 0.82%
```



5. Combination

- This simulation uses combination of all values in order to see their combined effect.

```
experiment(days=200, rI = 0.01, rS = 0.75, rQ = 0.3, lockdownStart=7, lockdownEnd=60, reducec
```

```
Final values:

Remaining Susceptible: 67.15%
Total Infected: 32.85%
Peak Infected: 9.98%
Total Deaths: 0.25%
```