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```
import networkx as nx
from scipy.io import loadmat
from scipy.linalg import eigh
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

a) Construct a network from the flight data

```
In [ ]:
         # Load data
         node metadata = pd.read csv('data/epidemics/airport Nodes GC.csv')
         edge_data = pd.read_csv('data/epidemics/airport_Edges_GC.csv')
         # map given node IDs to index order
         node_id_map = {given_id: node_id for (given_id, node_id) in zip(node_metadata.Id, node_
In [ ]:
         # build directed adjacency matrix from edge data
         A dir = np.zeros((len(node id map), len(node id map)))
         for i, row in edge data.iterrows():
             u, v = node_id_map[row.Source], node_id_map[row.Target]
             A dir[u][v] = row.Weight
         # Compute undirected A
         A = (A dir + A dir.T) / 2
         G = nx.from_numpy_matrix(A)
In [ ]:
         # confirm graph is connected
         print('Graph is connected: {}'.format(nx.is connected(G)))
```

Graph is connected: True

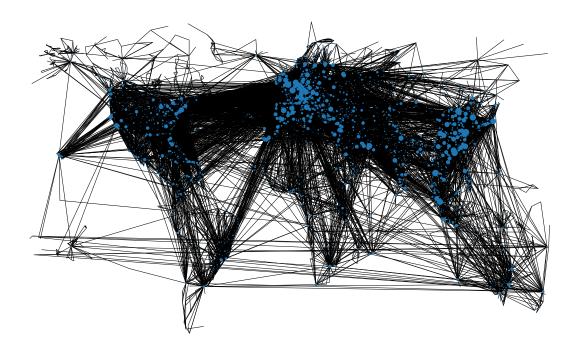
b) Plot the airport network

```
In []: # Compute top 2 e-val centralities as sanity check
    evec_centralities = nx.centrality.eigenvector_centrality(G, weight='weight')
    'Top 2 e-vec centralities: {}'.format(list(sorted(evec_centralities.values()))[-2:])

Out[]: 'Top 2 e-vec centralities: [0.16991022532548966, 0.1785292296913075]'

In []: # plot the network, using lat/long as node locations and e-vector centrality as node si
    pos = {idx: (row.Longitude, row.Latitude) for idx, row in node_metadata.iterrows()}
    node_size = [evec_centralities[n] * 1750 for n in G.nodes()]
    plt.figure(1, figsize=(25, 15))
    nx.draw(G, pos=pos, node_size=node_size, width=0.25)
```

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d) Mean-field approximation

```
In [ ]:
         def dp_dt(A, p_t, beta, gamma):
             The provided formula for dp/dt, computed using matrix operations
             left = beta * (1 - p_t)
             right = (A @ p_t) - (gamma * p_t)
             return left * right
         def infect(A, beta, gamma, dp_dt):
             Models the spread of infection throughout a graph over time
             beta, gamma: model parameters
             dp dt: function to compute change in infection probabilities across nodes
             Returns P; P[a][b] = infection probability for ath node at bth timestep
             # infect the first 20 nodes
             p_0 = np.zeros((len(A),))
             p_0[:20] = 1
             # compute infection probabilities over time
             t max = 5
             delta = 0.05
             P = np.zeros((len(p_0), int(t_max / delta)))
             P[:, 0] = p_0
             for i in range(1, int(t_max / delta)):
                 P[:, i] = P[:, i-1] + (delta * dp_dt(A, P[:, i-1], beta, gamma))
             return P
```

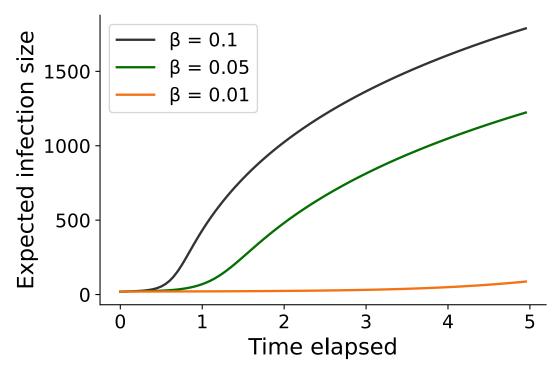
```
In []:
    gamma = 0.1

# test varying values of beta
P_bar_all = []
    for beta in (0.1, 0.05, 0.01):
        P = infect(A, beta, 0.1, dp_dt)
        P_bar_all.append(P.sum(axis=0))

# plot expected infected size over time for each beta value
x = np.array(range(0, int(5 / 0.05))) * 0.05
    [plt.plot(x, P_bar) for P_bar in P_bar_all]
    plt.legend(["β = 0.1", "β = 0.05", "β = 0.01"])
    plt.title("Expected infection size over time")
    plt.xlabel("Time elapsed")
    plt.ylabel("Expected infection size")
```

Out[]: Text(0, 0.5, 'Expected infection size')

Expected infection size over time



e) Minimum number of immunizations

```
A \text{ imm} = A.copy()
             for i in range(len(node_order)):
                 # remove a node
                 n = node_order[i]
                 # setting to 0 creates additional e-vals that are 0, but still produces valid L
                 # this is easier than deleting rows/columns
                 A_{imm}[n, :] = 0
                 A_{imm}[:, n] = 0
                  if i < start at:</pre>
                      continue
                  elif i == start at:
                      print('Starting with {} nodes removed'.format(i))
                  # recompute max e-val
                 w max = eigh(A imm, eigvals only=True, eigvals=(len(A imm) - 1, len(A imm) - 1)
                  if w max < eval thresh:</pre>
                      print('Max e-val after removing {} nodes: {}'.format(i+1, w_max))
                      print('Max e-val below threshold after removing {} nodes'.format(i+1))
                      break
                  if i % 5 == 4:
                      print('Max e-val after removing {} nodes: {}'.format(i+1, w_max))
             return A imm
In [ ]:
         # compute required threshold for \lambda max(A)
         beta = 0.01
         gamma = 0.4
         print('Must have λ max(A) < {}'.format(gamma / beta))</pre>
        Must have \lambda_{max}(A) < 40.0
In [ ]:
         # compute degree centrality
         degree_centralities = A.sum(axis=1) / (len(A) - 1)
         # order nodes by degree centrality
         node order = np.argsort(degree centralities)[::-1]
         # compute number of nodes necessary to remove
         immunize(A, node_order, gamma / beta, start_at=50); # start with 50 to speed up re-comp
        Starting with 50 nodes removed
        Max e-val after removing 55 nodes: 45.751362453969314
        Max e-val after removing 60 nodes: 45.749493453262154
        Max e-val after removing 65 nodes: 45.74924054241361
        Max e-val after removing 70 nodes: 41.151565542207784
        Max e-val after removing 73 nodes: 37.41654106581537
        Max e-val below threshold after removing 73 nodes
In [ ]:
         # compute e-val centrality
         eval centralities dict = nx.centrality.eigenvector centrality(G, weight='weight')
         eval_centralities = np.array([eval_centralities_dict[n] for n in G.nodes()])
```

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```
# order nodes by e-val centrality
node_order = np.argsort(eval_centralities)[::-1]
# compute number of nodes necessary to remove
immunize(A, node_order, gamma / beta, start_at=100);
```

```
Starting with 100 nodes removed

Max e-val after removing 105 nodes: 48.51744278279449

Max e-val after removing 110 nodes: 48.51591111485003

Max e-val after removing 115 nodes: 48.51590896694197

Max e-val after removing 120 nodes: 48.51590773253301

Max e-val after removing 125 nodes: 39.427119599712015

Max e-val below threshold after removing 125 nodes
```

Degree centrality only required 73 nodes to be removed, while e-val centrality required 125 nodes to be removed.