Homework 2: Models, Dynamics, Construction, Inference

Released: Sept 12, 2024; Due: **5pm ET, Sept 26, 2024**

Georgia Tech	CSE 8803 EPI Fall 2024
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Days Late: 1 day

Slip Time Left: 2 Days

Reminders:

1. *Out of 100 points. 4 Questions. Contains 6 pages.*
2. *If you use Late days, mark how many you are using (out of maximum 4 available) at the top of your answer PDF.*
3. *There could be more than one correct answer. We shall accept them all.*
4. *Whenever you are making an assumption, please state it clearly.*
5. *You will submit a solution pdf LASTNAME.pdf containing your answers and the plots as well as a tar-ball LASTNAME.tgz that contains your code and any output files.*
6. *Please type your answers either in LATEXdocument or in a separate file like a Word document and then convert it into a pdf file. Typed answers are strongly encouraged. Illegible handwriting may get no points,at the discretion of the grader. Only drawings may be hand-drawn, as long as they are neat and legible.*
7. *Additionally, you will submit one tar-ball LASTNAME.tgz that contains your code and any results files. Code and results for each question should be contained in a separate sub-directory (Eg: Q1) and there should be a README.txt file for each sub-directory explaining any packages to install, command to run the code files and location of the expected output. Please follow the naming convention* ***strictly****.*
8. *If a question asks you to submit code please enter the file path (Eg: Q1/Q-1.3.1.py) in the solution pdf.*
9. *You can download all the datasets needed for this homework from canvas files, you can check the information about the datasets in the README.txt file.*

1. (25 points) Metapopulation Model

We will model the SIR metapopulation model briefly introduced in Lecture 4 (Slide 5-6).

Let there be M regions with total populations $\{N_i\}_{i=1}^{M}$. We let $S_i(t), I_i(t), R_i(t)$ be the total population in respective component for region i at time t.

Assume that we σ_{ij} be the population flow from region i to j. Also, we assume the parameters β, γ are the same across all regions.

Q 1.1 (6 points) Similar to Lecture 4 Slide 5, write down the equations to derive effective population sizes $S_i^{eff}(t), I_i^{eff}(t), R_i^{eff}(t)$ at time t from $\{S_j(t), I_j(t), R_j(t)\}_{j=1}^{M}$ and flow parameters σ_{ij}.

Solution: https://drive.google.com/file/d/11Bv03Q8_TJ-RpgejE2jYZddHMTfrXuUz/view?usp=sharing

Since SIR parameters β, γ are the same across all regions we can write the change in S, I, R compartment sizes in 1 time-step as:

$$S_i(t+1) = S_i(t) - \beta S_i^{eff}(t) \sum_{j=1}^{M} \frac{I_j^{eff}(t)}{N_j}$$

$${}_i \qquad {}_i \qquad 1\,{}^i \qquad \overset{M}{\underset{j=1}{}} \frac{{}^{eff}}{N_j} \qquad {}_i$$

$$I\ (t+1) = I\ (t) + \beta S^{eff}(t) \sum I_j \quad (t) - \gamma I^{eff}(t)$$

$$R_i(t+1) = R_i(t) + \gamma I_i^{eff}(t)$$

Q 1.2 (6 points) Instead of 1 time-step, derive equations for change in Δt time; i.e., derive the formulas for $S_i(t + \Delta t) - S_i(t)$, $I_i(t + \Delta t) - I_i(t)$, $R_i(t + \Delta t) - R_i(t)$. *Hint:* This is similar in nature to Q1.2 in HW 1.

Solution: https://drive.google.com/file/d/1nCFhVwN05sCKdhAhD-hUfT47N9oYnkE_/view?usp=sharing

Q 1.3 (10 points) **[Bonus]** Implement the ODE of metapopulation model. The code should take the parameters β, γ, the flow parameters $\{\sigma_{i,j}\}_{i,j\in[1,M]\times[1,M]}$, total population $\{N_i\}_{i=1}^{M}$ and the initial population of each compartment for all regions $\{S_i(0), I_i(0), R_i(0)\}_{i=1}^{M}$ and max time and output the population sizes of $\{S_i(t), I_i(t), R_i(t)\}_{i=1}^{M}$ till max-time. We have provided a starter code in Python script metapop.py that implements the model. You have to fill in the missing parts of the method def ode(self, times, init, parms): that involves calculating the effective population.

Once you have completed the method, run the script to generate the SIR plots for each population. Submit the completed code and the plots.

Note: You don't need to change other functions in the script, only fill in the code in the space indicated.

Note: In case you are not comfortable with Python, you may translate the Python script into your language of choice and complete the implementation of the metapop- ulation model.

Solution: Code is in HW2 folder under Q1/metapop.py

2. (36 points) Viral propagation You are managing a network of devices inside your company connected to each other via a local intranet connection. Occasionally, some of thecomputers in the network get infected with a virus which can spread across the networkas users share information with each other. You job is to simulate the spread of the virus under different assumptions on the diffusion mechanism.

Network dataset: Your dataset contains multiple networks G = $\{G_1, G_2, \ldots, G_9\}$ between routers (this dataset is sourced from actual internet router dataset [1]. Each of the networks is a snapshot of the connections made across routers on some day collected over 3 months. The network files are named as network1.txt, network2.txt,..., network9.txt.

Aggregating all networks: We aggregate all the 9 snapshots of the networks into a single network $G(\rho)$. The aggregation process is simple: For each pair of nodes (u, v) if at least ρ networks in G have an edge between them, we add an edge (u, v) to $G(\rho)$. Here ρ isa parameter of our model.

We also assume an SIS network model with usual parameters β, γ on the graph $G(\rho)$.

Q 2.1 (10 points) Decreasing ρ will increase the number of edges in the graph and make it more denser and connected. In class we saw that λ, the highest eigenvalue of the adjacency matrix is a good proxy for the connectedness of the graph. Let us observethis empirically for this dataset.

[1] Collected by https://service.uoregon.edu/TDClient/2030/Portal/KB/ArticleDet?ID=53820 and downloaded from https://snap.stanford.edu/data/Oregon-1.html

For each value of ρ in $\{1, 2, 3, \ldots, 9\}$, write code to construct $G(\rho)$. Find the largest eigenvalues λ of the adjacency matrix for each graph $G(\rho)$. Submit the plot between ρ and λ. How does λ change with increase in ρ?

Hint: Since the graphs have over 10,000 nodes, please consider using sparse representations of adjacency matrix and efficient built-in methods to compute eigenvalues on the sparse graph. For example scipy.sparse.linalg module has efficient implementations to compute eigenvalues that enable you to perform the computations within fractions of a second.

Solution:
https://drive.google.com/file/d/1nqEEQ15SYGahurLhbozworIkPXi-rCz8/view?usp=sharing

The eigenvalues decrease as ρ increases. Since a higher ρ decreases the connectedness of the graph, the eigenvalue of the graph should also decrease when ρ increases which is shown in the program.

Q 2.2 (10 points) Set $\rho = 1$. Use the EoN package [2] to set up an SIS model on $G(\rho)$. Specifically use the EoN.fast SIS function_[3]. Set $\gamma = 0.08$, $\beta = 0.01$ and max time $T = 10$. Set node 1 as the only infected node at $t = 0$.

Now plot a curve with $I(t)$ on the y-axis vs t on the x-axis for $0 \leq t \leq T$ after simulating the model 50 times (similar to HW1 Q1.3). Now set $\beta = 0.001$ and plot the $I(t)$ vs t curve. Do you notice any difference? Explain.

Solution:
https://drive.google.com/file/d/1GCSmXpkPkki8nRHSHnB0zMIUJer3t0j3/view?usp=sharing

https://drive.google.com/file/d/1MjZlmoszoOO6O5ZGwvKnrvzuuXOLagcv/view?usp=sharing

Yes, there is a difference between the two plots. Plot 1, where beta = 0.01, seems to be an exponential function. In other words, the fraction of the population that is getting infected increases at an extremely high rate. On the other hand, in plot 2, where beta = 0.001, the function seems to be more linear and also drops off near the end of the time frame. This also makes sense since the rate of infection is almost a tenth of the first beta. Since this beta is a lot lower, the infection will spread a lot slower in comparison to the higher beta which the plots show.

Q 2.3 (10 points) Now set $\beta = 0.01$, $\gamma = 0.16$ and $\rho = 1$. We will try to reduce the effec-tive strength of the graph by another method of iteratively removing nodes using the following rule:

Find the node with the largest degree among all nodes (in case of a tie, choose the node with the highest index). Then remove the node.

Using this rule find the number of node removals required to reduce the effective strength of the graph to less than 1. Also, produce a plot of the number of nodes removed on the x-axis and effective strength on the y-axis till effective strength reduces to less than 1.

Solution: **42 nodes are required to reduce the effective strength of the graph to less than 1.**

https://drive.google.com/file/d/1KAsMmenyoLrHVX8fAic7cvyX1JS1P5e-/view?usp=sharing

(6 marks added to everyone).

Q 2.4 (6 points) **[Bonus]** We will denote as K the number of nodes you had to remove in Q2.3 before effective strength decreased below 1. Let $[G_0, G_1, G_2, \ldots, G_K]$ be the sequence of graphs after each removal of a node from Q 2.3 where $G_0 = G(\rho = 1)$. The effective strength of all G_i for $i < K$ is greater than 1 and G_K has effective strength ≤ 1.

For each graph G_K, G_{K-1} and G_{K-2} submit a plot of $I(t)$ vs t (3 plots in total).

Solution:

Gk: https://drive.google.com/file/d/1XL9wI0yGDPbfkz8gT4lAbABAUg7hkg48/view?usp=sharing

Gk-1:

https://drive.google.com/file/d/1XmRSdQqH3ehEGcfWO_isnAPXHbMhTNnD/view?usp=sharing

Gk-2:

https://drive.google.com/file/d/1F-jPqqJacj3W8HXnjuk_gfQvywQ_Cxqr/view?usp=sharing

3. (30 points) Finding Culprits

Let's use the k-regular Cayley tree we used in the previous HW.

[2] https://epidemicsonnetworks.readthedocs.io/en/latest/EoN.html

[3] See documentation in https://epidemicsonnetworks.readthedocs.io/en/latest/functions/EoN.fast_SIS.html

Q 3.1 (10 points) Let's consider the $k = 3$ tree with 22 nodes (see Figure 1). You can use edge list from cayley.txt to construct the graph.

Implement a simple SI model using *EoN.fast_SI* [4] or equivalent package in your language of choice. Set $\beta = 0.2$ in the SI model and run it on this graph. Let only the central node 0 be infected at $t = 0$. Run the SI model for 10 steps and record the set of nodes $\boldsymbol{I}$ that are infected at the end of 10 steps.

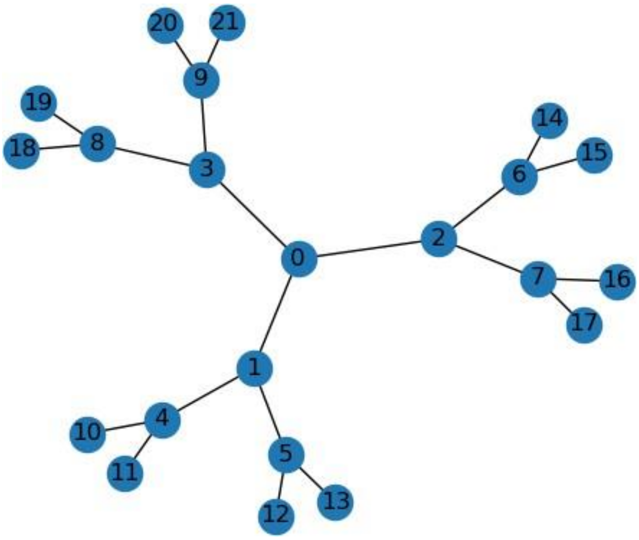


Figure 1: Cayley Tree

Repeat this for 100 times. Record these 100 sets of nodes as $X = \{I_1, I_2, \ldots, I_{100}\}$ in a file.

The file should contain 100 lines and each line i should contain the list of nodes infected $\boldsymbol{I}_i$ which are separated by a space.

Solution: **File is located in Q3/Q-3.1output.txt**

Q 3.2 (10 points) Now let's assume you are given the set X and you want to calculate the possible starting point of the epidemic. (we know it is node 0 but assume we don't know). Let's use a simple algorithm for this purpose. Let the inferred starting point be the centroid of the infected subgraph: u_i = Centroid(I_i). You may use networkx.center function.

Find the accuracy of this algorithm i.e., find the fraction of time the algorithm infers node 0 as the center of subgraph I_i over $X = \{I_1, I_2, \ldots, I_{100}\}$.

Solution: **File is located in Q3/Q-3.2.py**

Accuracy of algorithm hovers right around 0.88. The range is [0.85-0.93] after running program a couple of times.

Q 3.3 (6 points) Repeat the same steps as Q3.2 and Q3.3 except make node 1 (a point at depth 1) as the starting point. Compute the accuracy of the algorithm.

[4] https://epidemicsonnetworks.readthedocs.io/en/latest/functions/EoN.fast_SI.html

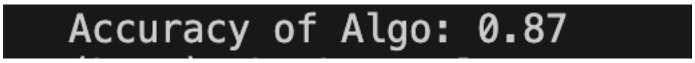
Solution: File is located in Q3/Q-3.3.py

Accuracy of algorithm hovers right around 0.6.

Q 3.4 (4 points) Does the accuracy of the estimator change (comparing the answer you get in Q3.2 and Q3.3)? Show your result and give the answer. If so, what does it tell you about the estimator on this type of graph (strengths and weaknesses; this is slightly an open-ended question). Do you think the rumor centrality metric we studied in class will probably perform better?

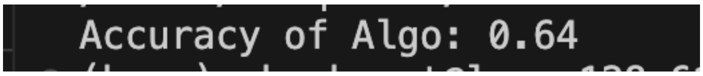
Solution:

Q3.2 Algo:



```
   Accuracy of Algo: 0.87
```

Q3.3 Algo:



```
   Accuracy of Algo: 0.64
```

Yes, the accuracy of the algorithm decreased in Q3.3 in comparison to Q3.2. It seems the estimator performs better when the source of the infection is a central node. The strength of this approach is that it chooses simplicity as the best explanation. Usually, this type of approach is great because the node that is the centermost of the graph and is extremely useful to use on graphs with a tree-like spread. However, since the initial-infected node isn't the centermost node and is less symmetric in Q3.3, the estimator doesn't predict it as often which can be detrimental since these types of scenarios can arise very easily in populations. I think the rumor centrality metric will perform better on this graph because the graph is acyclic. Furthermore, the rumor centrality metric is more robust when dealing with infections that start from non-central nodes, thereby maintaining the accuracy if the initial infected node is asymmetric.

4. (19 points) Steiner trees for Missing Infections

In this question, we will explore the use of Steiner trees for finding missing infections. Steiner trees are classic objects used for many 'facility location' problems. As we know many infections go unrecorded in real life, and it is helpful to understand which other nodesmay be infected but not recorded (the missing nodes). In class, we saw other types of methods for this problem. Here we will use the idea of a minimum Steiner tree over the known infected nodes as a way to approximate the unknown infected nodes in the graph.

if $G = (V, E)$ is our undirected social network with edge weights, and a set of terminals $I \subseteq V$, then a Steiner tree is a tree in G that spans I (i.e., contains at least all nodes in I; it might contain extra nodes from V not in $\boldsymbol{I}$ too, but at least it has to span all of I).

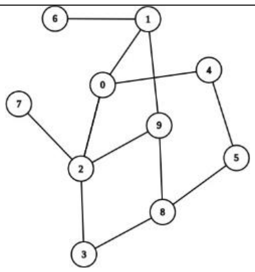
The minimum weighted Steiner tree is the Steiner tree for a given $\boldsymbol{I}$ that has the least sum of the weights of all the edges included in it. There are several algorithms for finding such a Steiner tree given the set of terminals $\boldsymbol{I}$ and graph G. See this link for more details on the Steiner tree problem https://en.wikipedia.org/wiki/Steiner_tree_problem.

For the following question, assume that all the edges have equal weights.

Q 4.1 (8 points) Let's try to compute a couple of minimum Steiner trees by hand. Feel free to use whatever method you want (except of course just using a software package). These can be done with intuition as well. Just draw and show us the final answer.

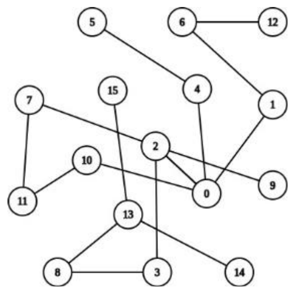
Q 4.1.1 (4 points) Terminal set = {7, 9, 3, 6} for graph below.

Solution: https://drive.google.com/file/d/17EJJhjmJUWLN_eJY-Q0A1UxnGCPVJwSv/view?usp=sharing



Q 4.1.2 (4 points) Terminal set = {12, 14, 9, 10} for graph below.

Solution: https://drive.google.com/file/d/1YyBHrv-dUkJsD36BVRa4pifs4KeYC8nO/view?usp=sharing



Q 4.2 (9 points) In the missing infections problem you are given a set of observed infections (the *known* set) *K*. For using Steiner trees to compute missing infections, the idea is very simple. Set *K* as the terminal nodes set *I* in the minimum weighted Steiner tree problem over the graph *G*. The resulting minimum-weighted Steiner tree is a good rough approximation of how the disease might have spread. In particular, the *extra* nodes you find in your min. Steiner tree are your missing nodes.

First generage the graph *G* as using the following function [5]:

G = networkx.random graphs.extended barabasi albert graph(50, 1, 0.2, 0.1, seed=10).

Obtain an approximate minimum Steiner tree using this existing Networkx function [6]. Submit both a visualization and the adjacency list of the minimum Steiner tree for each of the following initial known infected nodes.

1. *K* = {10, 14, 3}
2. *K* = {10, 14, 3, 4, 2}
3. *K* = {10, 14, 3, 4, 2, 31, 49}
4. *K* = {10, 14, 3, 4, 2, 31, 49, 21, 25, 36, 43}

Plot the visualization in the pdf and submit the adjacency file as a .npy 2-D numpy array file.

Solution: .npy files are in Q4/Npy_Files/

Plot 1:

https://drive.google.com/file/d/1u51urgdOzd7bkN4lmoHgt5cyiWgEPOxm/view?usp=sharing

Plot 2:
https://drive.google.com/file/d/1MakIWZfRjavVWAHlQN6fuQ_Dz3phr2rz/view?usp=sharing

Plot 3:

https://drive.google.com/file/d/1b137YTy2fAP0I27cWwig6U374BfxbOWT/view?usp=sharing

Plot 4:

https://drive.google.com/file/d/1bA_2bsNC5vktQ8SqUvvaej82KaqlVOZF/view?usp=sharing

Q 4.3 (2 points) Briefly in 1-2 lines, what maybe the pros and cons in using a min. Steiner tree to identify missing infections? Suggest improvements for the same. This is an open-ended question so feel free to give intuitive answers.

Solution: One pro is that min. Steiner trees provide a straightforward explanation for the missing infections. One con is that it can oversimplify the spread of infection as there are many nuances to the way an infection can spread. Incorporating specific infection beta values for edges could improve accuracy

[5] Checkout https://en.wikipedia.org/wiki/Barabasi-Albert_model for more details on the network model.

[6] See documentation at: https://networkx.org/documentation/stable/reference/algorithms/generated/networkx.algorithms.approximation.steinertree.steiner_tree.html.