Homework 2: Models, Dynamics, Construction, Inference

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CSE 8803 EPI Fall 2022
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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. (15 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 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 $\{S_j(t), R_j(t), R_j(t)\}_{j=1}^{M}$ and flow parameters σ_{ij}.

Solution:

The influx of susceptible population of city i when populace moves from city j to city i at time t =

$$S_j(t)\frac{\sigma_{ji}}{N_j}$$

The efflux of susceptible population of city i when populace moves from city i to city j at time t =

$$S_i(t)\frac{\sigma_{ij}}{N_i}$$

Total net flow of susceptible population and summation of M cities for city i at time t =

$$\sum_{j=1}^{M} S_j(t)\frac{\sigma_{ji}}{N_j} - \sum_{j=1}^{M} S_i(t)\frac{\sigma_{ij}}{N_i}$$

Thus effective susceptible population of city i at time t =

$$S_i^{eff}(t) = S_i(t) + \sum_{j=1}^{M} S_j(t) \times \frac{\sigma_{ji}}{N_j} - \sum_{j=1}^{M} S_i(t) \times \frac{\sigma_{ij}}{N_i}$$

Similarly for $I_i^{eff}(t)$ and $R_i^{eff}(t)$,

$$I_i^{eff}(t) = I_i(t) + \sum_{j=1}^{M} I_j(t) \times \frac{\sigma_{ji}}{N_j} - \sum_{j=1}^{M} I_i(t) \times \frac{\sigma_{ij}}{N_i}$$

$$R_i^{eff}(t) = R_i(t) + \sum_{j=1}^{M} R_j(t) \times \frac{\sigma_{ji}}{N_j} - \sum_{j=1}^{M} R_i(t) \times \frac{\sigma_{ij}}{N_i}$$

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

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

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

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

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:

Now, the previous values of $S(t)$, $I(t)$, $R(t)$ would be unchanged and wouldn't change with the change in the decrease of the time step. But β and γ would change with the change in the time step and become a fraction of itself as they are measured over a single time step. Considering a uniformity across the time-step, β would become $\beta\Delta t$ and γ would become $\gamma\Delta t$.

The flow parameters σ_{ij} on the other hand represents the flow of populace from city i to city j. This can also be said that this is the rate of populace migration and thus should be independent of time t.

Therefore the equations start looking a bit like this,

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

Thus the rate change of susceptible populations over a time step is,

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

Similarly for infected and recovered compartments,

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

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

Q 1.3 (3 points) Set $\Delta t \to 0$ and derive the ODE equations for the metapopulation model.

Solution: To derive standard ODE we reduce the Δt time step to the smallest possible value tending to 0. Therefore we will put the limit to 0.

$$\lim_{\Delta t \to 0} \frac{S_i(t+1) - S_i(t)}{\Delta t} = \beta S_i^{eff}(t) \sum_{j=1}^{M} \frac{I_j^{eff}(t)}{N_j}$$

$$\lim_{\Delta t \to 0} \frac{I_i(t+1) - I_i(t)}{\Delta t} = \beta S_i^{eff}(t) \sum_{j=1}^{M} \frac{I_j^{eff}(t)}{N_j} - \gamma I_i^{eff}(t)$$

$$\lim_{\Delta t \to 0} \frac{R_i(t+1) - R_i(t)}{\Delta t} = \gamma I_i^{eff}(t)$$

Solving the limits, we get

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

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

$$\frac{dR_i(t)}{dt} = \gamma I_i^{eff}(t)$$

Q 1.4 (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 metapopulation model.

Solution:
Code and plots in the tarball.

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 the computers in the network get infected with a virus which can spread across the network as 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 $\mathcal{G} = \{G_1, G_2, \ldots, G_9\}$ between routers (this dataset is sourced from actual internet router dataset [1]. Each of the networks are snapshots 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 $\mathcal{G}$ have an edge between them, we add an edge (u, v) to $G(\rho)$. Here ρ is a 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 observe this empirically for this dataset.

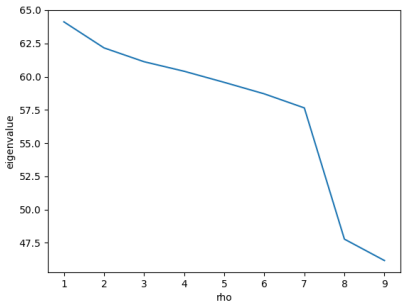
For each value of ρ in $\{1, 2, 3, \ldots, 9\}$, write code to construct $G(\rho)$. Find the largest eigenvalues λ of the adjacency matrix for each graph $G(\rho)$. Submit the plot between ρ and γ. How does λ change with increase in ρ?

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:
Code in the tarball as Q-2.1.ipynb.

[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`

Plot depicting the relation of ρ and λ.



The maximum eigenvalue λ decreases with the increase of ρ or sparseness of the network in a way such that ρ and λ are inversely related. The density of network is dependent on the maximum eigenvalue.

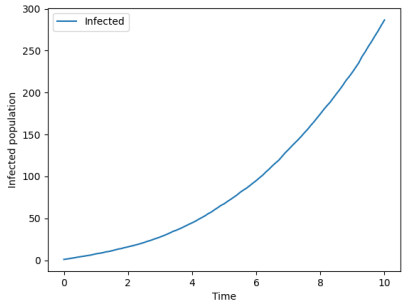
Q 2.2 (10 points) Set $\rho = 1$. Use the EoN package [2] to set up an SIS model on $G(\rho)$. Specifically use the `EoN.fast_SIS` function [3]. Set $\gamma = 0.08, \beta = 0.001$ and `max_time` $T = 10$. Set node 1 as the only infected node at $t = 0$.

Now plot a curve with $I(t)$ on y-axis vs t on x-axis for $0 \leq t \leq T$ after simulating the model 50 times (similar to HW1 Q1.3). Now set $\beta = 0.0001$ and plot the $I(t)$ vs t curve. Do you notice any difference? Explain.

Solution:

Code in the tarball under the name of Q-2.2.ipynb.

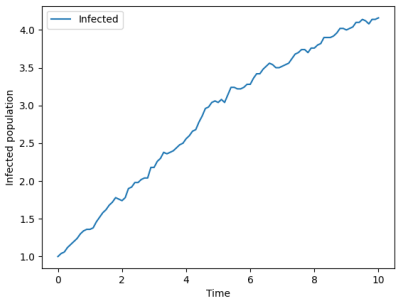
Plot for $\gamma = 0.08$, $\beta = 0.01$ with $T = 10$.



Plot for $\gamma = 0.08$, $\beta = 0.001$ with $T = 10$.

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

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



The figures represent a stark contrast in the sense, during the initiation of the infection, at $\beta = 0.01$ the infection shows a continuously increasing trend while the curve of infection with $\beta = 0.001$, has a discontinuous increasing trend and represents more uncertainty in the spread of the infection.
The rate of infection is proportional to β parameter and thus with β at 0.01, the infection spread is significant that it is continuously increasing with the value of γ we have. We can't say the same for infection spread with β at 0.001.

Q 2.3 (10 points) Now set $\beta = 0.001, \gamma = 0.16$ and $\rho = 1$. We will try to reduce the effective 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.

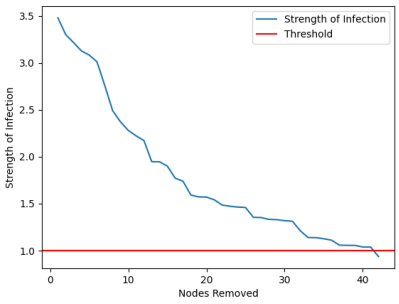
Using this rule find the number of node removals required to reduce the effective strength of the graph to less than 1. Also produce a plot of number of nodes removed in x-axis and effective strength on y-axis till effective strength reduces to less than 1.

Solution:

Code within the tarball under the name Q-2.3.ipynb.

After removing K = 42 nodes, we get a graph which has the effective strength less than 1.

Plot for the effective strength of the graph generated vs nodes removed.



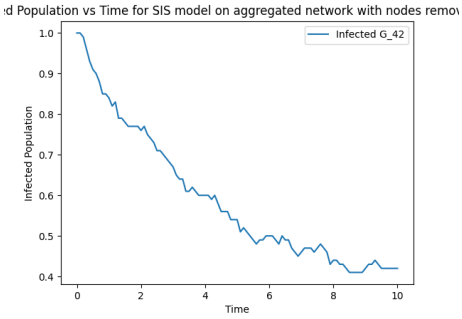
Q 2.4 (6 points) We will denote as K the number of nodes you had to remove in Q2.3 before effective strength decreased below 1. Consider the two graphs G_a and G_b where G_a is the initial graph you constructed by removing all K nodes and G_b the graph you constructed by removing $K - 1$ nodes (hence, effective strength is > 1). Simulate the

SIS model on G_a and G_b with the same parameters by randomly choosing a single node to be infected at $t = 0$. Perform 100 simulations for both G_a and G_b for $T = 10$ steps. Plot $I(t)$ vs t for both the graphs.

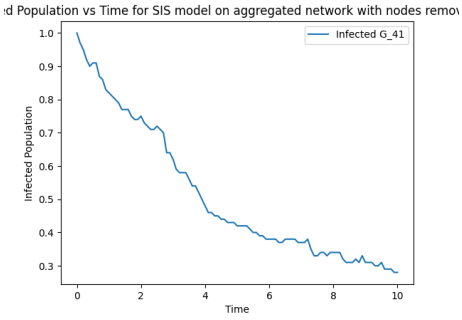
Solution:

Code within the tarball under the name Q-2.4.ipynb.

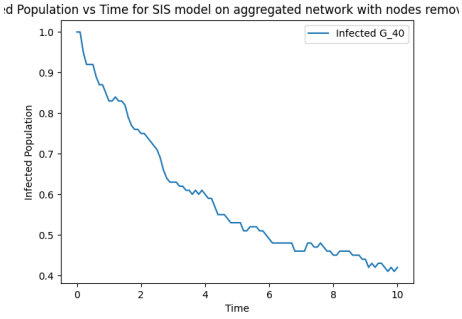
Plot for $I(t)$ vs t for G_{42}



Plot for $I(t)$ vs t for G_{41}



Plot for $I(t)$ vs t for G_{40}



3. (30 points) Finding Culprits

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

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

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

central node 0 be infected at $t = 0$. Run the SI model for 10 steps and record the set of nodes I which are infected at the end of 10 steps.

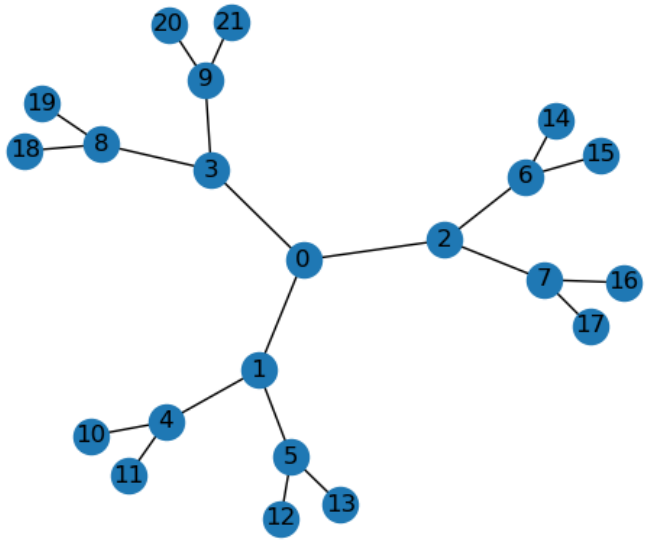


Figure 1: Cayley Tree

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 I_i which are separated by a space.

Solution:
Code and file in the tarball.

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: $u_i = \text{Centroid}(I_i)$. 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:
Code and file in the tarball.
Accuracy achieved = 91%

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.

Solution:
Code and file in the tarball.
Accuracy achieved = 69%

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:

The accuracy of the estimator decreases from 91% to 69%.

The central node being the patient zero or the initial node getting infected works the best for this algorithm. But, this is it's major limitation and the estimator will perform worse if the starting point of infection is in the deeper layer of the tree and thus estimator's accuracy would fail would not work properly. This estimator can only be helpful in determining whether the central node was the starting point of the infection spread.

Although computationally expensive the rumor centrality metric would perform better than just finding the center of infected sub-graph and provide a strong confidence in determining the starting point of the infection.

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 nodes may 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 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 I too, but at least it has to span all of I).

The minimum weighted Steiner tree, is the Steiner tree for a given 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 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.

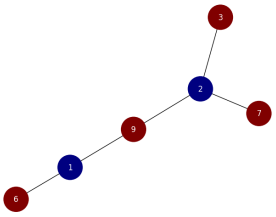
Q 4.1 (8 points) Let's try to compute a couple of minimum Steiner trees by hand. Feel free to use whatever method you want (except of course just using a software package). These can be done with intuition as well. Just draw and show us the final answer.

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

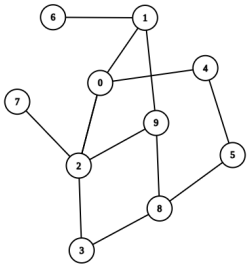
Solution:

By calculating the number of the minimum edge between the terminal node we get a distance matrix given below.

X	7	3	9	6
7	X	2	2	4
3	2	X	2	4
9	2	2	X	2
6	4	4	2	X



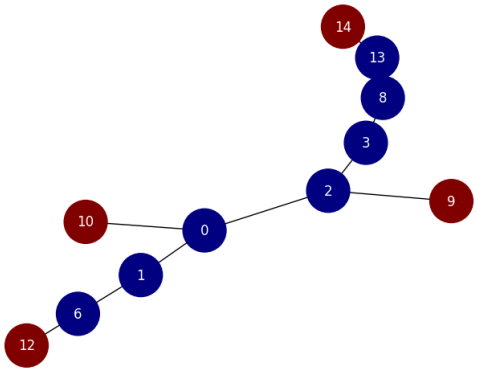
Used networkx only to draw the graph.



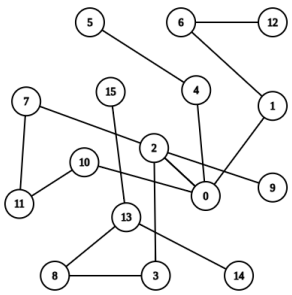
Q 4.1.2 (4 points) Terminal set = $\{12, 14, 9, 10\}$ for graph below.

Solution:
By calculating the number of the minimum edge between the terminal node we get a distance matrix given below.

X	12	14	9	10
12	X	8	5	4
14	8	X	5	6
9	5	5	X	3
10	4	6	3	X



Used networkx only to draw the graph.



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.

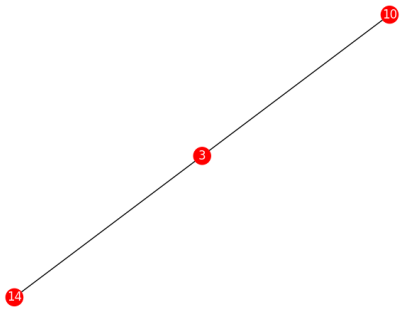
1. $K = \{10, 14, 3\}$
2. $K = \{10, 14, 3, 4, 2\}$
3. $K = \{10, 14, 3, 4, 2, 31, 49\}$
4. $K = \{10, 14, 3, 4, 2, 31, 49, 21, 25, 36, 43\}$

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

Solution:

Steiner trees plotted below .npy files in the tarball

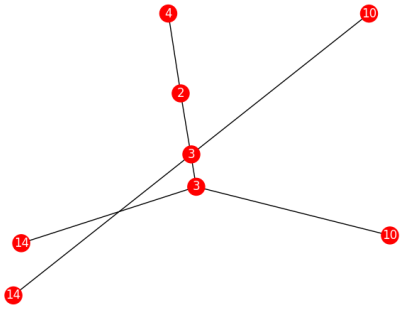
Steiner tree for terminal nodes 10, 14, 3



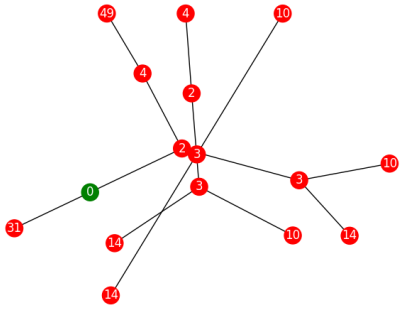
Steiner tree for terminal nodes 10, 14, 3, 4, 2

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

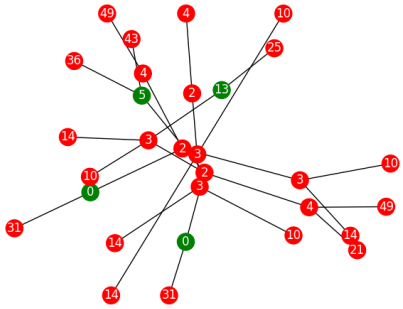
[6] See documentation at: `https://networkx.org/documentation/stable/reference/algorithms/generated/networkx.algorithms.approximation.steinertree.steiner_tree.html`.



Steiner tree for terminal nodes 10, 14, 3, 4, 2, 31, 49



Steiner tree for terminal nodes 10, 14, 3, 4, 2, 31, 49, 21, 25, 36, 43



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:

Steiner tree approximation of a graph sure does a decent job at explaining the infected sub-graph in use for transmission of infection. They can be used to identify the most susceptible or possibly asymptomatic nodes between the infected nodes and can use a probabilistic function to indicate the true risk of these nodes which belong in the Steiner tree with the terminal nodes.
They can also be used to identify with some certain probability whether a susceptible node is already infected or not. For nodes like these in an epidemic can be considered exposed or asymptomatic and can have a risk level assigned to them.

The major issue with the Steiner tree is the taken assumption that infection will

always travel the minimum distance between nodes and that will always need not be the actual case, although that happening might have a very less probability. But in a case like this, there is a chance for the network to miss out on the possible infected nodes. Thus it fails to identify the risk effect on the nodes which aren't part of Steiner tree yet, but chances are it was infected as well and went unreported. For this disadvantage one can go for Netfill coupling and decoupling to identify such nodes which are in closer proximity to the terminal nodes but are absent from the Steiner trees.
Steiner trees might also fail when there is a potential of multiple of infection starting points in a very sparse graph (imagining initial stages of the pandemic within a city) and we might see a surge of unreported infected nodes which aren't really infected. To avoid such an issue, sparsity between the clusters would be required to divide the static graph in two or more required sub-graphs and replicate the process from there.