

CS:4980 Homework 2

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1 Late day used.

1 Metapopulation Model

1.1

The formulae are:

$$S_i^{eff}(t) = S_i(t) + [\sum_j S_j(t) \frac{\delta_{ji}}{n_j} - \sum_j S_i(t) \frac{\delta_{ij}}{n_i}]$$

$$I_i^{eff}(t) = I_i(t) + [\sum_j I_j(t) \frac{\delta_{ji}}{n_j} - \sum_j I_i(t) \frac{\delta_{ij}}{n_i}]$$

$$R_i^{eff}(t) = R_i(t) + [\sum_j R_j(t) \frac{\delta_{ji}}{n_j} - \sum_j R_i(t) \frac{\delta_{ij}}{n_i}]$$

1.2

The formulae are:

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

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

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

1.3

Setting $\Delta t \rightarrow 0$, we get the Equations as follows:

$$S'_i(t) = -\beta S_i^{eff}(t) \sum_{j=1}^M \frac{I_j^{eff}(t)}{N_j}$$

$$I'_i(t) = \beta S_i^{eff} t \sum_{j=1}^M \frac{I_j^{eff}(t)}{N_j} - \gamma I_i^{eff}(t)$$

$$R'_i(t) = \gamma I_i^{eff}(t)$$

1.4

The plots for the Metapopulation Model are given in Figure 1,2 and 3.

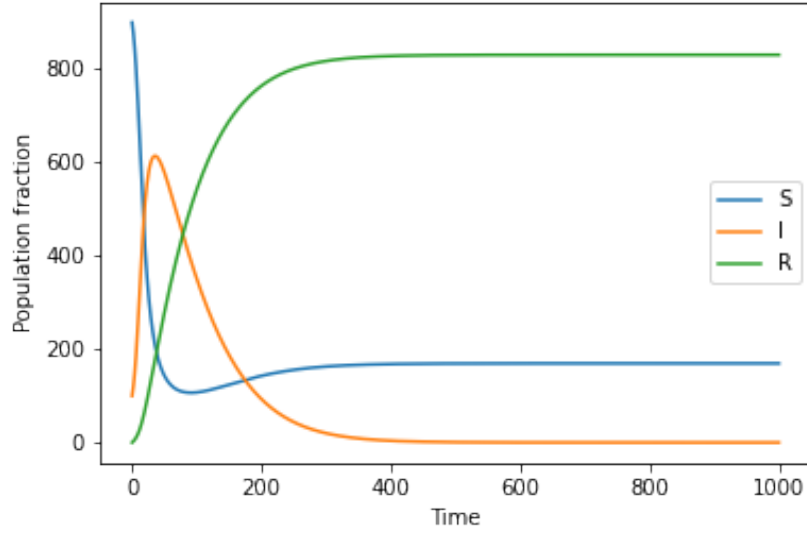


Figure 1: Metapop 1

2 Viral Propagation

2.1

The plot of λ with ρ is given in Figure 4.
It seems that λ decreases with increase of ρ .

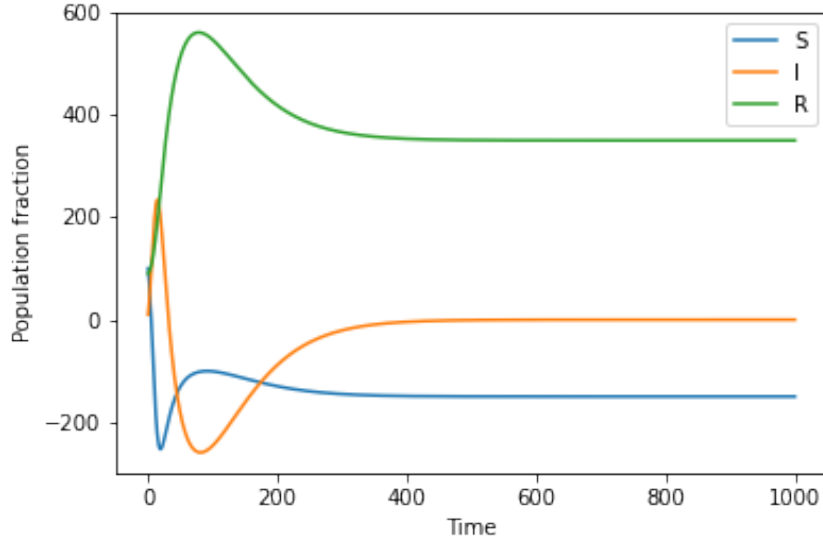


Figure 2: Metapop 2

2.2

The result of the SIS model with $\beta = 0.001$ is shown in Figure 5. The result of the SIS model with $\beta = 0.0001$ is shown in Figure 6.

From the 2 figures, we notice that the number of infections rise in Figure 5 and generally fall in Figure 6. This may be because for Figure 5, the effective strength was 0.8, which is much closer to the threshold value of 1, which means that the infection will initially spread and then will die off. While, the effective strength of the model for Figure 6 was 0.08, much lower than the threshold, which means that the disease did not get any chance to take off.

2.3

The total number of node removals was 42. The plot asked for is in Figure 7.

2.4

The plot of the k-1 graph with disease parameters from Q2.3 is given in Figure 8 while the plot of the k graph with disease parameters from Q2.3 is given in Figure 9.

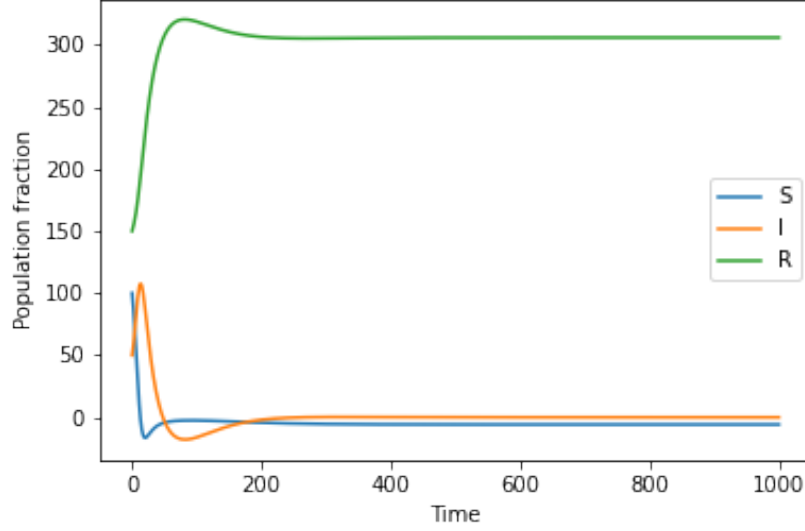


Figure 3: Metapop 3

3 Finding Culprits

3.1

The initial graph looked like Figure x1. The 100 sets of nodes file is stored in file 3.1.txt under directory 3.

3.2

The accuracy of the algorithm is 0.65.

3.3

The accuracy of the algorithm is 0.43.

3.4

Yes, the accuracy of the estimator changes. This result tells that the choice of estimator for generating simulations is extremely important as it will define the centrality of the disease spread. This particular estimator is extremely prone to initial point initialization and thus it does not do well in this kind of a graph. The rumor centrality metric will do well as it maximizes the likelihood of observed data through ripples in the Cayley tree.

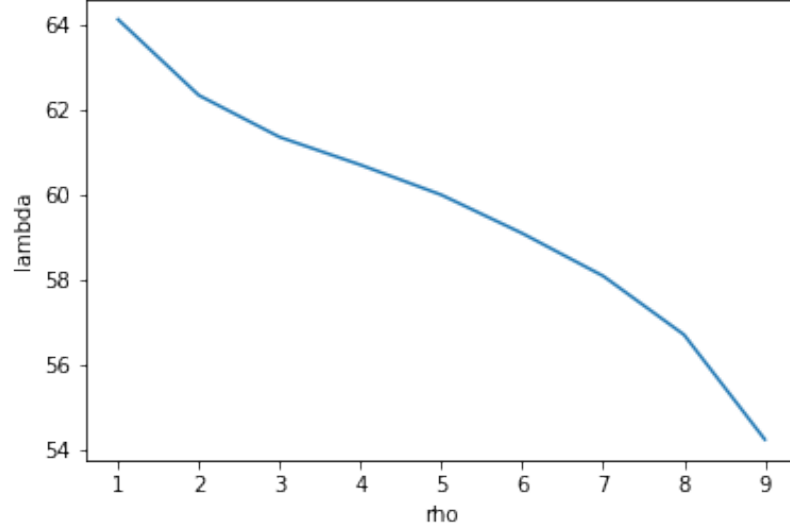


Figure 4: Variation of the eigenvalue with threshold

4 Steiner Tree for Missing Infections

4.1

4.1.1

The Minimum Steiner Tree is given in Figure 11 The weight is 5.

4.1.2

The Minimum Steiner Tree is given in Figure 12 The weight is 11.

4.2

The original Graph is given in Figure 13.

1. The visualization is given by Figure 14.
2. The visualization is given by Figure 15.
3. The visualization is given by Figure 16.
4. The visualization is given by Figure 17.

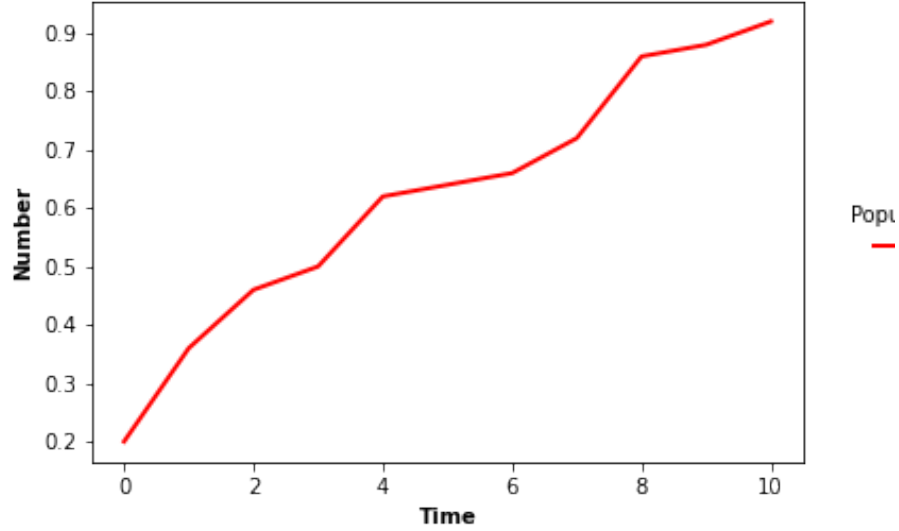


Figure 5: SIS model with the higher infectivity rate

4.3

The pros of using a minimum Steiner tree to detect missing infections is that it is intuitive. For simple graphs, it can be easily constructed to give infection cascades. Although it is NP- Hard, approximation algorithms can be made, which does well on average. The cons are that in dense graphs, it does very poorly. For example, take a clique with 2 observed infections. A minimum steiner tree formulation would only give 2 infections while in reality, the infection might have transmitted to numerous nodes. I think one improvement would be to not just consider the minimum lengthSteiner tree, but instead threshold the minimum steiner tree length so that the minimum Steiner Tree length would be greater than that threshold.

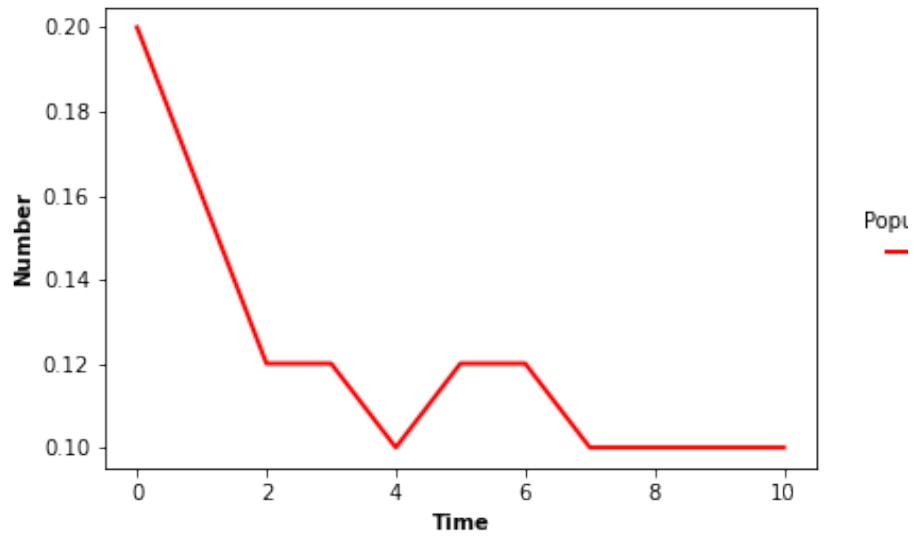


Figure 6: SIS model with the lower infectivity rate

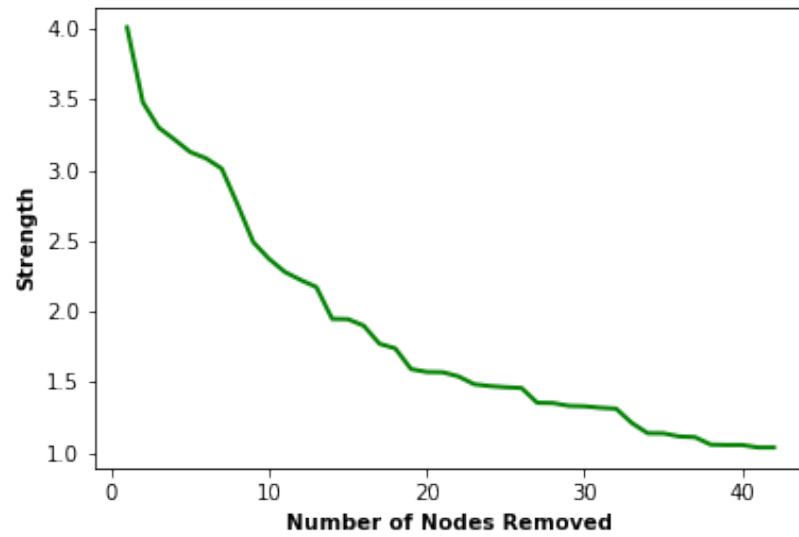


Figure 7: Variation of Strength vs number of node removals

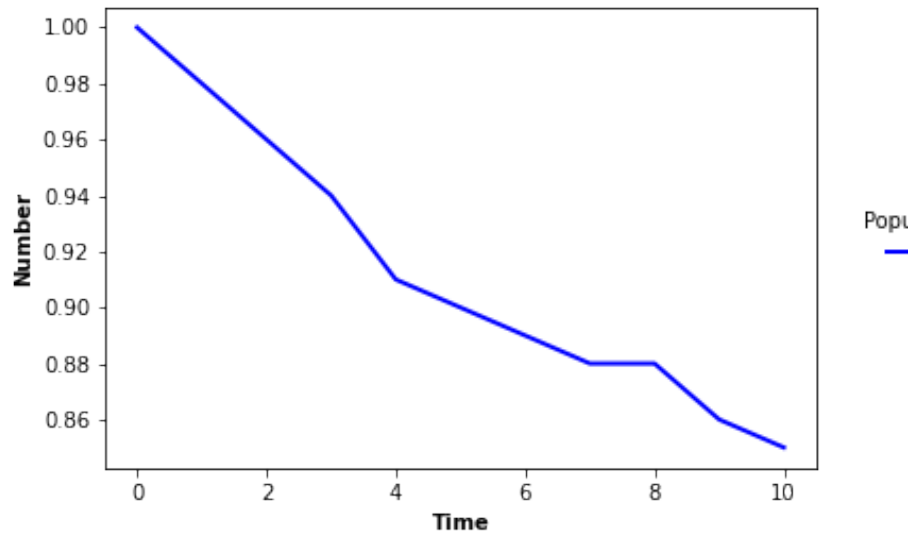


Figure 8: Disease Spread in K-1 removal graph

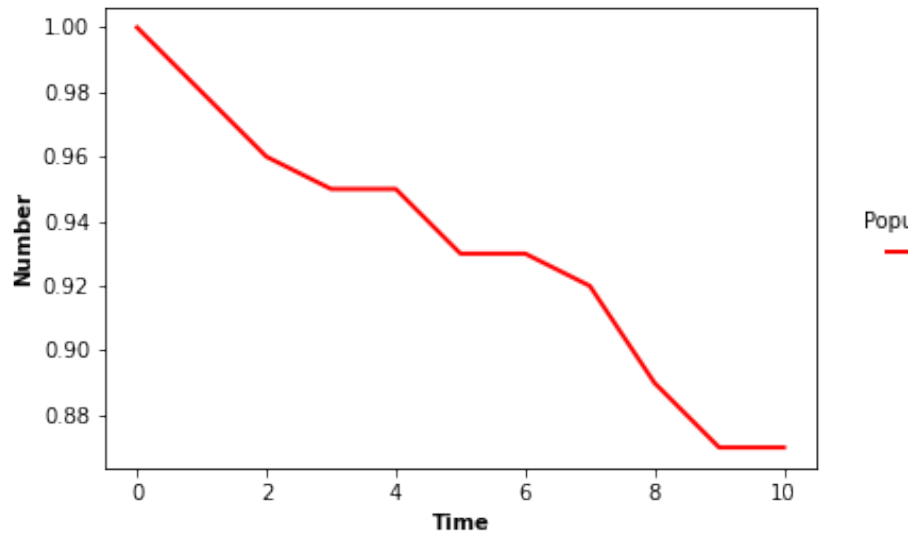


Figure 9: Disease Spread in K graph

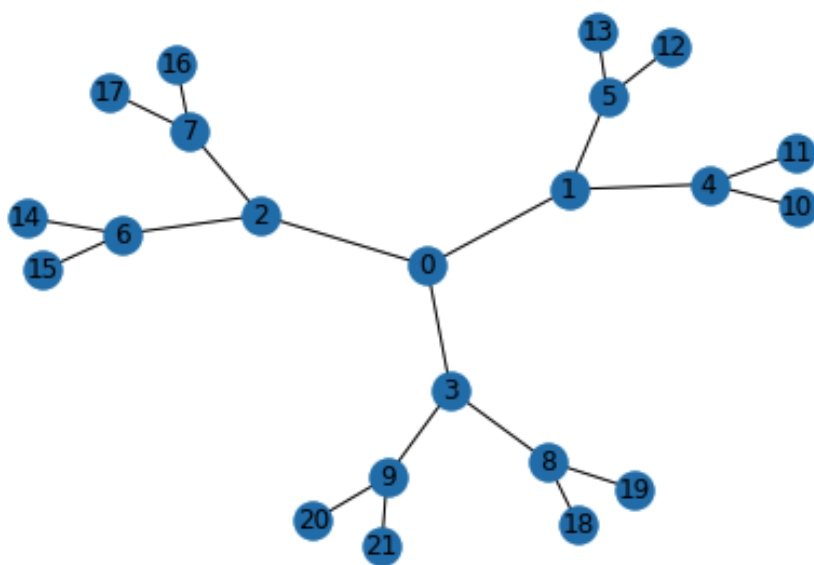


Figure 10: Cayley Tree

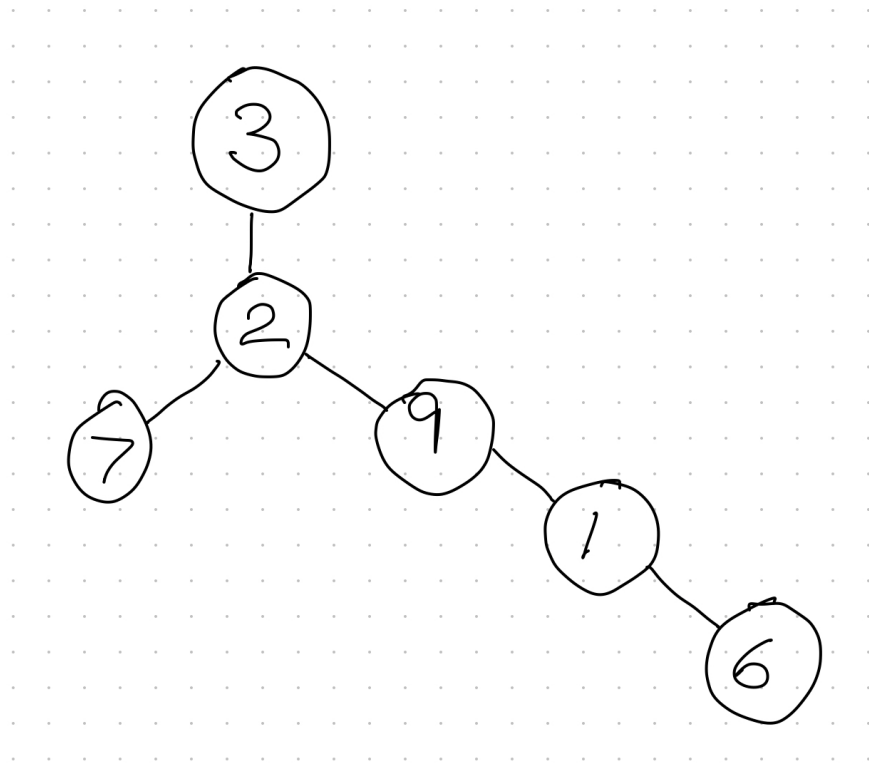


Figure 11: MST for 4.1.1

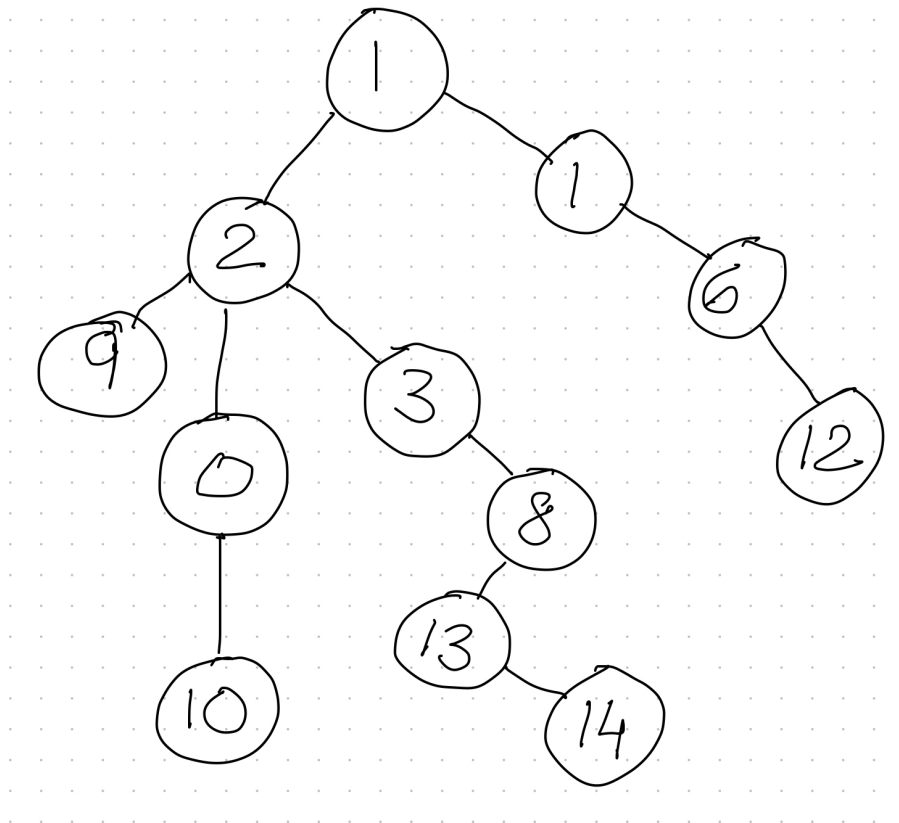


Figure 12: MST for 4.1.2

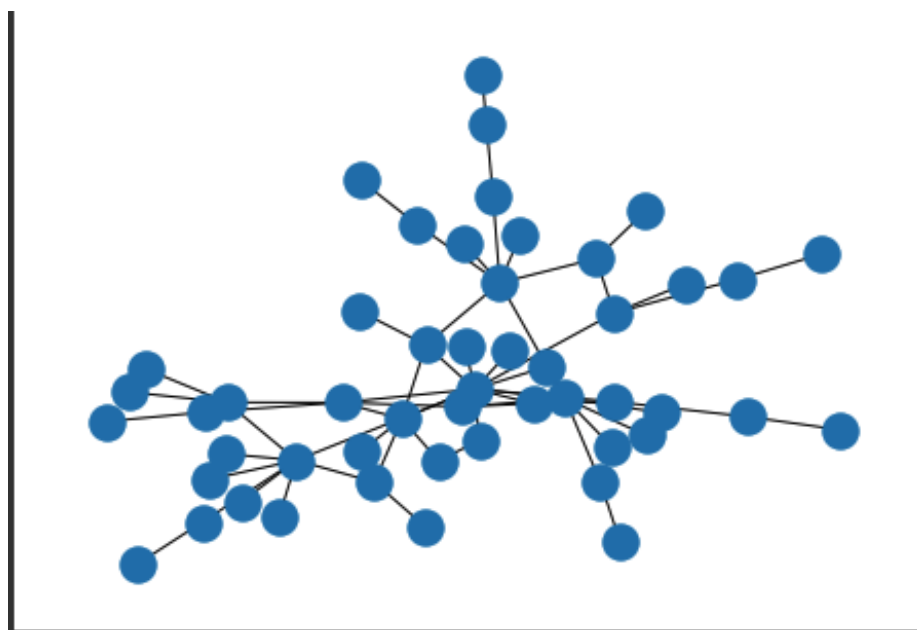


Figure 13: Original graph visualization for Q4.2

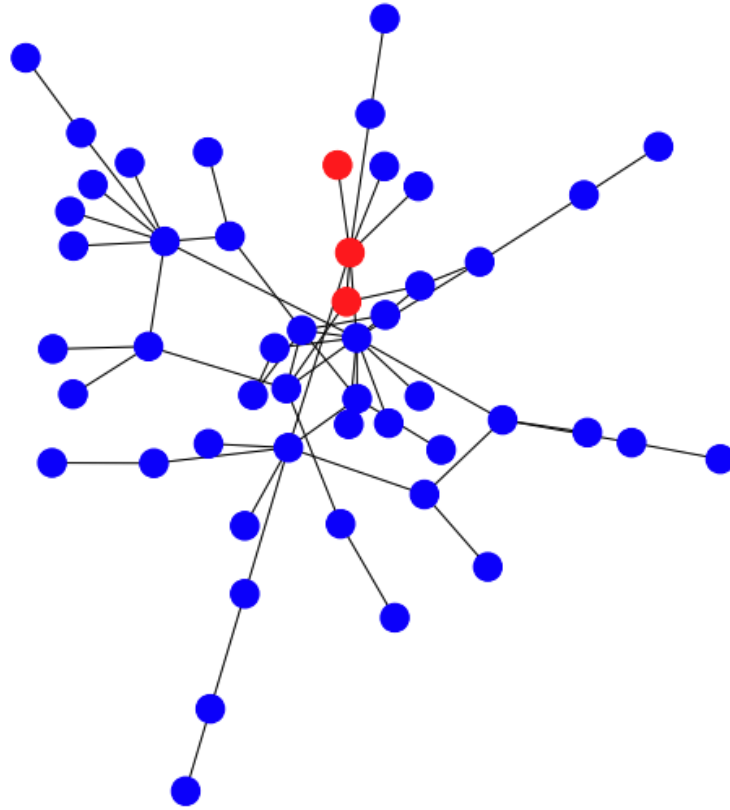


Figure 14: Original graph visualization for Q4.2 Part 1. The red colour denotes the nodes which are the part of the MST

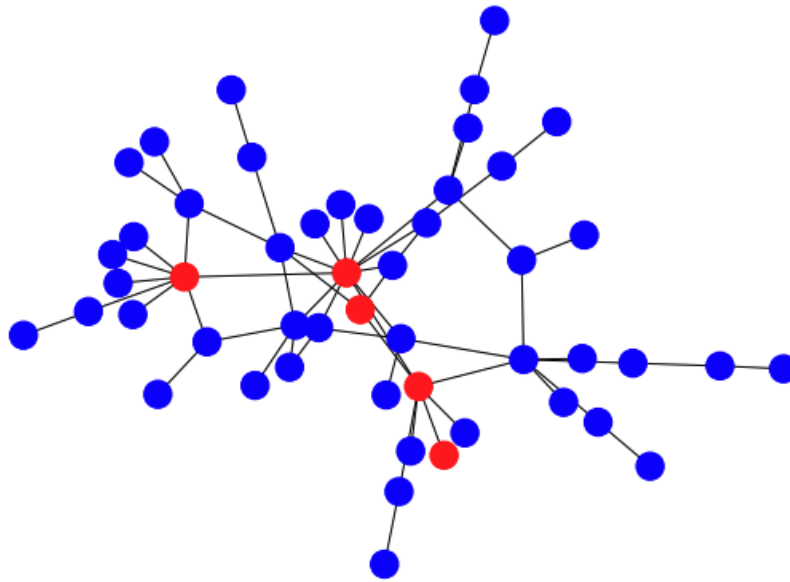


Figure 15: Original graph visualization for Q4.2 Part 2. The red colour denotes the nodes which are the part of the MST

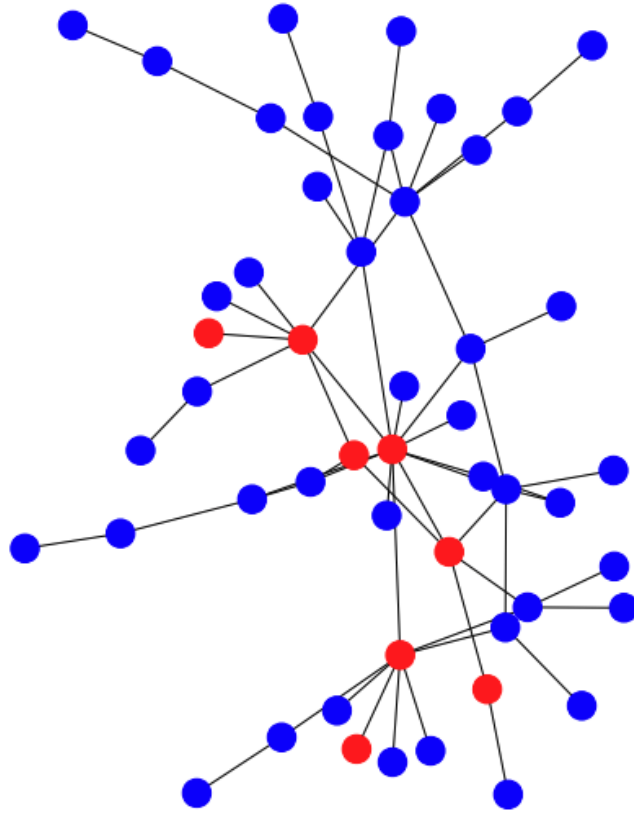


Figure 16: Original graph visualization for Q4.2 Part 3. The red colour denotes the nodes which are the part of the MST

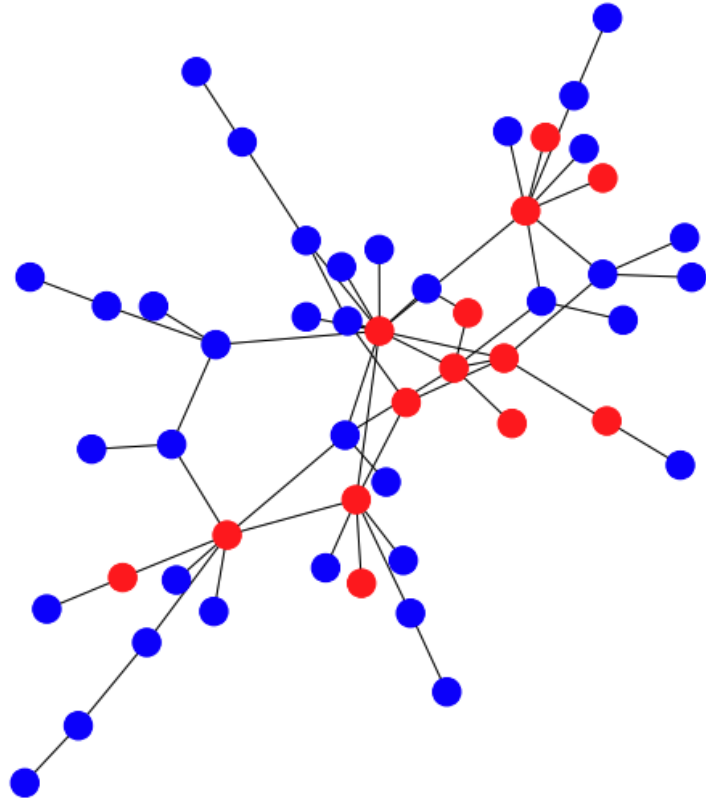


Figure 17: Original graph visualization for Q4.2 Part 4. The red colour denotes the nodes which are the part of the MST