COMP3340 Assignment 1 part 2

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# Question 1

## A).

## B).

1.

2.

3.

4.

5.

# Question 2

## Graphs

Proteins Relative neighbourhood graph



Samples Relative neighbourhood graph

Samples Minimum spanning tree.



Proteins Minimum spanning tree.



## Matrix’s

Proteins MST & RNG

Minimum spanning tree



Relative Neighbourhood Graph



Samples MST & RNG

Minimum spanning tree



Relative neighbourhood graph



## How was it done?

To generate the distance matrix I used the SCIPY euclidean() method. This checks the distance between two input arrays no matter of their contents. Where as with the hemming matrix it would only work properly for binary. I just used the same method I created in assignment 1 part 1 for question 1 retrofitted to generate a Euclidian matrix rather than a hemming matrix. For the samples I transposed the matrix using the numpy transpose() method.

To Actually generate the MST and RNG I used external libraries from SCIPY and relativeNeighborhoodGraph respectively. To generate the MST I parsed the distance matrix, index names and the export location to the generic method genMST() which used the SCIPY method minimum\_spanning\_tree() to generate a minimum spanning tree using Kruskal’s algorithm. The minimum\_spanning\_tree() method would return a sparse array which was then to be converted into a normal array. And exported to an XLSX file using pandas.  
To generate the RNG I used the same method as with he MST however with another step. The method returnRNG() returns a pandas data frame with duplicated lines, to fix this issue I created a method to loop through the matrix checking for duplicate lines (a line is duplicate if it appears in both x, y and y, x).

# Question 3

# Question 4

# Question 5