For the first part of the program:

Computing properties of biological networks.

Given n genes the co-expression graph is represented by an $n \times n$ matrix, Co-ex, whose element Co-ex[u,v] is the co-expression value of genes u and v. Co-expression values are in the range [0,1]. The graph is complete that is it has an edge connecting any two nodes. This graph is represented in the file in the data folder.

This program reads in input the Co-ex matrix. It then removes from the graph all edges with weight below 0.5. At this point, it generates a new graph Reduced_Unweighed_Graph which has the same set of genes and all remaining edges. It is unweighted and is represented by a binary adjacency matrix, ADJ, with ADJ[u,v]=1 if there is an edge between nodes u and v, 0 otherwise.

Of the network Reduced_Unweighed_Graph this program

1. a) Computes the degree distribution
2. b) Determines all cliques of size 3
3. c) Computes the neighborhood T2 of all nodes of the network. It determines the node whose neighborhood has the largest size among all nodes of the graph.

For the second part of the program:

This program generates a random graph in which each edge occurs with probability 0.5. The graph has the same number of nodes of the input PPI interaction network. Then, for the random graph it repeats tasks a), b) and c) as stated above. Finally the program generates a random graph in which each edge is present with probability $p = 0.1$ and another graph with probability $p = 0.8$. It then repeats for the random a), b) and c).