# **Cellular Networks with Cytoscape**

## Question 1

a) The average path length of the network

L = Total Length/Total Pair = 1,8667

A-B	1
A-C	1
A-D	1
A-E	2
A-F	3
B-C	2
B-D	2
B-E	3
B-F	4
C-D	2
C-E	1
C-F	2
D-E	1
D-F	2
E-F	1
Total Pairs: 15	Total Length: 28

#### b) The diameter of the network

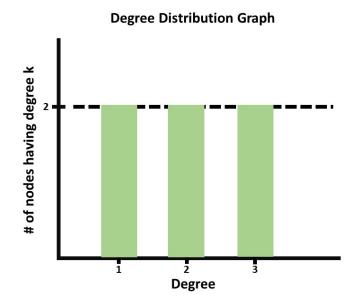
To find the shortest path between the two farthest points, you need to examine all possible routes between these two points. The length of a path is measured by the number of connections. For example, to go from A to F, we can consider different routes such as A-D-E-F or A-C-E-F. After examining all possible routes, you need to determine the shortest path between the two farthest points. We will calculate how many connections are on this path and its length.

When you find the length of the shortest path, you obtain the diameter of the network. The network's diameter is expressed as the length of the shortest path between these two farthest points. Assuming that the farthest two points are A and F, the shortest path would be A-C-E-F. This path has 3 connections (A-C, C-E, E-F), so the **diameter of the network is 3**.

### c) The degree distribution graph

Node	Degree
Α	3
В	1
С	2
D	2
Е	3
F	1

Degree	Node Count
1	2
2	2
3	2



# **Question 2**

**Goals:** We have quantified the data we have in the first question and manually obtained the average path length, network diameter values, and degree distribution graph. Now we will get the same values by using Analyze Network tools in Cytoscape and we will compare the results. Additionally, we will change the node color and node size based on the degrees of the nodes in the network.

Download the Cytoscape software in Figure 1.

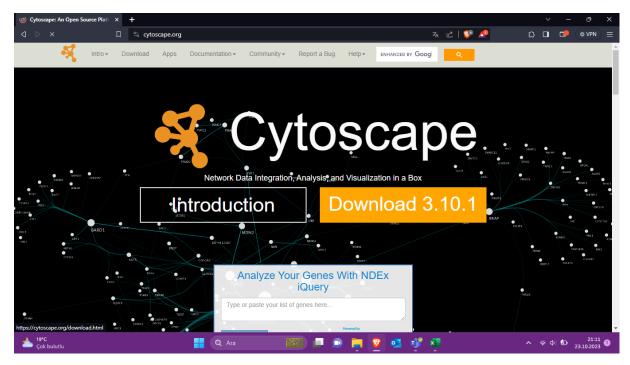


Figure 1. We have downloaded the Cytoscape software in <a href="https://cytoscape.org/">https://cytoscape.org/</a>.

We have created the excel file contain information the Node1 and Node2. This excel file including between nodes information; so it including Node1 and Node2 column. We will use this file in Cytoscape (Figure 2).

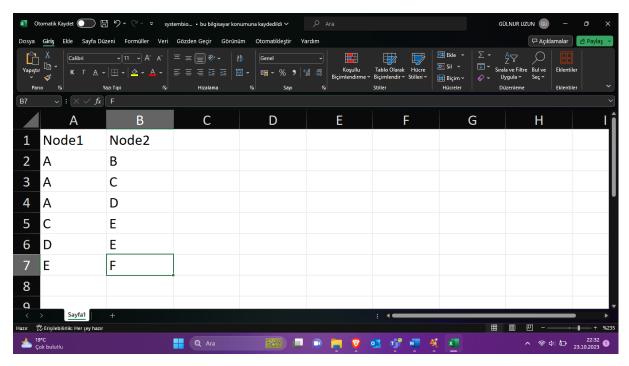


Figure 2. An excel file containing the Node1 and Node2 columns.

Then, we will import created the excel file in Figure 2 in Cytoscape. To do this, we will following these step: **File-Import-Network from File** (Figure 3).

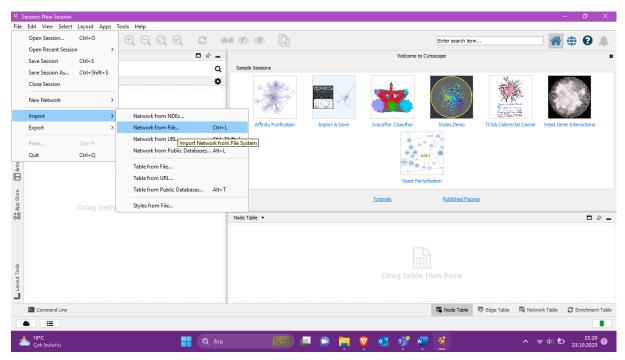


Figure 3. We import the created file by following the File-Import-Network from File path.

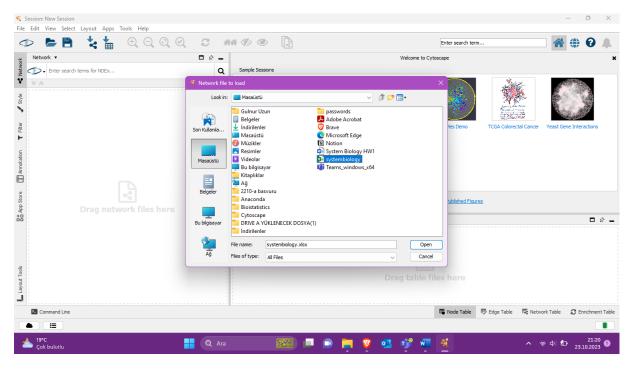


Figure 4. We have selected the systembiology.xlsx file.

After importing the file, according to the nodes information, we obtained an image of network connections, as in the Figure 5.

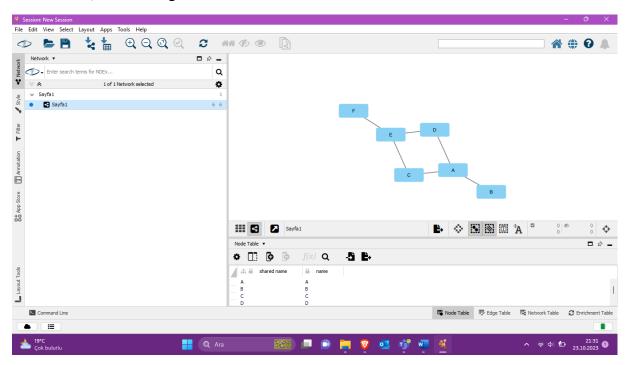


Figure 5. The image we got when we first opened the file in Cytoscape.

Afterward, we will perform network analysis by following the path **Tools-Analysis Network**. In the first question, we manually calculated certain values. We will obtain these manually calculated values here using the Network Analysis tool and compare the results.

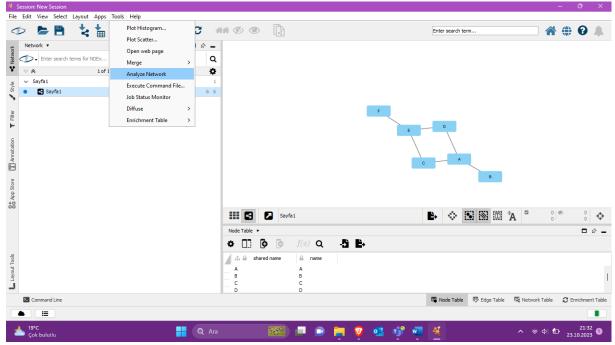


Figure 6. In this step, we following the Tools-Analyze Network pathway for average path length, diameter, and degree distribution graph.

We obtained the **Summary Statistics** (Figure 7) and the **Degree Distribution Graph** (Figure 8) results by following the path in Figure 6.

Summary Statistics	
Number of nodes	•
Number of edges	•
Avg. number of neighbors	2,000
Network diameter	:
Network radius	•
Characteristic path length	1,510
Clustering coefficient	0,000
Network density	0,200
Connected components	•
Multi-edge node pairs	(
Number of self-loops	(
Analysis time (sec)	0,044

Figure 7. Summary Statistics for our network.

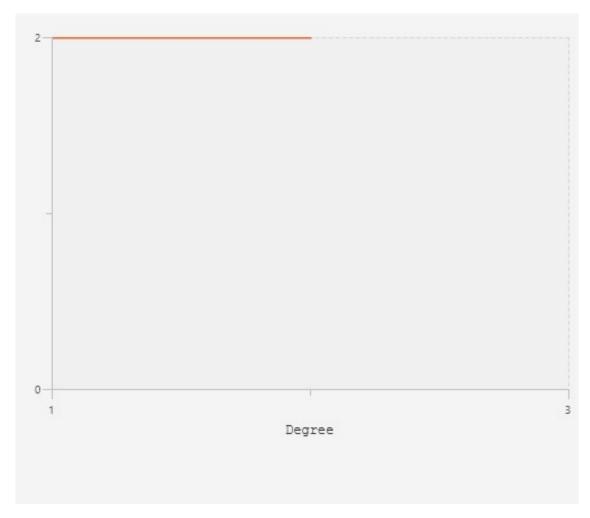


Figure 8. Degree Distribution Graph for our network.

In the final stage, an adjustment is required. We will modify the color tones and sizes based on the degrees of the nodes. For color adjustments, we selected the **Fill Color** section in the **Style tab** to determine the color tone. To make size adjustments, we made modifications on **the Height option** in the **Style tab**. As a result, we obtained a network with varying **sizes** and **color tones** based on their **degrees** (Figure 9).

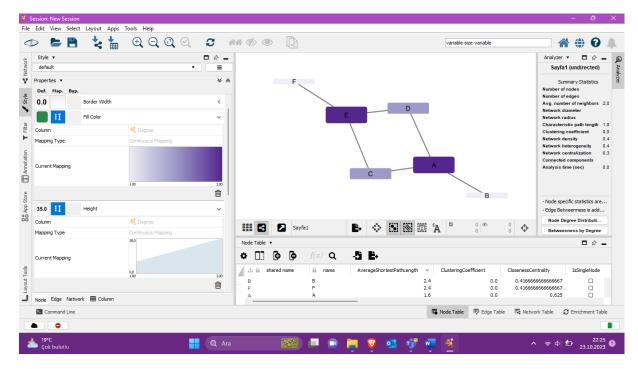


Figure 9. In this step, we change the node size and color suitable degree values.

Table 1 provides a comparison between the results of manual calculations and the results of the analyze network calculations. According to the obtained results, the diameter value is the same for both calculations, but there is a difference of 0.3 in the average path length value.

Table 1. We have compared the results of manual calculation and Network Analysis.

	Manual Calculation	Network Analyze Tool
Average Path Length	1,8667	1,510
Network Diameter	3	3

## **Question 3**

**Goals:** In this question, our objective is to download the .zip files (with .tab format being important) for the worm (*Caenorhabditis elegans*) and rat (*Rattus norvegicus*) organisms using the BioGRID database. Subsequently, we will perform Network Analysis using the Cytoscape software. Then, we will compare these results for two separate organisms.

Firstly, we accessed the BioGRID database (<a href="https://thebiogrid.org/">https://thebiogrid.org/</a>) and selected the downloads tab.

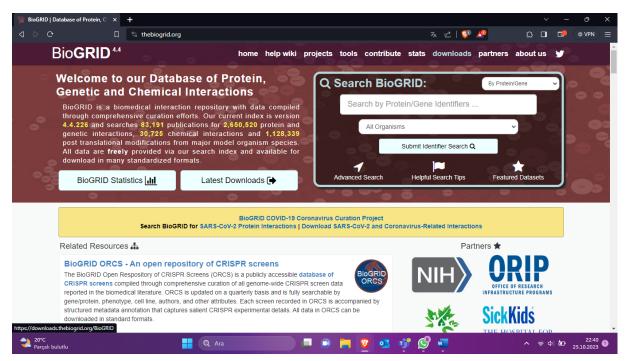


Figure 10. We have selected downloads tab in BioGRID database.

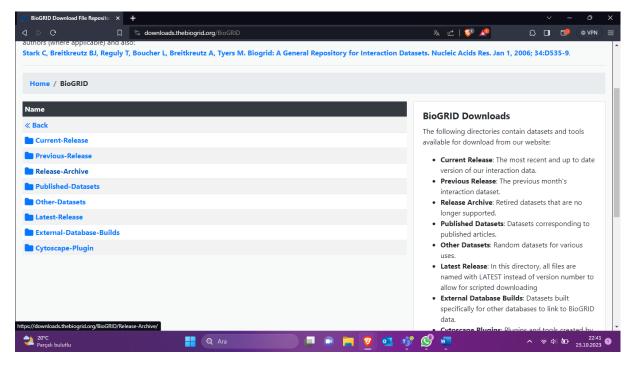


Figure 11. Then we have selected Release-Archive.

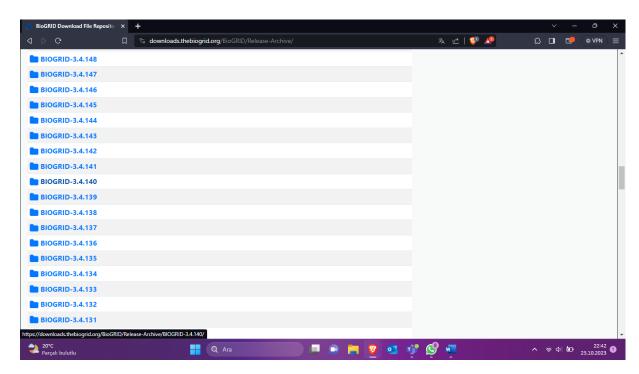


Figure 12. Then, we have opened the BioGRID-3.4.140 folder.

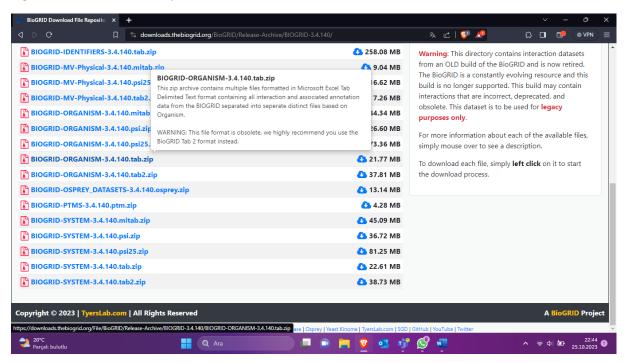


Figure 13. Then new step, we have downloaded BIOGRID-ORGANISM-3.4.140.tab.zip folder.

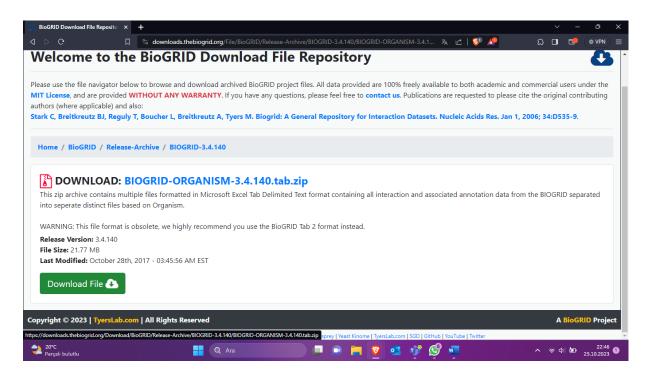


Figure 14. We have selected "Download File" tab, and have downloaded file.

When we opened the file, it contained data sets for various organisms, but the ones we are interested in are *C. elegans* and *R. norvegicus*. Therefore, we selected the files related to these two organisms and organized them in a new folder.

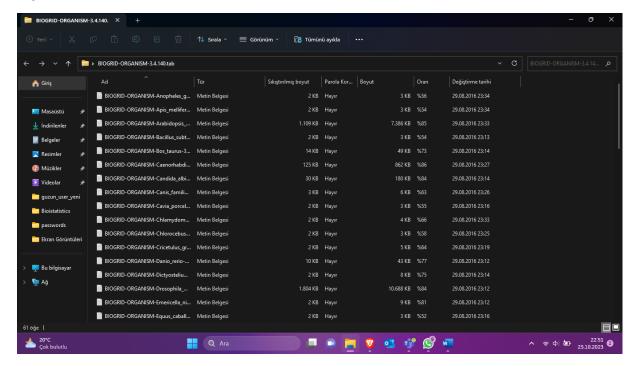


Figure 15. The contents of the file we downloaded.

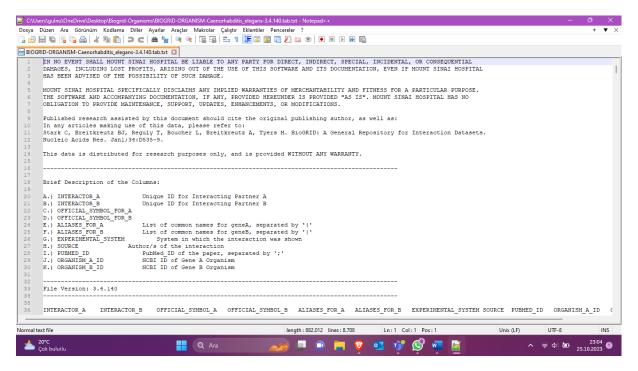


Figure 16. The initial view of the *C. elegans* file in Notepad++.

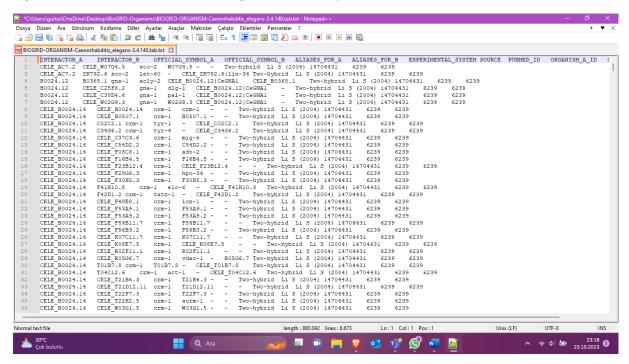


Figure 17. The updated version of the *C. elegans* file after removing the preceding descriptions before INTERACTOR\_A.

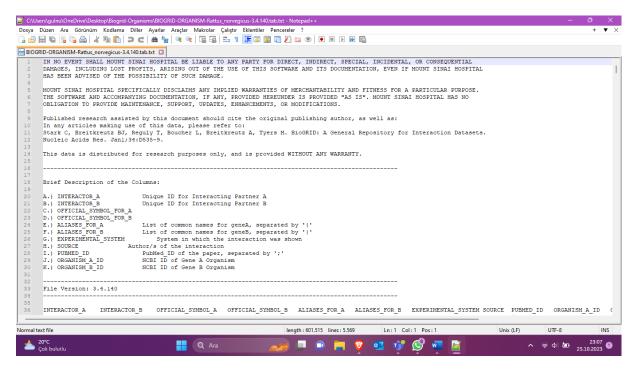


Figure 18. The initial view of the R. norvegius file in Notepad++.

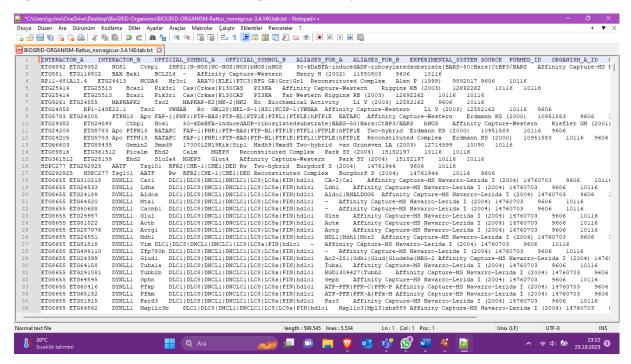


Figure 19. The updated version of the *R. norvegius* file after removing the preceding descriptions before INTERACTOR A.

We formatted the files to the required format. In the next steps, we will first import the file for the *C. elegans* organism and perform network analysis, and then we will import the file for the *R. norvegicus* organism and conduct network analysis.

Firstly we will import *C. elegans* file in Cytoscape.

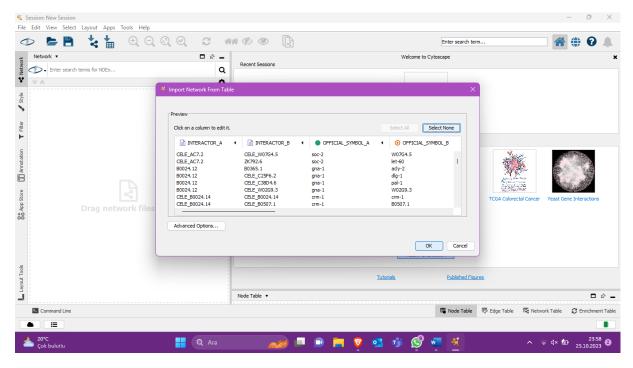


Figure 20. We determine the OFFICIAL\_SYMBOL\_A and OFFICIAL\_SYMBOL\_B columns as protein.

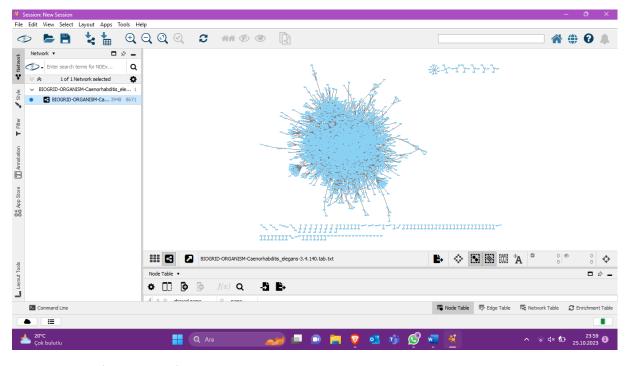


Figure 21. The first image of the *C. elegans* dataset in the Cytoscape.

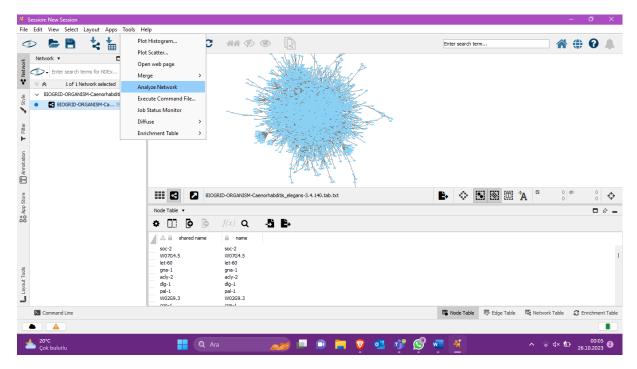


Figure 22. In this step, we following the Tools-Analyze Network pathway for average path length, diameter, and degree distribution graph.

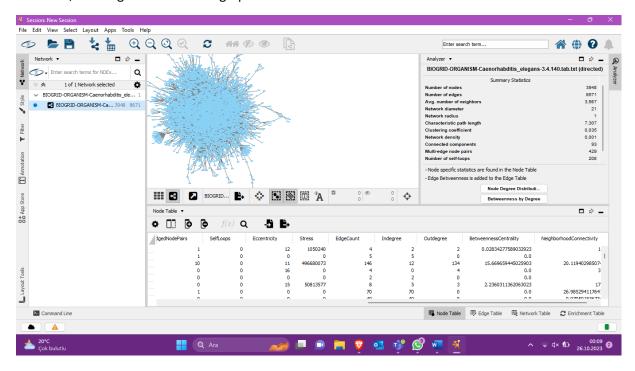


Figure 23. We obtained the analysis results for *C. elegans*.

### Analysis results for *C. elegans* organism

Number of nodes and edges: 3948 nodes and 8671.

Average path length: 7,307 Network

Diameter: 21

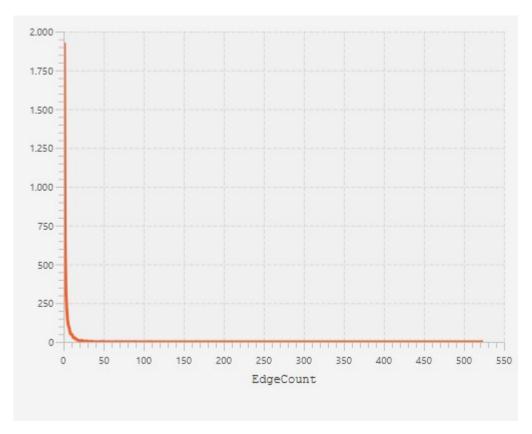


Figure 24. The degree distribution graph for the *C. elegans* dataset's network analysis.

Based on the results and graphs obtained for the *C. elegans* organism, we can say that some nodes have more connections and higher degrees, while others have fewer connections and a lower number of links compared to the rest. In this case, we can conclude that the network exhibits a scale-free smallworld property.

Secondly we will import *R. norvegius* file in Cytoscape.

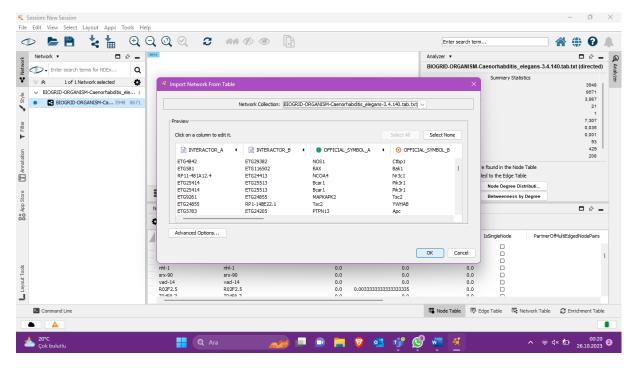


Figure 25. We determine the OFFICIAL\_SYMBOL\_A and OFFICIAL\_SYMBOL\_B columns as protein.

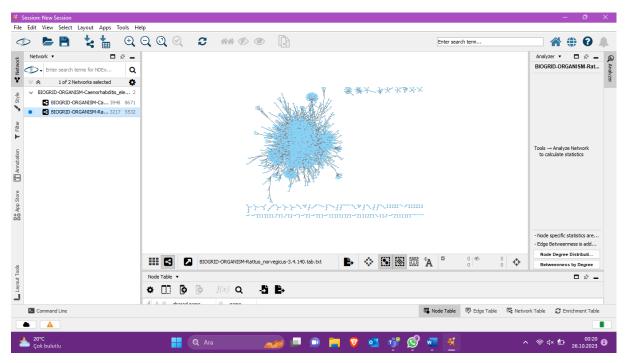


Figure 26. The first image of the *R. norvegius* dataset in the Cytoscape.

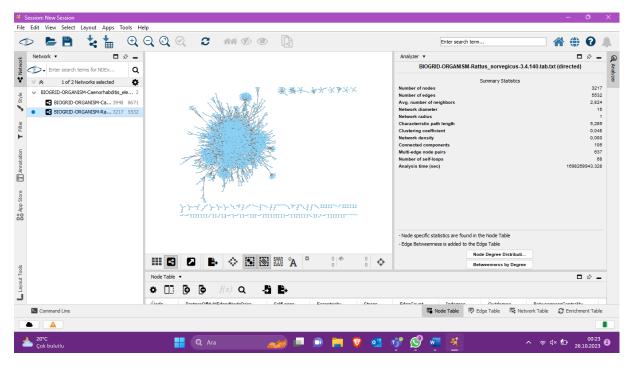


Figure 27. We obtained the analysis results for *R. norvegius*.

### Analysis results for *R. norvegius* organism

Number of nodes and edges: 3217 nodes and 5532 edges.

Average path length: 5,286

Network diameter: 15

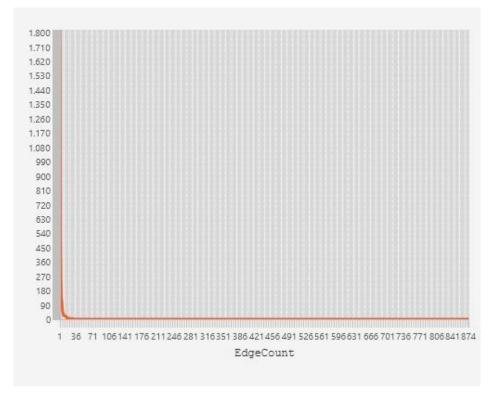


Figure 28. The degree distribution graph for the *R. norvegius* dataset's network analysis.

Based on the obtained results, we inferred that *C. elegans* and *R. norvegicus* exhibit similar characteristics in terms of the scale-free small-world property. So for *R. norvegius* organism, we can say that some nodes have more connections and higher degrees, while others have fewer connections and a lower number of links compared to the rest. In this case, we can conclude that the network exhibits a scale-free smallworld property.

When examining the directed and undirected nature for C. elegans and R. norvegius organisms (Figure 29-30), it can be observed that the network relationships have bidirectional connections. In other words, we can say that both organisms exhibit undirected characteristics.

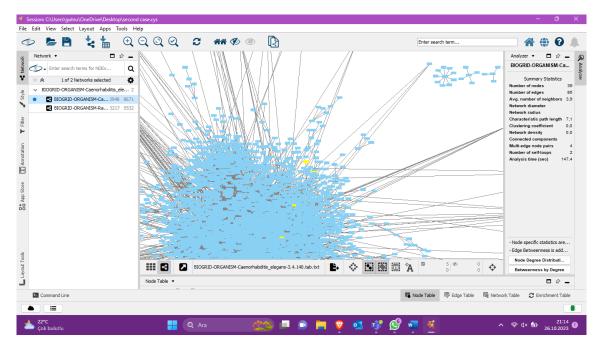


Figure 29. C. elegans organism is undirected feature.

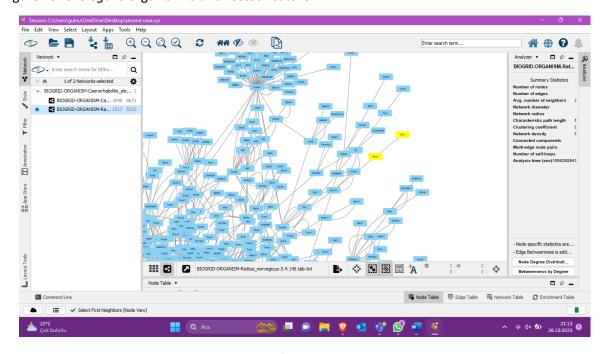


Figure 30. *R. norvegius* organism is undirected feature.