Analysis using Gephi on Biological Networks

Tharun Subramanian C

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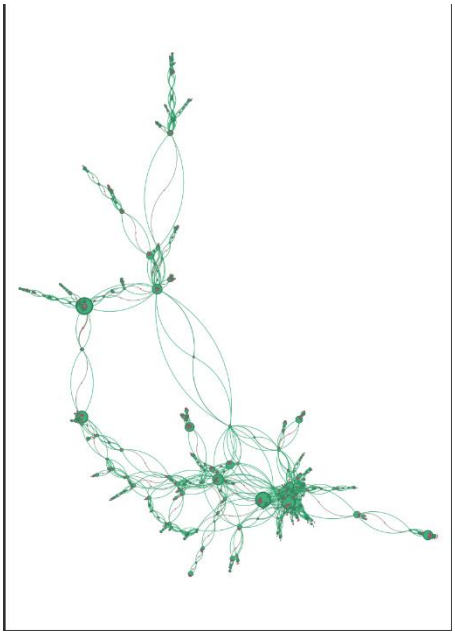
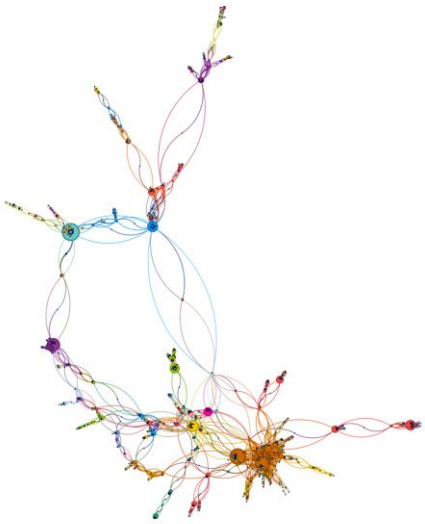
1. Dataset Overview

Description: GEXF. Diseasome: A network of disorders and disease genes linked by known disorder–gene associations, indicating the common genetic origin of many diseases. Genes associated with similar disorders show both higher likelihood of physical interactions between their products and higher expression profiling similarity for their transcripts, supporting the existence of distinct disease-specific functional modules. The original dataset can be found here: The Human Disease Network, Goh K-I, Cusick ME, Valle D, Childs B, Vidal M, Barabási A-L (2007), Proc Natl Acad Sci USA 104:8685-8690

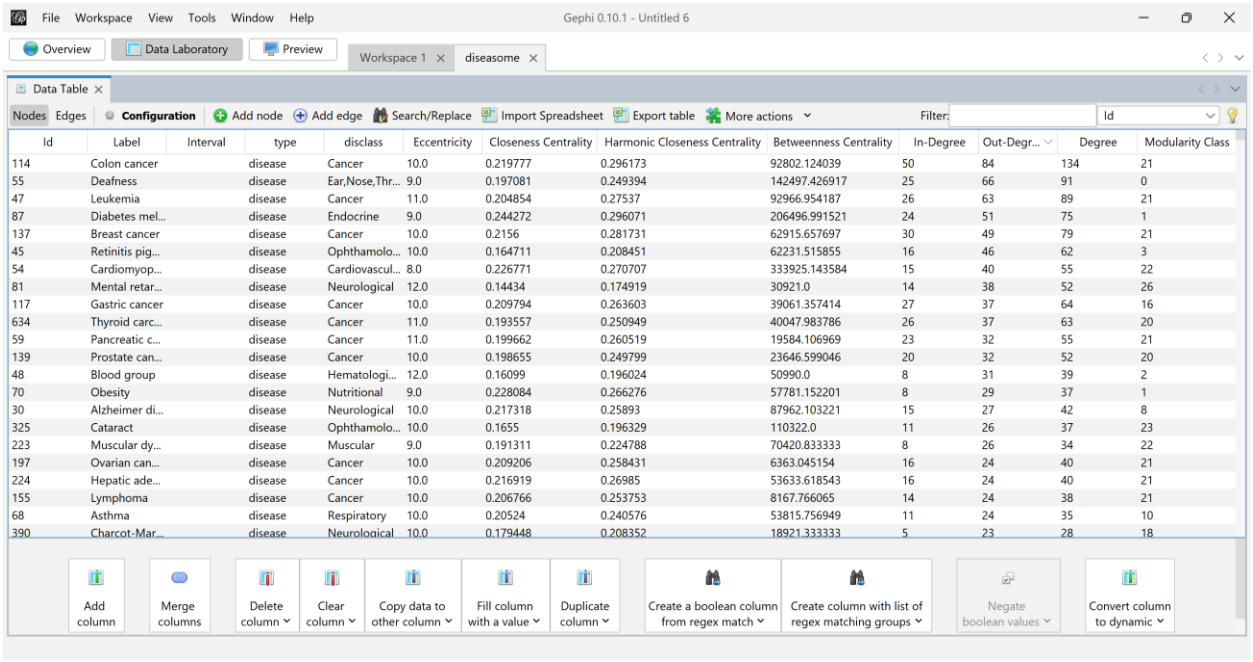




Format: The data was provided in `.gexf` format, a widely recognized format for exchanging graph structures, making it suitable for detailed analysis in tools like Gephi.

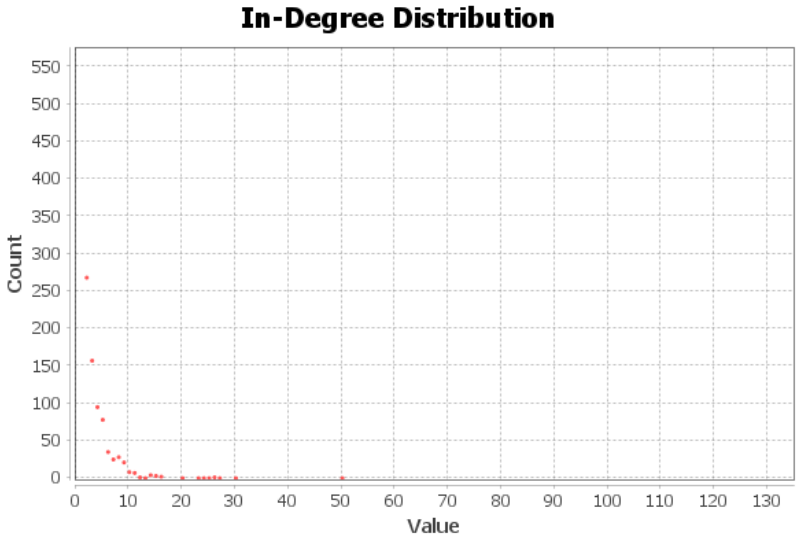
2. Degree Analysis

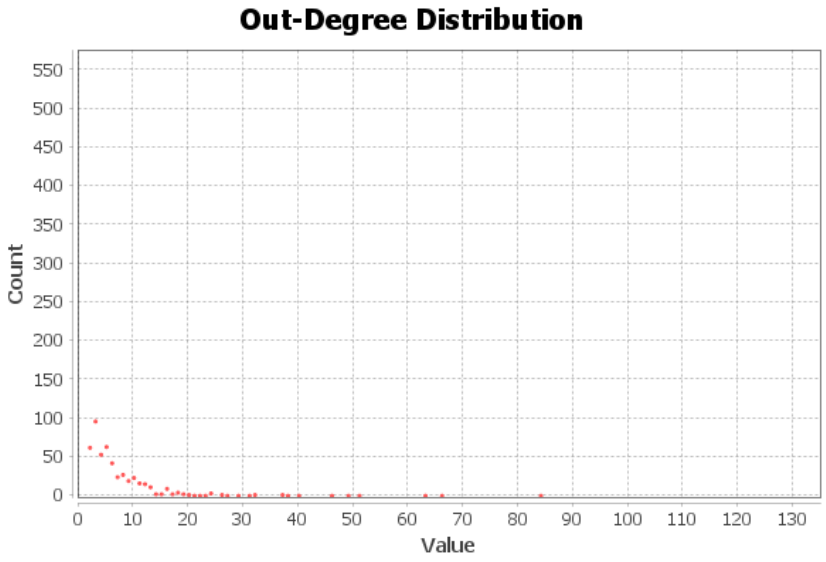
Degree Distribution: The degree of a node, representing the number of connections (edges) it has within the network, was calculated. The analysis showed that the degree varies across the network, with certain nodes displaying a high degree, indicating their significant connectivity and potential importance in the network structure.

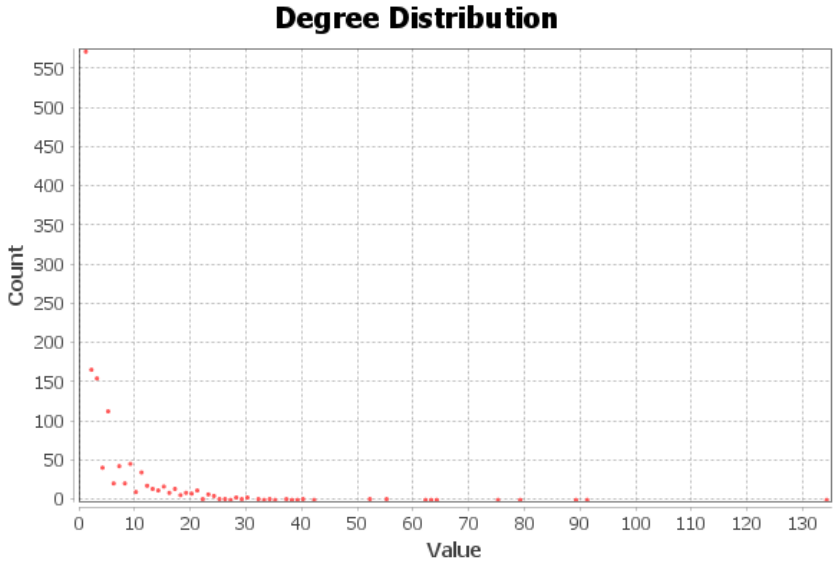


Id	Label	Interval	type	disclass	Eccentricity	Closeness Centrality	Harmonic Closeness Centrality	Betweenness Centrality	In-Degree	Out-Degr...	Degree	Modularity Class
114	Colon cancer		disease	Cancer	10.0	0.219777	0.296173	92802.124039	50	84	134	21
55	Deafness		disease	Ear,Nose,Thr...	9.0	0.197081	0.249394	142497.426917	25	66	91	0
47	Leukemia		disease	Cancer	11.0	0.204854	0.27537	92966.954187	26	63	89	21
87	Diabetes mel...		disease	Endocrine	9.0	0.244272	0.296071	206496.991521	24	51	75	1
137	Breast cancer		disease	Cancer	10.0	0.2156	0.281731	62915.657697	30	49	79	21
45	Retinitis pig...		disease	Ophthamolo...	10.0	0.164711	0.208451	62231.515855	16	46	62	3
54	Cardiomyop...		disease	Cardiovascul...	8.0	0.226771	0.270707	333925.143584	15	40	55	22
81	Mental retar...		disease	Neurological	12.0	0.14434	0.174919	30921.0	14	38	52	26
117	Gastric cancer		disease	Cancer	10.0	0.209794	0.263603	39061.357414	27	37	64	16
634	Thyroid carc...		disease	Cancer	11.0	0.193557	0.250949	40047.983786	26	37	63	20
59	Pancreatic c...		disease	Cancer	11.0	0.199662	0.260519	19584.106969	23	32	55	21
139	Prostate can...		disease	Cancer	10.0	0.198655	0.249799	23646.599046	20	32	52	20
48	Blood group		disease	Hematologi...	12.0	0.16099	0.196024	50990.0	8	31	39	2
70	Obesity		disease	Nutritional	9.0	0.228084	0.266276	57781.152201	8	29	37	1
30	Alzheimer di...		disease	Neurological	10.0	0.217318	0.25893	87962.103221	15	27	42	8
325	Cataract		disease	Ophthamolo...	10.0	0.1655	0.196329	110322.0	11	26	37	23
223	Muscular dy...		disease	Muscular	9.0	0.191311	0.224788	70420.833333	8	26	34	22
197	Ovarian can...		disease	Cancer	10.0	0.209206	0.258431	6363.045154	16	24	40	21
224	Hepatic ade...		disease	Cancer	10.0	0.216919	0.26985	53633.618543	16	24	40	21
155	Lymphoma		disease	Cancer	10.0	0.206766	0.253753	8167.766065	14	24	38	21
68	Asthma		disease	Respiratory	10.0	0.20524	0.240576	53815.756949	11	24	35	10
390	Charcot-Mar...		disease	Neurological	10.0	0.179448	0.208352	18921.333333	5	23	28	18

From the analysis and the provided screen-shot we can see conclude that ***Colon cancer*** has the highest In-Degree(50) and Out-Degree(84) with a degree of 134.

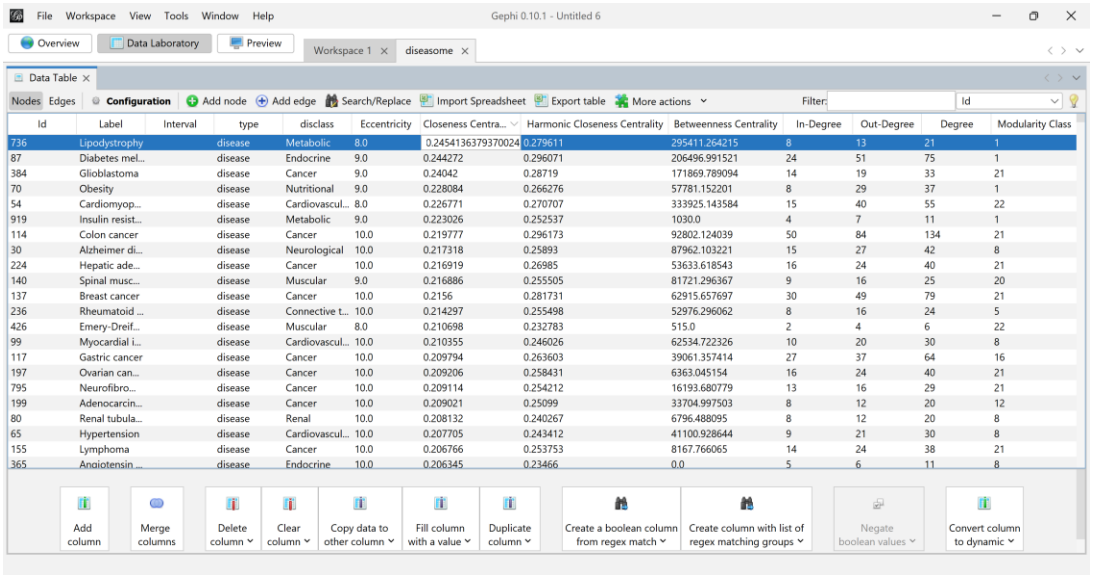




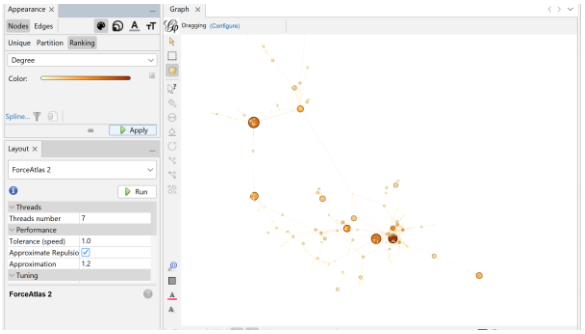


3. Node Centrality

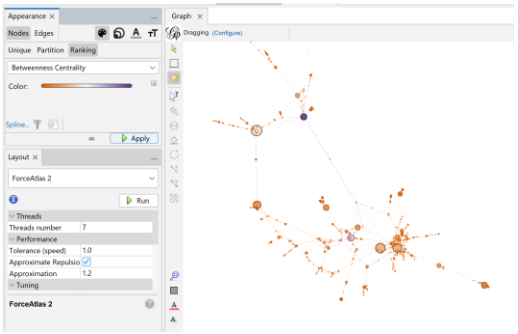
Centrality Measures: Several centrality measures were computed to identify the most influential nodes within the network:



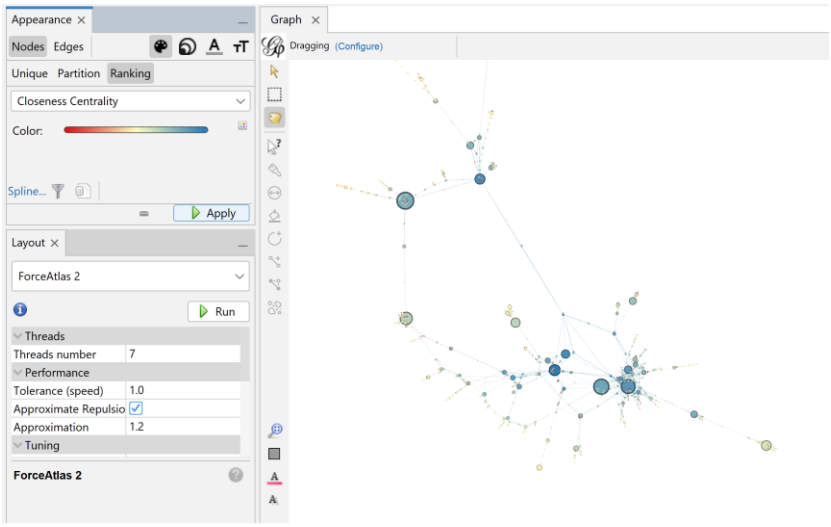
Degree Centrality: Nodes with the highest degree centrality were identified as critical hubs, having numerous connections within the network.



Betweenness Centrality: Key nodes with high betweenness centrality were found to act as bridges, frequently appearing on the shortest paths between other nodes.

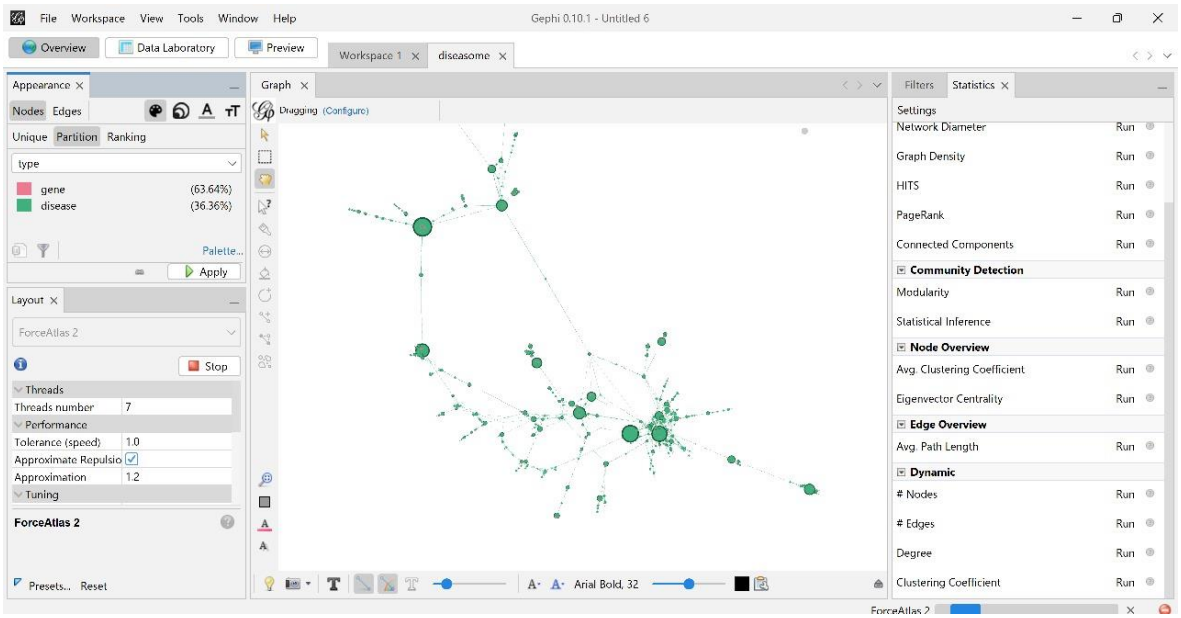


Closeness Centrality: Nodes with high closeness centrality were highlighted for their efficiency in interacting with all other nodes in the network.



4. Visualization and Analytical Steps

Dataset Loading: The `.gexf` file was successfully imported into Gephi for visualization and analysis.



Network Overview: The initial visualization provided a clear understanding of the overall structure, revealing key features of the biological network.

Degree Distribution Analysis: The degree distribution was analyzed to assess the spread of connectivity across the network. The results indicated a mix of highly connected hubs and sparsely connected nodes, suggesting a non-random network structure.

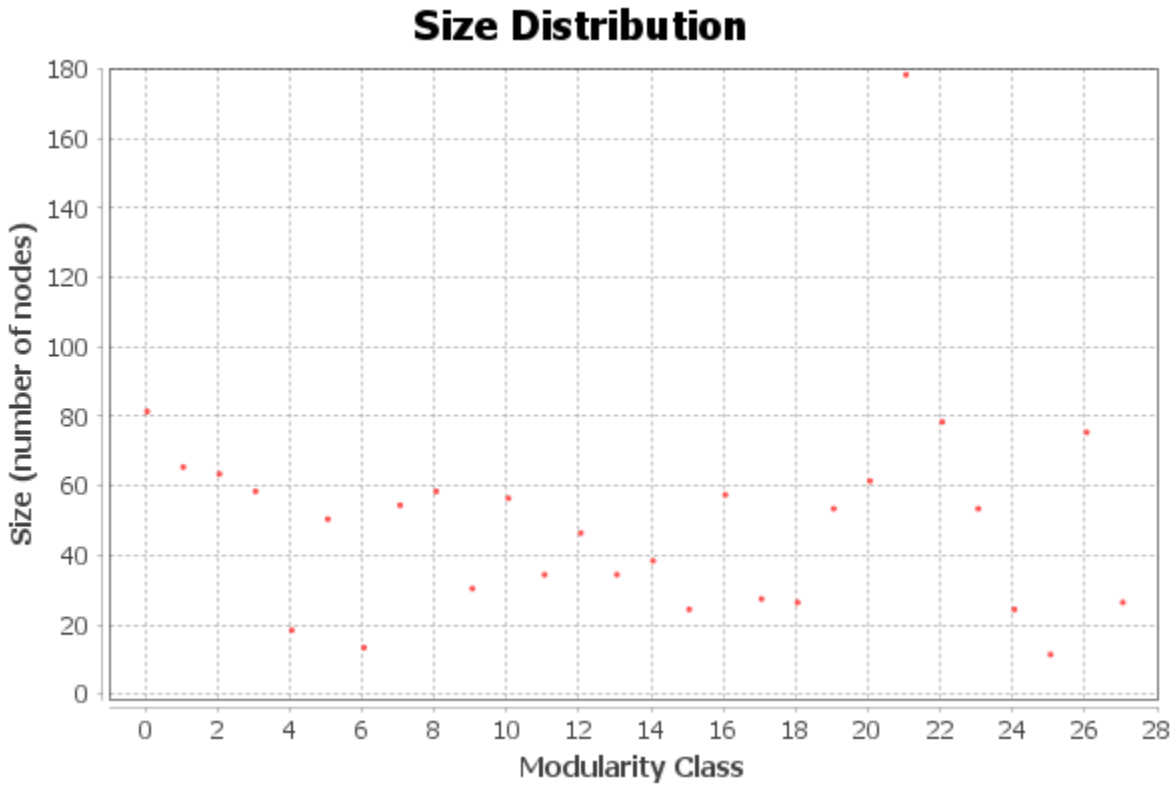
Centrality Visualization: Centrality measures were visualized, allowing for the identification of nodes that play crucial roles in the network's structure and function.

Modularity Analysis: Community detection using the modularity algorithm uncovered well-defined sub-communities within the network, highlighting areas of strong intra-community connections.

Visualization Refinement: The network visualization was refined by adjusting node sizes, colors, and layout, effectively emphasizing nodes with high degrees and centrality.

5. Insights from Data Laboratory

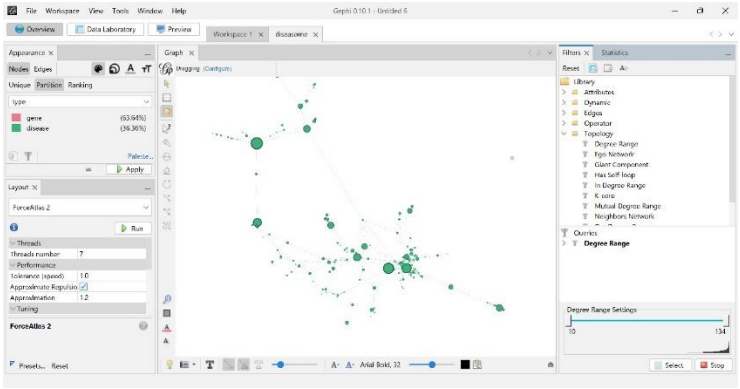
Highest Modularity: The community with the highest modularity score was identified, indicating the strongest and most distinct community structure within the network.



Largest Components: Nodes belonging to the largest connected components were analyzed, revealing their essential role in maintaining the network's overall connectivity and robustness.

6. Inference from Visualization

Degree Distribution: The analysis of node degrees confirmed that the network likely follows a scale-free model, characterized by a few highly connected hubs and many nodes with fewer connections.



Central Nodes: Nodes identified with high centrality measures were recognized as critical to the network's connectivity and influence, potentially representing key biological entities.

Modularity: The high modularity observed suggests that the network is organized into well-defined communities, which may correspond to functional clusters in the biological context.

Component Analysis: The analysis of the largest components underscored their importance in preserving the network's integrity, emphasizing their potential biological significance.