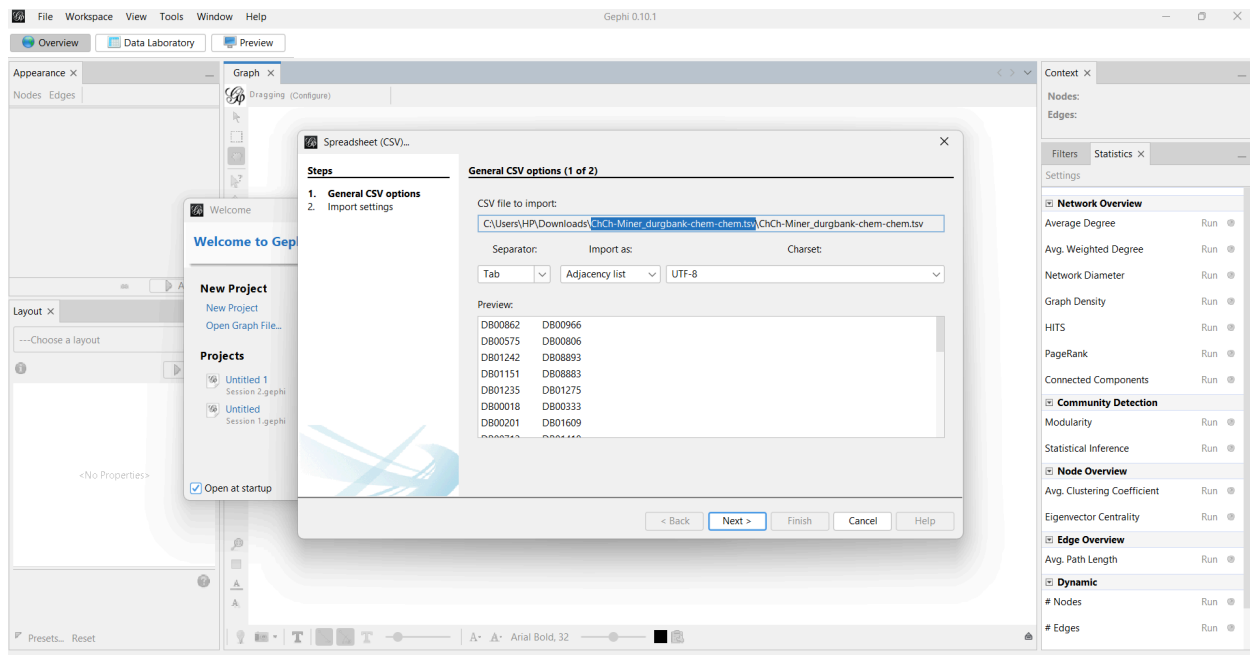


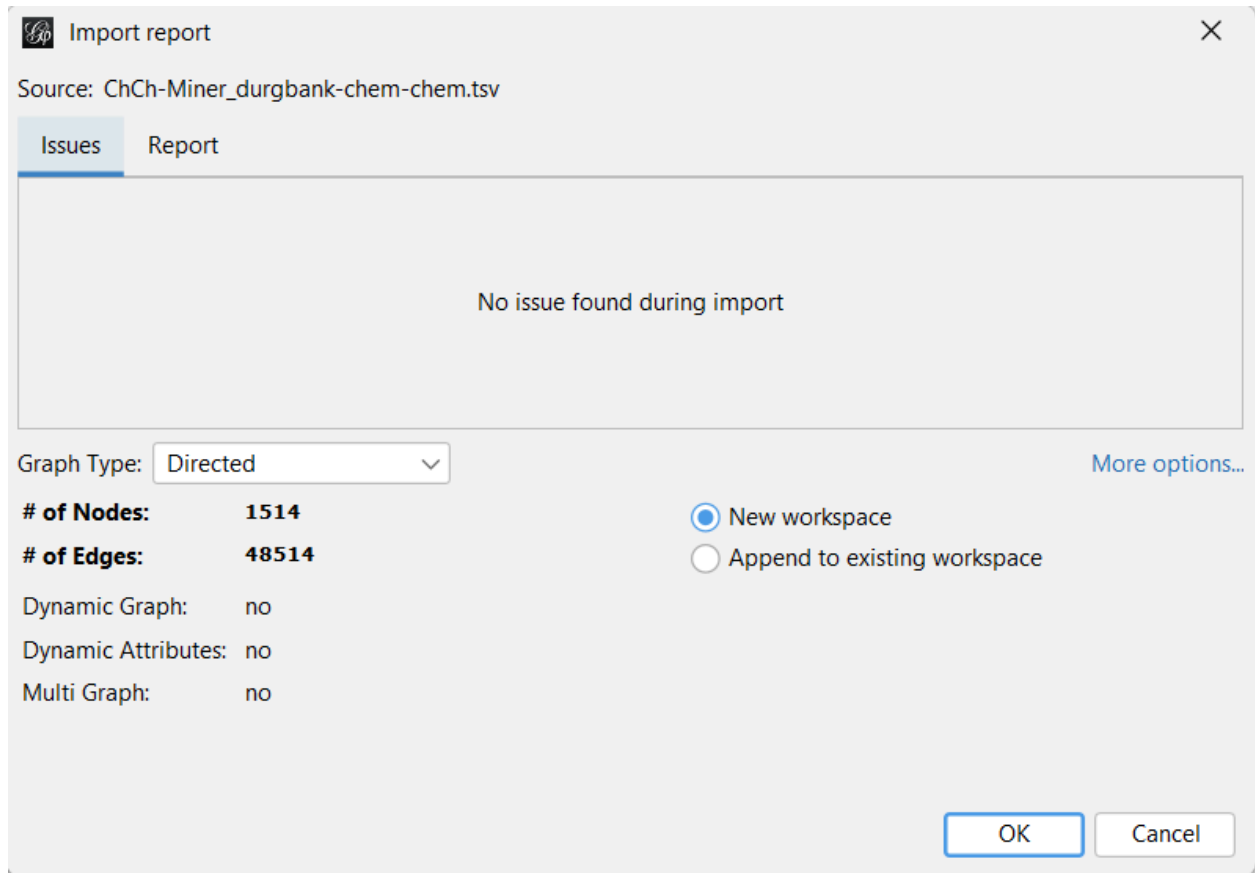
# Approved Drugs By FDA Analysis in Gephi

This is a network illustrating interactions between drugs approved by the U.S. Food and Drug Administration (FDA). Each node in the network represents a drug, and each edge indicates an interaction between drugs. Drug-drug interactions occur when the pharmacological effects of one drug are modified by another, potentially leading to unpredictable clinical outcomes like adverse reactions. The risk of such adverse reactions increases when multiple drugs are administered simultaneously, as one drug may enhance or diminish the effects of another. Therefore, it is vital to identify these interactions, particularly during the development of new drugs, to ensure they are safe to use alongside existing medications.

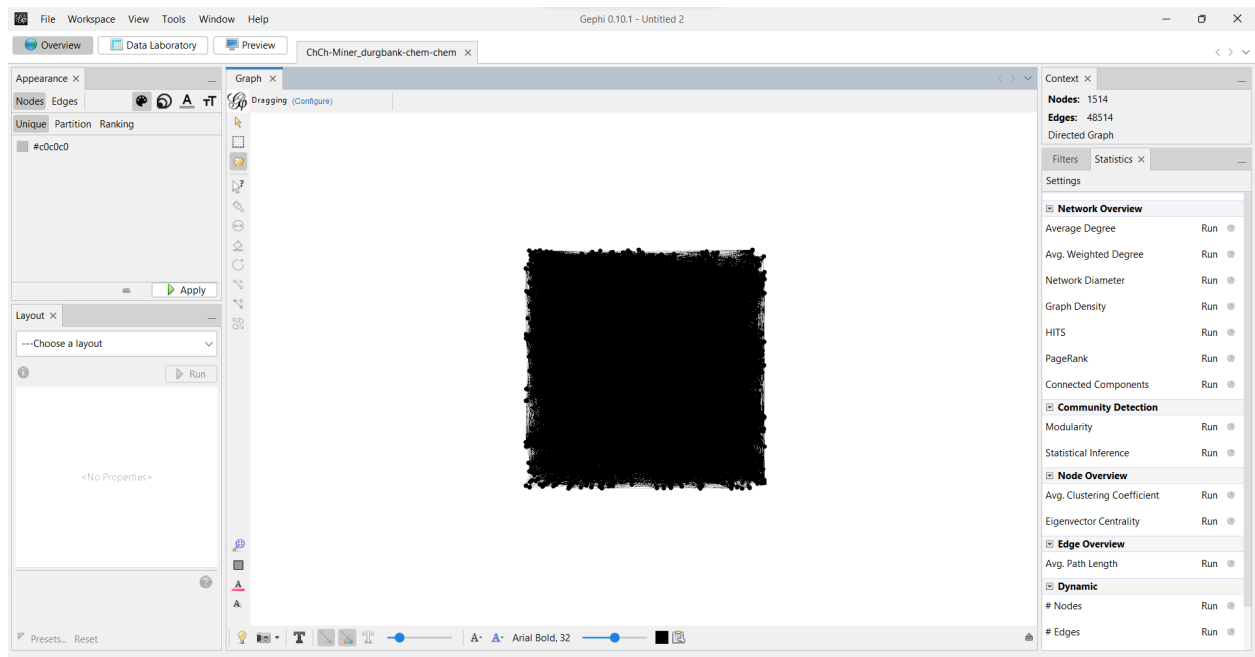
## Step 1: Importing the Dataset



After downloading the dataset, we will import it in Gephi.

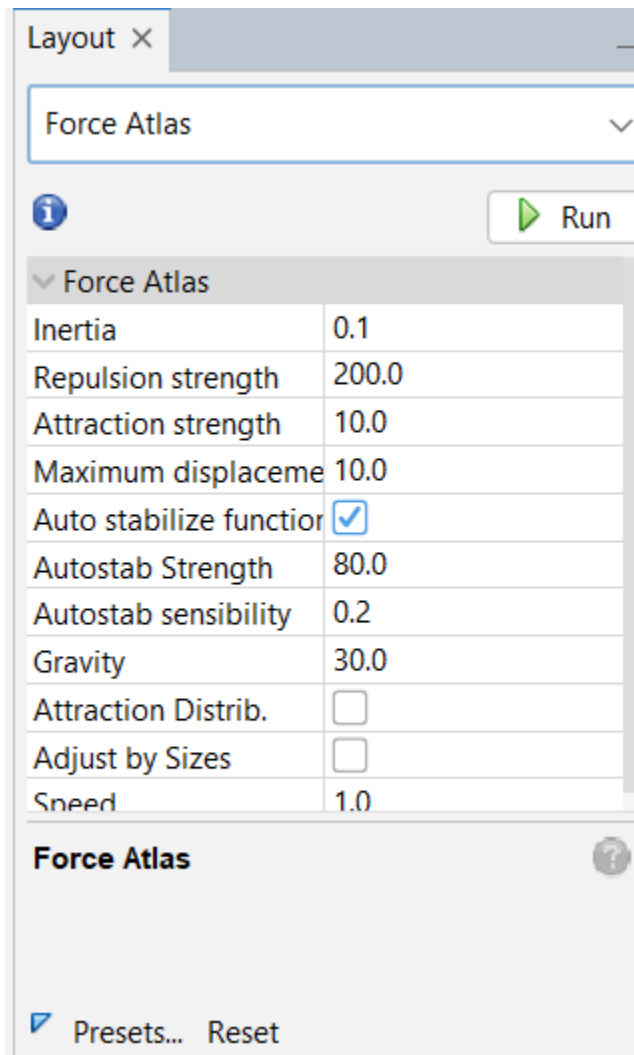


As we can see, in the network dataset there are 1514 nodes and 48514 edges. Hence, we will also select the directed graph option.

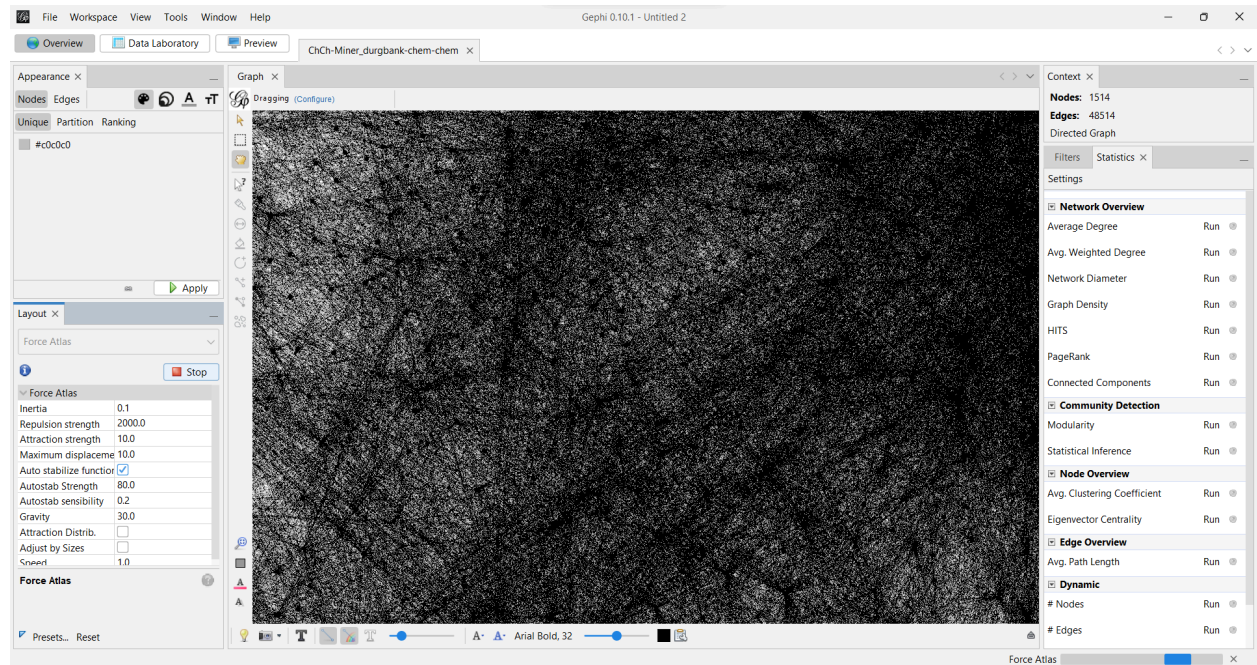


## Step 2: Modifying Force Atlas

We will see a graph full of nodes and edges after importing the file. However, we can still further modify it by changing the Force Atlas value.

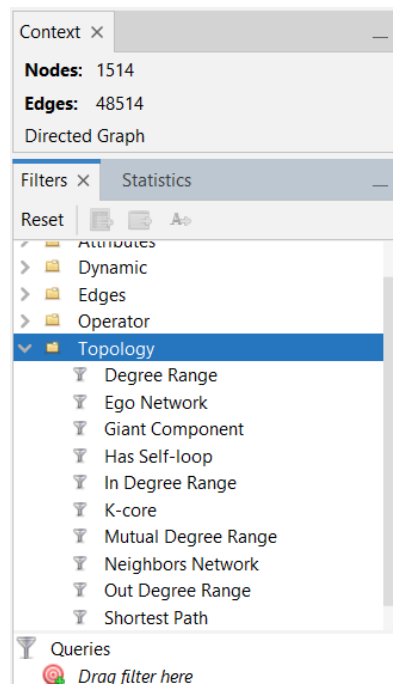


We will change the 'Repulsion strength' value from 200.0 to 2000.



We can further see the nodes and the edges after changing the repulsion strength value. To make it more presentable we could also go on and change the color of the edges and nodes.

### Step 3: Degree Range



We can go to filters and drag Degree Range under Queries in order to create a graph for Modularity Report.

## Modularity Report

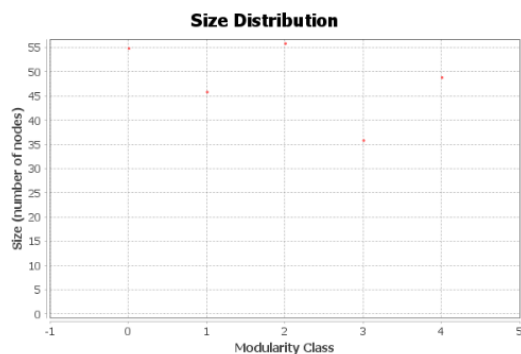
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### Parameters:

Randomize: On  
Use edge weights: On  
Resolution: 1.0

### Results:

Modularity: 0.366  
Modularity with resolution: 0.366  
Number of Communities: 5



### Algorithm:

Vincent D Blondel, Jean-Loup Guillaume, Renaud Lambiotte, Etienne Lefebvre, *Fast unfolding of communities in large networks*, in Journal of Statistical Mechanics: Theory and Experiment 2008 (10), P1000

### Resolution:

R. Lambiotte, J.-C. Delvenne, M. Barahona *Laplacian Dynamics and Multiscale Modular Structure in Networks* 2009

We will get a modularity report as shown above after following steps.

## Parameters:

- **Randomize:** On. This indicates that the network analysis included some randomization in the algorithm, which helps in avoiding local minima in community detection.
- **Use edge weights:** On. This suggests that the strength or weight of connections between nodes was considered in the modularity calculation.
- **Resolution:** 1.0. This parameter influences the granularity of community detection, with higher values leading to more but smaller communities.

## Results:

- **Modularity:** 0.366. This is a measure of the strength of division of a network into communities. A modularity value ranges from -1 to 1, where values closer to 1 indicate stronger community structure. A value of 0.366 suggests a moderate level of community structure in the network.
- **Modularity with resolution:** 0.366. This indicates the same modularity score when the resolution parameter is taken into account.
- **Number of Communities:** 5. The network was divided into five distinct communities based on the algorithm used.

## Size Distribution Chart:

- The chart shows the size distribution of nodes across the five modularity classes (communities). Each class appears to have a similar size, indicating a relatively balanced distribution of nodes across the communities.

The report indicates that the network has been analyzed using the Louvain method with consideration of edge weights and randomization. The network was partitioned into five communities with a moderate modularity score, suggesting a discernible but not overly strong community structure. The resolution setting played a role in determining the granularity of these communities.