**PPI network dataset**

1. Loading and understanding the dataset (attached notebook)
2. Visualization tasks
3. Calculate and Compare Different Centrality Measures:

* Task: Compute various centrality measures for all nodes in the network and compare their distributions and rankings.
* Steps:
  + Use the networkx library to calculate measures like:
    - Degree Centrality: Measures the number of direct connections a node has.
    - Betweenness Centrality: Measures how often a node lies on the shortest path between other nodes.
    - Closeness Centrality: Measures how quickly a node can spread information through the network.
    - Eigenvector Centrality: Measures the influence of a node based on the centrality of its neighbors.
  + Store these centrality values in a pandas DataFrame or dictionary, associated with the protein IDs.
  + Visualize the distribution of each centrality measure (e.g., using histograms).
  + Identify the top-k most central nodes based on each measure and compare these lists. Discuss why different measures might identify different nodes as most central.

1. Community detection:

* Task: Apply various community detection algorithms to the network and compare the resulting partitions.
* Steps:
  + Use libraries like networkx such as:
    - Louvain method: An iterative algorithm that optimizes modularity.
    - Girvan-Newman algorithm: A divisive algorithm based on edge betweenness.
  + Run several of these algorithms on your network.
  + Obtain the community assignments for each node.
* Task: Analyze the Properties of Identified Communities: such as their size, density, and internal structure.
* Steps:
  + Calculate the number of nodes and edges in each community.
  + Compute the density of each community (ratio of existing edges to possible edges).
  + Visualize individual communities or the network with nodes colored by their community membership
  + Analyze the distribution of community sizes.

* Task: Use metrics to assess the quality of the community structures found by different algorithms.
* Steps:
  + Calculate modularity: A widely used metric that measures how well a network is partitioned into communities. Higher modularity generally indicates a better partition.
* Task: Analyze the Role of Different Edge Types in Community Structure. Investigate how positive and negative edges contribute to the formation and structure of communities.
* Steps:
  + Consider applying community detection specifically to the subgraph of positive edges and the subgraph of negative edges.
  + Compare the community structures found in the positive and negative networks. Are the communities similar or different?
  + Analyze whether positive or negative edges play a more dominant role in holding communities together or in connecting different communities. Some algorithms might be designed to handle signed graphs, which could be explored.

1. Link Prediction:

Predicting Missing Positive Interactions:

* Task: Given the current network, predict which pairs of proteins are most likely to have a positive interaction that is currently missing from the observed data.
* Steps:
  + Consider the positive edges in your dataset as observed positive links.
  + Identify potential missing positive links between proteins that are not currently connected or are connected by negative edges.
  + Use link prediction methods based on network structure (e.g., common neighbors, Jaccard coefficient, Adamic-Adar index, preferential attachment [1]).
  + Evaluate the performance of your prediction model using appropriate metrics (e.g., Area Under the ROC Curve (AUC), Average Precision (AP)).
* Task: Similarly predict missing negative interactions.

1. Graphlets:

* Task: Identify graphlets.
  + Focus on smaller graphlets initially, such as 2-node graphlets (an edge), 3-node graphlets (a path and a triangle), and potentially some 4-node graphlets.
* Task: Compute Graphlet Frequency and Distribution. Count the occurrences of different graphlets in your network to understand its local structure.
  + Count the number of times each defined graphlet appears in your network.
  + Calculate the frequency of each graphlet type.
  + Visualize the distribution of graphlet counts.
* Task: Use Graphlet Features for Downstream Tasks:
  + Once you have the graphlet orbit count vectors for each node, use these vectors as features in a machine learning model.
  + For example, train a classifier to predict protein properties (as in node classification) using the graphlet features instead of or in addition to sequence-based features.
  + Apply clustering algorithms to the nodes using their graphlet feature vectors to see if similar graphlet patterns correspond to functional or structural groupings.

1. GNNs: Predict a property of each protein node in the network. For example, you could try to predict if a protein is involved in positive or negative interactions based on its sequence and the interactions it has.

* Steps:
  + Define a target variable for each node (protein). This could be derived from the 'edge\_type' of its interactions or external data if available.
  + Prepare node features. The protein sequences could be used to generate embeddings (e.g., using techniques like word2vec or bioBERT).
  + Split the nodes into training, validation, and test sets.
  + Build a simple GNN model (e.g., a Graph Convolutional Network - GCN) that takes node features and the graph structure as input.
  + Train the GNN model to predict the target variable for each node.
  + Evaluate the model's performance using metrics appropriate for classification.