Project Title: Protein Protein Interaction Prediction Using Graph Neural Networks
Faculty Information: Harun Pirim, Industrial and Manufacturing Engineering
e-mail: harun.pirim@ndsu.edu

Abstract

Protein-protein interaction (PPI) networks are essential to many biological processes and molecular functions within the cell. However, PPI networks derived from experimental techniques can be noisy and incomplete. Graph neural networks (GNNs) provide a promising approach to learn useful patterns and insights from PPI networks. GNNs can be used for a variety of tasks on PPI networks, including:

- Node-level prediction: imputing missing protein features,
- Edge-level prediction: predicting interaction strengths or confidence scores for noisy experimental PPI networks,
- Graph-level prediction: learning representations for drug response prediction or classifying disease networks.

By incorporating domain knowledge like node features, edge types, and graph topology, GNNs have the potential to make high-performance and interpretable predictions. Graph machine learning on PPI data can provide novel biological insights and drive discovery by improving our understanding of these foundational networks.

This research will contribute biomedical research skills and knowledge generation by:

- Retrieving PPI data from databases such as The Molecular INTeraction, IntAct Molecular Interaction, matrixDB, bioGRID and STRING databases.
- Performing centrality and cluster analysis of the PPI networks.
- Using Cytoscape BiNGO, ClueGO, and EnrichmentMap to determine functional annotations of protein clusters.
- Applying GNNs to predict protein-protein interactions and report accuracy scores.