**Disease Prediction from Protein-Protein Interactions Using Graph Neural Networks**

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Protein-protein interaction (PPI) networks play a fundamental role in understanding biological processes, yet experimental techniques often generate noisy and incomplete data. PPIs associated with various diseases can be merged for use in disease prediction. Graph neural networks (GNNs) offer a promising avenue for extracting meaningful insights from PPI networks by leveraging relevant knowledge and network topology. In this project, we aim to harness GNNs for node-level prediction tasks, aiming to improve the accuracy and interpretability of predictions on PPI networks. By integrating data from prominent databases such as STRING, UniProt, and DisGeNet, we retrieve comprehensive information to be integrated into the PPI data. Utilizing Cytoscape, we determine functional annotations of protein clusters, revealing their biological significance. Subsequently, we apply GNNs to predict childbirth disorders from protein-protein interactions, evaluating model performance through accuracy scores. This interdisciplinary approach combines biomedical research with machine learning techniques, offering new insights into biological systems. Our findings not only advance our understanding of PPI networks but also have practical implications in disease classification. Ultimately, this research contributes to the growing body of knowledge in biomedical research and paves the way for innovative applications in precision medicine.