With the advent of big data, researchers have been inundated with information. In an effort to find a way to analyze this data the analysis of complex networks has become a popular and ever-growing field. Complex networks are networks that contain non-trivial topological features. These features, which are not found in random graphs or lattices, allow for better modeling of numerous real-world systems including the Internet, scientist citation networks, and the focus of this presentation, protein-protein interaction (PPI) networks. Since structure implies function, knowledge of a PPI network's underlying structure may reveal functions and interactions that have previously gone unnoticed. Due to advances in biological technology, the accumulation of data involving PPIs has never been easier. Unfortunately these new technologies report numerous false-positives, i.e. identification of interactions that do not actually occur in vivo, which make it difficult to truly assess protein function. Thus the statistical analysis and classification of the network is necessary.

Determining the structure of a PPI network is done by comparing the empirical network to a variety of model graphs. We begin by examining properties of the model graphs to determine how accurately they mimic the features and structure of the real-world network under examination. Then four methods previously used to classify PPI networks are evaluated on their ability to accurately classify the model networks. Two of these methods rely on local structure for classification, relative graphlet frequency and graphlet degree distribution, while the other two, degree distribution distance and characteristic curve, rely on global properties.

In the final section, we propose a novel method for classifying networks referred to as Cross Scoring. This method works by comparing networks based on pre-selected network measures and ranking each type of model network by how close its value falls to the empirical value. Points are awarded to each model type and the model type with the fewest points at the end of the comparisons is considered the best fit.