Abstract: In the aspect of molecular medicine, the living system is regarded as a complex molecular network. All biochemical processes are connected as a whole network by molecular interactions. High throughput technologies enable us to screen all protein-protein interactions (PPI) of a cell in one test. The emerging challenge is to understand the function of the network components, answer the question about network evolution and how the network responds to diseases such as cancers. To come up with these problem, network alignment provides a promising framework to test hypotheses, identify functional orthologs and predict protein functions by using diverse high-throughput data.

This talk will be organized in two parts. In the first part, I will introduce a global network alignment algorithm IsoRank [1] and its improved version IsoRank-N [2] which integrate sequence information and network topology into one similarity measure. Incorporating network topology data in ortholog prediction results in improvements over existing sequence-only approaches and over predictions from local alignments of the yeast and fly networks. In the second part, I will briefly summarize the results and the contributions of my thesis.