Predicting Drug-Drug Interactions Using Meta-path Based Similarities

In study, drug-drug interactions with similarity matrix based network will be predicted. To achieve that embedding method via graph convolutional networks or concatenation methods can be used. On the other hand, to handle topological information obtained from similarity networks, path-based methods are introduced. In project, paths that can give powerful impression that specified two drugs are interacted can be used.

In study, different networks protein-protein-interaction, protein-drug-interaction disease and side effects were included to create heterogenous network. Then, paths between two drugs are found and feature vector was constructed by concatenation or embedding. Finally, interactions (binary: {True, False}) are predicted via these vectors.