

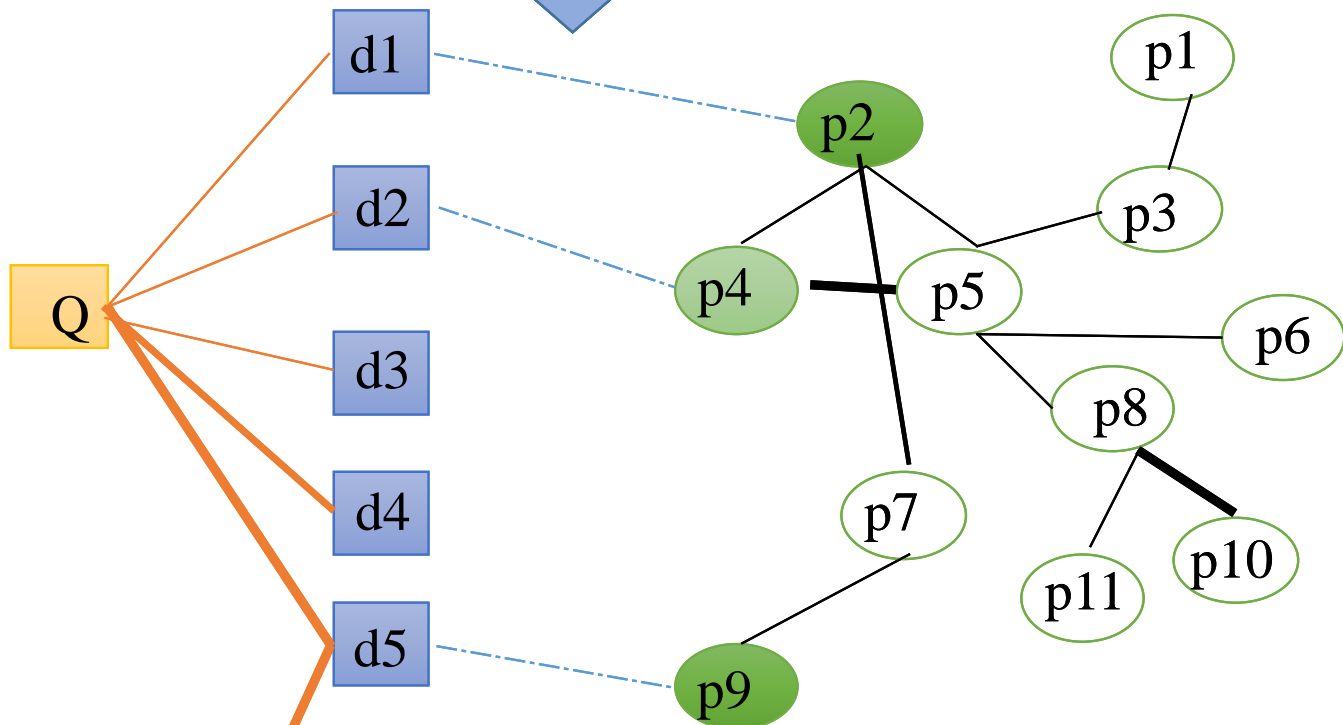


599 disease-protein interactions
1369 diseases
1043 proteins

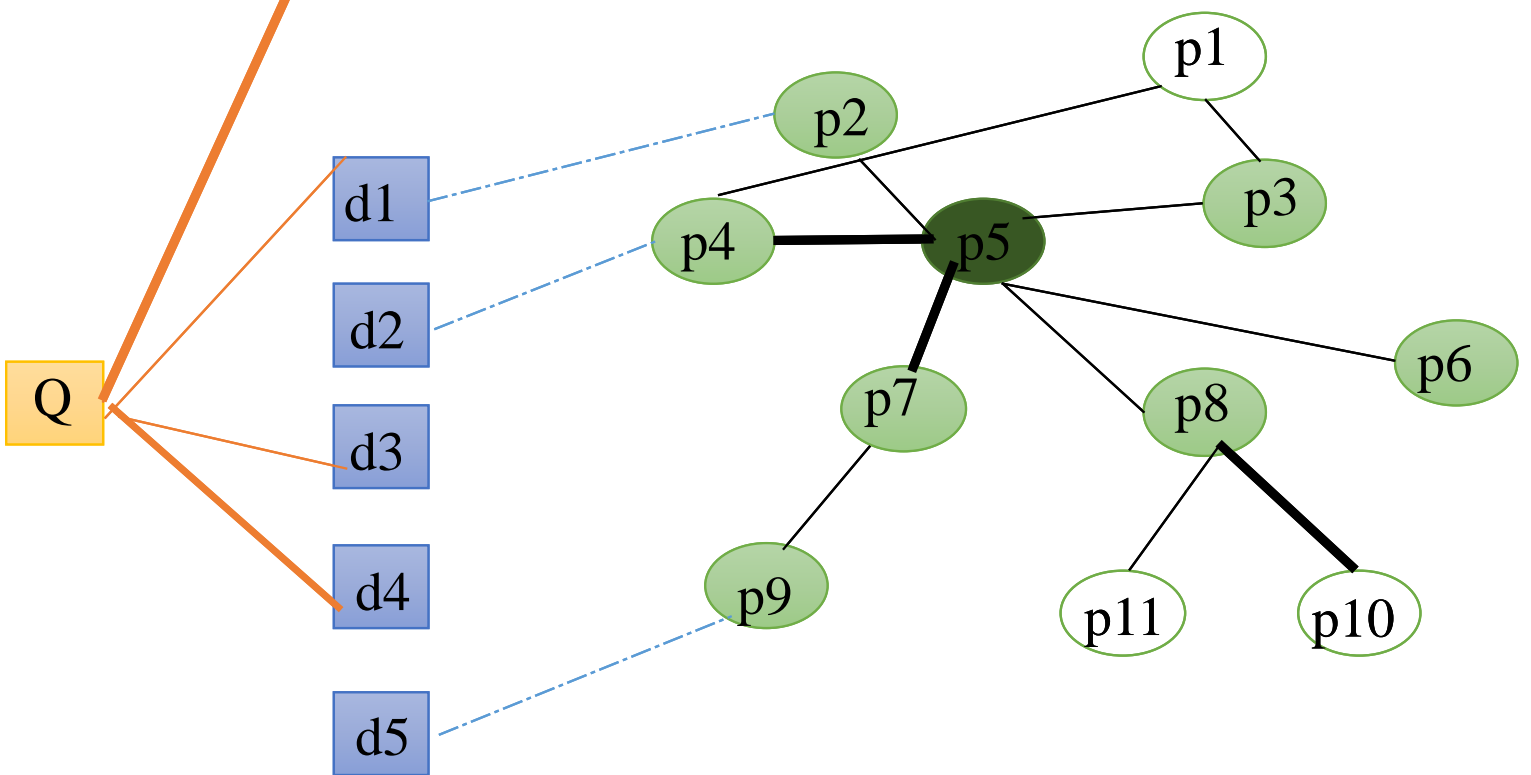
41072 protein-protein interactions
9998 proteins

A heterogenous disease-protein network based on protein-protein interaction (PPI) information with a disease similarity metric

A



B



Computing the prioritization function based on formulating constraints
Incorporating disease similarity information based on confidence scores with a logistic function

The prediction of disease-causing genes

Model validation

The leave-one-out cross validation (LOOCV)
Area under the curve (AUC) of receiver operation characteristic (ROC)
2-fold, 5-fold, 10-fold cross validation