Graduate School of Science and Technology Master's Thesis Abstract

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Thesis title	Drug repurposing for inflammatory bowel disease (IBD) based on similarity of disease related genes and bipartite relations between drugs and IBD related genes		

Abstract

Drug repurposing, which treats new and other diseases utilizing existing drugs, has turned into a much-valuable strategy. This strategy offers various advantages over developing an entirely new drug for a given indication. The present study focused on finding inflammatory bowel disease (IBD) associated drugs based on disease-disease relation and bi-clustering the drug-gene interactions aided by known IBD risk genes. First a comprehensive bipartite network is constructed involving the drug-gene-interaction (DGI) dataset collected from BioSNAP database. A bi-clustering algorithm BiClusO is then applied to the bipartite network for finding high density clusters. The presence of IBD risks genes in the clusters are examined and statistically significant clusters are determined which are then utilized for IBD drug repurposing. Second a clusterSim function is applied to the disease-gene association (DGA) network which is also collected from BioSNAP database to find the similarity score for each disease with Inflammatory Bowel Disease (IBD) using their corresponding genes. Diseases with high similarity scores are distinguished and then their corresponding drugs are identified using the drug-gene-interaction (DGI) dataset. We have identified some potential IBD drugs based on disease-disease relation and bi-clustering network analysis. The IBD drugs we have identified are: Cisplatin, Etanercept, Oxaliplatin, VX-702, Carboplatin, Adalimumab, AV411, CRx-139, SCIO-469, Chloroquine. These approaches can be generalized to find drugs for IBD diseases. Our proposed methods will be helpful to understand the mechanisms of the way the drugs work.