BIMC - We propose a drug repositioning computational approach based on the target microRNAs. The approach is able to predict the potential drug-disease associations along with the causal microRNAs.

Dataset

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1. Associations - Contains Drug-microRNA and microRNA-Disease association matrices and corresponding data.

2. Similarity Data – Contains Drug, microRNA and disease pairwise similarities.

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1. NamesToNumbrs.m – Code to convert existing associations to numbers for generating association

matrix.

2. Association.m – Code to generate association matrix.

In each matlab file, the commented portions represent code corresponding to Drug-microRNA associations.