**About the program:**

This package includes MATLAB codes for bi-relational graph based transductive multi-label function annotation (Bi-TMF) and three other methods it is compared to.

**Requirement:** the package was developed with MATLAB 7.1.1.0 (R2010b)

**How to use the program**

To run the program, open the folder Bi-TMF and add it to the MATLAB path. The main package that must be installed is:

Bi-TMF.m

**Description of other files in the folder:**

GRF.m: an independent model Bi-TMF is compared to. It is a classifier integration method that incorporates functional interrelationships and uses Jaccard coefficient to get the correlation matrix and to quantify interrelationships between functions.

PfunBG.m: an independent model Bi-TMF is compared to. It is a multi-label semi-supervised method that uses classifier integration to predict protein functions using a bi-relational graph of proteins and functions

TMEC.m: an independent model Bi-TMF is compared to. It uses ensemble classifier to integrate different data sources. It also uses bi-relational graph and graph-based multi-label classifier on the data sets

Datasets:

1. Yeast\_multigraph.mat
2. Human\_multigraph.mat
3. Mouse\_multigraph.mat

**Other codes:**

Gen\_train\_test.m: used for dividing training and testing set.