This program is to fuse peak tables from different peak matching software to enhance metabolic coverage. It can fuse more than two peak tables from any different peak matching software.

In the folder ‘data’, TTF\_cW.mat is the peak table from XCMS. TTF\_MZ.mat is the peak table from MZmine 2. TTF\_SI.mat is the peak table from SIEVE. Pk\_final.mat is the result after fusion.

The program has two parameters: two features with retention time difference smaller than *rt\_thresh* and m/z difference smaller than *mz\_thresh* are believed to be derived from the same metabolite. An example is created in the file ‘test\_f.m’, as following:

clear

rt\_thresh=6;

mz\_thresh=0.01;

load('E:\data\TTF\_cW.mat'); %load peak table form XCMS

load('E:\data\TTF\_MZ.mat'); %load peak table form MZmine 2

load('E:\data\TTF\_SI.mat'); %load peak table form SIEVE

pk=[TTF\_cW;TTF\_MZ;TTF\_SI]; %connect three different peak tables together

[pk\_final]=delete\_redundant\_features\_single\_pk(pk,rt\_thresh,mz\_thresh); % fuse different peak tables to enhance metabolic coverage.