

Manual for THDTricluster.exe

The manual for executing THDTricluster.exe is given here. This tool can be used for extracting biclusters from each GS plane of a GST dataset, considering SSSim threshold, minimum number of genes, and minimum number of samples and then merge them to find the triclusters across different time points, considering Inter-temporal threshold. This tool is developed in MATLAB environment using GUIDE.

Step-wise procedure to use the THDTricluster tool is explained below.

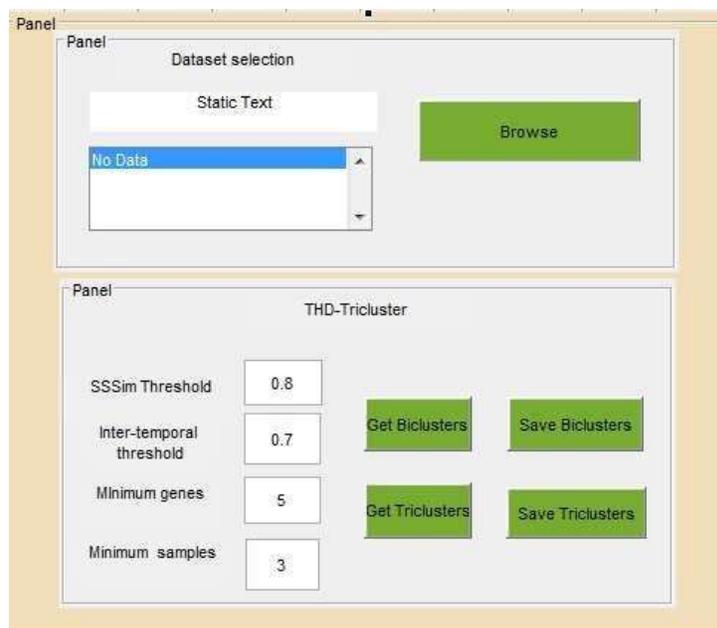
1. Download the THDTricluster.zip folder by clicking the link given below and extract the THDTricluster folder to a destination folder.

<http://agnigarh.tezu.ernet.in/~dkb/resources.html>

The THDTricluster.zip contains the following files:

- (i) THDTricluster.exe
- (ii) Datasets (data1,data2,data3, and data4)
- (iii) Screenshot of THDTricluster interface
- (iv) readme.txt file containing the instructions about the prerequisites for deploying the tool

2. Run the THDTricluster.exe file and the interface will appear as below.



3. First load the data by clicking the *Browse* button. To load the data for subsequent time points (GS planes), type 1 and click *YES* in the dialog box each time and select data from the desired location. If all data are uploaded, click *Cancel* button. The dataset with different time points will be loaded.
4. Extract the biclusters by setting the *SSSim Threshold*, *Minimum genes*, *Minimum samples* and clicking the *Get Biclusters* button. Extracted biclusters can be saved by clicking the *Save Biclusters* button.

Thereafter, the triclusters can be extracted by setting the *Inter-temporal threshold* and clicking the *Get Triclusters* button. These triclusters can be saved using the *Save Triclusters*. The extracted biclusters and triclusters are saved as *.mat* file. The *bicluser.mat* file is a cell array, containing the gene indices, sample indices of each bicluster obtained from different GS plane. The genes contained in each bicluster, are coexpressed across a subset of samples. Similarly, the *tricluster.mat* file is a cell array, containing the gene indices, sample indices, and time indices of each triclusters obtained across different GS plane. The genes contained in each tricluster are coexpressed across a subset of samples and time points.