**Instruction of NetworkConstruction package**

This package includes Matlab scripts and several datasets for demo of NetworkConstruction approach:

1. main\_NetworkConstruction.m is a Matlab function for the routine of experimental analysis. NetworkConstruction aims to construct the personalized gene interaction network.

**(b)**  main\_NetworkConstruction.m is the main script to call NetworkConstruction by supplying following parameters:

(1) **expression\_tumor\_fileName**: the directory locating of the gene expression data of tumor of tissue as the input data.

(2) **expression\_normal\_fileName**: the directory locating of the gene expression data of normal tissue as the input data.

(2) **mutation\_tumor\_fileName:** the directory locating of the copy number variations data as the input data.

**(c)** Algorithm\_NetworkConstruction directory includes Matlab scripts for each step of NetworkConstruction analysis, and called in main\_NetworkConstruction.m

(d) The input datasets include:

(1) **tumor.txt:** the tumor expression data in cancer.

(2) **normal.txt:** the normal expression data in cancer.

(2) **mutation.txt:** the gene mutation data in cancer.

**Note: Our NetworkConstruction outputs the information of samples with paired data in the both three files.**

(e) The analysis results are saved in directory pointed by fileName: The variable “**Result\_DNB\_score**”, and “**Result\_NetworkConstruction\_markers**” are the output of our NetworkConstruction, indicting the predicted early warning scores and multi-modal dynamic network biomakers.

(1) For “**Result\_DNB\_score**”, the first column is the sample name with paired data (normal and tumor) and the second column is the predicted early warning scores.

(2) For “**Result\_NetworkConstruction\_markers**”, the first colunm is the related combinational drugs (name in DCDB), the other colunms are different sets of multi-modal dynamic network biomakers.

(f) This package has been tested in different computer environments as: Window 7 or above; **Matlab 2014** or above.

(g) When users analyzed yourself new data, please:

(1) Prepare input datasets as introduced in (d).

(2) Clear the previous results.

(3) Set parameters in main\_NetworkConstruction.m as introduced in (b).

(4) Run main\_NetworkConstruction.m.

(5) Suggest that the users add all fille in our folders to your folder.

% $Id: main\_NetworkConstruction.m Created at 2021-07-22 16:25:22 $

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% $If any problem,pleasse contact **guowf@zzu.edu.cn** for help. $