**Instruction for constructing background network in PersonalizedGNN**

This package includes Matlab scripts and several datasets for demo:

1. Main\_construct\_background\_Network.m is a Matlab function for the routine of experimental analysis. This package aims to construct Personalzied Gene Interaction Network (for breast and lung cancer patients) .

**(b)**  Main\_construct\_background\_Network.m is the main script 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)** The input datasets include:

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

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

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

**Note: This package 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 “background.txt”, and “comutation.txt” are the output, indicting the edges of background network and node score.

(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\_construct\_background\_Network.m as introduced in (b).

(4) Run Main\_construct\_background\_Network.m.

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

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