**Instruction of Benchmark\_control package**

%Remaind: Please install gurobi before running our code (http://www.gurobi.com/)

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

1. main\_Benchmark\_control.m is a Matlab function for the routine of experimental analysis.

**(b)**  benchmark\_control.m is the main script to call Benchmark\_control

**(c)** The input datasets include:

% data:the tumor expression data

% gene\_list:the gene list name data

% ref\_data:the reference data used in SSN

% index:denotes we use which network construction method

%if index=1,we use CSN

%if index=2,we use SSN

%if index=3,we use SPCC

%if index=2,we use LIONESS

The output datasets include:

The sample-specific driver profiles (matrix) by using MMS,MDS,NCU,NCD；

For “MMS or MDS,NCU,NCD”, the column is the samples and the rows is the genes. The value “1” denoted that the gene is driver genes;

(d) As a demo, users can directly run main\_Benchmark\_control.m in Matlab. **We choose the single cell time cource data and BRCA cancer data as a test case in our demo.** This package has been tested in different computer environments as: Window 7 or above; **Matlab 2014** or above.

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

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

(2) Clear the previous results.

(3) Set parameters in benchmark\_control.m as introduced in (b).

(4) Run main\_Benchmark\_control.m.

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

% $Id: main\_Benchmark\_control.m Created by Weifeng Guo, Northwestern Polytechtical University, China at 2019-04-25 21:25:22 $

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% $If any problem, pleasse contact **shaonianweifeng@126.com** for help. $