**Instruction of PFApackage**

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

1. Main\_PFA.m is a Matlab function for the routine of experimental analysis.

(b) Main\_PFA.m is the main script to call CNS by supplying following parameters:

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

(2) methy\_fileName: the directory locating of the methylation expression data as the input data.

(3) mirna\_fileName: the directory locating of the miRNA expression data as the input data.

(4) res\_fileName: the directory locating of the global sample-spectrum as the output data.

(c) Algorithm\_PFA directory includes Matlab scripts for each step of PFA analysis, and called in Main\_PFA.m

(d) The input datasets include:

(1) **data\_gene\_expression.csv:** the dataset of gene expression, located in parameter gene\_fileName. Its format is: each row represents one gene exprssion; the first column are the name of genes;

(2) **data\_methy\_expression.csv:** the dataset of methylation expression, located in parameter methy\_fileName. Its format is: each row represents one methylation expression.

(3) **data\_mirna\_expression.csv:** the dataset of miRNA expression, located in parameter mirna\_fileName. Its format is: each row represents one miRNA expression.

(e) The analysis results are saved in directory pointed by parameter res\_fileName:

**global\_sample\_spectrum.csv:** the global sample spectrum by PFA in samples, located in parameter res\_fileName.

(f) As a demo, users can directly run Main\_PFA.m in Matlab. This package has been tested in different computer environments as: Window 7 or above; Matlab 2010 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\_PFA.m as introduced in (b).

(4) Run Main\_PFA.m.