```
% addpath('path_to_PBLR')
```

Import raw data

```
addpath(genpath('./'))
addpath PROPACK;
addpath Rank
addpath example_data
iniData = readtable('raw.txt','Delimiter','\t','ReadRowNames',true,...
    'ReadVariableNames',true);
```

Preprocessing data

```
tic;
minGenes = 0; minCells = 0; libararyflag = 0; logNormalize = 1;
proData = preprocessing(iniData, minCells, minGenes, libararyflag,logNormalize);
M = proData.data;
```

Select informative genes used for clustering

```
id = gene_selection(M);
```

Clustering

```
M0 = M(id,:);
K = []; % the cluster numbers can be given by user.
numCores = 1; % defined by user
system_used = 'Mac';
accelerate = 1;
label = [];
[group,coph] = clusteing(iniData,M0,K,numCores,system_used,accelerate,label);
```

```
Loading required package: ggplot2
Loading required package: cowplot

Attaching package: ‘cowplot’

The following object is masked from ‘package:ggplot2’:

    ggsave

Loading required package: Matrix

Attaching package: ‘dplyr’

The following objects are masked from ‘package:stats’:

    filter, lag
```

```
The following objects are masked from ‘package:base’:

    intersect, setdiff, setequal, union

------------------------------------------------------------------------------
You have loaded plyr after dplyr - this is likely to cause problems.
If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
library(plyr); library(dplyr)
------------------------------------------------------------------------------

Attaching package: ‘plyr’

The following objects are masked from ‘package:dplyr’:

    arrange, count, desc, failwith, id, mutate, rename, summarise,
    summarize


Attaching package: ‘data.table’

The following objects are masked from ‘package:dplyr’:

    between, first, last

Performing log-normalization
0%   10   20   30   40   50   60   70   80   90   100%
[----|----|----|----|----|----|----|----|----|----|
**************************************************|
Calculating gene means
0%   10   20   30   40   50   60   70   80   90   100%
[----|----|----|----|----|----|----|----|----|----|
**************************************************|
Calculating gene variance to mean ratios
0%   10   20   30   40   50   60   70   80   90   100%
[----|----|----|----|----|----|----|----|----|----|
**************************************************|
[1] 355
Scaling data matrix

  |
  |                                                                      |   0%
  |
  |======================================================================| 100%
```

Select boundary function through visualizing.

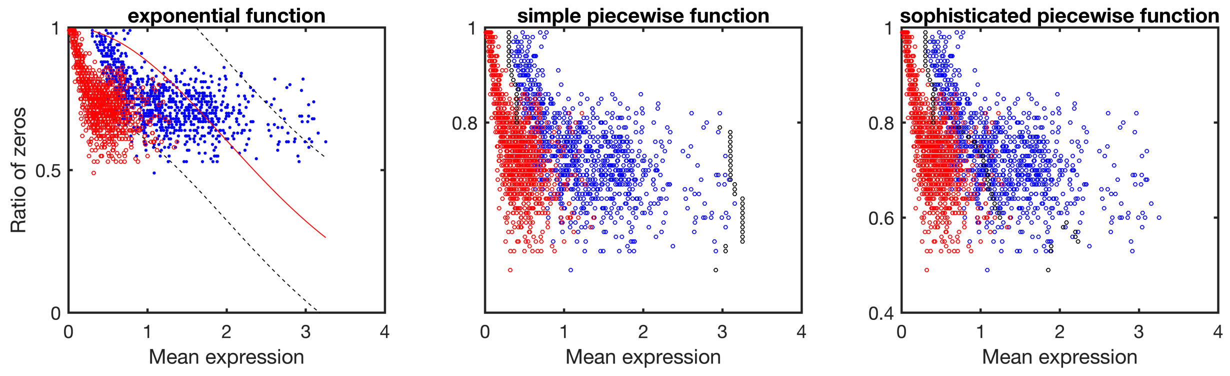
The boundary functions are divided into three categories:

1: exponetial function;

2: simple piecewise function;

3: sophisticated piecewise function.

```
boundary_selection(M);
```



Run PBLR with selected boundary function

```
boundary_function = 3;
imputation_all = 1;
accelate = true;
X = PBLR_main(M,id,group,boundary_function,imputation_all,numCores,accelate);
```

```
Imputing the submatrix of selected genes across cells of each cluster:
Imputing the remaining submatrix:
```

```
toc;
```

```
Elapsed time is 24.049764 seconds.
```

Export the imputed matrix

```
if isequal(imputation_all,true)
    id = 1:size(M,1);
end
T = array2table(X,'VariableNames',proData.cells,'RowNames',proData.genes(id));
writetable(T,'PBLR_impute.txt','Delimiter','\t','WriteRowNames',1);
```