LMGene User's Guide

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1 Introduction

This article introduces usage of the `LMGene` package. `LMGene` has been developed for analysis of microarray data using a linear model and glog data transformation in the R statistical package.

2 Data preparation

`LMGene` takes objects of class `ExpressionSet`, which is the standard data structure of the `Biobase` package. Therefore, the user who already has data that is of class `ExpressionSet` can jump to further steps, such as g-log transformation or looking for differentially expressed genes. Otherwise, the user needs to generate new objects of class `ExpressionSet`. For more detail, please see the vignette, 'An Introduction to Biobase and ExpressionSets' in the `Biobase` package.
Note: ExpressionSet. In this package, an object of class `ExpressionSet` must produce proper data using the commands `exprs(object)` and `phenoData(object)`.
`Example.` `LMGene` includes sample array data which is of class `ExpressionSet`. Let's take a look this sample data.

1. First, load the necessary packages in your R session.

```
> library(LMGene)
> library(Biobase)
> library(tools)
```

2. Load the sample `ExpressionSet` class data in the package `LMGene`.

```
> data(sample.eS)
```

3. View the data structure of the sample data and the details of `exprs` and `phenoData` slots in the data.

```
> slotNames(sample.eS)

[1] "experimentData"    "assayData"         "phenoData"
[4] "featureData"       "annotation"        "protocolData"
[7] ".__classVersion__"

> dim(exprs(sample.eS))

[1] 613  32

> exprs(sample.eS)[1:3,]

   p1d0 p1d1 p1d2 p1d3 p2d0 p2d1 p2d2 p2d3 p3d0 p3d1 p3d2 p3d3 p4d0 p4d1 p4d2
g1  216  149  169  113  193  172  167  168  151  179  142  156  160  214  157
g2  334  311  187  135  514  471  219  394  367  390  365  387  318  378  329
g3  398  367  351  239  712  523  356  629  474  438  532  427  429  574  419
   p4d3 p5d0 p5d1 p5d2 p5d3 p6d0 p6d1 p6d2 p6d3 p7d0 p7d1 p7d2 p7d3 p8d0 p8d1
g1  195  165  144  185  162  246  227  173  151  796  378  177  278  183  285
g2  450  293  285  390  428  645  631  324  343  852  451  259  379  259  386
g3  564  438  321  519  488  824  579  416  489 1046  501  375  388  373  509
   p8d2 p8d3
g1  275  202
g2  361  333
g3  468  436

> phenoData(sample.eS)

An object of class "AnnotatedDataFrame"
  sampleNames: p1d0 p1d1 ... p8d3 (32 total)
  varLabels: patient dose
  varMetadata: labelDescription

> slotNames(phenoData(sample.eS))

[1] "varMetadata"       "data"              "dimLabels"
[4] ".__classVersion__"
```

`Data generation.` If you don't have `ExpressionSet` class data, you need to make some. `LMGene` provides a function that can generate an object of class `ExpressionSet`, assuming that there are array data of `matrix` class and experimental data of `list` class.

1. The package includes sample array and experimental/phenotype data, `sample.mat` and `vlist`.

```
> data(sample.mat)
> dim(sample.mat)
```

```
[1] 613  32
```

```
> data(vlist)
> vlist
```

```
$patient
 [1] 1 1 1 1 2 2 2 2 3 3 3 3 4 4 4 4 5 5 5 5 6 6 6 6 7 7 7 7 8 8 8 8
Levels: 1 2 3 4 5 6 7 8

$dose
 [1] 0 1 2 3 0 1 2 3 0 1 2 3 0 1 2 3 0 1 2 3 0 1 2 3 0 1 2 3 0 1 2 3
```

2. Generate `ExpressionSet` class data using `neweS` function.

```
> test.eS<-neweS(sample.mat, vlist)
> class(test.eS)
```

```
[1] "ExpressionSet"
attr(,"package")
[1] "Biobase"
```

3 G-log transformation

1. `Estimating parameters for g-log transformation.` In `LMGene`, the linear model is not intended to be applied to the raw data, but to transformed and normalized data. Many people use a log transform. `LMGene` uses a log-like transform involving two parameters. We estimate the parameters λ and α of the generalized log transform $\log\left(y-\alpha+\sqrt{(y-\alpha)^2+\lambda}\right) = \sinh^{-1}(\frac{y-\alpha}{\lambda})+\log(\lambda)$ using the function tranest as follows:

```
> tranpar <- tranest(sample.eS)
> tranpar
```

```
$lambda
[1] 726.6187

$alpha
[1] 56.02754
```

The optional parameter `ngenes` controls how many genes are used in the estimation. The default is all of them (up to 100,000), but this option allows the use of less. A typical call using this parameter would be

```
> tranpar <- tranest(sample.eS, 100)
> tranpar
```

```
$lambda
[1] 379.7988

$alpha
[1] 44.13825
```

In this case, 100 genes are chosen at random and used to estimate the transformation parameter. The function returns a list containing values for lambda and alpha.

2. `G-log transformation.` Using the obtained two parameters, the g-log transformed expression set can be calculated as follows.

```
> trsample.eS <- transeS(sample.eS, tranpar$lambda, tranpar$alpha)
> exprs(sample.eS)[1:3,1:8]

   p1d0 p1d1 p1d2 p1d3 p2d0 p2d1 p2d2 p2d3
g1  216  149  169  113  193  172  167  168
g2  334  311  187  135  514  471  219  394
g3  398  367  351  239  712  523  356  629

> exprs(trsample.eS)[1:3,1:8]

       p1d0     p1d1     p1d2     p1d3     p2d0     p2d1     p2d2     p2d3
g1 5.843037 5.354315 5.526390 4.944695 5.700423 5.549855 5.510439 5.518445
g2 6.363679 6.281209 5.659645 5.213794 6.846015 6.750128 5.860234 6.551460
g3 6.562811 6.471281 6.420551 5.967929 7.197441 6.864973 6.436682 7.064800
```

3. `Tranest options: multiple alpha, lowessnorm, model`

Rather than using a single alpha for all samples, we can estimate a separate alpha for each sample. This allows for differences in chips, in sample concentration, or exposure conditions.

```
> tranparmult <- tranest(sample.eS, mult=TRUE)
> tranparmult

$lambda
[1] 689.2819

$alpha
 [1]  69.67146  37.02711  54.13904  69.35728  60.33270  60.75301  71.72965
 [8]  64.55506  58.63427  65.73625  48.40173  59.43778  76.34568  78.81046
[15]  82.20326  96.19938  77.60070  79.48089  73.63257  73.41650  33.86029
[22]  69.26448  55.75460  54.29840 139.89493  91.36521  46.46158  59.02056
[29]  73.60255  89.48728  57.13887  64.98866
```

For vector alphas, transeS uses exactly the same syntax:

```
> trsample.eS <- transeS (sample.eS, tranparmult$lambda, tranparmult$alpha)
> exprs(trsample.eS)[1:3,1:8]
```

```
       p1d0     p1d1     p1d2     p1d3     p2d0     p2d1     p2d2     p2d3
g1 5.686954 5.424873 5.449682 4.549380 5.590642 5.418542 5.268332 5.347915
g2 6.272797 6.308464 5.592073 4.915159 6.811348 6.710929 5.693269 6.492140
g3 6.488757 6.493737 6.388361 5.832776 7.173087 6.830052 6.345199 7.029530
```

It's also possible to estimate the parameters using the more accurate lowess normalization (as opposed to uniform normalization):

```
> tranparmult <- tranest(sample.eS, ngenes=100, mult=TRUE, lowessnorm=TRUE)
> tranparmult

$lambda
[1] 338.746

$alpha
 [1]  83.73783  57.44267  59.22589  66.03666  67.76811  64.93932  74.99275
 [8]  60.68315  69.53720  74.18539  69.88852  64.31053  63.31960  75.45773
[15]  61.72866  92.10563  64.28376  55.09079  65.02913  64.26601  58.10444
[22]  87.07437  59.49947  64.44771 183.50362 104.39813  58.44816  74.22959
[29]  56.99603  92.62905  60.06216  66.64911
```

One may also specify a model other than the default no-interaction model. For example, if we think that the interaction of variables in `vlist` is important, we can add interaction to the model:

```
> tranpar <- tranest(sample.eS, model='patient + dose + patient:dose')
> tranpar

$lambda
[1] 860.0836

$alpha
[1] 55.68625
```

The model is always specified in the same way as the right-hand side of an `lm` model. In the example above, we set the parameters to minimize the mean squared error for a regression of transformed gene expression against patient, log dose, and their interaction.

Be very careful of using interactions between factor variables. If you do not have enough replicates, you can easily overfit the data and have no degrees of freedom left for error.

Naturally, it's possible to use `mult`, `lowessnorm`, and `model` all together.

4 Finding differentially expressed genes

1. `Transformation and Normalization.` Before finding differentially expressed genes, the array data needs to be transformed and normalized.

```
> trsample.eS <- transeS (sample.eS, tranparmult$lambda, tranparmult$alpha)
> ntrsample.eS <- lnormeS (trsample.eS)
```

2. `Finding differentially expressed genes` The `LMGene` routine computes significant probes/genes by calculating gene-by-gene p-values for each factor in the model and adjusting for the specified false discovery rate (FDR). A typical call would be

   ```
   > sigprobes <- LMGene(ntrsample.eS)
   ```

   There is an optional argument, `level`, which is the FDR (default 5 percent). A call using this optional parameter would look like

   ```
   > sigprobes <- LMGene(ntrsample.eS,level=.01)
   ```

   The result is a list whose components have the names of the effects in the model. The values are the significant genes for the test of that effect or else the message "No significant genes".

   As with `tranest`, it's possible to specify a more complex model to `LMGene`:

   ```
   > sigprobes <- LMGene(ntrsample.eS, model='patient+dose+patient:dose')
   > sigprobes

   $patient
    [1] "g2"   "g3"   "g4"   "g9"   "g10"  "g15"  "g43"  "g54"  "g56"  "g84"
   [11] "g85"  "g86"  "g88"  "g93"  "g123" "g176" "g178" "g179" "g277" "g304"
   [21] "g305" "g310" "g336" "g375" "g399" "g405" "g406" "g407" "g408" "g409"
   [31] "g411" "g412" "g413" "g414" "g415" "g461" "g462" "g463" "g477" "g485"
   [41] "g503" "g520" "g528" "g544" "g566" "g607" "g612"

   $dose
   [1] "No significant genes"

   $`patient:dose`
   [1] "No significant genes"
   ```

References

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