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] "assayData"        "phenoData"          "featureData"
[4] "experimentData"   "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 and varMetadata description:
    patient: patient
    dose: dose

> 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] 436.8786

$alpha
[1] 43.14776
```

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 5.849220 5.364799 5.535081 4.961197 5.707626 5.558328 5.519282 5.527212
g2 6.367251 6.285102 5.667171 5.226030 6.848184 6.752521 5.866305 6.554398
g3 6.565715 6.474474 6.423918 5.973343 7.198954 6.867099 6.439992 7.066533
```

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] 788.9896


$alpha
 [1]  78.17234  54.69241  60.83804  62.75639  62.23945  65.22582  79.68228
 [8]  71.77268  63.39424  72.24447  68.35943  61.32813  65.32763  69.46020
[15]  59.30264  84.91039  61.37064  58.13618  60.45466  62.19224  57.43874
[22]  94.60027  53.90754  59.31561 212.24092 119.36359  59.46890  72.58829
[29]  54.25977  83.75370  66.43826  58.43802
```

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 = 0.01)
```

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" "g155" "g176" "g178" "g179" "g183"
[21] "g240" "g277" "g304" "g305" "g310" "g336" "g375" "g399" "g405" "g406"
[31] "g407" "g408" "g409" "g411" "g412" "g413" "g414" "g415" "g423" "g461"
[41] "g462" "g463" "g477" "g485" "g503" "g520" "g528" "g544" "g566" "g607"
[51] "g612"

$dose
[1] "No significant genes"

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

References

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