BLMA: A package for bi-level meta-analysis

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Abstract

This package provides a bi-level meta-analysis (BLMA) framework that can be applied in a wide range of applications: functional analysis, pathway analysis, differential expression analysis, and general hypothesis testing. The framework is able to integrate multiple studies to gain more statistical power, and can be used in conjunction with any statistical hypothesis testing method. It exploits not only the vast number of studies performed in independent laboratories, but also makes better use of the available number of samples within individual studies. In this document, we provide example code that applies BLMA in all of the areas mentioned above.

Contents

1   Introduction

This document provides an introductory description on how to use the package. For the extended description of the methods, please consult Nguyen et al. [1]. The bi-level meta-analysis (BLMA) framework integrates independent experiments at two levels: an intra-experiment analysis, and an inter-experiment analysis. First, for each experiment, the intra-experiment analysis splits the dataset into smaller datasets, performs a statistical test on each of the newly created small datasets, then combines the p-values. Next, the inter-experiment analysis combines those processed p-values, from each of the individual experiments.

In this package, we implement useful functions that allow users to integrate data in many applications. First, we implement classical methods for combining independent p-values, including Fisher's method [2], Stouffer's method [3]. We also implement our new method named addCLT [1, 4, 5, 6], which is based on the Irwin-Hall distribution [7, 8] and the Central Limit Theorem [9]. These methods of combining p-values (addCLT, Fisher's, Stouffer's, minP, and maxP) are the basic building blocks of the BLMA framework.

Second, we implement functions for BLMA that can be applied in conjunction with classical tests, such as t-test, Wilcoxon test, etc. We provide code and examples for applying the intra-experiment analysis and bi-level analysis in conjunction with t-test and Wilcoxon test. The functions are flexible and can be applied for one-sample, two-samples, one-tailed, and two-tailed tests. By default, addCLT [1, 4, 5, 6] is used to combine the p-values, but users can change it to Fisher's method [2], Stouffer's method [3], minP [10], or maxP [11], according to their preference.

Third, we implement functions for functional analysis and pathway analysis. Users can choose to apply the BLMA framework in conjunction with any of the 4 methods: Over-Representation Analysis (ORA) [12, 13], Gene Set Analysis (GSA) [14], Pathway Analysis with Down-weighting of Overlapping Genes (PADOG) [15], and Impact Analyis (IA) [16]. When there is only one dataset, the analysis is reduced to an intra-experiment analysis. The functions are flexible and easy to run.

Fourth, we implement functions for differential expression analysis. The package uses the moderated t-test (limma package [17]) as the test for differential expression. In the intra-experiment analysis, the framework splits a dataset into smaller datasets, performs the moderated t-test on these split datasets, and then combines the results. In the inter-experiment analysis, the framework combines the results obtained from the intra-experiment analysis of individual datasets. The output is a list of genes ranked according to how likely they are to be differentially expressed.

2   BLMA for classical hypothesis testing

Our bi-level meta-analysis framework is comprised of an intra-experiment and an inter-experiment analysis. The reasoning for the intra-experiment is that performing a statistical test on a large experiment is not as powerful as splitting it into smaller studies and then combining them. See Nguyen et al. [1] for a detailed explanation.

2.1   Intra-experiment analysis

We design the function *intraAnalysisClassic* in a way that it can be used in conjunction with classical tests without any restriction. For example, intead of calling one-sample left-tailed t-test or Wilcoxon test, users can call the function *intraAnalysisClassic* with the same parameters. Below are examples of how to use t-test and Wilcoxon test:

```
> # one-sample tests
> library(BLMA)
> set.seed(1)
> x <- rnorm(10, mean = 0)
> # one-sample left-tailed t-test
> t.test(x, mu=1, alternative = "less")$p.value

[1] 0.003280397

> # one-sample left-tailed intra-experiment analysis with t-test
> intraAnalysisClassic(x, func=t.test, mu=1, alternative = "less")

[1] 0.003090177

> # one-sample right-tailed t-test
> t.test(x, mu=1, alternative = "greater")$p.value

[1] 0.9967196

> # one-sample right-tailed intra-experiment analysis with t-test
> intraAnalysisClassic(x, func=t.test, mu=1, alternative = "greater")

[1] 0.9969098

> # one-sample two-tailed t-test
> t.test(x, mu=1)$p.value

[1] 0.006560794

> # one-sample two-tailed intra-experiment analysis with t-test
> intraAnalysisClassic(x, func=t.test, mu=1)

[1] 0.01236071

> # one-sample left-tailed Wilcoxon test
> wilcox.test(x, mu=1, alternative = "less")$p.value

[1] 0.006835938

> # one-sample left-tailed intra-experiment analysis with Wilcoxon test
> intraAnalysisClassic(x, func=wilcox.test, mu=1, alternative = "less")

[1] 0.004394531

> # one-sample right-tailed Wilcoxon test
> wilcox.test(x, mu=1, alternative = "greater")$p.value

[1] 0.9951172

> # one-sample right-tailed intra-experiment analysis with Wilcoxon test
> intraAnalysisClassic(x, func=wilcox.test, mu=1, alternative = "greater")
```

```
[1] 0.9995117

> # one-sample two-tailed Wilcoxon test
> wilcox.test(x, mu=1)$p.value

[1] 0.01367188

> # one-sample two-tailed intra-experiment analysis with Wilcoxon test
> intraAnalysisClassic(x, func=wilcox.test, mu=1)

[1] 0.01757812
```

Similarly, the intra-experiment analysis can be used with two-sample tests:

```
> # two-sample tests
> set.seed(1)
> x <- rnorm(20, mean=0); y=rnorm(20, mean=1)
> # two-sample left-tailed t-test
> t.test(x,y,alternative="less")$p.value

[1] 0.003561452

> # two-sample left-tailed intra-experiment analysis with t-test
> intraAnalysisClassic(x, y, func=t.test, alternative = "less")

[1] 0.0001387321

> # two-sample right-tailed t-test
> t.test(x,y,alternative="greater")$p.value

[1] 0.9964385

> # two-sample right-tailed intra-experiment analysis with t-test
> intraAnalysisClassic(x, y, func=t.test, alternative = "greater")

[1] 0.9998613

> # two-sample two-tailed t-test
> t.test(x,y)$p.value

[1] 0.007122904

> # two-sample two-tailed intra-experiment analysis with t-test
> intraAnalysisClassic(x, y, func=t.test)

[1] 0.002219713
```

2.2 Bi-level meta-analysis

Some example code for bi-level meta-analysis:

```
> # one-sample tests
> set.seed(1)
> l1 <- lapply(as.list(seq(3)),FUN=function (x) rnorm(n=10, mean=1))
> l0 <- lapply(as.list(seq(3)),FUN=function (x) rnorm(n=10, mean=0))
> # one-sample right-tailed t-test
> lapply(l1, FUN=function(x) t.test(x, alternative="greater")$p.value)

[[1]]
[1] 0.0006575675

[[2]]
[1] 0.002488991

[[3]]
[1] 0.009286192

> # combining the p-values of one-sample t-test:
> addCLT(unlist(lapply(l1, FUN=function(x)
+       t.test(x, alternative="greater")$p.value)))

[1] 3.202952e-07

> #Bi-level meta-analysis with one-sample right-tailed t-test
> bilevelAnalysisClassic(x=l1, func=t.test, alternative="greater")

[1] 2.765896e-07

> # two-sample left-tailed t-test
> lapply(seq(l1), FUN=function(i,l1,l0)
+       t.test(l1[[i]], l0[[i]], alternative="greater")$p.value, l1, l0)

[[1]]
[1] 0.005366316

[[2]]
[1] 0.006030029

[[3]]
[1] 0.05919203

> # combining the p-values of one-sample t-test:
> addCLT(unlist(lapply(seq(l1), FUN=function(i,l1,l0)
+       t.test(l1[[i]], l0[[i]], alternative="greater")$p.value, l1, l0)))

[1] 5.862034e-05
```

```
> #Bi-level meta-analysis with two-sample right-tailed t-test
> bilevelAnalysisClassic(x=l1, y=l0, func=t.test, alternative="greater")

[1] 7.899649e-06

> #Bi-level meta-analysis with two-sample left-tailed t-test
> bilevelAnalysisClassic(x=l1, y=l0, func=t.test, alternative="less")

[1] 0.9999921
```

3 BLMA for geneset/pathway analysis

For pathway/geneset analysis, the input of the framework is as follows. First, we have multiple studies (datasets) of the same disease. Each dataset consists of a group of control samples and a group of disease samples. Second, we have a list of genesets or pathways from an existing pathway database.

With the current implementation, the meta-analysis can be used in conjunction with the following approaches: Over-Representation Analysis (ORA) [12], Gene Set Analysis (GSA) [14], Pathway Analysis with Down-weighting of Overlapping Genes (PADOG) [15], and Impact Analyis (IA) [16]. By default, we use ORA as the enrichment method, which is very fast and is able to integrate hundreds of samples in a matter of seconds. Other enrichment methods are slower than ORA, and we encourage users to take advantage of our parallel computing by providing the number of processes via the *mc.cores* parameter.

3.1 Over-Representation Analysis (ORA)

We demonstrate this functionality using 4 acute myeloid leukemia (AML) datasets: GSE17054 (9 samples) [18], GSE57194 (12 samples) [19], GSE33223 (30 samples) [20], and GSE42140 (31 samples). The platform for all datasets is Affymetrix Human Genome U133 Plus 2.0 array. Affymetrix *CEL* files containing raw expression data were downloaded from GEO for each dataset and processed using *R* and *Bioconductor 2.13*. Quality control was performed using the *qc* method from the package *simpleaffy 2.38.0* [21]. Pre-processing was performed on individual datasets using the *threestep* function from the package *affyPLM version 1.38.0* [22, 23, 24]. We calculate the expression value of a gene by taking the median of the probesets that are mapped to the gene. Below is the code for performing BLMA in conjunction with ORA [12, 13] for the 4 datasets:

```
> library(BLMA)
> # load KEGG pathways and create genesets
> x=loadKEGGPathways()
> gslist <- lapply(x$kpg,FUN=function(y){return (nodes(y));})
> gs.names <- x$kpn[names(gslist)]
> # load the 4 AML datasets
> dataSets <- c("GSE17054", "GSE57194", "GSE33223", "GSE42140")
> data(list=dataSets, package="BLMA")
> # prepare dataList and groupList
> names(dataSets) <- dataSets
> dataList <- lapply(dataSets, function(dataset) get(paste0("data_", dataset)))
> groupList <- lapply(dataSets, function(dataset) get(paste0("group_", dataset)))
```

```
> # perform bi-level meta-analysis in conjunction with ORA
> system.time(ORAComb <- bilevelAnalysisGeneset(gslist, gs.names, dataList,
+                                               groupList, enrichment = "ORA"))

Working on dataset GSE17054, 9 samples
Working on dataset GSE57194, 12 samples
Working on dataset GSE33223, 30 samples
Working on dataset GSE42140, 31 samples
   user  system elapsed
  1.807   0.020   1.827

> #print the results
> options(digits=2)
> head(ORAComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])

                                      Name    pBLMA pBLMA.fdr rBLMA
path:hsa05200          Pathways in cancer 2.9e-05    0.0043     1
path:hsa04115         p53 signaling pathway 3.9e-04    0.0289     2
path:hsa05221       Acute myeloid leukemia 5.9e-04    0.0291     3
path:hsa04210                    Apoptosis 1.1e-03    0.0401     4
path:hsa04390       Hippo signaling pathway 4.8e-03    0.1288     5
path:hsa05169 Epstein-Barr virus infection 5.8e-03    0.1288     6
```

The running time for ORA is only 4 seconds. With a cutoff of 0.05, there are 4 significant pathways, among which the target pathway *Acute myeloid leukemia* is ranked 3rd with a FDR-corrected p-value 0.029.

3.2 Gene Set Analysis (GSA)

We can also perform BLMA in conjunction with GSA [14]. Since the function GSA (from the GSA package) is not as fast as ORA, we recommend users to take advantage of our parallel computing, by setting the number of cores using the *mc.cores* parameter:

```
> # perform bi-level meta-analysis in conjunction with GSA
> system.time(GSAComb <- bilevelAnalysisGeneset(gslist, gs.names, dataList,
+                                               groupList, enrichment = "GSA",
+                                               nperms=200, random.seed = 1))

Working on dataset GSE17054, 9 samples
Working on dataset GSE57194, 12 samples
Working on dataset GSE33223, 30 samples
Working on dataset GSE42140, 31 samples
   user  system elapsed
  18.51    0.15   18.66

> #print the results
> options(digits=2)
> head(GSAComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])
```

```
                              Name    pBLMA pBLMA.fdr rBLMA
path:hsa04210                Apoptosis 0.00056     0.042     1
path:hsa05161              Hepatitis B 0.00082     0.042     2
path:hsa05221 Acute myeloid leukemia 0.00086     0.042     3
path:hsa05222 Small cell lung cancer 0.00464     0.160     4
path:hsa05212        Pancreatic cancer 0.00570     0.160     5
path:hsa04012 ErbB signaling pathway 0.00648     0.160     6
```

The running time of the meta-analysis in conjunction with GSA is approximately 1 minutes with 1 core. With a cutoff of FDR=0.05, there are 2 significant pathways: *Apoptosis* and *Acute myeloid leukemia* . The target pathway *Acute myeloid leukemia* is ranked 2rd with a FDR-corrected p-value 0.023.

3.3 Pathway Analysis with Down-weighting of Overlapping Genes (PADOG)

Below is an example code for running BLMA in conjunction with PADOG [15]:

```
> set.seed(1)
> system.time(PADOGComb <- bilevelAnalysisGeneset(gslist, gs.names, dataList,
+                                  groupList, enrichment = "PADOG", NI=200))

Working on dataset GSE17054, 9 samples
Working on dataset GSE57194, 12 samples
Working on dataset GSE33223, 30 samples
Working on dataset GSE42140, 31 samples
   user  system elapsed
  44.85    0.33   45.18

> #print the results
> options(digits=2)
> head(PADOGComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])

                                   Name  pBLMA pBLMA.fdr rBLMA
path:hsa04012             ErbB signaling pathway 0.0031      0.18     1
path:hsa04390            Hippo signaling pathway 0.0033      0.18     2
path:hsa05221             Acute myeloid leukemia 0.0040      0.18     3
path:hsa04810 Regulation of actin cytoskeleton 0.0056      0.18     4
path:hsa04210                        Apoptosis 0.0068      0.18     5
path:hsa05031             Amphetamine addiction 0.0073      0.18     6
```

3.4 Impact Analysis (IA)

Impact Analysis (IA) is a topology-based pathway analysis approach that is able to take into consideration the interaction between genes [16]. Pathway information can be provided in the format of pathway graphs (e.g., graphNEL). Below is an example code for running BLMA in conjunction with IA:

```
> x <- loadKEGGPathways()
> system.time(IAComb <- bilevelAnalysisPathway(x$kpg, x$kpn, dataList, groupList))
```

```
Working on dataset GSE17054, 9 samples
Working on dataset GSE57194, 12 samples
Working on dataset GSE33223, 30 samples
Working on dataset GSE42140, 31 samples
   user  system elapsed
  47.06    0.18   47.24


> #print the results
> options(digits=2)
> head(IAComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])

                                                  Name    pBLMA pBLMA.fdr rBLMA
path:hsa05202    Transcriptional misregulation in cancer 6.0e-06   0.00088     1
path:hsa05221                     Acute myeloid leukemia 4.7e-05   0.00347     2
path:hsa04650 Natural killer cell mediated cytotoxicity 3.1e-03   0.11517     3
path:hsa05200                        Pathways in cancer 3.1e-03   0.11517     4
path:hsa04115                      p53 signaling pathway 4.8e-03   0.13996     5
path:hsa05212                         Pancreatic cancer 6.9e-03   0.16822     6
```

4 BLMA for differential expression analysis

The package also provides functions for differential expression analysis across multiple datasets. The input is a set of datasets from the same condition while the output is a list of genes ranked according to their p-values. Here we use the moderated t-test (limma package [17]) as the test for differential expression. As described above, BLMA performs the hypothesis testing at two levels: an intra-experiment analysis and an inter-experiment analysis. At the intra-experiment analysis, BLMA splits a dataset into smaller datasets, performs the moderated t-test for individual genes, and then combines the results obtained from these split datasets. At the inter-experiment analysis, the processed p-values from individual experiments are combined again. By default, the method addCLT is used to combine the p-values, but users can set it to Fisher's, Stouffer's method, minP, or maxP, according to their preference.

4.1 Intra-experiment analysis

The input for intra-experiment analysis is a dataset provided in a data frame. The output consists of the following information: i) logFC: log foldchanges, ii) pLimma: p-values calculated by limma without intra-experiment analysis, iii) FDR-correct p-values of pLimma, iv) pIntra: p-values obtained from the intra-experiment analysis, and v) FDR-corrected p-values of pIntra. The code for analyzing the dataset GSE33223 is as follows:

```
> #perform intra-experiment analysis of the dataset GSE33223 using addCLT
> library(BLMA)
> data(GSE33223)
> system.time(X <- intraAnalysisGene(data_GSE33223, group_GSE33223))

  user  system elapsed
  0.42    0.00    0.42
```

```
> X <- X[order(X$pIntra), ]
> # top 10 genes
> head(X)

          logFC  pLimma pLimma.fdr   pIntra pIntra.fdr
hsa:8761   0.88 2.9e-07    0.00040 9.3e-12    2.8e-08
hsa:801   -0.79 4.6e-08    0.00019 1.4e-11    2.8e-08
hsa:2744   0.80 7.7e-06    0.00291 3.0e-11    3.2e-08
hsa:3625  -0.47 1.2e-07    0.00025 3.1e-11    3.2e-08
hsa:5872  -2.33 2.8e-04    0.01561 6.4e-11    4.4e-08
hsa:81691  1.26 7.9e-07    0.00081 6.5e-11    4.4e-08

> # bottom 10 genes
> tail(X)

            logFC pLimma pLimma.fdr pIntra pIntra.fdr
hsa:26664 -0.0152   0.85       0.92      1          1
hsa:9451   0.0365   0.90       0.94      1          1
hsa:2961  -0.0131   0.94       0.96      1          1
hsa:712   -0.0295   0.92       0.95      1          1
hsa:904   -0.0119   0.96       0.97      1          1
hsa:655   -0.0065   0.93       0.96      1          1

> #perform intra-experiment analysis of GSE33223 using Fisher's method
> system.time(Y <- intraAnalysisGene(data_GSE33223, group_GSE33223,
+                        metaMethod=fisherMethod))

   user  system elapsed
   0.34    0.00    0.34

> Y = Y[order(Y$pIntra), ]
> # top 10 genes
> head(Y)

          logFC  pLimma pLimma.fdr   pIntra pIntra.fdr
hsa:81691  1.26 7.9e-07    0.00081 3.5e-11    1.4e-07
hsa:2744   0.80 7.7e-06    0.00291 1.6e-10    3.2e-07
hsa:5872  -2.33 2.8e-04    0.01561 3.5e-10    4.8e-07
hsa:3625  -0.47 1.2e-07    0.00025 1.1e-09    1.2e-06
hsa:8761   0.88 2.9e-07    0.00040 1.5e-09    1.2e-06
hsa:1029   1.29 4.1e-04    0.01821 1.7e-09    1.2e-06

> # bottom 10 genes
> tail(Y)

            logFC pLimma pLimma.fdr pIntra pIntra.fdr
hsa:26664 -0.0152   0.85       0.92      1          1
hsa:9451   0.0365   0.90       0.94      1          1
hsa:2961  -0.0131   0.94       0.96      1          1
hsa:712   -0.0295   0.92       0.95      1          1
hsa:904   -0.0119   0.96       0.97      1          1
hsa:655   -0.0065   0.93       0.96      1          1
```

4.2 Bi-level analysis

For bi-level analysis, the input is a list of multiple datasets. The ouput consists of the following information: i) pLimma: combined p-values of limma p-values obtained from individual expriments, ii) pLimma.fdr: FDR-correct p-values of pLimma, iii) pBilevel: combined p-values of pIntra obtained from individual experiments, and iv) pBilevel.fdr: FDR-corrected p-values of pBilevel. We demonstrate the bi-level analysis using the 8 example datasets as follows:

```
> system.time(Z <- bilevelAnalysisGene(dataList = dataList, groupList = groupList))

Working on dataset GSE17054, 9 samples
Working on dataset GSE57194, 12 samples
Working on dataset GSE33223, 30 samples
Working on dataset GSE42140, 31 samples
   user   system  elapsed
  1.622    0.032    1.654

> # top 10 genes
> head(Z)

           pLimma pLimma.fdr pBilevel pBilevel.fdr
hsa:3611  3.9e-06     0.0079  1.2e-06       0.0018
hsa:54407 1.4e-06     0.0058  1.4e-06       0.0018
hsa:55914 1.2e-05     0.0110  1.4e-06       0.0018
hsa:8660  1.3e-05     0.0110  1.7e-06       0.0018
hsa:4194  2.0e-05     0.0134  2.5e-06       0.0020
hsa:23237 2.5e-05     0.0148  6.2e-06       0.0042

> # bottom 10 genes
> tail(Z)

           pLimma pLimma.fdr pBilevel pBilevel.fdr
hsa:64106    0.96       0.97        1            1
hsa:259291   1.00       1.00        1            1
hsa:6572     1.00       1.00        1            1
hsa:347733   0.99       0.99        1            1
hsa:116443   0.98       0.98        1            1
hsa:3605     0.98       0.99        1            1
```

5 BLMA for network-based integrative analysis

BLMA also provides a function to estimate the effect sizes of genes across all studies (standardized mean difference) and their p-values. The function also performs classical hypothesis testing and meta-analysis to combine p-values for differential expressed genes across all studies. These statistics can be used as input of both geneset- and network-based analysis [25].

```
> allGenes <- Reduce(intersect, lapply(dataList, rownames))
> system.time(geneStat <- getStatistics(allGenes, dataList = dataList, groupList = groupList))
```

```
   user   system elapsed
   37.9     0.2    38.1


> # top 10 genes
> head(Z)


           pLimma pLimma.fdr pBilevel pBilevel.fdr
hsa:3611  3.9e-06     0.0079  1.2e-06       0.0018
hsa:54407 1.4e-06     0.0058  1.4e-06       0.0018
hsa:55914 1.2e-05     0.0110  1.4e-06       0.0018
hsa:8660  1.3e-05     0.0110  1.7e-06       0.0018
hsa:4194  2.0e-05     0.0134  2.5e-06       0.0020
hsa:23237 2.5e-05     0.0148  6.2e-06       0.0042


> # bottom 10 genes
> tail(Z)


           pLimma pLimma.fdr pBilevel pBilevel.fdr
hsa:64106    0.96       0.97        1            1
hsa:259291   1.00       1.00        1            1
hsa:6572     1.00       1.00        1            1
hsa:347733   0.99       0.99        1            1
hsa:116443   0.98       0.98        1            1
hsa:3605     0.98       0.99        1            1
```

For the details of each column, please consult the documentation of getStatistics function.

```
> ?getStatistics
```

Per form pathway analysis

```
> library(ROntoTools)
> # get gene network
> kpg <- loadKEGGPathways()$kpg
> # get gene network name
> kpn <- loadKEGGPathways()$kpn
> # get geneset
> gslist <- lapply(kpg,function(y) nodes(y))
> # get differential expressed genes
> DEGenes.Left <- rownames(geneStat)[geneStat$pLeft < 0.05 & geneStat$ES.pLeft < 0.05]
> DEGenes.Right <- rownames(geneStat)[geneStat$pRight < 0.05 & geneStat$ES.pRight < 0.05]
> DEGenes <- union(DEGenes.Left, DEGenes.Right)
> # perform pathway analysis with ORA
> oraRes <- lapply(gslist, function(gs){
+     pORACalc(geneSet = gs, DEGenes = DEGenes, measuredGenes = rownames(geneStat))
+ })
> oraRes <- data.frame(p.value = unlist(oraRes), pathway = names(oraRes))
> rownames(oraRes)  <- kpn[rownames(oraRes)]
> # print results
> print(head(oraRes))
```

```
                             p.value          pathway
Ribosome biogenesis in eukaryotes 8.6e-03 path:hsa03008
RNA transport                    1.5e-05 path:hsa03013
mRNA surveillance pathway        2.4e-03 path:hsa03015
RNA degradation                  3.2e-01 path:hsa03018
PPAR signaling pathway           8.5e-01 path:hsa03320
Fanconi anemia pathway           4.4e-04 path:hsa03460


> # perfrom pathway analysis with Pathway-Express from ROntoTools
> ES <- geneStat[DEGenes, "ES"]
> names(ES) <- DEGenes
> peRes = pe(x = ES, graphs = kpg, ref = allGenes, nboot = 1000, seed=1, verbose = F)
> peRes.Summary <- Summary(peRes, comb.pv.func = fisherMethod)
> peRes.Summary[, ncol(peRes.Summary) + 1] <- rownames(peRes.Summary)
> rownames(peRes.Summary) <- kpn[rownames(peRes.Summary)]
> colnames(peRes.Summary)[ncol(peRes.Summary)] = "pathway"
> # print results
> print(head(peRes.Summary))
```

	totalAcc	totalPert	totalAccNorm	totalPertNorm	pPert
RNA transport	2.1	26	1.51	0.71	0.495
Fanconi anemia pathway	4.2	14	2.86	2.10	0.033
Cell cycle	13.1	29	-0.54	-0.52	0.611
ErbB signaling pathway	21.9	31	4.49	4.57	0.003
Olfactory transduction	15.2	27	3.54	3.96	0.002
mRNA surveillance pathway	0.0	14	NA	0.95	0.356

	pAcc	pORA	pComb	pPert.fdr	pAcc.fdr	pORA.fdr
RNA transport	0.071	1.5e-05	9.6e-05	0.93	0.53	0.0022
Fanconi anemia pathway	0.007	4.4e-04	1.8e-04	0.40	0.16	0.0325
Cell cycle	0.603	7.1e-04	3.8e-03	0.94	0.82	0.0348
ErbB signaling pathway	0.003	1.8e-01	4.7e-03	0.15	0.16	0.9996
Olfactory transduction	0.002	3.9e-01	6.3e-03	0.15	0.16	0.9996
mRNA surveillance pathway	NA	2.4e-03	6.9e-03	0.82	NA	0.0897

	pComb.fdr	pathway
RNA transport	0.013	path:hsa03013
Fanconi anemia pathway	0.013	path:hsa03460
Cell cycle	0.169	path:hsa04110
ErbB signaling pathway	0.169	path:hsa04012
Olfactory transduction	0.169	path:hsa04740
mRNA surveillance pathway	0.169	path:hsa03015

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