

permPATH: Permutation Based Gene Expression Pathway Analysis

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1 Introduction

This vignette describes the R extension package `permPATH` for performing permutation based gene expression pathway analysis. The package works by computing a score for each group (pathway) of genes. The score is a function of the individual gene test statistics involved in the pathway. Currently, the package computes as the score the mean of the test statistics, the mean of the absolute values of the test statistics and the so called maxmean score [1]. The individual test statistics that the package currently supports are the t -test statistic, the Wilcoxon, Pearson, the Spearman and the Jonckheere-Terpstra (JT) test statistics.

2 Adjusting for Multiple Comparisons

In addition to computing individual test statistics and scores, the package also computes raw permutation p-values, false discovery (FDR) adjusted p-values, Bonferroni corrected p-values, as well as family wise error (FWER) adjusted two sided permutation p-values.

3 Data Format

The R package `permPATH` assumes that the gene expression data is in the form of a $K \times n$ matrix, where K is the number of genes and n is the number of samples. The row names of the data frame should be the gene symbols. The phenotype data should be in the form of a vector of length n . The user also needs to provide a list of pre-defined pathways with each list element containing the gene symbols associated with the pathway. The name of each list element should be the pathway name.

4 Input Parameters

The code requires that the user also specifies the type of local test statistic for each gene, the global test statistic used to compute the score and the number of random permutations. The user can specify the minimum number of genes that a pathway should contain, thus filtering out pathways with smaller number of genes. Likewise, the user can specify the maximum number of genes that a pathway should contain, thus filtering out pathways with

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larger number of genes. In case of missing values, the user can specify a value that can be imputed in the gene expression data. The package also allows for the user to specify a transformation to be applied to the gene expression data prior to the analysis.

5 Output

The output of `permPATH` is in the form of a list with the following elements:

- **res:** Data frame consisting of the pathway names (Pathway), the genes involved in each pathway (Genes), the number of genes in each pathway (Size), the score for each pathway (Score), the permutation raw p-value (pval), the FWER-adjusted permutation p-value (pfwer), the FDR-adjusted permutation p-value, the Bonferroni-adjusted permutation p-value (bonferroni). If specified by the user, annotation (anno) for each pathway.
- **stats:** The individual test statistic for each gene.
- **scores:** A matrix of scores. The matrix is of dimension $(B+1) \times M$, where M is the number of pathways. The first column contains the unpermuted scores, the remaining B columns contain the scores computed after each permutation.

The results can be sorted according to decreasing order of absolute score values or according to increasing order of raw p-values. This can be specified by the user.

6 Examples

6.1 Synthetic Data

In this section we demonstrate the use of `permPATH` on synthetically generated data.

```
# Generate toy phenotype and gene expression data sets
# This example consists of 40 genes grouped into 5 pathways and 100 patients
# grp is a binary trait (e.g., case vs control)
# bp is a continuous trait (e.g., blood pressure)
set.seed(1234)
library(permPATH)

## Loading required package: R2HTML
## Loading required package: xtable

n = 100
K = 40
grp = rep(1:0, each=n/2)
bp = rnorm(n)
g = rep(1:(n/20), rep(20, n/20))

pdat = data.frame(grp, bp, g)
rm(grp, bp)
expdat = matrix(rnorm(K*n), K, n)

## Assign marker names g1,...,gK to the expression data set and
## patient ids id1,...,idn to the expression and phenotype data
gnames = paste("g", 1:K, sep="")
rownames(expdat) = gnames
patid = paste("id", 1:n, sep="")
rownames(pdat) = patid
colnames(expdat) = patid

# Group the K genes into M pathways of sizes n1,...,nM
M = 5
p = runif(M)
p = p/sum(p)
nM = rmultinom(1, size=K, prob=p)
gset = lapply(nM, function(x){gnames[sample(x)]})
names(gset) = paste("pathway", 1:M, sep="")
names(gset)
```

```
## [1] "pathway1" "pathway2" "pathway3" "pathway4" "pathway5"

# Carry out permutation analysis with grp as the outcome
# using the two-sample Wilcoxon test with B=100 random permutations.
# The score is the maxmean test statistic
res = perm.path(expdat, y=pdcat[["grp"]], local.test="wilcoxon",
                global.test="maxmean", B=100, gset=gset, min.num=2,
                max.num=50, sort="score")

# Output results for top pathways
head(res[["res"]])

##          Pathway          Genes Size      Score pval
## pathway4 pathway4          g2;g1      2 -0.9754755 0.43
## pathway1 pathway1 g5;g3;g8;g4;g10;g6;g1;g9;g2;g7;g11 11 -0.8134707 0.68
## pathway2 pathway2 g3;g9;g10;g2;g7;g6;g8;g5;g4;g11;g1 11 -0.8134707 0.68
## pathway3 pathway3          g7;g1;g6;g5;g3;g6;g4;g2      8 -0.6783519 0.85
## pathway5 pathway5          g6;g5;g4;g8;g2;g3;g1;g7      8 -0.6783519 0.85
##          pwrer  fdr bonferroni
## pathway4  0.65 0.85          1
## pathway1  0.83 0.85          1
## pathway2  0.83 0.85          1
## pathway3  0.95 0.85          1
## pathway5  0.95 0.85          1

# Output individual test statistics
res[["stats"]]

##          g5          g3          g8          g4          g10          g6
## 0.28264661 -1.12369264 0.08961966 -0.30332807 1.06854208 -0.01378764
##          g1          g9          g2          g7          g11
## -0.42741683 -1.46838363 -1.52353419 1.17884320 -0.83415220

# Carry out permutation analysis with bp as the outcome
# using the Spearman test with B=100 random permutations.
# The score is the maxmean test statistic
res = perm.path(expdat, y=pdcat[["bp"]], local.test="spearman",
                global.test="maxmean", B=100, gset=gset, min.num=2,
                max.num=50, sort="score")

# Output results for top pathways
head(res[["res"]])

##          Pathway          Genes Size      Score pval
## pathway3 pathway3          g7;g1;g8;g5;g3;g6;g4;g2      8 -0.09945395 0.42
## pathway5 pathway5          g6;g5;g4;g8;g2;g3;g1;g7      8 -0.09945395 0.42
## pathway1 pathway1 g5;g3;g8;g4;g10;g6;g1;g9;g2;g7;g11 11 -0.07216322 0.78
## pathway2 pathway2 g3;g9;g10;g2;g7;g6;g8;g5;g4;g11;g1 11 -0.07216322 0.78
## pathway4 pathway4          g2;g1      2 0.02052205 0.97
##          pwrer  fdr bonferroni
## pathway3  0.62 0.97          1
## pathway5  0.62 0.97          1
## pathway1  0.84 0.97          1
## pathway2  0.84 0.97          1
## pathway4  1.00 0.97          1

# Output individual test statistics
res[["stats"]]

##          g5          g3          g8          g4          g10          g6
## 0.10024602 0.02095410 0.06522652 -0.09945395 0.02682268 0.03545155
##          g1          g9          g2          g7          g11
## 0.02653465 -0.04487249 0.01450945 0.06544254 0.11585959

# Carry out permutation analysis with g as the outcome
# using the JT test with B=100 random permutations.
# The score is the maxmean test statistic
res = perm.path(expdat, y=pdcat[["g"]], local.test="jt",
                global.test="maxmean", B=100, gset=gset, min.num=2,
                max.num=50, sort="score")

# Output results for top pathways
head(res[["res"]])

##          Pathway          Genes Size      Score pval
## pathway1 pathway1 g5;g3;g8;g4;g10;g6;g1;g9;g2;g7;g11 11 0.6674101 0.87
## pathway2 pathway2 g3;g9;g10;g2;g7;g6;g8;g5;g4;g11;g1 11 0.6674101 0.87
## pathway4 pathway4          g2;g1      2 0.5416368 0.73
## pathway3 pathway3          g7;g1;g8;g5;g3;g6;g4;g2      8 0.4944718 0.98
## pathway5 pathway5          g6;g5;g4;g8;g2;g3;g1;g7      8 0.4944718 0.98
##          pwrer  fdr bonferroni
## pathway1  0.95 0.98          1
## pathway2  0.95 0.98          1
## pathway4  0.99 0.98          1
## pathway3  1.00 0.98          1
## pathway5  1.00 0.98          1
```

```
# Output individual test statistics
res[["stats"]]
```

```
##           g5           g3           g8           g4           g10           g6
## 0.45643546 0.43817805 -0.31037612 -0.27386128 -0.06694387 -0.39557740
##           g1           g9           g2           g7           g11
## 0.76681158 1.51536574 0.31646192 -0.35297676 0.51120772
```

6.2 Incorporating Annotation

This subsection describes the use of `permPATH` with real gene symbols that can be mapped to a gene pathway data base supported by Broad Institute. The user can also create pathways on the bases of files from the Molecular Signatures Database[2].

```
# Generate gene symbols
set.seed(1234)
library(permPATH)

gnames = c("CCL13", "CCL19", "CCL2", "CCL3", "CCL3L1", "CCL4",
           "CCL5", "CCL7", "CCL8", "CCR1", "CCR2", "CCR3", "CCR5",
           "CD14", "CD180", "CD2", "CD209", "CD40", "CD44", "CD80",
           "CD86", "CD8A", "CDC42", "CEBPA", "CSF2", "CXCL1", "CXCL10",
           "CXCR4", "EIF2AK2", "ELK1", "ERBB2", "FCAR", "HLAA",
           "HLADQA1", "HLADQB1", "HSPA1A", "IFIT3", "IFNA1", "IFNB1",
           "IFNG", "IL10", "IL12A", "IL12B", "IL16", "IL1A", "IL1B",
           "IL2", "IL6", "IL8", "INHBA", "IRF1", "IRF3", "ITGAM",
           "LTA", "LYN", "MAP3K7", "MAP4K4", "MAPK8", "MAPK8IP3",
           "MYD88", "NFKB1", "NFKBIA", "NFKBIL1", "NFRKB", "PELI1",
           "PTGS2", "REL", "RELA", "RIPK2", "SARM1", "STK4", "TAP2",
           "TGFB1", "TIRAP", "TLR1", "TLR10", "TLR2", "TLR3", "TLR4",
           "TLR5", "TLR6", "TLR7", "TLR8", "TLR9", "TNF", "UBE2N", "B2M",
           "RPL13A", "ACTB", "HGDC", "RTC1", "RTC2", "RTC3", "PPC1", "PPC2", "PPC3")

# extract pathways available at "http://software.broadinstitute.org/gsea/resources/msigdb/4.0/c2.cp.reactome.v4.0.symbols.gmt"
xx = readLines("c2.cp.reactome.v4.0.symbols.gmt")
pnames = as.character(sapply(xx, function(x){unlist(strsplit(x, "\t", fixed=TRUE))[1]}))
anno = as.character(sapply(xx, function(x){unlist(strsplit(x, "\t", fixed=TRUE))[2]}))
gset = lapply(xx, function(x){unlist(strsplit(x, "\t", fixed=TRUE))[-c(1,2)]})
names(gset) = pnames
gset = list(gset, pnames, anno)

#intersect gene nsymbols with gene symbols from pathways
ind = unlist(lapply(gset[[1]], function(x){ifelse(length(intersect(x,gnames))>1, TRUE, FALSE)}))
gset[[1]] = gset[[1]][ind]
gset[[2]] = gset[[2]][ind]
gset[[3]] = gset[[3]][ind]
gset[[1]] = lapply(gset[[1]], function(x){intersect(x, gnames)})
names(gset[[1]]) = gset[[2]]
names(gset[[3]]) = gset[[2]]

#create gene expression data
n = 220
K = length(gnames)
expdat = matrix(abs(rnorm(K*n)), K, n)
rownames(expdat) = gnames
patid = paste("id",1:n,sep="")
colnames(expdat) = patid

grp = rep(1:0,each=n/2)
bp = abs(rnorm(n))
g = rep(1:(n/20), rep(20,n/20))

pdat = data.frame(grp, bp, g)
rm(grp, bp)

# Carry out permutation analysis with grp as the outcome
# using the two-sample Wilcoxon test with B=10000 random permutations.
# The score is the maxmean test statistic
res = perm.path(expdat, y=pdat[["grp"]], local.test="wilcoxon",
               global.test="maxmean", B=10^4, gset=gset[[1]], min.num=2,
               max.num=50, sort="score", anno=gset[[3]])

# Output results for top pathways
head(res[["res"]])

##                                     Pathway
## REACTOME_DEFENSINS                 REACTOME_DEFENSINS
## REACTOME_BETA_DEFENSINS            REACTOME_BETA_DEFENSINS
## REACTOME_DIABETES_PATHWAYS         REACTOME_DIABETES_PATHWAYS
## REACTOME_PERK_REGULATED_GENE_EXPRESSION REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE REACTOME_UNFOLDED_PROTEIN_RESPONSE
##                                     Genes Size      Score
## REACTOME_DEFENSINS                 CCR2;TLR1;TLR2      3 -1.806970
```

```

## REACTOME_BETA_DEFENSINS          CCR2;TLR1;TLR2      3 -1.806970
## REACTOME_DIABETES_PATHWAYS        IL8;CCL2         2 -1.652329
## REACTOME_PERK_REGULATED_GENE_EXPRESSION IL8;CCL2      2 -1.652329
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 IL8;CCL2      2 -1.652329
## REACTOME_UNFOLDED_PROTEIN_RESPONSE IL8;CCL2      2 -1.652329
##
##          pval pfwer  fdr bonferroni
## REACTOME_DEFENSINS                0.082 0.834 0.73      1
## REACTOME_BETA_DEFENSINS            0.082 0.834 0.73      1
## REACTOME_DIABETES_PATHWAYS        0.109 0.932 0.73      1
## REACTOME_PERK_REGULATED_GENE_EXPRESSION 0.109 0.932 0.73      1
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 0.109 0.932 0.73      1
## REACTOME_UNFOLDED_PROTEIN_RESPONSE 0.109 0.932 0.73      1
##
## REACTOME_DEFENSINS                http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_DEFENSINS
## REACTOME_BETA_DEFENSINS            http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_BETA_DEFENSINS
## REACTOME_DIABETES_PATHWAYS        http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_DIABETES_PATHWAYS
## REACTOME_PERK_REGULATED_GENE_EXPRESSION http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_UNFOLDED_PROTEIN_RESPONSE

# Carry out permutation analysis with bp as the outcome
# using the Spearman test with B=10000 random permutations.
# The score is the maxmean test statistic
res = perm.path(expdat, y=mdat[["grp"]], local.test="spearman",
                global.test="maxmean", B=10^4, gset=gset[[1]], min.num=2,
                max.num=50, sort="score", anno=gset[[3]])

# Output results for top pathways
head(res[["res"]])

##
## REACTOME_DEFENSINS                REACTOME_DEFENSINS
## REACTOME_BETA_DEFENSINS            REACTOME_BETA_DEFENSINS
## REACTOME_DIABETES_PATHWAYS        REACTOME_DIABETES_PATHWAYS
## REACTOME_PERK_REGULATED_GENE_EXPRESSION REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE REACTOME_UNFOLDED_PROTEIN_RESPONSE
##
##          Genes Size      Score
## REACTOME_DEFENSINS                CCR2;TLR1;TLR2      3 -0.1221037
## REACTOME_BETA_DEFENSINS            CCR2;TLR1;TLR2      3 -0.1221037
## REACTOME_DIABETES_PATHWAYS        IL8;CCL2         2 -0.1116540
## REACTOME_PERK_REGULATED_GENE_EXPRESSION IL8;CCL2      2 -0.1116540
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 IL8;CCL2      2 -0.1116540
## REACTOME_UNFOLDED_PROTEIN_RESPONSE IL8;CCL2      2 -0.1116540
##
##          pval pfwer  fdr bonferroni
## REACTOME_DEFENSINS                0.072 0.825 0.689      1
## REACTOME_BETA_DEFENSINS            0.072 0.825 0.689      1
## REACTOME_DIABETES_PATHWAYS        0.107 0.927 0.689      1
## REACTOME_PERK_REGULATED_GENE_EXPRESSION 0.107 0.927 0.689      1
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 0.107 0.927 0.689      1
## REACTOME_UNFOLDED_PROTEIN_RESPONSE 0.107 0.927 0.689      1
##
## REACTOME_DEFENSINS                http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_DEFENSINS
## REACTOME_BETA_DEFENSINS            http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_BETA_DEFENSINS
## REACTOME_DIABETES_PATHWAYS        http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_DIABETES_PATHWAYS
## REACTOME_PERK_REGULATED_GENE_EXPRESSION http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_UNFOLDED_PROTEIN_RESPONSE

# Carry out permutation analysis with grp as the outcome
# using the two-sample Wilcoxon test with B=10000 random permutations.
# The score is the maxmean test statistic
res = perm.path(expdat, y=mdat[["grp"]], local.test="wilcoxon",
                global.test="maxmean", B=10^4, gset=gset[[1]], min.num=2,
                max.num=50, sort="score", anno=gset[[3]])

# Output results for top pathways
head(res[["res"]])

##
## REACTOME_DEFENSINS                REACTOME_DEFENSINS
## REACTOME_BETA_DEFENSINS            REACTOME_BETA_DEFENSINS
## REACTOME_DIABETES_PATHWAYS        REACTOME_DIABETES_PATHWAYS
## REACTOME_PERK_REGULATED_GENE_EXPRESSION REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE REACTOME_UNFOLDED_PROTEIN_RESPONSE
##
##          Genes Size      Score
## REACTOME_DEFENSINS                CCR2;TLR1;TLR2      3 -1.806970
## REACTOME_BETA_DEFENSINS            CCR2;TLR1;TLR2      3 -1.806970
## REACTOME_DIABETES_PATHWAYS        IL8;CCL2         2 -1.652329
## REACTOME_PERK_REGULATED_GENE_EXPRESSION IL8;CCL2      2 -1.652329
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 IL8;CCL2      2 -1.652329
## REACTOME_UNFOLDED_PROTEIN_RESPONSE IL8;CCL2      2 -1.652329
##
##          pval pfwer  fdr bonferroni
## REACTOME_DEFENSINS                0.074 0.83 0.726      1
## REACTOME_BETA_DEFENSINS            0.074 0.83 0.726      1
## REACTOME_DIABETES_PATHWAYS        0.106 0.93 0.726      1
## REACTOME_PERK_REGULATED_GENE_EXPRESSION 0.106 0.93 0.726      1
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4 0.106 0.93 0.726      1

```

```
## REACTOME_UNFOLDED_PROTEIN_RESPONSE      0.106  0.93 0.726      1
##
## REACTOME_DEFENSINS                      http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_DEFENSINS
## REACTOME_BETA_DEFENSINS                 http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_BETA_DEFENSINS
## REACTOME_DIABETES_PATHWAYS              http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_DIABETES_PATHWAYS
## REACTOME_PERK_REGULATED_GENE_EXPRESSION http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4     http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE      http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_UNFOLDED_PROTEIN_RESPONSE

# Carry out permutation analysis with g as the outcome
# using the JT test with B=10000 random permutations.
# The score is the maxmean test statistic
res = perm.path(expdat, y=mdat[["g"]], local.test="jt",
               global.test="maxmean", B=10^4, gset=gset[[1]], min.num=2,
               max.num=50, sort="score", anno=gset[[3]])

# Output results for top pathways
head(res[["res"]])

##
## REACTOME_DIABETES_PATHWAYS              REACTOME_DIABETES_PATHWAYS
## REACTOME_PERK_REGULATED_GENE_EXPRESSION REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4     REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE        REACTOME_UNFOLDED_PROTEIN_RESPONSE
## REACTOME_IL_RECEPTOR_SHC_SIGNALING       REACTOME_IL_RECEPTOR_SHC_SIGNALING
## REACTOME_IL_2_SIGNALING                   REACTOME_IL_2_SIGNALING
##
## REACTOME_DIABETES_PATHWAYS              Genes Size      Score  pval  pfwer
## REACTOME_PERK_REGULATED_GENE_EXPRESSION IL8;CCL2      2 1.671291 0.104 0.917
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4     IL8;CCL2      2 1.671291 0.104 0.917
## REACTOME_UNFOLDED_PROTEIN_RESPONSE        IL8;CCL2      2 1.671291 0.104 0.917
## REACTOME_IL_RECEPTOR_SHC_SIGNALING       CSF2;IL2      2 1.599507 0.119 0.950
## REACTOME_IL_2_SIGNALING                   CSF2;IL2      2 1.599507 0.119 0.950
##
## REACTOME_DIABETES_PATHWAYS              fdr  bonferroni
## REACTOME_PERK_REGULATED_GENE_EXPRESSION 0.521      1
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4     0.521      1
## REACTOME_UNFOLDED_PROTEIN_RESPONSE        0.521      1
## REACTOME_IL_RECEPTOR_SHC_SIGNALING       0.521      1
## REACTOME_IL_2_SIGNALING                   0.521      1
##
## REACTOME_DIABETES_PATHWAYS              anno
## REACTOME_PERK_REGULATED_GENE_EXPRESSION http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_PERK_REGULATED_GENE_EXPRESSION
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4     http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_ACTIVATION_OF_GENES_BY_ATF4
## REACTOME_UNFOLDED_PROTEIN_RESPONSE        http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_UNFOLDED_PROTEIN_RESPONSE
## REACTOME_IL_RECEPTOR_SHC_SIGNALING       http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_IL_RECEPTOR_SHC_SIGNALING
## REACTOME_IL_2_SIGNALING                   http://www.broadinstitute.org/gsea/msigdb/cards/REACTOME_IL_2_SIGNALING
```

7 Exporting Results to HTML File

The user has the option to export the results of `permPATH` to an HTML file via the function `permPATH2HTML`. This option is useful when pathways have large number of genes and allows for improved readability of the results.

```
library(permPATH)
set.seed(1234)
n = 100
K = 40
grp = rep(1:0, each=n/2)
bp = rnorm(n)

pdat = data.frame(grp, bp)
rm(grp, bp)
expdat = matrix(rnorm(K*n), K, n)

## Assign marker names g1,...,gK to the expression data set and
## patient ids id1,...,idn to the expression and phenotype data
gnames = paste("g", 1:K, sep="")
rownames(expdat) = gnames
patid = paste("id", 1:n, sep="")
rownames(pdat) = patid
colnames(expdat) = patid

#Group the K genes into M pathways of sizes n1,...,nM
M = 5
p = runif(M)
p = p/sum(p)
nM = rmultinom(1, size=K, prob=p)
gset = lapply(nM, function(x){gnames[sample(x)]})
names(gset) = paste("pathway", 1:M, sep="")
```

```
## Carry out permutation analysis with grp as the outcome
## using the two-sample Wilcoxon with B=100 random permutations
res = perm.path(expdat, y=mdat[["grp"]], local.test="wilcoxon", global.test="maxmean", B=100, gset=gset,
  min.num=2, max.num=50, sort="score")

# create an html file
#permPATH2HTML(rstab, dir="/dir/", fname="tophits")

sessionInfo()

## R version 3.3.1 (2016-06-21)
## Platform: i686-pc-linux-gnu (32-bit)
## Running under: Ubuntu 16.04.1 LTS
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] permPATH_1.0 xtable_1.8-2 R2HTML_2.3.2
##
## loaded via a namespace (and not attached):
## [1] magrittr_1.5 formatR_1.4  tools_3.3.1 stringi_1.1.1 highr_0.6
## [6] knitr_1.13  stringr_1.0.0 evaluate_0.9
```

8 Acknowledgement

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