

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=mdat[["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 pfwer
## pathway4 pathway4          g1;g2         2 -0.9754755 0.43 0.70
## pathway1 pathway1 g6;g11;g3;g9;g8;g7;g2;g5;g1;g10;g4 11 -0.8134707 0.73 0.83
## pathway2 pathway2 g6;g3;g10;g8;g7;g11;g2;g4;g1;g9;g5 11 -0.8134707 0.73 0.83
## pathway3 pathway3          g8;g2;g4;g7;g1;g6;g3;g5     8 -0.6783519 0.80 0.92
## pathway5 pathway5          g8;g7;g4;g3;g1;g2;g5;g6     8 -0.6783519 0.80 0.92
##          fdr bonferroni
## pathway4 0.8          1
## pathway1 0.8          1
## pathway2 0.8          1
## pathway3 0.8          1
## pathway5 0.8          1

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

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

# 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=mdat[["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          g8;g2;g4;g7;g1;g6;g3;g5     8 -0.09945395 0.46
## pathway5 pathway5          g8;g7;g4;g3;g1;g2;g5;g6     8 -0.09945395 0.46
## pathway1 pathway1 g6;g11;g3;g9;g8;g7;g2;g5;g1;g10;g4 11 -0.07216322 0.81
## pathway2 pathway2 g6;g3;g10;g8;g7;g11;g2;g4;g1;g9;g5 11 -0.07216322 0.81
## pathway4 pathway4          g1;g2         2 0.02052205 1.00
##          pfwr fdr bonferroni
## pathway3 0.63 1          1
## pathway5 0.63 1          1
## pathway1 0.93 1          1
## pathway2 0.93 1          1
## pathway4 1.00 1          1

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

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

# 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=mdat[["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 pfwer
## pathway1 pathway1 g6;g11;g3;g9;g8;g7;g2;g5;g1;g10;g4 11 0.6674101 0.89 0.96
## pathway2 pathway2 g6;g3;g10;g8;g7;g11;g2;g4;g1;g9;g5 11 0.6674101 0.89 0.96
## pathway4 pathway4          g1;g2         2 0.5416368 0.75 0.99
## pathway3 pathway3          g8;g2;g4;g7;g1;g6;g3;g5     8 0.4944718 0.96 1.00
## pathway5 pathway5          g8;g7;g4;g3;g1;g2;g5;g6     8 0.4944718 0.96 1.00
##          fdr bonferroni
## pathway1 0.96          1
## pathway2 0.96          1
## pathway4 0.96          1
## pathway3 0.96          1
## pathway5 0.96          1

```

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

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

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", "HGD", "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          pval
## REACTOME_DEFENSINS          CCR2;TLR1;TLR2          3          -1.806970          0.082
```

```

## REACTOME_BETA_DEFENSINS          CCR2;TLR1;TLR2    3 -1.806970 0.082
## REACTOME_DIABETES_PATHWAYS      IL8;CCL2        2 -1.652329 0.109
## REACTOME_PERK_REGULATED_GENE_EXPRESSION  IL8;CCL2        2 -1.652329 0.109
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4  IL8;CCL2        2 -1.652329 0.109
## REACTOME_UNFOLDED_PROTEIN_RESPONSE  IL8;CCL2        2 -1.652329 0.109
##
##                                pfwere  fdr  bonferroni
## REACTOME_DEFENSINS              0.834 0.73    1
## REACTOME_BETA_DEFENSINS         0.834 0.73    1
## REACTOME_DIABETES_PATHWAYS     0.931 0.73    1
## REACTOME_PERK_REGULATED_GENE_EXPRESSION  0.931 0.73    1
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4  0.931 0.73    1
## REACTOME_UNFOLDED_PROTEIN_RESPONSE  0.931 0.73    1
##
##                                anno
## 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"]])

##                                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  pval
## REACTOME_DEFENSINS              CCR2;TLR1;TLR2    3 -0.1221037 0.072
## REACTOME_BETA_DEFENSINS         CCR2;TLR1;TLR2    3 -0.1221037 0.072
## REACTOME_DIABETES_PATHWAYS     IL8;CCL2        2 -0.1116540 0.107
## REACTOME_PERK_REGULATED_GENE_EXPRESSION  IL8;CCL2        2 -0.1116540 0.107
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4  IL8;CCL2        2 -0.1116540 0.107
## REACTOME_UNFOLDED_PROTEIN_RESPONSE  IL8;CCL2        2 -0.1116540 0.107
##                                pfwere  fdr  bonferroni
## REACTOME_DEFENSINS              0.825 0.689    1
## REACTOME_BETA_DEFENSINS         0.825 0.689    1
## REACTOME_DIABETES_PATHWAYS     0.927 0.689    1
## REACTOME_PERK_REGULATED_GENE_EXPRESSION  0.927 0.689    1
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4  0.927 0.689    1
## REACTOME_UNFOLDED_PROTEIN_RESPONSE  0.927 0.689    1
##
##                                anno
## 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"]])

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

```

```

## REACTOME_UNFOLDED_PROTEIN_RESPONSE      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"]])

##
##
## Pathway
## 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
##
## Genes Size Score pval pfwer
## REACTOME_DIABETES_PATHWAYS              IL8;CCL2 2 1.671291 0.104 0.917
## 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
##
## fdr bonferroni
## REACTOME_DIABETES_PATHWAYS              0.523      1
## REACTOME_PERK_REGULATED_GENE_EXPRESSION 0.523      1
## REACTOME_ACTIVATION_OF_GENES_BY_ATF4    0.523      1
## REACTOME_UNFOLDED_PROTEIN_RESPONSE      0.523      1
## REACTOME_IL_RECEPTOR_SHC_SIGNALING     0.523      1
## REACTOME_IL_2_SIGNALING                 0.523      1
##
##
## anno
## 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
## 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 4.4.1 (2024-06-14)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 24.04.1 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-r0.3.26.so; LAPACK version 3.12.0
##
## 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
##
## time zone: Etc/UTC
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats graphics grDevices utils datasets methods base
##
## other attached packages:
## [1] permPATH_1.3 xtable_1.8-4 R2HTML_2.3.4
##
## loaded via a namespace (and not attached):
## [1] compiler_4.4.1 tools_4.4.1 maketools_1.3.0 buildtools_1.0.0
## [5] highr_0.11 knitr_1.48 xfun_0.47 sys_3.4.2
## [9] evaluate_0.24.0

```

8 Acknowledgement

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References

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- [2] A. Subramanian, P. Tamayo, V. K. Mootha, S. Mukherjee, B. L. Ebert, M. A. Gillette, A. Paulovich, S. L. Pomeroy, T. R. Golub, E. S. Lander, and J. P. Mesirov. Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. *Proc. Natl. Acad. Sci. USA*, 102(43):15545–15550, 2005.