Package ‘MetaPath’

October 3, 2015

Type Package

Title Perform the Meta-Analysis for Pathway Enrichment Analysis (MAPE)

Version 1.0

Date 2015-09-28

Author Kui Shen and Geroge Tseng

Maintainer Kui Shen <kuishen@alumni.pitt.edu>

Depends R (>= 3.0.0), Biobase, GSEABase, genefilter, impute

Description Perform the Meta-analysis for Pathway Enrichment (MAPE) methods introduced by Shen and Tseng (2010). It includes functions to automatically perform MAPE_G (integrating multiple studies at gene level), MAPE_P (integrating multiple studies at pathway level) and MAPE_I (a hybrid method integrating MAEP_G and MAPE_P methods). In the simulation and real data analyses in the paper, MAPE_G and MAPE_P have complementary advantages and detection power depending on the data structure. In general, the integrative form of MAPE_I is recommended to use. In the case that MAPE_G (or MAPE_P) detects almost none pathway, the integrative MAPE_I does not improve performance and MAPE_P (or MAPE_G) should be used. Reference: Shen, Kui, and George C Tseng. Meta-analysis for pathway enrichment analysis when combining multiple microarray studies. Bioinformatics (Oxford, England) 26, no. 10 (April 2010): 1316-1323. doi:10.1093/bioinformatics/btq148. http://www.ncbi.nlm.nih.gov/pubmed/20410053.

License GPL (>= 2.0)

LazyLoad yes

NeedsCompilation no

Repository CRAN

Date/Publication 2015-10-03 07:57:54
R topics documented:

- MetaPath-package .......................................................... 2
- cor.func ................................................................. 3
- cox.perm.sample ...................................................... 3
- coxfunc ................................................................. 3
- coxscor ................................................................. 4
- coxstuff ................................................................. 4
- coxvar ................................................................. 4
- Enrichment_KS_gene .................................................... 5
- Enrichment_KS_sample .................................................. 5
- F.perm.sample ........................................................... 5
- MAPE ................................................................. 5
- MAPE_G_gene_KS ........................................................ 7
- MAPE_G_sample_KS ................................................... 7
- MAPE_I_KS ............................................................. 7
- MAPE_P_gene_KS ........................................................ 8
- MAPE_P_sample_KS .................................................... 8
- MAQC ................................................................. 8
- pathway.DB ............................................................ 8
- plotMAPE .............................................................. 9
- pqvalues.compute ..................................................... 9
- reg.perm.sample ...................................................... 10
- Tperm.sample ........................................................ 10

Index

MetaPath-package  Perform the Meta-Analysis for Pathway Enrichment (MAPE) analysis by combining multiple genomic studies

Description

Description: This R package was implemented to perform the Meta-analysis for Pathway Enrichment (MAPE) methods introduced by Shen and Tseng (2010). It includes functions to automatically perform MAPE_G (integrating multiple studies at gene level), MAPE_P (integrating multiple studies at pathway level) and MAPE_I (a hybrid method integrating MAEP_G and MAPE_P methods). In the simulation and real data analyses in the paper, MAPE_G and MAPE_P have complementary advantages and detection power depending on the data structure. In general, the integrative form of MAPE_I is recommended to use. In the case that MAPE_G (or MAPE_P) detects almost none pathway, the integrative MAPE_I does not improve performance and MAPE_P (or MAPE_G) should be used.

References

<table>
<thead>
<tr>
<th>cor.func</th>
<th><em>internal functions from Dr. Tibshirani’s software package GSA</em></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Description</strong></td>
<td>internal functions from Dr. Tibshirani’s software package GSA</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>cox.perm.sample</th>
<th><em>internal functions from Dr. Tibshirani’s software package GSA</em></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Description</strong></td>
<td>internal functions from Dr. Tibshirani’s software package GSA</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>cox.func</th>
<th><em>internal functions from Dr. Tibshirani’s software package GSA</em></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Description</strong></td>
<td>internal functions from Dr. Tibshirani’s software package GSA</td>
</tr>
</tbody>
</table>
**Description**

internal functions from Dr. Tibshirani’s software package GSA

**References**

Description

Enrichment_KS_gene

internal functions

Description

Enrichment_KS_sample

internal functions

Description

F.perm.sample

internal functions

Description

Perform the Meta-Analysis for Pathway Enrichment (MAPE) analysis.

MAPE

Usage

MAPE(arraydata,pathway,DB,resp.type=c('twoclass','multiclass','continuous','survival'), stat=c('maxP','minP','rth','Fisher'),rth.value=NULL, permutation=c('sample','gene'), nperm=500,size.min=15,size.max=500,knn.neighbors=10,qvalue.cal=c('permute','estimate'))
Arguments

arraydata

The arraydata is a list of microarray data sets. Each microarray data set can be either an ExpressionSet or a list. If the microarray data set is a list, then it includes five elements as follows: 1) x–exprs data 2) y– the phenotype of interests 3) z– censoring.status if applicable. 1 stands for the event occurred and 0 stands for censored. 4) geneid 5) samplename If the microarray data set is in an ExpressionSet format, the users need to 1) store the phenotype of interests in the slot 'label'. 2) store the censor data is the slot 'censoring.status' if applicable.

pathway.DB

The pathway database in a GeneSetCollection format defined by GSEABase. The pathway database can be downloaded from Broad institute (http://www.broadinstitute.org/gsea). PLEASE use the function 'getGmt' provided in the GSEABase package to load the pathway database.

resp.type

The phenotype of interest. It is one of the four values: 'twoclass', 'multiclass', 'continuous', 'survival'.

stat

The meta-analysis statistic to be used to combine two studies. It is one of the four values: 'minP', 'maxP', 'rth', 'Fisher'.

rth.value

The value of the rth statistic if the meta-analysis statistic is 'rth'. For example, rth.value=0.6.

permutation

The options for using sample permutation or gene permutation when performing enrichment analysis. It is one of the two values: 'gene' and 'sample'. The default option is sample permutation.

nperm

Number of permutations to be performed.

size.min

The minimum size of pathways to be considered. The default value is 15.

size.max

The maximum size of pathways to be considered. The default value is 500.

knn.neighbors

Number of neighbors to be used in the knn imputation method (default=10)

qvalue.cal

The method to calculate the q-values. The default method is to calculate the q-values based on the permutation method. If qvalue.cal='estimate', the q-values were estimated based on the Storey's method.

Value

The qvalue and pvalue of each pathway.

Author(s)

Kui Shen and George C Tseng.

References

Examples

```r
## Not run:
library(MetaPath)
data(MAQC)
data(pathway.DB)
## Supposed we are interested in the ER related pathways, we first store the ER
## information in the slot 'label'. Then perform MAPE on this data set.
MAQC[[1]]$label=MAQC[[1]]$ER_status
MAQC[[2]]$label=MAQC[[2]]$ER_status
nperm=10 ## nperm was set to 10 to save the computational time. The default value is 500.
MAPE.sample.obj=MAPE(arraydata=MAQC,pathway.DB=pathway.DB,resp.type="twoclasse",stat='maxP',
rth.value=NULL,nperm=nperm,permutation='gene',size.min=15,size.max=500)
cutoff=.1
subset(MAPE.sample.obj$qvalue,MAPE.I<=cutoff)
plotMAPE(MAPE.sample.obj,cutoff,MAPE.method='MAPE.I')
```

## End(Not run)

---

**MAPE_G_gene_KS**

internal functions

**Description**

internal functions

---

**MAPE_G_sample_KS**

internal functions

**Description**

internal functions

---

**MAPE_I_KS**

internal functions

**Description**

internal functions
MAPE_P_gene_KS  

**Description**

internal functions

MAPE_P_sample_KS  

**Description**

internal functions

MAQC  

**The data sets from MAQC project.**

**Description**

This is the microarray data sets from MAQC project.

**References**


**Examples**

data(MAQC)

pathway.DB  

**An example of pathway database.**

**Description**

This data set is an example of gene set database in a GeneSetCollection format defined by GSEABase. This database is the C2 collection of Molecular Signatures Database provided by Broad institute(http://www.broadinstitute.org/gsea).

**Usage**

data(pathway.DB)
**plotMAPE**

*Plot MAPE outcomes*

---

**Description**

This function will plot two figures. The first figure is the Venn diagram to show the overlapped enriched pathways identified by MAPE_G, MAPE_P and MAPE_I. The second figure is the heatmap of the q-values of enriched pathways.

**Usage**

```r
plotMAPE(mapeNobjL, cutoffL, MAPE.method = c("MAPE_I", "MAPE_P", "MAPE_G"))
```

**Arguments**

- `mapeNobj` The output of MAPE.
- `cutoff` The q-value cutoff.
- `MAPE.method` The MAPE method of interest.

**Value**

A heatmap of q-values of enriched pathways will be plotted. When plot the heatmap, if the MAPE.method is MAPE_I, it will plot the q-values of enriched pathways for each individual study and q-values computed by three MAPE methods. if the MAPE.method is MAPE_P, it will plot the q-values of enriched pathways for each individual study and q-values computed by the MAPE_P method. if the MAPE.method is MAPE_G, it will plot the q-values of enriched pathways for each individual study and q-values computed by the MAPE_G method.

**Examples**

```r
## Not run:
plot.MAPE(MAPE.obj, cutoff=0.05, MAPE.method = "MAPE_I")

## End(Not run)
```

---

**pqvalues.compute**

*internal functions*

---

**Description**

internal functions
<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>reg.perm.sample</code></td>
<td>internal functions</td>
</tr>
<tr>
<td><code>Tperm.sample</code></td>
<td>internal functions</td>
</tr>
</tbody>
</table>
Index

*Topic datasets
  MAQC, 8

  cor.func, 3
  cox.perm.sample, 3
  coxfunc, 3
  coxscor, 4
  coxstuff, 4
  coxvar, 4

  Enrichment_KS_gene, 5
  Enrichment_KS_sample, 5

  F.perm.sample, 5

  MAPE, 5
  MAPE_G_gene_KS, 7
  MAPE_G_sample_KS, 7
  MAPE_I_KS, 7
  MAPE_P_gene_KS, 8
  MAPE_P_sample_KS, 8
  MAQC, 8
  MetaPath (MetaPath-package), 2
  MetaPath-package, 2

  pathway.DB, 8
  plotMAPE, 9
  pqvalues.compute, 9

  reg.perm.sample, 10

  Tperm.sample, 10