Package ‘gageData’

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Type Package

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Description This is a supportive data package for the software package, gage. However, the data supplied here are also useful for gene set or pathway analysis or microarray data analysis in general. In this package, we provide two demo microarray dataset: GSE16873 (a breast cancer dataset from GEO) and BMP6 (originally published as an demo dataset for GAGE, also registered as GSE13604 in GEO). This package also includes commonly used gene set data based on KEGG pathways and GO terms for major research species, including human, mouse, rat and budding yeast. Mapping data between common gene IDs for budding yeast are also included.

biocViews ExperimentData, StemCell, CancerData, BreastCancerData, MicroarrayData, GEO

Suggests gage, pathview, genefilter

License GPL (>=2.0)

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A microarray dataset on BMP6 treated mesenchymal stem cells

Description

This dataset describes mesenchymal stem cell response to BMP6 treatment. This is a typical small dataset with as few as two samples per condition like in most experimental studies. BMP6 treated samples and controls are one-on-one matched. This data has been extensively analyzed in GAGE paper, and was used as the primary demo data in earlier versions of gage package.

Usage

data(bmp6)

Details

This dataset is also available through Gene Expression Omnibus (GEO) with accession number GSE13604. Notice that bmp6 dataset is processed differently than GSE13604. bmp6 dataset used a updated probe set definition (CDF) file based on Entrez Gene mapping, while GSE13604 used the original CDF based on UniGene mapping.

Source


References

Luo, W., Friedman, M., Shedden K., Hankenson, K. and Woolf, P GAGE: Generally Applicable Gene Set Enrichment for Pathways Analysis. BMC Bioinformatics 2009, 10:161

Examples

data(bmp6)
colnames(bmp6)

#kegg analysis
if(require(gage)){
data(kegg.gs)
lapply(kegg.gs[1:3],head)
head(rownames(bmp6))}
genesets

bpm6.kegg.p <- gage(bmp6, gsets = kegg.gs,
  ref = c(1,3), samp = c(2,4))
}

genesets

Common gene set data collections

Description

The gene set data collections derived from KEGG, GO and BioCarta databases.

Usage

data(kegg.sets.hs)
data(go.sets.hs)
data(carta.hs)
data(kegg.sets.mm)
data(go.sets.mm)
data(kegg.sets.rn)
data(go.sets.rn)
data(kegg.sets.sc)
data(go.sets.sc)
data(sigmet.idx.hs)
data(go.subs.hs)
data(sigmet.idx.mm)
data(go.subs.mm)
data(sigmet.idx.rn)
data(go.subs.rn)
data(sigmet.idx.sc)
data(go.subs.sc)

Format

kegg.sets.hs is a named list of 229 elements. Each element is a character vector of member gene
Entrez IDs for a single KEGG pathway. Type head(kegg.sets.hs, 3) for the first 3 gene sets or
pathways.

go.sets.hs is a named list of 17202 elements. Each element is a character vector of member gene
Entrez IDs for a single Gene Ontology term. Type head(go.sets.hs, 3) for the first 3 gene sets or
GO terms.

sigmet.idx.hs is a index numbers of sinaling and metabolic pathways in kegg.set.gs. In other words,
KEGG pathway include other types of pathway definitions, like "Global Map" and "Human Diseases",
which are frequently undesirable in pathway analysis. Therefore, kegg.sets.hs[sigmet.idx.hs]
gives you the "cleaner" gene sets of sinaling and metabolic pathways only.

go.subs.hs is a named list of three elements: "BP", "CC" and "MF", corresponding to biological
process, cellular component and molecular function subtrees. It may be more desirable to conduct
separated GO enrichment test on each of these 3 subtrees as shown in the example code.
carta.hs is a named list of 259 elements. Each element is a character vector of member gene Entrez IDs for a single BioCarta pathway. Type `head(carta.hs, 3)` for the first 3 gene sets or pathways. These are just KEGG, GO and BioCarta gene sets for the default species, i.e. human. KEGG or GO gene sets for other species including mouse (.mm), rat (.rn) and yeast (.sc) have similar structure as their counterparts for human. In addition to the individual species, KEGG gene sets for KEGG Orthology (.ko) is also provided. This is useful for metagenomics, microbiome and non-KEGG species data analysis.

**Details**

The human gene set data were compiled using Entrez Gene IDs, gene set names and mapping information from multiple Bioconductor packages, including: org.Hs.eg.db, KEGG.db, GO.db and cMAP. Please check the corresponding packages for more information.

Gene set for other 3 species included here, was built similarly. The users are encourage to build their own gene set collections for more species in a similar way or to use the Bioconductor package GSEABase.

**Source**

Human data come from multiple Bioconductor packages, including: org.Hs.eg.db, KEGG.db, GO.db and cMAP.

**References**


**Examples**

```r
if(require(gage)){
  #load expression and gene set data
data(gse16873)
cn=colnames(gse16873)
hn=grep('HN',cn, ignore.case =TRUE)
dcis=grep('DCIS',cn, ignore.case =TRUE)
data(kegg.sets.hs)
data(sigmet.idx.hs)
kegg.sigmet.hs=kegg.sets.hs[sigmet.idx.hs]

  #make sure the gene IDs are the same for expression data and gene set data
lapply(kegg.sets.hs[1:3],head)
head(rownames(gse16873))

  #GAGE analysis with signaling and metabolic pathways
gse16873.kegg.sets.p <- gage(gse16873, gsets = kegg.sigmet.hs, ref = hn[1:3], samp = dcis[1:3])
```
data(go.sets.hs)
data(go.subs.hs)
names(go.subs.hs)
go.mf.hs=go.sets.hs[go.subs.hs$MF]

#GAGE analysis with GO Molecular Function gene sets
gse16873.kegg.sets.p <- gage(gse16873, gsets = go.mf.hs,
  ref = hn[1:3], samp = dcis[1:3])

Description

GSE16873 is a breast cancer study (Emery et al, 2009) downloaded from Gene Expression Omnibus (GEO). GSE16873 covers twelve patient cases, each with HN (histologically normal), ADH (ductal hyperplasia), and DCIS (ductal carcinoma in situ) RMA samples. Hence, there are 12*3=36 microarray hybridizations or samples interesting to us plus 4 others less interesting in the full dataset, gse16873.full. Dataset gse16873 in gage and gse16873.2 in this package are half datasets each with only HN and DCIS samples of 6 patients. Dataset gse16873.affyid is similar to gse16873 in gage package, except that row IDs are Affymetrix probe set IDs instead of Entrez Gene IDs. This is because Affymetrix original CDF (hgu133a) instead of Entrez Gene based on CDF was used when processing the raw data.

Details section below gives more information on the datasets.

Usage

data(gse16873.full)
data(gse16873.2)
data(gse16873.affyid)

Details

Due to the size limit of the software package gage, we split GSE16873 into two halves, each including 6 patients with their HN and DCIS but not ADH tissue types. The gage package only includes the first half dataset for 6 patients as the example dataset gse16873. Most of our demo analyses are done on the first half dataset, except for the advanced analysis where we use both halves datasets with all 12 patients.

Raw data for these two half datasets were processed separately using two different methods, FARMS and RMA, respectively to generate the non-biological data heterogeneity. The first half dataset is named as gse16873, the second half dataset named gse16873.2. We also have this full dataset, gse16873.full, which includes all HN, ADH and DCIS samples of all 12 patients, processed together using FARMS.

Source

References


Examples

### usage of the full dataset
```r
data(gse16873.full)
#column/sample names
cn=colnames(gse16873.full)
hn=grep('HN', cn, ignore.case = TRUE)
sh=grep('SH', cn, ignore.case = TRUE)
adh=grep('ADH', cn, ignore.case = TRUE)
dcis=grep('DCIS', cn, ignore.case = TRUE)

# multi-state comparison based on f-test
fac=rep(NA, 40)
fac[hn]='hn'
fac[sh]='sh'
fac[adh]='adh'
fac[dcis]='dcis'
if (require(genefilter)){
  fstats=rowFtests(gse16873.full[, -sh],
                  as.factor(fac[-sh])[,1,drop=FALSE]
                  fstats=cbind(fstat=fstats)

  ## Not run:
  if(require(gage)){
    data(kegg.gs)
    lapply(kegg.gs[1:6], head)
    head(rownames(fstats))
    # feed fstats as single-column matrix into gage
    gse16873.fstats.kegg.p <- gage(fstats, gsets = kegg.gs,
                                  ref = NULL, samp = NULL)
    head(gse16873.fstats.kegg.p$greater)
  }
  ## End(Not run)
}
```

### for usage of the half datasets, check the help information for #heter.gage function in the gage package.

# use of gse16873.affyid
```r
# Not run:
if(require(hgu133a.db) & require(gage)){
data(gse16873.affyid)
affyid=rownames(gse16873.affyid)
egids2 <- hgu133aENTREZID[affyid]
annots=toTable(egids2)
str(annots)
```
hnrnp.cnts

**Description**

This dataset describes HeLa cell response to RNA-binding protein hnRNP C (HNRNPC) knockdown. There are two replicate samples from each HNRNPC knockdown condition/siRNA (KD1 and KD2). In addition, there are four control HeLa cell samples. This is a typical RNA-seq dataset with two experimental groups. Experiment and control samples in this study should be treated as unpaired. This data is used as the primary demo data in the RNA-seq pathway analysis workflow of gage package.

**Usage**

```r
data(hnrnp.cnts)
```

**Details**

This dataset is also available through EBI ArrayExpress with accession number E-MTAB-1147. The raw reads data in zipped FASTQ format (fastq.gz) were downloaded and mapped to human reference genome (hg19) using tophat2. Then reads mapped to annotated gene regions were counted using summarizeOverlaps function from GenomicRanges package.

**Source**

EBI ArrayExpress Experiment E-MTAB-1147: [URL: http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1147/]
References

Luo, W., Friedman, M., Shedden K., Hankenson, K. and Woolf, P. GAGE: Generally Applicable Gene Set Enrichment for Pathways Analysis. BMC Bioinformatics 2009, 10:161

Examples

```r
# data preparation
data(hnrnp.cnts)
cnts=hnrnp.cnts
libsizes=colSums(cnts)
size.factor=libsizes/exp(mean(log(libsizes)))
cnts.norm=t(t(cnts)/size.factor)

# selection
sel.rn=rownames(cnts) != 0
cnts.norm=cnts.norm[sel.rn,]
cnts.norm=log2(cnts.norm+8)

# kegg analysis
if(require(gage)){
data(kegg.gs)
lapply(kegg.gs[1:3],head)
head(rownames(cnts))
ref.idx=5:8
samp.idx=1:4
cnts.kegg.p <- gage(cnts.norm, gsets = kegg.gs,
                   ref = ref.idx, samp = samp.idx, compare ="unpaired")
}

# GO analysis
if(require(gage)){
data(go.sets.hs)
data(go.subs.hs)
cnts.mf.p <- gage(cnts.norm, gsets = go.sets.hs[go.subs.hs$MF],
                   ref = ref.idx, samp = samp.idx, compare ="unpaired")
}
```

---

**sc.gene**

*Common IDs used for budding yeast (Saccharomyces cerevisae) genes*

**Description**

These two data provide mapping between Entrez IDs, official symbols and ORF (open reading frame) IDs for budding yeast genes. These data are useful for yeast microarray data analysis. sc.gene is a 3-column matrix listing the Entrez IDs, official symbols and ORF (open reading frame) IDs for all known genes. orf2eg is a named vector mapping ORF IDs to Entrez IDs.
Usage

data(sc.gene)
data(orf2eg)

Details

These mapping data may be used together with functions eg2sym and sym2eg in the gage package or similar functions. Check the examples for these functions in gage package.

Source

These mapping data were compiled using the gene data from NCBI Entrez Gene database. Similar information can also be derived from Bioconductor package org.Sc.sgd.db. Please check the package for more information.

References


Examples

data(sc.gene)
head(sc.gene)
data(orf2eg)
head(orf2eg)

## for more example, check \code{eg2sym} and \code{sym2eg} funtions in
## the gage package.
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