Package ‘EmpiricalBrownsMethod’

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Title Uses Brown's method to combine p-values from dependent tests

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Author William Poole

Maintainer David Gibbs <dgibbs@systemsbiology.org>

Description Combining P-values from multiple statistical tests is common in bioinformatics. However, this procedure is non-trivial for dependent P-values. This package implements an empirical adaptation of Brown’s Method (an extension of Fisher’s Method) for combining dependent P-values which is appropriate for highly correlated data sets found in high-throughput biological experiments.

Depends R (>= 3.2.0)

Suggests BiocStyle, testthat, knitr, rmarkdown

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VignetteBuilder knitr

URL https://github.com/IlyaLab/CombiningDependentPvaluesUsingEBM.git

LazyData true

Encoding UTF-8

biocViews StatisticalMethod, GeneExpression, Pathways

NeedsCompilation no

R topics documented:

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ebmTestData

Data used in tests and examples.

Description

This data is used in the unit tests and usage examples. There are four items:

allPvals, dat, pathways, and randData. allPvals is a data.frame of p-values for the spearman correlation between CHD4 and each of the 45 genes. 

dat is the gene expression data corresponding to genes in allPvals. 

pathways is a data.frame listing gene membership for 3 biochemical pathways. 

randData is a gaussian generated data set, emphasizing dependence among variables. Independent Var [line 1] are 25 samples from a unit normal distribution. Dependent Var 1-10 [line 2-11] are each 25 samples drawn from a 10 dimensional normal distribution centered at the origin with off diagonal terms a=0.25. The P values from a pearson correlation between the independent var and each dependent var are combined. 

Usage

data(ebmTestData)

Format

Rdata object

Value

data objects in the environment

Source

GEO and generated.

empiricalBrownsMethod

The Empirical Browns Method For Combining P-values

Description

Combining P-values from multiple statistical tests is common in bioinformatics. However, this procedure is non-trivial for dependent P-values. This package provides an empirical adaptation of Brown’s Method (an extension of Fisher’s Method) for combining dependent P-values which is appropriate for highly correlated data sets, like those found in high-throughput biological experiments.

Usage

empiricalBrownsMethod(data_matrix, p_values, extra_info)
### kostsMethod

**The Kost Method For Combining P-values**

Combining P-values from multiple statistical tests is common in bioinformatics. However, this procedure is non-trivial for dependent P-values. This package provides an implementation of Kost’s Method for combining dependent P-values which is appropriate for highly correlated data sets, like those found in high-throughput biological experiments.

**Usage**

```
kostsMethod(data_matrix, p_values, extra_info)
```

**Arguments**

- `data_matrix`: An m x n numeric matrix with m variables in rows and n samples in columns.
- `p_values`: A numeric vector of p-values with length m.
- `extra_info`: boolean, TRUE additionally returns the p-value from Fisher’s method, the scale factor c, and the new degrees of freedom from Brown’s Method.

**Value**

The output is a list containing list(P_Brown=p_brown, P_Fisher=p_fisher, Scale_Factor_C=c, DF_Brown=df_brown)

- **P_test**: p-value for Brown’s method
- **P_Fisher**: p-value for Fisher’s method
- **Scale_Factor**: the scale factor c
- **DF**: the degrees of freedom used in Brown’s method

**Examples**

```r
## restore the saved values to the current environment
data(ebmTestData)
glypGenes <- pathways$gene[pathways$pathway == "GLYPICAN 3 NETWORK"]
glypPvals <- allPvals$pvalue.with.CHD4[match(glypGenes, allPvals$gene)];
glypDat <- dat[match(glypGenes, dat$V1), 2:ncol(dat)];
empiricalBrownsMethod(data_matrix=glypDat, p_values=glypPvals, extra_info=TRUE);
```
The output is a list containing list(P_test=p_brown, P_Fisher=p_fisher, Scale_Factor_C=c, DF=df)

**P_test**
- p-value for Kost’s method

**P_Fisher**
- p-value for Fisher’s method

**Scale_Factor**
- the scale factor c

**DF**
- the degrees of freedom

### Examples

```r
## restore the saved values to the current environment
data(ebmTestData)
glypGenes <- pathways$gene[pathways$pathway == "GLYPICAN 3 NETWORK"]
glypPvals <- allPvals$pvalue.with.CHD4[match(glypGenes, allPvals$gene)]
glypDat <- as.matrix(dat[match(glypGenes, dat$V1), 2:ncol(dat)])
kostsMethod(data_matrix=glypDat, p_values=glypPvals, extra_info=TRUE);
```
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