

Package ‘EmpiricalBrownsMethod’

September 25, 2024

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

Version 1.32.0

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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

git_url <https://git.bioconductor.org/packages/EmpiricalBrownsMethod>

git_branch RELEASE_3_19

git_last_commit cf3cd7e

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-09-25

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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)
```

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

```
## 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);
```

kostsMethod

The Kost 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 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_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

```
## 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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