Package 'EmpiricalBrownsMethod'

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

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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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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. Depedent 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);
```

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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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