

Package ‘EmpiricalBrownsMethod’

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

Version 1.14.0

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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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`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

| | |
|--------------------------|--|
| <code>data_matrix</code> | An $m \times n$ numeric matrix with m variables in rows and n samples in columns. |
| <code>p_values</code> | A numeric vector of p-values with length m . |
| <code>extra_info</code> | 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)`

| | |
|---------------------------|---|
| <code>P_test</code> | p-value for Brown's method |
| <code>P_Fisher</code> | p-value for Fisher's method |
| <code>Scale_Factor</code> | the scale factor c |
| <code>DF</code> | 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

| | |
|--------------------------|--|
| <code>data_matrix</code> | An $m \times n$ numeric matrix with m variables in rows and n samples in columns. |
| <code>p_values</code> | A numeric vector of p-values with length m . |
| <code>extra_info</code> | 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)])
kostaMethod(data_matrix=glypDat, p_values=glypPvals, extra_info=TRUE);
```

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