

Package: EmpiricalBrownsMethod (via r-universe)

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

Version 1.41.0

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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

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biocViews StatisticalMethod, GeneExpression, Pathways

Repository <https://bioc.r-universe.dev>

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ebmTestData	<i>Data used in tests and examples.</i>
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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 $\alpha=0.25$. 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	<i>The Empirical Browns Method For Combining P-values</i>
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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 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);
```

<code>kostsMethod</code>	<i>The Kost Method For Combining P-values</i>
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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 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)])
kostsMethod(data_matrix=glypDat, p_values=glypPvals, extra_info=TRUE);
```

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