

# Package ‘EmpiricalBrownsMethod’

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

**Version** 1.37.0

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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

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ebmTestData

*Data used in tests and examples.*


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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.

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empiricalBrownsMethod *The Empirical Browns Method For Combining P-values*


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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);
```

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kstsMethod

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*The Kost Method For Combining P-values*


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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**

```
kstsMethod(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)])
kotsMethod(data_matrix=glypDat, p_values=glypPvals, extra_info=TRUE);
```

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