Package ‘EmpiricalBrownsMethod’

May 15, 2024

Title  Uses Brown’s method to combine p-values from dependent tests
Version  1.32.0
Author  William Poole
Maintainer  David Gibbs <dgibbs@systemsbiology.org>
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
License  MIT + file LICENSE
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  2024-05-15

Contents

<table>
<thead>
<tr>
<th>Contents</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>ebmTestData</td>
<td>2</td>
</tr>
<tr>
<td>empiricalBrownsMethod</td>
<td>2</td>
</tr>
<tr>
<td>kostsMethod</td>
<td>3</td>
</tr>
</tbody>
</table>

Index 5
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)
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.

Examples
```r
## 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);
```
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
```r
## restore the saved values to the current environment
data(ebmTestData)
glypGenes <- pathways$gene[which(pathways$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);
```
Index

* datasets
  - ebmTestData, 2

* multivariate
  - empiricalBrownsMethod, 2
  - kostsMethod, 3

allPvals(ebmTestData), 2

dat(ebmTestData), 2

ebmTestData, 2
  - empiricalBrownsMethod, 2
  - kostsMethod, 3

pathways(ebmTestData), 2

randData(ebmTestData), 2