Package ‘GSAfisherCombined’

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*Gene Set Analysis with Fisher Combined Method*

**Description**


**Details**

Package: GSAfisherCombined Type: Package Version: 1.0 Date: 2018-02-10 License: GPL (>= 2)

**Author(s)**

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**References**


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GSAfisher

*GSAfisher*

**Description**

It is a generic function that dispatches different methods. It provides the p-value for a joint test of association between a phenotype and a set of genetic variants (SNPs) by combining marginal p-values using the Fisher method.

**Usage**

GSAfisher(x,...)

**Arguments**

- **x**: Set of marginal p-values.
- **...**: Further arguments passed to other methods.

**Details**

Use methods("GSAfisher") to get all the methods for the GSAfisher generic.
Value

UseMethod("GSAfisher")

Author(s)

Carlos Garcia Prieto

References


Description

Default method of GSAfisher function that computes the p-value for a joint test of association between a phenotype and a set of genetic variants (SNPs) by combining marginal p-values using the Fisher method.

Usage

## Default S3 method:
GSAfisher(x,...)

Arguments

x Numeric set of marginal p-values (one vector or a single p-value).

... Further arguments passed to or from other methods.

Value

p Fisher method combined p-value.

Author(s)

Carlos Garcia Prieto

References


Examples

# Generate 1000 random values from a Uniform distribution U (0, 0.25).
x<-runif(1000, 0, 0.25)
# Apply the GSAfisher.default function to this data vector.
GSAfisher(x)
GSAfisher.multiple

Description

Multiple method of GSAfisher function that computes the p-value for a joint test of association between a phenotype and multiple gene-sets of genetic variants (SNPs) by combining multiple marginal p-values data vectors using the Fisher method.

Usage

```r
## S3 method for class 'multiple'
GSAfisher(...)
```

Arguments

...  
Set of multiple marginal p-values data vectors or matrix.

Value

p.multiple  
Set of multiple Fisher method combined p-values for each data vector.

Author(s)

Carlos Garcia Prieto

Examples

```r
# Generate 3 vectors with 1000 random values from an Uniform distribution U (0, 0.25).
data.vector1<-runif(1000, 0, 0.25)
data.vector2<-runif(1000, 0, 0.25)
data.vector3<-runif(1000, 0, 0.25)
# Set data class to "multiple".
class(data.vector1)<-"multiple"
# Apply the GSAfisher.multiple function to these data vectors.
GSAfisher(data.vector1, data.vector2, data.vector3)

# You can also try:
# Generate 5000 vectors with 1000 random values from an Uniform distribution U(0,0.25).
data.vectors<-sapply(1:5000, function (x) runif(1000, 0, 0.25))
# Set data class to "multiple".
class(data.vectors)<-"multiple"
# Apply the GSAfisher.multiple function to these data vectors.
GSAfisher(data.vectors)
```
Description
Plot method of GSAfisher function that plots the p-values for a joint test of association between a phenotype and multiple gene-sets of genetic variants (SNPs) by combining multiple marginal p-values data vectors using the Fisher method.

Usage

```r
## S3 method for class 'plot'
GSAfisher(...)
```

Arguments

... Set of multiple marginal p-values data vectors or matrix.

Value

plot.p.multiple
Plot of a set of multiple Fisher method combined p-values for each data vector.

Author(s)

Carlos Garcia Prieto

Examples

#Generate 3 vectors with 1000 random values from an Uniform distribution U(0, 0.25).
data.vector1<-runif(1000, 0, 0.25)
data.vector2<-runif(1000, 0, 0.25)
data.vector3<-runif(1000, 0, 0.25)
#Set data class to "plot".
class(data.vector1)<-"plot"
#Apply the GSAfisher.plot function to these data vectors.
GSAfisher(data.vector1, data.vector2, data.vector3)

#You can also try:
#Generate 5000 vectors with 1000 random values from an Uniform distribution U(0,0.25).
data.vectors<-sapply(1:5000, function (x) runif(1000, 0, 0.25))
#Set data class to "plot".
class(data.vectors)<-"plot"
#Apply the GSAfisher.plot function to these data vectors.
GSAfisher(data.vectors)
### GSAfisher.print

#### Description

Print method of GSAfisher function that computes the p-value for a joint test of association between a phenotype and a set of genetic variants (SNPs) by combining marginal p-values using the Fisher method and prints the result.

#### Usage

```r
## S3 method for class 'print'
GSAfisher(x,...)
```

#### Arguments

- `x`: Numeric set of marginal p-values (one vector or a single p-value).
- `...`: Further arguments passed to or from other methods.

#### Value

- `print.p`: Displays Fisher method combined p-value.

#### Author(s)

Carlos Garcia Prieto

#### Examples

```r
# Generate 1000 random values from an Uniform distribution U(0, 0.25).
x<-runif(1000, 0, 0.25)
# Set data class to "print".
class(x)<-"print"
# Apply the GSAfisher.print function to this data vector.
GSAfisher(x)
```

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### GSAfisher.summary

#### Description

Summary method of GSAfisher function that computes a numerical summary of the marginal p-values.

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Usage

```r
## S3 method for class 'summary'
GSAfisher(x,...)
```

Arguments

- `x` Numeric set of marginal p-values (one vector or a single p-value).
- `...` Further arguments passed to or from other methods.

Value

- `summary.p` Summary statistics (min, 1st quantile, median, 3rd quantile, max) of a numerical set of marginal p-values.

Author(s)

Carlos Garcia Prieto

Examples

```r
# Generate 1000 random values from an Uniform distribution U (0, 0.25).
x<-runif(1000, 0, 0.25)
# Set data class to "summary"
class(x)<-"summary"
# Apply the GSAfisher.summary function to this data vector.
GSAfisher(x)
```
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