Package ‘GSAfisherCombined’

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Type Package

Title Gene Set Analysis with Fisher Combined Method

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Description 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. See Fisher, R.A. (1925,ISBN:0-05-002170-2) Statistical Methods for Research Workers.

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Contents

`GSAfisherCombined-package` *Gene Set Analysis with Fisher Combined Method*

Description

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Details

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

Author(s)

Carlos Garcia Prieto

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References

Fisher, R.A. (1925). Statistical Methods for Research Workers. ISBN 0-05-002170-2.

`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

Fisher, R.A. (1925). Statistical Methods for Research Workers. ISBN 0-05-002170-2.

`GSAfisher.default` *GSAfisher.default*

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 sinlge p-value).
`...`	Further arguments passed to or from other methods.

Value

`p`	Fisher method combined p-value.

Author(s)

Carlos Garcia Prieto

References

Fisher, R.A. (1925). Statistical Methods for Research Workers. ISBN 0-05-002170-2.

Examples

```
#Generate 1000 random values from an 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` *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

```
## 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

```
#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)
```

`GSAfisher.plot` *GSAfisher.plot*

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

```
## 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` *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

```
## 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 pvalue.

Author(s)

Carlos Garcia Prieto

Examples

```
#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)
```

`GSAfisher.summary` *GSAfisher.summary*

Description

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

Usage

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

Arguments

`x`	Numeric set of marginal p-values (one vector or a sinlge 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

```
#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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