

# 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.

**License** GPL (>= 2)

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## R topics documented:

GSAfisherCombined-package . . . . .	2
GSAfisher . . . . .	2
GSAfisher.default . . . . .	3
GSAfisher.multiple . . . . .	4
GSAfisher.plot . . . . .	5
GSAfisher.print . . . . .	6
GSAfisher.summary . . . . .	6
<b>Index</b>	<b>8</b>

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GSAfisherCombined-package

*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.

### Details

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

### Author(s)

Carlos Garcia Prieto

Maintainer: Carlos Garcia Prieto <carlosantonio.garcia@uvic.cat>

### References

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

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GSAfisher

*GSAfisher*

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### 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.

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GSAfisher.default      *GSAfisher.default*

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**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**

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*

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### 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)
```

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GSAfisher.plot	<i>GSAfisher.plot</i>
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### 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*

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**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*

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**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 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**

```
#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)
```

# Index

- \* **apply**
  - GSAfisher.multiple, 4
- \* **pchisq**
  - GSAfisher.default, 3
- \* **plot**
  - GSAfisher.plot, 5
- \* **summary**
  - GSAfisher.summary, 6
  
- GSAfisher, 2
- GSAfisher.default, 3
- GSAfisher.multiple, 4
- GSAfisher.plot, 5
- GSAfisher.print, 6
- GSAfisher.summary, 6
- GSAfisherCombined
  - (GSAfisherCombined-package), 2
- GSAfisherCombined-package, 2