# Package ‘GFisher’

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**Type** Package  
**Title** Generalized Fisher's Combination Tests Under Dependence  
**Version** 0.1.0  
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**Description** Accurate and computationally efficient p-value calculation methods for a general family of Fisher type statistics (GFisher). The GFisher covers Fisher's combination, Good's statistic, Lancaster's statistic, weighted Z-score combination, etc. It allows a flexible weighting scheme, as well as an omnibus procedure that automatically adapts proper weights and degrees of freedom to a given data. The new p-value calculation methods are based on novel ideas of moment-ratio matching and joint-distribution approximation. The technical details can be found in Hong Zhang and Zheyang Wu (2020) &lt;arXiv:2003.01286&gt;.

**License** GPL-2  
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Survival function of the generalized Fisher’s p-value combination statistic.

Usage

\[
p.GFisher(q, df, w, M, p.type = \text{"two"}, \text{method = \"HYB\"}, \text{nsim = NULL}, \\
\text{seed = NULL})
\]

Arguments

- **q**: observed GFisher statistic.
- **df**: vector of degrees of freedom for inverse chi-square transformation for each p-value. If all df’s are equal, it can be defined by the constant.
- **w**: vector of weights.
- **M**: correlation matrix of the input statistics.
- **p.type**: “two” = two-sided p-values, “one” = one-sided p-values.
- **nsim**: number of simulation used in the “MR” method, default = 5e4.
- **seed**: random seed used in the “MR” method

Value

p-value of the observed GFisher statistic.

References


Examples

```r
set.seed(123)
n = 10
M = matrix(0.3, n, n) + diag(0.7, n, n)
zsore = matrix(rnorm(n), nrow=1)%*%chol(M)
pval = 2*(1-pnorm(abs(zscore))
gf1 = stat.GFisher(pval, df=2, w=1)
gf2 = stat.GFisher(pval, df=1:n, w=1:n)
p.GFisher(gf1, df=2, w=1, M=M, method="HYB")
```
p.oGFisher

p.GFisher(gf1, df=2, w=1, M=M, method="MR", nsim=5e4)
p.GFisher(gf2, df=1:n, w=1:n, M=M, method="HYB")
p.GFisher(gf2, df=1:n, w=1:n, M=M, method="MR", nsim=5e4)

p.oGFisher  P-value of the omnibus generalized Fisher’s p-value combination test.

Description

P-value of the omnibus generalized Fisher’s p-value combination test.

Usage

p.oGFisher(p, DF, W, M, p.type = "two", method = "HYB",
combine = "cct", nsim = NULL, seed = NULL)

Arguments

- p: vector of input p-values.
- DF: matrix of degrees of freedom for inverse chi-square transformation for each p-value. Each row represents a GFisher test.
- W: matrix of weights. Each row represents a GFisher test.
- M: correlation matrix of the input statistics.
- p.type: "two" = two-sided p-values, "one" = one-sided p-values.
- combine: "cct" = oGFisher using the Cauchy combination method, "mvn" = oGFisher using multivariate normal distribution.
- nsim: number of simulation used in the "MR" method, default = 5e4.
- seed: random seed used in the "MR" method

Value

1. p-value of the oGFisher test. 2. individual p-value of each GFisher test.

References

Examples

```r
set.seed(123)
n = 10
M = matrix(0.3, n, n) + diag(0.7, n, n)
zs = matrix(rnorm(n), nrow=1)%*%chol(M)
pval = 2*(1-pnorm(abs(zs)))
DF = rbind(rep(1,n), rep(2,n))
W = rbind(rep(1,n), 1:10)
p.oGFisher(pval, DF, W, M, p.type="two", method="HYB", combine="cct")
```

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**stat.GFisher**  
*Generalized Fisher's p-value combination statistic.*

**Description**

Generalized Fisher's p-value combination statistic.

**Usage**

```r
stat.GFisher(p, df = 2, w = 1)
```

**Arguments**

- `p` - vector of input p-values.
- `df` - vector of degrees of freedom for inverse chi-square transformation for each p-value. If all df's are equal, it can be defined by the constant.
- `w` - vector of weights.

**Value**

GFisher statistic \( \sum_i w_i \cdot qchisq(1 - p_i, df_i) \).

**References**


**Examples**

```r
n = 10
pval = runif(n)
stat.GFisher(pval, df=2, w=1)
stat.GFisher(pval, df=rep(2,n), w=rep(1,n))
stat.GFisher(pval, df=1:n, w=1:n)
```
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