

# Package ‘GFisher’

July 21, 2025

**Type** Package

**Title** Generalized Fisher's Combination Tests Under Dependence

**Version** 0.2.0

**Author** Hong Zhang and Zheyang Wu

**Maintainer** Hong Zhang <hzhang@wpi.edu>

**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) <[doi:10.48550/arXiv.2003.01286](https://doi.org/10.48550/arXiv.2003.01286)>.

**License** GPL-2

**Imports** stats, methods, Matrix, mvtnorm

**Encoding** UTF-8

**RoxygenNote** 6.1.0

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2022-03-02 00:10:35 UTC

## Contents

p.GFisher	2
p.oGFisher	3
stat.GFisher	4
<b>Index</b>	<b>5</b>

---

p.GFisher	<i>Survival function of the generalized Fisher's p-value combination statistic.</i>
-----------	---

---

### Description

Survival function of the generalized Fisher's p-value combination statistic.

### Usage

```
p.GFisher(q, df, w, M, p.type = "two", method = "HYB", nsim = 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.
method	- "MR" = simulation-assisted moment ratio matching, "HYB" = moment ratio matching by quadratic approximation, "GB" = Brown's method with calculated variance. See details in the reference.
nsim	- number of simulation used in the "MR" method, default = 5e4.

### Value

p-value of the observed GFisher statistic.

### References

Hong Zhang and Zheyang Wu. "Accurate p-Value Calculation for Generalized Fisher's Combination Tests Under Dependence", <arXiv:2003.01286>.

### Examples

```
set.seed(123)
n = 10
M = matrix(0.3, n, n) + diag(0.7, n, n)
zscore = 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.GFisher(gf2, 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)
```

### 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.

**method** - "MR" = simulation-assisted moment ratio matching, "HYB" = moment ratio matching by quadratic approximation, "GB" = Brown's method with calculated variance. See details in the reference.

**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.

### Value

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

### References

Hong Zhang and Zheyang Wu. "Accurate p-Value Calculation for Generalized Fisher's Combination Tests Under Dependence", <arXiv:2003.01286>.

### Examples

```
set.seed(123)
n = 10
M = matrix(0.3, n, n) + diag(0.7, n, n)
zscore = matrix(rnorm(n),nrow=1)%*%chol(M)
pval = 2*(1-pnorm(abs(zscore)))
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")
```

---

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

---

**Description**

Generalized Fisher's p-value combination statistic.

**Usage**

```
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  $\sum_i w_i * qchisq(1 - p_i, df_i)$ .

**References**

Hong Zhang and Zheyang Wu. "Accurate p-Value Calculation for Generalized Fisher's Combination Tests Under Dependence", <arXiv:2003.01286>.

**Examples**

```
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)
```

# Index

p.GFisher, 2  
p.oGFisher, 3  
stat.GFisher, 4