

Package ‘TFisher’

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Type Package

Title Optimal Thresholding Fisher's P-Value Combination Method

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Description We provide the cumulative distribution function (CDF), quantile, and statistical power calculator for a collection of thresholding Fisher's p-value combination methods, including Fisher's p-value combination method, truncated product method and, in particular, soft-thresholding Fisher's p-value combination method which is proven to be optimal in some context of signal detection. The p-value calculator for the omnibus version of these tests are also included. For reference, please see Hong Zhang and Zheyang Wu. ``TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values'', submitted.

License GPL-2

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p.soft	<i>CDF of soft-thresholding Fisher's p-value combination statistic under the null hypothesis.</i>
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Description

CDF of soft-thresholding Fisher's p-value combination statistic under the null hypothesis.

Usage

p.soft(q, n, tau1, M = NULL)

Arguments

- q - quantile, could be a vector.
- n - dimension parameter, i.e. the number of p-values to be combined.
- tau1 - truncation parameter=normalization parameter. tau1 > 0.
- M - correlation matrix of the input statistics. Default = NULL assumes independence.

Value

The left-tail probability of the null distribution of soft-thresholding Fisher's p-value combination statistic at the given quantile.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.soft](#) for the definition of the statistic.

Examples

```
pval <- runif(100)
softstat <- stat.soft(p=pval, tau1=0.05)
p.soft(q=softstat, n=100, tau1=0.05)
M = matrix(0.3,100,100) + diag(1-0.3,100)
p.soft(q=softstat, n=100, tau1=0.05, M=M)
```

p.soft.omni	<i>CDF of omnibus soft-thresholding Fisher's p-value combination statistic under the null hypothesis.</i>
-------------	---

Description

CDF of omnibus soft-thresholding Fisher's p-value combination statistic under the null hypothesis.

Usage

```
p.soft.omni(q, n, TAU1, M = NULL)
```

Arguments

q	- quantile, could be a vector.
n	- dimension parameter, i.e. the number of p-values to be combined.
TAU1	- a vector of truncation parameters (=normalization parameters). Must be in non-descending order.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.

Value

The left-tail probability of the null distribution of omnibus soft-thresholding Fisher's p-value combination statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.soft.omni](#) for the definition of the statistic.

Examples

```
q = 0.01
n = 20
TAU1 = c(0.01, 0.05, 0.5, 1)
M = matrix(0.3,20,20) + diag(1-0.3,20)
p.soft.omni(q=q, n=n, TAU1=TAU1, M=M)
```

p.tfisher	<i>CDF of thresholding Fisher's p-value combination statistic under the null hypothesis.</i>
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Description

CDF of thresholding Fisher's p-value combination statistic under the null hypothesis.

Usage

```
p.tfisher(q, n, tau1, tau2, M = NULL, mu = NULL, sigma2 = NULL,
          p0 = NULL)
```

Arguments

q	- quantile, could be a vector.
n	- dimension parameter, i.e. the number of p-values to be combined.
tau1	- truncation parameter. $0 < \tau_1 \leq 1$.
tau2	- normalization parameter. $\tau_2 \geq \tau_1$.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.
mu	- the mean of TFisher statistics. Default = NULL.
sigma2	- the variance of TFisher statistics. Default = NULL.
p0	- the point masse of TFisher statistics. Default = NULL.

Value

The left-tail probability of the null distribution of thresholding Fisher's p-value combination statistic at the given quantile.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.tfisher](#) for the definition of the statistic.

Examples

```
pval <- runif(20)
tfstat <- stat.tfisher(p=pval, tau1=0.25, tau2=0.75)
p.tfisher(q=tfstat, n=20, tau1=0.25, tau2=0.75)
M = matrix(0.3,20,20) + diag(1-0.3,20)
p.tfisher(q=tfstat, n=20, tau1=0.25, tau2=0.75, M=M)
```

p.tfisher.omni	<i>CDF of omnibus thresholding Fisher's p-value combination statistic under the null hypothesis.</i>
----------------	--

Description

CDF of omnibus thresholding Fisher's p-value combination statistic under the null hypothesis.

Usage

```
p.tfisher.omni(q, n, TAU1, TAU2, M = NULL, P0 = NULL)
```

Arguments

q	- quantile, could be a vector.
n	- dimension parameter, i.e. the number of p-values to be combined.
TAU1	- a vector of truncation parameters. Must be in non-descending order.
TAU2	- a vector of normalization parameters. Must be in non-descending order.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.
P0	- a vector of point masses of TFisher statistics. Default = NULL.

Value

The left-tail probability of the null distribution of omnibus thresholding Fisher's p-value combination statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.tfisher.omni](#) for the definition of the statistic.

Examples

```
q = 0.05
n = 20
TAU1 = c(0.01, 0.05, 0.5, 1)
TAU2 = c(0.1, 0.2, 0.5, 1)
M = matrix(0.3,20,20) + diag(1-0.3,20)
p.tfisher.omni(q=q, n=n, TAU1=TAU1, TAU2=TAU2, M=M)
```

p.tpm

CDF of truncated product method statistic under the null hypothesis.

Description

CDF of truncated product method statistic under the null hypothesis.

Usage

```
p.tpm(q, n, tau1, M = NULL)
```

Arguments

q	- quantile, could be a vector.
n	- dimension parameter, i.e. the number of p-values to be combined.
tau1	- truncation parameter. $0 < \text{tau1} \leq 1$.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.

Value

The left-tail probability of the null distribution of truncated product method statistic at the given quantile.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.
2. Zaykin, D.V., Zhivotovsky, L. A., Westfall, P.H. and Weir, B.S. (2002), Truncated product method for combining P-values. Genet. Epidemiol., 22: 170–185. doi:10.1002/gepi.0042

See Also

[stat.tpm](#) for the definition of the statistic.

Examples

```
pval <- runif(100)
tpmstat <- stat.tpm(p=pval, tau1=0.05)
p.tpm(q=tpmstat, n=100, tau1=0.05)
M = matrix(0.3,100,100) + diag(1-0.3,100)
p.tpm(q=tpmstat, n=100, tau1=0.05, M=M)
```

p.tpm.omni	<i>CDF of omnibus truncated product method statistic under the null hypothesis.</i>
------------	---

Description

CDF of omnibus truncated product method statistic under the null hypothesis.

Usage

```
p.tpm.omni(q, n, TAU1, M = NULL)
```

Arguments

q	- quantile, could be a vector.
n	- dimension parameter, i.e. the number of p-values to be combined.
TAU1	- a vector of truncation parameters. Must be in non-descending order.
M	- correlation matrix of the input statistics. Default = NULL assumes independence

Value

The left-tail probability of the null distribution of omnibus truncated product method statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.tpm.omni](#) for the definition of the statistic.

Examples

```
q = 0.05
n = 20
TAU1 = c(0.01, 0.05, 0.5, 1)
M = matrix(0.3,20,20) + diag(1-0.3,20)
p.tpm.omni(q=q, n=n, TAU1=TAU1, M=M)
```

power.soft	<i>Statistical power of soft-thresholding Fisher's p-value combination test under Gaussian mixture model.</i>
------------	---

Description

Statistical power of soft-thresholding Fisher's p-value combination test under Gaussian mixture model.

Usage

```
power.soft(alpha, n, tau1, eps = 0, mu = 0)
```

Arguments

alpha	- type-I error rate.
n	- dimension parameter, i.e. the number of input p-values.
tau1	- truncation parameter=normalization parameter. tau1 > 0.
eps	- mixing parameter of the Gaussian mixture.
mu	- mean of non standard Gaussian model.

Details

We consider the following hypothesis test,

$$H_0 : X_i \sim F_0, H_a : X_i \sim (1 - \epsilon)F_0 + \epsilon F_1$$

, where ϵ is the mixing parameter, F_0 is the standard normal CDF and $F = F_1$ is the CDF of normal distribution with μ defined by mu and $\sigma = 1$.

Value

Power of the soft-thresholding Fisher's p-value combination test.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.soft](#) for the definition of the statistic.

Examples

```
alpha = 0.05
#If the alternative hypothesis Gaussian mixture with eps = 0.1 and mu = 1.2:#
power.soft(alpha, 100, 0.05, eps = 0.1, mu = 1.2)
```

power.tfisher	<i>Statistical power of thresholding Fisher's p-value combination test under Gaussian mixture model.</i>
---------------	--

Description

Statistical power of thresholding Fisher's p-value combination test under Gaussian mixture model.

Usage

```
power.tfisher(alpha, n, tau1, tau2, eps = 0, mu = 0)
```

Arguments

alpha	- type-I error rate.
n	- dimension parameter, i.e. the number of input p-values.
tau1	- truncation parameter. $0 < \tau_1 \leq 1$.
tau2	- normalization parameter. $\tau_2 \geq \tau_1$.
eps	- mixing parameter of the Gaussian mixture.
mu	- mean of non standard Gaussian model.

Details

We consider the following hypothesis test,

$$H_0 : X_i \sim F_0, H_a : X_i \sim (1 - \epsilon)F_0 + \epsilon F_1$$

, where ϵ is the mixing parameter, F_0 is the standard normal CDF and $F = F_1$ is the CDF of normal distribution with μ defined by mu and $\sigma = 1$.

Value

Power of the thresholding Fisher's p-value combination test.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.tfisher](#) for the definition of the statistic.

Examples

```
alpha = 0.05
#If the alternative hypothesis Gaussian mixture with eps = 0.1 and mu = 1.2:#
power.tfisher(alpha, 100, 0.05, 0.25, eps = 0.1, mu = 1.2)
```

power.tpm	<i>Statistical power of truncated product method test under Gaussian mixture model.</i>
-----------	---

Description

Statistical power of truncated product method test under Gaussian mixture model.

Usage

```
power.tpm(alpha, n, tau1, eps = 0, mu = 0)
```

Arguments

alpha	- type-I error rate.
n	- dimension parameter, i.e. the number of input p-values.
tau1	- truncation parameter. $0 < \tau_1 \leq 1$. $\tau_1 > 0$.
eps	- mixing parameter of the Gaussian mixture.
mu	- mean of non standard Gaussian model.

Details

We consider the following hypothesis test,

$$H_0 : X_i \sim F_0, H_a : X_i \sim (1 - \epsilon)F_0 + \epsilon F_1$$

, where ϵ is the mixing parameter, F_0 is the standard normal CDF and $F = F_1$ is the CDF of normal distribution with μ defined by mu and $\sigma = 1$.

Value

Power of the truncated product method test.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.soft](#) for the definition of the statistic.

Examples

```
alpha = 0.05
#If the alternative hypothesis Gaussian mixture with eps = 0.1 and mu = 1.2:#
power.tpm(alpha, 100, 0.05, eps = 0.1, mu = 1.2)
```

q.soft	<i>Quantile of soft-thresholding Fisher's p-value combination statistic under the null hypothesis.</i>
--------	--

Description

Quantile of soft-thresholding Fisher's p-value combination statistic under the null hypothesis.

Usage

```
q.soft(p, n, tau1, M = NULL)
```

Arguments

p	- a scalar left probability that defines the quantile.
n	- dimension parameter, i.e. the number of input p-values.
tau1	- truncation parameter=normalization parameter. tau1 > 0.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.

Value

Quantile of soft-thresholding Fisher's p-value combination statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.soft](#) for the definition of the statistic.

Examples

```
## The 0.05 critical value of soft-thresholding statistic when n = 10:
q.soft(p=.99, n=20, tau1 = 0.05)
M = matrix(0.9,20,20) + diag(1-0.9,20)
q.soft(p=.99, n=20, tau1 = 0.05, M=M)
```

q.tfisher	<i>Quantile of thresholding Fisher's p-value combination statistic under the null hypothesis.</i>
-----------	---

Description

Quantile of thresholding Fisher's p-value combination statistic under the null hypothesis.

Usage

```
q.tfisher(p, n, tau1, tau2, M = NULL)
```

Arguments

p	- a scalar left probability that defines the quantile.
n	- dimension parameter, i.e. the number of input p-values.
tau1	- truncation parameter. $0 < \text{tau1} \leq 1$.
tau2	- normalization parameter. $\text{tau2} \geq \text{tau1}$.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.

Value

Quantile of thresholding Fisher's p-value combination statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

See Also

[stat.tfisher](#) for the definition of the statistic.

Examples

```
## The 0.05 critical value of TFisher statistic when n = 10:
q.tfisher(p=.95, n=20, tau1=0.05, tau2=0.25)
## when correlated
M = matrix(0.3,20,20) + diag(1-0.3,20)
q.tfisher(p=.95, n=20, tau1=0.05, tau2=0.25, M=M)
```

q.tpm	<i>Quantile of truncated product method statistic under the null hypothesis.</i>
-------	--

Description

Quantile of truncated product method statistic under the null hypothesis.

Usage

```
q.tpm(p, n, tau1, M = NULL)
```

Arguments

- | | |
|------|--|
| p | - a scalar left probability that defines the quantile. |
| n | - dimension parameter, i.e. the number of input p-values. |
| tau1 | - truncation parameter. $0 < \text{tau1} \leq 1$. |
| M | - correlation matrix of the input statistics. Default = NULL assumes independence. |

Value

Quantile of truncated product method statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.
2. Zaykin, D.V., Zhivotovsky, L. A., Westfall, P.H. and Weir, B.S. (2002), Truncated product method for combining P-values. Genet. Epidemiol., 22: 170–185. doi:10.1002/gepi.0042

See Also

[stat.tpm](#) for the definition of the statistic.

Examples

```
## The 0.05 critical value of TPM statistic when n = 10:  
q.tpm(p=.95, n=20, tau1 = 0.05)  
M = matrix(0.3,20,20) + diag(1-0.3,20)  
q.tpm(p=.95, n=20, tau1 = 0.05, M=M)
```

stat.soft

Construct soft-thresholding Fisher's p-value combination statistic.

Description

Construct soft-thresholding Fisher's p-value combination statistic.

Usage

```
stat.soft(p, tau1)
```

Arguments

p - input p-values.
tau1 - truncation parameter=normalization parameter. tau1 > 0.

Details

Let $p_i, i = 1, \dots, n$ be a sequence of p-values, the soft-thresholding statistic

$$Soft = \sum_{i=1}^n -2 \log(p_i / \tau_1) I(p_i \leq \tau_1)$$

. Soft-thresholding is the special case of TFisher when tau1=tau2.

Value

Soft-thresholding Fisher's p-value combination statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

Examples

```
pval <- runif(100)
stat.soft(p=pval, tau1=0.05)
```

stat.soft.omni	<i>Construct omnibus soft-thresholding Fisher's p-value combination statistic.</i>
----------------	--

Description

Construct omnibus soft-thresholding Fisher's p-value combination statistic.

Usage

```
stat.soft.omni(p, TAU1, M = NULL)
```

Arguments

p	- input p-values.
TAU1	- a vector of truncation parameters (=normalization parameters). Must be in non-descending order.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.

Details

Let $x_i, i = 1, \dots, n$ be a sequence of individual statistics with correlation matrix M, p_i be the corresponding two-sided p-values, then the soft-thresholding statistics

$$Soft_j = \sum_{i=1}^n -2 \log(p_i / \tau_{1j}) I(p_i \leq \tau_{1j})$$

, $j = 1, \dots, d$. The omnibus test statistic is the minimum p-value of these soft-thresholding tests,

$$W_o = \min_j G_j(Soft_j)$$

, where G_j is the survival function of $Soft_j$.

Value

omni - omnibus soft-thresholding statistic.
pval - p-values of each soft-thresholding tests.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

Examples

```
pval = runif(20)
TAU1 = c(0.01, 0.05, 0.5, 1)
stat.soft.omni(p=pval, TAU1=TAU1)
M = matrix(0.3,20,20) + diag(1-0.3,20)
stat.soft.omni(p=pval, TAU1=TAU1, M=M)
```

stat.tfisher

Construct thresholding Fisher's p-value combination statistic.

Description

Construct thresholding Fisher's p-value combination statistic.

Usage

```
stat.tfisher(p, tau1, tau2)
```

Arguments

p - input p-values.
tau1 - truncation parameter. $0 < \text{tau1} \leq 1$.
tau2 - normalization parameter. $\text{tau2} \geq \text{tau1}$.

Details

Let $p_i, i = 1, \dots, n$ be a sequence of p-values, the thresholding Fisher's p-value combination statistic

$$TFisher = \sum_{i=1}^n -2 \log(p_i/\tau_2) I(p_i \leq \tau_2)$$

Value

Thresholding Fisher's p-value combination statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

Examples

```
pval <- runif(100)
stat.tfisher(p=pval, tau1=0.05, tau2=0.25)
```

stat.tfisher.omni	<i>Construct omnibus thresholding Fisher's (TFisher) p-value combination statistic.</i>
-------------------	---

Description

Construct omnibus thresholding Fisher's (TFisher) p-value combination statistic.

Usage

```
stat.tfisher.omni(p, TAU1, TAU2, M = NULL, MU = NULL, SIGMA2 = NULL,
  P0 = NULL)
```

Arguments

p	- input p-values from potentially correlated input statistics.
TAU1	- a vector of truncation parameters. Must be in non-descending order.
TAU2	- a vector of normalization parameters. Must be in non-descending order.
M	- correlation matrix of the input statistics. Default = NULL assumes independence
MU	- a vector of means of TFisher statistics. Default = NULL.
SIGMA2	- a vector of variances of TFisher statistics. Default = NULL.
P0	- a vector of point masses of TFisher statistics. Default = NULL.

Details

Let x_i , $i = 1, \dots, n$ be a sequence of individual statistics with correlation matrix M , p_i be the corresponding two-sided p-values, then the TFisher statistics

$$TFisher_j = \sum_{i=1}^n -2 \log(p_i / \tau_{2j}) I(p_i \leq \tau_{1j})$$

, $j = 1, \dots, d$. The omnibus test statistic is the minimum p-value of these thresholding tests,

$$W_o = \min_j G_j(Soft_j)$$

, where G_j is the survival function of $Soft_j$.

Value

omni - omnibus TFisher statistic.
 pval - p-values of each TFisher tests.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

Examples

```

pval = runif(20)
TAU1 = c(0.01, 0.05, 0.5, 1)
TAU2 = c(0.1, 0.2, 0.5, 1)
stat.tfisher.omni(p=pval, TAU1=TAU1, TAU2=TAU2)
M = matrix(0.3,20,20) + diag(1-0.3,20)
stat.tfisher.omni(p=pval, TAU1=TAU1, TAU2=TAU2, M=M)

```

stat.tpm

*Construct truncated product method statistic.***Description**

Construct truncated product method statistic.

Usage

```
stat.tpm(p, tau1)
```

Arguments

p - input p-values.
tau1 - truncation parameter. $0 < \text{tau1} \leq 1$.

Details

Let $p_i, i = 1, \dots, n$ be a sequence of p-values, the TPM statistic

$$TPM = \sum_{i=1}^n -2 \log(p_i) I(p_i \leq \tau_2)$$

. TPM is the special case of TFisher when $\text{tau2}=1$.

Value

Truncated product method statistic.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.
2. Zaykin, D.V., Zhivotovsky, L. A., Westfall, P.H. and Weir, B.S. (2002), Truncated product method for combining P-values. Genet. Epidemiol., 22: 170–185. doi:10.1002/gepi.0042

Examples

```

pval <- runif(100)
stat.tpm(p=pval, tau1=0.05)

```

stat.tpm.omni	<i>Construct omnibus truncated product method statistic.</i>
---------------	--

Description

Construct omnibus truncated product method statistic.

Usage

```
stat.tpm.omni(p, TAU1, M = NULL)
```

Arguments

p	- input p-values.
TAU1	- a vector of truncation parameters. Must be in non-descending order.
M	- correlation matrix of the input statistics. Default = NULL assumes independence.

Details

Let $x_i, i = 1, \dots, n$ be a sequence of individual statistics with correlation matrix M, p_i be the corresponding two-sided p-values, then the truncated product method statistics

$$TPM_j = \sum_{i=1}^n -2 \log(p_i) I(p_i \leq \tau_{1j})$$

, $j = 1, \dots, d$. The omnibus test statistic is the minimum p-value of these truncated product method tests,

$$W_o = \min_j G_j(TPM_j)$$

, where G_j is the survival function of TPM_j .

Value

omni - omnibus truncated product method statistic.

pval - p-values of each truncated product method tests.

References

1. Hong Zhang and Zheyang Wu. "TFisher Tests: Optimal and Adaptive Thresholding for Combining p-Values", submitted.

Examples

```
pval = runif(20)
TAU1 = c(0.01, 0.05, 0.5, 1)
stat.tpm.omni(p=pval, TAU1=TAU1)
M = matrix(0.3,20,20) + diag(1-0.3,20)
stat.tpm.omni(p=pval, TAU1=TAU1, M=M)
```

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