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

Usage

p.softert \( q, n, \tau_1, M = \text{NULL} \)

Arguments

- \( q \): quantile, could be a vector.
- \( n \): dimension parameter, i.e. the number of p-values to be combined.
- \( \tau_1 \): truncation parameter=normalization parameter. \( \tau_1 > 0 \).
- \( M \): 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


See Also

stat.softert for the definition of the statistic.
**Examples**

```r
pval <- runif(100)
softstat <- stat.soft(p=pval, tau1=0.05)
psoft(q=softstat, n=100, tau1=0.05)
m = matrix(c(0,3,100,100), 100, 100) + diag(1-0.3,100)
psoft(q=softstat, n=100, tau1=0.05, M=M)
``` 

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**p.soft.omni**

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

---

**Description**

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

**Usage**

```r
psoft.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**


**See Also**

- `stat.soft.omni` for the definition of the statistic.

**Examples**

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

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

Usage

\[ p.tfisher(q, n, \tau_1, \tau_2, M = \text{NULL}, \mu = \text{NULL}, \sigma^2 = \text{NULL}, p_\theta = \text{NULL}) \]

Arguments

- \( q \) - quantile, could be a vector.
- \( n \) - dimension parameter, i.e. the number of p-values to be combined.
- \( \tau_1 \) - truncation parameter. \( 0 < \tau_1 \leq 1 \).
- \( \tau_2 \) - 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.
- \( \sigma^2 \) - the variance of TFisher statistics. Default = NULL.
- \( p_\theta \) - 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


See Also

\[ \text{stat.tfisher} \] for the definition of the statistic.

Examples

\[
\begin{align*}
pval &<- \text{runif(20)} \\
tfstat &<- \text{stat.tfisher}(p=pval, \tau_1=0.25, \tau_2=0.75) \\
p.tfisher(q=tfstat, n=20, \tau_1=0.25, \tau_2=0.75) \\
M &<- \text{matrix}(0.3,20,20) + \text{diag}(1-0.3,20) \\
p.tfisher(q=tfstat, n=20, \tau_1=0.25, \tau_2=0.75, M=M)
\end{align*}
\]
CDF of omnibus thresholding Fisher's p-value combination statistic under the null hypothesis.

Usage

```r
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


See Also

`stat.tfisher.omni` for the definition of the statistic.

Examples

```r
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)
```
CDF of truncated product method statistic under the null hypothesis.

Description

CDF of truncated product method statistic under the null hypothesis.

Usage

\[ p.tpm(q, n, tau1, M = \text{NULL}) \]

Arguments

- **q**: quantile, could be a vector.
- **n**: dimension parameter, i.e. the number of p-values to be combined.
- **tau1**: truncation parameter. \(0 < \tau_1 \leq 1\).
- **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


See Also

- `stat.tpm` for the definition of the statistic.

Examples

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

Description

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

Usage

\[ p\text{.tpm.omni}(q, n, \text{TAU1}, M = \text{NULL}) \]

Arguments

- \( q \) - quantile, could be a vector.
- \( n \) - dimension parameter, i.e. the number of \( p \)-values to be combined.
- \( \text{TAU1} \) - 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


See Also

\[ \text{stat.tpm.omni} \] for the definition of the statistic.

Examples

\[ \begin{align*}
q &= 0.05 \\
n &= 20 \\
\text{TAU1} &= c(0.01, 0.05, 0.5, 1) \\
M &= \text{matrix}(0.3, 20, 20) + \text{diag}(1-0.3, 20) \\
p\text{.tpm.omni}(q=q, n=n, \text{TAU1}=\text{TAU1}, M=M)
\end{align*} \]
power.soft

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

Description

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

Usage

powerNsoft(alphaL nL tau1L eps = PL mu = PI)

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 \( \epsilon \) is the mixing parameter, \( F_0 \) is the standard normal CDF and \( F = F_1 \) is the CDF of normal distribution with \( \mu \) defined by \( \mu \) and \( \sigma = 1 \).

Value

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

References


See Also

statNsoft for the definition of the statistic.

Examples

alpha = 0.05
#If the alternative hypothesis Gaussian mixture with eps = 0.1 and mu = 1.2:
powerNsoft(alpha, 100, 0.05, eps = 0.1, mu = 1.2)
Description

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

Usage

\[ \text{powerNtfisher}(\alpha, n, \tau_1, \tau_2, \epsilon = \mu) \]

Arguments

- \( \alpha \) - type-I error rate.
- \( n \) - dimension parameter, i.e. the number of input p-values.
- \( \tau_1 \) - truncation parameter. \( 0 < \tau_1 \leq 1 \).
- \( \tau_2 \) - normalization parameter. \( \tau_2 \geq \tau_1 \).
- \( \epsilon \) - 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 \( \epsilon \) is the mixing parameter, \( F_0 \) is the standard normal CDF and \( F = F_1 \) is the CDF of normal distribution with \( \mu \) defined by \( \mu \) and \( \sigma = 1 \).

Value

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

References


See Also

- \text{statNtfisher} for the definition of the statistic.

Examples

\[ \alpha = 0.05 \]
\[ \text{#If the alternative hypothesis Gaussian mixture with } \epsilon = 0.1 \text{ and } \mu = 1.2:\# \]
\[ \text{powerNtfisher}(\alpha, 100, 0.05, 0.25, \epsilon = 0.1, \mu = 1.2) \]
Statistical power of truncated product method test under Gaussian mixture model.

Use

`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,

\[ H_0 : X_i \sim F_0, \quad H_a : X_i \sim (1 - \epsilon)F_0 + \epsilon F_1 \]

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

Value

Power of the truncated product method test.

References


See Also

`statNsoft` for the definition of the statistic.

Examples

```r
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

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

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.

Value

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

References


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

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

### 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 < tau1 <= 1.
- **tau2**: normalization parameter. tau2 >= tau1.
- **M**: correlation matrix of the input statistics. Default = NULL assumes independence.

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

### References

### 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

Quantile of truncated product method statistic under the null hypothesis.

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 < tau1 <= 1.

Value
Quantile of truncated product method statistic.

References

See Also
stat.tpm for the definition of the statistic.

Examples
```r
## 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)
```
Construct soft-thresholding Fisher’s p-value combination statistic.

Usage

\texttt{statNsoft(p, tau1)}

Arguments

\begin{itemize}
  \item \texttt{p} - input p-values.
  \item \texttt{tau1} - truncation parameter=normalization parameter. \( \text{tau1} > 0 \).
\end{itemize}

Details

Let \( p_i, i = 1, ..., n \) be a sequence of p-values, the soft-thresholding statistic

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

. Soft-thresholding is the special case of TFisher when \( \text{tau1}=\text{tau2} \).

Value

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

References


Examples

\begin{verbatim}
pval <- runif(100)
statNsoft(p=pval, tau1=0.05)
\end{verbatim}
`statNsoftNomni` Construct omnibus soft-thresholding Fisher’s p-value combination statistic.

**Description**

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

**Usage**

`statNsoftNomni(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 \( x_i, i = 1, ..., n \) be a sequence of individual statistics with correlation matrix M, \( p_i \) be the corresponding two-sided p-values, then the soft-thresholding statistics

\[
Soft_j = \sum_{i=1}^{n} -2 \log\left(\frac{p_i}{\tau_{1j}}\right) I(p_i \leq \tau_{1j})
\]

, \( j = 1, ..., d \). 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**

Examples

```r
pval = runif(20)
TAU1 = c(0.01, 0.05, 0.5, 1)
statNsoftNomni(p=pval, TAU1=TAU1)
M = matrix(0.3, 20, 20) + diag(1-0.3, 20)
statNsoftNomni(p=pval, TAU1=TAU1, M=M)
```

Description

Construct thresholding Fisher’s p-value combination statistic.

Usage

```r
statNtfisher(p, tau1, tau2)
```

Arguments

- `p` - input p-values.
- `tau1` - truncation parameter. 0 < tau1 <= 1.
- `tau2` - normalization parameter. tau2 >= tau1.

Details

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

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

Value

Thresholding Fisher’s p-value combination statistic.

References


Examples

```r
pval <- runif(100)
statNtfisher(p=pval, tau1=0.05, tau2=0.25)
```
Construct omnibus thresholding Fisher’s (TFisher) p-value combination statistic.

Usage

\[ \text{stat.tfisher.omi}(p, \text{Tau1, Tau2, M = NULL, Mu = NULL, Sigma2 = NULL,}\] 
\[ P0 = \text{NULL}) \]

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

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

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

\[ W_o = \min_j G_j(\text{Soft}_j) \]

where \( G_j \) is the survival function of \( \text{Soft}_j \).

Value

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

References

Examples

\begin{verbatim}
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(c(0.3, 20, 20) + diag(1-0.3, 20)
stat.tfisher.omni(p=pval, TAU1=TAU1, TAU2=TAU2, M=M)
\end{verbatim}

\section*{Description}
Construct truncated product method statistic.

\section*{Usage}
\begin{verbatim}
stat.tpm(p, tau1)
\end{verbatim}

\section*{Arguments}
\begin{itemize}
\item \texttt{p} - input p-values.
\item \texttt{tau1} - truncation parameter. 0 < tau1 <= 1.
\end{itemize}

\section*{Details}
Let $p_i$, $i = 1, ..., n$ 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 tau2=1.

\section*{Value}
Truncated product method statistic.

\section*{References}


\section*{Examples}
\begin{verbatim}
pval <- runif(100)
stat.tpm(p=pval, tau1=0.05)
\end{verbatim}
Construct omnibus truncated product method statistic.

Usage

statNtpmNomni(pL tau1L 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 \( x_i, i = 1, ..., n \) 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

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

\( j = 1, ..., d \). 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


Examples

```r
pval = runif(20)
tau1 = c(0.01, 0.05, 0.5, 1)
statNtpmNomni(p=pval, tau1=tau1)
M = matrix(0.3, 20, 20) + diag(1-.3, 20)
statNtpmNomni(p=pval, tau1=tau1, M=M)
```
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