

# Package ‘TFisher’

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**Type** Package

**Title** Optimal Thresholding Fisher's P-Value Combination Method

**Version** 0.2.0

**Author** Hong Zhang and Zheyang Wu

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

**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                      *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**

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

---

### 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.  $0 < \text{tau1} \leq 1$ .  
tau2                              - normalization parameter.  $\text{tau2} \geq \text{tau1}$ .  
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  $\epsilon$  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

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. $0 < \text{tau1} \leq 1$ .
tau2	- normalization parameter. $\text{tau2} \geq \text{tau1}$ .
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 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. $0 < \text{tau1} \leq 1$ . $\text{tau1} > 0$ .
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 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.  $\tau_1 > 0$ .

**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  $\tau_1 = \tau_2$ .

**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 sstatistics.
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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