

# Package ‘CTGSA’

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**Type** Package

**Title** CTGSA : Covariance Thresholding for Gene Set Analysis of Genetic Pathway Data

**Version** 0.1.0

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**Description** There have been many studies to reveal the outcome related genes associated with a disease or a trait. Unlike the methods to compare the gene expression levels with mean scale, our study is focusing the coexpression of genes by regulatory factors in a gene set. We propose the CTGSA which calculates a statistic with thresholded correlation matrix and gives the selection of tuning parameter through percentile of correlations. It also calculates p-values which control the type I error rate.

**License** GPL-2

**Depends** mnormt, stats

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

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## Description

CTGSA

CTGSA : Covariance Thresholding for Gene Set Analysis of Genetic Pathway Data

## Usage

```
CTGSA(x, y, out.type = c("stat", "pvalue"),
      percentile.type = c("case-control", "all", "user-defined"),
      percentile.user = NULL, nperm = NULL)
```

**Arguments**

<code>x</code>	an input matrix of dimension <code>nobs</code> x <code>nvars</code> .
<code>y</code>	a response variable where <code>y=1</code> is the case and <code>y=0</code> is control.
<code>out.type</code>	character of output type of statistic('stat') and p-value('pvalue').
<code>percentile.type</code>	three threshold calculating types are supported as 'case-control', 'all', and 'user-defined'. To choose the threshold, 'case-control' computes the percentile with the first singular value for case and control. Percentile.type 'all' calculates the percentile with whole samples. The percentile is given by user in 'user-defined', and the threshold is then calculated for case and control. The default is case-control.
<code>percentile.user</code>	a numeric value of percentile in [0, 1]. To specify the percentile, give the percentile.type 'user-defined', and the integer value taken here will be used.
<code>nperm</code>	number of permutation - default is 1000.

**Details**

See the reference below for more information.

**Value**

A list of a statistic, an optional pvalue and permuted statistics, and arguments used.

**Examples**

```
x <- replicate(5, rnorm(100, 0, 1))
y <- rep(0:1, each=50)
CTGSA( x = x, y = y, out.type="stat", percentile.type = "all")

require(mnormt)
x <- rbind(rmnorm(50, rep(0, 5), diag(5) ),
           rmnorm(50, rep(0, 5), outer(1:5, 1:5, function(i, j) 0.6^abs(i-j) ) ))
y <- rep(0:1, each=50)
CTGSA(x=x, y=y, out.type="pvalue", percentile.type = "case-control", nperm=1000)
```

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