Package 'MedOr'

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Title Median Ordering Statistical R package

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Depends R (>= 2.15.0)

Description This package contains the functions used to perform some confidence
statistics based in population median.

License GPL (>= 3)

Repository Google Code

URL http://code.google.com/p/medor/

R topics documented:

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| conf.interval | *Confidence Interval for Population Median* |

Description

Evaluates a confidence interval for population median.

Usage

```
conf.interval(x,alpha=0.95,verbose=TRUE)
```

Arguments

x	observed vector/sample.
alpha	confidence level.
verbose	print time elapsed (TRUE).

Details

Evaluates a confidence interval for population median based in the order statistics. It is considered the distribution of order statistics to evaluate the confidence level of the interval. It is not assumed any asymptotic distribution.

Value

A list with components:

cint1	A vector with the confidence interval limits, given by the biggest confidence level lower than or equal to alpha.
cint2	A vector with the confidence interval limits, given by the lowest confidence level bigger than or equal to alpha. If there is not interval with confidence level bigger than or equal to alpha, then cint2 is NULL.
alpha	Desired confidence level.
run.time	Time spent.
call	command evaluated.

Examples

```
x <- rnorm(10,0,1)
conf.interval(x)
```

`conf.statement`	*Confidence Statement for Ordered Population Median*

Description

Evaluates the Confidence Statement for Ordered Population Median.

Usage

```
conf.statement(data,verbose=TRUE)
```

Arguments

`data`	is a list of observed vectors/samples.
`verbose`	print the results (TRUE).

Details

The confidence statement is evaluated for the population median consedering: The population median of the group 1 is lower than the population median of the group 2, and this is lower than the population median of the group 3, and so... That is, M1 < M2 < ... < Mk, where Mj is the population median of the group j.

The group j is the j-th vector in the data (a list object).

Value

A list with components:

`call`	command evaluated.
`statement.level`	
	the confidence statement level.
`stat.order.i`	the numbers of the order statistics of i-th group.
`conf.statement.i`	
	the values of the order statistics of i-th group.
`total.groups`	the total number of groups.
`run.time`	Time spent.

Examples

```
set.seed(1234)
# Statement: M1 < M2 < M3, where Mj is the population
#    median of the group j.
data <- NULL
data$x1 <- rnorm(10,0,1)
data$x2 <- rnorm(10,1,1)
data$x3 <- rnorm(10,2,1)
conf.statement(data)
```

```
# Statement: M2 < M3 < M1, where Mj is the population
#   median of the group j.
data2 <- NULL
data2$g1 <- data$x2
data2$g2 <- data$x3
data2$g3 <- data$x1
conf.statement(data2)
```

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gleason7   *Data set Gleason 7*

Description

Pre-operative Gleason score provide valuable prognosis in cases of prostate cancer, in general. However, for patient's Gleason 7 it does not. This is because Gleason 7 tumors display great morphological heterogeneity among regions. The data set have the microarray data of gene RPS28 for recurrent (R) and non-recurrent (NR) Gleason 7 prostate cancer patients.

Value

The data variables are:

R	Recurrent cases.
NR	Non-recurrent cases.

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schizophrenia   *Data set Schizophrenia*

Description

Data extracted from study Altar A of the Stanley Medical Research Institute online genomics database (SMRIDB).

Value

The data variables are:

group	1: for control group, and 2: for schizophrenic.
others variables	each column represents the measure of a microarray probe.

Source

The Stanley Medical Research Institute online genomics database, www.stanleygenomics.org.

References

Higgs, B.W., Elashoff, M., Richman, S. and Barci, B. (2006) *An online database for brain disease research.* BMC Genomics 2006, 7:70, (DOI 10.1186/1471-2164-7-70).

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