

# 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/>

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

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**Description**

Evaluates a confidence interval for population median.

**Usage**

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

**Arguments**

<code>x</code>	observed vector/sample.
<code>alpha</code>	confidence level.
<code>verbose</code>	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:

<code>cint1</code>	A vector with the confidence interval limits, given by the biggest confidence level lower than or equal to alpha.
<code>cint2</code>	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 <code>cint2</code> is NULL.
<code>alpha</code>	Desired confidence level.
<code>run.time</code>	Time spent.
<code>call</code>	command evaluated.

**Examples**

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

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conf.statement	<i>Confidence Statement for Ordered Population Median</i>
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**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 considering: 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,  $M_1 < M_2 < \dots < M_k$ , where  $M_j$  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:  $M_1 < M_2 < M_3$ , where  $M_j$  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:  $M_2 < M_3 < M_1$ , where  $M_j$  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*

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### **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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