

# Package ‘ICtest’

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**Type** Package

**Title** Estimating and Testing the Number of Interesting Components in Linear Dimension Reduction

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**Description** For different linear dimension reduction methods like principal components analysis (PCA), independent components analysis (ICA) and supervised linear dimension reduction tests and estimates for the number of interesting components (ICs) are provided.

**License** GPL (>= 2)

**Suggests** knitr, rmarkdown, fICA

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**NeedsCompilation** yes

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components

*Generic Components Extraction Function*

---

### Description

Function to extract components from an object. If the object is of class `ictest` or `ladle` the user can choose if all components are extracted or only those which were interesting under the null hypothesis.

**Usage**

```

components(x, ...)
## S3 method for class 'icctest'
components(x, which = "all", ...)
## S3 method for class 'ladle'
components(x, which = "all", ...)

```

**Arguments**

**x** an object which has a components method, like for example an icctest object.

**which** for an object of class icctest. If "all", then all components S in the icctest object are extracted. If "k", then only the first k components are extracted, where the value of k is taken from the icctest object. This is only meaningful if k was at least 1.

**...** arguments passed on to other methods.

**Value**

a matrix with the components.

**Author(s)**

Klaus Nordhausen

**Examples**

```

n <- 200
X <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n), rnorm(n))

TestCov <- PCAasymp(X, k = 2)
head(components(TestCov))
head(components(TestCov, which = "k"))

```

---

 covSIR

---

*Supervised Scatter Matrix as Used in Sliced Inverse Regression*


---

**Description**

Sliced Inverse Regression (SIR) can be seen as special case of Supervised ICS (SICS) and this function gives the supervised scatter matrix for SIR

**Usage**

```

covSIR(X, y, h = 10, ...)

```

**Arguments**

X	a numeric data matrix.
y	a numeric response vector.
h	the number of slices.
...	arguments passed on to <a href="#">quantile</a> .

**Details**

This supervised scatter matrix is usually used as the second scatter matrix in SICS to obtain a SIR type supervised linear dimension reduction. For that purpose covSIR first divides the response y into h slices using the corresponding quantiles as cut points. Then for each slice the mean vector of X is computed and the resulting supervised scatter matrix consist of the covariance matrix of these mean vectors.

The function might have problems if the sample size is too small.

**Value**

a supervised scatter matrix

**Author(s)**

Klaus Nordhausen

**References**

- Liski, E., Nordhausen, K. and Oja, H. (2014), *Supervised invariant coordinate selection*, *Statistics: A Journal of Theoretical and Applied Statistics*, **48**, 711–731. <doi:10.1080/02331888.2013.800067>.
- Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, **188**, 104830. <doi:10.1016/j.jmva.2021.104830>.

**See Also**

[ics](#)

**Examples**

```
X <- matrix(rnorm(1000), ncol = 5)
eps <- rnorm(200, sd = 0.1)
y <- 2 + 0.5 * X[, 1] + 2 * X[, 3] + eps

covSIR(X, y)
```

FOBIasymp

*Testing for the Number of Gaussian Components in NGCA or ICA Using FOBI*

## Description

In non-gaussian component analysis (NGCA) and independent components analysis (ICA) gaussian components are considered as uninteresting. The function tests, based on FOBI, if there are  $p-k$  gaussian components where  $p$  is the dimension of the data. The function offers three different test versions.

## Usage

```
FOBIasymp(X, k, type = "S3", model = "NGCA", method = "satterthwaite")
```

## Arguments

<code>X</code>	numeric data matrix.
<code>k</code>	the number of non-gaussian components under the null.
<code>type</code>	which of the three tests to perform. Options are "S1", "S2" and "S3". For the differences see the details section.
<code>model</code>	What is the underlying assumption of the non-gaussian parts. Options are general "NGCA" model and "ICA" model.
<code>method</code>	if <code>type = "S1"</code> the teststatistic has as limiting distribution a weighted sum of chisquare distributions. To compute the p-value then the function used is <a href="#">pchisqsum</a> . The method argument specifies which method <a href="#">pchisqsum</a> uses for the computation. Options are "satterthwaite", "integration" and "saddlepoint".

## Details

The function jointly diagonalizes the regular covariance and the matrix of fourth moments. Note however that in this case the matrix of fourth moments is not made consistent under the normal model by dividing it by  $p + 2$ , as for example done by the function [cov4](#) where  $p$  denotes the dimension of the data. Therefore the eigenvalues of this generalized eigenvector-eigenvalue problem which correspond to normally distributed components should be  $p+2$ .

Given eigenvalues  $d_1, \dots, d_p$  the function thus orders the components in decending order according to the values of  $(d_i - (p + 2))^2$ .

Under the null it is then assumed that the first  $k$  interesting components are mutually independent and non-normal and the last  $p-k$  are gaussian.

Three possible tests are then available to test this null hypothesis for a sample of size  $n$ :

1. `type="S1"`: The test statistic  $T$  is the variance of the last  $p-k$  eigenvalues around  $p+2$ :

$$T = n \sum_{i=k+1}^p (d_i - (p + 2))^2$$

the limiting distribution of which under the null is the sum of two weighted chisquare distributions with weights:

$$w_1 = 2\sigma_1/(p - k) \text{ and } w_2 = 2\sigma_1/(p - k) + \sigma_2.$$

and degrees of freedom:

$$df_1 = (p - k - 1)(p - k + 2)/2 \text{ and } df_2 = 1.$$

2. type="S2": Another possible version for the test statistic is a scaled sum of the variance of the eigenvalues around the mean plus the variance around the expected value under normality ( $p+2$ ). Denote  $VAR_{dpk}$  as the variance of the last  $p-k$  eigenvalues and  $VAR2_{dpk}$  as the variance of these eigenvalues around  $p + 2$ . Then the test statistic is:

$$T = (n(p - k)VAR_{dpk})/(2\sigma_1) + (nVAR2_{dpk})/(2\sigma_1/(p - k) + \sigma_2)$$

This test statistic has a limiting chisquare distribution with  $(p - k - 1)(p - q + 2)/2 + 1$  degrees of freedom.

3. type="S3": The third possible test statistic just checks the equality of the last  $p-k$  eigenvalues using only the first part of the test statistic of type="S2". The test statistic is then:

$$T = (n(p - k)VAR_{dpk})/(2\sigma_1)$$

and has a limiting chisquare distribution with  $(p - k - 1)(p - q + 2)/2$  degrees of freedom.

The constants  $\sigma_1$  and  $\sigma_2$  depend on the underlying model assumptions as specified in argument `model` and are estimated from the data.

## Value

A list of class `ictest` inheriting from class `hctest` containing:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>parameter</code>	the degrees of freedom of the test or the degrees of freedoms and the corresponding weights of the test in case the test has as its limiting distribution a weighted sum of chisquare distributions.
<code>method</code>	character string denoting which test was performed.
<code>data.name</code>	character string giving the name of the data.
<code>alternative</code>	character string specifying the alternative hypothesis.
<code>k</code>	the number of non-gaussian components used in the testing problem.
<code>W</code>	the transformation matrix to the independent components. Also known as unmixing matrix.
<code>S</code>	data matrix with the centered independent components.
<code>D</code>	the underlying FOBI eigenvalues.
<code>MU</code>	the location of the data which was subtracted before calculating the independent components.
<code>sigma1</code>	the asymptotic constant <code>sigma1</code> needed for the asymptotic test(s).
<code>sigma2</code>	the asymptotic constant <code>sigma2</code> needed for the asymptotic test(s).
<code>type</code>	the value of <code>type</code> .
<code>model</code>	the value of <code>model</code> .

**Author(s)**

Klaus Nordhausen

**References**

Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, 188, 104830. <doi:10.1016/j.jmva.2021.104830>.

Nordhausen, K., Oja, H., Tyler, D.E. and Virta, J. (2017), *Asymptotic and Bootstrap Tests for the Dimension of the Non-Gaussian Subspace*, *Signal Processing Letters*, 24, 887–891. <doi:10.1109/LSP.2017.2696880>.

**See Also**

[FOBI](#), [FOBIboot](#)

**Examples**

```
n <- 1500
S <- cbind(runif(n), rchisq(n, 2), rexp(n), rnorm(n), rnorm(n), rnorm(n))
A <- matrix(rnorm(36), ncol = 6)
X <- S %*% t(A)

FOBIasympt(X, k = 2)
FOBIasympt(X, k = 3, type = "S1")
FOBIasympt(X, k = 0, type = "S2", model = "ICA")
```

FOBIboot

*Bootstrap-based Testing for the Number of Gaussian Components in ICA Using FOBI*

**Description**

In independent components analysis (ICA) gaussian components are considered as uninteresting. The function uses bootstrapping tests, based on FOBI, to decide if there are  $p-k$  gaussian components where  $p$  is the dimension of the data. The function offers two different bootstrapping strategies.

**Usage**

```
FOBIboot(X, k, n.boot = 200, s.boot = "B1")
```

**Arguments**

X	a numeric data matrix with $p > 1$ columns.
k	the number of non-gaussian components under the null.
n.boot	number of bootstrapping samples.
s.boot	bootstrapping strategy to be used. Possible values are "B1", "B2". See details for further information.

## Details

As in `FOBIasymp` the function jointly diagonalizes the regular covariance and the matrix of fourth moments. Note that in this case the matrix of fourth moments is not made consistent under the normal model by dividing it by  $p + 2$ , as for example done by the function `cov4` where  $p$  denotes the dimension of the data. Therefore the eigenvalues of this generalized eigenvector-eigenvalue problem which correspond to normally distributed components should be  $p+2$ . Given eigenvalues  $d_1, \dots, d_p$  the function thus orders the components in descending order according to the values of  $(d_i - (p + 2))^2$ .

Under the null it is then assumed that the first  $k$  interesting components are mutually independent and non-normal and the last  $p-k$  components are gaussian.

Let  $d_1, \dots, d_p$  be the ordered eigenvalues,  $W$  the correspondingly ordered unmixing matrix,  $s_i = W(x_i - MU)$  the corresponding source vectors which give the source matrix  $S$  which can be decomposed into  $S_1$  and  $S_2$  where  $S_1$  is the matrix with the  $k$  non-gaussian components and  $S_2$  the matrix with the gaussian components (under the null).

The test statistic is then  $T = n \sum_{i=k+1}^p (d_i - (p + 2))^2$

Two possible bootstrap tests are provided for testing that the last  $p-k$  components are gaussian and independent from the first  $k$  components:

1. `s.boot="B1"`: The first strategy has the following steps:
  - (a) Take a bootstrap sample  $S_1^*$  of size  $n$  from  $S_1$ .
  - (b) Take a bootstrap sample  $S_2^*$  consisting of a matrix of standard normally distributed elements.
  - (c) Combine  $S^* = (S_1^*, S_2^*)$  and create  $X^* = S^*W$ .
  - (d) Compute the test statistic based on  $X^*$ .
  - (e) Repeat the previous steps `n.boot` times.

Note that in this bootstrapping test the assumption of "independent components" is not used, it is only used that the last  $p - k$  components are gaussian and independent from the first  $k$  components. Therefore this strategy can be applied in an independent component analysis (ICA) framework and in a non-gaussian components analysis (NGCA) framework.

2. `s.boot="B2"`: The second strategy has the following steps:
  - (a) Take a bootstrap sample  $S_1^*$  of size  $n$  from  $S_1$  where the subsampling is done separately for each independent component.
  - (b) Take a bootstrap sample  $S_2^*$  consisting of a matrix of standard normally distributed elements.
  - (c) Combine  $S^* = (S_1^*, S_2^*)$  and create  $X^* = S^*W$ .
  - (d) Compute the test statistic based on  $X^*$ .
  - (e) Repeat the previous steps `n.boot` times.

This bootstrapping strategy assumes a full ICA model and cannot be used in an NGCA framework.

## Value

A list of class `ictest` inheriting from class `hctest` containing:

`statistic`          the value of the test statistic.



p.value	the p-value of the test.
parameter	the number of bootstrapping samples used to obtain the p-value.
method	character string which test was performed.
data.name	character string giving the name of the data.
alternative	character string specifying the alternative hypothesis.
k	the number of non-gaussian components used in the testing problem.
W	the transformation matrix to the independent components. Also known as un-mixing matrix.
S	data matrix with the centered independent components.
D	the underlying FOBI eigenvalues.
MU	the location of the data which was subtracted before calculating the independent components.
s.boot	character string which bootstrapping strategy was used.

**Author(s)**

Klaus Nordhausen

**References**

Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, 188, 104830. <doi:10.1016/j.jmva.2021.104830>.

Nordhausen, K., Oja, H., Tyler, D.E. and Virta, J. (2017), *Asymptotic and Bootstrap Tests for the Dimension of the Non-Gaussian Subspace*, *Signal Processing Letters*, 24, 887–891. <doi:10.1109/LSP.2017.2696880>.

**See Also**

[FOBI](#), [FOBIasymp](#)

**Examples**

```
n <- 1500
S <- cbind(runif(n), rchisq(n, 2), rexp(n), rnorm(n), rnorm(n), rnorm(n))
A <- matrix(rnorm(36), ncol = 6)
X <- S %*% t(A)

FOBIboot(X, k = 2)
FOBIboot(X, k = 3, s.boot = "B1")
FOBIboot(X, k = 0, s.boot = "B2")
```

---

FOBIladle	<i>Ladle Estimate to Estimate the Number of Gaussian Components in ICA or NGCA</i>
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---

**Description**

The ladle estimator uses the eigenvalues and eigenvectors of FOBI to estimate the number of Gaussian components in ICA or NGCA.

**Usage**

```
FOBIladle(X, n.boot = 200,
          ncomp = ifelse(ncol(X) > 10, floor(ncol(X)/log(ncol(X))), ncol(X) - 1))
```

**Arguments**

X	numeric data matrix.
n.boot	number of bootstrapping samples to be used.
ncomp	The number of components among which the ladle estimator is to be searched. The default here follows the recommendation of Luo and Li 2016.

**Details**

The model here assumes that in ICA or NGCA there are  $k$  non-gaussian components and  $p-k$  gaussian components. The idea is then to decide which eigenvalues differ from  $p+2$ . The ladle estimate for this purpose combines the values of the scaled eigenvalues and the variation of the eigenvectors based on bootstrapping. The idea there is that for distinct eigenvalues the variation of the eigenvectors is small and for equal eigenvalues the corresponding eigenvectors have large variation.

This measure is then computed assuming  $k=0, \dots, ncomp$  and the ladle estimate for  $k$  is the value where the measure takes its minimum.

**Value**

A list of class ladle containing:

method	the string FOBI.
k	the estimated number of non-gaussian components.
fn	vector giving the measures of variation of the eigenvectors using the bootstrapped eigenvectors for the different number of components.
phin	normalized eigenvalues of the FOBI matrix.
gn	the main criterion for the ladle estimate - the sum of fn and phin. k is the value where gn takes its minimum
lambda	the eigenvalues of the FOBI matrix.
W	the transformation matrix to the independent components. Also known as un-mixing matrix.

S	data matrix with the centered independent components.
MU	the location of the data which was subtracted before calculating the independent components.
data.name	the name of the data for which the ladle estimate was computed.

**Author(s)**

Klaus Nordhausen

**References**

Luo, W. and Li, B. (2016), *Combining Eigenvalues and Variation of Eigenvectors for Order Determination*, *Biometrika*, 103. 875–887. <doi:10.1093/biomet/asw051>

**See Also**

[ladleplot](#)

**Examples**

```
n <- 1000
X <- cbind(rexp(n), rt(n,5), rnorm(n), rnorm(n), rnorm(n), rnorm(n))

test <- FOBIladle(X)
test
summary(test)
plot(test)
ladleplot(test)
```

---

ggladleplot

*Ladle Plot for an Object of Class ladle Using ggplot2*

---

**Description**

The ladle plot is a measure to decide about the number of interesting components. Of interest for the ladle criterion is the minimum. The function here offers however also to plot other criterion values which are part of the actual ladle criterion.

**Usage**

```
ggladleplot(x, crit = "gn", type="l", ylab = crit,
            xlab = "component", main = deparse(substitute(x)), ...)
```

**Arguments**

x	an object of class ladle.
crit	the criterion to be plotted, options are "gn", "fn", "phin" and "lambda".
type	plotting type.
ylab	default ylab value.
xlab	default xlab value.
main	default title.
...	other arguments for the plotting functions.

**Details**

The main criterion of the ladle is the scaled sum of the eigenvalues and the measure of variation of the eigenvectors up to the component of interest.

The sum is denoted "gn" and the individual parts are "fn" for the measure of the eigenvector variation and "phin" for the scaled eigenvalues. The last option "lambda" corresponds to the unscaled eigenvalues yielding then a screeplot.

**Author(s)**

Klaus Nordhausen, Joni Virta

**References**

Luo, W. and Li, B. (2016), *Combining Eigenvalues and Variation of Eigenvectors for Order Determination*, *Biometrika*, 103. 875–887. <doi:10.1093/biomet/asw051>

**See Also**

[FOBIladle](#), [PCAladle](#), [SIRladle](#)

**Examples**

```
n <- 1000
X <- cbind(rexp(n), rt(n,5), rnorm(n), rnorm(n), rnorm(n), rnorm(n))
test <- FOBIladle(X)
ggladleplot(test)
ggladleplot(test, crit="fn")
ggladleplot(test, crit="phin")
ggladleplot(test, crit="lambda")
```

---

`ggplot.ictest`*Scatterplot Matrix for a ictest Object using ggplot2*

---

### Description

For an object of class `ictest`, plots either the pairwise scatter plot matrix using `ggpairs` from `GGally`, or the time series plots of the underlying components using `ggplot2`. The user can choose if only the components considered interesting or all of them should be plotted. Aesthetics can be passed to `ggpairs` as well.

### Usage

```
## S3 method for class 'ictest'  
ggplot(data, mapping = aes(), mapvar = NULL, which = "all", ...,  
        environment=parent.frame())
```

### Arguments

<code>data</code>	object of class <code>ictest</code>
<code>mapping</code>	aesthetic mapping, see documentation for <a href="#">ggpairs</a> . If <code>x</code> has the class <code>mts</code> then this argument is not used.
<code>mapvar</code>	<code>data.frame</code> of the external variables used by the aesthetic mappings. If <code>x</code> has the class <code>mts</code> then this argument is not used.
<code>which</code>	if <code>"all"</code> , then all components of <code>S</code> in the <code>ictest</code> object are plotted. If <code>"k"</code> , then only the first <code>k</code> components are plotted, where the value of <code>k</code> is taken from the <code>ictest</code> object. This is only meaningful if <code>k</code> was at least 2.
<code>...</code>	arguments passed on to <a href="#">ggpairs</a> . If the component matrix has the class <code>mts</code> , <code>xts</code> or <code>zoo</code> then this argument is not used.
<code>environment</code>	not used but needed for consistency.

### Details

If the component matrix has the class `mts`, `xts` or `zoo` then a time series plot will be plotted using `ggplot2`. Otherwise, a pairwise scatter plot matrix will be plotted using `GGally`.

### Author(s)

Klaus Nordhausen, Joni Virta

### See Also

[plot.ictest](#), [pairs](#)

**Examples**

```
# The data
X <- iris[, 1:4]

# The aesthetics variables
mapvar <- data.frame(iris[, 5])
colnames(mapvar) <- "species"

TestCov <- PCAasym(X, k = 2)
ggplot(TestCov)
ggplot(TestCov, aes(color = species), mapvar = mapvar, which = "k")
```

ggplot.ladle

*Scatterplot Matrix for a ladle Object using ggplot2***Description**

For an object of class `ladle`, plots either the pairwise scatter plot matrix using `ggpairs` from `GGally`, or the time series plots of the underlying components using `ggplot2`. The user can choose if only the components considered interesting or all of them should be plotted. Aesthetics can be passed to `ggpairs` as well.

**Usage**

```
## S3 method for class 'ladle'
ggplot(data, mapping = aes(), mapvar = NULL, which = "all", ...,
        environment=parent.frame())
```

**Arguments**

<code>data</code>	object of class <code>ladle</code>
<code>mapping</code>	aesthetic mapping, see documentation for <code>ggpairs</code> . If <code>x</code> has the class <code>mts</code> then this argument is not used.
<code>mapvar</code>	<code>data.frame</code> of the external variables used by the aesthetic mappings. If <code>x</code> has the class <code>mts</code> then this argument is not used.
<code>which</code>	if <code>"all"</code> , then all components of <code>S</code> in the <code>ladle</code> object are plotted. If <code>"k"</code> , then only the first <code>k</code> components are plotted, where the value of <code>k</code> is taken from the <code>ladle</code> object. This is only meaningful if <code>k</code> was at least 2.
<code>...</code>	arguments passed on to <code>ggpairs</code> . If the component matrix has the class <code>mts</code> , <code>xts</code> or <code>zoo</code> then this argument is not used.
<code>environment</code>	not used but needed for consistency.

**Details**

If the component matrix has the class `mts`, `xts` or `zoo` then a time series plot will be plotted using `ggplot2`. Otherwise, a pairwise scatter plot matrix will be plotted using `GGally`.

**Author(s)**

Klaus Nordhausen, Joni Virta

**See Also**

[plot.ladle](#), [pairs](#)

**Examples**

```
# The data
X <- as.matrix(iris[, 1:4])

# The aesthetics variables
mapvar <- data.frame(iris[, 5])
colnames(mapvar) <- "species"

ladle_res <- PCAladle(X)

# The estimate
summary(ladle_res)

# Plots of the components
ggplot(ladle_res)
ggplot(ladle_res, aes(color = species), mapvar = mapvar, which = "k")
```

---

`ggscreepplot`

*ggplot2-style screeplot*

---

**Description**

A generic method for ggplot2-style screeplots.

**Usage**

```
ggscreepplot(x, ...)
```

**Arguments**

<code>x</code>	An object of an appropriate class.
<code>...</code>	Additional arguments.

**Author(s)**

Joni Virta, Klaus Nordhausen

---

ggscreeplot.ictest      *Screeplot for an ictest Object Using ggplot2*

---

### Description

Plots the criterion values of an ictest object against its index number using ggplot2. Two versions of this screeplot are available.

### Usage

```
## S3 method for class 'ictest'  
ggscreeplot(x, type = "barplot", main = deparse(substitute(x)),  
            ylab = "criterion", xlab = "component", ...)
```

### Arguments

x	object of class ictest.
type	barplot if a barplot or lines if a line plot is preferred.
main	main title of the plot.
ylab	y-axis label.
xlab	x-axis label.
...	arguments passed to and from methods.

### Author(s)

Klaus Nordhausen, Joni Virta

### See Also

[screeplot.ictest](#)

### Examples

```
n <- 200  
X <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n), rnorm(n))  
  
TestCov <- PCAasymp(X, k = 2)  
ggscreeplot(TestCov)
```



---

ICSboot	<i>Bootstrap-based Testing for the Number of Gaussian Components in NGCA Using Two Scatter Matrices</i>
---------	---

---

### Description

In independent components analysis (ICA) gaussian components are considered as uninteresting. The function uses bootstrapping tests, based on ICS using any combination of two scatter matrices, to decide if there are  $p-k$  gaussian components where  $p$  is the dimension of the data. The function offers two different bootstrapping strategies.

### Usage

```
ICSboot(X, k, S1=cov, S2=cov4, S1args=NULL, S2args=NULL, n.boot = 200, s.boot = "B1")
```

### Arguments

X	a numeric data matrix with $p > 1$ columns.
k	the number of non-gaussian components under the null.
S1	name of the first scatter matrix function. Can only return a matrix. Default is <a href="#">cov</a>
.	.
S2	name of the second scatter matrix function. Can only return a matrix. Default is <a href="#">cov4</a>
S1args	list with optional additional arguments for S1.
S2args	list with optional additional arguments for S2.
n.boot	number of bootstrapping samples.
s.boot	bootstrapping strategy to be used. Possible values are "B1", "B2". See details for further information.

### Details

While in [FOBIasympt](#) and [FOBIboot](#) the two scatters used are always [cov](#) and [cov4](#) this function can be used with any two scatter functions. In that case however the value of the Gaussian eigenvalues are in general not known and depend on the scatter functions used. Therefore the test uses as test statistic the  $k$  successive eigenvalues with the smallest variance. Which means the default here might differ from [FOBIasympt](#) and [FOBIboot](#).

Given eigenvalues  $d_1, \dots, d_p$  the function thus orders the components in descending order according to the "variance" criterion .

Under the null it is then assumed that the first  $k$  interesting components are mutually independent and non-normal and the last  $p-k$  components are gaussian.

Let  $d_1, \dots, d_p$  be the ordered eigenvalues,  $W$  the correspondingly ordered unmixing matrix,  $s_i = W(x_i - MU)$  the corresponding source vectors which give the source matrix  $S$  which can be

decomposed into  $S_1$  and  $S_2$  where  $S_1$  is the matrix with the  $k$  non-gaussian components and  $S_2$  the matrix with the gaussian components (under the null).

Two possible bootstrap tests are provided for testing that the last  $p-k$  components are gaussian and independent from the first  $k$  components:

1. `s.boot="B1"`: The first strategy has the following steps:
  - (a) Take a bootstrap sample  $S_1^*$  of size  $n$  from  $S_1$ .
  - (b) Take a bootstrap sample  $S_2^*$  consisting of a matrix with gaussian random variables having  $cov(S_2)$ .
  - (c) Combine  $S^* = (S_1^*, S_2^*)$  and create  $X^* = S^*W$ .
  - (d) Compute the test statistic based on  $X^*$ .
  - (e) Repeat the previous steps `n.boot` times.

Note that in this bootstrapping test the assumption of "independent components" is not used, it is only used that the last  $p - k$  components are gaussian and independent from the first  $k$  components. Therefore this strategy can be applied in an independent component analysis (ICA) framework and in a non-gaussian components analysis (NGCA) framework.

2. `s.boot="B2"`: The second strategy has the following steps:
  - (a) Take a bootstrap sample  $S_1^*$  of size  $n$  from  $S_1$  where the subsampling is done separately for each independent component.
  - (b) Take a bootstrap sample  $S_2^*$  consisting of a matrix with gaussian random variables having  $cov(S_2)$ .
  - (c) Combine  $S^* = (S_1^*, S_2^*)$  and create  $X^* = S^*W$ .
  - (d) Compute the test statistic based on  $X^*$ .
  - (e) Repeat the previous steps `n.boot` times.

This bootstrapping strategy assumes a full ICA model and cannot be used in an NGCA framework. Note that when the goal is to recover the non-gaussian independent components both scatters used must have the independence property.

## Value

A list of class `ictest` inheriting from class `hctest` containing:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>parameter</code>	the number of bootstrapping samples used to obtain the p-value.
<code>method</code>	character string which test was performed and which scatters were used.
<code>data.name</code>	character string giving the name of the data.
<code>alternative</code>	character string specifying the alternative hypothesis.
<code>k</code>	the number of non-gaussian components used in the testing problem.
<code>W</code>	the transformation matrix to the independent components. Also known as un-mixing matrix.
<code>S</code>	data matrix with the centered independent components.
<code>D</code>	the underlying eigenvalues.
<code>MU</code>	the location of the data which was subtracted before calculating the independent components.
<code>s.boot</code>	character string which bootstrapping strategy was used.

**Author(s)**

Klaus Nordhausen

**References**

Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, 188, 104830. <doi:10.1016/j.jmva.2021.104830>.

Nordhausen, K., Oja, H., Tyler, D.E. and Virta, J. (2017), *Asymptotic and Bootstrap Tests for the Dimension of the Non-Gaussian Subspace*, *Signal Processing Letters*, 24, 887–891. <doi:10.1109/LSP.2017.2696880>.

Radojicic, U. and Nordhausen, K. (2020), *Non-Gaussian Component Analysis: Testing the Dimension of the Signal Subspace*. In Maciak, M., Pestas, M. and Schindler, M. (editors) "Analytical Methods in Statistics. AMISTAT 2019", 101–123, Springer, Cham. <doi:10.1007/978-3-030-48814-7\_6>.

**See Also**

[ics](#), [FOBIboot](#), [FOBIasympt](#)

**Examples**

```
n <- 750
S <- cbind(runif(n), rchisq(n, 2), rexp(n), rnorm(n), rnorm(n), rnorm(n))
A <- matrix(rnorm(36), ncol = 6)
X <- S %*% t(A)

# n.boot is small for demonstration purpose, should be larger
ICSboot(X, k=1, n.boot=10)

if(require("ICSNP")){
  myTyl <- function(X,...) HR.Mest(X,...)$scatter
  myT <- function(X,...) tM(X,...)$V

  # n.boot is small for demonstration purpose, should be larger
  ICSboot(X, k=3, S1=myT, S2=myTyl, s.boot = "B2", n.boot=4)
}
```

**Description**

Performs dimension estimation using various search strategies (forward, backward, binary) and hypothesis testing methods that evaluate whether the true dimension  $d \leq k$ . The search continues until a p-value exceeds the specified alpha threshold, which indicates that the null hypothesis is not rejected. The search can optionally continue to test all values, as there may not be a global optimum in the tested range.

**Usage**

```
kSearch(
  X,
  method,
  search = c("forward", "backward", "binary"),
  alpha = 0.05,
  early_stop = NULL,
  min_dim = NULL,
  max_dim = NULL,
  ...
)
```

**Arguments**

X	A data matrix with $p > 1$ columns.
method	A function that performs a hypothesis test given X and dimension k. For more details on supported tests, see the "Details" section below.
search	A character string specifying the search strategy. Options are forward (default), backward and binary. For more details on search techniques, see the "Details" section below.
alpha	A numeric significance level (default = 0.05) used as the threshold for rejecting the null hypothesis.
early_stop	Logical or NULL. Controls whether the search stops early once the null hypothesis is not rejected. If NULL (default), the behavior is determined by the selected search strategy: TRUE for "forward" and "backward", and FALSE for "binary". If explicitly set to TRUE or FALSE, this overrides the strategy's default behavior.
min_dim	Optional integer to limit the minimum dimension to search. By default, this is set according to the method being used.
max_dim	Optional integer to limit the maximum dimension to search. By default, this is set according to the method being used.
...	Additional arguments passed to the testing function method.

**Details**

This function is designed to work with the following tests:

- [FOBIasymp](#), [FOBIboot](#)
- [ICSboot](#)
- [NGPPsim](#)
- [PCAasymp](#), [PCAbboot](#), [PCAschott](#)
- [SIRasymp](#), [SIRboot](#)

These tests evaluate the null hypothesis that the true dimension  $d \leq k$ , and return a p-value indicating whether the null is rejected or not.

The search work as follows:

- "forward" (default) performs a linear search starting from the smallest possible value of  $k$  and incrementing upward. Returns the smallest  $k$  where the null is not rejected.
- "backward" performs a linear search starting from the largest possible value of  $k$  and decrementing downward. Returns  $k+1$ , where  $k$  is the largest dimension where the null is rejected.
- "binary" splits the possible range of  $k$ s in half and performs a binary search. This search may skip testing some possible  $k$  values, but it is typically faster than linear search.

### Value

An object of class `ictest` inheriting from `hctest`, with additional elements:

`tested.ks` An integer vector of all tested values of  $k$  during the search.

`tested.ks.pvals` A numeric vector of  $p$ -values corresponding to each tested  $k$ .

### Author(s)

Katariina Perkonjoja

### Examples

```
# Applying forward search with PCAasympt while evaluating
# all valid values of k (early_stop = FALSE)
n <- 200
S <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5),
           rnorm(n), rnorm(n), rnorm(n))
A <- rorth(5)
X <- S %*% t(A)
result <- kSearch(
  X = X,
  method = PCAasympt,
  alpha = 0.05,
  search = "forward",
  early_stop = FALSE
)

result
```

---

ladle

*Ladle estimate for an arbitrary matrix*

---

### Description

The `ladle` estimates the rank of a symmetric matrix  $S$  by combining the classical screeplot with an estimate of the rank from the bootstrap eigenvector variability of  $S$ .

### Usage

```
ladle(x, S, n.boots = 200, ...)
```

**Arguments**

x	n x p data matrix.
S	Function for computing a q x q symmetric matrix from the data x.
n.boots	The number of bootstrap samples.
...	Furhter parameters passed to S

**Details**

Assume that the eigenvalues of the population version of S are  $\lambda_1 \geq \dots \geq \lambda_k > \lambda_{k+1} = \dots = \lambda_p$ . The ladle estimates the true value of  $k$  (for example the rank of S) by combining the classical screeplot with estimate of  $k$  from the bootstrap eigenvector variability of S.

For applying the ladle to either PCA, FOBI or SIR, see the dedicated functions [PCAladle](#), [FOBIladle](#), [SIRladle](#).

**Value**

A list of class ladle containing:

method	The string “general”.
k	The estimated value of k.
fn	A vector giving the measures of variation of the eigenvectors using the bootstrapped eigenvectors for the different number of components.
phin	The normalized eigenvalues of the S matrix.
gn	The main criterion for the ladle estimate - the sum of fn and phin. k is the value where gn takes its minimum.
lambda	The eigenvalues of the covariance matrix.
data.name	The name of the data for which the ladle estimate was computed.

**Author(s)**

Joni Virta

**References**

Luo, W. and Li, B. (2016), Combining Eigenvalues and Variation of Eigenvectors for Order Determination, *Biometrika*, 103. 875-887. <doi:10.1093/biomet/asw051>

**See Also**

[PCAladle](#), [FOBIladle](#), [SIRladle](#)

**Examples**

```

# Function for computing the left CCA matrix
S_CCA <- function(x, dim){
  x1 <- x[, 1:dim]
  x2 <- x[, -(1:dim)]
  stand <- function(x){
    x <- as.matrix(x)
    x <- sweep(x, 2, colMeans(x), "-")
    eigcov <- eigen(cov(x), symmetric = TRUE)
    x%%(eigcov$vectors%%diag((eigcov$values)^(-1/2))%%t(eigcov$vectors))
  }

  x1stand <- stand(x1)
  x2stand <- stand(x2)

  crosscov <- cov(x1stand, x2stand)

  tcrossprod(crosscov)
}

# Toy data with two canonical components
n <- 200
x1 <- matrix(rnorm(n*5), n, 5)
x2 <- cbind(x1[, 1] + rnorm(n, sd = sqrt(0.5)),
            -1*x1[, 1] + x1[, 2] + rnorm(n, sd = sqrt(0.5)),
            matrix(rnorm(n*3), n, 3))
x <- cbind(x1, x2)

# The ladle estimate
ladle_1 <- ladle(x, S_CCA, dim = 5)
ladleplot(ladle_1)

```

---

ladleplot

*Ladle Plot for an Object of Class ladle*


---

**Description**

The ladle plot is a measure to decide about the number of interesting components. Of interest for the ladle criterion is the minimum. The function here offers however also to plot other criterion values which are part of the actual ladle criterion.

**Usage**

```

ladleplot(x, crit = "gn", type="l", ylab = crit,
          xlab = "component", main = deparse(substitute(x)), ...)

```

**Arguments**

x	an object of class ladle.
crit	the criterion to be plotted, options are "gn", "fn", "phin" and "lambda".
type	plotting type.
ylab	default ylab value.
xlab	default xlab value.
main	default title.
...	other arguments for the plotting functions.

**Details**

The main criterion of the ladle is the scaled sum of the eigenvalues and the measure of variation of the eigenvectors up to the component of interest.

The sum is denoted "gn" and the individual parts are "fn" for the measure of the eigenvector variation and "phin" for the scaled eigenvalues. The last option "lambda" corresponds to the unscaled eigenvalues yielding then a screeplot.

**Author(s)**

Klaus Nordhausen

**References**

Luo, W. and Li, B. (2016), *Combining Eigenvalues and Variation of Eigenvectors for Order Determination*, *Biometrika*, 103. 875–887. <doi:10.1093/biomet/asw051>

**See Also**

[FOBIladle](#), [PCAladle](#), [SIRladle](#)

**Examples**

```
n <- 1000
X <- cbind(rexp(n), rt(n,5), rnorm(n), rnorm(n), rnorm(n), rnorm(n))
test <- FOBIladle(X)
ladleplot(test)
ladleplot(test, crit="fn")
ladleplot(test, crit="phin")
ladleplot(test, crit="lambda")
```



**Description**

Estimates  $k$  non-Gaussian signal components using projection pursuit. The projection index can be chosen among convex combinations of squares of one or several standard projection indices used in ICA.

**Usage**

```
NGPP(X, k, nl = c("skew", "pow3"), alpha = 0.8, method = "symm", eps = 1e-6,
      verbose = FALSE, maxiter = 100)
```

**Arguments**

X	Numeric matrix with n rows corresponding to the observations and p columns corresponding to the variables.
k	Number of components to estimate, $1 \leq k \leq p$ .
nl	Vector of non-linearities, a convex combination of the corresponding squared objective functions of which is then used as the projection index. The choices include "skew" (skewness), "pow3" (excess kurtosis), "tanh" ( $\log(\cosh)$ ) and "gauss" (Gaussian function).
alpha	Vector of positive weights between 0 and 1 given to the non-linearities. The length of alpha should be either one less than the number of non-linearities in which case the missing weight is chosen so that alpha sums to one, or equal to the number of non-linearities in which case the weights are used as such. No boundary checks for the weights are done.
method	If "symm" the k signals are estimated simultaneously (symmetric projection pursuit) and if "defl" they are estimated one-by-one (deflation-based projection pursuit).
eps	Convergence tolerance.
verbose	If TRUE the numbers of iterations will be printed.
maxiter	Maximum number of iterations.

**Details**

It is assumed that the data is a random sample from the model  $x = m + As$  where the latent vector  $s = (s_1^T, s_2^T)^T$  consists of  $k$ -dimensional non-Gaussian subvector (the signal) and  $p-k$ -dimensional Gaussian subvector (the noise) and the components of  $s$  are mutually independent. Without loss of generality we further assume that the components of  $s$  have zero means and unit variances.

The objective is to estimate an inverse for the mixing matrix  $A$  and in non-Gaussian projection pursuit this is done by first standardizing the observations and then finding mutually orthogonal directions maximizing a convex combination of the chosen squared objective functions.

After estimation the found signals are ordered in decreasing order with respect to their objective function values.

**Value**

A list with class 'bss' containing the following components:

W	Estimated unmixing matrix
S	Matrix of size $n \times k$ containing the estimated signals.
D	Vector of the objective function values of the signals
MU	Location vector of the data which was subtracted before estimating the signal components.

**Author(s)**

Joni Virta

**References**

Virta, J., Nordhausen, K. and Oja, H., (2016), *Projection Pursuit for non-Gaussian Independent Components*, <<https://arxiv.org/abs/1612.05445>>.

**See Also**

[NGPPsim](#), [NGPPest](#), [fICA](#)

**Examples**

```
# Simulated data with 2 signals

n <- 500
S <- cbind(rexp(n), runif(n), rnorm(n))
A <- matrix(rnorm(9), ncol = 3)
X <- S %*% t(A)

res <- NGPP(X, 2)
res$W %*% A

# Iris data

X <- as.matrix(iris[, 1:4])

res <- NGPP(X, 2, nl = c("pow3", "tanh"), alpha = 0.5)
plot(res, col = iris[, 5])
```

---

NGPPest                      *Signal Subspace Dimension Testing Using non-Gaussian Projection Pursuit*

---

### Description

Estimates the dimension of the signal subspace using NGPP to conduct sequential hypothesis testing. The test statistic is a multivariate extension of the classical Jarque-Bera statistic and the distribution of it under the null hypothesis is obtained by simulation.

### Usage

```
NGPPest(X, nl = c("skew", "pow3"), alpha = 0.8, N = 500, eps = 1e-6,
        verbose = FALSE, maxiter = 100)
```

### Arguments

X	Numeric matrix with n rows corresponding to the observations and p columns corresponding to the variables.
nl	Vector of non-linearities, a convex combination of the corresponding squared objective functions of which is then used as the projection index. The choices include "skew" (skewness), "pow3" (excess kurtosis), "tanh" ( $\log(\cosh)$ ) and "gauss" (Gaussian function).
alpha	Vector of positive weights between 0 and 1 given to the non-linearities. The length of alpha should be either one less than the number of non-linearities in which case the missing weight is chosen so that alpha sums to one, or equal to the number of non-linearities in which case the weights are used as such. No boundary checks for the weights are done.
N	Number of normal samples to be used in simulating the distribution of the test statistic under the null hypothesis.
eps	Convergence tolerance.
verbose	If TRUE the numbers of iterations will be printed.
maxiter	Maximum number of iterations.

### Details

It is assumed that the data is a random sample from the model  $x = m + As$  where the latent vector  $s = (s_1^T, s_2^T)^T$  consists of  $k$ -dimensional non-Gaussian subvector (the signal) and  $p-k$ -dimensional Gaussian subvector (the noise) and the components of  $s$  are mutually independent. Without loss of generality we further assume that the components of  $s$  have zero means and unit variances.

The algorithm first estimates full  $p$  components from the data using deflation-based NGPP with the chosen non-linearities and weighting and then tests the null hypothesis  $H_0 : k_{true} \leq k$  for each  $k = 0, \dots, p-1$ . The testing is based on the fact that under the null hypothesis  $H_0 : k_{true} \leq k$  the distribution of the final  $p-k$  components is standard multivariate normal and the significance of the test can be obtained by comparing the objective function value of the  $(k+1)$ th estimated

components to the same quantity estimated from  $N$  samples of size  $n$  from  $(p - k)$ -dimensional standard multivariate normal distribution.

Note that if `maxiter` is reached at any step of the algorithm it will use the current estimated direction and continue to the next step.

### Value

A list with class `'icest'` containing the following components:

<code>statistic</code>	Test statistic, i.e. the objective function values of all estimated component.
<code>p.value</code>	Obtained vector of $p$ -values.
<code>parameter</code>	Number $N$ of simulated normal samples.
<code>method</code>	Character string "Estimation the signal subspace dimension using NGPP".
<code>data.name</code>	Character string giving the name of the data.
<code>W</code>	Estimated unmixing matrix
<code>S</code>	Matrix of size $n \times p$ containing the estimated signals.
<code>D</code>	Vector of the objective function values of the signals
<code>MU</code>	Location vector of the data which was subtracted before estimating the signal components.
<code>conv</code>	Boolean vector telling for which components the algorithm converged (TRUE) and for which not (FALSE).

### Author(s)

Joni Virta

### References

Virta, J., Nordhausen, K. and Oja, H., (2016), *Projection Pursuit for non-Gaussian Independent Components*, <<https://arxiv.org/abs/1612.05445>>.

### See Also

[NGPP](#), [NGPPsim](#)

### Examples

```
# Iris data

X <- as.matrix(iris[, 1:4])

# The number of simulations N should be increased in practical situations
# Now we settle for N = 100

res <- NGPPest(X, N = 100)
res$statistic
res$p.value
res$conv
```

---

NGPPsim                      *Signal Subspace Dimension Testing Using non-Gaussian Projection Pursuit*

---

### Description

Tests whether the true dimension of the signal subspace is less than or equal to a given  $k$ . The test statistic is a multivariate extension of the classical Jarque-Bera statistic and the distribution of it under the null hypothesis is obtained by simulation.

### Usage

```
NGPPsim(X, k, nl = c("skew", "pow3"), alpha = 0.8, N = 1000, eps = 1e-6,
        verbose = FALSE, maxiter = 100)
```

### Arguments

X	Numeric matrix with n rows corresponding to the observations and p columns corresponding to the variables.
k	Number of components to estimate, $1 \leq k \leq p$ .
nl	Vector of non-linearities, a convex combination of the corresponding squared objective functions of which is then used as the projection index. The choices include "skew" (skewness), "pow3" (excess kurtosis), "tanh" ( $\log(\cosh)$ ) and "gauss" (Gaussian function).
alpha	Vector of positive weights between 0 and 1 given to the non-linearities. The length of alpha should be either one less than the number of non-linearities in which case the missing weight is chosen so that alpha sums to one, or equal to the number of non-linearities in which case the weights are used as such. No boundary checks for the weights are done.
N	Number of normal samples to be used in simulating the distribution of the test statistic under the null hypothesis.
eps	Convergence tolerance.
verbose	If TRUE the numbers of iterations will be printed.
maxiter	Maximum number of iterations.

### Details

It is assumed that the data is a random sample from the model  $x = m + As$  where the latent vector  $s = (s_1^T, s_2^T)^T$  consists of  $k$ -dimensional non-Gaussian subvector (the signal) and  $p-k$ -dimensional Gaussian subvector (the noise) and the components of  $s$  are mutually independent. Without loss of generality we further assume that the components of  $s$  have zero means and unit variances.

To test the null hypothesis  $H_0 : k_{true} \leq k$  the algorithm first estimates  $k + 1$  components using deflation-based NGPP with the chosen non-linearities and weighting. Under the null hypothesis the distribution of the final  $p - k$  components is standard multivariate normal and the significance of the test is obtained by comparing the objective function value of the  $(k + 1)$ th estimated components to

the same quantity estimated from  $N$  samples of size  $n$  from  $(p-k)$ -dimensional standard multivariate normal distribution.

Note that if `maxIter` is reached at any step of the algorithm it will use the current estimated direction and continue to the next step.

### Value

A list with class `'ictest'`, inheriting from the class `'hctest'`, containing the following components:

<code>statistic</code>	Test statistic, i.e. the objective function value of the $(k + 1)$ th estimated component.
<code>p.value</code>	Obtained $p$ -value.
<code>parameter</code>	Number $N$ of simulated normal samples.
<code>method</code>	Character string denoting which test was performed.
<code>data.name</code>	Character string giving the name of the data.
<code>alternative</code>	Alternative hypothesis, i.e. "There are less than $p - k$ Gaussian components".
<code>k</code>	Tested dimension $k$ .
<code>W</code>	Estimated unmixing matrix
<code>S</code>	Matrix of size $n \times (k + 1)$ containing the estimated signals.
<code>D</code>	Vector of the objective function values of the signals
<code>MU</code>	Location vector of the data which was subtracted before estimating the signal components.

### Author(s)

Joni Virta

### References

Virta, J., Nordhausen, K. and Oja, H., (2016), *Projection Pursuit for non-Gaussian Independent Components*, <<https://arxiv.org/abs/1612.05445>>.

### See Also

[NGPP](#), [NGPPest](#)

### Examples

```
# Simulated data with 2 signals and 2 noise components

n <- 200
S <- cbind(rexp(n), rbeta(n, 1, 2), rnorm(n), rnorm(n))
A <- matrix(rnorm(16), ncol = 4)
X <- S %*% t(A)

# The number of simulations N should be increased in practical situations
# Now we settle for N = 100
```

```

res1 <- NGPPsim(X, 1, N = 100)
res1
screepplot(res1)

res2 <- NGPPsim(X, 2, N = 100)
res2
screepplot(res2)

```

---

PCAasympt	<i>Testing for Subsphericity using the Covariance Matrix or Tyler's Shape Matrix</i>
-----------	--

---

### Description

The function tests, assuming an elliptical model, that the last  $p-k$  eigenvalues of a scatter matrix are equal and the  $k$  interesting components are those with a larger variance. The scatter matrices that can be used here are the regular covariance matrix and Tyler's shape matrix.

### Usage

```
PCAasympt(X, k, scatter = "cov", ...)
```

### Arguments

<code>X</code>	a numeric data matrix with $p > 1$ columns.
<code>k</code>	the number of eigenvalues larger than the equal ones. Can be between 0 and $p-2$ .
<code>scatter</code>	the scatter matrix to be used. Can be "cov" or "tyler". For "cov" the regular covariance matrix is computed and for "tyler" the function <a href="#">HR.Mest</a> is used to compute Tyler's shape matrix.
<code>...</code>	arguments passed on to <a href="#">HR.Mest</a> if <code>scatter = "tyler"</code> .

### Details

The functions assumes an elliptical model and tests if the last  $p - k$  eigenvalues of PCA are equal. PCA can here be either be based on the regular covariance matrix or on Tyler's shape matrix.

For a sample of size  $n$ , the test statistic is

$$T = n / (2\bar{d}^2 \sigma_1) \sum_{k+1}^p (d_i - \bar{d})^2,$$

where  $\bar{d}$  is the mean of the last  $p - k$  PCA eigenvalues.

The constant  $\sigma_1$  is for the regular covariance matrix estimated from the data whereas for Tyler's shape matrix it is simply a function of the dimension of the data.

The test statistic has a limiting chisquare distribution with  $(p - k - 1)(p - k + 2)/2$  degrees of freedom.

Note that the regular covariance matrix is here divided by  $n$  and not by  $n - 1$ .

**Value**

A list of class `ictest` inheriting from class `hctest` containing:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>parameter</code>	the degrees of freedom of the test.
<code>method</code>	character string which test was performed.
<code>data.name</code>	character string giving the name of the data.
<code>alternative</code>	character string specifying the alternative hypothesis.
<code>k</code>	the number or larger eigenvalues used in the testing problem.
<code>W</code>	the transformation matrix to the principal components.
<code>S</code>	data matrix with the centered principal components.
<code>D</code>	the underlying eigenvalues.
<code>MU</code>	the location of the data which was subtracted before calculating the principal components.
<code>SCATTER</code>	the computed scatter matrix.
<code>sigma1</code>	the asymptotic constant needed for the asymptotic test.

**Author(s)**

Klaus Nordhausen

**References**

Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, 188, 104830. <doi:10.1016/j.jmva.2021.104830>.

**See Also**

[HR.Mest](#), [PCAboot](#)

**Examples**

```
n <- 200
X <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n), rnorm(n))

TestCov <- PCAasymp(X, k = 2)
TestCov
TestTyler <- PCAasymp(X, k = 1, scatter = "tyler")
TestTyler
```





**Value**

A list of class `ladle` containing:

<code>method</code>	the string <code>PCA</code> .
<code>k</code>	the estimated value of <code>k</code> .
<code>fn</code>	vector giving the measures of variation of the eigenvectors using the bootstrapped eigenvectors for the different number of components.
<code>phin</code>	normalized eigenvalues of the covariance matrix.
<code>gn</code>	the main criterion for the augmented estimate - the sum of <code>fn</code> and <code>phin</code> . <code>k</code> is the value where <code>gn</code> takes its minimum
<code>lambda</code>	the eigenvalues of the covariance matrix.
<code>W</code>	the transformation matrix to the principal components.
<code>S</code>	data matrix with the centered principal components.
<code>MU</code>	the location of the data which was subtracted before calculating the principal components.
<code>data.name</code>	the name of the data for which the augmented estimate was computed.
<code>sigma2</code>	the value used as noise variance when simulating the augmented components.

**Author(s)**

Klaus Nordhausen

**References**

- Luo, W. and Li, B. (2021), *On Order Determination by Predictor Augmentation*, *Biometrika*, 108, 557–574. <doi:10.1093/biomet/asaa077>
- Radojicic, U., Lietzen, N., Nordhausen, K. and Virta, J. (2021), *Dimension Estimation in Two-Dimensional PCA*. In S. Loncaric, T. Petkovic and D. Petrinovic (editors) "Proceedings of the 12 International Symposium on Image and Signal Processing and Analysis (ISPA 2021)", 16–22. <doi:10.1109/ISPA52656.2021.9552114>

**See Also**

[ladleplot](#), [PCAladle](#)

**Examples**

```
n <- 1000
Y <- cbind(rnorm(n, sd=2), rnorm(n, sd=2), rnorm(n), rnorm(n), rnorm(n), rnorm(n))

testPCA <- PCAaug(Y)
testPCA
summary(testPCA)
plot(testPCA)
ladleplot(testPCA)
ladleplot(testPCA, crit = "fn")
ladleplot(testPCA, crit = "lambda")
ladleplot(testPCA, crit = "phin")
```

### Description

The function tests, assuming an elliptical model, that the last  $p-k$  eigenvalues of a scatter matrix are equal and the  $k$  interesting components are those with a larger variance. To obtain  $p$ -values two different bootstrapping strategies are available and the user can provide the scatter matrix to be used as a function.

### Usage

```
PCABoot(X, k, n.boot = 200, s.boot = "B1", S = MeanCov, Sargs = NULL)
```

### Arguments

X	a numeric data matrix with $p > 1$ columns.
k	the number of eigenvalues larger than the equal ones. Can be between 0 and $p-2$ .
n.boot	number of bootstrapping samples.
s.boot	bootstrapping strategy to be used. Possible values are "B1", "B2". See details for further information.
S	A function which returns a list that has as its first element a location vector and as the second element the scatter matrix.
Sargs	list of further arguments passed on to the function specified in S.

### Details

Here the function S needs to return a list where the first argument is a location vector and the second one a scatter matrix.

The location is used to center the data and the scatter matrix is used to perform PCA.

Consider X as the centered data and denote by W the transformation matrix to the principal components. The corresponding eigenvalues from PCA are  $d_1, \dots, d_p$ . Under the null,  $d_k > d_{k+1} = \dots = d_p$ . Denote further by  $\bar{d}$  the mean of the last  $p-k$  eigenvalues and by  $D^* = \text{diag}(d_1, \dots, d_k, \bar{d}, \dots, \bar{d})$  a  $p \times p$  diagonal matrix. Assume that S is the matrix with principal components which can be decomposed into  $S_1$  and  $S_2$  where  $S_1$  contains the  $k$  interesting principal components and  $S_2$  the last  $p - k$  principal components.

For a sample of size  $n$ , the test statistic used for the bootstrapping tests is

$$T = n/(\bar{d}^2) \sum_{k+1}^p (d_i - \bar{d})^2.$$

The function offers then two bootstrapping strategies:

1. s.boot="B1": The first strategy has the following steps:

- (a) Take a bootstrap sample  $S^*$  of size  $n$  from  $S$  and decompose it into  $S_1^*$  and  $S_2^*$ .
  - (b) Every observation in  $S_2^*$  is transformed with a different random orthogonal matrix.
  - (c) Recombine  $S^* = (S_1^*, S_2^*)$  and create  $X^* = S^*W$ .
  - (d) Compute the test statistic based on  $X^*$ .
  - (e) Repeat the previous steps  $n.boot$  times.
2. `s.boot="B2"`: The second strategy has the following steps:
- (a) Scale each principal component using the matrix  $D$ , i.e.  $Z = SD$ .
  - (b) Take a bootstrap sample  $Z^*$  of size  $n$  from  $Z$ .
  - (c) Every observation in  $Z^*$  is transformed with a different random orthogonal matrix.
  - (d) Recreate  $X^* = Z^*D^{*-1}W$ .
  - (e) Compute the test statistic based on  $X^*$ .
  - (f) Repeat the previous steps  $n.boot$  times.

To create the random orthogonal matrices the function `rorth` is used.

## Value

A list of class `ictest` inheriting from class `hctest` containing:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>parameter</code>	the degrees of freedom of the test.
<code>method</code>	character string which test was performed.
<code>data.name</code>	character string giving the name of the data.
<code>alternative</code>	character string specifying the alternative hypothesis.
<code>k</code>	the number or larger eigenvalues used in the testing problem.
<code>W</code>	the transformation matrix to the principal components.
<code>S</code>	data matrix with the centered principal components.
<code>D</code>	the underlying eigenvalues.
<code>MU</code>	the location of the data which was subtracted before calculating the principal components.
<code>SCATTER</code>	The computed scatter matrix.
<code>scatter</code>	character string denoting which scatter function was used.
<code>s.boot</code>	character string denoting which bootstrapping test version was used.

## Author(s)

Klaus Nordhausen

## References

Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, 188, 104830. <doi:10.1016/j.jmva.2021.104830>.

**See Also**

[cov](#), [MeanCov](#), [PCAasymp](#)

**Examples**

```
n <- 200
X <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n), rnorm(n))

# for demonstration purpose the n.boot is chosen small, should be larger in real applications

TestCov <- PCAboot(X, k = 2, n.boot=30)
TestCov

TestTM <- PCAboot(X, k = 1, n.boot=30, s.boot = "B2", S = "tM", Sargs = list(df=2))
TestTM
```

---

PCAladle

*Ladle Estimate for PCA*


---

**Description**

For  $p$ -variate data, the Ladle estimate for PCA assumes that the last  $p-k$  eigenvalues are equal. Combining information from the eigenvalues and eigenvectors of the covariance matrix the ladle estimator yields an estimate for  $k$ .

**Usage**

```
PCAladle(X, n.boot = 200,
         ncomp = ifelse(ncol(X) > 10, floor(ncol(X)/log(ncol(X))), ncol(X) - 1))
```

**Arguments**

<code>X</code>	numeric data matrix.
<code>n.boot</code>	number of bootstrapping samples to be used.
<code>ncomp</code>	The number of components among which the ladle estimator is to be searched. The default here follows the recommendation of Luo and Li 2016.

**Details**

The model here assumes that the eigenvalues of the covariance matrix are of the form  $\lambda_1 \geq \dots \geq \lambda_k > \lambda_{k+1} = \dots = \lambda_p$  and the goal is to estimate the value of  $k$ . The ladle estimate for this purpose combines the values of the scaled eigenvalues and the variation of the eigenvectors based on bootstrapping. The idea there is that for distinct eigenvalues the variation of the eigenvectors is small and for equal eigenvalues the corresponding eigenvectors have large variation.

This measure is then computed assuming  $k=0, \dots, ncomp$  and the ladle estimate for  $k$  is the value where the measure takes its minimum.

**Value**

A list of class ladle containing:

method	the string PCA.
k	the estimated value of k.
fn	vector giving the measures of variation of the eigenvectors using the bootstrapped eigenvectors for the different number of components.
phin	normalized eigenvalues of the covariance matrix.
gn	the main criterion for the ladle estimate - the sum of fn and phin. k is the value where gn takes its minimum
lambda	the eigenvalues of the covariance matrix.
W	the transformation matrix to the principal components.
S	data matrix with the centered principal components.
MU	the location of the data which was subtracted before calculating the principal components.
data.name	the name of the data for which the ladle estimate was computed.

**Author(s)**

Klaus Nordhausen

**References**

Luo, W. and Li, B. (2016), *Combining Eigenvalues and Variation of Eigenvectors for Order Determination*, *Biometrika*, 103, 875–887. <doi:10.1093/biomet/asw051>

**See Also**

[ladleplot](#)

**Examples**

```
n <- 1000
Y <- cbind(rnorm(n, sd=2), rnorm(n,sd=2), rnorm(n), rnorm(n), rnorm(n), rnorm(n))

testPCA <- PCAladle(Y)
testPCA
summary(testPCA)
plot(testPCA)
ladleplot(testPCA)
ladleplot(testPCA, crit = "fn")
ladleplot(testPCA, crit = "lambda")
ladleplot(testPCA, crit = "phin")
```

PCAschott

*Testing for Subsphericity using the Schott's test***Description**

The test tests the equality of the last eigenvalues assuming normal distributed data using the regular covariance matrix.

**Usage**

```
PCAschott(X, k)
```

**Arguments**

X                    a numeric data matrix with  $p > 1$  columns.  
k                    the number of eigenvalues larger than the equal ones. Can be between 0 and  $p-2$ .

**Details**

The functions assumes multivariate normal data and tests if the last  $p - k$  eigenvalues of PCA are equal.

**Value**

A list of class `ictest` inheriting from class `hctest` containing:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>parameter</code>	the degrees of freedom of the test.
<code>method</code>	character string which test was performed.
<code>data.name</code>	character string giving the name of the data.
<code>alternative</code>	character string specifying the alternative hypothesis.
<code>k</code>	the number or larger eigenvalues used in the testing problem.
<code>W</code>	the transformation matrix to the principal components.
<code>S</code>	data matrix with the centered principal components.
<code>D</code>	the underlying eigenvalues.
<code>MU</code>	the mean vector of the data which was subtracted before calculating the principal components.
<code>SCATTER</code>	the computed covariance matrix matrix.

**Author(s)**

Klaus Nordhausen

## References

Schott, J.R. (2006), *A High-Dimensional Test for the Equality of the Smallest Eigenvalues of a Covariance Matrix*, *Journal of Multivariate Analysis*, 97, 827–843. <doi:10.1016/j.jmva.2005.05.003>

## See Also

[PCAasymp](#), [PCAbboot](#)

## Examples

```
n <- 200
X <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n), rnorm(n))
PCAschott(X, 2)
```

---

plot.ictest

*Scatterplot Matrix for a ictest Object*

---

## Description

For an object of class ictest, plots either the pairwise scatter plot matrix, or the time series plots of the underlying components. The user can choose if only the components considered interesting or all of them should be plotted.

## Usage

```
## S3 method for class 'icctest'
plot(x, which = "all", ...)
```

## Arguments

x	object of class ictest
which	if "all", then all components of S in the ictest object are plotted. If "k", then only the first k components are plotted, where the value of k is taken from the ictest object. This is only meaningful if k was at least 2.
...	other arguments passed on to <a href="#">pairs</a> if the components are a numeric matrix or to <a href="#">plot.ts</a> , <a href="#">plot.zoo</a> or <a href="#">plot.xts</a> if the components are from the corresponding class.

## Details

If the component matrix has the class mts, xts or zoo, then a time series plot will be plotted. Otherwise, the pairwise scatter plot matrix will be plotted.

## Author(s)

Klaus Nordhausen



**See Also**

[ggplot.icctest](#), [pairs](#), [plot.ts](#), [plot.zoo](#), [plot.xts](#)

**Examples**

```
n <- 200
X <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n), rnorm(n))

TestCov <- PCAasympt(X, k = 2)
plot(TestCov)
plot(TestCov, which = "k")
```

---

plot.ladle

*Plotting an Object of Class ladle*

---

**Description**

An object of class ladle contains always the source components as estimated by the corresponding statistical method. This function either plots all of the components or only this considered interesting according to the ladle estimate.

**Usage**

```
## S3 method for class 'ladle'
plot(x, which = "all", ...)
```

**Arguments**

x	an object of class ladle.
which	if "all", then all components of S in the ladle object are plotted. If "k", then only the k components are plotted, which are considered interesting according to the ladle estimator. This is only meaningful if the estimated 'k' is at least 2.
...	other arguments passed on to <a href="#">pairs</a> if the components are a numeric matrix or to <a href="#">plot.ts</a> , <a href="#">plot.zoo</a> or <a href="#">plot.xts</a> if the components are from the corresponding class.

**Details**

If the component matrix has the class mts, xts or zoo, then a time series plot will be plotted. Otherwise, the pairwise scatter plot matrix will be plotted.

**Author(s)**

Klaus Nordhausen

**See Also**

[pairs](#), [plot.ts](#), [plot.zoo](#), [plot.xts](#)

**Examples**

```
n <- 1000
X <- cbind(rexp(n), rt(n,5), rnorm(n), rnorm(n), rnorm(n), rnorm(n))
test <- FOBiladle(X)
plot(test)
```

---

print.kSearch

*Printing an Object of Class kSearch*


---

**Description**

Basic printing of an object of class kSearch. Prints the estimated dimension k along with all tested values and corresponding p-values.

**Usage**

```
## S3 method for class 'kSearch'
print(x, digits = getOption("digits"), ...)
```

**Arguments**

x	An object of class kSearch.
digits	Number of significant digits to use when printing p-values. Defaults to <code>getOption("digits")</code> .
...	Further arguments.

**Author(s)**

Katariina Perkonaja

**See Also**

[summary.kSearch](#), [kSearch](#)

**Examples**

```
n <- 500
S <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n))
A <- rorth(4)
X <- S %*% t(A)
result <- kSearch(X, method = PCAasymp)
result
```

---

print.ladle                      *Printing an Object of Class ladle*

---

**Description**

Basic printing of an object of class ladle. Prints basically everything but the estimated components.

**Usage**

```
## S3 method for class 'ladle'  
print(x, ...)
```

**Arguments**

x                      an object of class ladle.  
...                    further arguments to be passed to or from methods.

**Author(s)**

Klaus Nordhausen

**See Also**

[summary.ladle](#), [plot.ladle](#), [ladleplot](#), [FOBIladle](#), [PCAladle](#), [SIRladle](#)

**Examples**

```
n <- 1000  
X <- cbind(rexp(n), rt(n,5), rnorm(n), rnorm(n), rnorm(n), rnorm(n))  
test <- FOBIladle(X)  
test
```

---

rMU                      *Greek Letter mu Shaped Bivariate Data Generation*

---

**Description**

A function to generate bivariate data with the scatterplot resembling the greek letter mu.

**Usage**

```
rMU(n)
```

**Arguments**

n                      the sample size.

**Value**

A n times 2 matrix

**Author(s)**

Klaus Nordhausen, Joni Virta

**Examples**

```
x <- rMU(1000)
plot(x)
```

---

rOMEGA

*Greek Letter Omega Shaped Bivariate Data Generation*

---

**Description**

A function to generate bivariate data with the scatterplot resembling the greek letter Omega.

**Usage**

```
rOMEGA(n)
```

**Arguments**

n                    the sample size.

**Value**

A n times 2 matrix

**Author(s)**

Klaus Nordhausen, Joni Virta

**Examples**

```
x <- rOMEGA(1000)
plot(x)
```

---

rorth	<i>Random Orthogonal Matrix Creation Uniform WRT the Haar Measure.</i>
-------	--

---

### Description

A function to create a random orthogonal matrix uniformly distributed with respect to the Haar measure.

### Usage

```
rorth(k)
```

### Arguments

k                    the desired number of columns (=rows) of the orthogonal matrix.

### Details

The function fills a  $k \times k$  matrix with  $N(0,1)$  random variables and performs then a QR decomposition using `qr`. If the diagonal elements of  $R$  are all positive the resulting orthogonal matrix  $Q$  is uniform distributed wrt to the Haar measure. Note that the function currently does not check if all diagonal measurements are indeed positive (however this will happen with probability 1 in theory).

### Value

An orthogonal  $k$  times  $k$  matrix

### Author(s)

Klaus Nordhausen

### References

Stewart, G.W. (1980), *The efficient generation of random orthogonal matrices with an application to condition estimators*, SIAM Journal on Numerical Analysis, **17**, 403–409. <doi:10.1137/0717034>.

### Examples

```
Orth <- rorth(4)

crossprod(Orth)
tcrossprod(Orth)
```

---

screeplot.ictest      *Screeplot for an ictest Object*

---

### Description

Plots the criterion values of an ictest object against its index number. Two versions of this screeplot are available.

### Usage

```
## S3 method for class 'ictest'  
screeplot(x, type = "barplot", main = deparse(substitute(x)),  
          ylab = "criterion", xlab = "component", ...)
```

### Arguments

x	object of class ictest.
type	barplot if a barplot or lines if a line plot is preferred.
main	main title of the plot.
ylab	y-axis label.
xlab	x-axis label.
...	other arguments for the plotting functions.

### Author(s)

Klaus Nordhausen

### See Also

[ggscreeplot](#)

### Examples

```
n <- 200  
X <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n), rnorm(n))  
  
TestCov <- PCAasymp(X, k = 2)  
screeplot(TestCov)
```

**Description**

Using the two scatter matrices approach (SICS) for sliced inversion regression (SIR), the function tests if the last  $p-k$  components have zero eigenvalues, where  $p$  is the number of explaining variables. Hence the assumption is that the first  $k$  components are relevant for modelling the response  $y$  and the remaining components are not.

**Usage**

```
SIRasymp(X, y, k, h = 10, ...)
```

**Arguments**

<code>X</code>	a numeric data matrix of explaining variables.
<code>y</code>	a numeric vector specifying the response.
<code>k</code>	the number of relevant components under the null hypothesis.
<code>h</code>	the number of slices used in SIR. Passed on to function <code>covSIR</code> .
<code>...</code>	other arguments passed on to <code>covSIR</code> .

**Details**

Under the null the first  $k$  eigenvalues contained in  $D$  are non-zero and the remaining  $p-k$  are zero.

For a sample of size  $n$ , the test statistic  $T$  is then  $n$  times the sum of these last  $p-k$  eigenvalue and has under the null a chisquare distribution with  $(p-k)(h-k-1)$  degrees of freedom, therefore it is required that  $k < h-1$ .

**Value**

A list of class `ictest` inheriting from class `hctest` containing:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>parameter</code>	the degrees of freedom of the test.
<code>method</code>	character string which test was performed.
<code>data.name</code>	character string giving the name of the data.
<code>alternative</code>	character string specifying the alternative hypothesis.
<code>k</code>	the number of non-zero eigenvalues used in the testing problem.
<code>W</code>	the transformation matrix to the underlying components.
<code>S</code>	data matrix with the centered underlying components.
<code>D</code>	the underlying eigenvalues.
<code>MU</code>	the location of the data which was subtracted before calculating the components.

**Author(s)**

Klaus Nordhausen

**References**

Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, 188, 104830. <doi:10.1016/j.jmva.2021.104830>.

**See Also**

[covSIR](#), [SIRboot](#)

**Examples**

```
X <- matrix(rnorm(1000), ncol = 5)
eps <- rnorm(200, sd = 0.1)
y <- 2 + 0.5 * X[, 1] + 2 * X[, 3] + eps

SIRasyp(X, y, k = 0)
SIRasyp(X, y, k = 1)
```

---

SIRboot

*Testing the Subspace Dimension for Sliced Inverse Regression Using Bootstrapping.*

---

**Description**

Using the two scatter matrices approach (SICS) for sliced inversion regression (SIR) the function tests if the last  $p-k$  components have zero eigenvalues, where  $p$  is the number of explaining variables. Hence the assumption is that the first  $k$  components are relevant for modelling the response  $y$  and the remaining components are not. The function performs bootstrapping to obtain a  $p$ -value.

**Usage**

```
SIRboot(X, y, k, h = 10, n.boot = 200, ...)
```

**Arguments**

<code>X</code>	a numeric data matrix of explaining variables.
<code>y</code>	a numeric vector specifying the response.
<code>k</code>	the number of relevant components under the null hypothesis.
<code>h</code>	the number of slices used in SIR. Passed on to function <a href="#">covSIR</a> .
<code>n.boot</code>	number of bootstrapping samples.
<code>...</code>	other arguments passed on to <a href="#">covSIR</a> .



## Details

Under the null hypothesis the last  $p-k$  eigenvalue as given in  $D$  are zero. The test statistic is then the sum of these eigenvalues.

Denote  $W$  as the transformation matrix to the supervised invariant coordinates (SIC)  $s_i$ ,  $i = 1, \dots, n$ , i.e.

$$s_i = W(x_i - MU),$$

where  $MU$  is the location.

Let  $S_1$  be the submatrix of the SICs which are relevant and  $S_2$  the submatrix of the SICs which are irrelevant for the response  $y$  under the null.

The bootstrapping has then the following steps:

1. Take a bootstrap sample  $(y^*, S_1^*)$  of size  $n$  from  $(y, S_1)$ .
2. Take a bootstrap sample  $S_2^*$  of size  $n$  from  $S_2$ .
3. Combine  $S^* = (S_1^*, S_2^*)$  and create  $X^* = S^*W$ .
4. Compute the test statistic based on  $X^*$ .
5. Repeat the previous steps  $n$ .boot times.

## Value

A list of class `ictest` inheriting from class `hctest` containing:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>parameter</code>	the number of bootstrapping samples used to compute the p-value.
<code>method</code>	character string which test was performed.
<code>data.name</code>	character string giving the name of the data.
<code>alternative</code>	character string specifying the alternative hypothesis.
<code>k</code>	the number of non-zero eigenvalues used in the testing problem.
<code>W</code>	the transformation matrix to the underlying components.
<code>S</code>	data matrix with the centered underlying components.
<code>D</code>	the underlying eigenvalues.
<code>MU</code>	the location of the data which was subtracted before calculating the components.

## Author(s)

Klaus Nordhausen

## References

Nordhausen, K., Oja, H. and Tyler, D.E. (2022), *Asymptotic and Bootstrap Tests for Subspace Dimension*, *Journal of Multivariate Analysis*, 188, 104830. <doi:10.1016/j.jmva.2021.104830>.

**See Also**

[covSIR](#), [SIRasymp](#)

**Examples**

```
X <- matrix(rnorm(1000), ncol = 5)
eps <- rnorm(200, sd = 0.1)
y <- 2 + 0.5 * X[, 1] + 2 * X[, 3] + eps

SIRboot(X, y, k = 0)
SIRboot(X, y, k = 1)
```

---

SIRladle

*Ladle Estimate for SIR*


---

**Description**

In the supervised dimension reduction context with response  $y$  and explaining variables  $x$ , this functions provides the ladle estimate for the dimension of the central subspace for SIR.

**Usage**

```
SIRladle(X, y, h = 10, n.boot = 200,
         ncomp = ifelse(ncol(X) > 10, floor(ncol(X)/log(ncol(X))), ncol(X) - 1), ...)
```

**Arguments**

$X$	numeric data matrix.
$y$	numeric response vector.
$h$	number of slices in SIR.
$n.boot$	number of bootstrapping samples to be used.
$ncomp$	The number of components among which the ladle estimator is to be searched. The default here follows the recommendation of Luo and Li 2016.
$\dots$	arguments passed on to <a href="#">quantile</a> .

**Details**

The idea here is that the eigenvalues of the SIR-M matrix are of the form  $\lambda_1 \geq \dots \geq \lambda_k > 0 = \dots = 0$  and the eigenvectors of the non-zero eigenvalue span the central subspace.

The ladle estimate for  $k$  for this purpose combines the values of the scaled eigenvalues and the variation of the eigenvectors based on bootstrapping. The idea there is that for distinct eigenvalues the variation of the eigenvectors is small and for equal eigenvalues the corresponding eigenvectors have large variation.

This measure is then computed assuming  $k=0, \dots, ncomp$  and the ladle estimate for  $k$  is the value where the measure takes its minimum.

**Value**

A list of class ladle containing:

method	the string SIR.
k	the estimated value of k.
fn	vector giving the measures of variation of the eigenvectors using the bootstrapped eigenvectors for the different number of components.
phin	normalized eigenvalues of the M matrix in the SIR case.
gn	the main criterion for the ladle estimate - the sum of fn and phin. k is the value where gn takes its minimum
lambda	the eigenvalues of the M matrix in the SIR case.
W	the transformation matrix to supervised components.
S	data matrix with the centered supervised components.
MU	the location of the data which was subtracted before calculating the supervised components.
data.name	the name of the data for which the ladle estimate was computed.

**Author(s)**

Klaus Nordhausen

**References**

*Luo, W. and Li, B. (2016), Combining Eigenvalues and Variation of Eigenvectors for Order Determination, Biometrika, 103. 875–887. <doi:10.1093/biomet/asw051>*

**See Also**

[ladleplot](#)

**Examples**

```
n <- 1000
X <- cbind(rnorm(n), rnorm(n), rnorm(n), rnorm(n), rnorm(n))
eps <- rnorm(n, sd=0.02)
y <- 4*X[,1] + 2*X[,2] + eps

test <- SIRladle(X, y)
test
summary(test)
plot(test)
pairs(cbind(y, components(test)))
ladleplot(test)
ladleplot(test, crit = "fn")
ladleplot(test, crit = "lambda")
ladleplot(test, crit = "phin")
```

summary.kSearch      *Summarizing an Object of Class kSearch*

---

**Description**

Summarizes a kSearch object.

**Usage**

```
## S3 method for class 'kSearch'  
summary(object, ...)
```

**Arguments**

object      An object of class kSearch.  
...      Further arguments.

**Author(s)**

Katariina Perkonaja

**See Also**

[print.kSearch](#), [kSearch](#)

**Examples**

```
n <- 500  
S <- cbind(rnorm(n, sd = 2), rnorm(n, sd = 1.5), rnorm(n), rnorm(n))  
A <- rorth(4)  
X <- S %*% t(A)  
result <- kSearch(X, method = PCAasymp)  
summary(result)
```

---

summary.ladle      *Summarizing an Object of Class ladle*

---

**Description**

Summarizes an ladle object

**Usage**

```
## S3 method for class 'ladle'  
summary(object, ...)
```

**Arguments**

object            an object of class ladle.  
...                further arguments to be passed to or from methods.

**Author(s)**

Klaus Nordhausen

**See Also**

[print.ladle](#), [plot.ladle](#), [ladleplot](#), [FOBILadle](#), [PCAladle](#), [SIRladle](#)

**Examples**

```
n <- 1000
X <- cbind(rexp(n), rt(n,5), rnorm(n), rnorm(n), rnorm(n), rnorm(n))

test <- FOBILadle(X)
summary(test)
```

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