

Package ‘ICS’

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Description The package implements Tyler et al.’s and Oja et al.’s method of two different scatter matrices to obtain an invariant coordinate system or independent components, depending on the underlying assumptions.

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 ICS-package

Tools for Exploring Multivariate Data via ICS/ICA

Description

This package implements the 2 scatter matrix transformation to obtain an invariant coordinate system or independent components, depending on the underlying assumptions. The result of the transformation is an object of the S4 class `ics` which is provided by this package. Besides generic functions to create and work with an `ics` object the package contains also some scatter matrices.

Details

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Some multivariate tests and estimates are not affine equivariant by nature. A possible remedy for the lack of that property is to transform the data points to an invariant coordinate system, construct tests and estimates from the transformed data, and if needed, retransform the estimates back. The use of two different scatter matrices to obtain invariant coordinates is implemented in this package by the function `ics`. For an invariant coordinate selection no assumptions are made about the data or the scatter matrices and it can be seen as a data transformation method. If the data come, however, from a so called independent component model the `ics` function can recover the independent components and estimate the mixing matrix under general assumptions. Besides the function `ics`, which creates an S4 object of class `ics`, provides this package tools to work with objects of that class and some scatter matrices which can be used in the `ics` function. Furthermore are there also two tests for multinormality.

Author(s)

Klaus Nordhausen, Hannu Oja and David E. Tyler
 Maintainer: Klaus Nordhausen, <klaus.nordhausen@uta.fi>

`coef.ics`*Extracting the Unmixing Matrix*

Description

Function to extract the unmixing matrix of an class `ics` object.

Usage

```
## S4 method for signature 'ics':  
coef(object)
```

Arguments

`object` object of class `ics`.

Value

The unmixing matrix of an class `ics` object.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

[ics-class](#) and [ics](#)

`cov4`*Scatter Matrix based on Fourth Moments*

Description

Estimates the scatter matrix based on the 4th moments of the data.

Usage

```
cov4(X, location = "Mean", na.action = na.fail)
```

Arguments

`X` numeric data matrix or dataframe, missing values are not allowed.

`location` can be either `Mean`, `Origin` or numeric. If numeric the matrix is computed wrt to the given location.

`na.action` a function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

If location is `Mean` the scatter matrix of 4th moments is computed wrt to the sample mean. For location = `Origin` it is the scatter matrix of 4th moments wrt to the origin. The scatter matrix is standardized in such a way to be consistent for the regular covariance matrix at the multinormal model. It is given for $n \times p$ matrix X by

$$\frac{1}{p+2} \text{ave}_i \{ [(x_i - \bar{x})S^{-1}(x_i - \bar{x})]'(x_i - \bar{x})(x_i - \bar{x}) \},$$

where \bar{x} is the mean vector and S the regular covariance matrix.

Value

A matrix.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Cardoso, J.F. (1989), Source separation using higher order moments, in *Proc. IEEE Conf. on Acoustics, Speech and Signal Processing (ICASSP'89)*, 2109–2112.

Oja, H., Sirkiä, S. and Eriksson, J. (2006), Scatter matrices and independent component analysis, *Austrian Journal of Statistics*, **35**, 175–189.

Examples

```
set.seed(654321)
cov.matrix <- matrix(c(3,2,1,2,4,-0.5,1,-0.5,2), ncol=3)
X <- rmvnorm(100, c(0,0,0), cov.matrix)
cov4(X)
cov4(X, location="Origin")
rm(.Random.seed)
```

cov4.wt

Weighted Scatter Matrix based on Fourth Moments

Description

Estimates the weighted scatter matrix based on the 4th moments of the data.

Usage

```
cov4.wt(x, wt = rep(1/nrow(x), nrow(x)), location = TRUE,
        method = "ML", na.action = na.fail)
```

Arguments

<code>x</code>	numeric data matrix or dataframe.
<code>wt</code>	numeric vector of non-negative weights. At least some weights must be larger than zero.
<code>location</code>	TRUE if the weighted location vector should be computed. FALSE when taken wrt to the origin. If numeric the matrix is computed wrt to the given location.
<code>method</code>	Either ML or unbiased. Will be passed on to <code>cov.wt</code> when the Mahalanobis distance is computed.
<code>na.action</code>	a function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

If `location = TRUE`, then the scatter matrix is given for a $n \times p$ data matrix X by

$$\frac{1}{p+2} \text{ave}_i \{ w_i [(x_i - \bar{x}_w) S_w^{-1} (x_i - \bar{x}_w)'] (x_i - \bar{x}_w)' (x_i - \bar{x}_w) \},$$

where w_i are the weights standardized such that $\sum w_i = 1$, \bar{x}_w is the weighted mean vector and S_w the weighted covariance matrix. For details about the weighted mean vector and weighted covariance matrix see `cov.wt`.

Value

A matrix.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

[cov4](#), [cov.wt](#)

Examples

```

cov.matrix.1 <- matrix(c(3,2,1,2,4,-0.5,1,-0.5,2), ncol=3)
X.1 <- rmvnorm(100, c(0,0,0), cov.matrix.1)
cov.matrix.2 <- diag(1,3)
X.2 <- rmvnorm(50, c(1,1,1), cov.matrix.2)
X <- rbind(X.1, X.2)

cov4.wt(X, rep(c(0,1), c(100,50)))
cov4.wt(X, rep(c(1,0), c(100,50)))

```

covAxis

*One step Tyler Shape Matrix***Description**

This matrix can be used to get from [ics](#) the principal axes which is then known as principal axis analysis.

Usage

```
covAxis(X, na.action = na.fail)
```

Arguments

`X` numeric data matrix or dataframe.
`na.action` a function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

The `covAxis` matrix V is a given for a sample of size n as

$$p \text{ ave}_i \{ [(x_i - \bar{x})S^{-1}(x_i - \bar{x})']^{-1} (x_i - \bar{x})'(x_i - \bar{x}) \},$$

where \bar{x} is the mean vector and S the regular covariance matrix.

`covAxis` can be used to perform a Prinzipal Axis Analysis (Critchley et al. 2007) using the function [ics](#). In that case for a centered data matrix X `covAxis` can be used as `S2` in [ics](#), where `S1` should be in that case the regular covariance matrix.

Value

Matrix of the estimated scatter.

Author(s)

Klaus Nordhausen, klaus.nordhausen@uta.fi

References

Critchley, F., Pires, A. and Amado, C. (2007), *Principal axis analysis*, manuscript, ?, ?-?.
 Tyler, D.E., Critchley, F., Dümbgen, L. and Oja, H. (2009), *Invariant coordinate selection*, Journal of the Royal Statistical Society, Series B, ?, ?-?.

See Also

[ics](#)

Examples

```
data(iris)
iris.centered <- sweep(iris[,1:4], 2, colMeans(iris[,1:4]), "-")
iris.paa <- ics(iris.centered, cov, covAxis, stdKurt = FALSE)
summary(iris.paa)
plot(iris.paa, col=as.numeric(iris[,5]))
mean(iris.paa@gKurt)
emp.align <- iris.paa@gKurt
emp.align

screepplot(iris.paa)
abline(h = 1)
```

`covOrigin`*Covariance Matrix with Respect to the Origin*

Description

Estimates the covariance matrix with respect to the origin.

Usage

```
covOrigin(X, location = NULL, na.action = na.fail)
```

Arguments

<code>X</code>	a numeric data matrix or dataframe.
<code>location</code>	optional location value which serves then as the center instead of the origin.
<code>na.action</code>	a function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

The covariance matrix S_0 with respect to origin is given for a matrix X with n observations by

$$S_0 = \frac{1}{n} X'X.$$

Value

A matrix.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also[cov](#)**Examples**

```
set.seed(654321)
cov.matrix <- matrix(c(3,2,1,2,4,-0.5,1,-0.5,2), ncol=3)
X <- rmvnorm(100,c(0,0,0),cov.matrix)
covOrigin(X)
rm(.Random.seed)
```

`fitted.ics`*Fitted Values of an ICS Object*

Description

Function to compute the fitted values of a `ics` object.

Usage

```
## S4 method for signature 'ics':
fitted(object, index=NULL)
```

Arguments

<code>object</code>	object of class <code>ics</code> .
<code>index</code>	A vector which defines which components should be used to compute the fitted values. The default <code>NULL</code> uses all components.

Value

Returns a dataframe with the fitted values.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

[ics-class](#) and [ics](#)

Examples

```

set.seed(123456)
X1 <- rmvnorm(250, rep(0,8), diag(c(rep(1,6),0.04,0.04)))
X2 <- rmvnorm(50, c(rep(0,6),2,0), diag(c(rep(1,6),0.04,0.04)))
X3 <- rmvnorm(200, c(rep(0,7),2), diag(c(rep(1,6),0.04,0.04)))

X.comps <- rbind(X1,X2,X3)
A <- matrix(rnorm(64),nrow=8)
X <- X.comps %*% t(A)

ics.X.1 <- ics(X)
fitted(ics.X.1)
fitted(ics.X.1,index=c(1,2,3,6,7,8))

rm(.Random.seed)

```

 ics

Two Scatter Matrix ICS Transformation

Description

This function implements the 2 scatter matrix transformation to obtain an invariant coordinate system or independent components, depending on the underlying assumptions.

Usage

```

ics(X, S1 = cov, S2 = cov4, Slargs = list(), S2args = list(),
    stdB = "Z", stdKurt = TRUE, na.action = na.fail)

```

Arguments

X	numeric data matrix or dataframe.
S1	name of the first scatter matrix function or a scatter matrix. Default is the regular covariance matrix.
S2	name of the second scatter matrix or a scatter matrix. Default is the covariance matrix based on fourth order moments. Note that the type of S2 must be the same as S1.
Slargs	list with optional additional arguments for S1. Only considered if S1 is a function.
S2args	list with optional additional arguments for S2. Only considered if S2 is a function.
stdB	either "B" or "Z". Defines the way to standardize the matrix B. Default is "Z". Details are given below.
stdKurt	Logical, either "TRUE" or "FALSE". Specifies whether the product of the kurtosis values is 1 or not.
na.action	a function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

Seeing this function as a tool for data transformation the result is an invariant coordinate selection which can be used for testing and estimation. And if needed the results can be easily retransformed to the original scale. It is possible to use it also for dimension reduction, finding outliers or when searching for clusters in the data. The function can, however, also be used in a modelling framework. In this case it is assumed that the data were created by mixing independent components which have different kurtosis values. If the two scatter matrices used have then the so-called independence property the function can recover the independent components by estimating the unmixing matrix.

By default $S1$ is the regular covariance matrix `cov` and $S2$ the matrix of fourth moments `cov4`. However those can be replaced with any other scatter matrix the user prefers. The package **ICS** offers for example also `cov4.wt`, `covAxis`, `covOrigin` or `tM` and in the **ICSNP** are for example further scatters as `duembgen.shape`, `tyler.shape`, `HR.Mest` or `HP1.shape`. But of course also scatters from any other package can be used.

Note that when function names are submitted, the function should return only a scatter matrix. If the function returns more, the scatter should be computed in advance or a wrapper written that yields the required output. For example `tM` returns a list with four elements where the scatter estimate is called `V`. A simple wrapper would then be `my.tM <- function(x, ...) tM(x, ...) $V`.

For a given choice of $S1$ and $S2$ the general idea of the `ics` function is to find the unmixing matrix B and the invariant coordinates (independent coordinates) Z in such a way, that:

- (i) The elements of Z are standardized with respect to $S1$ ($S1(Z)=I$).
- (ii) The elements of Z are uncorrelated with respect to $S2$. ($S2(Z)=D$, where D is a diagonal matrix).
- (iii) The elements of Z are ordered according to their kurtosis.

Given those criteria, B is unique up to sign changes of its rows. The function provides two options to decide the exact form of B .

- (i) Method 'Z' standardizes B such, that all components are right skewed. The criterion used, is the sign of each componentwise difference of mean vector and transformation retransformation median. This standardization is preferred in an invariant coordinate framework.
- (ii) Method 'B' standardizes B independent of Z such that the maximum element per row is positive and each row has norm 1. Usual way in an independent component analysis framework.

In principal if $S1$ and $S2$ are true scatter matrices the order does not matter. It will just reverse and invert the kurtosis value vector. This is however not true when not both of them are scatter matrices but one or both are shape matrices. In this case the order of the kurtosis values is also reversed, the ratio however then is not 1 but only constant. This is due to the fact that when shape matrices are used, the kurtosis values are only relative ones. Therefore by the default the kurtosis values are standardized such that their product is 1. If no standardization is wanted, the 'stdKurt' argument should be used.

Value

an object of class `ics`.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Tyler, D.E., Critchley, F., Dümbgen, L. and Oja, H. (2009), *Invariant coordinate selection*, Journal of the Royal Statistical Society, Series B, ?, ?-?.

Oja, H., Sirkiä, S. and Eriksson, J. (2006), *Scatter matrices and independent component analysis*, Austrian Journal of Statistics, **35**, 175–189.

See Also

[ICS-package](#)

Examples

```
# example using two functions
set.seed(123456)
X1 <- rmvnorm(250, rep(0,8), diag(c(rep(1,6),0.04,0.04)))
X2 <- rmvnorm(50, c(rep(0,6),2,0), diag(c(rep(1,6),0.04,0.04)))
X3 <- rmvnorm(200, c(rep(0,7),2), diag(c(rep(1,6),0.04,0.04)))

X.comps <- rbind(X1,X2,X3)
A <- matrix(rnorm(64),nrow=8)
X <- X.comps %*% t(A)

ics.X.1 <- ics(X)
summary(ics.X.1)
plot(ics.X.1)

# compare to
pairs(X)
pairs(princomp(X,cor=TRUE)$scores)

# slow:

# library(ICSNP)
# ics.X.2 <- ics(X, tyler.shape, duembgen.shape, Slargs=list(location=0))
# summary(ics.X.2)
# plot(ics.X.2)

rm(.Random.seed)

# example using two computed scatter matrices for outlier detection

library(robustbase)
ics.wood<-ics(wood,tM(wood)$V,tM(wood,2)$V)
plot(ics.wood)

# example using three pictures
library(pixmap)

fig1 <- read.pnm(system.file("pictures/cat.pgm", package = "ICS")[1])
fig2 <- read.pnm(system.file("pictures/road.pgm", package = "ICS")[1])
fig3 <- read.pnm(system.file("pictures/sheep.pgm", package = "ICS")[1])
```

```

p <- dim(fig1@grey)[2]

fig1.v <- as.vector(fig1@grey)
fig2.v <- as.vector(fig2@grey)
fig3.v <- as.vector(fig3@grey)
X <- cbind(fig1.v,fig2.v,fig3.v)

set.seed(4321)
A <- matrix(rnorm(9), ncol = 3)
X.mixed <- X %*% t(A)

ICA.fig <- ics(X.mixed)

par.old <- par()
par(mfrow=c(3,3), omi = c(0.1,0.1,0.1,0.1), mai = c(0.1,0.1,0.1,0.1))

plot(fig1)
plot(fig2)
plot(fig3)

plot(pixmapGrey(X.mixed[,1],ncol=p))
plot(pixmapGrey(X.mixed[,2],ncol=p))
plot(pixmapGrey(X.mixed[,3],ncol=p))

plot(pixmapGrey(ics.components(ICA.fig)[,1],ncol=p))
plot(pixmapGrey(ics.components(ICA.fig)[,2],ncol=p))
plot(pixmapGrey(ics.components(ICA.fig)[,3],ncol=p))

par(par.old)
rm(.Random.seed)

```

 ics-class

Class ICS

Description

A S4 class to store results from an invariant coordinate system transformation or independent component computation based on two scatter matrices.

Objects from the Class

Objects can be created by calls of the form `new("ics", ...)`. But usually objects are created by the function `ics`.

Slots

gKurt: Object of class "numeric". Gives the generalized kurtosis measures of the components

UnMix: Object of class "matrix". The unmixing matrix.

S1: Object of class "matrix". The first scatter matrix.
S2: Object of class "matrix". The second scatter matrix.
S1name: Object of class "character". Name of the first scatter matrix.
S2name: Object of class "character". Name of the second scatter matrix.
Scores: Object of class "data.frame". The underlying components in the invariant coordinate system.
DataNames: Object of class "character". Names of the original variables.
StandardizeB: Object of class "character". Names standardization method for UnMix.
StandardizeKurt: Object of class "logical". States whether the generalized kurtosis is standardized or not.

Methods

For this class the following generic functions are available: `print.ics`, `summary.ics`, `coef.ics`, `fitted.ics` and `plot.ics`

Note

In case no extractor function for the slots exists, the component can be extracted the usual way using '@'.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

`ics`

`ics.components` *Extracting ICS Components*

Description

Function to extract the ICS components of a `ics` object.

Usage

```
ics.components(object)
```

Arguments

`object` object of class `ics`.

Value

Dataframe that contains the components.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

[ics-class](#) and [ics](#)

mean3

Location Estimate based on Third Moments

Description

Estimates the location based on third moments.

Usage

```
mean3(X, na.action = na.fail)
```

Arguments

`X` numeric data matrix or dataframe with at least two columns.
`na.action` a function which indicates what should happen when the data contain 'NA's.
 Default is to fail.

Details

This Location Estimate is defined for $n \times p$ matrix X as

$$\frac{1}{p} \text{ave}_i \{ [(x_i - \bar{x})S^{-1}(x_i - \bar{x})]' x_i \},$$

where \bar{x} is the mean vector and S the regular covariance matrix.

Value

A vector.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Oja, H., Sirkiä, S. and Eriksson, J. (2006), *Scatter matrices and independent component analysis*, Austrian Journal of Statistics, **35**, 175–189.

Examples

```
set.seed(654321)
cov.matrix <- matrix(c(3,2,1,2,4,-0.5,1,-0.5,2), ncol=3)
X <- rmvnorm(100, c(0,0,0), cov.matrix)
mean3(X)
rm(.Random.seed)
```

mvnorm.kur.test *Test of Multivariate Normality Based on Kurtosis*

Description

Test for multivariate normality which uses as criterion the kurtosis measured by the ratio of regular covariance matrix and matrix of fourth moments.

Usage

```
mvnorm.kur.test(X, method = "integration", n.simu = 1000,
               na.action = na.fail)
```

Arguments

X	a numeric data frame or matrix.
method	defines the method used for the computation of the p-value. The possibilities are "integration" (default), "satterthwaite" or "simulation". Details below.
n.simu	if 'method=simulation' this specifies the number of replications in the simulation.
na.action	a function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

This test implements the multivariate normality test based on kurtosis measured by two different scatter estimates as described in Kankainen, Taskinen and Oja. The choice here is based on the regular covariance matrix and matrix of fourth moments ([cov4](#)). The limiting distribution of the test statistic W is a linear combination of independent chi-square variables with different degrees of freedom. Exact limiting p-values or approximated p-values are obtained by using the function [pchisqsum](#). However Kankainen et al. mention that even for $n = 200$ the convergence can be poor, therefore also p-values simulated under the NULL can be obtained.

Value

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

statistic	the value of the test statistic W .
parameter	the degrees of freedom for the test statistic W with their weights or the number of replications depending on the chosen method.

p.value the p-value for the test.
method a character string indicating what type of test was performed.
data.name a character string giving the name of the data.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Kankainen, A., Taskinen, S. and Oja, H. (2007), Tests of multinormality based on location vectors and scatter matrices, Statistical Methods and Applications, 16, 357–379.

See Also

[mvnorm.skew.test](#)

Examples

```
X<-rmvnorm(100, c(2, 4, 5))
mvnorm.kur.test(X)
mvnorm.kur.test(X, method = "satt")
mvnorm.kur.test(X, method = "simu")
```

mvnorm.skew.test *Test of Multivariate Normality Based on Skewness*

Description

Test for multivariate normality which uses as criterion the skewness measured as the difference between location estimates based on first respectively third moments

Usage

```
mvnorm.skew.test(X, na.action = na.fail)
```

Arguments

X a numeric data frame or matrix.
na.action a function which indicates what should happen when the data contain 'NA's.
Default is to fail.

Details

This test implements the multivariate normality test based on skewness measured by two different location estimates as described in Kankainen, Taskinen and Oja. The choice here is based on the regular mean vector and the location estimate based on third moments ([mean3](#)). The scatter matrix used is the regular covariance matrix.

Value

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

statistic	the value of the test statistic U.
parameter	the degrees of freedom for the statistic U.
p.value	the p-value for the test.
method	a character string indicating what type of test was performed.
data.name	a character string giving the name of the data.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Kankainen, A., Taskinen, S. and Oja, H. (2007), Tests of multinormality based on location vectors and scatter matrices, Statistical Methods and Applications, 16, 357–379.

See Also

[mvnorm.kur.test](#)

Examples

```
X<-rmvnorm(100,c(2,4,5))
mvnorm.skew.test(X)
```

plot.ics

Scatterplot for a ICS Object

Description

Scatterplot matrix for a `ics` object.

Usage

```
## S4 method for signature 'ics, missing':
plot(x, index = NULL, ...)
```

Arguments

x	object of class <code>ics</code>
index	index vector of which components should be plotted. See details for further information
...	other arguments for <code>plot</code>

Details

If no index vector is given the function plots the full scatterplots matrix only if there are less than seven components. Otherwise the three first and three last components will be plotted. This is because the components with extreme kurtosis are the most interesting ones.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

[screepplot.ics](#), [ics-class](#) and [ics](#)

Examples

```
set.seed(123456)
X1 <- rmvnorm(250, rep(0,8), diag(c(rep(1,6),0.04,0.04)))
X2 <- rmvnorm(50, c(rep(0,6),2,0), diag(c(rep(1,6),0.04,0.04)))
X3 <- rmvnorm(200, c(rep(0,7),2), diag(c(rep(1,6),0.04,0.04)))

X.comps <- rbind(X1,X2,X3)
A <- matrix(rnorm(64),nrow=8)
X <- X.comps %*% t(A)

ics.X.1 <- ics(X)
plot(ics.X.1)
plot(ics.X.1,index=1:8)
rm(.Random.seed)
```

print.ics

Basic information of ICS Object

Description

Prints the minimal information of an `ics` object.

Usage

```
## S4 method for signature 'ics':
show(object)
```

Arguments

`object` object of class `ics`.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

[ics-class](#) and [ics](#)

screepLOT.ics *ScreepLOT for an ICS Object*

Description

Plots the kurtosis measures of an `ics` object against its index number. Two versions of this screepLOT are available.

Usage

```
## S3 method for class 'ics':
screepLOT(x, index = NULL, type = "barplot",
          main = deparse(substitute(x)), ylab = "generalized kurtosis",
          xlab = "component", ...)
```

Arguments

<code>x</code>	object of class <code>ics</code> .
<code>index</code>	index of the components to be plotted. If <code>NULL</code> all components are used.
<code>type</code>	<code>barplot</code> if a barplot or <code>lines</code> if a line plot is preferred.
<code>main</code>	main title of the plot.
<code>ylab</code>	y-axis label.
<code>xlab</code>	x-axis label.
<code>...</code>	other arguments for the plotting functions.

Author(s)

Klaus Nordhausen, klaus.nordhausen@uta.fi

See Also

[plot.ics](#), [ics-class](#) and [ics](#)

Examples

```
set.seed(654321)
A <- matrix(c(3,2,1,2,4,-0.5,1,-0.5,2), ncol=3)
eigen.A <- eigen(A)
sqrt.A <- eigen.A$vectors %*% (diag(eigen.A$values))^0.5 %*% t(eigen.A$vectors)
normal.ic <- cbind(rnorm(800), rnorm(800), rnorm(800))
mix.ic <- cbind(rt(800,4), rnorm(800), runif(800,-2,2))

data.normal <- normal.ic %*% t(sqrt.A)
```

```

data.mix <- mix.ic %*% t(sqrt.A)

par(mfrow=c(1,2))
screepplot(ics(data.normal))
screepplot(ics(data.mix), type="lines")
par(mfrow=c(1,1))
rm(.Random.seed)

```

summary.ics

Summarize a ICS object

Description

Summarizes and prints a `ics` object in an informative way.

Usage

```

## S4 method for signature 'ics':
summary(object, digits = 4)

```

Arguments

<code>object</code>	object of class <code>ics</code> .
<code>digits</code>	number of digits for the numeric output.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

See Also

[ics-class](#) and [ics](#)

tM

Joint M-estimation of Location and Scatter for a Multivariate t-distribution

Description

The functions implements three EM algorithms to M-estimate the location vector and scatter matrix of a multivariate t-distribution.

Usage

```

tM(X, df = 1, alg = "alg3", mu.init = NULL, V.init = NULL,
   gamma.init = NULL, eps = 1e-06, maxiter = 100,
   na.action = na.fail)

```

Arguments

<code>X</code>	numeric data matrix or dataframe.
<code>df</code>	assumed degrees of freedom of the t-distribution. Default is 1 which corresponds to the Cauchy distribution.
<code>alg</code>	specifies which algorithm to use. Options are <code>alg1</code> , <code>alg2</code> or <code>alg3</code> . <code>alg3</code> is the default.
<code>mu.init</code>	initial value for the location vector if available.
<code>V.init</code>	initial value for the scatter matrix if available.
<code>gamma.init</code>	initial value for gamma if available. Only needed for <code>alg2</code> .
<code>eps</code>	convergence tolerance.
<code>maxiter</code>	maximum number of iterations.
<code>na.action</code>	a function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

This implements the EM algorithms described in Kent et al. (1994). The norm used to define convergence is as in Arslan et al. (1995).

Algorithm 1 is valid for all degrees of freedom $df > 0$. Algorithm 2 is well defined only for degrees of freedom $df > 1$. Algorithm 3 is the limiting case of Algorithm 2 with degrees of freedom $df = 1$.

The performance of the algorithms are compared in Arslan et al. (1995).

Note that `cov.trob` in the MASS package implements also a covariance estimate for a multivariate t-distribution. That function provides for example also the possibility to fix the location. It requires however that the degrees of freedom exceeds 2.

Value

A list containing:

<code>mu</code>	vector with the estimated loaction.
<code>V</code>	matrix of the estimated scatter.
<code>gam</code>	estimated value of gamma. Only present when <code>alg2</code> is used.
<code>iter</code>	number of iterations.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Kent, J.T., Tyler, D.E. and Vardi, Y. (1994), A curious likelihood identity for the multivariate t-distribution, *Communications in Statistics, Theory and Methods*, **23**, 441–453.

Arslan, O., Constable, P.D.L. and Kent, J.T. (1995), Convergence behaviour of the EM algorithm for the multivariate t-distribution, *Communications in Statistics, Theory and Methods*, **24**, 2981–3000.

See Also[cov.trob](#)**Examples**

```
set.seed(654321)
cov.matrix <- matrix(c(3,2,1,2,4,-0.5,1,-0.5,2), ncol=3)
X <- rmvt(100, cov.matrix, 1)
tM(X)
rm(.Random.seed)
```

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