Package: ICSClust (via r-universe)

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Type Package

Title Tandem Clustering with Invariant Coordinate Selection

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Description Implementation of tandem clustering with invariant coordinate selection with different scatter matrices and several choices for the selection of components as described in Alfons, A., Archimbaud, A., Nordhausen, K.and Ruiz-Gazen, A. (2024) <doi:10.1016/j.ecosta.2024.03.002>.

License GPL (>= 3)

Encoding UTF-8

Depends ICS (>= 1.4-0), ggplot2

Imports cluster, fpc, GGally, heplots, mclust, moments, mvtnorm, otrimle, RcppRoll, rrcov, scales, tclust

LinkingTo Rcpp, RcppArmadillo

Suggests testthat (>= 3.0.0)

URL https://github.com/AuroreAA/ICSClust

BugReports https://github.com/AuroreAA/ICSClust/issues

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`ICSClust-package` *Tandem Clustering with Invariant Coordinate Selection*

Description

Implementation of tandem clustering with invariant coordinate selection with different scatter matrices and several choices for the selection of components as described in Alfons, A., Archimbaud, A., Nordhausen, K.and Ruiz-Gazen, A. (2024) <doi:10.1016/j.ecosta.2024.03.002>.

Details

The DESCRIPTION file:

Package:	ICSClust
Type:	Package
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Version:	0.1.1
Date:	2025-07-24
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License:	GPL (>= 3)
Encoding:	UTF-8
Depends:	ICS (>= 1.4-0), ggplot2
Imports:	cluster, fpc, GGally, heplots, mclust, moments, mvtnorm, otrimle, RcppRoll, rrcov, scales, tclust
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Suggests:	testthat (>= 3.0.0)
URL:	https://github.com/AuroreAA/ICSClust
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Index of help topics:


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                        Selection
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ICS_mlc                 Cauchy location and Scatter Estimates for ICS
ICS_tcov                Pairwise one-step M-estimate of scatter for ICS
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component_plot          Scatterplot Matrix with densities on the
                        diagonal
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                        discriminatory power
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plot.ICSClust	Scatterplot Matrix with densities on the diagonal
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select_plot	Plot of the Generalized Kurtosis Values of the ICS Transformation
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tcov	Pairwise one-step M-estimate of scatter
tkmeans_clust	Trimmed k-means clustering
ucov	Simple robust estimates of scatter
var_crit	Selection of Invariant components using the var criterion

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References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

See Also

Useful links:

- https://github.com/AuroreAA/ICSClust
- Report bugs at https://github.com/AuroreAA/ICSClust/issues

`component_plot` *Scatterplot Matrix with densities on the diagonal*

Description

Produces a gg-scatterplot matrix of the variables of a given dataframe or an invariant coordinate system obtained via an ICS transformation with densities on the diagonal for each cluster.

Usage

```
component_plot(
  object,
  select = TRUE,
  clusters = NULL,
  text_size_factor = 8/6.5,
  colors = NULL
)
```

Arguments

object	a dataframe or ICS-S3 class object.
select	a vector of indexes of variables to plot. If NULL or FALSE, all variables are selected. If TRUE only the first three and last three are considered.
clusters	a vector indicating the clusters of the data to color the plot. By default NULL.
text_size_factor	a numeric factor for controlling the axis.text and strip.text.
colors	a vector of colors to use. One color for each cluster.

Value

An object of class "ggmatrix" (see GGally::ggpairs()).

Author(s)

Andreas Alfons and Aurore Archimbaud

Examples

```
X <- iris[,1:4]
component_plot(X)
out <- ICS(X)
component_plot(out, select = c(1,4))
```

---

discriminatory_crit *Selection of ICS components based on discriminatory power*

Description

Identifies invariant coordinates associated to the highest discriminatory power. Currently, the implemented measure is "eta2" as quantified by the Wilks' partial eta-squared, computed using the heplots::etasq() function.

Usage

```
discriminatory_crit(object, ...)

## S3 method for class 'ICS'
discriminatory_crit(
  object,
  clusters,
  method = "eta2",
  nb_select = NULL,
  select_only = FALSE,
  ...
)

## Default S3 method:
discriminatory_crit(
  object,
  clusters,
  method = "eta2",
  nb_select = NULL,
  select_only = FALSE,
  gen_kurtosis = NULL,
  ...
)
```

Arguments

object	dataframe or object of class "ICS".
...	additional arguments are currently ignored.
clusters	a vector of the same length as the number of observations, indicating the true clusters. It is used to compute the discriminatory power based on it.
method	the name of the discriminatory power. Only "eta2" is implemented.
nb_select	the exact number of components to select. By default it is set to NULL, i.e the number of components to select is the number of clusters minus one.
select_only	boolean. If TRUE only the vector names of the selected invariant components are returned. If FALSE additional details are returned.
gen_kurtosis	vector of generalized kurtosis values.

Details

The discriminatory power is evaluated for each combination of the first and/or last combinations of nb_select components. The combination achieving the highest discriminatory power is selected.

More specifically, we compute $\eta^2 = 1 - \Lambda^{1/s}$, where Λ denotes Wilks' lambda:

$$\Lambda = \frac{\det(E)}{\det(T)},$$

where E is the within-group sum of squares and cross-products matrix, H is the between-group sum of squares and cross-products matrix and T is the total sum of squares and cross-products

matrix, with $T = H + E$, $s = min(p, df_h)$ with p being the number of latent roots of HE^{-1}. See `heplots::etasq()` for more details.

Value

If `select_only` is `TRUE` a vector of the names of the invariant components or variables to select. If `FALSE` an object of class `"ICS_crit"` is returned with the following objects:

- `crit`: the name of the criterion "discriminatory".
- `method`: the name of the discriminatory power.
- `nb_select`: the number of components to select.
- `select`: the names of the invariant components or variables to select.
- `power_combinations`: the discriminatory values for each of the considered combinations of `nb_select` components.
- `gen_kurtosis`: the vector of generalized kurtosis values in case of `ICS` object.

Author(s)

Aurore Archimbaud and Anne Ruiz-Gazen

References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

Muller, K. E. and Peterson, B. L. (1984). Practical methods for computing power in testing the Multivariate General Linear Hypothesis *Computational Statistics and Data Analysis*, **2**, 143-158.

See Also

`normal_crit()`, `med_crit()`, `var_crit()`, `heplots::etasq()`.

Examples

```
X <- iris[,-5]
out <- ICS(X)
discriminatory_crit(out, clusters = iris[,5], select_only = FALSE)
```

ICS_lcov *Local Shape Scatter Estimates for ICS*

Description

It is a wrapper for the local shape estimator of scatter as computed by `fpc::localshape()`.

Usage

```
ICS_lcov(x, mscatter = "cov", proportion = 0.1, ...)
```

Arguments

x	a numeric matrix or data frame.
mscatter	"mcd" or "cov" (default); specified minimum covariance determinant or classical covariance matrix to be used for Mahalanobis distance computation.
proportion	proportion of points to be considered as neighbourhood.
...	potential further arguments passed to fpc::localshape().

Value

An object of class "ICS_scatter" with the following components:

location	this is NULL as the estimator does not use a location estimate.
scatter	a numeric matrix giving the estimate of the scatter matrix.
label	a character string providing a label for the scatter matrix.

Author(s)

Andreas Alfons and Aurore Archimbaud

See Also

fpc::localshape()

ICS_mcd *MCD location and Scatter Estimates for ICS*

Description

It is a wrapper for the (reweighted) MCD estimators of location and scatter as computed by rrcov::CovMcd().

Usage

```
ICS_mcd_raw(x, location = FALSE, nsamp = "deterministic", alpha = 0.5, ...)

ICS_mcd_rwt(x, location = FALSE, nsamp = "deterministic", alpha = 0.5, ...)
```

Arguments

x	a numeric matrix or data frame.
location	a logical indicating whether to include the MCD-estimate of location (defaults to FALSE).
nsamp	number of subsets used for initial estimates or "best", "exact" or "deterministic" (default).
alpha	numeric parameter controlling the size of the subsets over which the determinant is minimized as in rrcov::CovMcd().
...	potential further arguments passed to rrcov::CovMcd().

Details

- `ICS_mcd_raw()`: computes the raw MCD estimates.
- `ICS_mcd_rwt()`: computes the reweighted MCD estimates.

Value

An object of class `"ICS_scatter"` with the following components:

`location`	if requested, a numeric vector giving the location estimate.
`scatter`	a numeric matrix giving the estimate of the scatter matrix.
`label`	a character string providing a label for the scatter matrix.

Author(s)

Andreas Alfons and Aurore Archimbaud

See Also

`rrcov::CovMcd()`

ICS_mlc *Cauchy location and Scatter Estimates for ICS*

Description

It is a wrapper for the Cauchy estimator of location and scatter for a multivariate t-distribution, as computed by `ICS::tM()`.

Usage

```
ICS_mlc(x, location = FALSE, ...)
```

Arguments

`x`	a numeric matrix or data frame.
`location`	a logical indicating whether to include the M-estimate of location (defaults to `FALSE`).
`...`	potential further arguments passed to `ICS::ICS_tM()`.

Value

An object of class `"ICS_scatter"` with the following components:

`location`	if requested, a numeric vector giving the location estimate.
`scatter`	a numeric matrix giving the estimate of the scatter matrix.
`label`	a character string providing a label for the scatter matrix.

Author(s)

Andreas Alfons and Aurore Archimbaud

See Also

ICS::tM(), ICS::ICS_tM()

ICS_tcov *Pairwise one-step M-estimate of scatter for ICS*

Description

Wrapper function for the pairwise one-step M-estimator of scatter with weights based on pairwise Mahalanobis distances, as computed by tcov(). Note that this estimator is based on pairwise differences and therefore no location estimate is returned.

Usage

```
ICS_tcov(x, beta = 2)
```

Arguments

x	a numeric matrix or data frame.
beta	a positive numeric value specifying the tuning parameter of the pairwise one-step M-estimator (default to 2), see tcov().

Value

An object of class "ICS_scatter" with the following components:

location	this is NULL as the estimator is based on pairwise differences and does not use a location estimate.
scatter	a numeric matrix giving the estimate of the scatter matrix.
label	a character string providing a label for the scatter matrix.

Author(s)

Andreas Alfons

See Also

ICS()

tcov(), ucov(), ICS_ucov()

ICS_ucov *Simple robust estimates of scatter for ICS*

Description

Wrapper functions for the one-step M-estimator of scatter with weights based on Mahalanobis distances as computed by `scov()`, or the simple related estimator that is based on a transformation as computed by `ucov()`.

Usage

```
ICS_scov(x, location = TRUE, beta = 0.2)

ICS_ucov(x, location = TRUE, beta = 0.2)
```

Arguments

`x`	a numeric matrix or data frame.
`location`	a logical indicating whether to include the sample mean as location estimate (defaults to `TRUE`).
`beta`	a positive numeric value specifying the tuning parameter of the estimator (default to 0.2), see `ucov()`.

Value

An object of class `"ICS_scatter"` with the following components:

`location`	if requested, a numeric vector giving the location estimate.
`scatter`	a numeric matrix giving the estimate of the scatter matrix.
`label`	a character string providing a label for the scatter matrix.

Author(s)

Andreas Alfons

See Also

`ICS()`

`tcov()`, `ICS_tcov()`, `ucov()`

ICSClust *Tandem clustering with ICS*

Description

Sequential clustering approach: (i) dimension reduction through the Invariant Coordinate Selection method using the ICS-S3 function and (ii) clustering of the transformed data.

Usage

```
ICSClust(
  X,
  nb_select = NULL,
  nb_clusters = NULL,
  ICS_args = list(),
  criterion = c("med_crit", "normal_crit", "var_crit", "discriminatory_crit"),
  ICS_crit_args = list(),
  method = c("kmeans_clust", "tkmeans_clust", "pam_clust", "mclust_clust",
    "rmclust_clust", "rimle_clust"),
  clustering_args = list(),
  clusters = NULL
)
```

Arguments

X	a numeric matrix or data frame containing the data.
nb_select	the number of components to select. It is used only in case criterion is either "med_crit", "var_crit" or "discriminatory_crit". By default it is set to NULL, i.e the number of components to select is the number of clusters minus one.
nb_clusters	the number of clusters searched for.
ICS_args	list of ICS-S3 arguments. Otherwise, default values of ICS-S3 are used.
criterion	criterion to automatically decide which invariant components to keep. Possible values are "med_crit", "normal_crit", "var_crit" and "discriminatory_crit". The default value is "med_crit". See med_crit(), normal_crit(), var_crit() or discriminatory_crit() for more details.
ICS_crit_args	list of arguments passed to med_crit(), normal_crit(), var_crit() or discriminatory_crit() for choosing the components to keep.
method	clustering method to perform. Currently implemented wrapper functions are "kmeans_clust", "tkmeans_clust", "pam_clust", "mclust_clust", "rmclust_clust" or "rimle_clust". The default value is "kmeans_clust".
clustering_args	list of kmeans_clust(), tkmeans_clust(), pam_clust(), rimle_clust(), mclust_clust() or rmclust_clust() arguments for performing cluster analysis.

clusters — a vector indicating the true clusters of the data. By default, it is NULL but it is required to choose the components based on the discriminatory criterion discriminatory_crit.

Details

Tandem clustering with ICS is a sequential method:

- ICS-S3 is performed.
- only a subset of the first and/or the last few components are selected based on a criterion.
- the clustering method is performed only on the subspace of the selected components.
- wrapper for several different clustering methods are provided. Users can however also write wrappers for other clustering methods.

Value

An object of class "ICSClust" with the following components:

- ICS_out: An object of class "ICS". See ICS-S3.
- select: a vector of the names of the selected invariant coordinates.
- clusters: a vector of the new partition of the data, i.e a vector of integers (from 1:k) indicating the cluster to which each observation is allocated. 0 indicates outlying observations.

summary() and plot() methods are available.

Author(s)

Aurore Archimbaud

References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

See Also

med_crit(), normal_crit(), var_crit(), ICS-S3, discriminatory_crit(), kmeans_clust(), tkmeans_clust(), pam_clust(), rimle_clust(), mclust_clust() summary() and plot() methods

Examples

```
X <- iris[,1:4]

# indicating the number of components to retain for the dimension reduction
# step as well as the number of clusters searched for.
out <- ICSClust(X, nb_select = 2, nb_clusters = 3)
summary(out)
plot(out)
```

```
# changing the scatter pair to consider in ICS
out <- ICSClust(X, nb_select = 1, nb_clusters = 3,
ICS_args = list(S1 = ICS_mcd_raw, S2 = ICS_cov,S1_args = list(alpha = 0.5)))
summary(out)
plot(out)

# changing the criterion for choosing the invariant coordinates
out <- ICSClust(X, nb_clusters = 3, criterion = "normal_crit",
ICS_crit_args = list(level = 0.1, test = "anscombe.test", max_select = NULL))
summary(out)
plot(out)

# changing the clustering method
out <- ICSClust(X, nb_clusters = 3, method  = "tkmeans_clust",
clustering_args = list(alpha = 0.1))
summary(out)
plot(out)
```

---

kmeans_clust k-*means clustering*

Description

Wrapper for performing k-means clustering from `stats::kmeans()`.

Usage

```
kmeans_clust(X, k, clusters_only = FALSE, iter.max = 100, nstart = 20, ...)
```

Arguments

`X`	a numeric matrix or data frame of the data. It corresponds to the argument `x`.
`k`	the number of clusters searched for. It corresponds to the argument `centers`.
`clusters_only`	boolean. If `TRUE` only the partition of the data is returned as a vector. If `FALSE` the usual output of the kmeans function is returned.
`iter.max`	the maximum number of iterations allowed.
`nstart`	if `centers` is a number, how many random sets should be chosen.
`...`	other arguments to pass to the `stats::kmeans()` function.

Value

If `clusters_only` is `TRUE` a vector of the new partition of the data is returned, i.e a vector of integers (from `1:k`) indicating the cluster to which each observation is allocated.

Otherwise a list is returned with the following components:

`clust_method`	the name of the clustering method, i.e. "kmeans".

clusters	the vector of the new partition of the data, i.e. a vector of integers (from 1:k) indicating the cluster to which each observation is allocated.
...	an object of class "kmeans"

.

Author(s)

Aurore Archimbaud

See Also

stats::kmeans()

Examples

```
kmeans_clust(iris[,1:4], k = 3, clusters_only = TRUE)
```

---

mclust_clust *Model-Based Clustering*

Description

Wrapper for performing Model-Based Clustering from mclust::Mclust() allowing noise or not.

Usage

```
mclust_clust(X, k, clusters_only = FALSE, ...)

rmclust_clust(X, k, clusters_only = FALSE, ...)
```

Arguments

X	a numeric matrix or data frame of the data. It corresponds to the argument data.
k	the number of clusters searched for. It corresponds to the argument G of function mclust::Mclust().
clusters_only	boolean. If TRUE only the partition of the data is returned as a vector. If FALSE the usual output of the mclust::Mclust() function is returned.
...	other arguments to pass to mclust::Mclust().

Details

- mclust_clust(): does not allow noise
- rmclust_clust(): allows noise

Value

If `clusters_only` is `TRUE` a vector of the new partition of the data is returned, i.e a vector of integers (from `1:k`) indicating the cluster to which each observation is allocated. 0 indicates trimmed observations.

Otherwise a list is returned with the following components:

`clust_method`	the name of the clustering method, i.e "rimle".
`clusters`	the vector of the new partition of the data, i.e a vector of integers (from `1:k`) indicating the cluster to which each observation is allocated. 0 indicates outlying observations for `rmclust_clust()` only.
`...`	an object of class "`mclust`"

Author(s)

Aurore Archimbaud

See Also

`mclust::Mclust()`

Examples

```
mclust_clust(iris[,1:4], k = 3, clusters_only = TRUE)
```

`med_crit` *Selection of Invariant components using the med criterion*

Description

Identifies as interesting invariant coordinates whose generalized eigenvalues are the furthermost away from the median of all generalized eigenvalues.

Usage

```
med_crit(object, ...)

## S3 method for class 'ICS'
med_crit(object, nb_select = NULL, select_only = FALSE, ...)

## Default S3 method:
med_crit(object, nb_select = NULL, select_only = FALSE, ...)
```

Arguments

object	object of class "ICS".
...	additional arguments are currently ignored.
nb_select	the exact number of components to select. By default it is set to NULL, i.e the number of components to select is the number of variables minus one.
select_only	boolean. If TRUE only the vector names of the selected invariant components is returned. If FALSE additional details are returned.

Details

If more than half of the components are "uninteresting" and have the same generalized eigenvalue then the median of all generalized eigenvalues corresponds to the uninteresting component generalized eigenvalue. The components of interest are the ones whose generalized eigenvalues differ the most from the median. The motivation of this criterion depends therefore on the assumption that at least half of the components have equal generalized eigenvalues.

Value

If select_only is TRUE a vector of the names of the invariant components or variables to select. If FALSE an object of class "ICS_crit" is returned with the following objects:

- crit: the name of the criterion "med".
- nb_select: the number of components to select.
- gen_kurtosis: the vector of generalized kurtosis values.
- med_gen_kurtosis: the median of the generalized kurtosis values.
- gen_kurtosis_diff_med: the absolute differences between the generalized kurtosis values and the median.
- select: the names of the invariant components or variables to select.

Author(s)

Andreas Alfons, Aurore Archimbaud and Klaus Nordhausen

References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

See Also

normal_crit(), var_crit(), discriminatory_crit().

Examples

```
X <- iris[,-5]
out <- ICS(X)
med_crit(out, nb_select = 2, select_only = FALSE)
```

`mixture_sim` *Simulation of a mixture of Gaussian distributions*

Description

Simulation of a $n \times p$ data frame according to a mixture of q Gaussian distributions with $q < p$, different location parameters $\mu_1, \ldots, \mu_q$, and the identity matrix as the covariance matrix.

Usage

```
mixture_sim(pct_clusters = c(0.5, 0.5), n = 500, p = 10, delta = 10)
```

Arguments

`pct_clusters`	a vector of marginal probabilities for each group, i.e mixture weights. Default is two balanced clusters.
`n`	integer. The number of observations.
`p`	integer. The number of variables.
`delta`	integer. The location shift.

Details

Let X be a p-variate real random vector distributed according to a mixture of q Gaussian distributions with $q < p$, different location parameters $\mu_1, \ldots, \mu_q$, and the same positive definite covariance matrix I_p:

$$X \sim \sum_{h=1}^{q} \epsilon_h \mathcal{N}(\mu_h, I_p),$$

where $\epsilon_1, \ldots, \epsilon_q$ are mixture weights with $\epsilon_1 + \cdots + \epsilon_q = 1$, $\mu_1 = 0_p$, and $\mu_{h+1} = \delta e_h$ with $h = 1, \ldots, q-1$.

Value

A dataframe of *n* observations and *p+1* variables with the first variable indicating the cluster assignment using a character string.

Author(s)

Aurore Archimbaud

References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

Examples

```
X <- mixture_sim()
summary(X)
```

`normal_crit` *Selection of Non-normal Invariant Components Using Marginal Normality Tests*

Description

Identifies invariant coordinates that are non normal using univariate normality tests as in the `comp.norm.test` function from the `ICSOutlier` package, with the difference that both the first and last few components are investigated.

Usage

```
normal_crit(object, ...)

## S3 method for class 'ICS'
normal_crit(
  object,
  level = 0.05,
  test = c("agostino.test", "jarque.test", "anscombe.test", "bonett.test",
    "shapiro.test"),
  max_select = NULL,
  select_only = FALSE,
  ...
)

## Default S3 method:
normal_crit(
  object,
  level = 0.05,
  test = c("agostino.test", "jarque.test", "anscombe.test", "bonett.test",
    "shapiro.test"),
  max_select = NULL,
  select_only = FALSE,
  gen_kurtosis = NULL,
  ...
)
```

Arguments

`object`	object of class `"ICS"` or a data frame or matrix.
`...`	additional arguments are currently ignored.
`level`	the initial level used to make a decision based on the test p-values. See details. Default is 0.05.

test	name of the normality test to be used. Possibilities are "jarque.test", "anscombe.test", "bonett.test", "agostino.test", "shapiro.test". Default is "agostino.test".
max_select	the maximal number of components to select.
select_only	boolean. If TRUE only the vector names of the selected invariant components is returned. If FALSE additional details are returned.
gen_kurtosis	vector of generalized kurtosis values.

Details

The procedure sequentially tests the first and the last components until finding no additional components as non-normal. The quantile levels are adjusted for multiple testing by taking the level as level/*j* for the *j*th component.

Value

If select_only is TRUE a vector of the names of the invariant components or variables to select. If FALSE an object of class "ICS_crit" is returned with the following objects:

- crit: the name of the criterion "normal".
- level: the level of the test.
- max_select: the maximal number of components to select.
- test: name of the normality test to be used.
- pvalues: the p-values of the tests.
- adjusted_levels: the adjusted levels.
- select: the names of the invariant components or variables to select.
- gen_kurtosis: the vector of generalized kurtosis values in case of ICS object.

Author(s)

Andreas Alfons, Aurore Archimbaud, Klaus Nordhausen and Anne Ruiz-Gazen

References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

Archimbaud, A., Nordhausen, K., and Ruiz-Gazen, A. (2018). ICSOutlier: Unsupervised Outlier Detection for Low-Dimensional Contamination Structure, The RJournal, Vol. 10(1):234–250. doi:10.32614/RJ2018034

Archimbaud, A., Nordhausen, K., and Ruiz-Gazen, A. (2016). ICSOutlier: Outlier Detection Using Invariant Coordinate Selection. R package version 0.3-0

See Also

med_crit(), var_crit(), discriminatory_crit(), moments::jarque.test(), moments::anscombe.test(), moments::bonett.test(), moments::agostino.test(), stats::shapiro.test().

Examples

```
X <- iris[,-5]
out <- ICS(X)
normal_crit(out, level = 0.1, select_only = FALSE)
```

---

pam_clust *Partitioning Around Medoids clustering*

Description

Wrapper for performing Partitioning Around Medoids clustering from `cluster::pam()`.

Usage

```
pam_clust(X, k, clusters_only = FALSE, ...)
```

Arguments

X	a numeric matrix or data frame of the data. It corresponds to the argument x.
k	the number of clusters searched for. It corresponds to the argument k.
clusters_only	boolean. If TRUE only the partition of the data is returned as a vector. If FALSE the usual output of the `cluster::pam()` function is returned.
...	other arguments to pass to the `cluster::pam()`.

Value

If `clusters_only` is TRUE a vector of the new partition of the data is returned, i.e a vector of integers (from `1:k`) indicating the cluster to which each observation is allocated. 0 indicates trimmed observations.

Otherwise a list is returned with the following components:

clust_method	the name of the clustering method, i.e "clara_pam".
clusters	the vector of the new partition of the data, i.e a vector of integers (from `1:k`) indicating the cluster to which each observation is allocated. 0 indicates outlying observations.
...	an object of class "pam"

.

Author(s)

Aurore Archimbaud

See Also

`cluster::pam()`

Examples

```
pam_clust(iris[,1:4], k = 3, clusters_only = TRUE)
```

`plot.ICSClust` *Scatterplot Matrix with densities on the diagonal*

Description

Wrapper for `component_plot()`.

Usage

```
## S3 method for class 'ICSClust'
plot(x, ...)
```

Arguments

`x`	an object of class `"ICSClust"`.
`...`	additional arguments to be passed down to `component_plot()`

Value

An object of class `"ggmatrix"` (see `GGally::ggpairs()`).

Author(s)

Aurore Archimbaud

`print.ICSClust_summary`
Print of an `ICSClust_summary` *object*

Description

Prints an `ICSClust_summary` object in an informative way.

Usage

```
## S3 method for class 'ICSClust_summary'
print(x, info = FALSE, digits = 4L, ...)
```

Arguments

x	object of class "ICSClust_summary".
info	logical, either TRUE or FALSE. If TRUE, prints additional information on arguments used for computing scatter matrices (only named arguments that contain numeric, character, or logical scalars) and information on the parameters of the algorithm. Default is FALSE.
digits	number of digits for the numeric output.
...	additional arguments are ignored.

Value

The supplied object of class "ICSClust_summary" is returned invisibly.

Author(s)

Aurore Archimbaud

---

rimle_clust *Robust Improper Maximum Likelihood Clustering*

Description

Wrapper for performing Robust Improper Maximum Likelihood Clustering clustering from otrimle::rimle().

Usage

```
rimle_clust(X, k, clusters_only = FALSE, ...)
```

Arguments

X	a numeric matrix or data frame of the data. It corresponds to the argument data.
k	the number of clusters searched for. It corresponds to the argument G.
clusters_only	boolean. If TRUE only the partition of the data is returned as a vector. If FALSE the usual output of the otrimle::rimle() function is returned.
...	other arguments to pass to otrimle::rimle().

Value

If clusters_only is TRUE a vector of the new partition of the data is returned, i.e a vector of integers (from 1:k) indicating the cluster to which each observation is allocated. 0 indicates trimmed observations.

Otherwise a list is returned with the following components:

clust_method	the name of the clustering method, i.e, "rimle".
clusters	the vector of the new partition of the data, i.e. a vector of integers (from 1:k) indicating the cluster to which each observation is allocated. 0 indicates outlying observations.
...	an object of class "rimle"

Author(s)

Aurore Archimbaud

See Also

otrimle::rimle()

Examples

```
rimle_clust(iris[,1:4], k = 3, clusters_only = TRUE)
```

---

runif_outside_range *Uniform distribution outside a given range*

Description

Draw from a multivariate uniform distribution outside a given range. Intuitively speaking, the observations are drawn from a multivariate uniform distribution on a hyperrectangle with a hole in the middle (in the shape of a smaller hyperrectangle). This is useful, e.g., for adding random noise to a data set such that the noise consists of large values that do not overlap the initial data.

Usage

```
runif_outside_range(n, min = 0, max = 1, mult = 2)
```

Arguments

n	an integer giving the number of observations to generate.
min	a numeric vector giving the minimum of each variable of the initial data set (outside of which to generate random noise).
max	a numeric vector giving the maximum of each variable of the initial data set (outside of which to generate random noise).
mult	multiplication factor (larger than 1) to expand the hyperrectangle around the initial data (which is given by min and max). For instance, the default value 2 gives a hyperrectangle for which each side is twice as long as the range of the initial data. The data are then drawn from a uniform distribution on the expanded hyperrectangle from which the smaller hyperrectangle around the data is cut out. See the examples for an illustration.

Value

A matrix of generated points.

Author(s)

Andreas Alfons

References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

Examples

```
## illustrations for argument 'mult'

# draw observations with argument 'mult = 2'
xy2 <- runif_outside_range(1000, min = rep(-1, 2), max = rep(1, 2),
                           mult = 2)
# each side of the larger hyperrectangle is twice as long as
# the corresponding side of the smaller rectanglar cut-out
df2 <- data.frame(x = xy2[, 1], y = xy2[, 2])
ggplot(data = df2, mapping = aes(x = x, y = y)) +
  geom_point()

# draw observations with argument 'mult = 4'
xy4 <- runif_outside_range(1000, min = rep(-1, 2), max = rep(1, 2),
                           mult = 4)
# each side of the larger hyperrectangle is four times as long
# as the corresponding side of the smaller rectanglar cut-out
df4 <- data.frame(x = xy4[, 1], y = xy4[, 2])
ggplot(data = df4, mapping = aes(x = x, y = y)) +
  geom_point()
```

---

select_plot *Plot of the Generalized Kurtosis Values of the ICS Transformation*

Description

Extracts the generalized kurtosis values of the components obtained via an ICS transformation and draws either a screeplot or a specific plot for a given criterion. If an object of class `"ICS_crit"` is given, then the selected components are shaded on the plot.

Usage

```
select_plot(object, ...)

## Default S3 method:
select_plot(
  object,
  select = NULL,
  scale = FALSE,
  screeplot = TRUE,
  type = c("dots", "lines"),
  width = 0.2,
```

```
  color = "grey",
  alpha = 0.3,
  size = 3,
  ...
)

## S3 method for class 'data.frame'
select_plot(
  object,
  type = c("dots", "lines"),
  width = 0.2,
  color = "grey",
  alpha = 0.3,
  ...
)

## S3 method for class 'ICS_crit'
select_plot(
  object,
  type = c("dots", "lines"),
  width = 0.2,
  color = "grey",
  alpha = 0.3,
  size = 3,
  screeplot = TRUE,
  ...
)
```

Arguments

object	an object inheriting from class "ICS" and containing results from an ICS transformation or from class "ICS_crit".
...	additional arguments are currently ignored.
select	an integer, character, or logical vector specifying for which components to extract the generalized kurtosis values, or NULL for extracting the generalized kurtosis values of all components.
scale	a logical indicating whether to scale the generalized kurtosis values to have product 1 (defaults to FALSE).
screeplot	boolean. If TRUE a plot of the generalized kurtosis values is drawn. Otherwise it is context specific to the ICS_crit object. For "med" criterion, the differences between the kurtosis values and the median are plotted in absolute values. For "discriminatory" the discriminatory power associated to the evaluated combinations are drawn.
type	either "dots" or "lines" for the type of plot.
width	the width for shading the selected components in case an ICS_crit object is given.

color	the color for shading the selected components in case an ICS_crit object is given.
alpha	the transparency for shading the selected components in case an ICS_crit object is given.
size	size of the points. Only relevant for "discriminatory" criteria.

Value

An object of class "ggplot" (see ggplot2::ggplot()).

Author(s)

Andreas Alfons and Aurore Archimbaud

Examples

```
X <- iris[,-5]
out <- ICS(X)

# on an ICS object
select_plot(out)
select_plot(out, type = "lines")

# on an ICS_crit object
# median criterion
out_med <- med_crit(out, nb_select = 1, select_only = FALSE)
select_plot(out_med, type = "lines")
select_plot(out_med, screeplot = FALSE, type = "lines",
color = "lightblue")

# discriminatory criterion
out_disc <- discriminatory_crit(out, clusters = iris[,5],
 select_only = FALSE)
select_plot(out_disc)
```

---

summary.ICSClust *Summary of an* ICSClust *object*

Description

Summarizes an ICSClust object in an informative way.

Usage

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

Arguments

`object`	object of class `"ICSClust"`.
`...`	additional arguments passed to `summary()`

Value

An object of class `"ICSClust_summary"` with the following components:

- `ICS_out`: `ICS_out` object
- `nb_comp`: number of selected components
- `select`: vector of names of selected components
- `nb_clusters`: number of clusters
- `table_clusters`: frequency table of clusters

Author(s)

Aurore Archimbaud

---

tcov *Pairwise one-step M-estimate of scatter*

Description

Computes a pairwise one-step M-estimate of scatter with weights based on pairwise Mahalanobis distances. Note that it is based on pairwise differences and therefore does not require a location estimate.

Usage

```
tcov(x, beta = 2)
```

Arguments

`x`	a numeric matrix or data frame.
`beta`	a positive numeric value specifying the tuning parameter of the pairwise one-step M-estimator (defaults to 2), see 'Details'.

Details

For a sample $\boldsymbol{X}_n = (\mathbf{x}_1, \ldots, \mathbf{x}_n)^\top$, a positive and decreasing weight function w, and a tuning parameter $\beta > 0$, the pairwise one-step M-estimator of scatter is defined as

$$\mathrm{TCOV}_\beta(\boldsymbol{X}_n) = \frac{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} w(\beta\, r^2(\mathbf{x}_i, \mathbf{x}_j))(\mathbf{x}_i - \mathbf{x}_j)(\mathbf{x}_i - \mathbf{x}_j)^\top}{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} w(\beta\, r^2(\mathbf{x}_i, \mathbf{x}_j))},$$

where

$$r^2(\mathbf{x}_i, \mathbf{x}_j) = (\mathbf{x}_i - \mathbf{x}_j)^\top \mathrm{COV}(\boldsymbol{X}_n)^{-1}(\mathbf{x}_i - \mathbf{x}_j)$$

denotes the squared pairwise Mahalanobis distance between observations $\mathbf{x}_i$ and $\mathbf{x}_j$ based on the sample covariance matrix $\mathrm{COV}(\boldsymbol{X}_n)$. Here, the weight function $w(x) = \exp(-x/2)$ is used.

Value

A numeric matrix giving the pairwise one-step M-estimate of scatter.

Author(s)

Andreas Alfons and Aurore Archimbaud

References

Caussinus, H. and Ruiz-Gazen, A. (1993) Projection Pursuit and Generalized Principal Component Analysis. In Morgenthaler, S., Ronchetti, E., Stahel, W.A. (eds.) *New Directions in Statistical Data Analysis and Robustness*, 35-46. Monte Verita, Proceedings of the Centro Stefano Franciscini Ascona Series. Springer-Verlag.

Caussinus, H. and Ruiz-Gazen, A. (1995) Metrics for Finding Typical Structures by Means of Principal Component Analysis. In *Data Science and its Applications*, 177-192. Academic Press.

See Also

`ICS_tcov()`, `ucov()`, `ICS_ucov()`

---

tkmeans_clust *Trimmed k-means clustering*

Description

Wrapper for performing trimmed k-means clustering from `tclust::tkmeans()`.

Usage

```
tkmeans_clust(X, k, clusters_only = FALSE, alpha = 0.05, ...)
```

Arguments

`X`	a numeric matrix or data frame of the data. It corresponds to the argument `x`.
`k`	the number of clusters searched for. It corresponds to the argument `k`.
`clusters_only`	boolean. If `TRUE` only the partition of the data is returned as a vector. If `FALSE` the usual output of the tkmeans function is returned.
`alpha`	the proportion of observations to be trimmed.
`...`	other arguments to pass to the `tclust::tkmeans()`

Value

If `clusters_only` is `TRUE` a vector of the new partition of the data is returned, i.e a vector of integers (from `1:k`) indicating the cluster to which each observation is allocated. 0 indicates trimmed observations.

Otherwise a list is returned with the following components:

`clust_method`	the name of the clustering method, i.e. "tkmeans".
`clusters`	the vector of the new partition of the data, i.e. a vector of integers (from `1:k`) indicating the cluster to which each observation is allocated. 0 indicates trimmed observations.
`...`	an object of class `"tkmeans"`

.

Author(s)

Aurore Archimbaud

See Also

`tclust::tkmeans()`

Examples

```
tkmeans_clust(iris[,1:4], k = 3, alpha = 0.1, clusters_only = TRUE)
```

---

ucov *Simple robust estimates of scatter*

Description

Compute a one-step M-estimator of scatter with weights based on Mahalanobis distances, or a simple related estimator that is based on a transformation.

Usage

```
scov(x, beta = 0.2)

ucov(x, beta = 0.2)
```

Arguments

`x`	a numeric matrix or data frame.
`beta`	a positive numeric value specifying the tuning parameter of the estimator (defaults to 0.2), see 'Details'.

Details

For a sample $\boldsymbol{X}_n = (\mathbf{x}_1, \ldots, \mathbf{x}_n)^\top$, a positive and decreasing weight function w, and a tuning parameter $\beta > 0$, the one-step M-estimator of scatter is defined as

$$\mathrm{SCOV}_\beta(\boldsymbol{X}_n) = \frac{\sum_{i=1}^n w(\beta\, r^2(\mathbf{x}_i))(\mathbf{x}_i - \bar{\mathbf{x}}_n)(\mathbf{x}_i - \bar{\mathbf{x}}_n)^\top}{\sum_{i=1}^n w(\beta\, r^2(\mathbf{x}_i))},$$

where

$$r^2(\mathbf{x}_i) = (\mathbf{x}_i - \bar{\mathbf{x}}_n)^\top \mathrm{COV}(\boldsymbol{X}_n)^{-1}(\mathbf{x}_i - \bar{\mathbf{x}}_n)$$

denotes the squared Mahalanobis distance of observation $\mathbf{x}_i$ from the sample mean $\bar{\mathbf{x}}_n$ based on the sample covariance matrix $\mathrm{COV}(\boldsymbol{X}_n)$. Here, the weight function $w(x) = \exp(-x/2)$ is used.

A simple robust estimator that is consistent under normality is obtained via the transformation

$$\mathrm{UCOV}_\beta(\boldsymbol{X}_n) = (\mathrm{SCOV}_\beta(\boldsymbol{X}_n)^{-1} - \beta\, \mathrm{COV}(\boldsymbol{X}_n)^{-1})^{-1}.$$

Value

A numeric matrix giving the estimate of the scatter matrix.

Author(s)

Andreas Alfons and Aurore Archimbaud

References

Caussinus, H. and Ruiz-Gazen, A. (1993) Projection Pursuit and Generalized Principal Component Analysis. In Morgenthaler, S., Ronchetti, E., Stahel, W.A. (eds.) *New Directions in Statistical Data Analysis and Robustness*, 35-46. Monte Verita, Proceedings of the Centro Stefano Franciscini Ascona Series. Springer-Verlag.

Caussinus, H. and Ruiz-Gazen, A. (1995) Metrics for Finding Typical Structures by Means of Principal Component Analysis. In *Data Science and its Applications*, 177-192. Academic Press.

Ruiz-Gazen, A. (1996) A Very Simple Robust Estimator of a Dispersion Matrix. *Computational Statistics & Data Analysis*, **21**(2), 149-162. doi:10.1016/01679473(95)000097.

See Also

`ICS_ucov()`, `tcov()`, `ICS_tcov()`

var_crit *Selection of Invariant components using the var criterion*

Description

Identifies the interesting invariant coordinates based on the rolling variance criterion as used in the ICSboot function of the ICtest package. It computes rolling variances on the generalized eigenvalues obtained through ICS::ICS().

Usage

```
var_crit(object, ...)

## S3 method for class 'ICS'
var_crit(object, nb_select = NULL, select_only = FALSE, ...)

## Default S3 method:
var_crit(object, nb_select = NULL, select_only = FALSE, ...)
```

Arguments

object	object of class "ICS".
...	additional arguments are currently ignored.
nb_select	the exact number of components to select. By default it is set to NULL, i.e the number of components to select is the number of variables minus one.
select_only	boolean. If TRUE only the vector names of the selected invariant components is returned. If FALSE additional details are returned.

Details

Assuming that the generalized eigenvalues of the uninformative components are all the same means that the variance of these generalized eigenvalues must be minimal. Therefore when nb_select components should be selected, the method identifies the p - nb_select neighboring generalized eigenvalues with minimal variance, where p is the total number of components. The number of interesting components should be at most p-2 as at least two uninteresting components are needed to compute a variance.

Value

If select_only is TRUE a vector of the names of the invariant components or variables to select. If FALSE an object of class "ICS_crit" is returned with the following objects:

- crit: the name of the criterion "var".
- nb_select: the number of components to select.
- gen_kurtosis: the vector of generalized kurtosis values.
- select: the names of the invariant components or variables to select.

- `RollVarX`: the rolling variances of order d-`nb_select`.
- `Order`: indexes of the ordered invariant components such that the ones associated to the smallest variances of the eigenvalues are at the end.

Author(s)

Andreas Alfons, Aurore Archimbaud and Klaus Nordhausen

References

Alfons, A., Archimbaud, A., Nordhausen, K., & Ruiz-Gazen, A. (2024). Tandem clustering with invariant coordinate selection. Econometrics and Statistics. doi:10.1016/j.ecosta.2024.03.002.

Radojicic, U., & Nordhausen, K. (2019). Non-gaussian component analysis: Testing the dimension of the signal subspace. In Workshop on Analytical Methods in Statistics (pp. 101–123). Springer. doi:10.1007/9783030488147_6.

See Also

`normal_crit()`, `med_crit()`, `discriminatory_crit()`.

Examples

```
X <- iris[,-5]
out <- ICS(X)
var_crit(out, nb_select = 2, select_only = FALSE)
```

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