

Package ‘ClusBoot’

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Title Bootstrap a Clustering Solution to Establish the Stability of the Clusters

Version 1.2.2

Description Providing a cluster allocation for n samples, either with an $n \times p$ data matrix or an $n \times n$ distance matrix, a bootstrap procedure is performed. The proportion of bootstrap replicates where a pair of samples cluster in the same cluster indicates how tightly the samples in a particular cluster cluster together.

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Encoding UTF-8

RoxygenNote 7.2.3

Depends R (≥ 2.10)

LazyData true

Imports graphics, grDevices, stats

Suggests fpc, testthat ($\geq 3.0.0$)

Config/testthat/edition 3

NeedsCompilation no

Author Sugnet Lubbe [aut, cre, cph] (ORCID:
<<https://orcid.org/0000-0003-2762-9944>>)

Maintainer Sugnet Lubbe <slubbe@sun.ac.za>

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boot.proportions	<i>Heatmap of the proportion of bootstrap replicates where objects cluster together</i>
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Description

Heatmap of the proportion of bootstrap replicates where objects cluster together

Usage

```
boot.proportions(  
  x,  
  col = grDevices::heat.colors(101, rev = TRUE),  
  show.vals = F,  
  text.col = "black",  
  cluster.col = "firebrick",  
  ...  
)
```

Arguments

x	an object of class clusboot
col	vector of colours for shading to indicate proportion values
show.vals	logical value indicating whether proportion values should be added to individual cells
text.col	colour of text for show.vals if TRUE
cluster.col	colour of lines demarcating cluster membership
...	more arguments to be passed to plot()

Examples

```
out <- clusboot (scale(case.study.psychiatrist), B=100, k=6, clustering.func=complete.linkage)  
boot.proportions(out)
```

boot.silhouette	<i>Produces silhouette plots</i>
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Description

Produces silhouette plots

Usage

```
boot.silhouette(clusboot.out, ...)
```

Arguments

clusboot.out	an object of class clusboot
...	more arguments to be passed to barplot()

Value

list of silhouette widths

Examples

```
out <- clusboot (scale(case.study.psychiatrist), B=100, k=6, clustering.func=complete.linkage)
boot.silhouette(out)
```

calc.silhouette	<i>Computes the silhouette vales based on proportion of times items cluster together</i>
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Description

Computes the silhouette vales based on proportion of times items cluster together

Usage

```
calc.silhouette(clusboot.out)
```

Arguments

clusboot.out	an object of class clusboot
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Value

an object of class clusboot

`case.study.psychiatrist`*Patient by psychiatric symptom data*

Description

Presence/absence ratings of 24 psychiatric symptoms in 30 psychiatric inpatients made by an individual psychiatrist. The data have been collected in a case study of an individual psychiatrist to identify his implicit taxonomy.

Usage

`case.study.psychiatrist`

Format

`case.study.psychiatrist:`

A data frame with 30 observations on the following 28 variables:

V1 inappropriate affect, appearance or behavior; binary vector

V2 interview belligerence - negativism; binary vector

V3 agitation - excitement; binary vector

V4 retardation; binary vector

V5 lack of emotions; binary vector

V6 speech disorganization; binary vector

V7 grandiosity; binary vector

V8 suspicion - ideas of persecution; binary vector

V9 hallucinations - delusions; binary vector

V10 overt anger; binary vector

V11 depression; binary vector

V12 anxiety; binary vector

V13 obsession - compulsion; binary vector

V14 suicide; binary vector

V15 self injury; binary vector

V16 somatic concerns; binary vector

V17 social isolation; binary vector

V18 daily routine impairment; binary vector

V19 leisure time impairment; binary vector

V20 antisocial impulses or acts; binary vector

V21 alcohol abuse; binary vector

V22 drug abuse; binary vector

V23 disorientation; binary vector

V24 memory impairment; binary vector

- V25 rating on Global Assessment Scale, a 101-point scale for overall severity of psychiatric disturbance; a numeric vector
- V26 Affective (Affective Disorder or Anxiety Disorder); binary vector
- V27 Psychotic (Schizophrenic Disorder or Paranoid Disorder); binary vector
- V28 Substance abuse (Substance Use Disorder or Substance-Induced Disorder); binary vector

Details

The data set forms part of the International Federation of Classification Societies Cluster Benchmark Data Repository

Source

Van Mechelen, I., & De Boeck, P. (1989). Implicit taxonomy in psychiatric diagnosis: A case study. *Journal of Social and Clinical Psychology*, 8, 276-287. https://ifcs.boku.ac.at/repository/data/case_study_psychiatrist/index.html

clusboot	<i>Performs bootstrap on a cluster analysis output</i>
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Description

Performs bootstrap on a cluster analysis output

Usage

```
clusboot(datmat, B = 1000, clustering.func = complete.linkage, ...)
```

Arguments

datmat	a data matrix or distance object which will be the input to the clustering function
B	number of bootstrap replicates
clustering.func	the function which will perform the clustering and output a vector of cluster memberships
...	more arguments to be passed to the clustering function

Details

Any R function performing cluster analysis can be specified in `clustering.func` although a wrapper function is typically needed to isolate only the vector output of cluster memberships. See `?complete.linkage` as an example. Should users prefer to use alternative resampling schemes, other than the bootstrap, Hennig (2007) discuss a variety of options which could be accessed by specifying `clustering.func = fpc.clusterboot`. In addition, the sampling method is specified in the argument `bootmethod` and additional arguments for the function `clusterboot` in the package `fpc` must be given. Note that only the resampling facilities of `clusterboot` is utilised while the computation of proportions and silhouette widths remain unchanged. The output object of class `clusboot` will remain unchanged as only the resampling section of `clusterboot` is used.

Value

an object of class `clusboot` which is a list with the following components:

<code>proportions</code>	matrix of size <code>n</code> x <code>n</code> with cell <code>ij</code> containing the proportion of bootstrap replicates in which object <code>i</code> and object <code>j</code> clustered together.
<code>clustering</code>	a vector of length <code>n</code> containing the cluster membership of the <code>n</code> input objects.
<code>sil</code>	a vector of length the number of clusters containing the bootstrap-silhouette values for the clusters.
<code>indv.sil</code>	a vector of length <code>n</code> containing the bootstrap-silhouette values for the individual objects.
<code>sil.order</code>	a vector of length <code>n</code> containing the ordering of the <code>n</code> objects used by the functions <code>boot.silhouette</code> and <code>boot.proportions</code> to order objects in the same cluster adjacent and clusters in decreasing order of cluster tightness.
<code>ave.sil.width</code>	the overall stability of the clustering solution, obtained by averaging over the individual object bootstrap-silhouette values.

References

Hennig, C., 2007. Cluster-wise assessment of cluster stability. Computational Statistics & Data Analysis, 52(1), pp.258-271. Lubbe, S., 2024. Bootstrapping Cluster Analysis Solutions with the R Package `ClusBoot`. Austrian Journal of Statistics, 53(3), pp.1-19.

Examples

```
clusboot (scale(case.study.psychiatrist), B=100, k=6, clustering.func=complete.linkage)
library(fpc)
clusboot (scale(case.study.psychiatrist), B=100, k=6, clustering.func=fpc.clusterboot,
          clustermethod=hclustCBI, method="complete", bootmethod="subset", subtuning=10)
```

<code>complete.linkage</code>	<i>Wrapper function for performing complete linkage clustering</i>
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Description

Wrapper function for performing complete linkage clustering

Usage

```
complete.linkage(X, k)
```

Arguments

<code>X</code>	samples x variables data matrix
<code>k</code>	number of clusters

Value

vector of cluster memberships

Examples

```
complete.linkage(scale(case.study.psychiatrist), k=6)
```

fpc.clusterboot

Resampling according to the methods discussed in Hennig (2007)

Description

Resampling according to the methods discussed in Hennig (2007)

Usage

```
fpc.clusterboot(
  data,
  B,
  distances = (inherits(data, "dist")),
  bootmethod = "boot",
  bscompare = TRUE,
  multipleboot = FALSE,
  jittertuning = 0.05,
  noisetuning = c(0.05, 4),
  subtuning = floor(nrow(data)/2),
  clustermethod,
  noisemethod = FALSE,
  count = TRUE,
  seed = NULL,
  datamatrix = TRUE,
  ...
)
```

Arguments

data	a data matrix or distance object which will be the input to the clustering function
B	number of bootstrap replicates
distances	see ?fpc::clusterboot
bootmethod	see ?fpc::clusterboot
bscompare	see ?fpc::clusterboot
multipleboot	see ?fpc::clusterboot
jittertuning	see ?fpc::clusterboot
noisetuning	see ?fpc::clusterboot

subtuning	see ?fpc::clusterboot
clustermethod	see ?fpc::clusterboot
noisemethod	see ?fpc::clusterboot
count	see ?fpc::clusterboot
seed	see ?fpc::clusterboot
datatomatrix	see ?fpc::clusterboot
...	additional arguments to be sent to the function specified in clustermethod

Value

a list with two components; boot.out contains the computations for clusboot and out contains the clustering solution of the original data set

plot.clusboot	<i>MDS plot of similarities given by the proportion of bootstrap replicates where objects cluster together</i>
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Description

MDS plot of similarities given by the proportion of bootstrap replicates where objects cluster together

Usage

```
## S3 method for class 'clusboot'
plot(x, col, show.silhouette = TRUE, ...)
```

Arguments

x	an object of class clusboot
col	single colour or a vector specifying a colour for each object
show.silhouette	logical indicating whether plotting character size should represent the individual silhouette values
...	more arguments to be passed to plot()

Value

matrix of similarities (proportions)

Examples

```
out <- clusboot(scale(case.study.psychiatrist), B=100, k=6, clustering.func=complete.linkage)
plot(out)
```

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