Package ‘psy’

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R topics documented:

  ckappa .......... 2
cronbach .......... 3
ehd ................. 4
expsy ............... 5
f pca ............... 6
icc ................. 8
lkappa ............. 9
mdspca ............. 11
mtmm ............... 12
psy .................. 13
scree.plot .......... 14
sleep ............... 15
sp h pca ............. 16
wkappa ............. 18

Index 20
Cohen’s Kappa for 2 raters

Description
Computes Cohen’s Kappa for agreement in the case of 2 raters. The diagnosis (the object of the rating) may have k possible values.

Usage
ckappa(r)

Arguments
r
n*2 matrix or dataframe, n subjects and 2 raters

Details
The function deals with the case where the two raters have not exactly the same scope of rating (some software associate an error with this situation). Missing value are omitted.

Value
A list with:
$table the 2*k table of raw data (first rater in rows, second rater in columns)
$kappa Cohen’s Kappa

Author(s)
Bruno Falissard

References

Examples
data(expsy)
## Cohen's kappa for binary diagnosis
ckappa(expsy[,c(12,14)])

##to obtain a 95%confidence interval:
#library(boot)
#ckappa.boot <- function(data,x) {ckappa(data[x,])[[2]]}
#res <- boot(expsy[,c(12,14)],ckappa.boot,1000)
## two-sided bootstrapped confidence interval of kappa
#quantile(res$t,c(0.025,0.975))
cronbach

```r
## adjusted bootstrap percentile (BCa) confidence interval (better)
#boot.ci(res,type="bca")
##Cohen's kappa for non binary diagnosis
#ckappa(expsy[,c(11,13)])
```

<table>
<thead>
<tr>
<th>cronbach</th>
<th>Cronbach's coefficient alpha</th>
</tr>
</thead>
</table>

### Description

Computes the Cronbach’s reliability coefficient alpha. This coefficient may be applied to a series of items destined to be aggregated in a single score. It estimates reliability in the framework of the domain sampling model.

### Usage

```r
cronbach(v1)
```

### Arguments

- `v1`  
  n*p matrix or dataframe, n subjects and p items

### Details

Missing value are omitted in a "listwise" way (all items are removed even if only one of them is missing).

### Value

A list with:

- `$sample.size`  
  Number of subjects under study
- `$number.of.items`  
  Number of items of the scale or questionnaire
- `$alpha`  
  alpha

### Author(s)

Bruno Falissard

### References

Examples

data(expsy)
cronbach(expsy[,1:10])  ## not good because item 2 is reversed (1 is high and 4 is low)
cronbach(cbind(expsy[,c(1,3:10)],-1*expsy[,2]))  ## better

#to obtain a 95% confidence interval:
datafile <- cbind(expsy[,c(1,3:10)],-1*expsy[,2])
library(boot)
cronbach.boot <- function(data,x) {cronbach(data[x,])[3]}</crunch>
res <- boot(datafile,cronbach.boot,1000)
quantile(res$t,c(0.025,0.975))  ## two-sided bootstrapped confidence interval of Cronbach's alpha
boot.ci(res,type="bca")  ## adjusted bootstrap percentile (BCa) confidence interval (better)

---

**ehd**

*Depressive Mood Scale*

Description


Usage

data(ehd)

Format

This data frame contains the following columns:

- **e1** Observed painful sadness
- **e2** Emotional hyperexpressiveness
- **e3** Emotional instability
- **e4** Observed monotony
- **e5** Lack spontaneous expressivity
- **e6** Lack affective reactivity
- **e7** Emotional incontinence
- **e8** Affective hyperesthesia
- **e9** Observed explosive mood
- **e10** Worried gesture
- **e11** Observed anhedonia
- **e12** Felt sadness
- **e13** Situational anhedonia
- **e14** Felt affective indifference
e15 Hypersensibility unpleasant events
e16 Sensory anhedonia
e17 Felt affective monotony
e18 Felt hyperemotionalism
e19 Felt irritability
e20 Felt explosive mood

Source

Examples
data(ehd)
str(ehd)

<table>
<thead>
<tr>
<th>expsy</th>
<th>Data set related to psychometry</th>
</tr>
</thead>
</table>

Description
The expsy data frame has 30 rows and 16 columns with missing data. it1-it10 correspond to the rating of 30 patients with a 10 items scale. r1, r2, r3 to the rating of item 1 by 3 different clinicians of the same 30 patients. rb1, rb2, rb3 to the binary transformation of r1, r2, r3 (1 or 2 -> 0; and 3 or 4 -> 1).

Usage
data(expsy)

Format
This data frame contains the following columns:

it1 a numeric vector corresponding to item 1 (rated from 1:low to 4:high)
it2 a numeric vector corresponding to item 2 (rated from 1:high to 4:low)
it3 a numeric vector corresponding to item 3 (rated from 1:low to 4:high)
it4 a numeric vector corresponding to item 4 (rated from 1:low to 4:high)
it5 a numeric vector corresponding to item 5 (rated from 1:low to 4:high)
it6 a numeric vector corresponding to item 6 (rated from 1:low to 4:high)
it7 a numeric vector corresponding to item 7 (rated from 1:low to 4:high)
it8 a numeric vector corresponding to item 8 (rated from 1:low to 4:high)
it9 a numeric vector corresponding to item 9 (rated from 1:low to 4:high)
### Examples

```r
data(expsy)
expsy[1:4,]
```

### Description

Graphical representation similar to a principal components analysis but adapted to data structured with dependent/independent variables

### Usage

```r
fpca(formula=NULL, y=NULL, x=NULL, data, cx=0.75, pvalues="No", partial="Yes", input="data", contraction="No", sample.size=1)
```

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>formula</code></td>
<td>&quot;model&quot; formula, of the form <code>y ~ x</code></td>
</tr>
<tr>
<td><code>y</code></td>
<td>column number of the dependent variable</td>
</tr>
<tr>
<td><code>x</code></td>
<td>column numbers of the independent (explanatory) variables</td>
</tr>
<tr>
<td><code>data</code></td>
<td>name of datafile</td>
</tr>
<tr>
<td><code>cx</code></td>
<td>size of the lettering (0.75 by default, 1 for bigger letters, 0.5 for smaller)</td>
</tr>
<tr>
<td><code>pvalues</code></td>
<td>vector of prespecified pvalues (pvalues=&quot;No&quot; by default) (see below)</td>
</tr>
<tr>
<td><code>partial</code></td>
<td>partial=&quot;Yes&quot; by default, corresponds to the original method (see below)</td>
</tr>
<tr>
<td><code>input</code></td>
<td>input=&quot;Cor&quot; for a correlation matrix (input=&quot;data&quot; by default)</td>
</tr>
<tr>
<td><code>contraction</code></td>
<td>change the aspect of the diagram, contraction=&quot;Yes&quot; is convenient for large data set (contraction=&quot;No&quot; by default)</td>
</tr>
<tr>
<td><code>sample.size</code></td>
<td>to be specified if input=&quot;Cor&quot;</td>
</tr>
</tbody>
</table>

---

*Source*

artificial data

*Examples*

data(expsy)
expsy[1:4,]

---

*Description*

Graphical representation similar to a principal components analysis but adapted to data structured with dependent/independent variables

*Usage*

```r
fpca(formula=NULL, y=NULL, x=NULL, data, cx=0.75, pvalues="No", partial="Yes", input="data", contraction="No", sample.size=1)
```

*Arguments*

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>formula</code></td>
<td>&quot;model&quot; formula, of the form <code>y ~ x</code></td>
</tr>
<tr>
<td><code>y</code></td>
<td>column number of the dependent variable</td>
</tr>
<tr>
<td><code>x</code></td>
<td>column numbers of the independent (explanatory) variables</td>
</tr>
<tr>
<td><code>data</code></td>
<td>name of datafile</td>
</tr>
<tr>
<td><code>cx</code></td>
<td>size of the lettering (0.75 by default, 1 for bigger letters, 0.5 for smaller)</td>
</tr>
<tr>
<td><code>pvalues</code></td>
<td>vector of prespecified pvalues (pvalues=&quot;No&quot; by default) (see below)</td>
</tr>
<tr>
<td><code>partial</code></td>
<td>partial=&quot;Yes&quot; by default, corresponds to the original method (see below)</td>
</tr>
<tr>
<td><code>input</code></td>
<td>input=&quot;Cor&quot; for a correlation matrix (input=&quot;data&quot; by default)</td>
</tr>
<tr>
<td><code>contraction</code></td>
<td>change the aspect of the diagram, contraction=&quot;Yes&quot; is convenient for large data set (contraction=&quot;No&quot; by default)</td>
</tr>
<tr>
<td><code>sample.size</code></td>
<td>to be specified if input=&quot;Cor&quot;</td>
</tr>
</tbody>
</table>
Details

This representation is close to a Principal Components Analysis (PCA). Contrary to PCA, correlations between the dependent variable and the other variables are represented faithfully. The relationships between non dependent variables are interpreted like in a PCA: correlated variables are close or diametrically opposite (for negative correlations), independent variables make a right angle with the origin. The focus on the dependent variable leads formally to a partialisation of the correlations between the non dependent variables by the dependent variable (see reference). To avoid this partialisation, the option partial="No" can be used. It may be interesting to represent graphically the strength of association between the dependent variable and the other variables using p values coming from a model. A vector of pvalue may be specified in this case.

Value

A plot (q plots in fact).

Author(s)

Bruno Falissard, Bill Morphey, Adeline Abbe

References


Examples

data(sleep)
fpca(Paradoxical.sleep~Body.weight+Brain.weight+Slow.wave.sleep+Maximum.life.span+
    Gestation.time+Predation+Sleep.exposure+Danger,data=sleep)
fpca(y="Paradoxical.sleep",x=c("Body.weight","Brain.weight","Slow.wave.sleep",
    "Maximum.life.span","Gestation.time","Predation","Sleep.exposure","Danger"),data=sleep)

## focused PCA of the duration of paradoxical sleep (dreams, 5th column)
## against constitutional variables in mammals (columns 2, 3, 4, 7, 8, 9, 10, 11).
## Variables inside the red cercle are significantly correlated
## to the dependent variable with p<0.05.
## Green variables are positively correlated to the dependent variable,
## yellow variables are negatively correlated.
## There are three clear clusters of independent variables.

corsleep <- as.data.frame(cor(sleep[,2:11],use="pairwise.complete.obs"))
fpca(Paradoxical.sleep~Body.weight+Brain.weight+Slow.wave.sleep+Maximum.life.span+
    Gestation.time+Predation+Sleep.exposure+Danger,
data=corsleep,input="Cor",sample.size=60)

## when missing data are numerous, the representation of a pairwise correlation
## matrix may be preferred (even if mathematical properties are not so good...)

umer <- c(2:4,7:11)
l <- length(numer)
resu <- vector(length=l)
for(i in 1:l)
{
  int <- sleep[,numer[i]]
  mod <- lm(sleep$Paradoxical.sleep~int)
  resu[i] <- summary(mod)[[4]][2,4]*sign(summary(mod)[[4]][2,1])
}
fpca(Paradoxical.sleep~Body.weight+Brain.weight+Slow.wave.sleep+Maximum.life.span+
     Gestation.time+Predation+Sleep.exposure+Danger,
     data=sleep,pvalues=resu)
## A representation with p values
## When input="Cor" or pvalues="Yes" partial is turned to "No"

mod <- lm(sleep$Paradoxical.sleep~sleep$Body.weight+sleep$Brain.weight+
          sleep$Slow.wave.sleep+sleep$Maximum.life.span+sleep$Gestation.time+
          sleep$Predation+sleep$Sleep.exposure+sleep$Danger)
resu <- summary(mod)[[4]][2:9,4]*sign(summary(mod)[[4]][2:9,1])
fpca(Paradoxical.sleep~Body.weight+Brain.weight+Slow.wave.sleep+Maximum.life.span+
     Gestation.time+Predation+Sleep.exposure+Danger,
     data=sleep,pvalues=resu)
## A representation with p values which come from a multiple linear model
## (here results are difficult to interpret)

---

**icc**

**Intraclass correlation coefficient (ICC)**

**Description**

Computes the ICC of several series of measurements, for example in an interrater agreement study. Two types of ICC are proposed: consistency and agreement.

**Usage**

`icc(data)`

**Arguments**

- `data` n*p matrix or dataframe, n subjects p raters

**Details**

Missing data are omitted in a listwise way. The "agreement" ICC is the ratio of the subject variance by the sum of the subject variance, the rater variance and the residual; it is generally preferred. The "consistency" version is the ratio of the subject variance by the sum of the subject variance and the residual; it may be of interest when estimating the reliability of pre/post variations in measurements.
lkappa

Value
A list with :

$\text{nb.subjects}$  number of subjects under study

$\text{nb.raters}$  number of raters

$\text{subject.variance}$  subject variance

$\text{rater.variance}$  rater variance

$\text{residual}$  residual variance

$\text{icc.consistency}$  Intra class correlation coefficient, "consistency" version

$\text{icc.agreement}$  Intra class correlation coefficient, "agreement" version

Author(s)
Bruno Falissard

References

Examples

data(expsy)

icc(expsy[,c(12,14,16)])

# to obtain a 95% confidence interval:
library(boot)
#icc.boot <- function(data,x) {icc(data[x,][[7]])}
#res <- boot(expsy[,c(12,14,16)],icc.boot,1000)
#quantile(res$t,c(0.025,0.975))  # two-sided bootstrapped confidence interval of icc (agreement)
#boot.ci(res,type="bca")  # adjusted bootstrap percentile (BCa) confidence interval (better)

---

lkappa  

Light’s kappa for n raters

Description
Computes Light’s Kappa for agreement in the case of n raters. The diagnosis (the object of the rating) may have k possible values (ordered or not).

Usage

lkappa(r, type="Cohen", weights="squared")
Arguments

- \( r \)  
  \( m \times n \) matrix, \( m \) subjects and \( n \) raters

- \textit{type}  
  type="Cohen" for a categorical diagnosis. If not, the diagnosis is supposed to be ordered

- \textit{weights}  
  weight="squared" for a weighted kappa with squared weights. If not, weights are computed with absolute values.

Details

Light's Kappa is equal to the mean of the \( n(n-1)/2 \) kappas obtained from each pair of raters. Missing values are omitted locally when considering each pair of raters. If type="Cohen" the diagnosis is considered as a categorical variable. If not, the diagnosis is considered as an ordered variable and weighted kappas are computed. In this last situation, the type of weights that is used (squared or absolute values) is given by the variable \textit{weights}.

Value

kappa (mean of the \( n(n-1)/2 \) kappas obtained from each pair of raters)

Author(s)

Bruno Falissard

References


Examples

data(expsy)
lkappa(expsy[,c(11,13,15)])  # Light's kappa for non binary diagnosis
lkappa(expsy[,c(12,14,16)])  # Light's kappa for binary diagnosis
lkappa(expsy[,c(11,13,15)], type="weighted")  # Light's kappa for non binary ordered diagnosis

# to obtain a 95% confidence interval:
#library(boot)
#lkappa.boot <- function(data,x) {lkappa(data[,], type="weighted")}
#res <- boot(expsy[,c(11,13,15)],lkappa.boot,1000)
#quantile(res$t[,c(0.025,0.975)])  # Bootstrapped confidence interval of Light's kappa
#boot.ci(res,type="bca")  # adjusted bootstrap percentile (BCa) confidence interval
mdspca

Graphical representation of a correlation matrix using a Principal Component Analysis

Description

Similar to many routines, the interest is in the possible representation of both variables and subjects (and by the way categorical variables) with active and supplementary points. Missing data are omitted.

Usage

mdspca(datafile, supvar="no", supsubj="no", namesupvar=colnames(supvar, do.NULL=FALSE), namesupsubj=colnames(supsubj, do.NULL=FALSE), dimx=1, dimy=2, cx=0.75)

Arguments

datafile name of datafile
supvar matrix corresponding to supplementary variables (if any), supvar="no" by default
supsubj matrix corresponding to supplementary subjects (if any), supsubj="no" by default
namesupvar names of the points corresponding to the supplementary variables
namesupsubj names of the points corresponding to the supplementary subjects
dimx rank of the component displayed on the x axis (1 by default)
dimy rank of the component displayed on the y axis (2 by default)
cx size of the lettering (0.75 by default, 1 for bigger letters, 0.5 for smaller)

Value

A diagram (two diagrams if supplementary subjects are used)

Author(s)

Bruno Falissard

Examples

data(sleep)

mdspca(sleep[,c(2:5,7:11)])
## three consistent groups of variables, paradoxical sleep (in other words: dream)
## is negatively correlated with danger

mdspca(sleep[,c(2:5,7:11)], supvar=sleep[,6], namesupvar="Total.sleep", supsubj=sleep[,1], namesupsubj="", cx=0.5)
## Total.sleep is here a supplementary variable since it is deduced
## from Paradoxical.sleep and Slow.wave.sleep
## The variable Species is displayed in the subject plane,
## Rabbit and Cow have a high level of danger

### Description

This function is destined to assess the convergent and discriminant validity of subscales of a given scale. Items belonging to the same subscale should correlate highly amongst themselves. Items belonging to different subscales should not correlate highly. This approach is simpler and more robust than confirmatory factor analysis (CFA). It can be interesting to verify (at least approximately) the proposed structure of an existing instrument in a new population. Most psychometricians will however prefer CFA.

### Usage

```r
mtmm(datafile,x,color=FALSE,itemTot=FALSE,graphItem=FALSE,stripChart=FALSE,namesDim=NULL)
```

### Arguments

- **datafile**
  - name of datafile
- **x**
  - a list of variable names (as many elements as there are subscales)
- **color**
  - boxplot are in colour: FALSE = colourless just in grey and white (by default), TRUE = with colours
- **itemTot**
  - if TRUE, for subscale i (i=1,...,n), boxplot of Pearson’s correlations between total score of subscale i and the items of subscale j (j=1,...,n). If j=i, the item is omitted in the computation of the total score. If FALSE, for subscale i (i=1,...,n), boxplot of Pearson’s correlations between the items of subscale i and the items of subscale j (j=1,...,n)
- **graphItem**
  - if TRUE represents graphically each correlation
- **stripChart**
  - if TRUE, dot charts are preferred to boxplots. Used with small number of items
- **namesDim**
  - Labels foreach boxplots

### Value

For subscale i (i=1,...,n), displays the n boxplots of the distributions of the Pearson’s correlations between items of subscale i and items of subscale j (j=1,...,n). If j=i, the correlation of a given item with itself is omitted. Boxplot for i=j (grey by default) should be above boxplots for i!=j. Likewise, the correlation of an item with the global score of its subscale should be above its correlations with the global score of the other subscales.
Various procedures used in psychometry

Description

Kappa, Intra class correlation coefficient, Cronbach alpha, Scree plot, Multitraits multimethods, Spherical representation of a correlation matrix

Details

<table>
<thead>
<tr>
<th>Package:</th>
<th>psy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type:</td>
<td>Package</td>
</tr>
<tr>
<td>Version:</td>
<td>1.0</td>
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<td>License:</td>
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<tr>
<td>LazyLoad:</td>
<td>yes</td>
</tr>
</tbody>
</table>

Author(s)

Bruno Falissard <falissard_b@wanadoo.fr>
**References**


Horn, JL (1965) A Rationale and Test for the Number of Factors in Factor Analysis, Psychometrika, 30, 179-185.


**Examples**

```r
data(sleep)
spheca(sleep[,c(2:5,7:11)])
data(expsy)
scree.plot(expsy[,1:10],simu=20,use="P")
data(ehd)
par(mfrow=c(1,5))
mtmm(ehd,list(c("e15","e18","e19","e20"),c("e4","e5","e6","e14","e17"),c("e11","e13","e16"),c("e1","e10","e12"),c("e2","e3","e7","e8","e9")))
```

**Description**

Graphical representation of the eigenvalues of a correlation/covariance matrix. Usefull to determine the dimensional structure of a set of variables. Simulation are proposed to help the interpretation.

**Usage**

```r
scree.plot(namefile, title = "Scree Plot", type = "R", use = "complete.obs", simu = "F")
```

**Arguments**

- **namefile**: dataset
- **title**: Title
- **type**: type="R" to obtain the eigenvalues of the correlation matrix of dataset, type="V" for the covariance matrix, type="M" if the input data is directly the matrix, type="E" if the input data are directly the eigenvalues
- **use**: omit missing values by default, use="P" to analyse the pairwise correlation/covariance matrix
- **simu**: simu=p to add p screeplots of simulated random normal data (same number of patients and variables as in the original data set, same pattern of missing data if use="P")
Details

Simulations lead sometimes to underestimate the actual number of dimensions (as opposed to Kayser rule: eigen values superior to 1). Basically, simu=20 is enough.

Value

a plot

Author(s)

Bruno Falissard

References


Examples

data(expsy)
scree.plot(expsy[,1:10],simu=20,use="P") #no obvious structure with such a small sample

sleep

Ecological and Constitutional Data in Mammals

Description

Data from which conclusions were drawn in the article Mammals: Ecological and Constitutional Correlates, by Allison, T. and Cicchetti, D. (1976) Science, November 12, vol. 194, pp.732-734

Usage

data(sleep)

Format

This data frame contains the following columns:

Species  a factor with levels
Body.weight  a numeric vector, body weight in kg
Brain.weight  a numeric vector, Brain weight in g
Slow.wave.sleep  a numeric vector, nondreaming sleep (hrs/day)
Paradoxical.sleep  a numeric vector, dreaming sleep (hrs/day)
Total.sleep  a numeric vector, nondreaming + "dreaming" (hrs/day)
Maximum.life.span  a numeric vector (in years)
**Gestation.time**  a numeric vector (in days)
**Predation**  a numeric vector, Predation index (1 min - 5 max)
**Sleep.exposure**  a numeric vector, Sleep exposure index (1 min - 5 max)
**Danger**  a numeric vector, Overall danger index (1 min - 5 max)

**Source**
http://lib.stat.cmu.edu/datasets/sleep

**References**

**Examples**
```r
data(sleep)
str(sleep)
```

---

`sphpca`  *Spherical Representation of a Correlation Matrix*

**Description**
Graphical representation of a correlation matrix, similar to principal component analysis (PCA) but the mapping is on a sphere. The information is close to a 3d PCA, the picture is however easier to interpret since the variables are in fact on a 2d map.

**Usage**
```r
sphpca(datafile, h=0, v=0, f=0, cx=0.75, nbsphere=2, back=FALSE, input="data", method="approx", maxiter=500, output=FALSE)
```

**Arguments**
- **datafile**  name of datafile
- **h**  rotation of the sphere on a horizontal plane (in degrees)
- **v**  rotation of the sphere on a vertical plane (in degrees)
- **f**  rotation of the sphere on a frontal plane (in degrees)
- **cx**  size of the lettering (0.75 by default, 1 for bigger letters, 0.5 for smaller)
- **nbsphere**  two by default: front and back
- **back**  "FALSE" by default: the back sphere is not seen through
- **input**  "data" by default: raw data are analysed, if not "data": correlation matrix is expected
**sphpc**a

- **method**
  "approx" by default: the estimation is based on a principal component analysis approximation. If "exact" the "approx" estimation is optimized (may be computationally consuming). If "rscal" a multidimensional scaling approach is used: distances between points on the sphere are optimized so that they represent at best the original correlations. The scaling that is used leads to angles on the sphere proportional to correlation between variables

- **maxiter**
  maximum number of iterations in the optim process

- **output**
  FALSE by default: if TRUE and method="rscal" numerical results are proposed

**Details**

There is an isophormism between a correlation matrix and points on the unit hypersphere of R^n. It can be shown that a 3d spherical representation of a correlation matrix is statistically and cognitively interesting (see reference). The default option method="approx" is based on a principal components approximation (see reference). It is fast and gives rather good results. If method="exact" the representation is slighty improved in terms of fit (the sphere minimizes the sum of squared distances between the original variables on the hypersphere and their projections on the sphere). The option method="rscal" optimizes the representation of correlations between variables with distances between points (in a least squares sense). For convenience, the scaling of points on the sphere is chosen so that angles between points are linearly related to correlations between variables (this is not the case on the hypersphere were d=[2*(1-r)]^0.5). For method="exact" or method="rscal" computations may be rather lengthy (and not sensible for more than 20-40 variables). The sphere may be rotated to help in visualising most of variables on a same side (front for example). By default, the back of the sphere (right plot) is not seen showing through.

**Value**

A plot. If method="rscal" and output=TRUE, a list with :

- **$stress.before.optim**
  Stress before optimization. The stress is equal to the sum of squares of differences between distances on the 3d sphere and distances on the hypersphere.

- **$stress.after.optim**
  Stress after optimization.

- **$convergence**
  If 0, convergence is OK. If not, maxiter may be increased.

- **$correlations**
  Correlation matrix of variables (Pearson).

- **$residuals**
  Differences between observed correlations (hypersphere) and correlations estimated from points on the 3d sphere.

- **$mean.abs.resid**
  Mean of absolute values of residuals.

**Author(s)**

Bruno Falissard

**References**

Examples

data(sleep)
sphpca(sleep[,c(2:5,7:11)])
## spherical representation of ecological and constitutional correlates in mammals

sphpca(sleep[,c(2:5,7:11)],method="rscal",output=TRUE)
## idem, but optimizes the representation of correlations between variables with distances
## between points

corsleep <- as.data.frame(cor(sleep[,c(2:5,7:11)],use="pairwise.complete.obs"))
sphpca(corsleep,input="Cor")
sphpca(corsleep,method="rscal",input="Cor")
## when missing data are numerous, the representation of a pairwise correlation
## matrix may be preferred (even if mathematical properties are not so good...)

sphpca(corsleep,method="rscal",input="Cor",h=180,f=180,nbsphere=1,back=TRUE)
## other option of presentation

##
## # library(polycor)
## # sleep$Predation <- as.ordered(sleep$Predation)
## # sleep$Sleep.exposure <- as.ordered(sleep$Sleep.exposure)
## # sleep$Danger <- as.ordered(sleep$Danger)
## # corsleeph <- as.data.frame(hetcor(sleep[,c(2:5,7:11)])$correlations)
## # sphpca(corsleeph,input="Cor",f=180)
## # sphpca(corsleeph,method="rscal",input="Cor",f=180)
## # --> Correlations between discrete variables may appear shocking to some statisticians (?)
## # --> Representation of polychoric/polyserial correlations could be preferred in this situation

---

wkappa

**weighted Kappa for 2 raters**

**Description**

Computes a weighted Kappa for agreement in the case of 2 raters. The diagnosis (the object of the rating) may have k possible ordered values.

**Usage**

wkappa(r,weights="squared")

**Arguments**

- **r**
  - n*2 matrix or dataframe, n subjects and 2 raters
- **weights**
  - weights="squared" to obtain squared weights. If not, absolute weights are computed (see details)
Details

Diagnoses have to be coded by numbers (ordered naturally). For `weights="squared"`, weights are related to squared differences between rows and columns indices (in this situation `wkappa` is close to an ICC). For `weights!="squared"`, weights are related to absolute values of differences between rows and columns indices. The function is supposed to deal with the case where the two raters have not exactly the same scope of rating. Missing value are omitted.

Value

A list with:

- `$table` the 2*k table of raw data (first rater in rows, second rater in columns)
- `$weights` "squared" or "absolute"
- `$kappa` Weighted Kappa

Author(s)

Bruno Falissard

References


Examples

data(expsy)
wkappa(expsy[,c(11,13)]) # weighted kappa (squared weights)

# to obtain a 95% confidence interval:
#library(boot)
#wkappa.boot <- function(data,x) {wkappa(data[,x][[3]])}  
#res <- boot(expsy[,c(11,13)],wkappa.boot,1000)
#quantile(res$t,c(0.025,0.975)) # two-sided bootstrapped confidence interval of weighted kappa
#boot.ci(res,type="bca") # adjusted bootstrap percentile (BCa) confidence interval (better)
Index

* datasets
  ehd, 4
  expsy, 5
  sleep, 15
* multivariate
  fpca, 6
  mdspca, 11
  scree.plot, 14
  sphpca, 16
* package
  psy, 13
* univar
  ckappa, 2
  cronbach, 3
  icc, 8
  lkappa, 9
  wkappa, 18

c kappa, 2
cronbach, 3
ehd, 4
expsy, 5
fpca, 6
icc, 8
lkappa, 9
mdspca, 11
mtmm, 12
psy, 13
scree.plot, 14
sleep, 15
sphpca, 16
wkappa, 18