Package 'clinsig'

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Title Clinical Significance Functions

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Description Functions for calculating clinical significance.

Imports graphics, stats

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Contents

`clinsig` *Calculate clinical significance criteria.*

Description

Calculates one or more parametric or non-parametric criteria for clinical significance.

Usage

```
clinsig(pre.x,post.x,dys.mct=NA,func.mct=NA,dys.disp=NA,func.disp=NA,
mct="mean",disp="sd",disp.mult=c(2,2),dys.qnts=NA,
dir.effect=NA,xlim=range(c(pre.x,post.x),na.rm=TRUE),
ylim=range(c(pre.x,post.x),na.rm=TRUE),pch=par("pch"),
do.plot=TRUE,point.id=NA,which.crit="c",coef.alpha=NA,rc.mult=1.96,...)
```

Arguments

pre.x	A vector of pre-intervention assessment scores.
post.x	A vector of post-intervention assessment scores for the same measure as 'pre.x'.
dys.mct	A Measure of Central Tendency (MCT) for the scores of the population of dysfunctional persons on the measure used. If absent, it will be estimated from 'pre.x'.
func.mct	A Measure of Central Tendency for the normative ("functional") scores on the measure.
dys.disp	A measure of DISPersion for the scores of the population of dysfunctional persons on the measure. If missing, it will also be estimated.
func.disp	A measure of DISPersion for the normative scores on the measure.
mct	The name of a Measure of Central Tendency to be used. Defaults to the mean.
disp	The name of a measure of DISPersion to be used. Defaults to the standard deviation.
disp.mult	The multiple(s) of the dispersion measure to be used in calculations. If different multiples are to be used for the pre/post measures and the normative scores, pass a two element vector containing the multipliers for the pre/post and then the normative dispersions. Defaults to 2 for both.
dys.qnts	The lower and upper quantiles of the pre-assessment intervention scores to be used in calculating the "a" criterion. If a two element vector of quantiles such as 'c(0.16,0.84)' is passed, this will be used instead of 'dys.disp' or the dispersion calculated for 'pre.x'. See Details.
dir.effect	The direction of effect expected of the intervention. This argument should only take the values of -1 or 1. see Details.
xlim, ylim	Allows the user to set the x and y axes to the range desired. Defaults to range(pre.x) and range(post.x) respectively.
pch	Symbols to use in the plot.
do.plot	Whether to display a significance plot.
point.id	Optional text to be displayed instead of symbols for each score pair.
which.crit	Which criterion should be used if reliable change measure is to be calculated.
coef.alpha	sample Cronbach's alpha for the instrument used to measure the dysfunction. If NOT NA, this causes the reliable change measure to be calculated.
rc.mult	The multiplier for the standard error in the reliable change measure. See Details.
...	Additional arguments passed to 'plot'.

Details

The 'clinsig' function calculates both parametric and non-parametric versions of the Jacobson-Truax estimates of clinical significance. The number of estimates produced will depend upon which arguments are supplied. The '"a"' estimate is always calculated as it only requires the measure of central tendency (MCT) and dispersion of the pre-intervention scores. The 'c' estimate requires that the normal (non-pathologic) measure of central tendency be specified. The '"b"' estimate requires the dispersion of the normal MCT. If the dispersion of the dysfunctional scores is not supplied, the function will estimate this with the function named in 'disp'. The user can calculate a measure of dispersion and pass it as 'dys.disp' or write a function and pass the name of that function as 'disp'. Note that the use of non- parametric estimates is not included in the work Jacobson and colleagues.

Using the '"a"' cutoff means that post-intervention scores are significant if they are at least a specified distance from the MCT of pre-intervention scores in the direction of the normal MCT (i.e. they are "far enough" from the dysfunctional MCT). The '"b"' cutoff means that post-intervention scores are significant if they are within a specified distance of the normal MCT (i.e. they are "close enough" to the normal MCT). This criterion is typically used with overlapping distributions. The '"c"' cutoff means that post-intervention scores are in the direction of the normal MCT and beyond the weighted mean of the two MCTs (i.e. they are "on the normal side" of the average of the MCTs). The "c" criterion is usually recommended for non-overlapping distributions of pre- and post-scores. Look at the second plot in the examples for an illustration of this in which there is a large effect and a clear separation of pre- and post-scores.

The direction of effect is calculated as the sign of the functional (normal) MCT minus the dysfunctional MCT. If one or both of these are missing, the pre- and post-MCTs are substituted. This assumes that the post-MCT is in the expected direction toward the functional MCT. If this is not the case, the user should set 'dir.effect' to 1 (higher scores = improvement) or -1 (lower scores = improvement) or the function may report improvement when the scores are actually indicating deterioration.

If only the pre-intervention and post-intervention scores are provided, the function calculates a cutoff score for significant change based upon 'disp.mult' times the measure of dispersion for the pre-intervention scores if 'dys.disp' is specified. However, if 'dys.qnts' is not NA, the '"a"' cutoff score is set to one of the quantiles of the pre-intervention score distribution. If the normal MCT is supplied and it is less than the pre-intervention MCT, or 'dir.effect' is -1, the lower quantile is used. In all other cases, the upper cutoff is calculated. Remember that the quantile is not adjusted for 'disp.mult'.

The reliable change measure is calculated following Evans, Margison & Barkham (1998). This calculation assumes that the sample score distribution is normal. It will be calculated with the measures specified in sampmct and sampdisp, but unless these are the defaults, it is not guaranteed to be correct.

Value

A list containing:

pre.x	the pre-assessment scores
post.x	the post-assessment scores
crit	the three estimated criteria, some of which may be NA

sigsums	the number of scores that met each of the three criteria
pre.mct	the pre-intervention MCT
post.mct	the post-intervention MCT
func.mct	the normative MCT
mct	the name of the function used to calculate the MCTs
disp	the name of the function used to calculate the dispersions
post.n	the number of post-intervention assessments
passed	a vector of three logicals indicating whether the post-intervention MCT met the respective criteria
relchng	the reliable change measure calculated. NA if not.
dir.effect	the direction of effect. see Details.
which.crit	which of the three criteria should be used in calculating the reliable change measure.

As a side effect, a scatterplot of the pre- and post-scores and MCTs with the calculated cutoff scores as lines is displayed if 'do.plot' is TRUE.

Author(s)

Jim Lemon - thanks to Elisa Napoleone for requesting the reliable change measure.

References

Evans, C., Margison, F. & Barkham, M. (1998) The contribution of reliable and clinically significant change methods to evidence-based mental health. Evidence Based Mental Health, 1: 70-72.

Jacobson, N.S. & Truax, P. (1991) Clinical significance: a statistical approach to defining meaningful change in psychotherapy research. Journal of Consulting and Clinical Psychology, 59(1): 12-19.

Examples

```
pre.x<-runif(30,3,6)
post.x<-runif(30,1,4)
clinsig(pre.x,post.x,func.mct=1,func.disp=1,xlim=c(1,6),ylim=c(1,6))
# simulate scores on a typical psychological assessment with a limited
# range and a large separation between the pre- and post- assessments
pre.x<-c(3,3,4,5,5,6,6,6,6,7,7,7,8,8,8,8,9,9,10,10)
post.x<-c(13,12,15,14,12,18,13,17,NA,20,16,22,23,15,19,17,18,21,13,15)
big.sep<-clinsig(pre.x,post.x,mct="median",disp="mad",func.mct=19,func.disp=2,
 do.plot=FALSE)
hist(big.sep,main="Widely separated samples")
legend(20,3.8,c("Pre","Post"),fill=c("red","green"))
# now squeeze the two samples together to show how the criteria change positions
post.x<-post.x-7
little.sep<-clinsig(pre.x,post.x,mct="median",disp="mad",func.mct=15,func.disp=2,
 do.plot=FALSE)
hist(little.sep,main="Closely spaced samples")
```

```
legend(12.5,3.8,c("Pre","Post"),fill=c("red","green"))
# example from Evans, Margison & Barkham, 1998 with simulated data
set.seed(12345)
# values from EMB
pre_mct<-1.81
pre_disp<-0.53
post_mct<-0.79
post_disp<-0.5
func_mct<-0.72
func_disp<-0.57
# accept EMB's normality of distribution
pre_treat<-rnorm(40,pre_mct,pre_disp)
post_treat<-rnorm(40,post_mct,post_disp)
# make sure that no scores go below zero
post_treat[post_treat<0]<-0
emb<-clinsig(pre_treat,post_treat,
 dys.mct=pre_mct,func.mct=func_mct,
 dys.disp=pre_disp,func.disp=func_disp,
 coef.alpha=0.89,
 main="Clinical significance plot with reliable change window")
print(emb)
hist(emb)
```

`hist.clinsig` *Plot a histogram of a clinsig list*

Description

Displays a histogram of the result of the 'clinsig' function.

Usage

```
 ## S3 method for class 'clinsig'
hist(x,breaks=NA,main="",xlab="Score",ylab="Frequency",
  xlim=NA,ylim=NA,col=2:3,border=par("fg"),only.pairs=FALSE,...)
```

Arguments

x	a clinsig table produced by clinsig
breaks	The breaks to be used in categorizing scores.
main	The title for the plot.
xlab, ylab	The labels for the axes.
xlim, ylim	The limits for the plot.
col	The colors of the paired bars, pre- first, post- second.
border	The border color for the bars.
only.pairs	Whether to display counts only for clients with both pre and post scores.
...	additional arguments passed to 'plot'.

Details

'hist.clinsig' displays a histogram of the counts of scores in the categories defined by 'breaks' and other information in the object returned by 'clinsig'.

The default is to display all pre and post scores. This may lead to plots that look wrong because the measures of central tendency were calculated for pairs rather than all scores. Setting 'only.pairs' will display only the pairs of scores.

Value

nil

Author(s)

Jim Lemon

See Also

clinsig

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plot.clinsig *Plot a clinsig list*

Description

Displays a scatterplot of the result of the 'clinsig' function.

Usage

```
 ## S3 method for class 'clinsig'
plot(x,main="Clinical significance plot",
  xlab="Pre-intervention score",ylab="Post-intervention score",
  xlim=NA,ylim=NA,pch=par("pch"),point.id=NA,...)
```

Arguments

x	a clinsig table produced by clinsig
main	The title for the plot.
xlab, ylab	The labels for the axes.
xlim, ylim	The limits for the plot.
pch	The symbols to be used in plotting the score pairs.
point.id	Optional text to be used instead of symbols for the points.
...	additional arguments passed to 'print'.

Details

'plot.clinsig' displays a scatterplot and other information in the object returned by 'clinsig'.

Value

nil

Author(s)

Jim Lemon

See Also

clinsig

`print.clinsig` *Display a clinsig list*

Description

Displays the result of the 'clinsig' function.

Usage

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

Arguments

x	a clinsig table produced by clinsig
...	additional arguments passed to 'print'.

Details

'print.clinsig' displays a list produced by 'clinsig'.

Value

nil

Author(s)

Jim Lemon

See Also

clinsig

spreadout *Spread numeric values out to a minimum spacing.*

Description

Spreads a vector of numeric values out by increasing any intervals smaller than 'mindist'.

Usage

```
spreadout(x,mindist)
```

Arguments

x	A numeric vector that may contain NAs.
mindist	The minimum interval allowed in the output.

Details

'spreadout' orders the vector 'x' and begins at the middle, increasing any intervals between values to 'mindist'. The function is designed to avoid crowding of labels on a plot, but may have other uses.

Value

New values with a minimum interval of 'mindist'. NAs are preserved.

Author(s)

Jim Lemon

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