

Package: psycho (via r-universe)

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Type Package

Title Efficient and Publishing-Oriented Workflow for Psychological Science

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URL <https://github.com/neuropsychology/psycho.R>

BugReports <https://github.com/neuropsychology/psycho.R/issues>

Description The main goal of the psycho package is to provide tools for psychologists, neuropsychologists and neuroscientists, to facilitate and speed up the time spent on data analysis. It aims at supporting best practices and tools to format the output of statistical methods to directly paste them into a manuscript, ensuring statistical reporting standardization and conformity.

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LazyData true

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Suggests knitr, rmarkdown, testthat, covr, GPArotation

VignetteBuilder knitr

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Repository <https://neuropsychology.r-universe.dev>

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affective	<i>Data from the Affective Style Questionnaire (ASQ - French Validation)</i>
-----------	--

Description

This is data from the French validation of the Affective Style Questionnaire.

Usage

affective

Format

A data frame with 1277 rows and 8 variables:

- Sex** Sex (F or M)
- Birth_Season** Season of birth
- Age** Current age
- Salary** Salary in euros

- Life_Satisfaction** General life satisfaction
- Concealing** Concealing score
- Adjusting** Adjusting score
- Tolerating** Tolerating score

assess	<i>Compare a patient's score to a control group</i>
--------	---

Description

Compare a patient's score to a control group.

Usage

```
assess(  
  patient,  
  mean = 0,  
  sd = 1,  
  n = NULL,  
  controls = NULL,  
  CI = 95,  
  treshold = 0.05,  
  iter = 10000,  
  color_controls = "#2196F3",  
  color_CI = "#E91E63",  
  color_score = "black",  
  color_size = 2,  
  alpha_controls = 1,  
  alpha_CI = 0.8,  
  verbose = TRUE  
)
```

Arguments

- | | |
|----------------|--------------------------------------|
| patient | Single value (patient's score). |
| mean | Mean of the control sample. |
| sd | SD of the control sample. |
| n | Size of the control sample. |
| controls | Vector of values (control's scores). |
| CI | Credible interval bounds. |
| treshold | Significance treshold. |
| iter | Number of iterations. |
| color_controls | Color of the controls distribution. |

color_CI	Color of CI distribution.
color_score	Color of the line representing the patient's score.
color_size	Size of the line representing the patient's score.
alpha_controls	Alpha of the CI distribution.
alpha_CI	Alpha of the controls distribution.
verbose	Print possible warnings.

Details

Until relatively recently the standard way of testing for a difference between a case and controls was to convert the case's score to a z score using the control sample mean and standard deviation (SD). If z was less than -1.645 (i.e., below 95

Value

output

Author(s)

Dominique Makowski

Examples

```
result <- assess(patient = 124, mean = 100, sd = 15, n = 100)
print(result)
plot(result)
```

crawford.test

Crawford-Garthwaite (2007) Bayesian test for single-case analysis.

Description

Neuropsychologists often need to compare a single case to a small control group. However, the standard two-sample t-test does not work because the case is only one observation. Crawford and Garthwaite (2007) demonstrate that the Bayesian test is a better approach than other commonly-used alternatives. .

Usage

```
crawford.test(
  patient,
  controls = NULL,
  mean = NULL,
  sd = NULL,
  n = NULL,
  CI = 95,
```

```

    treshold = 0.1,
    iter = 10000,
    color_controls = "#2196F3",
    color_CI = "#E91E63",
    color_score = "black",
    color_size = 2,
    alpha_controls = 1,
    alpha_CI = 0.8
  )

```

Arguments

patient	Single value (patient's score).
controls	Vector of values (control's scores).
mean	Mean of the control sample.
sd	SD of the control sample.
n	Size of the control sample.
CI	Credible interval bounds.
treshold	Significance treshold.
iter	Number of iterations.
color_controls	Color of the controls distribution.
color_CI	Color of CI distribution.
color_score	Color of the line representing the patient's score.
color_size	Size of the line representing the patient's score.
alpha_controls	Alpha of the CI distribution.
alpha_CI	lpha of the controls distribution.

Details

The p value obtained when this test is used to test significance also simultaneously provides a point estimate of the abnormality of the patient's score; for example if the one-tailed probability is .013 then we know that the patient's score is significantly ($p < .05$) below the control mean and that it is estimated that 1.3

Author(s)

Dominique Makowski

Examples

```

library(psycho)

crawford.test(patient = 125, mean = 100, sd = 15, n = 100)
plot(crawford.test(patient = 80, mean = 100, sd = 15, n = 100))

crawford.test(patient = 10, controls = c(0, -2, 5, 2, 1, 3, -4, -2))
test <- crawford.test(patient = 7, controls = c(0, -2, 5, -6, 0, 3, -4, -2))
plot(test)

```

crawford.test.freq	<i>Crawford-Howell (1998) frequentist t-test for single-case analysis.</i>
--------------------	--

Description

Neuropsychologists often need to compare a single case to a small control group. However, the standard two-sample t-test does not work because the case is only one observation. Crawford and Garthwaite (2012) demonstrate that the Crawford-Howell (1998) t-test is a better approach (in terms of controlling Type I error rate) than other commonly-used alternatives. .

Usage

```
crawford.test.freq(patient, controls)
```

Arguments

patient	Single value (patient's score).
controls	Vector of values (control's scores).

Value

Returns a data frame containing the t-value, degrees of freedom, and p-value. If significant, the patient is different from the control group.

Author(s)

Dan Mirman, Dominique Makowski

Examples

```
library(psycho)

crawford.test.freq(patient = 10, controls = c(0, -2, 5, 2, 1, 3, -4, -2))
crawford.test.freq(patient = 7, controls = c(0, -2, 5, 2, 1, 3, -4, -2))
```

crawford_dissociation.test	<i>Crawford-Howell (1998) modified t-test for testing difference between a patient's performance on two tasks.</i>
----------------------------	--

Description

Assessing dissociation between processes is a fundamental part of clinical neuropsychology. However, while the detection of suspected impairments is a fundamental feature of single-case studies, evidence of an impairment on a given task usually becomes of theoretical interest only if it is observed in the context of less impaired or normal performance on other tasks. Crawford and Garthwaite (2012) demonstrate that the Crawford-Howell (1998) t-test for dissociation is a better approach (in terms of controlling Type I error rate) than other commonly-used alternatives. .

Usage

```
crawford_dissociation.test(
  case_X,
  case_Y,
  controls_X,
  controls_Y,
  verbose = TRUE
)
```

Arguments

case_X	Single value (patient's score on test X).
case_Y	Single value (patient's score on test Y).
controls_X	Vector of values (control's scores of X).
controls_Y	Vector of values (control's scores of Y).
verbose	True or False. Prints the interpretation text.

Value

Returns a data frame containing the t-value, degrees of freedom, and p-value. If significant, the dissociation between test X and test Y is significant.

Author(s)

Dominique Makowski

Examples

```
library(psycho)

case_X <- 142
case_Y <- 7
controls_X <- c(100, 125, 89, 105, 109, 99)
controls_Y <- c(7, 8, 9, 6, 7, 10)

crawford_dissociation.test(case_X, case_Y, controls_X, controls_Y)
```

dprime

Dprime (d') and Other Signal Detection Theory indices.

Description

Computes Signal Detection Theory indices, including d', beta, A', B''D and c.

Usage

```
dprime(
  n_hit,
  n_fa,
  n_miss = NULL,
  n_cr = NULL,
  n_targets = NULL,
  n_distractors = NULL,
  adjusted = TRUE
)
```

Arguments

<code>n_hit</code>	Number of hits.
<code>n_fa</code>	Number of false alarms.
<code>n_miss</code>	Number of misses.
<code>n_cr</code>	Number of correct rejections.
<code>n_targets</code>	Number of targets (<code>n_hit + n_miss</code>).
<code>n_distractors</code>	Number of distractors (<code>n_fa + n_cr</code>).
<code>adjusted</code>	Should it use the Hautus (1995) adjustments for extreme values.

Value

Calculates the d' , the β , the A' and the $B''D$ based on the signal detection theory (SRT). See Pallier (2002) for the algorithms.

Returns a list containing the following indices:

- **dprime (d')**: The sensitivity. Reflects the distance between the two distributions: signal, and signal+noise and corresponds to the Z value of the hit-rate minus that of the false-alarm rate.
- **beta**: The bias (criterion). The value for beta is the ratio of the normal density functions at the criterion of the Z values used in the computation of d' . This reflects an observer's bias to say 'yes' or 'no' with the unbiased observer having a value around 1.0. As the bias to say 'yes' increases (liberal), resulting in a higher hit-rate and false-alarm-rate, beta approaches 0.0. As the bias to say 'no' increases (conservative), resulting in a lower hit-rate and false-alarm rate, beta increases over 1.0 on an open-ended scale.
- **c**: Another index of bias. the number of standard deviations from the midpoint between these two distributions, i.e., a measure on a continuum from "conservative" to "liberal".
- **aprim (A')**: Non-parametric estimate of discriminability. An A' near 1.0 indicates good discriminability, while a value near 0.5 means chance performance.
- **bppd (B''D)**: Non-parametric estimate of bias. A $B''D$ equal to 0.0 indicates no bias, positive numbers represent conservative bias (i.e., a tendency to answer 'no'), negative numbers represent liberal bias (i.e. a tendency to answer 'yes'). The maximum absolute value is 1.0.

Note that for d' and β , adjustment for extreme values are made following the recommendations of Hautus (1995).

Author(s)

Dominique Makowski

Examples

```
library(psycho)

n_hit <- 9
n_fa <- 2
n_miss <- 1
n_cr <- 7

indices <- psycho::dprime(n_hit, n_fa, n_miss, n_cr)

df <- data.frame(
  Participant = c("A", "B", "C"),
  n_hit = c(1, 2, 5),
  n_fa = c(6, 8, 1)
)

indices <- psycho::dprime(
  n_hit = df$n_hit,
  n_fa = df$n_fa,
  n_targets = 10,
  n_distractors = 10,
  adjusted = FALSE
)
```

emotion

Emotional Ratings of Pictures

Description

Emotional ratings of neutral and negative pictures by healthy participants.

Usage

emotion

Format

A data frame with 912 rows and 11 variables:

Participant_ID Subject's number

Participant_Age Subject's age

Participant_Sex Subject's sex

Item_Category Picture's category

Item_Name Picture's name
Trial_Order Trial order (1-48)
Emotion_Condition Picture's emotional category (Neutral or Negative)
Subjective_Arousal Participant's rating of arousal (0-100)
Subjective_Valence Participant's rating of valence (-100: negative, 100: positive, 0: neutral)
Autobiographical_Link Participant's rating of autobiographical connection (is the picture's content associated with memories)
Recall Whether the participant recalled the picture 20min after presentation

find_combinations	<i>Generate all combinations.</i>
-------------------	-----------------------------------

Description

Generate all combinations.

Usage

```
find_combinations(object, ...)
```

Arguments

object	Object
...	Arguments passed to or from other methods.

Author(s)

Dominique Makowski

find_combinations.formula	<i>Generate all combinations of predictors of a formula.</i>
---------------------------	--

Description

Generate all combinations of predictors of a formula.

Usage

```
## S3 method for class 'formula'
find_combinations(object, interaction = TRUE, fixed = NULL, ...)
```

Arguments

object	Formula.
interaction	Include interaction term.
fixed	Additional formula part to add at the beginning of each combination.
...	Arguments passed to or from other methods.

Value

list containing all combinations.

Author(s)

Dominique Makowski

Examples

```
library(psycho)

f <- as.formula("Y ~ A + B + C + D")
f <- as.formula("Y ~ A + B + C + D + (1|E)")
f <- as.formula("Y ~ A + B + C + D + (1|E) + (1|F)")

find_combinations(f)
```

find_matching_string *Fuzzy string matching.*

Description

Fuzzy string matching.

Usage

```
find_matching_string(x, y, value = TRUE, step = 0.1, ignore.case = TRUE)
```

Arguments

x	Strings.
y	List of strings to be matched.
value	Return value or the index of the closest string.
step	Step by which decrease the distance.
ignore.case	if FALSE, the pattern matching is case sensitive and if TRUE, case is ignored during matching.

Author(s)

Dominique Makowski

Examples

```
library(psycho)
find_matching_string("Hwo rea ouy", c("How are you", "Not this word", "Nice to meet you"))
```

find_season	<i>Find season of dates.</i>
-------------	------------------------------

Description

Returns the season of an array of dates.

Usage

```
find_season(
  dates,
  winter = "12-21",
  spring = "3-20",
  summer = "6-21",
  fall = "9-22"
)
```

Arguments

dates	Array of dates.
winter	month-day of winter solstice.
spring	month-day of spring equinox.
summer	month-day of summer solstice.
fall	month-day of fall equinox.

Value

season

Author(s)

Josh O'Brien

See Also

<https://stackoverflow.com/questions/9500114/find-which-season-a-particular-date-belongs-to>

Examples

```
library(psycho)

dates <- c("2012-02-15", "2017-05-15", "2009-08-15", "1912-11-15")
find_season(dates)
```

golden	<i>Golden Ratio.</i>
--------	----------------------

Description

Returns the golden ratio (1.618034...).

Usage

```
golden(x = 1)
```

Arguments

x	A number to be multiplied by the golden ratio. The default (x=1) returns the value of the golden ratio.
---	---

Author(s)

Dominique Makowski

Examples

```
library(psycho)

golden()
golden(8)
```

is.psychobject	<i>Creates or tests for objects of mode "psychobject".</i>
----------------	--

Description

Creates or tests for objects of mode "psychobject".

Usage

```
is.psychobject(x)
```

Arguments

x	an arbitrary R object.
---	------------------------

is.standardized	<i>Check if a dataframe is standardized.</i>
-----------------	--

Description

Check if a dataframe is standardized.

Usage

```
is.standardized(df, tol = 0.1)
```

Arguments

df	A dataframe.
tol	The error threshold.

Value

bool.

Author(s)

Dominique Makowski

Examples

```
library(psycho)
library(effectsize)

df <- psycho::affective
is.standardized(df)

dfZ <- effectsize::standardize(df)
is.standardized(dfZ)
```

mellenbergh.test	<i>Mellenbergh & van den Brink (1998) test for pre-post comparison.</i>
------------------	---

Description

Test for comparing post-test to baseline for a single participant.

Usage

```
mellenbergh.test(t0, t1, controls)
```

Arguments

t0	Single value (pretest or baseline score).
t1	Single value (posttest score).
controls	Vector of scores of the control group OR single value corresponding to the control SD of the score.

Value

Returns a data frame containing the z-value and p-value. If significant, the difference between pre and post tests is significant.

Author(s)

Dominique Makowski

Examples

```
library(psycho)

mellenbergh.test(t0 = 4, t1 = 12, controls = c(0, -2, 5, 2, 1, 3, -4, -2))
mellenbergh.test(t0 = 8, t1 = 2, controls = 2.6)
```

percentile	<i>Transform z score to percentile.</i>
------------	---

Description

Transform z score to percentile.

Usage

```
percentile(z_score)
```

Arguments

z_score	Z score.
---------	----------

Author(s)

Dominique Makowski

Examples

```
library(psycho)
percentile(-1.96)
```

percentile_to_z	<i>Transform a percentile to a z score.</i>
-----------------	---

Description

Transform a percentile to a z score.

Usage

```
percentile_to_z(percentile)
```

Arguments

percentile	Percentile
------------	------------

Author(s)

Dominique Makowski

Examples

```
library(psycho)
percentile_to_z(95)
```

plot.psychobject	<i>Plot the results.</i>
------------------	--------------------------

Description

Plot the results.

Usage

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

Arguments

x	A psychobject class object.
...	Arguments passed to or from other methods.

Author(s)

Dominique Makowski

power_analysis	<i>Power analysis for fitted models.</i>
----------------	--

Description

Compute the n models based on n sampling of data.

Usage

```
power_analysis(  
  fit,  
  n_max,  
  n_min = NULL,  
  step = 1,  
  n_batch = 1,  
  groups = NULL,  
  verbose = TRUE,  
  CI = 90  
)
```

Arguments

fit	A lm or stanreg model.
n_max	Max sample size.
n_min	Min sample size. If null, take current nrow.
step	Increment of the sequence.
n_batch	Number of iterations at each sample size.
groups	Grouping variable name (string) to preserve proportions. Can be a list of strings.
verbose	Print progress.
CI	Confidence level.

Value

A dataframe containing the summary of all models for all iterations.

Author(s)

Dominique Makowski

Examples

```
## Not run:  
library(dplyr)  
library(psycho)  
  
fit <- lm(Sepal.Length ~ Sepal.Width, data = iris)
```

```

results <- power_analysis(fit, n_max = 300, n_min = 100, step = 5, n_batch = 20)

results %>%
  filter(Variable == "Sepal.Width") %>%
  select(n, p) %>%
  group_by(n) %>%
  summarise(
    p_median = median(p),
    p_mad = mad(p)
  )

## End(Not run)

```

print.psychobject	<i>Print the results.</i>
-------------------	---------------------------

Description

Print the results.

Usage

```

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

```

Arguments

x	A psychobject class object.
...	Further arguments passed to or from other methods.

Author(s)

Dominique Makowski

remove_empty_cols	<i>Remove empty columns.</i>
-------------------	------------------------------

Description

Removes all columns containing any NaNs.

Usage

```
remove_empty_cols(df)
```

Arguments

df Dataframe.

Author(s)

Dominique Makowski

summary.psychobject *Print the results.*

Description

Print the results.

Usage

```
## S3 method for class 'psychobject'  
summary(object, round = NULL, ...)
```

Arguments

object A psychobject class object.
round Round the output.
... Further arguments passed to or from other methods.

Author(s)

Dominique Makowski

values *Extract values as list.*

Description

Extract values as list.

Usage

```
values(x)
```

Arguments

x A psychobject class object.

Author(s)

Dominique Makowski

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