

Package ‘singlecase’

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Type Package

Title statistical tests for single case studies in neuropsychology

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Description The singlecase package implements various functions for the single-case research in neuropsychology. Currently, the functions that are implemented were all originally developed by John Crawford, Paul Garthwaite and colleagues. These functions mainly deal with the comparison of a patient’s test score (or score difference) to a control or normative sample. These methods also provide a point estimate of the percentage of the population that would obtain a more extreme score (or score difference) and, for some problems, an accompanying interval estimate (i.e., confidence limits) on this percentage.

License GPL (>= 2)

URL http://www.code.ucl.ac.be/MatthieuDubois/r_code.html

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singlecase-package *Single-case inferential methods*

Description

The package implement frequentist and Bayesian inferential methods for use in single-case studies in which a patient is compared to a small control sample.

Details

Package: singlecase
Type: Package
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License: GPL 2 or newer
LazyLoad: yes

At this stage of development, the package contains implementation of functions for: (1) comparison of an individual's score on a single test with the score of a small normative or control sample: `crawford.t.test` and `SingleBayes`; (2) test whether the difference between scores on two tests observed for a patient is significantly greater than the differences observed for a small control or normative sample: `crawford.diff.test` and `DiffBayes`.

`crawford.t.test`, and `crawford.diff.test` rely upon the t -distribution and treat summary statistics from the control group as estimates rather than parameters. `SingleBayes` and `DiffBayes` are Bayesian inferential alternatives, based on a Monte Carlo process. All methods may take either the raw data or summary statistics from the control population as inputs.

Author(s)

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References

Crawford, J. and Garthwaite, P. (2002) Investigation of the single case in neuropsychology: Confidence limits on the abnormality of test scores and test score differences. *Neuropsychologia*, **40(8)**, 1196–1208.

Crawford, J. and Garthwaite, P. (2005) Testing for suspected impairments and dissociations in single-case studies in neuropsychology: Evaluation of alternatives using Monte Carlo simulations and revised tests for dissociations. *Neuropsychology*, **19(3)**, 318–331.

Crawford, J. and Garthwaite, P. (2007) Comparison of a single case to a control or normative sample in neuropsychology: Development of a bayesian approach. *Cognitive Neuropsychology*, **24(4)**, 343–372.

Crawford, J. and Howell, D. (1998) Comparing an individual's test score against norms derived from small samples. *Clinical Neuropsychologist*, **12**(4), 482–486.

Crawford, J., Howell, D., and Garthwaite, P. (1998) Payne and Jones revisited: Estimating the abnormality of test score differences using a modified paired samples *t*-test. *Journal of clinical and experimental neuropsychology*, **20**(6), 898–905.

.crawford.CI

Confidence Intervals based on a non-central t distribution

Description

.crawford.CI is an internal function that computes 95% confidence intervals around the rarity of a score (Crawford & Garthwaite, 2002). These confidence intervals are based on non-central *t*-distributions.

Usage

```
.crawford.CI(c, n)
```

Arguments

c	test statistics
n	number of control subjects

Details

c is an observation from a non-central *t*-distribution on $n - 1$ degrees of freedom. Confidence intervals are based on two values of the non-centrality parameter of non-central *t*-distribution, such that the resulting non-central *t*-distribution has $c\sqrt{n}$ as its $100\alpha/2$ percentile (value 1) or as its $100(1 - \alpha/2)$ (value 2) (for details, see Crawford & Garthwaite, 2002). The purpose of the .crawford.CI function is to find those values.

Value

2.5%	Lower bound of the confidence interval.
97.5%	Upper bound of the confidence interval.

Author(s)

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References

Crawford, J. R., & Garthwaite, P. H. (2002). Investigation of the single case in neuropsychology: Confidence limits on the abnormality of test scores and test score differences. *Neuropsychologia*, **40**(8), 1196–208.

See Also

`crawford.t.test`, `crawford.diff.test`

DiffTest

Difference between patient's scores on two tasks

Description

These functions test whether the difference between scores on two tests observed for a patient is significantly greater than the differences observed for a small control or normative sample. `crawford.diff.test` implements Crawford's Unstandardized Difference Test and Crawford's Revised Standardized Difference Test (Crawford & Garthwaite, 2005). `DiffBayes` corresponds to a Bayesian alternative (Crawford & Garthwaite, 2007).

Usage

```
crawford.diff.test(patient, controls, mean.c = 0, sd.c = 0, r = 0,
                  n = 0, na.rm = FALSE, standardized=FALSE)
DiffBayes(patient, controls, mean.c = 0, sd.c = 0, r = 0, n = 0,
          na.rm = FALSE, n.simul = 1e+05, standardized = TRUE)
```

Arguments

<code>patient</code>	a vector containing the patient's two scores
<code>controls</code>	a $n \times 2$ matrix/data-frame containing the control subjects raw scores, one column for each task
<code>mean.c</code>	a vector containing the control group's two means, one for each task
<code>sd.c</code>	a vector containing the control group's two standard deviations, one for each task
<code>r</code>	the correlation coefficient between the two tasks in the control group
<code>n</code>	size of the control group
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds
<code>n.simul</code>	a numerical value indicating the number of observations generated for the Monte Carlo estimation. Set at 100.000 by default
<code>standardized</code>	a logical value indicating whether the data should be standardized (TRUE, the default in function <code>DiffBayes</code>) or not (FALSE, the default in function <code>crawford.diff.test</code>).

Details

These functions examine the difference between a patient's score on two tasks, relative to the difference observed between the same tasks within the control group. `crawford.diff.test` implements a modified *t*-test that treat summary statistics from the control group as estimates rather than parameters. `DiffBayes` uses Bayesian Monte Carlo methods as an alternative to the *t*-test. Both methods may take either the raw data (using the argument `controls`) or summary statistics from the control population as inputs. In this later case, the controls' means (`mean.c`), standard deviations (`sd.c`), correlation between tasks (`r`) and sample size (`n`) are required.

When it is sensible to examine the raw differences between a patient's scores on two tasks against the raw differences in controls, then the argument `standardized=FALSE` can be applied. In this case, the frequentist and Bayesian alternatives are converging (Crawford and Garthwaite, 2007). However, it is usually necessary to standardize the patient's scores on each task (using the data from the controls). The `DiffBayes` function (with argument `standardized=TRUE`, the default) should be applied in these circumstances. This test does not exhibit convergence with its frequentist alternative, the `crawford.diff.test(standardized=TRUE)`, which is deprecated. Indeed, the Bayesian alternative has a number of advantages (see Crawford & Garthwaite, 2007, for details) including the fact that it factors in the uncertainty over the standard deviations of the two tasks used to standardize the patient's scores.

Those tests further include a point estimate of the rarity of the patient's score, as well as an interval estimate around this quantity (with the exception of `crawford.diff.test`, with argument `standardized` set to `TRUE`). Rarity (or abnormality) of the score corresponds to the percentage of the population that would exhibit a difference between scores *lower* than the patient's.

Value

`crawford.diff.test` returns a list with class "htest" containing all the following components. `DiffBayes` only returns a list with `p-value` and `rarity`:

<code>statistic</code>	the one-tailed value of the test statistic.
<code>df</code>	the degrees of freedom for the <i>t</i> -statistic.
<code>p.value</code>	the two-tailed <i>p</i> -value for the test.
<code>rarity</code>	a vector containing the point estimate of the rarity of the score and a 95% confidence interval around the rarity estimate (additional 5% and 95% bounds are also provided in the case of <code>DiffBayes</code>). It captures the percentage of the population that will obtain a difference more <i>extreme</i> than the patient's and in the same direction.
<code>method</code>	a character string indicating what type of <i>t</i> -test was performed.

Author(s)

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References

Crawford, J. and Garthwaite, P. (2005) Testing for suspected impairments and dissociations in single-case studies in neuropsychology: Evaluation of alternatives using Monte Carlo simulations and revised tests for dissociations. *Neuropsychology*, **19**(3), 318–31.

Crawford, J. and Garthwaite, P. (2007) Comparison of a single case to a control or normative sample in neuropsychology: Development of a bayesian approach. *Cognitive Neuropsychology*, **24(4)** 343–372.

John Crawford's website: <http://www.abdn.ac.uk/~psy086/dept/SingleCaseMethodology.htm>

See Also

`crawford.t.test`, `SingleBayes`

Examples

```
#Both methods can take either raw data or summary measures as arguments
controls <- as.data.frame(matrix(rnorm(50,100,10),ncol=2))
crawford.diff.test(patient=c(95,105), controls)
crawford.diff.test(patient=c(95,105), mean.c=mean(controls),
  sd.c=sd(controls), r = cor(controls[,1],controls[,2]),
  n = dim(controls)[1])

#In the case of unstandardized tests, the methods are converging
# Note that the default is unstandardized for crawford.t.test,
#       and standardized for DiffBayes
controls <- as.data.frame(matrix(rnorm(50,100,10),ncol=2))
X <- crawford.diff.test(patient=c(95,105), controls)
X
X$rarity
DiffBayes(patient=c(95,105), controls=controls,standardized=FALSE)

#In the case of standardized tests, the methods are not converging
#DiffBayes has to be preferred
crawford.diff.test(patient=c(90,110), mean.c=c(100,100), sd.c=c(10,10),
  n=5, r=.6, standardized=TRUE)
DiffBayes(patient=c(90,110), mean.c=c(100,100), sd.c=c(10,10), n=5, r=.6)
```

SingleTest

Single score comparison

Description

`crawford.t.test` and `SingleBayes` are for comparison of an individual's score on a single test with the score of a small normative or control sample. They provide a significance test, point estimate of the abnormality of the individual's score, and confidence limits on the abnormality. `crawford` t-test is based on the *t* distribution, `SingleBayes` is a Bayesian alternative.

Usage

```
crawford.t.test(patient, controls, mean.c = 0, sd.c = 0, n = 0, na.rm = FALSE)
SingleBayes(patient, controls, mean.c = 0, sd.c = 0, n = 0,
  na.rm = FALSE, n.simul = 1e+05)
```

Arguments

<code>patient</code>	a vector with the patient's score
<code>controls</code>	a vector with the control subjects raw scores
<code>mean.c</code>	mean of the control group
<code>sd.c</code>	standard deviation of the control group
<code>n</code>	size of the control group
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds
<code>n.simul</code>	a numerical value indicating the number of observations generated for the Monte Carlo estimation. Set at 100.000 by default

Details

`crawford.t.test` is a modified *t*-test that compare a patient's score to that of a control sample of small size. The test treats the mean and standard deviation from the control group as estimates rather than parameters. It provides a significance test, point estimate of the abnormality of the individual's score, and 95% confidence limits on the abnormality. Abnormality (or rarity) is defined as the percentage of the population that would obtain a score *lower* than the patient's.

`SingleBayes` uses Bayesian Monte Carlo methods to test if a patient's score is sufficiently below the scores of controls such that the null hypothesis that it is an observation from the control population can be rejected (i.e., it is used to test for a deficit). It also provides a point estimate of the percentage of the control population that would obtain a lower score (i.e., a point estimate of the abnormality of the score) and a 95% credible interval for this quantity.

Bayesian and frequentist methods provide converging results. Both methods may take either the raw data (using the argument `controls`) or summary statistics from the control population as inputs. In this later case, the control mean (`mean.c`), standard deviation (`sd.c`) and sample size (`n`) are required.

Value

`crawford.t.test` returns a list with class "htest" containing all the following components. `SingleBayes` only returns a list with `p-value` and `rarity`:

<code>statistic</code>	the one-tailed value of the <i>t</i> -statistic.
<code>df</code>	the degrees of freedom for the <i>t</i> -statistic.
<code>p.value</code>	the <i>p</i> -value of the one-tailed hypothesis that patient's score is <i>lower</i> than that of the control participants.
<code>rarity</code>	a vector containing the point estimate of the rarity of the score and a 95% interval around the rarity estimate (additional 5% and 95% bounds are also provided in the case of <code>SingleBayes</code>).
<code>method</code>	a character string indicating the test used.

Author(s)

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References

Crawford, J. and Howell, D. (1998) Comparing an individual's test score against norms derived from small samples. *Clinical Neuropsychologist*, **12(4)**,482–486.

Crawford, J. and Garthwaite, P. (2002) Investigation of the single case in neuropsychology: Confidence limits on the abnormality of test scores and test score differences. *Neuropsychologia*, **40(8)**, 1196–208.

Crawford, J. and Garthwaite, P. (2007) Comparison of a single case to a control or normative sample in neuropsychology: Development of a bayesian approach. *Cognitive Neuropsychology*, **24(4)**, 343–372.

John Crawford's website: <http://www.abdn.ac.uk/~psy086/dept/SingleCaseMethodology.htm>

See Also

`crawford.diff.test`, `DiffBayes`

Examples

```
#function provided with either raw data or summary statistics
controls <- rnorm(15,50,10)
crawford.t.test(patient=30, controls=controls)
crawford.t.test(patient=30, mean.c = mean(controls),
                sd.c = sd(controls), n = length(controls))

#results provided by the two methods are converging
X <- crawford.t.test(patient=30, mean.c=50, sd.c=10, n=15)
X
X$rarity
SingleBayes(patient=30, mean.c=50, sd.c=10, n=15)
```

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