Package ‘correctR’

March 13, 2024

Type Package

Title Corrected Test Statistics for Comparing Machine Learning Models on Correlated Samples

Version 0.2.1

Date 2024-03-14

Maintainer Trent Henderson <then6675@uni.sydney.edu.au>

Description Calculate a set of corrected test statistics for cases when samples are not independent, such as when classification accuracy values are obtained over resamples or through k-fold cross-validation, as proposed by Nadeau and Bengio (2003) <doi:10.1023/A:1024068626366> and presented in Bouckaert and Frank (2004) <doi:10.1007/978-3-540-24775-3_3>.

BugReports https://github.com/hendersontrent/correctR/issues

License MIT + file LICENSE

Encoding UTF-8

Depends R (>= 3.5.0)

Imports stats

Suggests knitr, markdown, rmarkdown, pkgdown, testthat (>= 3.0.0)

RoxygenNote 7.2.2

VignetteBuilder knitr

Config/testthat/edition 3

URL https://hendersontrent.github.io/correctR/

NeedsCompilation no

Author Trent Henderson [cre, aut]

Repository CRAN

Date/Publication 2024-03-13 22:30:02 UTC
R topics documented:

- correctR .......................... 2
- kfold_ttest .......................... 2
- repkfold_ttest ......................... 3
- resampled_ttest ....................... 4

Index 6

**correctR**  
*Corrections For Correlated Test Statistics*

**kfold_ttest**  
*Compute correlated t-statistic and p-value for k-fold cross-validated results*

**Description**  
Compute correlated t-statistic and p-value for k-fold cross-validated results

**Usage**  
kfold_ttest(x, y, n, k, tailed = c("two", "one"), greater = NULL)

**Arguments**  
- **x** numeric vector of values for model A
- **y** numeric vector of values for model B
- **n** integer denoting total sample size
- **k** integer denoting number of folds used in k-fold
- **tailed** character denoting whether to perform a two-tailed or one-tailed test. Can be one of "two" or "one". Defaults to "two"
- **greater** character specifying whether "x" or "y" is greater for the one-tailed test if tailed = "one". Defaults to NULL

**Value**  
data.frame containing the test statistic and p-value

**Author(s)**  
Trent Henderson
References


Examples

\[
x <- \text{rnorm}(100, \text{mean} = 95, \text{sd} = 0.5) \\
y <- \text{rnorm}(100, \text{mean} = 90, \text{sd} = 1) \\
kfold_ttest(x = x, y = y, n = 100, k = 5, \text{tailed} = \text{"two"})
\]

repkfold_ttest

Compute correlated t-statistic and p-value for repeated k-fold cross-validated results

Description

Compute correlated t-statistic and p-value for repeated k-fold cross-validated results

Usage

repkfold_ttest(data, n1, n2, k, r, tailed = c("two", "one"), greater = NULL)

Arguments

data data.frame of values for model A and model B over repeated k-fold cross-validation. Four named columns are expected: "model", "values", "k", and "k"
n1 integer denoting train set size
n2 integer denoting test set size
k integer denoting number of folds used in k-fold
r integer denoting number of repeats per fold
tailed character denoting whether to perform a two-tailed or one-tailed test. Can be one of "two" or "one". Defaults to "two"
greater value specifying which value in the "model" column is greater for the one-tailed test if tailed = "one". Defaults to NULL

Value

data.frame containing the test statistic and p-value

Author(s)

Trent Henderson
References


Examples

tmp <- data.frame(model = rep(c(1, 2), each = 60),
  values = c(stats::rnorm(60, mean = 0.6, sd = 0.1),
  stats::rnorm(60, mean = 0.4, sd = 0.1)),
  k = rep(c(1, 1, 2, 2), times = 15),
  r = rep(c(1, 2), times = 30))
repkfold_ttest(data = tmp, n1 = 80, n2 = 20, k = 2, r = 2, tailed = "two")

---

resampled_ttest

Compute correlated t-statistic and p-value for resampled data

Description

Compute correlated t-statistic and p-value for resampled data

Usage

resampled_ttest(x, y, n, n1, n2, tailed = c("two", "one"), greater = NULL)

Arguments

x numeric vector of values for model A
y numeric vector of values for model B
n integer denoting number of repeat samples. Defaults to length(x)
n1 integer denoting train set size
n2 integer denoting test set size
tailed character denoting whether to perform a two-tailed or one-tailed test. Can be one of "two" or "one". Defaults to "two"
greater character specifying whether "x" or "y" is greater for the one-tailed test if tailed = "one". Defaults to NULL

Value

data.frame containing the test statistic and p-value
**Author(s)**
Trent Henderson

**References**

**Examples**
```r
x <- rnorm(100, mean = 95, sd = 0.5)
y <- rnorm(100, mean = 90, sd = 1)
resampled_ttest(x = x, y = y, n = 100, n1 = 80, n2 = 20, tailed = "two")
```
Index

correctR, 2
correctR-package (correctR), 2

kfold_ttest, 2

repkfold_ttest, 3
resampled_ttest, 4