Package 'mcBFtest'

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Type Package

Title Monte Carlo Based Tests for the Behrens Fisher Problem as an
Alternative to Welch's t-Approximation

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Imports stats, MASS

Description Monte Carol based tests for the Behrens Fisher Problem enhance the statistical power
and performs better than Welch's t-approximation, see Ullah et al. (2019).

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LazyData true

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R topics documented:

MC-internal   *Internal Functions*

Description

Internal functions not to be used by the user.

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mcBFtest   *Monte Carlo based tests as an alternative of Welch's t-approximation*

Description

In the t test, it is usually the case that the assumption of equal variances on the two groups is violated. The test problem is known as the Behrens-Fisher (BF) problem when no assumption of equal population variances can be made. For the BF problem, the T statistic provides value for a given dataset and its statistical distribution is not easy to characterise.

To our knowledge, the best approximation thus far is due to Welch (1938). The Welch's test involves two layers of approximations: approximating the distribution of the statistic by a t-distribution, which in turn depends on an approximate degrees of freedom.

The Monte Carlo based tests improve upon Welch's approximate test by avoiding one layer of approximation, resulting in enhancement in statistical power than Welch's t-approximation.

Usage

```
mcBFtest(x, y, method, MC)
```

Arguments

x	a (non-empty) numeric vector of data values
y	a (non-empty) numeric vector of data values
method	if "t" is used, we will use t-test assuming equal variance and df=n+m-2. If "W" is used, we assume unequal variance and the Welch approximation is used. If "Monte Carlo", the Monte Carlo procedure is applied.
MC	a number for Monte Carlo procedure

Value

The function returns a list including

p.value	the p-value for the test.

Author(s)

You-Gan Wang, Na Wang

References

Welch, B.L. (1938). The significance of the difference between two means when the population variances are unequal. Biometrika, 29 (3/4), 350–362.

Ullah, I., Paul, S., Hong, Z., & Wang, Y-G. (2019). Significance tests for analyzing gene expression data with small sample sizes. Bioinformatics, in press.

See Also

`t.test` function from package `stats`

Examples

```
library(mcBFtest)

x <- sleep[1:10,1]
y <- sleep[11:20,1]

mcBFtest(x, y, method = "t")
mcBFtest(x, y, method = "W")
mcBFtest(x, y, method = "Monte Carlo", MC = 100000)
```

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