Package: homnormal (via r-universe)

September 13, 2024

Title Tests of Homogeneity of Variances

Version 0.1

Description Most common exact, asymptotic and resample based tests are
provided for testing the homogeneity of variances of k normal
distributions under normality. These tests are Barlett,
Bhandary & Dai, Brown & Forsythe, Chang et al., Gokpinar &
Gokpinar, Levene, Liu and Xu, Gokpinar. Also, a data generation
function from multiple normal distribution is provided using
any multiple normal parameters. Bartlett, M. S. (1937)
<doi:10.1098/rspa.1937.0109> Bhandary, M., & Dai, H. (2008)
<doi:10.1080/03610910802431011> Brown, M. B., & Forsythe, A. B.
(1974).<doi:10.1080/01621459.1974.10482955> Chang, C. H., Pal,
N., & Lin, J. J. (2017) <doi:10.1080/03610918.2016.1202277>
Gokpinar E. & Gokpinar F. (2017)
<doi:10.1080/03610918.2014.955110> Liu, X., & Xu, X. (2010)
<doi:10.1016/j.spl.2010.05.017> Levene, H. (1960)
<https://cir.nii.ac.jp/crid/1573950400526848896> Gökpınar, E.
(2020) <doi:10.1080/03610918.2020.1800037>.

License GPL-2

Depends R (>= 3.5.0), huxtable (>= 5.4.0)

Imports stats, graphics

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NeedsCompilation no

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Contents

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bart   *Bartlett Test for Homogeniety*

Description

Tests the homogeniety of variances for more than two normal groups.

Usage

```
bart(x1, x2, alfa = 0.05, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Bartlett, M. S. (1937). "Properties of sufficiency and statistical tests". Proceedings of the Royal Statistical Society, Series A 160, 268–282 JSTOR.

See Also

levene Brown_Forsythe, Cat_GG, Cat_LR, genp, slrt, bdai

Examples

```
 data(FH_data)
x1=FH_data$SurvivalTime
x2=FH_data$HospitalNo
bart(x1,x2)
readline(prompt = "Pause. Press <Enter> to continue...")
bart(x1,x2,alfa=0.10)
readline(prompt = "Pause. Press <Enter> to continue...")
 bart(x1,x2,alfa=0.10,table=FALSE)
 readline(prompt = "Pause. Press <Enter> to continue...")
 bart(x1,x2,alfa=0.10,table=FALSE,graph="centerized")
  readline(prompt = "Pause. Press <Enter> to continue...")
 bart(x1,x2,alfa=0.10,table=FALSE,graph="none")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#  #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

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bdai	*Bahandary-Dai Test for Homogeniety*

Description

Tests the homogeniety of variances for more than two normal groups using Bahandary-Dai test.

Usage

```
bdai(x1, x2, alfa = 0.05, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Bhandary, M., & Dai, H. (2008). An alternative test for the equality of variances for several populations when the underlying distributions are normal. Communications in Statistics-Simulation and Computation, 38(1), 109-117.

See Also

Brown_Forsythe, Cat_GG, Cat_LR, genp, slrt, levene

Examples

```
    data(FH_data)
    x1=FH_data$SurvivalTime
    x2=FH_data$HospitalNo
    bdai(x1,x2)
    readline(prompt = "Pause. Press <Enter> to continue...")
    bdai(x1,x2,alfa=0.10)
    readline(prompt = "Pause. Press <Enter> to continue...")
     bdai(x1,x2,alfa=0.10,table=FALSE)
     readline(prompt = "Pause. Press <Enter> to continue...")
     bdai(x1,x2,alfa=0.10,table=FALSE,graph="raw")
     readline(prompt = "Pause. Press <Enter> to continue...")
     bdai(x1,x2,alfa=0.10,table=FALSE,graph="none")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#   #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

| Brown_Forsythe | *Brown-Forsythe Test for Homogeniety* |

Description

Tests the homogeniety of variances for more than two normal groups.

Usage

```
Brown_Forsythe(x1, x2, alfa = 0.05, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Brown, M. B., & Forsythe, A. B. (1974). Robust tests for the equality of variances. Journal of the American Statistical Association, 69(346), 364-367.

See Also

bdai, Cat_GG, Cat_LR, genp, slrt, levene,

Examples

```
 data(FH_data)
x1=FH_data$SurvivalTime
x2=FH_data$HospitalNo
Brown_Forsythe(x1,x2)
readline(prompt = "Pause. Press <Enter> to continue...")
Brown_Forsythe(x1,x2,alfa=0.10)
readline(prompt = "Pause. Press <Enter> to continue...")
 Brown_Forsythe(x1,x2,alfa=0.10,table=FALSE)
 readline(prompt = "Pause. Press <Enter> to continue...")
 Brown_Forsythe(x1,x2,alfa=0.10,table=FALSE,graph="raw")
 readline(prompt = "Pause. Press <Enter> to continue...")
 Brown_Forsythe(x1,x2,alfa=0.10,table=FALSE,graph="none")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#  #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

Cat_GG   *Computational Approach Test for Homogeniety*

Description

Tests the homogeniety of variances for more than two normal groups using standartized likelihood ratio test.

Usage

```
Cat_GG(x1, x2, alfa = 0.05, m = 2000, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
m	number of resampling.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Gokpinar, E., & Gokpinar, F. (2017). Testing equality of variances for several normal populations. Communications in Statistics-Simulation and Computation, 46(1), 38-52.

See Also

Brown_Forsythe, bdai, Cat_LR, genp, slrt, levene

Examples

```
 data(FH_data)
x1=FH_data$SurvivalTime
x2=FH_data$HospitalNo
Cat_GG(x1,x2)
readline(prompt = "Pause. Press <Enter> to continue...")
Cat_GG(x1,x2,alfa=0.10)
readline(prompt = "Pause. Press <Enter> to continue...")
 Cat_GG(x1,x2,alfa=0.10,table=FALSE)
 readline(prompt = "Pause. Press <Enter> to continue...")
 Cat_GG(x1,x2,alfa=0.10,table=FALSE,graph="raw")
 readline(prompt = "Pause. Press <Enter> to continue...")
 Cat_GG(x1,x2,alfa=0.10,table=FALSE,graph="none")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#  #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

Cat_LR *Computational Approach Test for Homogeniety*

Description

Tests the homogeniety of variances for more than two normal groups using standartized likelihood ratio test.

Usage

```
Cat_LR(x1, x2, alfa = 0.05, m = 2000, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
m	number of resampling.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Chang, C. H., Pal, N., & Lin, J. J. (2017). A revisit to test the equality of variances of several populations. Communications in Statistics-Simulation and Computation, 46(8), 6360-6384.

See Also

Brown_Forsythe, Cat_GG, bdai, genp, slrt, levene

Examples

```
 data(FH_data)
x1=FH_data$SurvivalTime
x2=FH_data$HospitalNo
Cat_LR(x1,x2)
readline(prompt = "Pause. Press <Enter> to continue...")
Cat_LR(x1,x2,alfa=0.10)
readline(prompt = "Pause. Press <Enter> to continue...")
 Cat_LR(x1,x2,alfa=0.10,table=FALSE)
 readline(prompt = "Pause. Press <Enter> to continue...")
 Cat_LR(x1,x2,alfa=0.10,table=FALSE,graph="raw")
```

```
      readline(prompt = "Pause. Press <Enter> to continue...")
      Cat_LR(x1,x2,alfa=0.10,m=5000,table=FALSE,graph="none")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#   #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

---

datagen   *Multiple Normal Distribution Data Generation*

Description

This function generates data from multiple normal distribution.

Usage

```
datagen(n, mu, sigma, tn = 1)
```

Arguments

n	Sample sizes of each group. n=c(n1,n2,...nk); for example: n=c(3, 4, 5).
mu	Mean of each group.mu=c(mu1,mu2,...muk); for example: mu=c(3, 4, 5).
sigma	Standard deviation of each group.sigma=c(sigma1,sigma2,...sigmak); for example: sigma=c(1, 2, 3).
tn	Trial number for all groups. Default of the parameter is 1. This parameter for use more than 1, is especially useful for resampling such as Monte Carlo, Parametric Bootstrap.

Value

a data matrix with size (n1,n2,...nk) with group number 1,2,...k at first row and random number with mnean mu=(mu1,mu2,...muk) and standard deviation sigma=(sigma1,sigma2,...sigmak)

Examples

```
n=c(3, 4, 5)
mu=c(3, 4, 5)
sigma=c(3, 4, 5)
F=datagen(n,mu,sigma);muh=F[1];S2h=F[2];x=F[3]
muh
S2h
x

# Following example especially useful for simulation based tecnhiques
# such as Monte Carlo, Parametric Bootstrap and comparison studies
# by using simulation.

 Fm=datagen(c(3, 4, 5),c(3, 4, 5),c(3, 4, 5),10);muhm=Fm[1];S2hm=Fm[2];xm=Fm[3]
```

```
muhm
S2hm
xm
```

FH_data   *Fleming and Harrington Data*

Description

The data related to survival times of patients was collected from 4 hospitals, which was a part of the data by given Fleming and Harrington(1991). The data contain failure time of the patients.

Usage

```
data(FH_data)
```

Format

A dataframe with 21 rows 2 variables

HospitalNo Hospital No

SurvivalTime Survival Time of Patients

Source

T.R. Fleming and D.P. Harrington, Counting processes and survival analysis. Wiley Online Library, Vol. 8., 1991.

Examples

```
 data("FH_data")
   x1=FH_data$SurvivalTime
   x2=FH_data$HospitalNo
```

---

genp   *Generalized p value Test for Homogeniety*

Description

Tests the homogeniety of variances for more than two normal groups using generalized p value test.

Usage

```
genp(x1, x2, alfa = 0.05, m = 2000, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
m	number of resampling.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Liu, X., & Xu, X. (2010). A new generalized p-value approach for testing the homogeneity of variances. Statistics & probability letters, 80(19-20), 1486-1491.

See Also

Brown_Forsythe, Cat_GG, Cat_LR, bdai, slrt, levene

Examples

```
  data(FH_data)
   x1=FH_data$SurvivalTime
   x2=FH_data$HospitalNo
   genp(x1,x2)
   readline(prompt = "Pause. Press <Enter> to continue...")
   genp(x1,x2,alfa=0.10)
   readline(prompt = "Pause. Press <Enter> to continue...")
   genp(x1,x2,alfa=0.10,m=5000)
   readline(prompt = "Pause. Press <Enter> to continue...")
    genp(x1,x2,alfa=0.10,table=FALSE)
    readline(prompt = "Pause. Press <Enter> to continue...")
    genp(x1,x2,alfa=0.10,table=FALSE,graph="raw")
    readline(prompt = "Pause. Press <Enter> to continue...")
    genp(x1,x2,alfa=0.10,table=FALSE,graph="none")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#   #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

---

levene	*Levene Test for Homogeniety*

Description

Tests the homogeniety of variances for more than two normal groups.

Usage

```
levene(x1, x2, alfa = 0.05, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Levene, H. (1960). Robust tests for equality of variances, p 278–292. Contributions to probability and statistics: essays in honor of Harold Hotelling. Stanford University Press, Palo Alto, CA.

See Also

Brown_Forsythe, Cat_GG, Cat_LR, genp, slrt, bdai

Examples

```
 data(FH_data)
x1=FH_data$SurvivalTime
x2=FH_data$HospitalNo
levene(x1,x2)
readline(prompt = "Pause. Press <Enter> to continue...")
levene(x1,x2,alfa=0.10)
readline(prompt = "Pause. Press <Enter> to continue...")
 levene(x1,x2,alfa=0.10,table=FALSE)
 readline(prompt = "Pause. Press <Enter> to continue...")
 levene(x1,x2,alfa=0.10,table=FALSE,graph="raw")
 readline(prompt = "Pause. Press <Enter> to continue...")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#  #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

slrt   *Standartized Likelihood Ratio Test for Homogeniety*

Description

Tests the homogeniety of variances for more than two normal groups using standartized likelihood ratio test.

Usage

```
slrt(x1, x2, alfa = 0.05, table = TRUE, graph = "none")
```

Arguments

x1	a numeric matrix containing the values of groups.
x2	numeric matrix containing the values of group numbers.
alfa	significance level of the test. Default number is 0.05.
table	a logical variable that indicates table will appear or not. Default is TRUE.
graph	box plot of groups of raw or centered data.

Value

if table is TRUE, then it gives a detailed table, else it gives a vector of r value(r=1 when null hypothesis was rejected and r=0 when null hypothesis was accepted) p-value and test statistic value.

References

Gökpınar, E. (2020). Standardized likelihood ratio test for homogeneity of variance of several normal populations. Communications in Statistics-Simulation and Computation, 1-11.

See Also

Brown_Forsythe, datagen, levene, Cat_LR, genp

Examples

```
data(FH_data)
x1=FH_data$SurvivalTime
x2=FH_data$HospitalNo
slrt(x1,x2)
readline(prompt = "Pause. Press <Enter> to continue...")
slrt(x1,x2,alfa=0.10)
readline(prompt = "Pause. Press <Enter> to continue...")
 slrt(x1,x2,alfa=0.10,table=FALSE)
 readline(prompt = "Pause. Press <Enter> to continue...")
 slrt(x1,x2,alfa=0.10,table=FALSE,graph=FALSE)
 readline(prompt = "Pause. Press <Enter> to continue...")
```

```
    slrt(x1,x2,alfa=0.10,table=FALSE,graph="none")
# ---THIS VERSION IS ESPECIALLY USEFUL FOR COMPARISON STUDIES BY SIMULATION---
#   #first value of the vector is r value(r=1 when rejected and r=0 when accepted null hypothesis)
# second value of the vector is the p-value and third value is the tests statistic value
```

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