

Package ‘homnormal’

July 22, 2025

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 Bar-

lett, 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](https://doi.org/10.1098/rspa.1937.0109)>

Bhandary, M., & Dai, H. (2008) <[doi:10.1080/03610910802431011](https://doi.org/10.1080/03610910802431011)>

Brown, M. B., & Forsythe, A. B. (1974).<[doi:10.1080/01621459.1974.10482955](https://doi.org/10.1080/01621459.1974.10482955)>

Chang, C. H., Pal, N., & Lin, J. J. (2017) <[doi:10.1080/03610918.2016.1202277](https://doi.org/10.1080/03610918.2016.1202277)>

Gokpinar E. & Gokpinar F. (2017) <[doi:10.1080/03610918.2014.955110](https://doi.org/10.1080/03610918.2014.955110)>

Liu, X., & Xu, X. (2010) <[doi:10.1016/j.spl.2010.05.017](https://doi.org/10.1016/j.spl.2010.05.017)>

Levene, H. (1960) <<https://cir.nii.ac.jp/crid/1573950400526848896>>

Gokpinar, E. (2020) <[doi:10.1080/03610918.2020.1800037](https://doi.org/10.1080/03610918.2020.1800037)>.

License GPL-2

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bart	<i>Bartlett Test for Homogeniety</i>
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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

```

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. $n=c(n_1, n_2, \dots, n_k)$; for example: $n=c(3, 4, 5)$.
mu	Mean of each group. $\mu=c(\mu_1, \mu_2, \dots, \mu_k)$; for example: $\mu=c(3, 4, 5)$.
sigma	Standard deviation of each group. $\sigma=c(\sigma_1, \sigma_2, \dots, \sigma_k)$; 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 $(n_1, n_2, \dots, n_k)$ with group number 1, 2, ..., k at first row and random number with mean $\mu=(\mu_1, \mu_2, \dots, \mu_k)$ and standard deviation $\sigma=(\sigma_1, \sigma_2, \dots, \sigma_k)$

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 techniques
# 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	<i>Levene Test for Homogeneity</i>
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Description

Tests the homogeneity 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

Standardized Likelihood Ratio Test for Homogeneity

Description

Tests the homogeneity of variances for more than two normal groups using standardized 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

Gökpinar, 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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