Package ‘svplots’

April 7, 2021

Type Package
Title Sample Variance Plots (Sv-Plots)
Version 0.1.0
Author Uditha Amarananda Wijesuriya <u.wijesuriya@usi.edu>
Maintainer Uditha Amarananda Wijesuriya <u.wijesuriya@usi.edu>
Description Two versions of sample variance plots, Sv-plot1 and Sv-plot2, will be provided illustrating the squared deviations from sample variance. Besides indicating the contribution of squared deviations for the sample variability, these plots are capable of detecting characteristics of the distribution such as symmetry, skewness and outliers. A remarkable graphical method based on Sv-plot2 can determine the decision on testing hypotheses over one or two population means. In sum, Sv-plots will be appealing visualization tools. Complete description of this methodology can be found in the article, Wijesuriya (2020) <doi:10.1080/03610918.2020.1851716>.
License GPL-3
Encoding UTF-8
RoxygenNote 7.1.1
Depends R (>= 3.0.2)
Imports ggplot2
Suggests testthat (>= 3.0.0), knitr, rmarkdown, stats
Config/testthat/edition 3
VignetteBuilder knitr
NeedsCompilation no
Repository CRAN
Date/Publication 2021-04-07 08:40:02 UTC

R topics documented:

svplot1 ................................................................. 2
svplot2 ................................................................. 3
test1mu ................................................................. 4
svplot1

Creates Sv-plot1, the first version of the sample variance plots.

Description

Sv-plot1 identifies the characteristics of the distribution illustrating squared deviations in the sample variance by squares for each data value.

Usage

svplot1(X,title="Sv-plot1",xlab="x",lbcol="grey5",lscol="grey60",
rbcol="grey45",rscol="grey75",...)

Arguments

X  
an n by 1 matrix, equivalently, a column vector of length n, where n is number of observations.
title  
title of the plot, Sv-plot1 by default.
xlab  
x-axis label, x by default.
lbcol  
left bound color, grey5 by default.
lscolor  
left square color, grey60 by default.
rbcol  
right bound color, grey45 by default.
rscolor  
right square color, grey75 by default.
...  
other graphical parameters.

Value

Sv-plot1

References

Examples

```r
set.seed(0)
X1 <- matrix(rnorm(50,mean=2,sd=5))
svplot1(X1)
X2 <- matrix(rf(50,df1=10,df2=5))
svplot1(X2)
X3 <- matrix(rbeta(50,shape1=10,shape2=2))
svplot1(X3,title="",lbcol="blue",lscol="blue",rbcol="red",rscol="grey75")
```

svplot2

*Creates Sv-plot2, the second version of the sample variance plots.*

Description

Sv-plot2 identifies the characteristics of the distribution illustrating squared deviation values in the sample variance against each data value.

Usage

```r
svplot2(X,title="Sv-plot2",xlab="x",lbcol="grey5", lsdcol="grey60", rbcol="grey45",rsdcol="grey75",...)
```

Arguments

- `X` an `n` by 1 matrix, equivalently, a column vector of length `n`, where `n` is number of observations.
- `title` title of the plot, *Sv-plot2* by default.
- `xlab` `x`-axis label, `x` by default.
- `lbcol` left bound color, `grey5` by default.
- `lsdcol` left squared deviation color, `grey60` by default.
- `rbcol` right bound color, `grey45` by default.
- `rsdcol` right squared deviation color, `grey75` by default.
- `...` other graphical parameters.

Value

*Sv-plot2*

References

Examples

```r
set.seed(0)
X1 <- matrix(rnorm(50, mean=2, sd=5))
svplot2(X1)

X2 <- matrix(rf(50, df1=10, df2=5))
svplot2(X2)

X3 <- matrix(rbeta(50, shape1=10, shape2=2))
svplot2(X3, lbcol="blue", lsdcol="blue", rbcol="red", rsdcol="red")
```

test1mu

Tests the hypothesis over population mean based on one sample by Sv-plot2.

Description

Decision on hypothesis testing over single mean is made by graphing sample and population Sv-plot2s along with the threshold line. If the intersection point of two Sv-plot2s locates on or above the threshold line, the null hypothesis is rejected at specified significance level, otherwise, failed to reject.

Usage

```r
test1mu(X, mu0=3.5, alpha=0.05, unkwnsigma=TRUE, sigma=NULL, xlab="x", title="Single mean: Hypothesis testing by Sv-plot2", samcol="grey5", popcol="grey45", thrcol="black", ...)
```

Arguments

- **X**: an \( n \) by 1 matrix, equivalently, a column vector of length \( n \), where \( n \) is number of observations.
- **mu0**: hypothesized population mean, \( mu0=3.5 \) by default.
- **alpha**: significance level, \( alpha=0.05 \) by default.
- **unkwnsigma**: population standard deviation is unknown, \( TRUE \) by default.
- **sigma**: population standard deviation, \( NULL \) by default.
- **xlab**: \( x \)-axis label, \( x \) by default.
- **title**: title of the plot, \( Single mean: Hypothesis testing by Sv-plot2 \) by default.
- **samcol**: sample Sv-plot2 color, \( grey5 \) by default.
- **popcol**: sample Sv-plot2 color, \( grey45 \) by default.
- **thrcol**: threshold color, \( black \) by default.
- **...**: other graphical parameters.
Value

Decision on testing hypotheses over single population mean by Sv-plot2.

References


Examples

```r
set.seed(5)
X = matrix(rnorm(20, mean=3, sd=2))
test1mu(X, mu0=3.5, alpha=0.05, unkwnsigma=TRUE, sigma=NULL, xlab="x",
    title="Single mean: Hypothesis testing by Sv-plot2",
    samcol="grey5", popcol="grey45", thrcol="black")
```

```
test1musm
Tests the hypothesis over population mean based on one sample summary statistics by Sv-plot2.
```

Description

Decision on hypothesis testing over single mean is made by graphing sample and population Sv-plot2s along with the threshold line. Intersecting Sv-plots on or above the horizontal line concludes the alternative hypothesis.

Usage

```r
test1musm(n=20, xbar=3, s=2, mu0=4.5, alpha=0.05, unkwnsigma=TRUE, sigma=NULL, xlab="x",
    title="Single mean summary: Hypothesis testing by Sv-plot2",
    samcol="grey5", popcol="grey45", thrcol="black",...)
```

Arguments

- `n`: sample size, `n=20` by default.
- `xbar`: sample average, `xbar=3` by default.
- `s`: sample standard deviation, `s=2` by default.
- `mu0`: hypothesized population mean, `mu0=4.5` by default.
- `alpha`: significance level, `alpha=0.05` by default.
- `unkwnsigma`: population standard deviation is unknown, `TRUE` by default.
- `sigma`: population standard deviation, `NULL` by default.
- `xlab`: `x`-axis label, `x` by default.
- `title`: title of the plot, `Single mean: Hypothesis testing by Sv-plot2` by default by default.
test2mu

`samcol` sample Sv-plot2 color, *grey5* by default.
`popcol` sample Sv-plot2 color, *grey45* by default.
`thrcol` threshold color, *black*.
...
other graphical parameters.

**Value**

Decision on testing hypotheses over single population mean by Sv-plot2.

**References**


**Examples**

```r
## For summary data
test1musm(n=20,xbar=3,s=2,mu0=4.5,alpha=0.05, unkwnsigma=TRUE,sigma=NULL,xlab="x", title="Single mean summary: Hypothesis testing by Sv-plot2", samcol="grey5",popcol="grey45",thrcol="black")
```

**Description**

Decision on hypothesis testing over two means is made by graphing two sample Sv-plot2s along with the threshold line. If the intersection point of two Sv-plot2s locates on or above the threshold line, the null hypothesis is rejected at specified significance level, otherwise, failed to reject.

**Usage**

```r
test2mu(X1,X2,paired=FALSE,eqlvar=FALSE,unkwnsigmas=TRUE, sigma1=NULL,sigma2=NULL,alpha=0.05,xlab="x", title="Two means: Hypothesis testing by Sv-plot2", sam1col="grey5",sam2col="grey45",thrcol="black",...)
```

**Arguments**

- **X1** an \( n_1 \) by 1 matrix, equivalently, a column vector of length \( n_1 \), where \( n_1 \) is number of observations.
- **X2** an \( n_2 \) by 1 matrix, equivalently, a column vector of length \( n_2 \), where \( n_2 \) is number of observations.
- **paired** for dependent samples TRUE, *FALSE* by default.
- **eqlvar** population variances are equal, *FALSE* by default.
unkwnsigmas  population standard deviations are unknown, **TRUE** by default.
sigma1  population1 standard deviation, **NULL** by default.
sigma2  population2 standard deviation, **NULL** by default.
alpha  significance level, **alpha=0.05** by default.
xlab  x-axis label, **x** by default.
title  title of the plot, **Two means: Hypothesis testing by Sv-plot2** by default.
sam1col  sample1 Sv-plot2 color, **grey5** by default.
sam2col  sample2 Sv-plot2 color, **grey45** by default.
thrcol  threshold color, **black** by default.
...  other graphical parameters.

**Value**

Decision on testing hypotheses over two population means by Sv-plot2.

**References**


**Examples**

```r
test2mu(X1=matrix(rnorm(10,mean=3,sd=2)),X2=matrix(rnorm(20,mean=4,sd=2.5)),
  paired=FALSE,eqlvar=FALSE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,alpha=0.05,
sam1col="grey5",sam2col="grey45",thrcol="black")
```

```r
test2mu(X1=matrix(rnorm(10,mean=3,sd=2)),X2=matrix(rnorm(20,mean=4,sd=2.5)),
  paired=FALSE,eqlvar=TRUE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,alpha=0.05,
sam1col="grey5",sam2col="grey45",thrcol="black")
```

```r
test2mu(X1=matrix(rnorm(50,mean=3,sd=2)),X2=matrix(rnorm(30,mean=4,sd=2.5)),
  xlab="x",title="Two means: Hypothesis testing by Sv-plot2",
  paired=FALSE,eqlvar=FALSE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,alpha=0.05,
sam1col="grey5",sam2col="grey45",thrcol="black")
```

```r
test2mu(X1=matrix(rnorm(50,mean=3,sd=2)),X2=matrix(rnorm(30,mean=4,sd=2.5)),
  paired=FALSE,eqlvar=FALSE,unkwnsigmas=FALSE,
sigma1=2,sigma2=4.920782,alpha=0.05,
sam1col="grey5",sam2col="grey45",thrcol="black")
```

X1=matrix(rnorm(10,mean=3,sd=2))
X2=2*X1
test2mu(X1,X2,
  paired=TRUE,eqlvar=FALSE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,alpha=0.05,
sam1col="blue",sam2col="red",thrcol="black")
**test2musm**

Tests the hypothesis over two population means based on two samples summary statistics by Sv-plot2.

**Description**

Decision on hypothesis testing over two means is made by graphing two sample Sv-plot2s along with the threshold line. Intersecting Sv-plots on or above the horizontal line concludes the alternative hypothesis.

**Usage**

```r
test2musm(n1=20, n2=25, xbar1=3, xbar2=4, s1=1, s2=1.5, 
  paired=FALSE, eqlvar=FALSE, unkwnsigmas=TRUE, 
  sigma1=NULL, sigma2=NULL, sdevdif=NULL, alpha=0.05, 
  xlab="x", title="Two means summary: Hypothesis testing by Sv-plot2", 
  sam1col="grey5", sam2col="grey45", thrcol="black", ...)
```

**Arguments**

- **n1**: sample1 size, *n1*=20 by default.
- **n2**: sample2 size, *n2*=25 by default.
- **xbar1**: sample1 average, *xbar1*=3 by default.
- **xbar2**: sample2 average, *xbar2*=4 by default.
- **s1**: sample1 standard deviation, *s1*=1 by default.
- **s2**: sample2 standard deviation, *s2*=1.5 by default.
- **paired**: for dependent samples TRUE, FALSE by default.
- **eqlvar**: population variances are equal, FALSE by default.
- **unkwnsigmas**: population standard deviations are unknown, TRUE by default.
- **sigma1**: population1 standard deviation, *NULL* by default.
- **sigma2**: population2 standard deviation, *NULL* by default.
- **sdevdif**: standard deviation of the differences, *NULL* by default.
- **alpha**: significance level, *alpha*=0.05 by default.
- **xlab**: *x*-axis label, *x* by default.
- **title**: title of the plot, *Two means: Hypothesis testing by Sv-plot2* by default.
- **sam1col**: sample1 Sv-plot2 color, *grey5* by default.
- **sam2col**: sample2 Sv-plot2 color, *grey45* by default.
- **thrcol**: threshold color, *black* by default.
- **...**: other graphical parameter.
Value

Decision on testing hypotheses over two population means by Sv-plot2.

References


Examples

```r
# For summary data
test2musm(n1=20,n2=25,xbar1=3,xbar2=4,s1=1,s2=1.5,
paired=FALSE,eqlvar=FALSE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,sdevdif=NULL,alpha=0.05,
lab="x",title="Two means summary: Hypothesis testing by Sv-plot2",
sam1col="grey5",sam2col="grey45",thrcol="black")

test2musm(n1=20,n2=25,xbar1=3,xbar2=4,s1=1.5,s2=1.5,
paired=FALSE,eqlvar=TRUE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,sdevdif=NULL,alpha=0.05,
lab="x",title="Two means summary: Hypothesis testing by Sv-plot2",
sam1col="grey5",sam2col="grey45",thrcol="black")

test2musm(n1=50,n2=35,xbar1=3,xbar2=4,s1=1,s2=1.5,
paired=FALSE,eqlvar=FALSE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,sdevdif=NULL,alpha=0.05,
lab="x",title="Two means summary: Hypothesis testing by Sv-plot2",
sam1col="grey5",sam2col="grey45",thrcol="black")

test2musm(n1=50,n2=35,xbar1=3,xbar2=4,s1=1,s2=1.5,
paired=FALSE,eqlvar=FALSE,unkwnsigmas=FALSE,
sigma1=2,sigma2=3,sdevdif=NULL,alpha=0.05,
lab="x",title="Two means summary: Hypothesis testing by Sv-plot2",
sam1col="grey5",sam2col="grey45",thrcol="black")

test2musm(n1=20,n2=20,xbar1=3,xbar2=4,s1=1,s2=1.5,
paired=TRUE,eqlvar=FALSE,unkwnsigmas=TRUE,
sigma1=NULL,sigma2=NULL,sdevdif=2,alpha=0.05,
lab="x",title="Two means summary: Hypothesis testing by Sv-plot2",
sam1col="grey45",sam2col="grey5",thrcol="black")
```
Index

svplot1, 2
svplot2, 3
test1mu, 4
test1musm, 5
test2mu, 6
test2musm, 8