

Package ‘jocre’

October 5, 2016

Type Package

Title Joint Confidence Regions

Version 0.1

Date 2016-10-07

Description Computing and plotting joint confidence regions and intervals. Regions include classical ellipsoids, minimum-volume or minimum-length regions, and an empirical Bayes region. Intervals include the TOST procedure with ordinary or expanded intervals and a fixed-sequence procedure. Such regions and intervals are useful e.g., for the assessment of multi-parameter (bio-)equivalence. Joint confidence regions for the mean and variance of a normal distribution are available as well.

License GPL-2

Imports boot, KernSmooth

Suggests mvtnorm

BugReports <https://github.com/PhilipPallmann/jocre/issues>

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NeedsCompilation no

Repository CRAN

Date/Publication 2016-10-05 22:33:58

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jocre-package

Joint confidence regions

Description

This package provides functions for computing and plotting joint confidence regions as well as (simultaneous) confidence intervals, with a focus on multivariate normal parameter vectors and parameters of the normal distribution i.e., mean and variance.

Details

Package: jocre
Type: Package
Version: 0.1
Date: 2016-09-27
License: GPL-2

`plot2D` generates plots of joint confidence regions or (simultaneous) confidence intervals in two dimensions and allows for fine tuning e.g., shading of an equivalence region. The confidence region's boundaries can be found with `confset`, whereas `confints` computes (simultaneous) confidence intervals.

`plotMV2D` produces graphics of joint confidence regions for the mean and variance (or standard deviation) of a normal distribution.

Insights into the conservativeness of the two one-sided test procedure can be obtained with `iutsize`.
CIGE ...

Author(s)

Philip Pallmann (<p.pallmann@lancaster.ac.uk>)

References

Philip Pallmann (2016) Joint confidence regions with the R package jocre. In preparation.

Examples

```
data("marzo")
#plot2D()

data("wires")
#plotMV2D()
```

`confints`*Confidence intervals around multivariate normal means*

Description

Computes boundaries of (simultaneous) confidence intervals around multivariate normal means using different methods.

Usage

```
confints(dat, method, alpha=0.1, steps=100)
```

Arguments

<code>dat</code>	A matrix or <code>data.frame</code> with independent units in rows and multivariate outcomes in columns.
<code>method</code>	A character string specifying the method to be used. See details for available methods.
<code>alpha</code>	A numeric value giving the type I error level to be controlled. Default is 0.1 .
<code>steps</code>	An integer setting the initial number of steps for the search algorithm.

Details

Available methods are: `expanded` for the two one-sided test (TOST) procedure (Schuirmann 1987) using the expanded intervals described e.g., in Bofinger (1992) and Hsu et al. (1994); `fixseq` for the fixed sequence intervals described in Maurer et al (1995) and Hsu & Berger (1999); `tost` for the two one-sided test (TOST) intervals described in Schuirmann (1987).

Value

A matrix of parameter estimates and confidence bounds.

Note

Warning: please use with care! Some of the functionality has not yet been thoroughly tested.

Author(s)

Philip Pallmann (<p.pallmann@lancaster.ac.uk>)

References

Eve Bofinger (1992) Expanded confidence intervals, one-sided tests, and equivalence testing. *Journal of Biopharmaceutical Statistics*, 2(2), 181–188.

Jason C. Hsu & Roger L. Berger (1999) Stepwise confidence intervals without multiplicity adjustment for dose-response and toxicity studies. *Journal of the American Statistical Association*, 94(446), 468–482.

Jason C. Hsu, J. T. Gene Hwang, Hung-Kung Liu, Stephen J. Ruberg (1994) Confidence intervals associated with tests for bioequivalence. *Biometrika*, 81(1), 103–114.

Willi Maurer, Ludwig A. Hothorn, Walter Lehmacher (1995) Multiple comparisons in drug clinical trials and preclinical assays: a priori ordered hypotheses. In: Joachim Vollmar (editor), *Biometrie in der Chemisch-Pharmazeutischen Industrie*, vol. 6, pp. 3–18. Fischer-Verlag, Stuttgart, Germany.

Philip Pallmann & Thomas Jaki (2016) Simultaneous confidence regions and intervals for multivariate bioequivalence. Submitted to *Statistics in Medicine*.

Donald J. Schuirmann (1987) A comparison of the two one-sided tests procedure and the power approach for assessing the equivalence of average bioavailability. *Journal of Pharmacokinetics and Biopharmaceutics*, 15(6), 657–680.

See Also

[plot2D](#) for plots.

Examples

```
## Not run:
# Generate trivariate normal data

mydata <- mvtnorm::rmvnorm(n=50, mean=rep(0.1, 3), sigma=diag(3) * 0.05)
colnames(mydata) <- LETTERS[1:3]

# Compute 90

confints(dat=mydata, method="tost", alpha=0.1)
confints(dat=mydata, method="expanded", alpha=0.1)
confints(dat=mydata, method="fixseq", alpha=0.1)

## End(Not run)
```

confset

Confidence regions around multivariate normal means

Description

Computes boundaries of (simultaneous) confidence regions around multivariate normal means using different methods, and projects the boundaries onto the axes.

Usage

```
confset(dat, method, alpha=0.1, steps=100, TsengBrownA=1, TsengBrownB=1)
```

Arguments

<code>dat</code>	A matrix or <code>data.frame</code> with independent units in rows and multivariate outcomes in columns.
<code>method</code>	A character string specifying the method to be used. See details for available methods.
<code>alpha</code>	A numeric value giving the type I error level to be controlled. Default is 0.1.
<code>steps</code>	An integer setting the initial number of steps for the search algorithm.
<code>TsengBrownA</code>	A numeric giving the parameter A to be used when <code>method="tseng.brown"</code> (ignored otherwise). Default is 1.
<code>TsengBrownB</code>	A numeric giving the parameter B to be used when <code>method="tseng.brown"</code> (ignored otherwise). Default is 1.

Details

Available methods are: `emp.bayes` for the empirical Bayes region described in Casella & Hwang (1983); `fixseq` for the fixed sequence intervals described in Maurer et al (1995) and Hsu & Berger (1999); `hotelling` for the Hotelling-type region described in Wang et al (1999); `limacon.asy` for the limaçon-shaped minimum expected volume region described in Brown et al (1995); `limacon.fin` for the finite-sample variant of the minimum expected volume region described in Berger & Hsu (1996); `standard.cor` for the standard region incorporating correlation between parameters; `standard.ind` for the standard region ignoring correlation between parameters; `tost` for the two one-sided test (TOST) intervals described in Schuirmann (1987); `tseng` for the minimum expected interval length region described in Tseng (2002); `tseng.brown` for the pseudo-empirical Bayes region described in Tseng & Brown (1997). See also an overview and comparison of all methods in Pallmann & Jaki (2016).

Value

A matrix of parameter estimates and confidence bounds.

Note

Warning: please use with care! Some of the functionality has not yet been thoroughly tested.

Author(s)

Philip Pallmann (<p.pallmann@lancaster.ac.uk>)

References

- Roger L. Berger & Jason C. Hsu (1996) Bioequivalence trials, intersection-union tests and equivalence confidence sets. *Statistical Science*, 11(4), 283–319.
- Lawrence D. Brown, George Casella, J. T. Gene Hwang (1995) Optimal confidence sets, bioequivalence, and the limaçon of Pascal. *Journal of the American Statistical Association*, 90(431), 880–889.
- George Casella & Jiunn T. Hwang (1983) Empirical Bayes confidence sets for the mean of a multivariate normal distribution. *Journal of the American Statistical Association*, 78(383), 688–698.

Jason C. Hsu & Roger L. Berger (1999) Stepwise confidence intervals without multiplicity adjustment for dose-response and toxicity studies. *Journal of the American Statistical Association*, 94(446), 468–482.

Willi Maurer, Ludwig A. Hothorn, Walter Lehmacher (1995) Multiple comparisons in drug clinical trials and preclinical assays: a priori ordered hypotheses. In: Joachim Vollmar (editor), *Biometrie in der Chemisch-Pharmazeutischen Industrie*, vol. 6, pp. 3–18. Fischer-Verlag, Stuttgart, Germany.

Philip Pallmann & Thomas Jaki (2016) Simultaneous confidence regions and intervals for multivariate bioequivalence. Submitted to *Statistics in Medicine*.

Donald J. Schuurmann (1987) A comparison of the two one-sided tests procedure and the power approach for assessing the equivalence of average bioavailability. *Journal of Pharmacokinetics and Biopharmaceutics*, 15(6), 657–680.

Yu-Ling Tseng (2002) Optimal confidence sets for testing average bioequivalence. *Test*, 11(1), 127–141.

Yu-Ling Tseng & Lawrence D. Brown (1997) Good exact confidence sets for a multivariate normal mean. *The Annals of Statistics*, 25(5), 2228–2258.

Weizhen Wang, J. T. Gene Hwang, Anirban DasGupta (1999) Statistical tests for multivariate bioequivalence. *Biometrika*, 86(2), 395–402.

bootkern not included so far

See Also

[plot2D](#) for plots.

Examples

```
## Not run:
# Generate trivariate normal data

mydata <- mvtnorm::rmvnorm(n=50, mean=rep(0.1, 3), sigma=diag(3) * 0.05)
colnames(mydata) <- LETTERS[1:3]

# Compute boundaries of simultaneous 90

confset(dat=mydata, method="standard.ind", alpha=0.1)
confset(dat=mydata, method="standard.cor", alpha=0.1)
confset(dat=mydata, method="hotelling", alpha=0.1)
confset(dat=mydata, method="limacon.asy", alpha=0.1)
confset(dat=mydata, method="limacon.fin", alpha=0.1)
confset(dat=mydata, method="tseng", alpha=0.1)

## End(Not run)
```

iutsize	<i>Size of intersection union tests derived from confidence sets</i>
---------	--

Description

Computes the actual size of a intersection union test procedure that corresponds to a $(1 - \alpha)$ confidence set.

Usage

```
iutsize(p, n, alpha=0.1, sim=1e6)
```

Arguments

p	An integer giving the number of dimensions.
n	An integer giving the sample size.
alpha	A numeric value specifying the type I error level to be controlled. Default is 0.1.
sim	An integer giving the number of simulations to be carried out. Default is 1 million.

Details

A $(1 - \alpha)$ confidence set can be used to derive a two one-sided tests (TOST) procedure (Schuirmann 1987) whereby type I error rate control is ensured at level α due to the intersection union principle (Berger 1982). The actual test size, however, is often substantially lower than α i.e., the approach is conservative. It is well known for the one-dimensional case that the TOST corresponding to a $(1 - \alpha)$ confidence interval has size $(1 - \alpha/2)$. This function computes the achieved test size with dimension p and n according to the formula on p. 399 of Wang et al (1999).

Value

A numeric value giving the actual size of the test.

Author(s)

Philip Pallmann (<p.pallmann@lancaster.ac.uk>)

References

- Roger L. Berger (1982) Multiparameter hypothesis testing and acceptance sampling. *Technometrics*, 24(4), 295–300.
- Donald J. Schuirmann (1987) A comparison of the two one-sided tests procedure and the power approach for assessing the equivalence of average bioavailability. *Journal of Pharmacokinetics and Biopharmaceutics*, 15(6), 657–680.
- Weizhen Wang, J. T. Gene Hwang, Anirban DasGupta (1999) Statistical tests for multivariate bioequivalence. *Biometrika*, 86(2), 395–402.

Examples

```
# For p=1 we get the well-known result that the 90% CI corresponds to the TOST at 5%:

#iutsize(p=1, n=20)

# With increasing dimension the test gets conservative:

#iutsize(p=2, n=20)
#iutsize(p=3, n=20)

# For p>1 the conservativeness also depends on sample size:

#iutsize(p=2, n=10)
#iutsize(p=2, n=1000)
```

marzo

Bioequivalence study of ticlopidine hydrochloride

Description

Pharmacokinetic data from a study on the bioequivalence of a test and a reference formulation of ticlopidine hydrochloride in 24 healthy male volunteers, using a randomised crossover design (Marzo et al. 2002).

Usage

```
data("marzo")
```

Format

A data frame with 24 observations on the following 8 variables.

Volunteer A numeric vector giving the volunteer ID.

Sequence A factor with levels RT and TR specifying the sequence a volunteer was randomised to (R=reference, T=test).

Cmax_T A numeric vector of the maximum concentration (Cmax) with the test product.

Cmax_R A numeric vector of the maximum concentration (Cmax) with the reference product.

AUC_T A numeric vector of the area under the concentration-time curve (AUC) from zero to the last observed time point with the test product.

AUC_R A numeric vector of the area under the concentration-time curve (AUC) from zero to the last observed time point with the reference product.

AUCinf_T A numeric vector of the area under the concentration-time curve (AUC) from zero to infinity with the test product.

AUCinf_R A numeric vector of the area under the concentration-time curve (AUC) from zero to infinity with the reference product.

Details

The pharmacokinetic parameters (Cmax and AUC) were calculated using a non-compartmental approach. The data were taken from Tables I and II of Marzo et al. (2002).

Source

Antonio Marzo, Lorenzo Dal Bo, Antonio Rusca, Pierangelo Zini (2002) Bioequivalence of ticlopidine hydrochloride administered in single dose to healthy volunteers. *Pharmacological Research*, 46(5), 401–407.

References

Philip Pallmann & Thomas Jaki (2016) Simultaneous confidence regions and intervals for multivariate bioequivalence. Submitted to *Statistics in Medicine*.

Examples

```
data(marzo)

## An example analysis of Cmax assuming log-normality

# Difference of log(Cmax)
marzo$deltalogCmax <- log(marzo$Cmax_T) - log(marzo$Cmax_R)

# Estimated mean treatment effect with SE
mean(marzo$deltalogCmax)
sd(marzo$deltalogCmax) / sqrt(nrow(marzo))

# Two one-sided test (TOST) p-values
t.test(x=marzo$deltalogCmax, alternative="less", mu=log(1.25))$p.value
t.test(x=marzo$deltalogCmax, alternative="greater", mu=log(0.80))$p.value

# 90% confidence interval
t.test(x=marzo$deltalogCmax, conf.level=0.9)$conf.int[1:2]
```

plot2D

Plotting 2D confidence sets

Description

Creates graphs of (simultaneous) confidence regions and intervals around multivariate normal means using different methods for computing the confidence sets.

Usage

```
plot2D(dat, method, alpha=0.1, equi=log(c(0.8, 1.25)), axnames=NULL, main="Title",
       xlim=log(c(0.77, 1.3)), ylim=log(c(0.77, 1.3)), col="black", steps=400,
       nboot=1e4, TsengBrownA=1, TsengBrownB=1)
```

Arguments

<code>dat</code>	A matrix or <code>data.frame</code> with independent units in rows and multivariate outcomes in columns. It must have two columns.
<code>method</code>	A character string specifying the method to be used. See details for available methods.
<code>alpha</code>	A numeric value giving the type I error level to be controlled. Default is 0.1.
<code>equi</code>	A numeric vector of length 2 specifying the equivalence region (lower and upper equivalence threshold) to be shaded in grey. When set to NULL no equivalence region is drawn. Default is $\log(c(0.8, 1.25))$.
<code>axnames</code>	A vector of two character strings giving the x and y axis labels. When set to NULL the column names of <code>dat</code> are used as axis labels. Default is NULL.
<code>main</code>	A character string giving the plot title.
<code>xlim</code>	A numeric vector of length two specifying the plotting range on the x-axis. Default is $\log(c(0.77, 1.3))$.
<code>ylim</code>	A numeric vector of length two specifying the plotting range on the y-axis. Default is $\log(c(0.77, 1.3))$.
<code>col</code>	A character string specifying the colour of the plotted region or intervals.
<code>steps</code>	An integer setting the initial number of steps for the search algorithm.
<code>nboot</code>	An integer giving the number of bootstrap replications, which is only required for <code>method="bootkern"</code> . Default is 10000.
<code>TsengBrownA</code>	A numeric giving the parameter A to be used when <code>method="tseng.brown"</code> (ignored otherwise). Default is 1.
<code>TsengBrownB</code>	A numeric giving the parameter B to be used when <code>method="tseng.brown"</code> (ignored otherwise). Default is 1.

Details

Available methods are: `bootkern` for the bootstrap kernel density region described in Pallmann & Jaki (2016); `emp.bayes` for the empirical Bayes region described in Casella & Hwang (1983); expanded for the two one-sided test (TOST) procedure (Schuirmann 1987) using the expanded intervals described e.g., in Bofinger (1992) and Hsu et al. (1994); `fixseq` for the fixed sequence intervals described in Maurer et al (1995) and Hsu & Berger (1999); `hotelling` for the Hotelling-type region described in Wang et al (1999); `limacon.asy` for the limaçon-shaped minimum expected volume region described in Brown et al (1995); `limacon.fin` for the finite-sample variant of the minimum expected volume region described in Berger & Hsu (1996); `standard.cor` for the standard region incorporating correlation between parameters; `standard.ind` for the standard region ignoring correlation between parameters; `tost` for the two one-sided test (TOST) intervals described in Schuirmann (1987); `tseng` for the minimum expected interval length region described in Tseng (2002); `tseng.brown` for the pseudo-empirical Bayes region described in Tseng & Brown (1997). See also an overview and comparison of all methods in Pallmann & Jaki (2016).

The default choices of `equi`, `xlim`, and `ylim` are convenient for many bioequivalence settings but can of course be modified as needed.

White dot and white cross (the latter only where `theta0` appears).

Value

A graphical display of a (simultaneous) confidence set in two dimensions.

Note

Warning: please use with care! Some of the functionality has not yet been thoroughly tested.

Author(s)

Philip Pallmann (<p.pallmann@lancaster.ac.uk>)

References

- Roger L. Berger & Jason C. Hsu (1996) Bioequivalence trials, intersection-union tests and equivalence confidence sets. *Statistical Science*, 11(4), 283–319.
- Eve Bofinger (1992) Expanded confidence intervals, one-sided tests, and equivalence testing. *Journal of Biopharmaceutical Statistics*, 2(2), 181–188.
- Lawrence D. Brown, George Casella, J. T. Gene Hwang (1995) Optimal confidence sets, bioequivalence, and the limaçon of Pascal. *Journal of the American Statistical Association*, 90(431), 880–889.
- George Casella & Jiunn T. Hwang (1983) Empirical Bayes confidence sets for the mean of a multivariate normal distribution. *Journal of the American Statistical Association*, 78(383), 688–698.
- Jason C. Hsu & Roger L. Berger (1999) Stepwise confidence intervals without multiplicity adjustment for dose-response and toxicity studies. *Journal of the American Statistical Association*, 94(446), 468–482.
- Jason C. Hsu, J. T. Gene Hwang, Hung-Kung Liu, Stephen J. Ruberg (1994) Confidence intervals associated with tests for bioequivalence. *Biometrika*, 81(1), 103–114.
- Willi Maurer, Ludwig A. Hothorn, Walter Lehmacher (1995) Multiple comparisons in drug clinical trials and preclinical assays: a priori ordered hypotheses. In: Joachim Vollmar (editor), *Biometrie in der Chemisch-Pharmazeutischen Industrie*, vol. 6, pp. 3–18. Fischer-Verlag, Stuttgart, Germany.
- Philip Pallmann & Thomas Jaki (2016) Simultaneous confidence regions and intervals for multivariate bioequivalence. Submitted to *Statistics in Medicine*.
- Donald J. Schuurmann (1987) A comparison of the two one-sided tests procedure and the power approach for assessing the equivalence of average bioavailability. *Journal of Pharmacokinetics and Biopharmaceutics*, 15(6), 657–680.
- Yu-Ling Tseng (2002) Optimal confidence sets for testing average bioequivalence. *Test*, 11(1), 127–141.
- Yu-Ling Tseng & Lawrence D. Brown (1997) Good exact confidence sets for a multivariate normal mean. *The Annals of Statistics*, 25(5), 2228–2258.
- Weizhen Wang, J. T. Gene Hwang, Anirban DasGupta (1999) Statistical tests for multivariate bioequivalence. *Biometrika*, 86(2), 395–402.

See Also

[confset](#) and [confints](#) for confidence boundaries; [plotMV2D](#) for confidence regions for a normal mean and variance.

Examples

```
## Not run:
# Generate bivariate normal data

mydata <- mvtnorm::rmvnorm(n=50, mean=rep(0.1, 2), sigma=diag(2) * 0.05)

# Specify axis labels

ax <- c(expression(paste(Delta, " log(AUC)")), expression(paste(Delta, " log(Cmax)")))

# Plot simultaneous 90

plot2D(dat=mydata, method="standard.ind", alpha=0.1, axnames=ax, main="Standard")
plot2D(dat=mydata, method="standard.cor", alpha=0.1, axnames=ax, main="Standard")
plot2D(dat=mydata, method="hotelling", alpha=0.1, axnames=ax, main="Hotelling")
plot2D(dat=mydata, method="limacon.asy", alpha=0.1, axnames=ax, main="Limacon")
plot2D(dat=mydata, method="limacon.fin", alpha=0.1, axnames=ax, main="Limacon")
plot2D(dat=mydata, method="tseng", alpha=0.1, axnames=ax, main="Tseng")
plot2D(dat=mydata, method="bootkern", alpha=0.1, axnames=ax, main="Bootstrap")

# Plot simultaneous 90

plot2D(dat=mydata, method="tost", alpha=0.1, axnames=ax, main="TOST")
plot2D(dat=mydata, method="expanded", alpha=0.1, axnames=ax, main="Expanded TOST")
plot2D(dat=mydata, method="fixseq", alpha=0.1, axnames=ax, main="Fixed Sequence")

## End(Not run)
```

plotMV2D

Plotting 2D confidence sets for normal mean and variance

Description

Creates graphs of (simultaneous) confidence regions for the mean and variance of a normal distribution using different methods.

Usage

```
plotMV2D(dat, n, method, alpha=0.1, scale="var", axnames=NULL,
         main="Title", xlim=NULL, ylim=NULL, col="black", steps=400)
```

Arguments

dat	A vector of numeric values assumed to follow a normal distribution. Not required for method="cheng.iles" or "min.area".
n	A numeric value giving the sample size. Only required for method="cheng.iles" or "min.area".
method	A character string specifying the method to be used. See details for available methods.

alpha	A numeric value giving the type I error level to be controlled. Default is 0.1.
scale	A character string specifying whether the variance (<code>var</code>) or standard deviation (<code>sd</code>) is to be plotted on the y axis. Not required for <code>method="cheng.iles"</code> or <code>"min.area"</code> .
axnames	A vector of two character strings giving the x and y axis labels. Default is NULL.
main	A character string giving the plot title.
xlim	A numeric vector of length two specifying the plotting range on the x-axis. Default is NULL.
ylim	A numeric vector of length two specifying the plotting range on the y-axis. Default is NULL.
col	A character string specifying the colour of the plotted region or intervals.
steps	An integer setting the initial number of steps for the search algorithm.

Details

Available methods are: `mood` for the classical region described in Mood (1950); `large` for the large-sample approximation region described in section 4.1 of Arnold & Shavelle (1998); `plugin` for a plug-in variant of the large-sample approximation region described in section 4.2 of Arnold & Shavelle (1998); `pluginF` for the plug-in variant of the large-sample approximation region described in section 4.3 of Arnold & Shavelle (1998) using an asymptotic F distribution as in Douglas (1993); `lrt` for the likelihood ratio test region described in section 4.4 of Arnold & Shavelle (1998); `cheng.iles` for the region described in Cheng & Iles (1983); `min.area` for the minimum-area region described in Frey et al. (2009).

Value

A graphical display of a (simultaneous) confidence set in two dimensions.

Note

Warning: please use with care! Some of the functionality has not yet been thoroughly tested.

Author(s)

Philip Pallmann (<p.pallmann@lancaster.ac.uk>) using code from xxxxx

References

- Barry C. Arnold & Robert M. Shaville (1998) Joint confidence sets for the mean and variance of a normal distribution. *The American Statistician*, 52(2), 133–140.
- R. C. H. Cheng & T. C. Iles (1983) Confidence bands for cumulative distribution functions of continuous random variables. *Technometrics*, 25(1), 77–86.
- J. B. Douglas (1993) Confidence regions for parameter pairs. *The American Statistician*, 47(1), 43–45.
- Jesse Frey, Osvaldo Marrero, Douglas Norton (2009) Minimum-area confidence sets for a normal distribution. *Journal of Statistical Planning and Inference*, 139(3), 1023–1032.
- Alexander M. Mood (1950) *Introduction to the Theory of Statistics*. McGraw-Hill, New York, NY.

See Also

[plot2D](#) for confidence regions and intervals around (multivariate) normal means.

Examples

```
## Not run:
# Generate normal data

mydata <- rnorm(n=50)

# Plot simultaneous 90

plotMV2D(dat=mydata, method="mood", alpha=0.1, main="Mood")
plotMV2D(dat=mydata, method="large", alpha=0.1, main="Large-sample")
plotMV2D(dat=mydata, method="plugin", alpha=0.1, main="Plug-in")
plotMV2D(dat=mydata, method="pluginF", alpha=0.1, main="Plug-in (F distribution)")
plotMV2D(dat=mydata, method="lrt", alpha=0.1, main="Likelihood ratio test")

## End(Not run)
```

wires

Quality control study of wire connections

Description

Data from a study in quality control assessing the breaking strengths of 20 wire connections between a semiconductor wafer and a terminal post (King 1971).

Usage

```
data("wires")
```

Format

A data frame with 20 observations on the following 2 variables.

Strength A numeric vector giving the strength at which the connection failed.

Failure A factor with levels b and w specifying whether the bond or wire failed.

Details

The data were taken from Table 4.1 of Nelson (1982).

Source

James R. King (1971) Probability Charts for Decision Making. Industrial Press, New York, NY.

References

Wayne B. Nelson (1982) Applied Life Data Analysis. Wiley, Hoboken, NJ.

Examples

```
data(wires)

# Simultaneous confidence regions for the mean and variance
plotMV2D(wires$Strength, method="mood", main="Mood")
plotMV2D(wires$Strength, method="lrt", main="LRT")
```

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