

Package ‘equivalence’

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Type Package

Title Provides tests and graphics for assessing tests of equivalence

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Depends lattice, boot, grid, PairedData

Description This package provides some statistical tests and graphics for assessing tests of equivalence. Such tests have similarity as the alternative hypothesis instead of the null. Sample data sets are included.

License GPL-2

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equiv.boot	<i>Regression-based TOST using bootstrap</i>
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Description

This function wraps the regression-based TOST equivalence test inside a bootstrap, extracts and reports the useful quantities, and reports the outcome of the test. The function was written for validating models, and requires paired data points. To use it for this purpose, pass the model predictions as the predictor variable, and the observations (which the predictions are intended to match) as the response variable.

Usage

```
equiv.boot(x, y, alpha = 0.05, b0.ii = 0.25, b1.ii = 0.25, reps = 100,
          b0.ii.absolute = FALSE)
```

Arguments

x	the predictor variable (commonly predictions)
y	the response variable (commonly observations)
alpha	the size of the test
b0.ii	the half-length of the region of similarity for the intercept, expressed as a proportion of the estimate or in the same units as the estimate (see b0.ii.absolute).
b1.ii	the half-length of the region of similarity for the slope, expressed as a proportion of the estimate.
reps	the number of bootstrap replicates required
b0.ii.absolute	option to express b0.ii in the same units as the estimate of the intercept.

Details

In each case, if the two one-sided confidence interval is inside the region of similarity then the null hypothesis of dissimilarity is *rejected*.

Value

A list of length 10, comprising

n	The effective (non-missing) sample size
ci.b0	The intercept TOST confidence interval
rs.b0	The intercept region of similarity
q.b0	The proportions of simulations below, within, and above, the intercept region of similarity
Test.b0	The outcome of the test of the null hypothesis of dissimilarity for the intercept (Reject/Not Reject)

ci.b1	The slope TOST confidence interval
rs.b1	The slope region of similarity
q.b1	The proportions of simulations below, within, and above, the slope region of similarity
Test.b1	The outcome of the test of the null hypothesis of dissimilarity for the slope (Reject/Not Reject)
eff.alpha	The corrected alpha for each of the two independent tests.

Acknowledgements

Feedback from Mohammad Al-Ahmadi has been very useful for this function.

Author(s)

Andrew Robinson <A.Robinson@ms.unimelb.edu.au>

References

Robinson, A.P., R.A. Duursma, and J.D. Marshall. 2005. A regression-based equivalence test for model validation: shifting the burden of proof. *Tree Physiology* 25, 903-913.

See Also

[lm](#), [boot](#), [tost](#)

Examples

```
# Approximately reproduces the first row from Table 2 of Robinson et al. (2005)

data(pref.4PG)
equiv.boot(pref.4PG$volinc4PG, pref.4PG$stemvolinc)
```

equiv.p

Inverts the regression-based TOST equivalence test

Description

This function generates the TOST intervals for the intercept and the slope of the regression of y on x, and determines the smallest region of indifference in each case that would reject the null hypothesis of dissimilarity.

Usage

```
equiv.p(x, y, alpha = 0.05)
```

Arguments

x	The predictor variable - perhaps the model predictions
y	The response variable - perhaps the observations
alpha	The size of the test

Details

The generated confidence intervals are corrected for experiment-level size of alpha using Bonferoni.

Value

A list of two items:

Intercept	The smallest half-length of the interval that leads to rejection of the null hypothesis of dissimilarity for the intercept, in the units of y.
Slope	The smallest half-length of the interval that leads to rejection of the null hypothesis of dissimilarity for the slope, in the units of the slope.

Note

The accuracy of the output of this function is contingent on the usual regression assumptions, which are not checked here. Caveat emptor!

Author(s)

Andrew Robinson <A.Robinson@ms.unimelb.edu.au>

References

- Robinson, A.P., and R.E. Froese. 2004. Model validation using equivalence tests. *Ecological Modelling* 176, 349–358.
- Robinson, A.P., R.A. Duursma, and J.D. Marshall. 2005. A regression-based equivalence test for model validation: shifting the burden of proof. *Tree Physiology* 25, 903-913.

See Also

[tost.data](#)

Examples

```
data(ufc)
equiv.p(ufc$Height.m.p, ufc$Height.m)
```

equivalence

Equivalence Tests

Description

This package provides tools to perform several equivalence tests.

Note

Recent changes: the `tost.data` function is deprecated as of version 0.5.0; please use `tost`, which provides more functionality.

Author(s)

Andrew Robinson <A.Robinson@ms.unimelb.edu.au>

References

Schuirmann, D.L. 1981. On hypothesis testing to determine if the mean of a normal distribution is contained in a known interval. *Biometrics* 37 617.

Robinson, A.P., and R.E. Froese. 2004. Model validation using equivalence tests. *Ecological Modelling* 176, 349–358.

Wellek, S. 2003. Testing statistical hypotheses of equivalence. Chapman and Hall/CRC. 284 pp.

Westlake, W.J. 1981. Response to T.B.L. Kirkwood: bioequivalence testing - a need to rethink. *Biometrics* 37, 589-594.

Examples

```
data(ufc)

### Tost

tost(ufc$Height.m.p, ufc$Height.m, epsilon = 1)

### equivalence plot

ufc.ht <- ufc[!is.na(ufc$Height),]
equivalence.xyplot(ufc.ht$Height.m ~ ufc.ht$Height.m.p,
  alpha=0.05, b0.ii=0.1, b1.ii=0.2,
  xlab="Predicted height (m)",
  ylab="Measured height (m)")
```

equivalence-deprecated

Deprecated Functions in Equivalence package

Description

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as the next release.

Usage

```
tost.data(x, null = 0, alpha = 0.05, Epsilon = 0.36, absolute = FALSE)
```

Arguments

x	the sample of paired differences
null	the value of the parameter in the null hypothesis
alpha	test size
Epsilon	magnitude of region of similarity
absolute	choose units: absolute (TRUE) or relative to the standard deviation (FALSE).

Details

The original help page for these functions is available at `help("oldName-deprecated")` (note the quotes). Functions in packages other than the base package are listed in `help("pkg-deprecated")`. `tost.data` is superseded by [tost](#).

See Also

[Deprecated](#)

equivalence.xyplot	<i>Constructs graphical regression-based tests of equivalence inside a lattice coplot</i>
--------------------	---

Description

Implements regression-based tests of equivalence within lattice graphics.

Usage

```
equivalence.xyplot(formula, alpha, b0.ii, b1.ii,
  add.smooth=FALSE, b0.absolute=FALSE, ...)
```

Arguments

formula	a formula describing the form of conditioning plot. See the manual entry for xyplot for more details.
alpha	the size of the test
b0.ii	the half-length of the region of similarity for the intercept, can be relative or absolute (see below).
b1.ii	the half-length of the region of similarity for the slope.
add.smooth	adds a loess smooth to the graph.
b0.absolute	is b0.ii in absolute or relative units?
...	extra arguments passed on to xyplot

Details

The graphic created by this function was proposed by Robinson et al. (2005) as a visual summary of the regression-based TOST. At first glance the graph will look messy; interpretation eases with practice. The following points should be noted.

- LS line: A black, solid line of best fit is added.
- Mean: A grey vertical bar indicates the mean of x and the TOST confidence interval for the intercept.
- b0 R.S.: A shaded polygon is the region of similarity of the intercept, to test the model bias.
- Test b0: If the grey vertical bar is within the shaded polygon then reject the null hypothesis of dissimilarity. This is a test of *bias*.
- ...1 -If the *region* is too low then the predictions are too low.
- ...2 -If the *region* is too high then the predictions are too high.
- ...3 -If the *region* is too narrow then the predictions are too variable.
- b1 C.I.: A black vertical bar underneath the grey bar represents a confidence interval for the slope of the line of best fit.
- b1 R.S.: Two black dashed lines are added representing the region of similarity.
- Test b1: If the black bar is within the angle described by the dashed black lines then the slope of the observed/predicted regression is significantly similar to 1. This is a test of *proportionality*.
- ...1 -If the *bar* is too high then the slope is too high; the model over-predicts the higher observations and under-predicts the lower observations.
- ...2 -If the *bar* is too low then the slope is too low; the model underpredicts the higher observations and overpredicts the lower observations (analogous to regression to the mean).
- ...3 -If the *region* is too narrow then the predictions are too variable.

The implementation in Robinson et al. (2005) required shifting so that the predictor has 0 mean. This hack has been removed here so that the basic graph object is a plot of the two variables being compared.

Value

Run for its side effect of producing a lattice plot object.

Warning

The accuracy of the output of this function is contingent on the usual regression assumptions, which are not checked here. *Caveat emptor!* Consider using `equiv.boot()` for a bootstrap-based solution. Transforming either variable will probably complicate the analysis considerably.

Acknowledgements

Feedback from Mohammad Al-Ahmadi has been very useful for this function.

Note

This version produces a regression-based TOST for each level of the conditioning factor. There may be an argument for pooling the test across these levels, in which case some prepanel computations will be helpful.

The TOST requires only estimates and standard errors from the data. Therefore the linear model used in the panel function can be replaced by any model that will produce suitable estimates. For example, in applying this function to hierarchical data we have had success using `lme()` instead.

I'm not entirely convinced that all these lines on one image are a good idea. It's straightforward to remove some, or change the colours. Recommendations for graphics that are visually cleaner are welcome.

Author(s)

Andrew Robinson <A.Robinson@ms.unimelb.edu.au>

References

Robinson, A.P., R.A. Duursma, and J.D. Marshall. 2005. A regression-based equivalence test for model validation: shifting the burden of proof. *Tree Physiology* 25, 903-913.

See Also

[tost.stat](#), [xyplot](#), [equiv.boot](#)

Examples

```
data(pref.4PG)
equivalence.xyplot(pref.4PG$stemvolinc ~ pref.4PG$volinc4PG,
  alpha=0.05, b0.ii=0.25, b1.ii=0.25, add.smooth=TRUE,
  xlab=expression(paste("4PG decadal volume growth (", m^3,
    ha^-1, decade^-1, ")", sep="")),
  ylab=expression(paste("Measured decadal volume growth (",
    m^3, ha^-1, decade^-1, ")", sep="")))

data(pref.LAI)
equivalence.xyplot(pref.LAI$lai.pa ~ pref.LAI$lai.bl,
  alpha=0.05, b0.ii=0.25, b1.ii=0.25,
  xlab=expression(paste("LAI Beer-Lambert (", m^2, m^-2, ")",
    sep="")),
```



```

ylab=expression(paste("LAI Ceptometer (", m^2, m^-2, ") ",
                      sep=""))

data(ufc)
ufc.ht <- ufc[!is.na(ufc$Height),]
equivalence.xyplot(ufc.ht$Height.m ~ ufc.ht$Height.m.p,
                  alpha=0.05, b0.ii=0.1, b1.ii=0.2,
                  xlab="Predicted height (m)",
                  ylab="Measured height (m)")

equivalence.xyplot(ufc.ht$Height.m ~ ufc.ht$Height.m.p | ufc.ht$Species,
                  alpha=0.05, b0.ii=0.1, b1.ii=0.2,
                  xlab="Predicted height (m)",
                  ylab="Measured height (m)",
                  subset=ufc.ht$Species %in%
                      levels(ufc.ht$Species)[table(ufc.ht$Species)>5])

```

pref.4PG

Measured and simulated data from PREF, northern Idaho, USA, and 4-PG

Description

These data are the juxtaposition of model output and field measurements for the Priest River Experimental Forest in northern Idaho, USA. The model was a process-based aspatial forest stand model called 4-PG, developed from 3-PG by Duursma (2004). The data were used to demonstrate a regression-based TOST in Robinson et al (2005).

Usage

```
data(pref.4PG)
```

Format

A dataset with 35 observations on 33 variables, of which the following two were used for the model validation exercise.

stemvolinc measured decadal stem growth in m^3/ha

volinc4PG predicted decadal stem growth in m^3/ha

Details

Nothing in particular. Devil's club (*Oplopanax horridus*) is very painful.

Source

The data are documented in Duursma (2004) and Robinson et al (2005).

References

Duursma, R.A. 2004. A simple process-based model of forest growth, and a test for the Priest River Experimental Forest. Ph.D. Thesis, University of Idaho, 169 p.

Robinson, A.P., R.A. Duursma, and J.D. Marshall. 2005. A regression-based equivalence test for model validation: shifting the burden of proof. *Tree Physiology* 25, 903-913

Examples

```
data(pref.4PG)
```

pref.LAI

Measured Leaf Area Index data from PREF, northern Idaho, USA

Description

These data are the juxtaposition of model output and field measurements for 36 forest plots in the Priest River Experimental Forest in northern Idaho, USA. The model was based on the Beer-Lambert model (Duursma et al. 2003). The data were used to demonstrate a regression-based TOST in Robinson et al (2005).

Usage

```
data(pref.LAI)
```

Format

A dataset with 36 observations on 8 variables, the following two of which were used for the test of equivalence:

`lai.pa` LAI as estimated using allometric functions applied to measurements of trees within the sample plot.

`lai.bl` LAI as estimated using the Beer-Lambert model from measurements of interception using a hand-held ceptometer.

Details

Nothing in particular. PREF, and northern Idaho, are very attractive.

Source

The data are documented in Duursma et al. (2003) and Robinson et al (2005).

References

Duursma, R.A., J.D. Marshall, and A.P. Robinson. 2003. Leaf area index inferred from solar beam transmission in mixed conifer forests on complex terrain. *Agricultural and Forest Meteorology* 118, 221-236.

Robinson, A.P., R.A. Duursma, and J.D. Marshall. 2005. A regression-based equivalence test for model validation: shifting the burden of proof. *Tree Physiology* 25, 903-913.

Examples

```
data(pref.LAI)
```

ptte.data	<i>Computes a paired t-test for equivalence from a single sample of a normally-distributed population</i>
-----------	---

Description

This function computes the test and key test quantities for the paired t-test for equivalence, as documented in Wellek (2003, pp 77-80). This function computes the test from a sample of a normally-distributed population.

Usage

```
ptte.data(x, alpha = 0.05, Epsilon = 0.25)
```

Arguments

x	paired differences
alpha	test size
Epsilon	magnitude of region of similarity

Details

This test requires the assumption of normality of the population. Under that assumption the test is the uniformly most powerful invariant test (Wellek, 2003, pp. 78-79).

The function as documented by Wellek (2003) uses units relative to the standard deviation, noting (p. 12) that 0.25 corresponds to a strict test and 0.5 to a liberal test.

Value

A list with the following components

Dissimilarity	the outcome of the test of the null hypothesis of dissimilarity
Mean	the mean of the sample
StdDev	the standard deviation of the sample
n	the sample size
alpha	the size of the test
missing	the number of observations missing
Epsilon	the magnitude of the region of similarity
cutoff	the critical value
Tstat	the test statistic; if Tstat < cutoff then the null hypothesis is rejected.
Power	the power of the test evaluated at the observed value

Note

This test requires the assumption of normality of the population. Under that assumption the test is the uniformly most powerful invariant test (Wellek, 2003, pp. 78-79). The exposition in Robinson and Froese (2004) mistakenly omits the square root of the F-quantile.

Author(s)

Andrew Robinson<A.Robinson@ms.unimelb.edu.au>

References

Robinson, A.P., and R.E. Froese. 2004. Model validation using equivalence tests. *Ecological Modelling* 176, 349–358.

Wellek, S. 2003. *Testing statistical hypotheses of equivalence*. Chapman and Hall/CRC. 284 pp.

See Also

[ptte.stat](#), [tost.data](#)

Examples

```
data(ufc)
ptte.data(ufc$Height.m.p - ufc$Height.m)
```

ptte.stat

Computes a paired t-test for equivalence from the mean and standard deviation of a sample from a normally-distributed population

Description

This function computes the test and key test quantities for the paired t-test for equivalence, as documented in Wellek (2003, pp 77-80). This function computes the test from the mean and standard deviation of a sample of paired differences from a normally-distributed population.

Usage

```
ptte.stat(mean, std, n, alpha = 0.05, Epsilon = 0.25)
```

Arguments

mean	the sample mean
std	the sample standard deviation
n	sample size
alpha	test size
Epsilon	magnitude of region of similarity

Details

This test requires the assumption of normality of the population. Under that assumption the test is the uniformly most powerful invariant test (Wellek, 2003, pp. 78-79). This version of the test can be applied post-hoc to any testing situation in which you have the mean, standard deviation, and sample size, and are confident that the sample is drawn from a normally-distributed population.

The function as documented by Wellek (2003) uses units relative to the standard deviation, noting (p. 12) that 0.25 corresponds to a strict test and 0.5 to a liberal test.

Value

A list with the following components

Dissimilarity	the outcome of the test of the null hypothesis of dissimilarity
Mean	the mean of the sample
StdDev	the standard deviation of the sample
n	the sample size
alpha	the size of the test
Epsilon	the magnitude of the region of similarity
cutoff	the critical value
Tstat	the test statistic; if Tstat < cutoff then the null hypothesis is rejected.
Power	the power of the test evaluated at the observed value

Note

The exposition in Robinson and Froese (2004) mistakenly omits the square root of the F-quantile.

Author(s)

Andrew Robinson <A.Robinson@ms.unimelb.edu.au>

References

Robinson, A.P., and R.E. Froese. 2004. Model validation using equivalence tests. *Ecological Modelling* 176, 349–358.

Wellek, S. 2003. *Testing statistical hypotheses of equivalence*. Chapman and Hall/CRC. 284 pp.

See Also

[ptte.data](#), [tost.stat](#)

Examples

```
data(ufc)
ptte.stat(mean(ufc$Height.m.p - ufc$Height.m, na.rm=TRUE),
          sd(ufc$Height.m.p - ufc$Height.m, na.rm=TRUE),
          sum(!is.na(ufc$Height.m.p - ufc$Height.m)))
```


result	the outcome of the test of the null hypothesis of dissimilarity
p.value	the p-value of the significance test
check.me	the confidence interval corresponding to the p-value

Note

This test is the `tost` for equivalence (`tost` equivalence) wrapped around the robust, trimmed mean, winsorized variance `yuen.t.test` (`yuen PairedData`).

Author(s)

Gregory Belenky <belenky@wsu.edu>

References

- Schuirmann, D.L. 1981. On hypothesis testing to determine if the mean of a normal distribution is contained in a known interval. *Biometrics* 37, 617.
- Robinson, A.P., and R.E. Froese. 2004. Model validation using equivalence tests. *Ecological Modelling* 176, 349–358.
- Wellek, S. 2003. Testing statistical hypotheses of equivalence. Chapman and Hall/CRC. 284 pp.
- Westlake, W.J. 1981. Response to T.B.L. Kirkwood: bioequivalence testing - a need to rethink. *Biometrics* 37, 589-594.
- Yuen, K.K. (1974) The two-sample trimmed t for unequal population variances. *Biometrika*, 61, 165-170.
- Yuen, K.K., and Dixon, W.J. (1973) The approximate behavior and performance of the two-sample trimmed t. *Biometrika*, 60, 369-374.

See Also

[tost](#), [yuen.t.test](#)

Examples

```
data(ufc)
rtost(ufc$Height.m.p, ufc$Height.m, epsilon = 1, tr = 0.2)
```

tost

Computes a TOST for equivalence from paired or unpaired data

Description

This function computes the test and key test quantities for the two one-sided test for equivalence, as documented in Schuirmann (1981) and Westlake (1981). This function computes the test for a sample of paired differences or two samples, assumed to be from a normally-distributed population.

Usage

```
tost(x, y = NULL, alpha = 0.05, epsilon, ...)
```

Arguments

x	the first (or only) sample
y	the second sample
alpha	test size
epsilon	magnitude of region of similarity
...	arguments to be passed to <code>t.test</code>

Details

This test requires the assumption of normality of the population, or an invocation of large-sample theory. The function wraps around the `t.test` function, so it provides `tosts` for the same range of designs, accepts the same arguments, and handles missing values the same way.

Value

A list with the following components

<code>mean.diff</code>	the mean of the difference
<code>se.diff</code>	the standard error of the difference
<code>alpha</code>	the size of the test
<code>ci.diff</code>	the 1-alpha confidence interval for the difference
<code>df</code>	the degrees of freedom used for the confidence interval
<code>epsilon</code>	the magnitude of the region of similarity
<code>result</code>	the outcome of the test of the null hypothesis of dissimilarity
<code>p.value</code>	the p-value of the significance test
<code>check.me</code>	the confidence interval corresponding to the p-value

Note

This test requires the assumption of normality of the population. The components of the test are t-based confidence intervals, so the Central Limit Theorem and Slutsky's Theorem may be relevant to its application in large samples.

Author(s)

Andrew Robinson <A.Robinson@ms.unimelb.edu.au>

References

- Schuirmann, D.L. 1981. On hypothesis testing to determine if the mean of a normal distribution is contained in a known interval. *Biometrics* 37 617.
- Robinson, A.P., and R.E. Froese. 2004. Model validation using equivalence tests. *Ecological Modelling* 176, 349–358.
- Wellek, S. 2003. Testing statistical hypotheses of equivalence. Chapman and Hall/CRC. 284 pp.
- Westlake, W.J. 1981. Response to T.B.L. Kirkwood: bioequivalence testing - a need to rethink. *Biometrics* 37, 589-594.

See Also

[tost.stat](#), [ptte.data](#)

Examples

```
data(ufc)
tost(ufc$Height.m.p, ufc$Height.m, epsilon = 1)
```

tost.stat

Computes a TOST for equivalence from sample statistics

Description

This function computes the test and key test quantities for the two one-sided test for equivalence, as documented in Schuirmann (1981) and Westlake (1981). This function computes the test from the statistics of a sample of paired differences of a normally-distributed population.

Usage

```
tost.stat(mean, std, n, null = 0, alpha = 0.05, Epsilon = 0.36)
```

Arguments

mean	sample mean
std	sample standard deviation
n	sample size
null	the value of the parameter in the null hypothesis
alpha	test size
Epsilon	magnitude of region of similarity

Details

This test requires the assumption of normality of the population.

Value

A list with the following components

Dissimilarity	the outcome of the test of the null hypothesis of dissimilarity
Mean	the mean of the sample
StdDev	the standard deviation of the sample
n	the non-missing sample size
alpha	the size of the test
Epsilon	the magnitude of the region of similarity
Interval	the half-length of the two one-sided interval

Note

This test requires the assumption of normality of the population. The components of the test are t-based confidence intervals, so the Central Limit Theorem and Slutsky's Theorem may be relevant to its application in large samples.

Author(s)

Andrew Robinson <A.Robinson@ms.unimelb.edu.au>

References

- Schuurmann, D.L. 1981. On hypothesis testing to determine if the mean of a normal distribution is contained in a known interval. *Biometrics* 37 617.
- Wellek, S. 2003. Testing statistical hypotheses of equivalence. Chapman and Hall/CRC. 284 pp.
- Westlake, W.J. 1981. Response to T.B.L. Kirkwood: bioequivalence testing - a need to rethink. *Biometrics* 37, 589-594.

See Also

[tost.data](#), [ptte.stat](#)

Examples

```
data(ufc)
tost.stat(mean(ufc$Height.m.p - ufc$Height.m, na.rm=TRUE),
          sd(ufc$Height.m.p - ufc$Height.m, na.rm=TRUE),
          sum(!is.na(ufc$Height.m.p - ufc$Height.m)))
```

ufc

Upper Flat Creek cruise data

Description

These are forest measurement data from the Upper Flat Creek unit of the University of Idaho Experimental Forest, measured in 1991. The inventory was based on variable radius plots with 6.43 sq. m. per ha. BAF (Basal Area Factor). The forest stand was 121.5 ha.

Usage

`data(ufc)`

Format

A data frame with 633 observations on the following 12 variables.

Plot plot label

Tree tree label

Species species kbd

Dbh tree diameter at 1.37 m. from the ground, measured in millimetres.

Height tree height measured in decimetres

Height.ft tree height converted to feet

Dbh.in tree diameter converted to inches

Height.ft.p predicted tree height in feet

Height.m tree height in metres

Height.m.p predicted tree height in metres

Details

Plots that were measured with no trees are signified in the dataset by lines that have blank species codes and missing DBH.

Source

The data are provided courtesy of Harold Osborne and Ross Appelgren of the University of Idaho Experimental Forest. The predicted height comes from the height/diameter model documented in Wykoff et al. (1982). The data and model were used in Robinson et al. (2005).

References

- Robinson, A.P., R.A. Duursma, and J.D. Marshall. 2005. A regression-based equivalence test for model validation: shifting the burden of proof. *Tree Physiology* 25, 903-913.
- Wykoff, W.R., N.L. Crookston, and A.R. Stage. 1982. User's guide to the stand Prognosis model. GTR-INT 133, USDA Forest Service, Intermountain Research Station, Ogden, UT, 113 p.

Examples

```
data(ufc)
```

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