

# Package ‘lmfor’

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**Description** Functions for different purposes related to Forest biometrics, including illustrative graphics, numerical computation, modeling height-diameter relationships, prediction of tree volumes, modelling of diameter distributions and estimation off stand density using ITD. Several empirical datasets are also included.

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Imfor-package	<i>Functions of Lauri Mehtatalo</i>
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## Description

Functions for different purposes related to Forest biometrics, including illustrative graphics, numerical computation, modeling height-diameter relationships, prediction of tree volumes, modeling of diameter distributions and estimation off stand density using ITD. Several empirical datasets are also included.

## Details

Package:	Imfor
Type:	Package
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## Author(s)

Lauri Mehtatalo <lauri.mehtatalo@uef.fi>

## References

Mehtatalo, L. and Lappi, J. forthcoming. Forest Biometrics with examples in R. Textbook in preparation. Available at <http://cs.uef.fi/~lamehtat/>.

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afterthin

*Increment core data of Scots pine trees*

---

### Description

Post-thinning growth ring measurements of 88 trees of a long-term thinning experiment on a naturally regenerated Scots pine stand in Eastern Finland.

### Usage

```
data(afterthin)
```

### Format

A data frame with 1319 observations on the following 7 variables.

Plot Sample plot id, a factor with 10 levels.

Tree Tree id, a factor with 55 levels (same tree id may occur on different plots!).

Year Calendar year of the ring.

SDAfterThin Stand density (trees per ha) of the sample plot.

SDClass Thinning treatment, factor with 4 levels (1=Control, 2=Light, 3=Moderate, 4=Heavy).

CA Current tree age in years.

RBA Ring Basal area,  $mm^2$

### Details

Long-term thinning experiment on a naturally regenerated Scots pine stand in Eastern Finland. The experiment consists of 10 sample plots, in four different classes according to the post-thinning stand density. The plots were thinned in winter 1986-1987. In winter 2006 -2007, 10 trees were felled from each plot. A radial 5mm by 5mm segment from pith to bark was cut from each tree at height 1.3 meter height. Ring widths from pith to bark were analyzed for each sample, using an ITRAX X-ray microdensitometer and post-processed to create ring widths from pith to bark were determined for each disc. The ring widths were further transformed to ring basal areas by assuming circular growth rings. For 12 trees, ring widths could not be extracted. The data includes ring widths for a total of 88 trees between years 1991-2005. The original data is available in data set [patti](#).

### References

Mehtatalo, L., Peltola, H., Kilpelainen, A. and Ikonen, V.-P. 2014. The response of basal area growth of Scots pine to thinning: A longitudinal analysis of tree-specific series using a nonlinear mixed-effects model. *Forest Science* 60 (4): pp. 636-644. DOI: <http://dx.doi.org/10.5849/forsci.13-059>.

### See Also

[patti](#).

**Examples**

```

data(afterthin)
par(mfcol=c(2,1),cex=0.7,mai=c(0.8,0.8,0.5,0.1))
linesplot(afterthin$CA,
  afterthin$RBA,
  group=afterthin$Plot:afterthin$Tree,
  col.lin=as.numeric(afterthin$SDClass),cex=0,
  xlab="Tree age",
  ylab=expression("Ring basal area, " *mm^2))

linesplot(afterthin$Year,
  afterthin$RBA,
  group=afterthin$Plot:afterthin$Tree,
  col.lin=as.numeric(afterthin$SDClass),cex=0,
  xlab="Year",
  ylab=expression("Ring basal area, " *mm^2))

```

---

alsTree

*Individual tree characteristics and ALS data*


---

**Description**

Field-measured and remotely sensed characteristics of 1510 individual Scots Pine trees from 56 sample plots in Kiihtelysvaara, Eastern Finland.

**Usage**

```
data(alsTree)
```

**Format**

A data frame with 1510 observations on the following 15 variables.

plot Sample plot id, integer

tree Tree id, integer

DBH Tree diameter at breast height, cm

H Tree height, m

V Tree volume, m<sup>2</sup>)

HDB Height of lowest dead branch, m

HCB Crown base height, m

hmax Maximum return height, m

h20 20th percentile of return heights within the tree crown, m

h30 30th percentile of return heights within the tree crown, m

h70 70th percentile of return heights within the tree crown, m

h80 80th percentile of return heights within the tree crown, m

a\_hmean Mean height of returns in the 250m<sup>2</sup> neighbourhood of the tree, m  
 a\_veg Proportion of returns from vegetation in the 250m<sup>2</sup> neighbourhood of the tree, m  
 a\_h30 30th percentile of returns in the 250m<sup>2</sup> neighbourhood around the tree, m  
 a\_h70 70th percentile of returns in the 250m<sup>2</sup> neighbourhood around the tree, m

### Details

Field measurements of tree diameter and height, height of dead branch and crown base height and tree location were taken from the trees in a field campaign. Volume was estimated based on diameter, height and upper stem diameter. In addition, the area was remotely sensed using airborne laser scanning. Detectable individual trees were delineated from the ALS point cloud and associated with the field measurements. From a large set of tree-specific ALS characteristics, the data includes those that were used in the final models of stand characteristics in Maltamo et al (2012).

### References

Maltamo, M., Mehtatalo, L., Vauhkonen, J. and Packalen, P. 2012. Predicting and calibrating tree attributes by means of airborne laser scanning and field measurements. Canadian Journal of Forest Research 42: 1896-1907

### Examples

```
data(alsTree)
```

---

circle	<i>Plot circles of a specified radius</i>
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### Description

Adds circles of radii *r* at coordinates specified by *x* and *y* onto an existing plot.

### Usage

```
circle(x,y,r,border="black",lty="solid",lwd=1,fill=NULL)
```

### Arguments

<i>x</i> , <i>y</i> , <i>r</i>	Vectors of the <i>x</i> - and <i>y</i> - coordinates of the midpoints and the associated radii. Vectors <i>x</i> , <i>y</i> and <i>r</i> should be of the same length
<i>border</i> , <i>lty</i> , <i>lwd</i>	the draving color, line type and line width of the perimeter line. Use <i>border</i> =NA to omit the perimeter.
<i>fill</i>	The color used to fill the circles. <i>fill</i> =NULL does not fill at all.

### Value

This function is used for its side effects on the graphical display.

**Author(s)**

Lauri Mehtatalo

**Examples**

```
plot(0,type="n",xlim=c(-2,12),ylim=c(-2,12))
#Plot on average 7 tree crowns of Weibull-distributed radius at random locations
n<-rpois(1,7)
circle(x=runif(n,0,10),
       y=runif(n,0,10),
       r=rweibull(n,6,2))
```

ddcomp

*Evaluate the fit of a tree diameter distribution***Description**

A function to compare the fit of the observed tree diameter data (d) to a specified diameter distribution (density).

**Usage**

```
ddcomp(d,density="dweibull",power=0,limits=seq(0,100),limitsd=limits,plot=FALSE,...)
```

**Arguments**

d	numeric vector of observed diameters
density	either a valid name for a probability density function in R or a vector of diameter class densities for diameter classes whose limits are given in vector limitsd
power	gives the weights (2 gives BA weight, 0 (default) the unweighted)
limits	the diameter class limits to compute the error index
limitsd	see the description of argument density
plot	logical. Should a graph be produced to illustrate the ecdf of d and the cdf corresponding to density
...	additional arguments passed to function specified by a character-type density. e.g. Weibull shape and scale of if density="dweibull"

**Details**

The comparison is first done for mean, variance and standard deviation. Thereafter, a location switch and rescaling is done to the predicted density so that it has exactly same mean and variance as the given diameter data, but the shape is not changed. The shape is thereafter compared by computing the sum of absolute differences (error index) in densities for the observed data and rescaled density in diameter classes specified by "limits". The error index has therefore a value between 0 (complete match) and 2 (complete mismatch).

**Value**

A list of components

mudif	The difference in means
vardif	The difference in variances
sddif	The difference in standard deviations
errorindex	the error index (see details)

**Author(s)**

Lauri Mehtatalo

**Examples**

```
# Example
# Observed diameters
d<-c(18.8,24.2,18.7,13.0,18.9,22.4,17.6,22.0,18.8,22.9,
     16.7,13.7,20.6,15.1,31.8,17.2,19.6,16.8,19.3,27.4,
     23.7,18.2,19.7,18.9,23.0,21.4,23.8,22.1,24.2,20.9)

# Weibull(5,20) distribution in 1 cm classes (class limits from 0,...,60)
f<-pweibull(1:60,5,20)-pweibull(0:59,5,20)

# compare using the classified true distribution (approximate)
ddcomp(d,density=f,limitsd=0:60,limits=0:100,plot=TRUE)

# compare b specifying a Weibull dsitribution (accurate)
ddcomp(d,density="dweibull",shape=5,scale=20,plot=TRUE)
```

---

fithd	<i>Fit a Height-Diameter model to forest tree data using functions of package nlme.</i>
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---

**Description**

Fits either linear or nonlinear Height-Diameter (H-D) model into a dataset of tree heights and diameters. Possible hierarchy of the data can be taken into account through random effects. Several commonly used nonlinear two-parameter H-D functions are available. Linear functions can be used as well.

**Usage**

```
fithd(d, h, plot=c(), modelName="naslund", nranp=2,
      random=NA, varf=0, na.omit=TRUE, start=NA, bh=1.3,
      control = list(), SubModels=NA, vfstart=0)
```

**Arguments**

d	A numerical vector of tree diameters, usually given in cm.
h	A numerical vector of tree heights, usually given in meters. Should be of the same length as d.
plot	A vector of type <code>numeric</code> or <code>factor</code> , defining the groups of the data; usually the plot indices. Should be of the same length as d and h.
modelName	Either (i) a character vector specifying the name of the nonlinear function or (ii) the formula specifying a linear model. In case (i) the name should be one of the functions documented on the help page of <a href="#">HDmodels</a> . In case (ii), it should be the linear formula in the form that is entered to the function <a href="#">lme</a> , for example <code>model=h~d+I(d^2)-1</code>
nranp, random	Parameters <code>nranp</code> and <code>random</code> specify two alternative ways to specify the random effects of the model. An easy but restricted way is to use argument <code>nranp</code> . It is an integer between 0 and the number of fixed parameters, and has the the following meaning in the case of nonlinear model: <ul style="list-style-type: none"> <li>• If <code>nranp=0</code>, then a model without random parameters is fitted. Results to a fixed-effects model, and argument <code>plot</code> is not used.</li> <li>• If <code>nranp=1</code>, then parameter <code>a</code> of a nonlinear function or the first coefficient of the linear formula is assumed to vary among plots.</li> <li>• If <code>nranp=2</code>, then <code>a</code> and <code>b</code> or the first two terms of the linear formula are assumed to vary among plots or</li> <li>• If <code>nranp=3</code>, then <code>a</code>, <code>b</code>, and <code>c</code> of a three-parameter nonlinear model or three first coefficients of a linear model are assumed to vary among plots</li> </ul> <p>In the case of linear model, the constant (if exists) it always counted as the first term.</p> <p>As an alternative to <code>nranp</code>, argument <code>random</code> can be used to express the random part as a <code>nlme</code> formula, but without specification of the grouping structure. The provided formula is passed to the <code>lme</code> or <code>nlme</code> function. Argument <code>random</code> is always used when provided, so <code>nranp</code> has effect only if <code>random=NA</code> (the default).</p>
varf	Numeric with values 0, 1 or 2. If 0 or <code>FALSE</code> , no variance function is used. If <code>varf=1, 2</code> or <code>TRUE</code> , then the power- type variance function $\text{var}(e)=\sigma^2*w^{(2*\delta)}$ is used. where weight <code>w</code> is the raw diameter (when <code>varf=1</code> or <code>TRUE</code> ), or $w=\max(1, \text{dsd}+3)$ (when <code>varf=2</code> ), where $\text{dsd}=(d-D)/SDD$ . Here <code>d</code> is tree diameter, <code>D</code> and <code>SDD</code> are the mean and standard deviation of diameters on the plot in question.
na.omit	Should missing heights be omitted. Defaults to <code>TRUE</code> .
start	A vector of the starting values of the parameters of the <code>nlme</code> fit. If <code>NA</code> , then the starting values are computed using the function computing the starting values (e.g., <code>startHDnaslund</code> , see <a href="#">HDmodels</a> ).
bh	The applied breast height. Defaults to 1.3 (meters).
control	Parameters to control of the model fitting algorithm, see <a href="#">nlmeControl</a> for details.
SubModels	Implemented only for nonlinear models. A character vector of length 2 or 3, according to the number of parameters in the model. It allows submodels for parameters <code>a</code> , <code>b</code> (and <code>c</code> ), where the parameter is explained by plot-specific mean



diameter (" $\sim$ dmean"), plot-specific standard deviation " $\sim$ dsd", or diameter standardized at plot level (" $\sim$ dstd"), when the predictor is (d-D)/SDD (see the documentation of argument varf). Defaults to NA, which corresponds to no submodels, or submodels=c(" $\sim$ 1", " $\sim$ 1", "1")

vfstart Starting value of the power parameter delta of the variance function. Defaults to 0.

### Details

Depending on the model (nonlinear or linear, mixed-effects model or marginal), the the model is fitted using one of the following functions functions of the nlme package: nlme, lme, gls or gnls.

See available H-D functions at [HDmodels](#). The user can define her own new functions as specified at [HDmodels](#).

### Value

An object of class hmod, inheriting from class nlme.

### Author(s)

Lauri Mehtatalo

### References

Mehtatalo, L., Gregoire, T.G., and de Miguel, S. Modeling Height-diameter curves for height prediction. Manuscript.

Mehtatalo, L. 2004. A longitudinal height-diameter model for Norway spruce in Finland. Canadian Journal of Forest Research 34(1): 131-140.

Mehtatalo, L. 2005. Height-diameter models for Scots pine and birch in Finland. Silva Fennica 39(1): 55-66.

### See Also

[HDmodels](#) for the available functions, Functions [nlme](#), [lme](#), [gls](#) or [gnls](#) for details on model fitting, [ImputeHeights](#) for imputing unobserved tree heights.

### Examples

```
data(spati)

fithd(spati$d,spati$h,spati$plot)
fithd(spati$d,spati$h,spati$plot,SubModels=c("dmean", "log(dmean)"),varf=2)
```

foto

*CO<sub>2</sub> exchange of transplanted Sphagnum fuscum moss in a chronosequence of mires.*

### Description

The net carbon dioxide exchange of late successional moss species (*Sphagnum fuscum*) samples under seven levels of photosynthetic photon flux density in chronosequence of land uplift mires on the Finnish side of Bothnia Bay in Siikajoki, Finland. Moss samples were transplanted from the late succession site (Site 6) to all sites and photosynthetic activity was measured one year later for those samples which had survived.

### Usage

data(foto)

### Format

A data frame with 455 observations on the following 8 variables.

Site a factor with levels 1,...,6 from the earliest successional stage to the latest

Treatment a factor with value 1 for samples with competitor removal treatment and 0 for untreated control.

sample a factor with unique value for each of the 72 survived samples

moisture moisture of the sample

PARtop Photosynthetically active radiation (photon flux density  $\mu\text{mol}/\text{m}^2/\text{s}^2$ )

WT water table, cm

A Net CO<sub>2</sub> exchange,  $\mu\text{mol}/\text{g}/\text{h}$ ,

subplot a factor with unique value for each replicate

### Details

The number of transplanted replicates per site was 12, with two samples per replicate. One of the samples was treated with competing vegetation removal before transplanting whereas the other was left untreated. The 12 replicates per site were planted in locations with 2 to 3 different ground water table levels. A year after the transplanting, the photosynthetic activity (A) of the survived transplanted samples was recorded using seven artificially created light conditions ranging from complete darkness (PPFD=0) to extreme light conditions (PPFD=2000) using an open, fully controlled flow-through gas exchange fluorescence measurement system (GFS-3000; Walz, Effeltrich, Germany).

### References

Laine, A.M., Ehonen, S., Juurola, E., Mehtatalo, L., and Tuittila, E-S. 2015. Performance of late succession species along a chronosequence: Environment does not exclude *Sphagnum fuscum* from the early stages of mire development. *Journal of Vegetation Science* 26(2): 291-301. DOI: 10.1111/jvs.12231

**Examples**

```

data(foto)

LightResp<-function(PPFD,alpha=0.1,Pmax=10,A0=0) {
  A0+Pmax*PPFD/(alpha+PPFD)
}

library(nlme)

model5<-nlme(A~LightResp(PARtop,alpha,Pmax,A0),
fixed=list(alpha~Site+Treatment+moisture,Pmax~Site+Treatment,A0~Site),
random=list(sample=Pmax+alpha~1),
data=foto,
start=c(c(80,0,0,0,0,0,0,0),c(100,0,0,0,0,0,0),c(-20,0,0,0,0,0)),
verbose=TRUE)

```

---

HD models

*Available 2- and 3- parameter H-D model functions to be used by function fithd.*


---

**Description**

Nonlinear functions for modeling tree height on diameter. Usually called using `fithd`.

**Usage**

```

HDnaslund(d, a, b, bh=1.3)
HDcurtis(d, a, b, bh=1.3)
HDmichailoff(d, a, b, bh=1.3)
HDmeyer(d, a, b, bh=1.3)
HDpower(d, a, b, bh=1.3)
HDnaslund2(d, a, b, bh=1.3)
HDnaslund3(d, a, b, bh=1.3)
HDnaslund4(d, a, b, bh=1.3)
HDmicment(d, a, b, bh=1.3)
HDmicment2(d, a, b, bh=1.3)
HDwykoff(d, a, b, bh=1.3)

HDprodan(d, a, b, c, bh=1.3)
HDlogistic(d, a, b, c, bh=1.3)
HDrichards(d, a, b, c, bh=1.3)
HDweibull(d, a, b, c, bh=1.3)
HDgomperz(d, a, b, c, bh=1.3)
HDSibbesen(d, a, b, c, bh=1.3)
HDkorf(d, a, b, c, bh=1.3)
HDratkowsky(d, a, b, c, bh=1.3)
HDhossfeldIV(d, a, b, c, bh=1.3)

```

```

startHDnaslund(d, h, bh=1.3)
startHDcurtis(d, h, bh=1.3)
startHDmichailoff(d, h, bh=1.3)
startHDMeyer(d, h, bh=1.3)
startHDPower(d, h, bh=1.3)
startHDnaslund2(d, h, bh=1.3)
startHDnaslund3(d, h, bh=1.3)
startHDnaslund4(d, h, bh=1.3)
startHDMicment(d, h, bh=1.3)
startHDMicment2(d, h, bh=1.3)
startHDwykoff(d, h, bh=1.3)

startHDprodan(d, h, bh=1.3)
startHDlogistic(d, h, bh=1.3)
startHDRichards(d, h, bh=1.3, b=0.04)
startHDweibull(d, h, bh=1.3)
startHDgomperz(d, h, bh=1.3)
startHDSibbesen(d, h, bh=1.3, a=0.5)
startHDKorf(d, h, bh=1.3)
startHDratkowsky(d, h, bh=1.3, c=5)
startHDhossfeldIV(d, h, bh=1.3, c=5)

```

### Arguments

d	A vector of tree diameters, usually in cm
h	A vector of tree heights, usually in m. The observed heights should be always above or equal to bh.
a, b, c	Parameters a, b (and c for 3- parameter functions) of the applied function. See details for expressions of different functions.
bh	The applied height for the measurement of tree diameter (so called breast height). Of the same unit as h.

### Details

The available 2- parameter functions are

- Naslund:  $h(d) = bh + \frac{d^2}{(a+bd)^2}$
- Curtis:  $h(d) = bh + a \left( \frac{d}{1+d} \right)^b$
- Michailoff:  $h(d) = bh + ae^{-bd^{-1}}$
- Meyer:  $h(d) = bh + a(1 - e^{-bd})$
- Power:  $h(d) = bh + ad^b$
- Naslund2:  $h(d) = bh + \frac{d^2}{(a+e^b d)^2}$
- Naslund3:  $h(d) = bh + \frac{d^2}{(e^a + bd)^2}$

- Naslund4:  $h(d) = bh + \frac{d^2}{(e^a + e^b d)^2}$
- Michaelis-Menten:  $h(d) = bh + \frac{ad}{b+d}$
- Michaelis-Menten2:  $h(d) = bh + \frac{d}{a+b*d}$
- Wykoff:  $h(d) = bh + \exp\left(a + \frac{b}{d+1}\right)$

The available 3- parameter functions are

- Prodan:  $h(d) = bh + \frac{d^2}{a+bd+cd^2}$
- Logistic:  $h(d) = bh + \frac{a}{1+be^{-cd}}$
- Chapman-Richards:  $h(d) = bh + a(1 - e^{-bd})^c$
- Weibull:  $h(d) = bh + a(1 - e^{-bd^c})$
- Gompertz:  $h(d) = bh + a \exp(-b \exp(-cd))$
- Sibbesen:  $h(d) = bh + ad^{bd^{-c}}$
- Korf:  $h(d) = bh + a \exp(-bd^{-c})$
- Ratkowsky:  $h(d) = bh + a \exp\left(\frac{-b}{d+c}\right)$
- Hossfeld IV:  $h(d) = bh + \frac{a}{1+\frac{1}{bd^c}}$

For each model, two functions are provided: one computing the value of the H-D model for given diameters using given values of parameters a, b (and c), and another returning the initial guesses of a, b (and c) for given h-d data.

The initial guesses are in most cases computed by fitting a linearized version of the model into the provided h-d data using `lm`. For some 3- parameter versions, no straightforward linearization is possible and one of the parameters is set to a fixed sensible constant. Those values can be seen as additional arguments in the corresponding `startHD` - functions. Details can be seen directly from the function definitions.

The user can define her own functions to be used with `fithd`. The case-sensitive naming of the functions should follow exactly the naming convention shown above. In addition, the names of the of arguments, as well as their order, should be the same as in the functions above.

The models are named according to references in

- Zeide, B. 1993. Analysis of growth equations. *Forest Science* 39(3):594-616.
- Huang, S., Titus, S.J., and Wiens, D.P. 1992. Comparison of nonlinear height-diameter function for major Alberta tree species. *Can J. For. Res.* 22: 1297-1304.

Suggestions on naming and references on the functions are welcome.

### Value

For functions `HDxxx`, a vector of tree heights corresponding diameters `d` is returned. For functions `startHDxxx`, a named vector of initial estimates of a, b and (c).

### Author(s)

Lauri Mehtatalo lauri.mehtatalo@uef.fi

## References

Mehtatalo, L., de Miguel, S. and Gregoire, T.G. Modeling Height-diameter curves for prediction. Canadian Journal of Forest Research, 45(7): 826-837, 10.1139/cjfr-2015-0054.

## Examples

```
data(spati)
theta<-startHDnaslund(spati$d,spati$h)
plot(spati$d,spati$h)
d<-seq(0,50)
lines(d,HDnaslund(d,a=theta[1],b=theta[2]),col="red",lwd=5)
```

---

HTest

*Estimate stand density using a Horvitz–Thompson-like estimator*


---

## Description

HTest calculates the Horvitz–Thompson-like stand density estimate (number of trees) in a specified area based on a collection of detected trees.

area\_esh is an internal function for surface area calculations that can handle empty sets.

gg\_wind is an internal function that forms a union of discs based on their center points and radii.

## Usage

```
HTest(treelist, plotwindow, alpha)
```

```
area_esh(W)
```

```
gg_wind(treelist)
```

## Arguments

treelist	A 3-column matrix containing the x and y coordinates of detected trees and their crown radii.
plotwindow	A spatstat object of class "owin", representing the area where stand density estimation is done.
alpha	A tuning parameter that controls the calculation of detection probabilities, or detectabilities. Must have a value from -1 to 1.
W	A spatstat object of class "owin" or NULL.

## Details

HTest is the Horvitz–Thompson-like stand density estimator presented by Kansanen et al. (2016) to adjust individually detected trees for non-detection. It uses individual tree detection data, namely the locations and crown radii of detected trees, to calculate detection probabilities, or detectabilities, for every detected tree, and produces an estimate based on the detectabilities. The detectability for a certain tree is based on the planar set formed by the larger trees. The parameter alpha controls how easy it is to detect a tree of certain size from under the larger trees. If alpha=1, then the tree will be detected if it is not fully covered by the larger crowns. If alpha=0, the tree will be detected if its center point is not covered. If alpha=-1, the tree will be detected if it is fully outside the larger tree crowns.

The object `treelist` can include trees that are not in the estimation area specified by `plotwindow`. This can be useful to take into account possible edge effects, by including trees with center points outside `plotwindow` that have crown discs that intersect `plotwindow`. The estimate is calculated only using those trees that have crown center points in `plotwindow`.

`area_esh` and `gg_wind` are internal helper functions used by HTest. First one is a shell for the `spatstat` function `area.owin` that takes into account that an intersection of two sets can be empty, represented in the calculations as NULL. The function returns 0 in this case. Otherwise, it returns the surface area of the window `W`. The latter function forms a union of discs that is needed in the detectability calculations.

## Value

HTest returns a list with two components:

N	The estimated number of trees in <code>plotwindow</code>
<code>treelist</code>	matrix with columns "r" and "detectability", giving the tree crown radii that have been used in the estimation, as well as the detectabilities for trees with those crown radii.

`area_esh` returns 0, if `W` is NULL; otherwise, the surface area of `W`.

`gg_wind` returns a `spatstat` object of class "owin" representing a set formed as a union of discs.

## Note

These functions require the package `spatstat` (Baddeley et al. 2015) to work.

## Author(s)

Kasper Kansanen, [kasperkansanen@gmail.com](mailto:kasperkansanen@gmail.com)

## References

Kansanen, K., Vauhkonen, J., Lahivaara, T., and Mehtatalo., L. (2016) *Stand density estimators based on individual tree detection and stochastic geometry*. Canadian Journal of Forest Research 46(11):1359–1366. <http://dx.doi.org/10.1139/cjfr-2016-0181>.

Baddeley, A., Rubak, E. and Turner, R. (2015) *Spatial Point Patterns: Methodology and Applications with R*. Chapman and Hall/CRC Press, London. <http://www.crcpress.com/Spatial-Point-Patterns-Methodology-and-Applications-with-R/Baddeley-Rubak-Turner/9781482210200/>

Kansanen, K., Packalen, P., Lahivaara, T., Seppanen, A., Vauhkonen, J., Maltamo, M., and Mehtatalo., L. (2019) *Horvitz–Thompson-like stand density estimation and functional k-NN in individual tree detection*. Submitted manuscript.

### Examples

```
require(spatstat)

# Generate a 10x10 meter square window:
w<-square(10)

# Generate 6 detected trees, 5 located in the window:
x<-cbind(c(6.75, 8.65, 3.95, 2, 2, 11),
         c(1.36, 3.10, 6.66, 2, 4, 11),
         c(1.29, 2.31, 1.80, 2, 1.5, 3))

# Draw the set formed by the detected tree crowns:
plot(w)
plot(gg_wind(x), add=TRUE)

# Calculate the results with different alpha:
HTest(x, w, 1)
HTest(x, w, 0)
HTest(x, w, -0.75)
```

---

ImputeHeights	<i>Impute missing tree heights into a forest data using a nonlinear (mixed-effects) model.</i>
---------------	------------------------------------------------------------------------------------------------

---

### Description

A function to impute tree heights in a forest inventory situation where all trees have been measured for diameter but only some trees have been measured for height.

### Usage

```
ImputeHeights(d, h, plot, modelName = "naslund", nranp = 2, varf = TRUE,
              addResidual = FALSE, makeplot=TRUE, level = 1,
              start=NA, bh=1.3, control=list(),random=NA)
```

### Arguments

d	A numerical vector of tree diameters, usually given in cm.
h	A numerical vector of tree heights, usually given in meters. Should be of the same length as d.
plot	A vector of type numeric or factor, defining the groups of the data; usually the plot indices. Should be of the same length as d and h.



modelName	Either (i) a character vector specifying the name of the nonlinear function or (ii) the formula specifying a linear model. In case (i) the name should be one of the functions documented on the help page of <a href="#">HDmodels</a> . In case (ii), it should be the linear formula in the form that is entered to the function <a href="#">lme</a> , for example $model=h\sim d+I(d^2)-1$
nranp	Parameters nranp and random specify two alternative ways to specify the random effects of the model. An easy but restricted way is to use argument nranp. It is an integer between 0 and the number of fixed parameters, and has the the following meaning in the case of nonlinear model: <ul style="list-style-type: none"> <li>• If nranp=0, then a model without random parameters is fitted. Results to a fixed-effects model, and argument plot is not used.</li> <li>• If nranp=1, then parameter a of a nonlinear function or the first coefficient of the linear formula is assumed to vary among plots.</li> <li>• If nranp=2, then a and b or the first two terms of the linear formula are assumed to vary among plots or</li> <li>• If nranp=3, then a, b, and c of a three-parameter nonlinear model or three first coefficients of a linear model are assumed to vary among plots</li> </ul> <p>In the case of linear model, the constant (if exists) it always counted as the first term.</p> <p>As an alternative to nranp, argument random can be used to express the random part as a nlme formula, but without specification of the grouping structure. The provided formula is passed to the lme or nlme function. Argument random is always used when provided, so nranp has effect only if random=NA (the default).</p>
varf	Numeric with values 0, 1 or 2. If 0 or FALSE, no variance function is used. If varf=1, 2 or TRUE, then the power- type variance function $var(e)=\sigma^2*w^{(2*\delta)}$ is used. where weight w is the raw diameter (when varf=1 or TRUE), or $w=\max(1,dsd+3)$ (when varf=2), where $dsd=(d-D)/SDD$ . Here d is tree diameter, D and SDD are the mean and standard deviation of diameters on the plot in question.
addResidual	Boolean. If TRUE, a random residual is added to the imputed height from a normal distribution using the estimated variance function. If also level=0 or if the plot did not include any measured heights to predict the random effects, then also a randomly selected plot effect from among the predicted plot effects is added. The added plot effect is the same for all trees of a given plot.
makeplot	Should a residual plot of the fitted model be produced for evaluation of goodness of fit? The plot is produced using the default arguments of function <a href="#">plot.hdmod</a> , and is not affected by the value of arguments level and addResidual.
level	The level of prediction. 0 means fixed-effect prediction and 1 means plot-level prediction using the random effects. Has no effect if nranp=0.
start, bh, control, random	Arguments passed to <a href="#">fithd</a> . See documentation of <a href="#">fithd</a> .

## Details

The function predicts the missing heights using a nonlinear mixed-effects model or a nonlinear fixed-effects model. In mixed-effects model, plot-specific random effects can be used if other tree heights have been measured from the same plot. Also random, normally distributed residual can

be added to the heights according to the estimated constant or heteroscedastic residual variance structure.

### Value

A list of components

h	A vector of tree heights, including the measured heights for the trees with known height and imputed heights for the others.	
imputed	A boolean vector of the same length as h, having value TRUE for imputed heights. Produced as <code>is.na(data\$h)</code>	
model	The fitted model that was used in imputation. Fitted using <code>fi<th>d</th></code> which in turn calls <code>nlme</code> or <code>gnls</code>	d
predType	A vector of the same length as h, including information on the level of prediction. Value 0 means a measured height (no model prediction is used), value 1 means the plot-level prediction has been done using the estimated plot effects. Value 2 means that no sample trees were available and the prediction is based on fixed part only (if <code>level=0</code> ) or on a simulated plot effect (if <code>level=1</code> ).	
hpred	Predicted heights for all trees. Equals to vector h for trees that had missing heights.	

### Note

Works only with the nonlinear functions specified in `HDmodels`; does not work if the `modelName` is specified as a linear expression.

### Author(s)

Lauri Mehtatalo <lauri.mehtatalo@uef.fi>

### References

Mehtatalo, L., de Miguel, S. and Gregoire, T.G. Modeling Height-diameter curves for prediction. Canadian Journal of Forest Research, 45(7): 826-837, 10.1139/cjfr-2015-0054.

### See Also

`fi d |` for model fitting and `plot.hdmod` for plotting.

### Examples

```
data(spati)

ImpFixed<-ImputeHeights(spati$d, spati$h, spati$plot, level=0)
ImpRandom<-ImputeHeights(spati$d, spati$h, spati$plot, level=1, makeplot=FALSE)
# Try also
# ImpRanRes<-ImputeHeights(spati$d, spati$h, spati$plot, level=1, addResidual=TRUE, makeplot=FALSE)

plot(spati$d[!is.na(spati$h)],
      spati$h[!is.na(spati$h)],
```

```

col=spati$plot[!is.na(spati$h)],
main="Observations", xlab="d, cm", ylab="h, m",
ylim=c(0,30))

plot(spati$d[ImpFixed$imputed],
     ImpFixed$h[ImpFixed$imputed],
     col=spati$plot[ImpFixed$imputed],
     main="Imputed, Naslund, Fixed", xlab="d, cm", ylab="h, m",
     ylim=c(0,30))

plot(spati$d[ImpRandom$imputed],
     ImpRandom$h[ImpRandom$imputed],
     col=spati$plot[ImpRandom$imputed],
     main="Imputed, Naslund, Fixed + Plot", xlab="d, cm", ylab="h, m",
     ylim=c(0,30))

# Try also
# plot(spati$d[ImpRanRes$imputed],
#       ImpRanRes$h[ImpRanRes$imputed],
#       col=spati$plot[ImpRanRes$imputed],
#       main="Imputed, Naslund, Fixed + Plot + Tree", xlab="d, cm", ylab="h, m",
#       ylim=c(0,30))

```

---

ips	<i>Wood-decaying fungi carried by bark beetle individuals and their mites.</i>
-----	--------------------------------------------------------------------------------

---

## Description

The total number of fungal species (ophistomatoid and non-ophistomatoid fungi are coded separately) associated with *Ips typographus* bark beetle individuals and their mites.

## Usage

```
data(ips)
```

## Format

A data frame with 298 observations (bark beetle individuals) on the following 5 variables.

**Fungi** The total number of fungal species associated with the individual bark beetle.

**Ophi** The number of ophistomatoid fungal species.

**Other** The number of non-ophistomatoid fungal species. The three first variables are related through  $Other + Ophi = Fungi$ .

**Season** Categorical time of data collection with three levels: spring, summer or fall. The default is spring.

**Mites** The number of mites found in the bark beetle.

## Details

The ophiostomatoid fungal families *Microascales* and *Ophiostomatales* are common associates of bark beetle *Ips typographus*, which they use to spread within the wood material. The number of fungal species in these families is high, and a certain beetle individual can carry several fungal species with it. The bark beetles may have mites attached to them, and it may be possible that some fungal species are associated to the beetles only through the mites.

The dataset includes measurements of 289 bark beetle individuals from a storm-felled Norway spruce forest in eastern Finland. For each individual, the number of attached mites was determined using a microscope. In addition the number of fungal species per bark beetle was determined genetically. However, it was not possible to determine whether the fungi were associated with the mites or the bark beetle itself. The observations were collected at three different seasons: spring, summer and fall of the same year, approximately 100 individuals in each season. The data are used to analyze the effects of season and number of mites on the number of fungal species per bark beetle.

## References

Linnakoski, R., Mahilainen, S., Harrington, A., Vanhanen, H., Eriksson, M., Mehtatalo, L., Pappinen, A., Wingfield, M.J. 2016. The seasonal succession of fungi associated with *Ips typographus* beetles and their phoretic mites in an outbreak region of Finland. PLOS ONE. 10.1371/journal.pone.0155622.

## Examples

```
data(ips)

ips$Mites2<-ips$Mites-mean(ips$Mites)

mod1<-glm(Fungi~Season+Mites,family=poisson,data=ips)
```

---

linesplot

*A spaghetti plot of grouped data*

---

## Description

Orders the observations by x and thereafter plots y on x and connects observations of the same group by lines. Useful, for example, to plot a longitudinal dataset.

## Usage

```
linesplot(x, y, group, xlab = "x", ylab = "y",
          main = "", cex = 0.5, pch = 19, col = 1, col.lin = 1,
          lw = FALSE, ylim = NULL, xlim = NULL, add = FALSE, lty = "solid", lwd=1)
```

**Arguments**

x, y	Numerical vectors of the same length including the x and y variables.
group	The variable specifying the group. Should be of the same length as vectors x and y.
xlab, ylab, main, cex, pch, col, col.lin, xlim, ylim, lty, lwd	Graphical parameters, see <a href="#">par</a>
lw	Boolean. Whether a loess smoother to be added onto the plot.
add	Boolean. Whether to add to an existing plot or to open a new window.

**Details**

The observations within the group are connected at the increasing order of x.

**Value**

Used for its side effects.

**Author(s)**

Lauri Mehtatalo

**References**

For graphs using this function, see e.g.,

Mehtatalo, L., de Miguel, S. and Gregoire, T.G. Modeling Height-diameter curves for prediction. Canadian Journal of Forest Research, 45(7): 826-837, 10.1139/cjfr-2015-0054.

Mehtatalo, L. 2004. A longitudinal height-diameter model for Norway spruce in Finland. Canadian Journal of Forest Research 34(1): 131-140.

Mehtatalo, L. 2005. Height-diameter models for Scots pine and birch in Finland. Silva Fennica 39(1): 55-66.

**Examples**

```
D<-rep(seq(10,30),10)
H<-(20+rep(rnorm(10,0,0.5),each=21))*exp(-1.5*D^(-1.3))
plot<-rep(1:10,each=21)
linesplot(D,H,plot)
```

---

mywhiskers

*A whiskers type residual plot*


---

## Description

A function for adding vertical lines onto residual plots to show

1. 95% confidence intervals of means or
2. 95% confidence intervals for individual observations

in the classes of the variable on the x-axis. Plot of the first type is useful for analyzing the fit of the assumed fixed part and plots of type b can be used to analyze the homogeneity of residuals.

## Usage

```
mywhiskers(x, y,
           nclass = 10,
           limits = NA,
           add = FALSE,
           se = TRUE,
           main = "",
           xlab = "x",
           ylab = "y",
           ylim = NA,
           lwd = 1,
           highlight = "red")
```

## Arguments

x	The variable on the x-axis. Usually one of the predictors or the predicted value.
y	The variable on the y-axis. Usually model residual.
nclass	The maximum number of classes to be used.
limits	The class limits. Alternative to nclass.
add	logical. Whether a new graphic window is opened or the lines will be added into an exosting plot.
se	Logical. Use standard errors of means (se=TRUE, option (a) above) or class-specific standard deviations (se=FALSE, option (b) above).
main, xlab, ylab, ylim, lwd	Graphical parameters of the plot. ignored if add=TRUE.
highlight	The color for lines that do not cross the y-axis.

**Details**

The function first classifies the data in `nclass` classes of variable `x` so that each class has approximately equal number of observations. Then the class mean and deviation `s` is computed for each class, where `s` is either the standard error of the mean (if `se=TRUE`) or standard deviation (if `se=FALSE`). A vertical line is plotted at the middle of each class showing the class mean by a dot and lines of length  $3.92*s$ . If the line does not cross the `x`- axis, then the highlight color is used in the line. With small number of observations (or lot of ties), the number of classes is decreased until each class includes the minimum of 2 observations.

**Value**

The function is usually used for its side effects (i.e., the plot). However, the values used in producing the plot are returned in a list of elements

- `x`: the class midpoint `x` values.
- `m`: class-specific means of `y`.
- `s`: class-specific standard deviations or standard errors of `y` (see details).
- `lb`: lower ends of the class-specific lines.
- `ub`: upper ends of the lines.

**Author(s)**

Lauri Mehtatalo

**References**

Mehtatalo, L. 2010. Forest biometrics with R. Lecture notes.

**Examples**

```
x<-seq(1,100,1)
y<-x+10*log(x)+rnorm(100,0,5)
fm1<-lm(y~x)
plot(x,resid(fm1))
mywhiskers(x,resid(fm1),se=FALSE,add=TRUE)
mywhiskers(x,resid(fm1),se=TRUE,lwd=2,add=TRUE)
abline(h=0)
```

---

 NR

*Solve simple equations using Newton-Raphson algorithm.*

---

**Description**

Solves equations of form  $f(x) = 0$ , for scalar  $x$  using the Newton-Raphson algorithm.

**Usage**

```
NR(init, fn, gr, crit = 6, range = c(-Inf, Inf))
```

**Arguments**

<code>init</code>	Numeric scalar, The initial guess for $x$ .
<code>fn</code>	An R-function returning the scalar value of $f(x)$ , with $x$ as the only argument.
<code>gr</code>	An R-function returning the first derivative of $f(x)$ , with $x$ as the only argument.
<code>crit</code>	Convergence criteria. The upper limit for the absolute value of $f(x)$ at an accepted the solution.
<code>range</code>	A two-unit vector giving the upper and lower bounds for $x$ . The solution is searched from within this range.

**Details**

The function is a straightforward implementation of the well-known Newton-Raphson algorithm.

**Value**

A list of components

<code>par</code>	the value of $x$ in the solution
<code>crit</code>	the value of $f(x)$ at the solution

If estimation fails (no solution is found during 100000 iterations), both elements of the solution are NA's.

**Author(s)**

Lauri Mehtatalo <lauri.mehtatalo@uef.fi>

**See Also**

See [NRnum](#) for a vector-valued  $x$  without analytical gradients.

**Examples**

```
## Numerically solve Weibull shape for a stand
## where DGM=15cm, G=15m^2/ha and N=1000 trees per ha
func<-function(shape,G,N,DGM) {
  ##   print(G,DGM,N)
  val<-pi/(4*gamma(1-2/shape)*log(2)^(2/shape))-G/(N*DGM^2)
  val
}

grad<-function(shape) {
  pi/4*(-1)*
  (gamma(1-2/shape)*log(2)^(2/shape))^(-2)*
  (gamma(1-2/shape)*digamma(1-2/shape)*2*shape^(-2)*log(2)^(2/shape)+
  log(2)^(2/shape)*log(log(2))*(-2)*shape^(-2)*gamma(1-2/shape))
}

shape<-NR(5,fn=function(x) func(x,G=10000*15,1000,15),gr=grad,crit=10,range=c(2.1,Inf))$par
```



NRnum

*Solve systems of equations using the Gauss-Newton algorithm***Description**

Solves systems of functions of form  $f_1(x) = 0, f_2(x) = 0, \dots$  for vector  $x$  using the Gauss-Newton algorithm (the multidimensional version of the Newton-Raphson algorithm). The gradients are solved numerically within the function using R-function `numericDeriv`.

**Usage**

```
NRnum(init, fnlist, crit = 6, ...)
```

**Arguments**

<code>init</code>	A vector of initial values for $x$ .
<code>fnlist</code>	a list of R-functions for $f_1(x), f_2(x), \dots$ the functions get a vector-valued argument $x$ and return a scalar value.
<code>crit</code>	The maximum accepted value of the convergence criteria. The applied criteria is the sum of absolute function values at the solution ( $ f_1(x)  +  f_2(x) + \dots $ )
<code>...</code>	Other arguments passed to the functions of <code>fnlist</code>

**Value**

A list of components

<code>par</code>	the value of vector $x$ in the solution
<code>crit</code>	the value of the convergence criterion at the solution

If estimation fails (no solution is found during 100 iterations), both elements of the solution are NA's.

**Author(s)**

Lauri Mehtatalo, lauri.mehtatalo@uef.fi

**See Also**

Function [NR](#).

**Examples**

```
# Moment-based recovery of Weibull parameters
mu<-14
mu2<-210
muf<-function(theta) theta[2]*gamma(1+1/theta[1])-mu
mu2f<-function(theta) theta[2]^2*gamma(1+2/theta[1])-mu2
functions<-list(muf,mu2f)
```

```
momrec<-NRnum(c(3,13),functions)
momrec$par
```

---

patti

*Increment core data of Scots pine trees*

---

### Description

Growth ring measurements of 88 trees of a long-term thinning experiment on a naturally regenerated Scots pine stand in Eastern Finland.

### Usage

```
data(patti)
```

### Format

A data frame with 3604 observations on the following 9 variables.

Plot Sample plot id, a factor with 10 levels.

Tree Tree id, a factor with 55 levels (same tree id may occur on different plots!).

SDClass Thinning treatment, factor with 4 levels (1=Control, 2=Light, 3=Moderate, 4=Heavy).

Diam1986 Tree diameter in year 1986, just before the thinning.

Year Calendar year of the ring.

CA Current tree age in years.

RW Ring width, *mm*

RD Ring density, *g/cm<sup>3</sup>*

RBA Ring Basal area, *mm<sup>2</sup>*

### Details

Long-term thinning experiment on a naturally regenerated Scots pine stand in Eastern Finland. The experiment consists of 10 sample plots, in four different classes according to the post-thinning stand density. The plots were thinned in winter 1986-1987. In winter 2006-2007, 10 trees were felled from each plot. A radial 5mm by 5mm segment from pith to bark was cut from each tree at height 1.3 meter height. Ring widths from pith to bark were analyzed for each sample, using an ITRAX X-ray microdensitometer a post-processed to create ring widths from pith to bark were determined for each disc. The ring widths were further transformed to ring basal areas by assuming circular, growth rings. For 12 trees, ring widths could not be extracted. The data includes ring widths for a total of 88 trees between years 1991-2005.

### References

Mehtatalo, L., Peltola, H., Kilpelainen, A. and Ikonen, V.-P. 2014. The response of basal area growth of Scots pine to thinning: A longitudinal analysis of tree-specific series using a nonlinear mixed-effects model. *Forest Science* 60 (4): pp. 636-644. DOI: <http://dx.doi.org/10.5849/forsci.13-059>.

**See Also**

[afterthin.](#)

**Examples**

```
data(afterthin)
par(mfcol=c(2,1),cex=0.7,mai=c(0.8,0.8,0.5,0.1))
linesplot(afterthin$CA,
  afterthin$RBA,
  group=afterthin$Plot:afterthin$Tree,
  col.lin=as.numeric(afterthin$SDClass),cex=0,
  xlab="Tree age",
  ylab=expression("Ring basal area, " *mm^2))

linesplot(afterthin$Year,
  afterthin$RBA,
  group=afterthin$Plot:afterthin$Tree,
  col.lin=as.numeric(afterthin$SDClass),cex=0,
  xlab="Year",
  ylab=expression("Ring basal area, " *mm^2))
```

---

 plants

---

*Sapling counts from sample plots of sapling stands in Finland.*


---

**Description**

Grouped Norway Spruce regeneration establishment data.

**Usage**

```
data(plants)
```

**Format**

A data frame with 1926 observations (fixed-area sample plots) from a total of 123 forest stands, with the following 8 variables.

spruces The number of spruce saplings (both planted and natural)

stand The stand id)

hdecid The mean height of deciduous tree species

prepar Site preparation method, categorical with 4 levels

stones Binary indicator for stoniness

wet Binary indicator for wetness

**Details**

The data are collected from 123 fixed-area sample plots with similar age of planted spruce saplings. The variables have been measured on fixed-area plots.

## References

Miina, J. and Saksa, T. 2006. Predicting regeneration establishment in Norway spruce plantations using a multivariate multilevel model. *New Forests* 32: 265-283.

## Examples

```
data(plants)
library(lme4)
glmm1<-glmer(spruces ~ (1|stand)+hdecid+as.factor(prepar)+as.factor(stones)+as.factor(wet),
             family=poisson(),
             data=plants)
```

---

plants2

*Sapling counts from sample plots of sapling stands in Finland.*

---

## Description

Independent Norway Spruce regeneration establishment data.

## Usage

```
data(plants2)
```

## Format

A data frame with 123 observations on the following 8 variables.

planted The number of planted spruce saplings on the plot  
 pines The number of natural pine saplings  
 spruces The number of natural spruce saplings  
 birches The number natural birch saplings  
 othersp The number of natural saplings of other species  
 hcrop The mean height of crop species  
 hdecid The mean height of deciduous tree species  
 sitetype Site fertility class (small number indicates more fertile site)

## Details

The data are collected from 123 fixed-area sample plots with similar age of planted spruce saplings. The number of saplings per species and the height of crop species (spruce and pine) and competing vegetation (birch and other broadleaved trees) has been recorded for all plots. The data includes one plot per forest stand.

## References

Miina, J. and Saksa, T. 2006. Predicting regeneration establishment in Norway spruce plantations using a multivariate multilevel model. *New Forests* 32: 265-283.

**Examples**

```
data(plants2)

glm1 <- glm(spruces ~ hdecid, family=quasipoisson(), data=plants2)
```

---

plot.hdmod	<i>Diagnostic plot a Height-Diameter model residuals</i>
------------	----------------------------------------------------------

---

**Description**

Plotting method for class hdmod

**Usage**

```
## S3 method for class 'hdmod'
plot(x, col.point = "blue", highlight = "red", standd = TRUE,
      cex=1, corD=FALSE, ask=TRUE, ...)
```

**Arguments**

x	A H-D model model fitted by <a href="#">fithd</a> .
col.point	The color used for data points
highlight	The color used to highlight classes with mean significantly different from zero
standd	Plot residuals against diameter standardized using the plot-specific mean and diameter (standd=TRUE) or against raw diameter (standd=FALSE)
cex	See <a href="#">par</a>
corD	should predictions of random effects be plotted on mean diameter of the plot.
ask	ask before new plot.
...	Other arguments, currently ignored.

**Details**

The function makes residual plots on a fitted H-D model, which can be used to explore whether the fixed part satisfactorily models the shape of H-D models. The residuals are plotted on diameters standardized at plot level (dsd) or on raw diameters (d) according to argument standd. Here  $dsd = (d - D)/SDD$ , where  $d$  is tree diameter,  $D$  and  $SDD$  are the mean and standard deviation of diameters on the plot in question. Using plot-specific standardized diameter ensures that e.g., the medium-sized trees of the plot are always in the middle of the plot, which provides a better graph to explore the fit at the plot level in a dataset where the diameter range varies between plots.

**Author(s)**

Lauri Mehtatalo (lauri.mehtatalo@uef.fi)

**See Also**

The function plots model residuals on the required type of diameter and adds a whiskers plot using `mywhiskers` with argument `se=TRUE`.

**Examples**

```
data(spati)

model<-fithd(spati$d,spati$h,spati$plot)

plot(model)
```

---

predvol

*Individual tree volume functions for Finland*

---

**Description**

Predict individual tree volumes using the functions of Laasasenaho(1982). The volume prediction can be based on tree diameter or tree diameter and height. The functions applying upper stem diameter have not (yet) been implemented.

**Usage**

```
predvol(species,d,h=0,model=1)
```

**Arguments**

species	The vector of tree species. 1:Pine, 2:Spruce, 3: Silver birch. 4: Downy birch. Other codes than 1-4 are accepted but return NA as the volume prediction.
d	The vector of tree diameters at breast height (cm)
h	The vector of tree heights. Used only if model=2.
model	The model used. If model is 1, the prediction is based on tree diameter only. If model=2, then diameter and height are used.

**Details**

Vectors species, dbh and height should be either scalars or vectors of the same length so that each element corresponds to one individual tree.

**Value**

A vector of tree volumes (in liters).

**Author(s)**

Lauri Mehtatalo

## References

Laasasenaho, Jouko 1982. Taper curve and volume functions for pine, spruce and birch. Comm. Inst. For. Fenn 108: 1-74.

## Examples

```
d<-c(15,18.3,29.3,22.4)
h<-c(13,18,22,19)
species<-c(1,1,1,3)
predvol(species,d,h,model=2)
predvol(species,d,model=1)
```

---

qqplotHD

*Normal QQ-plot of a fitted H-D model*

---

## Description

Produces a panel of graphs including the Normal qq-plot of a H-D model residuals and of the predicted random effects.

## Usage

```
qqplotHD(model, startnew=TRUE)
```

## Arguments

model	A nonlinear H-D model fitted by <a href="#">fithd</a> .
startnew	Should a new plotting window be opened?

## Details

The function extracts the residuals and the random effects of the fitted Height-Diameter model and produces a panel of plots including univariate Normal qq-plots of the model.

## Author(s)

Lauri Mehtatalo (lauri.mehtatalo@uef.fi)

## Examples

```
data(spati)

model<-fithd(spati$d,spati$h,spati$plot)

qqplotHD(model)
```

---

recweib	<i>Recovery of Weibull parameters of tree diameter distribution using measured stand characteristics</i>
---------	----------------------------------------------------------------------------------------------------------

---

### Description

The function finds such parameters shape and scale of the Weibull diameter distribution that yield the given basal area, number of stems and weighted/unweighted mean/median diameter.

### Usage

```
recweib(G, N, D, Dtype, init=NA, trace=FALSE)
func.recweib(lshape, G, N, D, Dtype, trace=FALSE)
```

### Arguments

G	The basal area in $m^2/ha$ , scalar.
N	The number of stems per ha, scalar.
D	Either A: The arithmetic mean diameter, B: The basal-area weighted mean diameter, C: median diameter or D: The basal-area weighted median diameter of the stand, cm.
Dtype	One of characters "A", "B", "C", "D", indicating which type of mean diameter was given in argument D.
init	The initial guess for the shape parameter (scalar). If not given, a simple model (see Siipilehto and Mehtatalo 2013, appendix) is used to compute the initial guess.
trace	if TRUE, some output on the convergence of the algorithm is printed on the screen.
lshape	logarithmic shape parameter, $(\log(\text{shape}+0.01))$

### Details

The recovery is based on the solution of the equation  $DQMW(\text{shape}, \text{scale}(\text{D}, \text{shape})) - DQM = 0$ , where  $DQMW(\text{shape}, \text{scale}(\text{D}, \text{shape}))$  expresses the DQM of The Weibull distribution for the given value of the shape parameter and using the scale parameter that corresponds to the given combination of the shape parameter and the mean/median diameter given in D. The function which is set to zero is implemented in `func.recweib`. The Gauss-Newton method implemented in `NRnum` is used for solving the equation.

### Value

A list of components

shape, scale	The value of the shape and scale parameters at the solution.
G, N, D, Dtype	The input arguments.
val	The value of the equation $DQMW(\text{shape}, \text{scale}(\text{D}, \text{shape})) - DQM$ at the solution



**Author(s)**

Lauri Mehtatalo and Jouni Siipilehto

**References**

Siipilehto, J. and Mehtatalo, L. 2013. Parameter recovery vs. parameter prediction for the Weibull distribution validated for Scots pine stands in Finland. *Silva Fennica* 47(4), article id 1057.

**See Also**

The mean diameters for options A, B, C and D are computed by functions documented at [scaledMean](#).

**Examples**

```
# Demonstration with 3 example stands.
# Example stand 1. Uneven-aged stand in Finland (Vesijako, Kailankulma, stand no 1):
G_ha<-17.0
N_ha<-1844
D<-7.9
DG<-19.6
DM<-8.1
DGM<-19.1
recweib(G_ha,N_ha,D,"A") # 1.066123, 8.099707
recweib(G_ha,N_ha,DG,"B") # 1.19316 8.799652
recweib(G_ha,N_ha,DM,"C") # 1.601795 10.18257
recweib(G_ha,N_ha,DGM,"D") # 1.095979 8.280063

# Example 2. Even aged stand in Finland (see Siipilehto & Mehtatalo, Fig 2):
G_ha<-9.6
N_ha<-949
D<-11.0
DG<-12.3
DM<-11.1
DGM<-12.4
recweib(G_ha,N_ha,D,"A") # 4.465673 12.05919
recweib(G_ha,N_ha,DG,"B") # 4.463991 12.05912
recweib(G_ha,N_ha,DM,"C") # 4.410773 12.05949
recweib(G_ha,N_ha,DGM,"D") # 4.448272 12.05924

# Example 3. Assumed peaked even aged stand (see Siipilehto & Mehtatalo, Fig 1):
G_ha<-10.0
N_ha<-1300
D<-9.89
DG<-10.0
DM<-9.89
DGM<-10.0
recweib(G_ha,N_ha,D,"A") # 34.542 10.04978
recweib(G_ha,N_ha,DG,"B") # 14.23261 10.22781
recweib(G_ha,N_ha,DM,"C") # 6.708882 10.44448
recweib(G_ha,N_ha,DGM,"D") # 24.45228 10.10607
```

---

scaleDMean	<i>The Weibull scale parameter for the given mean/median diameter and shape parameter.</i>
------------	--------------------------------------------------------------------------------------------

---

### Description

The function finds such scale parameter of the Weibull distribution that yields the given mean/median diameter. Function `scaleDMean` is used for arithmetic mean, `scaleDGMean` for the mean of basal-area weighted distribution, `scaleDMed` for median and `scaleDGMed` for the median of the basal-area weighted diameter distribution.

The functions are used in the recovery of Weibull parameters using function [recweib](#).

### Usage

```
scaleDMean(D, shape)
scaleDGMean(D, shape)
scaleDMed(D, shape)
scaleDGMed(D, shape)
```

### Arguments

D	The diameter
shape	The Weibull shape parameter

### Value

scale	The value of the Weibull scale parameter.
-------	-------------------------------------------

### Author(s)

Lauri Mehtatalo and Jouni Siipilehto

### References

Siipilehto, J. and Mehtatalo, L. 2013. Parameter recovery vs. parameter prediction for the Weibull distribution validated for Scots pine stands in Finland. *Silva Fennica* 47(4), article id 1057.

### See Also

[recweib](#)

### Examples

```
scaleDMean(15, 3)
scaleDGMean(15, 3)
scaleDMed(15, 3)
scaleDGMed(15, 3)
```

spati

*Raw sample plot data of Scots pine in Ilomantsi, Finland.***Description**

A dataset of Scots pine growth. The trees were collected on 56 fixed-area sample plots. The data includes no remeasurements. The growth data are based on measurements of increment borer chips.

**Usage**

```
data(spati)
```

**Format**

A data frame with 9913 observations on the following 3 variables.

plot A unique sample plot id.

X x-coordinate of the plot

Y Y-coordinate of the plot

N Stand density, trees per ha

G Basal area,  $m^2/ha$

V Plot volume,  $m^3/ha$

Dg Basal area median diameter, cm

Hg Height of basal area median diameter tree, m

Tg Age of basal area median tree, yr

Hdom Dominant height, m

maos percentage of Scots pines of the total volume

kuos percentage of Norway spruces of the total volume

kanro A unique sample plot id (same as plot).

puunro Tree id within plot.

p1 tree species. 1=Scots Pine

xk x- coordinates of trees within plot

yk y- coordinates of trees within plot

d Tree diameter at breast height (1.3 meters above the ground) in cm.

h Tree height, m.

t Tree age, years

dk Tree diameter at stump height, cm. there seems to be some unclear issues.

X2b Double bark thickness, mm

id1 Tree diameter growth within the 5 year period prior to the measurement. Missing data coded as -1.

id2 Tree diameter growth within the period 6-10 years prior to the measurement. Missing data coded as -1.

**Author(s)**

The data were collected by Timo Pukkala.

**References**

Pukkala, T. 1989. Prediction of tree diameter and height in a Scots pine stand as a function of the spatial pattern of trees. *Silva Fennica* 23(2): 83-99.

---

spati2

*Heights and diameters of Scots pine trees in Ilomantsi, Finland.*

---

**Description**

A dataset of Scots pine tree heights and diameters. The trees were collected on 56 fixed-area sample plots. This is a subset of the larger data set `spati`.

**Usage**

```
data(spati2)
```

**Format**

A data frame with 1678 observations on the following 3 variables.

`plot` A unique sample plot id.

`d` Tree diameter at breast height (1.3 meters above the ground) in cm.

`h` Tree height, m.

`n` The total number of trees on the plot.

`dvar` The variance of tree diameters on the plot.

`dmean` The mean of tree diameters on the plot.

**Author(s)**

The data were collected by Timo Pukkala.

**References**

Pukkala, T. 1989. Prediction of tree diameter and height in a Scots pine stand as a function of the spatial pattern of trees. *Silva Fennica* 23(2): 83-99.

**Examples**

```
data(spati2)
fithd(spati2$d,spati2$h,spati2$plot)
```

stumplift

*Productivity of stump lifting machines.***Description**

The productivity of stump lifting machines on three Norway Spruce (*Picea Abies*) clearcut areas (sites). Stumps are lifted for use as bioenergy. The data were collected from three sites in Central Finland.

**Usage**

```
data(stumplift)
```

**Format**

A data frame with 485 observations on the following 5 variables.

**Stump** A unique stump id based on the order of processing. The successive numbers are usually close to each other in the clearcut area, but nearby trees do not necessarily have small difference in stump id.

**Machine** The machine/clearcut/driver combination. A factor with three levels.

**Diameter** Stump diameter, cm.

**Time** Processing time, seconds.

**Productivity** Productivity,  $m^3$ /effective working hour

**Details**

Each site was operated with different machine and driver so that the effect of site, machine and driver cannot be separated. The volume of each stump was estimated using the function of Laitila (2008), based on the stump diameter. A work system study was conducted to measure the processing time (seconds) and productivity ( $m^3$ /hour) for each stump.

**References**

Teijo Palander, Kalle Karha, Lauri Mehtatalo 2016. Applying polynomial regression modeling to productivity analysis of sustainable stump harvesting. *Scandinavian Journal of Forest Research* (Accepted). doi:10.1080/02827581.2016.1238957

Teijo Palander, Janne Smolander, Kalle Karha, 2015. Work system study of three stump-lifting devices in Finland. *Scandinavian Journal of Forest Research* 30(6) 558-567, doi:10.1080/02827581.2015.1027731

**Examples**

```
data(stumplift)
library(nlme)
```

```
modConstPow<-gls(Productivity~Machine+Machine*I((Diameter-70)^2),
  data=stumplift,
```

```
weights=varPower(),
corr=corAR1(form=~Stump|Machine))
```

---

updown

---

*Solve a simple equation using a step halving algorithm.*


---

### Description

Solves equations of form  $f(x) = 0$ , for scalar  $x$  ( $l \leq x \leq u$ ) using a simple step halving algorithm, where  $f(x)$  is a monotonic continuous function. Initial finite upper and lower bounds for  $x$  are required. The algorithm first computes  $f$  for  $x = u$  and  $x = l$ . If the sign was different then another call is performed at the midpoint  $x = (u + l)/2$ , and the midpoint is taken as a new upper or lower bound, according to the location of sign change. The upper or lower bound are repeatedly updated until the absolute value of  $f$  at the midpoint is below a specified criteria.

### Usage

```
updown(l, u, fn, crit = 6)
```

### Arguments

<code>l</code>	The initial lower bound
<code>u</code>	The initial upper bound
<code>fn</code>	R-function for $f(x)$
<code>crit</code>	The convergence criteria (Maximum accepted value of $f$ at the solution is $10^{-\text{crit}}$ ).

### Value

A scalar giving the value of  $x$  at the solution. If the sign did not change between  $l$  and  $u$ , NA is returned.

### Warning

May lead to infinite loop for non-continuous functions. Works only with monotonic functions.

### Author(s)

Lauri Mehtatalo <lauri.mehtatalo@uef.fi>

### Examples

```
## Compute the median of Weibull distribution
fn<-function(x) pweibull(x,5,15)-0.5
updown(1,50,fn)
```

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