Package ‘biometrics’

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Title A Package for Biometrics and Modelling

Version 1.0.4

Description A system of functions and datasets to carry out quantitative analyses in the biological sciences. The package facilitates data management, exploratory analyses, and model assessment. Although it currently focuses on forest ecology, silviculture and decision-making, most of the package functions are applicable across several disciplines, including economics, environmental science, and healthcare.

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URL `https://eljatib.com`, `https://biometriaforestal.uchile.cl`

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LazyData true

Imports graphics, grDevices, gtools, nlme, stats, utils

Suggests datana, lattice

NeedsCompilation no

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Contents

`assignspp` *Assign species botanical information to a data frame*

Description

Assigns species botanical attributes to a dataset, based upon a reference column (`refcol`). The attributes can be any of the fields available in the spplist dataframe, such as: `spp.ci.name` (genus and epitetus name of the species), `spp.name` (common name), and `spp.ci.abb` (abbreviated scientific name).

Usage

```
assignspp(
  data,
  attri = c("spp.name", "spp.ci.name"),
  refcol = "sppcode",
  all.x = TRUE,
  attri.all = FALSE,
  ...
)
```

Arguments

`data`	A dataframe where to assign the species information.
`attri`	A string vector having the attributes of the species to be assigned from the species list contained in spplist. This vector, by default, has two attributes: `spp.name` and `spp.ci.name`, representing the common name and the scientific name, respectively. Other alternatives are, among others, `spp.ci.abb` (abbreviated scientific name), `genus` (genus of the species), and `family` (family of the species).
`refcol`	A string having the common column name to be used for linking both the dataset and the species list. In spplist, all the attributes available for the species list are detailed, showing all the information that can be joined to the dataset. Notice that the `refcol` has to exist in both the dataset and the species list. Additional options of the `base::merge()` function can be passed to the current `assignspp()` function.
`all.x`	Whether to preserve not finded values (`TRUE`, default) or not (`FALSE`).
`attri.all`	By default is set to `FALSE`, otherwise, will overwrite the vector provided in option `attri`, with all the attributes available in the species list.
`...`	Other options for controlling the `base::merge()` function, which is internally loaded.

Value

A dataframe object including the attributes defined in the parameter `attri`.

See Also

spplist and `base::merge()`.

Examples

```
## example data frame
myData <- data.frame(narb = c(1, 2, 3),
                     sppcode = c("nob", "np", "nd"),
                     dbh = c(20, 14, 23))
myData


## assign common, scientific and abbreviated name, based on `esp` value (default)
assignspp(myData)

## Assign more than one attribute based on common name
## just to remember, adding a single attribute (different from the default)
assignspp(myData, attri = "spp.ci.name")
## now, a more real example
newData <- assignspp(myData, attri = c("spp.name","genus","spp.ci.abb"))
newData
## by default this function preserve names not found in biometrics::spplist
missingData <- rbind(myData, c(4, "notFoundData", 30))
missingData
assignspp(missingData, attri = "spp.name")
##the latter can be modified with option `all.x` of the `merge()` function
assignspp(missingData, attri = "spp.name", all.x = FALSE)
## In the case of wanting all the attributes to be merged, set option
## `attri.all` to `TRUE`, which willl overwrite the vector `attri`.
assignspp(missingData, attri = "spp.name", attri.all=TRUE, all.x =
FALSE)
```

`asymreg.fx` *Function to compute the result of the asymptotic regression model, as an allometric functional form.*

Description

Function of the asymptotic regression model, based upon its parameters and a variable, as follows

$$y_i = \alpha + (\beta - \alpha)\left\{ \mathrm{e}^{\left[-\left(\mathrm{e}^{-\gamma}\right)x_i\right]} \right\},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
asymreg.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \alpha + (\Upsilon - \alpha)\left\{e^{\left[-\left(e^{-\beta}\right)x_i\right]}\right\}$, thus the model will have only two parameters. By default Υ is set to `0`.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Pinheiro JC, DM Bates. 2000. Mixed-effects Models in S and Splus. New York, USA. Springer-Verlag. 528 p.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
#---------------------
# 2-parameters variant
# Predictor variable values to be used
time<-seq(0,50,by=0.1)
# Using the function, upsilon must be provided
y<-asymreg.fx(x=time,alpha=20,beta=2.5,upsilon =5)
plot(time,y,type="l",ylim=c(0,20))
```

`bankfit` *Function that fits a list of models on a given dataframe.*

Description

Function that fits a list of models on a given dataframe.

Usage

```
bankfit(modlist, data, file = NULL, file.full = FALSE, trace = FALSE, ...)
```

Arguments

`modlist`	List that contains the models to be fitted. To know the structure, see examples below.
`data`	`dataframe` that contains the values that correspond to observed values and variables as columns.
`file`	a (writable binary-mode) connection or the name of the file where the data will be saved (when tilde expansion is done).
`file.full`	wheter to include all output (`TRUE`) or just the fitted models plus their respective `pred.f` field (`FALSE`, default).
`trace`	logical value indicating if a trace of the iteration progress of `stats::nls()` should be printed (`TRUE`) or not (`FALSE`, default).
`...`	Other options used to control de behavior of `stats::nls()`.

Examples

```
model.list <- list(
    mod1 = list(expr = vtot ~ I(dap^2) + I(dap^2 * atot^2) +I(d6),
                pred.f = function(x, ...) x,
                type = "lm"),
    mod2 = list(expr = I(log(vtot)) ~ I(log(dap)) + I(log(atot)),
                pred.f = function(x, ...) exp(x),
                type = "lm"))

## example dataframe
df <- treevolruca2
head(df)

## fitting models to dataframe
bankfit(modlist = model.list, data = df)
```

`bankpred` *Predicts the variable of interest for each model of the list*

Description

The function predicts the variable of biometrics-interest for each model belonging to the list previously fitted, as well as, generates a dataframe with the results.

Usage

```
bankpred(
  file = stop("You must provide a bankfit output object"),
  data = stop("You must provide a dataframe")
)
```

Arguments

`file`	The output from `bankfit()` as a file path or object.
`data`	A dataframe for the prediction of the response variable's values using the models fitted in `file`.

Examples

```
## Not run:
## list of example models
model.list <- list(
    mod1 = list(expr = vtot ~ I(dap^2) + I(dap^2 * atot^2) +I(d6),
                pred.f = function(x, ...) x,
                summodel = function(x, ...) datana::modresults(x)),
    mod2 = list(expr = I(log(vtot)) ~ I(log(dap)) + I(log(atot)),
                pred.f = function(x, ...) exp(x),
                summodel = function(x, ...) datana::modresults(x)))

## example dataframe
df <- treevolruca2
head(df)

## fitting models to dataframe and saving them
bankfit(models = model.list, data = df, file = "out.rdata")


## using fitted models file from biometrics::bankfit()
bankpred(file = "out.rdata", data = df)

## End(Not run)
```

`barplotgr` *Function for building a barplot for one or two factors*

Description

The function creates a barplot of numeric vector by one or two factor.

Usage

```
barplotgr(
  yvar,
  factors,
  data = data,
  percentage = FALSE,
  errbar = !percentage,
  half.errbar = TRUE,
  conf.level = 0.95,
  xlab = NULL,
```

```
  ylab = NULL,
  main = NULL,
  names.arg = NULL,
  bar.col = "black",
  whisker = 0.015,
  args.errbar = NULL,
  legend = TRUE,
  legend.text = NULL,
  args.legend = NULL,
  legend.border = FALSE,
  box = TRUE,
  args.yaxis = NULL,
  mar = c(5, 4, 3, 2),
  ...
)
```

Arguments

`yvar`	The column having the variable to represent the height of the bars.
`factors`	A vector having the columns with the factors to be used in the resulting plot. Notice that the last listed factor, will be used in X-axis plot.
`data`	A data frame having the above described columns.
`percentage`	Logical value, set to `FALSE`.
`errbar`	Please set this option to `FALSE`.
`half.errbar`	Optional, default set to `TRUE`.
`conf.level`	Optional, a numeric value for the confidence interval, the default is 0.95.
`xlab`	Optional, as in the generic barplot function.
`ylab`	Optional, as in the generic barplot function.
`main`	Optional, as in the generic barplot function.
`names.arg`	Optional, as in the generic barplot function.
`bar.col`	Optional, as in the generic barplot function.
`whisker`	Optional, A numeric value, the default is 0.015.
`args.errbar`	Optional, as in the generic barplot function.
`legend`	Optional, as in the generic barplot function.
`legend.text`	Optional, as in the generic barplot function.
`args.legend`	Optional, as in the generic barplot function.
`legend.border`	Optional, as in the generic barplot function.
`box`	Optional, as in the generic barplot function.
`args.yaxis`	Optional, as in the generic barplot function.
`mar`	Optional, as in the generic barplot function.
`...`	list of columns to sort on

Value

The function returns the above described graph.

Author(s)

Christian Salas-Eljatib

References

The present function was modified from a similar one available at `https://github.com/mrxiaohe/R_Functions/blob/master/functions/bar`

Examples

```
data(standtabRauli2)
df <- standtabRauli2
head(df)
barplotgr(yvar = nha.cd, factors = c(bosque.id,cd), data = df,
errbar = FALSE, ylim=c(0, 640))
```

`bertarich.fx` *A function having the mathematical expression of the Bertalanffy-Richards model.*

Description

Function of the Bertalanffy-Richards model, based upon three parameters and a single predictor variable as follows

$$y_i = \alpha \left(1 - \mathrm{e}^{-\beta x_i}\right)^{1/\gamma},$$

where: y_i and x_i are the response and predictor variable, respectively for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
bertarich.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Richards FJ. 1959. A flexible growth function for empirical use. J. of Experimental Botany 10(29):290-300.
- von Bertalanffy L. 1957. Quantitative laws in metabolism and growth. The Quarterly Review of Biology 32(3):217-231.
- Salas-Eljatib C. 2020. Height growth-rate at a given height: a mathematical perspective for forest productivity. Ecological Modelling 431:109198. doi:10.1016/j.ecolmodel.2020.109198 `https://eljatib.com/myPubs/2020hgrate_ecoModelling.pdf`
- Salas-Eljatib C, Mehtatalo L, Gregoire TG, Soto DP, Vargas-Gaete R. 2021. Growth equations in forest research: mathematical basis and model similarities. Current Forestry Reports 7:230-244. doi:10.1007/s40725021001458
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-bertarich.fx(x=time,alpha=23,beta=0.08,gamma=0.89)
plot(time,y,type="l")
```

`biging.fx` *Taper equation by Biging*

Description

Tree taper equation proposed by Biging (1984), that depends on model parameters and tree size variables: diameter, total height, and stem height. The mathematical model is:

$$d_{l_i} = d_i(\beta_0 + \beta_1 ln(1 - \lambda(h_{l_i}/h_i)^{\frac{1}{3}}))$$

where: d_{l_i} is the stem diameter at stem-height h_{l_i} for the *i*-th tree; d_i and h_i are the tree-level variables diameter at breast height and total height, respectively, and

$$\lambda = 1 - e^{(\frac{-\beta_0}{\beta_1})}$$

Usage

```
biging.fx(d, hl, h, paramod)
```

Arguments

`d`	is the diameter at breast height (1.3 m) of the tree. The measurement unit is cm in the metric system, but ultimately it will depend on how the model was previously fitted, because of the measurement unit of the variables included.
`hl`	hl is stem height within the tree, thus $h_l \leq h$.
`h`	is total height of the tree.
`paramod`	paramod is a vector having the coefficients of the model in the following order: β_0, β_1.

Value

Returns the diameter of the stem at the stem-height h_l, thus d_l, for the Biging (1984) functional form, based upon tree diameter d and total height h.

References

- Biging GS. 1984. Taper equations for second-growth mixed conifers of northern California. Forest Science 30(4): 1103–1117. doi:10.1093/forestscience/30.4.1103

Examples

```
## Parameters
b0 <- 1.016215
b1 <- 0.332529
coefs <- c(b0, b1)

## Tree attributes
dbh <- 40
toth <- 25

## Using the function
hl.int <- c(0.3, 1.3, 5)
dl.hat <- biging.fx(d = dbh, h = toth, hl = hl.int, paramod=coefs)
cbind(hl.int, dl.hat)
```

`biomass` *Contains tree-level biomass data for four species in Canada.*

Description

These are tree-level variables for four species in Canada.

Usage

```
biomass
```

Format

Data contain the following columns:

tree Tree number code.

spp Species common name, as follows: `Balsam fir` is *Abies balsamea*, `Black spruce` is *Picea mariana*, `White birch` is *Betula papyrifera*, and `White spruce` is *Picea glauca*.

dbh Diameter at breast height, in cm.

toth Total height, in m.

totbiom Total biomass, in kg.

bolebiom Stem biomass, in kg.

branchbiom Branches biomass, in kg.

foliagebiom Foliage biomass, in kg.

Source

Data were provided by Prof. Timothy Gregoire, School of Forestry and Environmental Studies, Yale University (New Haven, CT, USA).

Examples

```
data(biomass)
head(biomass)
tapply(biomass$totbiom,biomass$spp,summary)
```

`biomass2` *Biomasa a nivel de árbol para cuatro especies arbóreas de Canadá*

Description

Biomasa a nivel de árbol y otras variables, para cuatro especies que crecen en bosques de Canadá.

Usage

```
biomass2
```

Format

Los datos contienen las siguientes columnas:

arbol Número del árbol.

spp Nombre común de la especie, como sigue: `Balsam fir` es *Abies balsamea*, `Black spruce` es *Picea mariana*, `White birch` es *Betula papyrifera*, y `White spruce` es *Picea glauca*.

dap Diámetro a la altura del pecho (1.3 m), en cm.

atot Altura total, en m.

wtot Biomasa total, en kg.

wfus Biomasa del fuste, en kg.

wramas Biomasa de las ramas, en kg.

whojas Biomasa del follaje, en kg.

Source

Los datos fueron cedidos cortesía del profesor Timothy Gregoire, School of Forestry and Environmental Studies, Yale University (New Haven, CT, USA).

Examples

```
data(biomass2)
head(biomass2)
tapply(biomass2$wtot,biomass2$spp,summary)
```

`cubica` *Compute taper volume*

Description

Performs the cubication of taper data. If the data corresponds to a full tree, and `pred == FALSE` the calculation is performed as a cilinder for the stump, smalian for each section in the stem and a cone for the crown. Otherwise, just smalian is used and a sum is performed up to the corresponding heights.

Usage

```
cubica(
  dl,
  hl,
  hstump = NA,
  htop = NA,
  dlu = NA,
  hlu = NA,
  full.tree = TRUE,
  pred = FALSE,
  rel.vol = c(25, 30, 40, 50, 90),
  ...
)
```

Arguments

`dl`	`vector` of diameters. Has to have the same length as `hl`
`hl`	`vector` of heights. Has to have the same length as `dl`
`hstump`	a numeric value indicating the stump height. If missing and `pred == FALSE` it defaults to the height of the first section.
`htop`	a numeric value indicating the height to crown base. If missing and `pred == FALSE` it defaults to the height of the next to last section.
`dlu`	numeric values indicating comercial diameters. If the values doesn't exists in the data they are interpolated via datana::interp.
`hlu`	numeric values indicating comercial heights. If the values doesn't exists in the data they are interpolated via datana::interp.
`full.tree`	wheter the data comes from a full tree having stump, stemp and crown (`TRUE`, default) or just stem data (`FALSE`).
`pred`	wheter the data comes from measured data (`FALSE`, default) or from predicted values (`TRUE`).
`rel.vol`	numerical values of relative volumes, used to compute the corresponding height and diameter.
`...`	optional parameters to pass to `datana::interp()`.

Value

A list with data.frames with the different volumes calculated.

Author(s)

Christian Salas-Eljatib and Nicolás Campos

Examples

```
## Not run:
## generating suitable data
df <- data.frame(dl = c(31.1, 25.8, 21.2, 19.6, 17.9, 15.9, 13.5,  9.8,  7.3, 0),
                 hl = c(0.30, 0.80, 1.30, 4.88, 9.76, 12.20, 14.64, 19.52, 24.40, 31.1),
                 hstump = c(0.30, 0.30, 0.30, 0.30, 0.30, 0.30, 0.30, 0.30, 0.30, 0.30),
            htop = c(24.40, 24.40, 24.40, 24.40, 24.40, 24.40, 24.40, 24.40, 24.40, 24.40))
df

cubica(dl = df$dl,
       hl = df$hl,
       hstump = unique(df$hstump),
       htop = unique(df$htop))

## adding commercial volumes
cubica(dl = df$dl,
       hl = df$hl,
       dlu = c(20, 15, 21.2),
       hstump = unique(df$hstump),
```

```
        htop = unique(df$htop))

## End(Not run)
```

`curtis.fx` *Function to computes the result of the Curtis's allometric model.*

Description

Function of the traditional Curtis' allometric model, based upon two parameters, and a single predictor variable as follows

$$y_i = \alpha \left(\frac{x_i}{1 + x_i} \right)^{\beta},$$

where: y_i and x_i are the response and predictor variable, respectively for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
curtis.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Curtis RO. 1967. Height-diameter and height-diameter-age equations for second-growth Douglas-fir. Forest Sci. 13(4):365-375.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-curtis.fx(x=time,alpha=20,beta=8)
plot(time,y,type="l")
```

`curtisori.fx` *Function to computes the result of the original Curtis's allometric model.*

Description

Function of the originally proposed allometric model by Curtis, based upon two parameters, and a single predictor variable as follows

$$y_i = \frac{x_i}{\alpha + \beta x_i},$$

where: y_i and x_i are the response and predictor variable, respectively for the *i*-th observation; and the rest are parameters (i.e., coefficients). Please read the details on this model in Salas-Eljatib (2025).

Usage

```
curtisori.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Curtis RO. 1967. Height-diameter and height-diameter-age equations for second-growth Douglas-fir. Forest Sci. 13(4):365-375.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Parameters
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-curtisori.fx(x=time,alpha=20,beta=8)
plot(time,y,type="l")
```

`cwd` *Contains coarse woody debris measurement in a unit of line intersect sampling.*

Description

These are log-level variables measured in the field in a single line intersect sampling (LIS) unit. The length of the line or transect is 30 m. Details on this type of sampling strategy can be reviewed in Gregoire and Valentine (2008).

Usage

```
cwd
```

Format

Data contains the following columns:

element Element (i.e., log) number with the LIS sample.

diam Diameter of the element, in cm.

len Length, in m.

ang Angle of the element with respect to the line sampling, in degrees.

Source

Data from Marshall et al 2000.

References

- Marshall PL, G Davis, VM LeMay. 2000. Using line intersect sampling for coarse woody debris. Technical Report 3, British Columbia Forest Service, Nanaimo, BC, Canada. 34 p.
- Gregoire TG, HT Valentine. 2008. Sampling Strategies for Natural Resources and the Environment. New York, USA. Chapman & Hall/CRC. 474 p.

Examples

```
data(cwd)
cwd
```

`cwd2` *Contiene mediciones de material leñoso muerto en una unidad de muestreo de linea.*

Description

Son variables medidas a nivel de trozo en la unidad de muestreo (LIS). El largo de la línea de muestreo o transecto es de 30 m. Detalles sobre este tipo de estrategia de muestreo se pueden revisar en Gregoire and Valentine (2008).

Usage

```
cwd2
```

Format

Data contiene las siguientes columnas:

elemento Número del elemento (i.e., trozo) medido dentro de la muesta de LIS.

diam Diámetro en la mitad del elemento, en cm.

lar Largo, en m.

ang Ángulo de intersección del elemento con la línea de muestreo LIS, en grados.

Source

Datos digitados desde Marshall et al (2000).

References

- Marshall PL, G Davis, VM LeMay. 2000. Using line intersect sampling for coarse woody debris. Technical Report 3, British Columbia Forest Service, Nanaimo, BC, Canada. 34 p.
- Gregoire TG, HT Valentine. 2008. Sampling Strategies for Natural Resources and the Environment. New York, USA. Chapman & Hall/CRC. 474 p.

Examples

```
data(cwd2)
cwd2
```

`deadlianas` *Mortality of lianas (vines) in tropical forests*

Description

This study is part of the project "Diversity and dynamics of vascular epiphytes in Colombian Andes" supported by `COLCIENCIAS` (contract 2115-2013). The data corresponds to the first large-scale assessment of vascular epiphyte mortality in the neotropics. Based on two consecutive annual surveys, we followed the fate of 4247 epiphytes to estimate the epiphyte mortality rate on 116 host trees at nine sites. Additional variables were taken from the area of study in order to find relationships with epiphyte mortality.

Usage

```
data(deadlianas)
```

Format

The data frame contains four variables as follows:

PlotSite Municipality name of the 9 study sites

Y.Plot Latitude of the plot in decimal degrees

X.Plot Longitude of the plot in decimal degrees

PhoroNo ID number of the sampled host trees in each site

EpiFam Epiphyte taxonomic family

EpiGen Epiphyte taxonomic genus

cf.aff Abbreviations of Latin terms in the context of taxonomy. cf. "confer" meaning "compare with". aff.: "affinis" meaning "similar to".

Species Epiphyte (morpho) species name

Author Author of the scientific name

EpiAzi Azimuth of the epiphyte individual on each host tree

BraAzi Azimuth of the branch in which the epiphyte individual was found

EpiDisTru Distance in meters from the trunk to the epiphyte attachment site on a branch

EpiSize Estimated size of the epiphyte individual, in cm.

EpiAttHei Epiphyte attachment height in meters

Date0 Date of the first census

Date1 Date of the final census

Location Section (roots, trunks, branches) of the host tree in which theepiphyte individual was found

Mortality Dichotomous variable. 0 if the epiphyte individual was dead in the final census and 1 if otherwise

MorCat Mechanical or non-mechanical cause of mortality

Elevation Elevation (m a.s.l.) of the plot

AP_bio12 Annual precipitation in the plot (mm yr-1)

PDM_bio14 Precipitation of driest month in the plot (mm)

PS_bio15 Precipitation seasonality in the plot (coefficient of variation)

MDT_bio2 Mean Diurnal Range (Mean of monthly (max temp - min temp)) in the plot (oC * 10)

TS_bio4 Temperature seasonality in the plot (standard deviation * 100)

ATR_bio7 Annual temperature range in the plot (10 celsius degrees)

AET Actual evapotranspiration in the plot (mm yr-1)

BasAre Basal area of trees with DBH major or equal to 5 cm (AB) in the plot (m^2/ha)

BasAre5_10 Basal area of trees with greater or equal than 5 DBH and less than 10 cm in the plot (m^2/ha)

BasAre10 Basal area of trees with greater or equal than 10 cm DBH in the plot (m^2/ha)

Ind10 Number of canopy trees (with greater or equal than 10 cm DBH) in the plot

Ind5 Number of understory trees (with greater or equal than 5 DBH and less than 10 cm) in the plot

Ind5_10 Number of trees with greater or equal than 5 DBH and less than 10 cm in the plot

Ind10_15 Number of trees with greater or equal than 10 DBH and less than 15 cm in the plot

Ind15_20 Number of trees with greater or equal than 15 DBH and less than 20 cm in the plot

Ind20_25 Number of trees with greater or equal than 20 DBH and less than 25 cm in the plot

Ind25_30 Number of trees with greater or equal than 25 DBH and less than 30 cm in the plot

Ind30 Number of trees with DBH major or equal to 30 cm in the plot

TreeHei Total tree height in meters

MedHei Median height of trees in each plot

MaxHei Maximum height of trees in each plot

BranchNumb Number of branches of the host tree

Obs Observations and notes in Spanish

Source

Data were retrieved from the DRYAD repository at doi:10.5061/dryad.g5510.

References

Zuleta D, Benavides AM, Lopez-Rios V, Duque A. 2016. Local and regional determinants of vascular epiphyte mortality in the Andean mountains of Colombia. Journal of Ecology 104(3): 841-843. doi:10.1111/13652745.12563

Examples

```
data(deadlianas)
head(deadlianas)
```

`deadlianas2` *Datos de mortalidad de lianas en árboles tropicales*

Description

Los datos provienen de un estudio que fue parte del proyecto "Diversidad y dinámica de epífitas vasculares en los Andes colombianos". apoyado por COLCIENCIAS (contrato 2115-2013). Este conjunto de datos tiene 43 columnas y 4247 filas. Cada fila corresponde a un individuo epifito ubicado en secciones confiables de los árboles hospedantes Los datos corresponden a la primera gran escala evaluación de la mortalidad de epífitas vasculares en los neotrópicos. Basado en dos encuestas anuales consecutivas, Seguimos el destino de 4247 epífitas para estimar la tasa de mortalidad de epífitas en 116 árboles hospedantes. en nueve sitios. Se tomaron variables adicionales del area de estudio para encontrar relaciones con mortalidad de epifitas.

Usage

```
data(deadlianas2)
```

Format

Variables se describen a continuación::

PlotSite Nombre del municipio de los 9 sitios de estudio.

Y.Plot Latitud del grafico en grados decimales.

X.Plot Longitud de la grafica en grados decimales.

PhoroNo número de identificacion de los árboles hospedantes muestreados en cada sitio

EpiFam Familia taxonomica de epifitas.

EpiGen Genero taxonomico de epifitas.

cf.aff Abreviaturas de terminos latinos en el contexto de la taxonomia. cf. "conferir" que significa "comparar con". aff .: "affinis" que significa "similar a".

Species Nombre de la especie epifita (morfo)

Author Autor del nombre científico.

EpiAzi Azimut del individuo epifito en cada árbol huesped.

BraAzi Azimut de la rama en la que se encontro el individuo epifito.

EpiDisTru Distancia en metros desde el tronco hasta el sitio de union de la epifita en una rama.

EpiSize Tamaño estimado del individuo epifito en centimetros.

EpiAttHei Altura del accesorio de la epifita en metros.

Date0 Fecha del primer censo.

Date1 Fecha del censo final.

Location Seccion (raices, troncos, ramas) del árbol anfitrion en el que se encontro el individuo epifito.

Mortality Variable dicotomica. 0 si el individuo epifito estaba muerto en el censo final y 1 si no.

MorCat Causa de mortalidad mecanica o no mecánica.

Elevation Elevacion (msnm) de la parcela.

AP_bio12 Precipitación anual en la parcela, en mm.

PDM_bio14 Precipitación del mes más seco en la parcela, en mm.

PS_bio15 Estacionalidad de la precipitacion en la parcela (coeficiente de variacion)

MDT_bio2 Rango diurno medio (Media mensual (temperatura maxima - temperatura minima)) en la grafica (10°C)

TS_bio4 Estacionalidad de la temperatura en la grafica (desviacion estandar * 100)

ATR_bio7 Rango de temperatura anual en la parcela (10 grados centigrados)

AET Evapotranspiración anual en la parcela, en mm.

BasAre Area basal de árboles con DAP mayor o igual a 5 cm en la parcela, en m^2/ha.

BasAre5_10 Area basal de árboles con DAP mayor o igual a 5 y menor a 10 cm en la parcela (m^2/ha)

BasAre10 Area basal de árboles con DAP mayor o igual a 10 cm en la parcela (m^2/ha)

Ind10 Número de árboles del dosel (con un DAP superior o igual a 10 cm) en la parcela

Ind5 Número de árboles de sotobosque (con DAP mayor o igual a 5 y menor a 10 cm) en la parcela

Ind5_10 Número de árboles con un DAP mayor o igual a 5 y menos de 10 cm en la parcela

Ind10_15 Número de árboles con un DAP mayor o igual a 10 y menos de 15 cm en la parcela

Ind15_20 Número de árboles con un DAP mayor o igual a 15 y menos de 20 cm en la parcela

Ind20_25 Número de árboles con un DAP mayor o igual a 20 y menos de 25 cm en la parcela

Ind25_30 Número de árboles con un DAP mayor o igual a 25 y menos de 30 cm en la parcela

Ind30 Número de árboles con DAP mayor o igual a 30 cm en la parcela

TreeHei Altura total del árbol en metros

MedHei Altura media de los árboles en cada parcela

MaxHei Altura maxima de los árboles en cada parcela

BranchNumb Número de ramas del árbol anfitrion

Obs Observaciones y notas en español

Source

Los datos fueron obtenidos desde el repositorio DRYAD doi:10.5061/dryad.g5510.

References

Zuleta D, Benavides AM, Lopez-Rios V, Duque A. 2016. Local and regional determinants of vascular epiphyte mortality in the Andean mountains of Colombia. Journal of Ecology 104(3): 841-843. doi:10.1111/13652745.12563

Examples

```
data(deadlianas2)
head(deadlianas2)
```

`dg.fx` *Function to computes the diameter of the tree of average basal area.*

Description

Function to compute the diameter of the tree of average basal area ($D_{\overline{g}}$), which depends on stand density (N) and stand basal area (G). The aforementioned stand diameter is computed as

$$D_{\overline{g}} = \sqrt{\frac{G}{N}\frac{k}{pi}}$$

where the constant k depends on whether the variables are in the units of measurement of the metric or imperial system.

Usage

```
dg.fx(n = n, g = g, metrics = TRUE)
```

Arguments

`n`	is stand tree density. By default the unit of measurement is trees/ha, but if the option 'metrics' is set to `FALSE`, the unit is trees/acre.
`g`	is stand basal area. By default the unit of measurement must be entered in m^2/ha, but if the option 'metrics' is set to `FALSE`, the unit must be ft^2/ha.
`metrics`	is a logic value, the default is set to `TRUE`, thus both variables must be entered in the metric system, i.e., N in 'trees/ha', and G in m^2/ha. If metrics is `FALSE`, N must be in trees/acre, and G in ft^2/acre.

Value

Returns the diameter of the tree of average basal area.

Author(s)

Christian Salas-Eljatib.

Examples

```
##Using the function
dg.fx(n=1000, g=55)
dg.fx(n=210, g=160, metrics=FALSE)
```

domvar *Function to compute a dominant stand-level variable based on a sample plot data.*

Description

Computes the so-called dominant stand-level variable, corresponding to the average of a tree-level variable for the `nref.ha` largest sorting-tree-level diameter trees in 1-ha.

Usage

```
domvar(data, varint, varsort, plot.area, ndom.ha = 100)
```

Arguments

`data`	the tree-list dataframe of a sample plot, having at least column `varint`.
`varint`	The column name of the data having the tree-level variable of interest (e.g., "toth"). Can be entered as the actual name, without the need of using quotation marks.
`varsort`	The column name of the data having the tree-level variable to be used as reference (e.g., "dbh") for defining the sorting variable of interest. If there is only data for the `varint` column, colum `varsort` can be the same as in `varint`.
`plot.area`	A numeric value of the plot area in m^2. Notice that in a tree list, the plot area is also a column, thus, the option `plot.area` can also be the column name where the surface of the plot is keept. In such a case, the area to be used for the computation is the average of the plot.
`ndom.ha`	It is the number of trees/ha used as reference. By default `ndom.ha` is set to 100..

Details

The original function was written by Dr Oscar García for computing top height, and the corresponding reference is provided. Nevertheless, several changes were applied, to make the current function provide a broader application. Regardless, the function aims to calculate a "dominant" stand-level variable by taking into account the plot area. Thus, requires having a dataframe having both the variable of interest (e.g., height) and the sorting variable used for the computation (e.g., diameter) for all trees in a sample plot, as well as, the plot area.

Value

The main output is the calculated dominant stand-variable for the given sample plot. The unit of the computed variable is the same as the one used as variable of interest.

Author(s)

Christian Salas-Eljatib.

References

- García O, Batho A. 2005. Top height estimation in lodgepole pine sample plots. Western Journal of Applied forestry 20(1):64-68.

Examples

```
# Dataframe to be used
df<-biometrics::eucaplot2
#' ?eucaplot2
#' head(df)
datana::descstat(df[,c("dap","atot")])
#' # Using the domvar function
domvar(data=df,varint = "atot",varsort = "atot",plot.area = 500)
domvar(data=df,varint = "atot",varsort = "dap",plot.area = 500)
domvar(data=df,varint = "atot",varsort = "dap",plot.area = 500,ndom.ha = 50)
```

`eucaplot` *Tree-level data from a sample plot established in a* Eucalyptus globulus *plantation*

Description

Tree-level variables collected for all trees (even the variable height) within a sample plot in a forestry plantation of *Eucalyptus globulus* near Gorbea, southern Chile. The plot size is 500 m^2. The plantation is 15 yr-old and had been subject to three thinnings.

Usage

```
data(eucaplot)
```

Format

The dataframe contains four variables as follows:

dbh Diameter at breast height, in cm.

health health status (1: good, 2: medium, 3: bad).

shape stem shape for timber purposes (1: good, 2: medium, 3: bad).

crown.class Crown class (1: superior, 2: intermedium, 3: lower).

toth Total height, in m.

Source

The data were provided courtesy of Dr Christian Salas-Eljatib (Universidad de Chile, Santiago, Chile).

References

- Forest biometrics lecture notes, Prof. Christian Salas-Eljatib, Universidad de Chile. Santiago, Chile

Examples

```
data(eucaplot)
table(eucaplot$health)
library(datana)
descstat(eucaplot[,c("dbh","toth")])
```

`eucaplot2` *Lista de árboles con todas las variables medidas en una parcela de muestreo, establecida en una plantación de* Eucalyptus globulus.

Description

Variables a nivel individual medidas en todos los árboles (incluso la variable altura) encontrados en una parcela de muestreo en una plantación forestal de *Eucalyptus globulus* cerca de Gorbea, en el sur de Chile. La superficie de la parcela es de 500 m^2. La plantación tiene 15 años de edad y ha estado sujeta a tres raleos.

Usage

```
data(eucaplot2)
```

Format

Los datos contienen las siguientes cuatro columnas:

dap Diámetro a la altura del pecho, en cm.

sanidad Evaluación cualitativa de la sanidad del árbol (1: buena, 2: media, 3: mala).

forma Evaluación cualtitativa de la forma del fuste (1: buena, 2: media, 3: mala).

clase.copa Clase de copa (1: superior, 2: intermedio, 3: inferior).

atot Altura total, en m.

Source

Los datos fueron cedidos por el Prof. Christian Salas (Universidad de Chile, Santiago, Chile), y colectados por él mientras fue Profesor del Departamento de Ciencias Forestales en la Universidad de La Frontera (Temuco, Chile). La plantación se encontraba dentro de un predio del colega (QEPD) Hugo Castro.

References

- Apuntes de Biometría y Modelación Forestal, Prof. Christian Salas-Eljatib, Universidad de Chile. Santiago, Chile

Examples

```
data(eucaplot2)
table(eucaplot$forma)
library(datana)
descstat(eucaplot2[,c("dap","atot")])
```

`eucaplotr` *Tree-list (realistic-) data in a sample plot established in a* Eucalyptus globulus *plantation in southern Chile.*

Description

Tree-level variables collected in a sample plot (area=500 m^2) in a forestry plantation of *Eucalyptus globulus* near Gorbea, in southern Chile. The variable height, was only measured in a sub-sample of trees within the plot. The plantation is 15 yr-old and had been subject to three thinnings.

Usage

```
data(eucaplotr)
```

Format

The dataframe contains four variables as follows:

dbh Diameter at breast height, in cm.

health health status (1: good, 2: medium, 3: bad).

shape stem shape for timber purposes (1: good, 2: medium, 3: bad).

crown.class Crown class (1: superior, 2: intermedium, 3: lower).

toth Total height (in m), only available for some trees. Otherwise missing values are denoted by `NA`.

Source

The data were provided courtesy of Dr Christian Salas-Eljatib (Universidad de Chile, Santiago, Chile).

References

- Forest biometrics lecture notes, Prof. Christian Salas-Eljatib, Universidad de Chile. Santiago, Chile

Examples

```
data(eucaplotr)
table(eucaplotr$shape)
library(datana)
descstat(eucaplotr[,c("dbh","toth")])
```

`eucaplotr2` *Lista de árboles con variables medidas (más realista) en una parcela de muestreo, establecida en una plantación de Eucalyptus globulus.*

Description

Variables a nivel individual medidas en los árboles encontrados en una parcela de muestreo (de 500 m^2) en una plantación forestal de *Eucalyptus globulus*, cerca de Gorbea (Sur de Chile). La variable altura fue medida solo en una sub-muestra de árboles. La plantación tiene 15 años de edad y ha estado sujeta a tres raleos. Este set de datos es similar al de la dataframe `eucaplot2`, pero siendo más realista en el sentido que no es comun que la altura se mida en todos los árboles como es el caso de los dataframe `eucaplot2`.

Usage

```
data(eucaplotr2)
```

Format

Los datos contienen las siguientes cuatro columnas:

dap Diámetro a la altura del pecho, en cm.

sanidad Evaluación cualitativa de la sanidad del árbol (1: buena, 2: media, 3: mala).

forma Evaluación cualtitativa de la forma del fuste (1: buena, 2: media, 3: mala).

clase.copa Clase de copa (1: superior, 2: intermedio, 3: inferior).

atot Altura total, en m. Esta variable fue medida solo en una submuestra de árboles, y los registros vacíos estan denotados por `NA`.

Source

Los datos fueron cedidos por el Prof. Christian Salas-Eljatib (Universidad de Chile, Santiago, Chile), y colectados por él mientras fue Profesor del Departamento de Ciencias Forestales en la Universidad de La Frontera (Temuco, Chile). La plantación se encontraba dentro de un predio del colega (QEPD) Hugo Castro.

References

- Forest biometrics lecture notes, Prof. Christian Salas-Eljatib, Universidad de Chile. Santiago, Chile

Examples

```
data(eucaplotr2)
table(eucaplotr2$sanidad)
library(datana)
descstat(eucaplotr2[,c("dap","atot")])
```

`expogral.fx` *Function that computes the result of the Stage allometric model.*

Description

Function of the generalized-exponential allometric model, based upon four parameters (i.e., coefficients) and a variable, as defined by the mathematical expression

$$y_i = \mathrm{e}^{\left(\alpha + \frac{\beta}{x_i^{\gamma} + \delta}\right)},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this function can be found in Salas-Eljatib (2025).

Usage

```
expogral.fx(x, alpha, beta, gamma, delta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`delta`	is the coefficient-parameter δ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-expogral.fx(x=time,alpha=3,beta=8,gamma=1,delta=1)
plot(time,y,type="l",col="blue")
```

`expogralfull.fx` *Function that computes the result of the Stage allometric model.*

Description

Function of the fully generalized-exponential allometric model, based upon five parameters (i.e., coefficients) and a variable, as defined by the mathematical expression

$$y_i = \alpha \mathrm{e}^{\left(\beta + \frac{\gamma}{x_i^{\delta}+\epsilon}\right)},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this function can be found in Salas-Eljatib (2025).

Usage

```
expogralfull.fx(x, alpha, beta, gamma, delta, epsilon, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`delta`	is the coefficient-parameter δ.
`epsilon`	is the coefficient-parameter ϵ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-expogralfull.fx(x=time,alpha=20,beta=.1,gamma=10,delta=1,
epsilon=1)
plot(time,y,type="l",col="red")
```

`gompertz.fx` *Function to compute the result of the Gompertz allometric model.*

Description

Function of the Gompertz model, depending on its three parameters and a variable, defined by the following mathematical expression

$$y_i = \alpha \mathrm{e}^{\left(-\beta \mathrm{e}^{-\gamma x_i}\right)},$$

where: y_i and x_i are the response and predictor variable, respectively for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
gompertz.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Gompertz B. 1825. On the nature of the function expressive of the law of human mortality, and on a new mode of determining the value of life contingencies. Philosophical Transactions of the Royal Society of London 115:513–583.
- Salas-Eljatib C, Mehtatalo L, Gregoire TG, Soto DP, Vargas-Gaete R. 2021. Growth equations in forest research: mathematical basis and model similarities. Current Forestry Reports 7:230-244. doi:10.1007/s40725021001458
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-gompertz.fx(x=time,alpha=25,beta=.22,gamma=16)
plot(time,y,type="l")
```

`gompertzm.fx` *Function that computes the result of the modified Gompertz's model.*

Description

Function of the Gompertz modified model, based upon parameters (i.e., coefficients) and a variable, as follows

$$y_i = \alpha \mathrm{e}^{\left(-\beta \mathrm{e}^{-\gamma x_i}\right)},$$

where: y_i and x_i are the response and predictor variable, respectively for the *i*-th observation; and the rest are parameters (i.e., coefficients). The Gompertz equation is a widely used allometric mathematical function.

Usage

```
gompertzm.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Gompertz B. 1825. On the nature of the function expressive of the law of human mortality, and on a new mode of determining the value of life contingencies. Philosophical Transactions of the Royal Society of London 115:513–583.
- Salas-Eljatib C, Mehtatalo L, Gregoire TG, Soto DP, Vargas-Gaete R. 2021. Growth equations in forest research: mathematical basis and model similarities. Current Forestry Reports 7:230-244. doi:10.1007/s40725021001458
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-gompertzm.fx(x=time,alpha=25,beta=3.6,gamma=0.17)
plot(time,y,type="l")
```

`gtree` *Function to compute basal area of a tree*

Description

The function computes the basal area of a tree (g), which only depends on its diameter at breast-height (d). The basal area of a tree is computed as

$$g = \left(\frac{\pi}{k}\right) d^2$$

where the constant k depends on whether the diameter and the resulting basal area are in the units of the metric or imperial system.

Usage

```
gtree(x, metric = TRUE)
```

Arguments

`x`	is the object (i.e., vector or scalar) having tree diameter. By default the function assumes that the unit of measurement of this variable is cm.
`metric`	is a logic value, the default is to `TRUE`, thus the diameter has to be expressed in cm, and the resulting basal area will be expressed in m^2. If `metric` is `FALSE`, the diameter has to be in inches and the resulting basal area will be in ft^2.

Value

The value of basal area in m^2 or in ft^2, depending on the units of measurement being defined.

Author(s)

Christian Salas-Eljatib

Examples

```
#Using the function
 gtree(40)
 gtree(x=30)
gtree(x=11.81,metric=FALSE)
```

`hawaii` *Diameter growth increments of a tropical tree species in Hawaii*

Description

Tree size, competition, and diameter growth increment of *Metrosideros polymorpha* trees collected in the Kilauea Volcano, Hawaii. Data containing 64 observations at the current annual growth rate (defined as `dbh` increment within one calendar year) of each tree. Measurements were made from 1986 to 1988.

Usage

```
data(hawaii)
```

Format

The dataframe has the following columns:

tree.code Tree number identification. The first letter of the ID represents a cohort. Six cohorts representing a chronosequence were sampled.

dbh Diameter at breast height, in cm.

toth Total height, in m.

crown.area Crown outline area, in square meters.

comp.ind Competition index (Basal area of nearest neighbor divided by square of distance to nearest neighbor plus basal area of second nearest neighbor divided by square of distance to second nearest neighbor).

cai.1986 Current annual stem diameter increment during 1986, in mm.

cai.1987 Current annual stem diameter increment during 1987, in mm.

cai.1988 Current annual stem diameter increment during 1988, in mm.

Source

The data were obtained from Gerrish and Mueller-Dombois (1999).

References

- Gerrish G, Mueller-Dombois D. 1999. Measuring stem growth rates for determining age and cohort analysis of a tropical evergreen tree. Pacific Science. 53(4): 418-429.

Examples

```
data(hawaii)
head(hawaii)
```

`hawaii2` *Incremento corriente anual en diámetro de una especie tropical en Hawaii*

Description

Tamaño del árbol, competencia, e incremento corriente anual de árboles de *Metrosideros polymorpha* colectado en el volcán Kilauea, Hawaii. Los datos contienen 64 observaciones de incremento corriente anual (definido como el incremento en `dap` en un año calendario) de cada árbol. Estos incrementos fueron medidos desde el año 1986 a 1988.

Usage

```
data(hawaii)
```

Format

Estos datos contienen las siguientes columnas:

arb.id Código identificador del árbol. La primera letra del ID representa una cohorte. Hay seis cohortes que representan una cronosecuencia.

dap Diámetro a la altura del pecho, en cm.

atot Altura total, en m.

area.copa Área de copa, en metros cuadrados.

ind.comp Índice de competencia (Área basal del vecino más cercano dividido por la distancia al vecino más cercano al cuadrado más el área basal del segundo vecino más cercano dividio por la distancia al segundo vecino más cercano al cuadrado)

ica.1986 Incremento corriente anual durante el año 1986, en mm.

ica.1987 Incremento corriente anual durante el año 1987, en mm.

ica.1988 Incremento corriente anual durante el año 1988, en mm.

Source

Los datos fueron obtenidos desde Gerrish and Mueller-Dombois (1999).

References

- Gerrish G, Mueller-Dombois D. 1999. Measuring stem growth rates for determining age and cohort analysis of a tropical evergreen tree. Pacific Science. 53(4): 418-429.

Examples

```
data(hawaii2)
head(hawaii2)
```

`hossfeld.fx` *Function that computes the result of the Hossfeld allometric model.*

Description

Function of the Hossfeld (actually it is "Hoßfeld") allometric model, based upon parameters (i.e., coefficients) and a variable, as defined by the mathematical expression

$$y_i = \alpha \left(\frac{1}{1 + \frac{\beta}{x_i^{\gamma}}} \right),$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this function can be found in Salas-Eljatib (2025).

Usage

```
hossfeld.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Hoßfeld JW. 1822. Mathematik für Forstmänner, Oekonomen und Cameralisten. Dresden, Germany. Gotha:Hennings. 472 p.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-hossfeld.fx(x=time,alpha=31,beta=38,gamma=1.4)
plot(time,y,type="l")
```

`interpy1` *A simple linear interpolation function applicable to two vectors (X and Y), when the first element of Y is missing.*

Description

A simple linear interpolation function applicable to two vectors (e.g., X and Y) of length three, suitable when the first element of Y is missing.

Usage

```
interpy1(xs = xs, ys = ys)
```

Arguments

`xs`	A numeric vector of length 3
`ys`	A numeric vector of length 3, with the first position empty.

Value

The interpolated value for the first element of vector Y.

Author(s)

Christian Salas-Eljatib.

Examples

```
x<-c(0.2,0.8,1.3)
y<-c(NA,41,38)
interpy1(xs=x,ys=y)
```

`interpy2` *A simple linear interpolation function applicable to two vectors (X and Y), when the second element of Y is missing.*

Description

A simple linear interpolation function applicable to two vectors (e.g., X and Y) of length three, suitable when the second element of Y is missing.

Usage

```
interpy2(xs = xs, ys = ys)
```

Arguments

`xs`	A numeric vector of length 3.
`ys`	A numeric vector of length 3, with the second position empty.

Value

The interpolated value for the second element of vector Y.

Author(s)

Christian Salas-Eljatib.

Examples

```
x<-c(0.2,0.8,1.3)
y<-c(48,NA,41)
interpy2(xs=x,ys=y)
```

`inv.fx` *Function to compute the result of the simple linear inverse model.*

Description

Function of the inverse model, based upon its two parameters and a variable, as follows

$$y_i = \alpha - \left(\frac{\beta}{x_i}\right),$$

where: y_i and x_i are the response and predictor variable, respectively for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
inv.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0. Note that this restriction must be imposed during the fitting of the model.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable to be used is 40
# Using the function
inv.fx(x=40,alpha=25,beta=115)
# The effect of the constant term phi
inv.fx(x=40,alpha=25,beta=115, upsilon=2.5)
```

`kozak.fx` *Function to computes the stem diameter of a tree according to the Kozak (1988) taper equation.*

Description

Function of the Kozak (1988) taper equation model, based upon the model parameters, and the tree variables: diameter, total height, and stem height. The mathematical expression is as follows

$$d_{l_i} = \alpha_0 d_i^{\alpha_1} \alpha_2^{d_i} X_{l_i}^{\left[\beta_1 z_{l_i}^2 + \beta_2 \ln{(z_{l_i} + 0.001)} + \beta_3 \sqrt{z_{l_i}} + \beta_4 \mathrm{e}^{z_{l_i}} + \beta_5 (d_i/h_i)\right]},$$

where: d_{l_i} is the stem diameter at stem-height h_{l_i} for the *i*-th tree; and d_i and h_i are the tree-level variables diameter at breast height and total height, respectively, for tje *i*-th tree. The other terms are

$$z_{l_i} = \frac{h_{l_i}}{h_i},$$

$$X_{l_i} = \frac{1 - \sqrt{z_{l_i}}}{1 - \sqrt{p}},$$

with *p* being the inflextion point.

Usage

```
kozak.fx(d, h, hl, paramod, p = 0.2, c0 = 0.001)
```

Arguments

`d`	is the diameter at breast height (1.3 m) of the tree. The measurement unit is cm in the metric system, but ultimately it will depend on how the model was previously fitted, because of the measurement unit of the variables included.
`h`	is total height of the tree.
`hl`	is stem height within the tree, thus $h_l \leq h$.
`paramod`	is a vector having the eight coefficients of the taper model in the following order: $\alpha_0, \alpha_1, \alpha_2, \beta_1, \beta_2, \beta_3, \beta_4$, and β_5.
`p`	is the inflextion height. By default is set to 0.2
`c0`	is a constant build-in the model. By default is set to 0.001.

Value

Returns the diameter of the stem at the stem-height h_l, thus d_l, for the Kozak (1988) functional form, based upon tree diameter d and total height h.

Author(s)

Christian Salas-Eljatib.

References

Kozak A. 1988. A variable-exponent taper equation. Canadian Journal of Forest Research 18: 1363-1368. doi:10.1139/x88213

Examples

```
# Parameters
a0<- 1.02453; a1<- 0.88809; a2<- 1.00035
b1<- 0.95086; b2<- -0.18090; b3<- 0.61407;
b4<- -0.35105; b5 <- 0.05686;
coefs<-c(a0,a1,a2,b1,b2,b3,b4,b5);p.coef <- 0.25
# Tree attributes
dbh <- 45; toth <- 27

# Using the function
hl.int <- c(0.3, 1.3, 5)
dl.hat <- kozak.fx(d=dbh,h=toth,hl=hl.int,paramod=coefs,p=p.coef)
cbind(hl.int,dl.hat)
```

`kozaklast.fx` *Function to computes the stem diameter of a tree according to the Kozak (2004) taper equation.*

Description

Function of the Kozak (2004) taper equation model, based upon the model parameters, and the tree variables: diameter, total height, and stem height. The mathematical expression is as follows (escribir la correcta)

$$d_{l_i} = \alpha_0 d_i^{\alpha_1} \alpha_2^{d_i} X_{l_i}^{\left[\beta_1 z_{l_i}^2 + \beta_2 \ln\left(z_{l_i} + 0{,}001\right) + \beta_3 \sqrt{z_{l_i}} + \beta_4 e^{z_{l_i}} + \beta_5 (d_i/h_i)\right]},$$

where: d_{l_i} is the stem diameter at stem-height h_{l_i} for the *i*-th tree; and d_i and h_i are the tree-level variables diameter at breast height and total height, respectively, for tje *i*-th tree. The other terms are

$$z_{l_i} = \frac{h_{l_i}}{h_i},$$

$$X_{l_i} = \frac{1 - \sqrt{z_{l_i}}}{1 - \sqrt{p}},$$

with *p* being the inflextion point.

Usage

```
kozaklast.fx(d, h, hl, paramod)
```

Arguments

`d`	is the diameter at breast height (1.3 m) of the tree. The measurement unit is cm in the metric system, but ultimately it will depend on how the model was previously fitted, because of the measurement unit of the variables included.
`h`	is total height of the tree.
`hl`	is stem height within the tree, thus $h_l \leq h$.
`paramod`	is a vector having the nine coefficients of the taper model in the following order: $\alpha_0, \alpha_1, \alpha_2, \beta_1, \beta_2, \beta_3, \beta_4, \beta_5$, and β_6.

Value

Returns the diameter of the stem at the stem-height h_l, thus d_l, for the Kozak (1988) functional form, based upon tree diameter d and total height h.

Author(s)

Christian Salas-Eljatib.

References

Kozak A. 2004. My last words on taper equations. The Forestry Chronicle 80: 507–515. doi:10.1139/x88213

Examples

```
# Parameters
a0<- 0.80; a1<- 0.88809; a2<- 0.2
b1<- 0.95086; b2<- -0.18090; b3<- 0.61407;
b4<- -0.35105; b5 <- 0.05686; b6 <- 0.001;
coefs<-c(a0,a1,a2,b1,b2,b3,b4,b5,b6);
# Tree attributes
dbh <- 45; toth <- 27

# Using the function
hl.int <- c(0.3, 1.3, 5)
dl.hat <- kozaklast.fx(d=dbh,h=toth,hl=hl.int,paramod=coefs)
cbind(hl.int,dl.hat)
```

`kozakln.fx` *Function to computes the stem diameter of a tree according to the log-transformed Kozak (1988) taper equation.*

Description

Function of the natural log-transformed Kozak (1988) taper equation model, based upon the model parameters, and the tree variables: diameter, total height, and stem height. The mathematical expression is as follows

$$\ln d_{l_i} = \alpha_0+\alpha_1 \ln d_i+\alpha_2 d_i+\beta_1 \ln(X_{l_i}) z_{l_i}^2+\beta_2 \ln(X_{l_i}) \ln(z_{l_i}+0.001)+\beta_3 \ln(X_{l_i})\sqrt{z_{l_i}}+\beta_4 \ln(X_{l_i}) e^{z_{l_i}}+\beta_5 \ln(X_{l_i})\frac{d_i}{h_i},$$

where: d_{l_i} is the stem diameter at stem-height h_{l_i} for the *i*-th tree; and d_i and h_i are the tree-level variables diameter at breast height and total height, respectively, for tje *i*-th tree. The other terms are

$$z_{l_i} = \frac{h_{l_i}}{h_i},$$

$$X_{l_i} = \frac{1-\sqrt{z_{l_i}}}{1-\sqrt{p}},$$

with *p* being the inflextion point.

Usage

```
kozakln.fx(d, h, hl, paramod, p = 0.2, c0 = 0.001)
```

Arguments

`d`	is the diameter at breast height (1.3 m) of the tree. The measurement unit is cm in the metric system, but ultimately it will depend on how the model was previously fitted, because of the measurement unit of the variables included.
`h`	is total height of the tree.
`hl`	is stem height within the tree, thus $h_l \leq h$.
`paramod`	is a vector having the eight coefficients of the taper model in the following order: $\alpha_0, \alpha_1, \alpha_2, \beta_1, \beta_2, \beta_3, \beta_4$, and β_5.
`p`	is the inflextion height. By default is set to 0.2
`c0`	is a constant build-in the model. By default is set to 0.001.

Value

Returns the diameter of the stem at the stem-height h_l, thus d_l, for the natural log-transformed Kozak (1988) functional form, based upon tree diameter d and total height h. Therefore, the result applies the back-transformation by using the anti-log function, i.e., `exp()`.

Author(s)

Christian Salas-Eljatib.

References

Kozak A. 1988. A variable-exponent taper equation. Canadian Journal of Forest Research 18: 1363-1368. doi:10.1139/x88213

Examples

```
# Parameters
a0<- 0.04338410; a1<- 0.88657485; a2<- 0.00446052;b1<- 1.978196;
b2<- -0.40676847; b3<- 3.50815520; b4<- -1.84177070;b5<- 0.19647175
coefs<-c(a0,a1,a2,b1,b2,b3,b4,b5);p.coef <- 0.25
# Tree attributes
dbh <- 40; toth <- 25

# Using the function
hl.int <- c(0.3, 1.3, 5)
dl.hat <- kozakln.fx(d=dbh,h=toth,hl=hl.int,paramod=coefs,p=p.coef)
cbind(hl.int,dl.hat)
```

`lang.fx` *Function to computes the result of the Curtis's allometric model.*

Description

Function of the Langhmuir model, based upon two parameters, and a single predictor variable, as follows

$$y_i = \alpha \left(\frac{1}{1 + \frac{1}{\beta x_i}} \right),$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details of this function can be found in Salas-Eljatib (2025).

Usage

```
lang.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Khayyun TS, Mseer AH. 2019. Comparison of the experimental results with the Langmuir and Freundlich models for copper removal on limestone adsorbent. Applied Water Science 9(8):170.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(.1,60,by=0.01)
# Using the function
y<-lang.fx(x=time, alpha=37,beta=0.05)
plot(time,y,type="l")
```

`largeplot` *Tree spatial coordinates in a large sample plot in Fennoscandia*

Description

Data from a large (8.8 ha) fully mapped plot in a Norway spruce (*Picea abies*) dominated old-growth forest in the subarctic region of Fennoscandia.

Usage

```
data(largeplot)
```

Format

Contains Cartesian position of trees and other variables in a large sample plot, as follows:

tree Tree ID.

spp.code Species code as follows: 1=Pinus sylvestris,2=Picea abies,3=Betula pubescens, 5=Salix caprea, 8: Sorbus aucuparia.

x.coord Cartesian position in the X-axis, in m.

y.coord Cartesian position in the Y-axis, in m.

status Measurement year.

dbh Diameter at breast-height, in cm.

toth Total height, in m.

Source

Data were retrieved from the paper cited below, where several details might be worth reading.

References

- Pouta P, Kulha N, Kuuluvainen T, Aakala T. 2022. Partitioning of space among trees in an old-growth spruce forest in subarctic Fennoscandia. Frontiers in Forests and Global Change 5: 817248. doi:10.3389/ffgc.2022.817248

Examples

```
data(largeplot)
head(largeplot)
df<-largeplot
pine <- df[df$spp.code==1,]
spruce <- df[df$spp.code==2,]
birch <- df[df$spp.code==3,]
plot(spruce$x.coord,spruce$y.coord,cex=(spruce$dbh)/30,col="blue")
points(birch$x.coord,birch$y.coord,cex=(birch$dbh)/30,col="green")
points(pine$x.coord,pine$y.coord,cex=(pine$dbh)/30,col="red")
```

`logist.fx` *A function having the mathematical expression of the Logistic model.*

Description

Function of the Logistic model, based upon three parameters and a single predictor variable as follows

$$y_i = \frac{\alpha}{1 + \mathrm{e}^{\beta - \gamma x_i}},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
logist.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f\,(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Pearl R. 1909. Some recent studies on growth. The American Naturalist 43(509):302-316.
- Salas-Eljatib C, Mehtatalo L, Gregoire TG, Soto DP, Vargas-Gaete R. 2021. Growth equations in forest research: mathematical basis and model similarities. Current Forestry Reports 7:230-244. doi:10.1007/s40725021001458
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-logist.fx(x=time,alpha=22,beta=1.4,gamma=.1)
plot(time,y,type="l")
#'
```

`logistm.fx` *A function having the mathematical expression of the Logistic modified model.*

Description

Function of the Logistic modified model, based upon three parameters and a single predictor variable as follows

$$y_i = \frac{\alpha}{1 + \mathrm{e}^{-(x_i - \beta)/\gamma}},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
logistm.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f\,(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Pearl R. 1909. Some recent studies on growth. The American Naturalist 43(509):302-316.
- Pinheiro JC, DM Bates. 2000. Mixed-effects Models in S and Splus. New York, USA. Springer-Verlag. 528 p.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(0.1,65,by=0.01)
# Using the function
y<-logistm.fx(x=time,alpha=22,beta=8.59,gamma=4.72)
plot(time,y,type="l")
#'
```

`meyer.fx` *A function having the mathematical expression of the Meyer model.*

Description

Function of the Meyer model, based upon two parameters and a single predictor variable as follows

$$y_i = \alpha \left(1 - \mathrm{e}^{-\beta x_i}\right),$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
meyer.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Meyer HA. 1940. A mathematical expression for height curves. Journal of Forestry 38(5):415-420.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-meyer.fx(x=time,alpha=20,beta=.07)
plot(time,y,type="l")
```

`mmenten.fx` *A function having the mathematical expression of the Michaelis-Menten model.*

Description

Function of the Michaelis-Menten model, based upon two parameters and a single predictor variable as follows

$$y_i = \alpha \left(\frac{x_i}{\beta + x_i} \right),$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
mmenten.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Michaelis L, ML Menten. 1913. Die kinetik der invertinwirkung. Biochemische Zeitschrift 49:333–369.
- Salas-Eljatib C, P Corvalán, N Pino, PJ Donoso, DP Soto.

1. Modelos de efectos mixtos de altura-diámetro para *Drimys winteri* en el sur (41-43 S) de Chile. Bosque 40(1):71-80.

- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-mmenten.fx(x=time,alpha=30,beta=13)
plot(time,y,type="l")
```

`mmweibull` *Function to estimates the parameters of the Weibull probability density function using the method of moments*

Description

Estimates the parameters of the Weibull probability density function based on the method of moments. It is based on the 2-parameter reparemetrization of the function, i.e., the `shape` and `scale` parameters.

Usage

```
mmweibull(y)
```

Arguments

`y`	a vector having the randon variable values.

Details

Althought the original function was written by Dr Oscar García, and the corresponding reference is provided, the current function has some changes to make it of a broader use.

Value

The main output is a list with the two estimated parameters and the number of observations being used for estimating the parameters.

Author(s)

Dr Oscar García and Christian Salas-Eljatib.

References

- García, O. 1981. Simplified method-of-moments estimation for the Weibull distribution. New Zealand Journal of Forestry Science 11(3): 304-306.

Examples

```
# Random variable to be studied
library(datana)
yvar<-llancahue$dbh
summary(yvar)
hist(yvar)
# Using the  function
mmweibull(y=yvar)
```

`mortaforest` *Climatic, forest structure and forest mortality variables in California (USA)*

Description

The data file contains one row per unique 3.5km grid cell by year combination. The data frame covers all grid cells within the state of California where at least one Aerial Detection Survey (ADS) flight was taken between 2009 and 2015, so each grid cell position has between 1 and 7 years of data (reflected as 1 to 7 rows in the data file per grid cell position). The main response variables are `mort.bin` (presence of any mortality) and `mort.tph` (number of dead trees/ha within the given grid cell by year).

Usage

```
data(mortaforest)
```

Format

The data frame contains four variables as follows:

live.bah Live basal area from the GNN dataset

live.tph Live trees per hectare from the GNN dataset

pos.x rank-order x-position of the grid cell (position `1` is western-most)

pos.y rank-order y-position of the grid cell (position `1` is northern-most)

alb.x x-coordinate of the grid cell centroid in California Albers (EPSG 3310)

alb.y y-coordinate of the grid cell centroid in California Albers (EPSG 3310)

mort.bin `1`= dead trees observed in grid cell. `0`= no dead trees observed

mort.tph Dead trees per hectare from the aggregated ADS dataset

mort.tpa Dead trees per acre from the aggregated ADS dataset

year Year of the ADS flight. Most flights occurred from May-August.

Defnorm Mean annual climatic water deficit for the grid cell, for Oct 1-Sept 31 water year, averaged from 1981-2015

Def0 Climatic water deficit for the grid cell during the Oct-Sept water year overlapping the summer ADS flight of the given year

Defz0 Z-score for climatic water deficit for the given grid cell/water year. Calculated as (`Def0`–`Defnorm`)/(standard deviation in deficit among all years 1981-2015 for the given grid cell)

Defz1 Z-score for climatic water deficit for the given grid cell in the preceeding water year.

Defz2 Z-score for climatic water deficit for the given grid cell two water years prior.

Tz0 Z-score for temperature for the given grid cell/year.

Pz0 Z-score for precipitation for the given grid cell/year.

Defquant FDCI variable. Quantile of `Defnorm` of the given grid cell, relative to the `Defnorm` of all other grid cells with a basal area within 2.5 m^2/ha of the given cell is basal area.

Source

The data were obtained from the DRYAD repository doi:10.5061/dryad.7vt36

References

- Young DJN, Stevens JS, Earles JM, Moore J, Ellis A, Jirka AM, Latimer ML. 2017. Long-term climate and competition explain forest mortality patterns under extreme drought. Ecology Letters 20(1):78-86. doi:10.1111/ele.12711
- Salas-Eljatib C, Fuentes-Ramírez A, Gregoire TG, Altamirano A, Yaitul V. A study on the effects of unbalanced data when fitting logistic regression models in ecology. Ecological Indicators 85:502-508. doi:10.1016/j.ecolind.2017.10.030

Examples

```
data(mortaforest)
head(mortaforest)
```

`mortaforest2` *Mortalidad en bosques, y variables climáticas y de estructura forestal en California (USA)*

Description

El archivo de datos contiene una fila por combinación única de celda de cuadrícula de 3,5 km por año. El marco de datos cubre todas las celdas de la cuadrícula dentro del estado de California donde se tomo al menos un vuelo de la Encuesta de deteccion aérea (ADS) entre 2009 y 2015, por lo que cada posición de celda de la cuadrícula tiene entre 1 y 7 años de datos (reflejados como 1 a 7 filas en el archivo de datos por posición de celda de cuadrícula). Las principales variables de respuesta son `mort.bin` (presencia de alguna mortalidad) y `mort.tph` (número de árboles muertos /ha dentro de la celda de la cuadrícula por año).

Usage

```
data(mortaforest2)
```

Format

Las variables se describen a continuación::

live.bah Área basal viva del conjunto de datos GNN

live.tph Árboles vivos por hectárea del conjunto de datos GNN

pos.x Posición `X` del orden de clasificación de la celda de la cuadrícula (la posición `1` es la más occidental)

pos.y Posición `Y` del orden de clasificación de la celda de la cuadrícula (la posición `1` es la más al norte)

alb.x Coordenada `X` del centroide de la celda de la cuadrícula en California Albers (EPSG 3310)

alb.y Coordenada `Y` del centroide de la celda de la cuadrícula en California Albers (EPSG 3310)

mort.bin Codificación para identificar mortalidad. `1` = árboles muertos observados en la celda de la cuadrícula. `0` = no se observaron árboles muertos

mort.tph Árboles muertos por hectárea del conjunto de datos ADS agregado

mort.tpa Árboles muertos por acre del conjunto de datos ADS agregado

year año del vuelo de ADS. La mayoría de los vuelos se realizaron entre mayo y agosto

Defnorm Déficit hídrico climático anual medio para la celda de la cuadrícula, para el año hídrico del 1 de octubre al 31 de septiembre, promediado de 1981 a 2015

Def0 Déficit de agua climática para la celda de la cuadrícula durante el año hidrológico de octubre a septiembre que se superpone al vuelo ADS de verano del año dado

Defz0 Puntaje Z para el déficit hídrico climático para la celda de cuadrícula / año hídrico dado. Calculado como (`Def0`–`Defnorm`) / (desviación estándar en el déficit entre todos los años 1981-2015 para la celda de la cuadrícula dada)

Defz1 Puntuación Z para el déficit hídrico climático para la celda de la cuadrícula dada en el año hidrológico anterior.

Defz2 Puntuación Z para el déficit hídrico climático para la celda de la cuadrícula dada dos años antes.

Tz0 Puntaje Z para la temperatura para la celda de cuadrícula / año dado.

Pz0 Puntaje Z para la precipitación para la celda / año de la cuadrícula dado.

Defquant Variable FDCI. Cuantil de `Defnorm` de la celda de la cuadrícula dada, en relación con la `Defnorm` de todas las demás celdas de la cuadrícula con un área basal dentro de 2.5 m^2/ha de la celda dada

Source

Los datos fueron obtenidos desde el repositorio DRYAD en doi:10.5061/dryad.7vt36

References

- Young DJN, Stevens JS, Earles JM, Moore J, Ellis A, Jirka AM, LatimerML. 2017. Long-term climate and competition explain forest mortality patterns under extreme drought. Ecology Letters 20(1):78-86. doi:10.1111/ele.12711
- Salas-Eljatib C, Fuentes-Ramírez A, Gregoire TG, Altamirano A, and Yaitul V. 2018. A study on the effects of unbalanced data when fitting logistic regression models in ecology. Ecological Indicators 85:502-508. doi:10.1016/j.ecolind.2017.10.030

Examples

```
data(mortaforest2)
head(mortaforest2)
```

`naslund.fx` *A function having the mathematical expression of the Naslund model.*

Description

Function of the Naslund model, based upon two parameters and a single predictor variable as follows

$$y_i = \frac{x_i^2}{(\alpha + \beta x_i)^2},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
naslund.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Näslund M. 1947. Skogsförsöksanstaltens gallringsförsök i tallskog. Technical report. Biochemische Zeitschrift 49:333–369.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-naslund.fx(x=time,alpha=1.5,beta=.37)
plot(time,y,type="l")
```

`nele.list` *Extract the n-th element from a list*

Description

Extract the n-th element from a list

Usage

```
nele.list(lst, n)
```

Arguments

`lst`	is the list object
`n`	is the position of the element in the list to be retrieved

Value

object with elements of each list

Author(s)

Christian Salas-Eljatib

Examples

```
x <- list(list("z","x","y"), list(3,4,99,23,45), list(1,67,5,6,89))
nele.list(x,1)
nele.list(x,2)
nele.list(x,3)
```

`ogawa.fx` *Function that computes the result of the Ogawa allometric model.*

Description

Function of the Ogawa allometric model, based upon parameters (i.e., coefficients) and a variable, as defined by the mathematical expression

$$y_i = \left(\frac{1}{\alpha} + \frac{1}{\beta {x_i}^{\gamma}} \right)^{-1},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this function can be found in Salas-Eljatib (2025).

Usage

```
ogawa.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the inverse of the response variable based upon the predictor variable and the coefficients shown above.

Author(s)

Christian Salas-Eljatib.

References

- Kohyama T, T Hara, T Tadaki. 1990. Patterns of trunk diameter, tree height and crown depth in crowded abies stands. Annals of Botany 65(5):567–574.
- Salas-Eljatib C. 2026. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 53 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
d<-ogawa.fx(x=time,alpha=22,beta=0.013,gamma=1.13)
plot(time,d,type="l")
```

`pinaster` *Tree volume for Pinus pinaster in the Baixo-Mino, Galicia, Spain*

Description

These are volume measurements data of sample trees in the Baixo-Mino region in Galicia, Spain.

Usage

```
data(pinaster)
```

Format

Contains tree-level variables, as follows:

stand Stand number from the sample tree was selected.

si Site index of the stand.

tree.no Tree number.

dbh Diameter at breast height, in cm.

toth Total height, in m.

d4 Upper-stem diameter at 4 m, in cm.

volwb Tree gross volume, in m^3 with bark.

volwob Tree gross volume, in m^3 without bark.

Source

The data are provided courtesy of Dr. Christian Salas-Eljatib at the Universidad de Chile (Santiago, Chile).

References

- Salas C, Nieto L, Irisarri A. 2005. Modelos de volumen para Pinus pinaster Ait. en la comarca del Baixo Mino, Galicia, España. Quebracho 12: 11-22. https://eljatib.com/publication/2005-12-01_modelos_de_volumen_p/

Examples

```
data(pinaster)
head(pinaster)
```

`pinaster2` *Volumen individual de árboles de Pinus pinaster en Galicia, España*

Description

Variables de volumen y otras a nivel de árbol para una muestra de árboles de Pinus pinaster en la comarca del Baixo-Mino en Galicia, España.

Usage

```
data(pinaster2)
```

Format

Contiene las siguientes variables a nivel de árbol:

rodal Rodal desde donde el árbol fue muestreado

ind.sitio Índice de sitio del rodal, en m.

arbol Número del árbol.

dap Diámetro a la altura del pecho, en cm.

atot Altura total, en m.

d4 Diámetro fustal a los 4 m, en cm.

vtcc Volumen bruto total con corteza, en m^3.

vtsc Volumen bruto total sin corteza, en m^3.

Source

Lo datos fueron cedidos cortesía del Dr. Christian Salas-Eljatib de la Universidad de Chile (Santiago, Chile).

References

- Salas C, Nieto L, Irisarri A. 2005. Modelos de volumen para Pinus pinaster Ait. en la comarca del Baixo Miño, Galicia, España. Quebracho 12: 11-22. `https://eljatib.com/publication/2005-12-01_modelos_de_volumen_p/`

Examples

```
data(pinaster2)
head(pinaster2)
```

`pinusSpp` *Tree-level variables of several sample plots of invasive Pinus spp in Chile*

Description

These are tree-lavel measurement data from Pinus spp invasion in *Araucaria-Nothofagus* forests in the Malalcahuello National Reserve in La Araucanía region in southhern Chile, measured in 2012. There are 26 plots and plot size is 100 m².

Usage

```
data(pinusSpp)
```

Format

Contains eight variables, as follows:

plot.id Plot sample ID.

plot.size Plot size, en m^2.

lat.s Decimal coordinate of S latitude.

long.w Decimal coordinate of W longitude.

indv.id Tree identificator number in each plot. Same `indv.id` for multi-stem trees.

stem.id Stem identificator number in each plot.

spp Species.

dbh Diameter at breast-height, in cm.

toth Total height, in m.

hcb Height to crown base, in m.

crown.lenght Crown lenght, in m.

Source

The data is provided courtesy of Drs. Aníbal Pauchard and Rafael García at the Laboratorio de Invasiones Biológicas, Universidad de Concepción (Concepción, Chile).

References

- Cobar-Carranza A, Garcia R, Pauchard A, Pena E. 2014. Effect of *Pinus contorta* invasion on forest fuel properties and its potential implications on the fire regime of *Araucaria araucana* and *Nothofagus antarctica* forests. Biological Invasions. 16(11): 2273-2291. doi:10.1007/s1053001406638

Examples

```
data(pinusSpp)
head(pinusSpp)
length(unique(pinusSpp$plot.id))
boxplot(dbh~plot.id, data=pinusSpp)
```

`pinusSpp2` *Variables a nivel de árbol en parcelas de muestreo de Pinus spp en Chile.*

Description

Mediciones a nivel de árbol para estudiar la invasión de Pinus spp en bosques de *Araucaria-Nothofagus* en la Reserva Nacional Malalcahuello en la región de la Araucanía en el sur de Chile. Hay 26 parcelas, y la superficie de cada una es de 100 m^2.

Usage

```
data(pinusSpp2)
```

Format

Los datos contienen ocho columnas que se detallan a continuación:

parcela Número de la parcela.

sup.parcela Superficie de la parcela, en m^2.

lat.s Coordenada decimal latitud S.

long.w Coordenada decimal longitud W.

indv.id Identificador del árbol en la parcela. Mismo `indv.id` para árboles multi-fustales

fuste.id Identificador del fuste.

espe Especie.

dap Diámetro a la altura del pecho, en cm.

atot Altura total, en m.

hcc Altura comienzo de copa, en m.

largo.copa Largo de copa, en m.

Source

Los datos fueron cedidos por los Drs. Aníbal Pauchard y Rafael García del Laboratorio de Invasiones Biológicas, Universidad de Concepción (Concepción, Chile).

References

- Cobar-Carranza A, Garcia R, Pauchard A & Pena E. 2014. Effect of Pinus contorta invasion on forest fuel properties and its potential implications on the fire regime of *Araucaria araucana* and Nothofagus antarctica forests. Biological Invasions. 16(11):2273-2291. doi:10.1007/s1053001406638

Examples

```
data(pinusSpp2)
head(pinusSpp2)
length(unique(pinusSpp2$parce))
boxplot(dap~parce, data=pinusSpp2)
```

`plantshawaii` *Maximum plant size in the Hawaiian archipelago*

Description

Maximum plant size of 58 tree species, shrub and tree fern species that occur in 530 forest plots across the Hawaiian archipelago.

Usage

```
data(plantshawaii)
```

Format

Contains six columns, as follows:

species Genus and epithet of the species.

family Family of each species.

native.status Categorical variable (`native`, `alien`, `uncertain`) indicating alien status of each individual following Wagner *et al.* (2005).

n Number of individuals used to estimate maximum plant size.

d95 Maximum plant size, estimated as `D950.1` (King *et al.* 2006).

dmax3 Maximum plant size, estimated as `Dmax3` (King *et al.* 2006).

Source

The data were obtained from the DRYAD repository at doi:10.5061/dryad.1kk02qr.

References

- Craven D, Knight T, Barton K, Bialic-Murphy L, Cordell S, Giardina C, Gillespie T, Ostertag R, Sack L,Chase J. 2018. OpenNahele: the open Hawaiian forest plot database. Biodiversity Data Journal 6: e28406.

Examples

```
data(plantshawaii)
head(plantshawaii)
tapply(plantshawaii$d95,plantshawaii$native.status,summary)
```

`popvol` *Population of stand-volume for 400 elements.*

Description

The data corresponds to a list of 400 elements of a population of the variable forest volume (in m^3/ha) measured in field plots of 0.1 ha of area. Therefore, the data emerge from a grid of 20 rows by 20 columns, completely covering a forest of 40 ha.

Usage

```
data(popvol)
```

Format

Contains two variables, as follows:

plot.id Plot number, or ID.

vol Stand volume, in m^3/ha

Source

The values were digitized from Table No. 11 of Zohrer (1980), which is actually based upon Loetsch and Haller (1964).

References

- Zohrer F. 1980. Forstinventur. Ein Leitfaden fur Studium und Praxis. Pareys Studientexte Nr. 26. Parey. Berlin, Germany. 207
- Loetsch F, Haller KE. 1964. Forest inventory. Volume 1. Bayerischer Landwirtschaftsverlag Gmbh. Munchen, Germany. 436 p.

Examples

```
data(popvol)
sum(popvol$vol)
mean(popvol$vol)
hist(popvol$vol)
```

`popvol2` *Población de 400 elementos de la variable volumen de bosque*

Description

Los datos corresponden a una lista de 400 elementos de un población de la variable volumen de bosque (en m^3/ha), medida en parcelas de 0.1 ha de superficie. Por lo tanto, los datos provienen de una grilla de 20 filas por 20 columnas, que cubren por completo un bosque de 40 ha de superficie.

Usage

```
data(popvol2)
```

Format

Contiene las siguientes dos columnas:

plot.id Número de parcela (*i.e.*, elemento de la población).

vol Volumen en m^3/ha

Source

Datos digitados desde el cuadro No. 11 de Zohrer (1980), el cual es en realidad un cuadro citado del libro de Loetsch y Haller (1964).

References

- Zohrer F. 1980. Forstinventur. Ein Leitfaden fur Studium und Praxis. Pareys Studientexte Nr. 26. Parey. Berlin, Germany. 207
- Loetsch F, Haller KE. 1964. Forest inventory. Volume 1. Bayerischer Landwirtschaftsverlag Gmbh. Munchen, Germany. 436 p.

Examples

```
data(popvol2)
sum(popvol2$vol)
mean(popvol2$vol)
hist(popvol2$vol)
```

`power.fx` *Function to computes the result of the power model, as a classical allometric functional form.*

Description

Function of the power model, based upon the model parameters, and a single predictor variable as follows

$$y_i = \alpha x_i^{\beta}$$

where: y_i and x_i are the response and predictor variable, respectively for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
power.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable to be used is 30
# Using the function
power.fx(x=30,alpha=2.86,beta=.49)
```

`prodan.fx` *A function having the mathematical expression of the Naslund model.*

Description

Function of the Naslund model, based upon three parameters and a single predictor variable as follows

$$y_i = \frac{x_i^2}{\left(\alpha + \beta x_i\right)^2},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
prodan.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f\left(x_i, \theta\right)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Näslund M. 1947. Skogsförsöksanstaltens gallringsförsök i tallskog. Technical report. Biochemische Zeitschrift 49:333–369.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-prodan.fx(x=time,alpha=2.06,beta=.41,gamma=.03)
plot(time,y,type="l")
```

`radiatapl` *Sampling plots data from a Pinus radiata plantation near Capitán Pastene, La Araucanía region, Chile.*

Description

Tree-level information collected within sample plots in a forestry 13 years-old plantation of *Pinus radiata* near Capitán Pastene, Southern Chile. The sample plots size is 150 m², and the total area of the plantation is 45 ha.

Usage

```
data(radiatapl)
```

Format

The data frame contains four variables as follows:

plot Plot number identification.

tree Tree number identification.

dbh Diameter at breast height (1.3 m), in cm.

heigth Total height, in m. Not measured for all trees.

sanity Tree-health clasification, assigned to any of the following levels: good, medium, and bad.

Source

The data are provided courtesy of Mr. Mauricio Lobos-Beneventi (Temuco, Chile), and were collected with the help of his colleague, Christian Salas-Eljatib.

Examples

```
data(radiatapl)
head(radiatapl)
```

`radiatapl2` *Datos a nivel de árbol de parcelas de muestreo en plantaciones de Pinus radiata*

Description

Es un listado de árboles con características de árboles medidos dentro de unidades de muestreo en una plantación de 13 años de edad de *Pinus radiata* ubicada cerca a Capitán Pastene, región de la Araucanía, Chile. Las parcelas de muestreo tienen 150 m², y la plantación cubre una superficie total de 45 ha.

Usage

```
data(radiatapl2)
```

Format

Los datos contienen las siguientes columnas

parce Número de identificación de la parcela de muestreo.

arbol Número de identificación del árbol dentro de la parcela.

dap Diámetro a la altura del pecho (1.3 m), en cm.

atot Altura total, en m. Solo registrada para algunos árboles muestra.

sanidad Clasificación sobre el estado sanitario del árbol, en tres niveles: buena, media, y mala.

Source

Los datos son cortesía del Ing. Forestal Mauricio Lobos-Beneventi (Temuco, Chile), y fueron recolectados en conjunto con su colega Christian Salas-Eljatib.

Examples

```
data(radiatapl2)
head(radiatapl2)
```

`ratkow.fx` *Function that computes the result of the Ratkowsky allometric model.*

Description

Function of the Ratkowsky allometric model, based upon parameters (i.e., coefficients) and a variable, as defined by the mathematical expression

$$y_i = \alpha \mathrm{e}^{\left(\frac{-\beta}{x_i+\gamma}\right)},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this function can be found in Salas-Eljatib (2025).

Usage

```
ratkow.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Zhang L. 1997. Cross-validation of non-linear growth functions for modelling tree height-diameter relationships. Annals of Botany 79(3):251–257.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
d<-seq(5,60,by=0.01)
# Using the function
h<-ratkow.fx(x=d,alpha=28,beta=34,gamma=.85)
plot(d,h,type="l")
```

`schnute.fx` *Function that computes the result of the Schnute allometric model.*

Description

Function of the Schnute allometric model, based upon parameters (i.e., coefficients) and a variable, as defined by the mathematical expression

$$y_i = \left\{ \Upsilon^{\alpha} + (\gamma^{\alpha} - \Upsilon^{\alpha}) \frac{1 - \mathrm{e}^{-\beta(x_i)}}{1 - \mathrm{e}^{-\beta(x_2)}} \right\}^{1/\alpha},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this function can be found in Salas-Eljatib et al (2021).

Usage

```
schnute.fx(x, alpha, beta, gamma, upsilon = 0, x1 = min(x), x2 = max(x))
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. The default value for Υ is 0.
`x1`	is the minimum value for the x variable. The default value is internally computed from the sample.
`x2`	is the maximumvalue for the x variable. The default value is internally computed from the sample.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Schnute I. 1981. A versatile growth model with statistically stable parameters. Can. J. Fish. Aquat. Sci. 38(9):1128-1140.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
d<-seq(5,60,by=0.01)
# Using the function
h<-schnute.fx(x=d,alpha=1.77,beta=0.01,gamma=28)
plot(d,h,type="l")
```

`schuma.fx` *A function having the mathematical expression of the Johnson-Schumacher model.*

Description

Function of the Johnson-Schumacher model, based upon two parameters and a single predictor variable as follows

$$y_i = \alpha \mathrm{e}^{(-\beta/x_i)},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this model can be found in Salas-Eljatib et al (2021) and Salas-Eljatib (2025).

Usage

```
schuma.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Johnson NO. 1935. A trend line for growth series. J. Am. Stat. Assoc. 30(192):717-717.
- Schumacher FX. 1939. A new growth curve and its application to timber yield studies. J. of Forestry 37(10):819-820.
- Salas-Eljatib C, Mehtatalo L, Gregoire TG, Soto DP, Vargas-Gaete R. 2021. Growth equations in forest research: mathematical basis and model similarities. Current Forestry Reports 7:230-244. doi:10.1007/s40725021001458
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
d<-seq(5,60,by=0.01)
# Using the function
h<-schuma.fx(x=d,alpha=3.87,beta=4.38)
plot(d,h,type="l")
```

`sibbesen.fx` *A function having the mathematical expression of the Sibbesen model.*

Description

Function of the Sibbesen model, based upon three parameters and a single predictor variable as follows

$$y_i = \alpha \left(x_i\right)^{-\beta x_i{}^{-\gamma}},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
sibbesen.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Sibbesen E. 1981. Some new equations to describe phosphate sorption by soils. Journal of Soil Science 32:67-74.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-sibbesen.fx(x=time,alpha=32,beta=0.52,gamma=4.83)
plot(time,y,type="l")
```

`spataustria` *Tree locations within sample plots in an experimental forest in Austria*

Description

The Austrian Research Center for Forests established a spacing experiment with Norway spruce (*Picea abies*) in the Vienna Woods. In the “Hauersteig” experiment, several tree-level variables were measured within four sample plots over time. **The current dataframe has only the measurements carried out in 1944**, for all years see `biometrics::spatimepsp`.

Usage

```
data(spataustria)
```

Format

Contains cartesian position of trees, and covariates, in sample plots, as follows:

plot Plot number.

tree Tree number.

species Species code as follows: PCAB=*Picea abies*, LADC=*Larix decidua*, PNSY=*Pinus sylvestris*, FASY=*Fagus Sylvatica*, QCPE=*Quercus petraea*, BTPE=*Betula pendula*.

x.coord Cartesian position in the X-axis, in m.

y.coord Cartesian position in the Y-axis, in m.

year Measurement year.

dbh Diameter at breast-height, in cm.

Source

Data were retrieved from the paper cited below, where several details might be worth reading. For instance, plot size slightly varies among plots: Plot No. 1=2509.7 m^2, Plot No. 2=2474.8 m^2, Plot No. 3=2415.9 m^2, and Plot No. 4=2482.8 m^2.

References

- Kindermann G. Kristofel F, Neumann M, Rossler G, Ledermann T & Schueler. 2018. 109 years of forest growth measurements from individual Norway spruce trees. Sci. Data 5:180077 doi:10.1038/sdata.2018.77

Examples

```
data(spataustria)
head(spataustria)
df<-spataustria
oldpar<-par(mar=c(4,4,0,0))
bord<-data.frame(
 x=c(min(df$x.coord),max(df$x.coord),min(df$x.coord),max(df$x.coord)),
 y=c(min(df$y.coord),min(df$y.coord),max(df$y.coord),min(df$y.coord))
 )
plot(bord,type="n", xlab="x (m)", ylab="y (m)", asp=1, bty='n')
points(df$x.coord,df$y.coord,col=df$plot,cex=0.5)
par(oldpar)
```

`spatimepsp` *Temporal tree locations within a sample plot in the Vienna woods*

Description

The Austrian Research Center for Forests established a spacing experiment with Norway spruce (*Picea abies*) in the Vienna Woods. In the “Hauersteig” experiment, several tree-level variables were measured within four sample plots over time.

Usage

```
data(spatimepsp)
```

Format

Contains cartesian position of trees, and covariates, in a sample plot, as follows:

plot Plot number.

tree Tree number.

species Species code as follows: PCAB=*Picea abies*, LADC=*Larix decidua*, PNSY=*Pinus sylvestris*, FASY=*Fagus Sylvatica*, QCPE=*Quercus petraea*, BTPE=*Betula pendula*.

x.coord Cartesian position in the X-axis, in m.

y.coord Cartesian position in the Y-axis, in m.

year Measurement year.

dbh diameter at breast-height, in cm.

Source

Data were retrieved from the paper cited below, where several details might be worth reading.

References

- Kindermann G. Kristofel F, Neumann M, Rossler G, Ledermann T & Schueler. 2018. 109 years of forest growth measurements from individual Norway spruce trees. Sci. Data 5:180077 doi:10.1038/sdata.2018.77

Examples

```
data(spatimepsp)
head(spatimepsp)
df<-spatimepsp
lattice::xyplot(y.coord~x.coord|as.factor(year),
data=df,as.table=TRUE)
```

`spplist` *List of botanical attributes of plant species*

Description

List of botanical attributes of plant species

Usage

```
data(spplist)
```

Format

The list contains the following fields:

numtaxon Unique number of the taxon (i.e., species).

kingdom Taxonomic rank Kingdom. In this datase, all species belong to the Kingdom Plantae.

division Taxonomic rank division or phylum within the Kingdom.

class Taxonomic rank Class within the Kingdom.

orden Taxonomic rank Order within the Class.

family Taxonomic rank Family within the Order.

spp.ci.full Full scientific name including author.

spp.ci.gen Solely the genus of the scientific name.

spp.ci.epi Solely the epithet of the scientific name.

authorspp Species botanical-author.

subspp Subspecies: one of two or more populations of a species varying from one another by morphological characteristics.

authorsubspp Sub-species botanical-author.

variety

authorvar

shape Shape

authorshape Shape's author.

comnames Species common name(s). With blank spaces, no special characters.

synonymy Synonyms of the scientific name by which the species has been or is known.

borcount Border countries given the species distribution range.

habit The general appearance, growth form, or architecture e.g., tree, shrub, grass.

lifecycle Life cycle.

statusori Status according to the species origin: Native or Endemic

regdist Distribution range of the species, within Chile administrative regions

elerange Elevation range of the species, in meters above sea level.

note

sppcode Abreviattion of the species according to the Forest Biometrics and Modelling Lab at the Universidad de Chile (`https://biometriaforestal.uchile.cl`). For instance, `ap` stands for the species *Aextoxicon punctatum*, `lh` for *Lomatia hirsuta*, and alike. Meanwhile `nob` is *Nothofagus obliqua* and `nal` to *Nothofagus alpina*.

spp.name Species common name. No blank spaces, no special characters.

spp.ci.abb Species scientific name abbreviation.

spp.ci.name Species scientific name.

spp.co.name.latex Species common name in LaTeX

spp.co.name Species single common name.

`stage.fx` *Function that computes the result of the Stage allometric model.*

Description

Function of the Stage allometric model, based upon parameters (i.e., coefficients) and a variable, as defined by the mathematical expression

$$y_i = \alpha \mathrm{e}^{\left(-\beta ({x_i}^{-\gamma})\right)},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients). Further details on this function can be found in Salas-Eljatib (2025).

Usage

```
stage.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Stage AR. 1963. A mathematical approach to polymorphic site index curves for Grand Fir. Forest Sci. 9(2):167-180. doi:10.1093/forestscience/9.2.167
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
d<-stage.fx(x=time,alpha=28,beta=56,gamma=1.19)
plot(time,d,type="l")
```

`standtab` *Function to creates a stand for a given imputed-tree-list of a sample plot.*

Description

Creates a stand table, i.e. a table that describes the tree density of a forest segregated by a tree-size variable `y`. The most common example is to use diameter at breast-heigth (i.e., d) as the variable, thus the resulting table is a way to describe the diameter distribution.

Usage

```
standtab(
  data,
  plot.area,
  y.for.class,
  yclass.amp,
  metric = TRUE,
  want.basal.area = FALSE,
  ...
)
```

Arguments

`data`	data frame having the tree list of a sample plot.
`plot.area`	column name having the plot area in m^2.
`y.for.class`	a text of the column-name having the tree-size variable to be used to segregated the tree density.
`yclass.amp`	a numeric value establishing the width of each class of the variable `y.for.class`. The measurement unit must be the same as the one of the variable `y.for.class`.
`metric`	is a logic value, the default is to `TRUE`, thus the diameter `d` has to be in cm, and the resulting tree-level basal area will be in m^2. If `metric` is `FALSE`, the diameter `d` has to be in inches, and the computed tree basal area will be in ft^2.
`want.basal.area`	is a logic value, if set to `TRUE`, the stand basal area, segregated by the classes of they`.for.class` is added as a column, next to the tree density one. The basal area column by class is expressed in m^2/ha. The default for this option is `FALSE`.
`...`	aditional options for basic stats functions.

Details

For a given imputed tree list of a sample plot, tree density is computed by classes of the tree-size variable. Note that the imputed-tree list must have all the tree-level variables needed to compute stand-level variables, such as, diameter and plot size.

Value

Returns a stand table.

Author(s)

Christian Salas-Eljatib.

References

- Salas-Eljatib C. 2025. Biometría y Modelación Forestal. Borrador de libro, en revisión. 352 p.

Examples

```
## Dataframe to be used
df<-biometrics::eucaplot2
#see the metadata by typing ?eucaplot2
head(df)
datana::descstat(df[,c("dap","atot")])
## Preparing the treelist, in the required format
df$parce<-1;df$sup.plot<-500;amp.diam=2;
out<-standtab(data=df,plot.area="sup.plot",y.for.class = "dap",
              yclass.amp = amp.diam)
out
#the following sum
sum(out$nha.class)
# must be equal to the stand-level density (in trees/ha)
df$expf<-10000/df$sup.plot;sum(df$expf)
# Do you want to add the stand basal area segregated by `y.for.class`
out2<-standtab(data=df,plot.area="sup.plot",y.for.class = "dap",
               yclass.amp = amp.diam, want.basal.area = TRUE)
out2
#the following sum
sum(out2$gha.class)
# must be equal to the stand-level basal area (in m2/ha)
df$g<-gtree(x=df$dap);df$gtree.ha<-df$g*df$expf;sum(df$gtree.ha)
```

`standtabCoihue` *Stand table for a* Nothofagus dombeyi *(coihue) forest*

Description

Stand table for a secondary forest of *Nothofagus dombeyi* (coihue) en Chile.

Usage

```
data(standtabCoihue)
```

Format

The data has the following columns

diam.cl Diameter class, in cm.

nha Density for the respective diameter class, in trees/ha.

gha Basal area for the respective diameter class, in m^2/ha.

Source

The forest was located in the Andean foothills in the Araucanía region in southern Chile. Data from Prof. Christian Salas-Eljatib, Universidad de Chile, Santiago, Chile.

References

- Donoso C. 1995. Bosques Templados de Chile y Argentina. Editorial Universitaria. Santiago, Chile.

Examples

```
data(standtabCoihue)
df<-standtabCoihue
df<-df[-nrow(df),]
# Diameter distribution plot
barplot(df$nha, legend = TRUE, beside = TRUE, las=1,
        names.arg = as.numeric(df$diam.cl),
        ylab="Density (trees/ha)",xlab="Diameter class (cm)")
abline(h=0)
```

`standtabCoihue2` *Tabla de rodal para bosque de* Nothofagus dombeyi *(coihue)*

Description

Tabla de rodal para un bosque secundario de *Nothofagus dombeyi* (coihue) en Chile.

Usage

```
data(standtabCoihue2)
```

Format

Los datos tienen las siguientes columnas

cd Marca de la clase diamétrica, en cm.

nha Densidad de la clase diamétrica, en arb/ha.

gha Área basal de la clase diamétrica, en m^2/ha.

Source

Bosque ubicado en sector Andino de la Región de la Araucanía en el sur de Chile. Cuadro cedido por el Prof. Christian Salas-Eljatib, Universidad de Chile, Santiago, Chile.

References

- Donoso C. 1995. Bosques Templados de Chile y Argentina. Editorial Universitaria. Santiago, Chile.

Examples

```
data(standtabCoihue2)
df<-standtabCoihue2
df<-df[-nrow(df),]
# Diameter distribution plot
barplot(df$nha, legend = TRUE, beside = TRUE, las=1,
        names.arg = as.numeric(df$cd),
        ylab="Densidad (arb/ha)",xlab="Clase diametrica (cm)")
abline(h=0)
```

`standtabRauli` *Stand tables for* Nothofagus alpina *(raulí) forests*

Description

Stand tables for secondary *Nothofagus alpina*-dominated forests in different locations in southern Chile.

Usage

```
data(standtabRauli)
```

Format

The data has the following columns

site Study site.

sector Location within a study site.

low.cd Lower limit of the diameter class, in cm.

upp.cd Upper limit of the diameter class, in cm.

dclass Diameter class, in cm.

nha.dcl Tree density for the respective diameter class, in trees/ha.

forest.id Forest ID code, a combination of columns `site` and `sector`.

Source

Tree density by diameter classes (i.e., stand table). Data were digitized from table No. 4 of Wadsworth (1976).

References

- Wadsworth RK. 1976. Aspectos ecologicos y crecimiento del raulí (*Nothofagus alpina*) y sus asociados en bosques de segundo crecimiento de las provincias de Bío-Bío, Malleco y Cautín, Chile. Boletin Técnico No. 37, Fac. Cs. Forestales, Universidad de Chile, Santiago, Chile.

Examples

```
data(standtabRauli)
head(standtabRauli)
df<-standtabRauli
table(df$site,df$sector,df$dclass)
```

`standtabRauli2` *Tablas de rodal para bosques de* Nothofagus alpina *(raulí)*

Description

Tablas de rodal para bosques secundarios dominados por *Nothofagus alpina* en diferentes localidades del sur de Chile.

Usage

```
data(standtabRauli2)
```

Format

Los datos tienen las siguientes columnas

sitio Nombre del sitio de estudio.

sector Código identificador de un sector específico dentro del sitio en estudio.

linf.cd Límite inferior de la clase diamétrica, en cm.

lsup.cd Límite superior de la clase diamétrica, en cm.

cd Marca de la clase diamétrica, en cm.

nha.cd Densidad de la clase diamétrica, en arb/ha.

bosque.id Identificador del bosque, combinación de `sitio` y `sector`.

Source

Densidad de árboles por clase diamétrica, i.e., tabla de rodal. Datos digitados desde el cuadro No. 4 de Wadsworth (1976).

References

- Wadsworth RK. 1976. Aspectos ecologicos y crecimiento del raulí (*Nothofagus alpina*) y sus asociados en bosques de segundo crecimiento de las provincias de Bío-Bío, Malleco y Cautín, Chile. Boletin Técnico No. 37, Fac. Cs. Forestales, Universidad de Chile, Santiago, Chile.

Examples

```
data(standtabRauli2)
head(standtabRauli2)
df<-standtabRauli2
table(df$sitio,df$sector,df$cd)
```

`standtabRoble` *Stand table for* Nothofagus obliqua *(roble) secondary forests*

Description

Average stand table for secondary forests of *Nothofagus obliqua* (roble) forests, between 40 and 50 years-old, in the Malleco, Cautín, and Valdiva provinces in southern Chile.

Usage

```
data(standtabRoble)
```

Format

The data has the following columns

diam.cl Diameter class, in cm.

nha Density for the respective diameter class, in trees/ha.

Source

The stand table is from Puente et al. (1979), as a part of a study regarding secondary *Nothofagus* forests in southern Chile.

References

- Puente M, C Donoso, R Peñaloza, E Morales. 1979. Estudio de raleo y otras técnicas para el manejo de renovales de raulí (*Nothofagus alpina*) y roble (*Nothofagus obliqua*). Etapa I: Identificación y caracterización de renovales de raulí y roble. Informe de convenio No. 5, Proyecto CONAF/PNUD/FAO-CHI/76/003, Santiago, Chile. 88 p.

Examples

```
data(standtabRoble)
df<-standtabRoble
df<-df[-nrow(df),]
# Diameter distribution plot
barplot(df$nha, legend = TRUE, beside = TRUE, las=1,
        names.arg = df$diam.cl,
        ylab="Density (trees/ha)",xlab="Diameter class (cm)")
abline(h=0)
```

`standtabRoble2` *Tabla de rodal media para renovales de* Nothofagus obliqua *(roble)*

Description

Tabla de rodal media para renovales dominados por *Nothofagus obliqua* (roble), que tienen entre 40 y 50 años, en las provincias de Malleco, Cautín, y Valdiva, en el sur de Chile.

Usage

```
data(standtabRoble2)
```

Format

Las columnas son las siguientes

cd Clase diamétrica, en cm.

nha Densidad para la respectiva clase diamétrica, en arb/ha.

Source

La tabla de rodal proviene de Puente et al. (1979), y es el resultado de un estudio sobre los bosques secundarios de *Nothofagus* en el sur de Chile.

References

- Puente M, C Donoso, R Peñaloza, E Morales. 1979. Estudio de raleo y otras técnicas para el manejo de renovales de raulí (*Nothofagus alpina*) y roble (*Nothofagus obliqua*). Etapa I: Identificación y caracterización de renovales de raulí y roble. Informe de convenio No. 5, Proyecto CONAF/PNUD/FAO-CHI/76/003, Santiago, Chile. 88 p.

Examples

```
data(standtabRoble2)
df<-standtabRoble2
df<-df[-nrow(df),]
# Grafico de distribucion diametrica
barplot(df$nha, legend = TRUE, beside = TRUE, las=1,
```

```
        names.arg = df$cd,
        ylab="Densidad (arb/ha)",xlab="Clase diametrica (cm)")
abline(h=0)
```

`standvar` *Function to compute stand-level variables for a given imputed-tree-list.*

Description

Computes stand-level variables for a given sample plot. The variables are the following: density, basal area, quadratic diameter diameter, average height, top height, and stand volume.

Usage

```
standvar(
  data,
  plot.id,
  plot.area,
  time = NA,
  d,
  y,
  h = NA,
  factvar = NA,
  metric = TRUE,
  eng = TRUE,
  ...
)
```

Arguments

`data`	data frame having the tree list of a sample plot.
`plot.id`	a string having the plot code-number or unique identificator.
`plot.area`	column name having the plot area in m^2.
`time`	a number of year of measurement, if not provided the current year is assigned by default.
`d`	a text of the column-name having the diameter at breast-heigth. By default is assumed to be in cm. See option `metrics` to change it to the imperial system.
`y`	a string-vector with the name(s) of the tree-level variable(s) to which aggregated stand variables are needed to be computed. For example, volume is such a variable. By default is set to `NA`, thus only stand basal area will be computed. For instance, if is a vector, `y=c("vgross","vnet")`, those variables must be present in the tree list as column names. Notice that the resulting stand variable accronimg for each variable will be "vgross.ha" and "vnet.ha", by default.

`h`	a text of the column-name having the total height of the tree. By default is set to NA. If provided this variable is assumed to be measured in meters. See option `metrics` to use the imperial system.
`factvar`	a string having de name of the variable used as factor. Each level of the 'factvar' is a category.
`metric`	is a logic value, the default is to `TRUE`, thus the diameter `d` has to be in cm, and the resulting tree-level basal area will be in m^2. If `metric` is `FALSE`, the diameter `d` has to be in inches, and the computed tree basal area will be in ft^2.
`eng`	logical; if `TRUE` (by default), the language of some of the output-column names will be English; if "FALSE" will be Spanish. For instance, the levels of the factor-variable (`factvar`) is named "level"; otherwise will be "nivel".
`...`	aditional options for basic stats functions.

Details

For a given imputed tree list of a sample plot, several stand-level variales are computed. Note that the imputed-tree list must have all the tree-level variables needed to obtain the stand-level ones, such as, height, and volume. If there remeasurement for a plot, the computation is by plot and measurement year.

Value

Returns a data frame with the the stand variables per plot. If `factvar` is provided, the stand variables will be a also computed for each level of the `factvar`. Dominant diameter and dominant height are computed using the function `domvar()`.

Author(s)

Christian Salas-Eljatib.

References

- Salas-Eljatib C. 2025. Biometría y Modelación Forestal. Borrador de libro, en revisión. 352 p.

Examples

```
df<-biometrics::eucaplot2
#see the metadata by typing ?eucaplot2
head(df)
datana::descstat(df[,c("dap","atot")])
## Preparing the treelist, in the required format
df$parce<-1;df$sup.plot<-500
## Estimating tree-volume using an artifical factor form
df$vol<-gtree(x=df$dap)*df$atot*0.35
## Using the function
standvar(data=df,plot.id="parce",plot.area="sup.plot",
         d="dap",h="atot",y="vol")
# Do the same as before, but adding the computation by a factor
```

```
standvar(data=df,plot.id="parce",plot.area="sup.plot",
         d="dap",h="atot",y="vol",factvar = "clase.copa")
## More than one aggregated variable. For instance, adding biomass
##  and tree carbon, aside of volume. A naive estimation
##  of tree-biomass and carbon, could be
df$biom<-df$v*420 #(kg/m3)
df$carb<-df$biom*0.5 #50% of biomass is carbon
df
standvar(data=df,plot.id="parce",plot.area="sup.plot",
         d="dap",h="atot",y=c("vol","biom","carb"))
 #what if the sample plot has a remeasurement
df$measu.yr<-2025;df$measu.yr[1:5]<-2020
df
#' ## Using the function per measurement year
standvar(data=df,plot.id="parce",plot.area="sup.plot",
         d="dap",h="atot",y=c("vol","biom","carb"),time="measu.yr")
# Do the same as before, but adding the computation by a factor
standvar(data=df,plot.id="parce",plot.area="sup.plot",
         d="dap",h="atot",y=c("vol","biom","carb"),time="measu.yr",
         factvar = "clase.copa")
# More than one plot
df<-biometrics::radiatapl2
table(df$parce)
## naive imputation of tree-height
df[is.na(df$atot),"atot"]<-df[is.na(df$atot),"dap"]*0.8
## Estimating tree-volume using an artifical factor form
df$vtot<-gtree(x=df$dap)*df$atot*0.35
datana::descstat(df[,c("dap","atot","vtot")])
df$sup.plot<-150
standvar(data=df,plot.id="parce",plot.area="sup.plot",
         d="dap",h="atot",y="vtot")
standvar(data=df,plot.id="parce",plot.area="sup.plot",
             d="dap",h="atot",y="vtot",factvar = "sanidad")
```

`strand.fx` *A function having the mathematical expression of the Strand model.*

Description

Function of the Strand model, based upon two parameters and a single predictor variable as follows

$$y_i = \left(\frac{x_i}{\alpha + \beta x_i}\right)^3,$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
strand.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Strand L. 1964. Numerical constructions of site-index curves. Forest Sci. 10(4):410-414.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-strand.fx(x=time,alpha=1.15,beta=.37)
plot(time,y,type="l")
```

`strandg.fx` *A function having the mathematical expression of the Strand model.*

Description

Function of the Strand generalized model, based upon three parameters and a single predictor variable as follows

$$y_i = \left(\frac{x_i}{\alpha + \beta x_i}\right)^{\gamma},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
strandg.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Strand L. 1964. Numerical constructions of site-index curves. Forest Sci. 10(4):410-414.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-strandg.fx(x=time,alpha=0.98,beta=0.52,gamma=4.83)
plot(time,y,type="l")
```

`tapereuca2` *Datos de ahusamiento de Eucalyptus regnans*

Description

Corresponde a mediciones de diámetros fustales, con y sin corteza, para árboles muestra en plantaciones de *Eucalyptus regnans* en la comuna de Gorbea, región de la Araucanía, Chile. Note que existen por lo tanto, varias mediciones para cada árbol.

Usage

```
data(tapereuca2)
```

Format

Contiene las siguientes variables:

narb Número del árbol.

sec Número de sección del árbol `narb`.

hl Altura fustal de la sección `sec`, en m.

dlcc Diámetro de la sección `sec` con corteza, en cm.

dlsc Diámetro de la sección `sec` sin corteza, en cm.

ec Espesor de corteza de la sección `sec`.

forma Forma del árbol, en donde `1` = Fuste cilíndrico y `2` = Fuste acilíndrico (pequeña curvatura).

dap Diámetro a la altura del pecho (1.3 m) en cm.

decdap Doble espesor de corteza en el `dap`.

htot Altura total del árbol `narb`, en m.

dtoc Diámetro con corteza en `hcc`.

hcc Altura de comienzo de copa del árbol `narb`, m.

Source

Los datos provienen de la Tesis de Ingeniero Forestal de Manuel Morales, UFRO.

References

- Morales, M. (2003). Modelos fustales para *Eucalyptus regnans* F. Muell., en la comuna de Gorbea, Novena Región. Tesis Ingeniero Forestal. Universidad de La Frontera. Temuco, Chile. 43p.

Examples

```
data(tapereuca2)
lattice::xyplot(dlcc~hl, data=tapereuca2, type = "l", groups = narb)
```

`taperpoly.fx` *Carrasco polynomial function*

Description

Polynomial function of Carrasco (1986)

Usage

```
taperpoly.fx(hl = hl, hcc = hcc, paramod = paramod, n = (length(paramod) - 1))
```

Arguments

`hl`	is stem height within the tree, thus $h_l \leq h$.
`hcc`	is height to crown base.
`paramod`	is a vector having the coefficients of the taper model in the following order up to `n`: $\beta_0, \beta_1, \beta_2, ..., \beta_n$
`n`	degree of the polynomic function

Details

This function takes the form of

$$\frac{d_{l_i}}{d_i} = \beta_0 + \beta_1 X + \beta_2 X^2 + \beta_3 X^3 + \cdots + \beta_n X^n,$$

where: d_{l_i} is the stem diameter at stem-height h_{l_i} for the *i*-th tree; d_i and h_i are the tree-level variables diameter at breast height and total height respectively for the *i*-th tree, and n is the degree of the polynomial. The other term is

$$X = \frac{hcc_i - h_{l_i}}{hcc_i - 1.3},$$

Value

Returns the diameter of the stem at the stem-height h_l, thus d_l, divided by the diameter at breast height (1.3). This is

$$\frac{d_{l_i}}{d_i}$$

Author(s)

Christian Salas-Eljatib and Nicolás Campos

References

- Carrasco, J. 1986. Estudio Comparativo de dos Métodos para Evaluar la Calidad a árboles en pie y para representar la Forma del Fuste en el Bosque Siempreverde valdiviano. Tesis Ingeniero Forestal. Universidad Austral de Chile. Valdivia, Chile. 117 p.

Examples

```
dl <- seq(40, 0, -5)
hl <- seq(0, 16, 2)
d <- 30
hcc <- 12
h <- max(hl)
df <- data.frame(dl = dl,
                 hl = hl,
                 d = d,
                 hcc = hcc,
                 h = h)
df

myparams <- c(0.3, 0.8, 0.00003)

taperpoly.fx(hl = df$hl, hcc = df$hcc, paramod = myparams, n = 2)

df$y <- taperpoly.fx(hl = df$hl, hcc = df$hcc, paramod = myparams, n = 2)
## the n parameter is not necesary
df$y2 <- taperpoly.fx(hl = df$hl, hcc = df$hcc, paramod = myparams)
df$dl.h <- df$y * df$d
df
```

`thinningtrial` *Stand variables by thinning treatment for secondary forests of* Drymis winteri *near Valdivia, Chile.*

Description

The average of stand variables per thinning treatments applied to secondary forest of *Drymis winteri* in Hueicolla, in the Coastal range of Valdivia (Chile). Data are measurements carried out during 1986 and 1990. The thinning treatments are as follows: distance among trees of 2 m, 3 m, y 4 m; release thinning, and control (i.e., no thinning). The values are the mean of the following stand variables: density (trees/ha), basal area (^{2}/ha) and volume (^{3}/ha).

Usage

```
data(thinningtrial)
```

Format

The dataframe has the following columns:

treat Thinning treatment: distance among trees of 2m, 3m, and 4m; release thinning; and control.

time Year of measurement (1986 o 1990)

nha Average density, in arb/ha.

gha Average basal area, in m^2/ha

vha Average volume, in m^3/ha.

Source

Data were derived from the tables number 4, 6 and 7, of the paper of Navarro et al. (1997).

References

Navarro, C., Donoso, P., y Rosas, M. (1997). Crecimiento de renovales de *Drymis winteri* sometidos a distintos tratamientos de raleo. En: Donoso, C. (Ed.), Bosques templados de Chile y Argentina. Editorial Universitaria, Santiago de Chile.

Examples

```
data(thinningtrial)
head(thinningtrial)
df<-thinningtrial
require(lattice)
xyplot(nha~time|treat, data=df, type="b",as.table=TRUE)
xyplot(nha~time,groups=treat, data=df, type="b",auto.key = TRUE)
xyplot(gha~time|treat, data=df, type="b",as.table=TRUE)
```

`thinningtrial2` *Variables de estado segun tratamiento de raleo en renovales de* Drymis winteri *en Valdivia, Chile.*

Description

Valores medios de variables de estado de rodal en un ensayo de raleo de renovales de *Drymis winteri* en Hueicolla, en la Cordillera de la costa de Valdivia (Chile). Las mediciones se realizaron los años 1986 y 1990. Los tratamientos de raleo son: distanciamiento entre árboles de 2 m, 3 m, y 4 m; raleo de liberación, y testigo (i.e., sin intervención). Los valores son la media de las siguientes variables de rodal: densidad (arb/ha), area basal (^{2}/ha) y volumen (^{3}/ha).

Usage

```
data(thinningtrial2)
```

Format

Los datos contienen las siguientes columnas:

trat Tratamiento de raleo: distanciamiento a 2m, 3m, y 4m; raleo de liberación; y testigo.

tiempo Año de evaluación (1986 o 1990)

nha Densidad media, en arb/ha.

gha Área basal media, en m^2/ha

vha Volumen medio, en m^3/ha.

Source

Datos digitados desde los cuadro 4, 6 y 7 de Navarro et al. (1997).

References

Navarro, C., Donoso, P., y Rosas, M. (1997). Crecimiento de renovales de *Drymis winteri* sometidos a distintos tratamientos de raleo. En: Donoso, C. (Ed.), Bosques templados de Chile y Argentina. Editorial Universitaria, Santiago de Chile.

Examples

```
data(thinningtrial2)
head(thinningtrial2)
df<-thinningtrial2
require(lattice)
xyplot(nha~tiempo|trat, data=df, type="b",as.table=TRUE)
xyplot(nha~tiempo,groups=trat, data=df, type="b",auto.key = TRUE)
xyplot(gha~tiempo|trat, data=df, type="b",as.table=TRUE)
```

`treegrowth` *Diameter and height growth of Grand-fir sample trees.*

Description

Diameter and height growth of 66 Grand-fir trees. Data derived from stem analysis sample trees collected by Dr. Albert Stage (US Forest Service, Moscow, ID, USA.)

Usage

```
data(treegrowth)
```

Format

Contains seven column, as follows:

tree.no Tree number identificator. An unique number to each sample tree.

forest Forest type.

habitat Forest habitat type.

tree.code A composite tree code representing the following columns: `tree.id-forest-habitat`

age Age, in yr

dbh Diameter at breast-height, in cm. Originally measured in inches, and was converted to cm using a single decimal.

toth Total height, in m. Originally measured in feet, and was converted to m using a single decimal.

Source

Originally, the data were provided by Dr. Albert Stage (R.I.P) to Professor Andrew Robinson (University of Idaho, USA), whom used them to explain the fitting of statistical models. Dr Christian Salas-Eljatib was a former graduate student of Statistics of Prof. Robinson at the Univ. of Idaho.

References

- Stage, A. R., 1963. A mathematical approach to polymorphic site index curves for Grand fir. Forest Science 9 (2), 167–180.

Examples

```
data(treegrowth)
df<-treegrowth
head(df)
require(lattice)
xyplot(dbh~age, groups = tree.code,data=df, type="b")
```

`treegrowth2` *Crecimiento en diámetro y altura de árboles muestra de Grand-fir.*

Description

Crecimiento en diámetro y altura de 66 árboles de Grand-fir. Los datos fueron derivados a partir de árboles muestras de análisis fustal colectados por el Dr. Albert Stage (US Forest Service, Moscow, ID, USA.)

Usage

```
data(treegrowth)
```

Format

Contiene las siguientes siete columnas:

num.arb Número identificador del árbol. Único para cada árbol muestra.

bosque Tipo forestal.

habitat Clasificacion de tipo de hábitat.

cod.arb Un código que combina a las siguientes columnas: `num.arb-bosque-habitat`

edad Edad, en años.

dap Diámetro a la altura del pecho, en cm. Originalmente fue medido en pulgadas, y acá se transformó empleando un solo decimal.

atot Altura total, in m. Originalmente esta variable fue medido en pies, y acá se transformó empleando un solo decimal.

Source

En un principio los datos fueron cedidos por el Dr. Albert Stage (Q.E.P.D) al Profesor Andrew Robinson (University of Idaho, USA), quien los usaba para explicar el ajuste de modelos estadísticos. El Dr. Christian Salas-Eljatib fue un estudiante de postgrado en estadistica del Prof. Robinson en la Univ. of Idaho.

References

- Stage, A. R., 1963. A mathematical approach to polymorphic site index curves for Grand fir. Forest Science 9 (2), 167–180.

Examples

```
data(treegrowth2)
df<-treegrowth2
head(df)
require(lattice)
xyplot(dap~edad, groups = cod.arb,data=df, type="b")
```

`treelistinve` *Tree-list data from a forest sampling work*

Description

Tree-level variables measured within three sample plots in a forest sampling effort. This sort of work is commonly referred as a forest inventory. Notice that plots might have different areas. The sampling was carried out in a secondary forest of *Nothofagus obliqua* in the Rucamanque experimental station, near the city of Temuco, in southern Chile.

Usage

```
data(treelistinve)
```

Format

Contains tree-level variables, as follows:

plot Plot number.

plot.size Plot size, in m^2.

tree Tree identificator

species Species common name as follows: Olivillo=*Aextocicon puncatatum*, Tepa=*Laureliopsis philippiana*, Lingue=*Persea lingue*, Coigue=*Nothofagus dombeyi*, Roble=*Nothofagus obliqua*, Other=Other

dbh Diameter at breast-height, in cm.

toth Total height, in m. Only measured for some sample trees.

Source

The data is provided courtesy of Prof. Christian Salas-Eljatib, Universidad de Chile (Santiago, Chile).

References

- Salas C. 2001. Caracterización básica del relicto de Biodiversidad Rucamanque. Bosque Nativo, 29:3-9. `https://eljatib.com/publication/2001-06-01_caracterizacion_basi/`
- Salas C. 2002. Ajuste y validación de ecuaciones de volumen para un relicto del bosque de Roble-Laurel-Lingue. Bosque 23(2): 81-92. doi:10.4067/S0717920020020002000009 `https://eljatib.com/publication/2002-07-01_ajuste_y_validacion_/`

Examples

```
data(treelistinve)
head(treelistinve)
tapply(treelistinve$dbh,treelistinve$species,summary)
```

`treelistinve2` *Lista de árboles en un muestreo forestal*

Description

Variables a nivel de árbol medidas en tres unidades de muestreo (*i.e.*, parcelas) establecidas en un muestreo forestal. Este tipo de muestreo de bosques, es comunmente conocido como "inventario forestal". Note que las parcelas podrían tener diferentes superficies. El muestreo fue realizado en un bosque secundario dominado por *Nothofagus obliqua* en el predio Rucamanque, en las cercanías de la ciudad de Temuco, en el sur de Chile.

Usage

```
data(treelistinve2)
```

Format

Contiene variables a nivel de árbol dentro de parcelas.

parce Número de la parcela de muestreo.

sup.parce Superficie de la parcela, en m^2.

arbol Número identificador del árbol.

spp Nombre común de especies como sigue: Olivillo=*Aextocicon puncatatum*, Tepa=*Laureliopsis philippiana*, Lingue=*Persea lingue*, Coigue=*Nothofagus dombeyi*, Roble=*Nothofagus obliqua*, Other=Other

dap Diámetro a la altura del pecho, en cm.

atot Altura total, en m. Solo medida en algunos árboles muestra.

Source

Los datos fueron cedidos por el Prof. Christian Salas-Eljatib, Universidad de Chile (Santiago, Chile).

References

- Salas C. 2001. Caracterización básica del relicto de Biodiversidad Rucamanque. Bosque Nativo, 29:3-9. `https://eljatib.com/publication/2001-06-01_caracterizacion_basi/`
- Salas C. 2002. Ajuste y validación de ecuaciones de volumen para un relicto del bosque de Roble-Laurel-Lingue. Bosque 23(2): 81-92. doi:10.4067/S0717920020020002000009 `https://eljatib.com/publication/2002-07-01_ajuste_y_validacion_/`

Examples

```
data(treelistinve2)
unique(treelistinve2$parce)
table(treelistinve2$parce,treelistinve2$sup.parce)
tapply(treelistinve2$dap,treelistinve2$spp,summary)
```

`treestat` *Function to compute descriptive statistics at tree-level, segregated by a factor (`factvar`) per sample plot.*

Description

Computes several descriptive statistics of variables at the tree-level per sample plot. It can also be be applied to compute them by levels of factor within each available plot.

Usage

```
treestat(
  data,
  plot.id,
  t = NA,
  y,
  d = NA,
  factvar = NA,
  full = FALSE,
  short.names = TRUE,
  metric = TRUE,
  eng = TRUE,
  want.add.d = FALSE,
  want.add.g = FALSE,
  ...
)
```

Arguments

`data`	data frame having the tree list of a sample plot.
`plot.id`	a string having the plot code-number or unique identificator.
`t`	(optional) a time variable having the the measurement year (in numeric or character format). The default is `NA`, in which case the current year is assigned.

`y`	a string-vector with the name(s) of the random variable(s) to which the descriptive statistics will be computed. By default uses `dbh` as the name of the variable.
`d`	(optional) a text with the name of the column of the `data` having the diameter at breast-heigth. The default is `NA`. If provided, it is assumed to be in cm. See option `metrics` to change it to the imperial system.
`factvar`	a string having de name of the variable used as factor. Each level of the 'factvar' is a category.
`full`	logical; if `TRUE`, the output includes some extra descriptive statistics as explained in the datana::descstat() function. The default is `FALSE`.
`short.names`	logical; if `TRUE`, the name of the statistics are short names as explained in the datana::descstat() function. The default is `FALSE`.
`metric`	is a logic value, the default is `TRUE`, thus the diameter `d` has to be in cm, and the resulting tree-level basal area will be in m^2. If `metric` is `FALSE`, the diameter `d` has to be in inches, and the computed tree basal area will be in ft^2.
`eng`	logical; if `TRUE` (by default), the language of some of the output-column names will be English; if "FALSE" will be Spanish. For instance, the levels of the factor-variable (`factvar`) is named "level"; otherwise will be "nivel".
`want.add.d`	logical; if `TRUE`, the computations will include the diameter at breast-heigth defined in option `d`, as an extra random variable to be added at the end of the vector `y`. The default is `FALSE`.
`want.add.g`	logical; if `TRUE`, the computations will include the tree basal area, only possible if option `d` was defined, as an extra random variable to be added at the end of the vector `y`. The default is `FALSE`.
`...`	aditional options for basic stats functions.

Details

For a given tree list of a sample plot, several descriptive statistics are computed for the selected random variables, by plot and measurement year.

Value

Returns a data frame with the statistics per plot and time for the selected `y` variables. If `factvar` is given, the same statistics will be added but segregated by each level (or category) of the `factvar`.

Author(s)

Christian Salas-Eljatib.

References

- Salas-Eljatib C. 2025. Biometría y Modelación Forestal. Borrador de libro, en revisión. 352 p.

Examples

```
# Dataframe to be used
df<-biometrics::eucaplot2
#?eucaplot2
head(df)
datana::descstat(df[,c("dap","atot")])
df$parce<-1
## Using the function
treestat(data=df,plot.id="parce",y="atot")
# Now, for two random variables, instead of a single one
treestat(data=df,plot.id="parce",y=c("dap","atot"))
# If the d is provided, Do you want to add both the diameter
# and the basal area (g), as random variables?
treestat(data=df,plot.id="parce",y="atot",d="dap",want.add.d=TRUE,want.add.g=TRUE)
## Do the same as before, but adding the computation by a factor

treestat(data=df,plot.id="parce",y="atot",factvar="clase.copa")
df$time<-2025;df$time[1:5]<-2020
df
## Using the function per measurement year
treestat(data=df,plot.id="parce",y="atot",t="time",full=TRUE)
# Do the same as before, but adding the computation by a factor
treestat(data=df,plot.id="parce",y="atot",t="time",
         factvar="clase.copa",full = TRUE)
## same as before, but for two random variables
treestat(data=df,plot.id="parce",y=c("dap","atot"),t="time",
          factvar="clase.copa",full = TRUE)
```

`treevolruca` *Tree-level volume by species in the Rucamanque forest*

Description

These is tree-level measurement data of sample trees in the Rucamanque experimental forest, near Temuco, in the Araucanía region in south-central Chile. Data were measured in 1999.

Usage

```
data(treevolruca)
```

Format

Contains tree-level variables, as follows:

- **tree** Tree number identification.
- **spp** Tree species common name as follows: "Laurel" is *Laurelia sempervirens*, "Lingue" is *Persea lingue*, "Olivillo" is *Aextoxicon punctatum*, "Tepa" is *Laureliopsis philippiana*, "Tineo" is *Weinmannia trichosperma*, y "Ulmo" is *Eucryphia cordifolia*.
- **dbh** Diameter at breast height, in cm.

toth Total height, in m.

d6 Upper-stem diameter at 6 m, in cm.

totv Tree gross volume, in m^3 with bark.

Source

The data were provided courtesy of Dr. Christian Salas-Eljatib, Universidad de Chile (Santiago, Chile).

References

- Salas C. 2002. Ajuste y validación de ecuaciones de volumen para un relicto del bosque de Roble-Laurel-Lingue. Bosque 23(2): 81-92. doi:10.4067/S071792002002000200009 `https://eljatib.com/publication/2002-07-01_ajuste_y_validacion_/`

Examples

```
data(treevolruca)
head(treevolruca)
table(treevolruca$spp)
```

`treevolruca2` *Volumen a nivel de árbol para especies nativas del bosque de Rucamanque*

Description

Volumen, altura y diámetro, entre otras para árboles muestra en el bosque de Rucamanque, cerca de Temuco, en la región de la Araucanía, en el sur de Chile.

Usage

```
data(treevolruca2)
```

Format

Las siguientes columnas son parte de la dataframe:

arbol Número del árbol.

spp Codificación de la especie como sigue: "Laurel" es *Laurelia sempervirens*, "Lingue" es *Persea lingue*, "Olivillo" es *Aextoxicon punctatum*, "Tepa" es *Laureliopsis philippiana*, "Tineo" es *Weinmannia trichosperma*, y "Ulmo" es *Eucryphia cordifolia*.

dap Diámetro a la altura del pecho, en cm.

atot Altura total, en m.

d6 Diámetro fustal a los 6 m, en cm.

vtot Volumen bruto total, en m^3 con corteza.

Source

Los datos fueron cedidos por el Dr. Christian Salas-Eljatib, Universidad de Chile (Santago, Chile).

References

- Salas C. 2002. Ajuste y validación de ecuaciones de volumen para un relicto del bosque de Roble-Laurel-Lingue. Bosque 23(2): 81-92. doi:10.4067/S0717920020020002000009 `https://eljatib.com/publication/2002-07-01_ajuste_y_validacion_/`

Examples

```
data(treevolruca2)
head(treevolruca2)
table(treevolruca2$spp)
```

`trlhawaii` *Tree-level information of forest plots across the Hawaiian archipelago.*

Description

Diameter at breast height (or occurrence) of individual trees, shrubs and tree ferns across 530 plots across the Hawaiian archipelago and includes native status and cultivated status of the 185 species.

Usage

```
data(trlhawaii)
```

Format

Contains 18 variables, as follows:

island Island name.

plot.id Unique numeric identifier for each plot.

study Brief name of study.

plot.area Plot area in m^2.

longitude Longitude of plot in decimal degrees; WGS84 coordinate system.

latitude Latitude of plot in decimal degrees; WGS84 coordinate system.

year Year in which plot data was collected.

census Numeric identifier for each census.

tree.id Unique numeric identifier for each individual.

scientific.name Genus and species of each individual following TPL v. 1.1.

family Family of each individual following TPL v. 1.1.

angiosperm Binary variable (`1` = yes, `0` = no) indicating whether an individual is classified as an angiosperm following APG III.

monocot Binary variable (`1` = yes, `0` = no) indicating whether an individual is classified as a monocot following APG III.

native.status Categorical variable (`native`, `alien`, `uncertain`) indicating alien status of each individual following Wagner *et al.* (2005).

cultivated.status Binary variable (`1` = yes, `0` = no, `NA` = not applicable) indicating if species is cultivated following PIER.

abundance Number of individuals (all = 1).

abundance.ha Abundance of each individual on a per hectare basis.

dbh Diameter at 1.3 m (in cm) for each individual; `NA` indicates that size was not measured, but was classified by size class.

Source

The data were obtained from the DRYAD repository at doi:10.5061/dryad.1kk02qr.

References

- Craven D, Knight T, Barton K, Bialic-Murphy L, Cordell S, Giardina C, Gillespie T, Ostertag R, Sack L,Chase J. 2018. OpenNahele: the open Hawaiian forest plot database. Biodiversity Data Journal 6: e28406.

Examples

```
data(trlhawaii)
table(trlhawaii$island,trlhawaii$study)
unique(trlhawaii$plot.id)
table(trlhawaii$plot.id)
tapply(trlhawaii$plot.area,trlhawaii$study,summary)
```

`trlpsptime` *Long term tree-list data from permanent sample plots*

Description

Temporal tree-level data within four sample plots in an experimental forest in Austria. The dataframe contains several tree-level variables. Plot sizes are 2500 m^2 (approx.).

Usage

```
data(trlpsptime)
```

Format

Contains tree-level variables, as follows:

plot Plot number.

tree Tree identificator.

species Species code as follows: PCAB=*Picea abies*, LADC=*Larix decidua*, PNSY=*Pinus sylvestris*, FASY=*Fagus Sylvatica*, QCPE=*Quercus petraea*, BTPE=*Betula pendula*.

year Year of measurement.

obs Observation.

dbh Diameter at breast-height, in mm.

dbh2 Orthogonal measured second diameter, in mm.

hmk Selection criteria to measure tree height. `1`=systematic, `2`=systematic and in the group of the 100 thickest, `3`=belongs to the 100 thickest, `4`=lying tree, `5`=Standing tree with a ladder, `6`=outlier, `7`=from stem analysis.

kh Type of the height measurement. `0`=tree height, `1`=angle and distances.

ho Tree height in dm when `kh=0`. When `kh=1` then distance to the tree in dm or in 1977 length of the base bar in cm.

ka Height to the crown base in dm when `kh=0`. When `kh=1` then angle to the tree top in 1/10 degree.

kb Crown width in dm when `kh=0`. When `kh=1` then angle to 1.3 m above tree base in 1/10 degree.

wka Angle to crown base in 1/10 degree.

crown.cl Crown class according to Kraft. `1`=predominant, `2`=dominant, `3`=co-dominant, `4`=dominated, `5`=overtopped.

crown Crown quality. `0`=normal, `1`=broken in the crown region, `2`=substituted tree top, `3`=forked, `4`=bushy, stork nest, witches' broom, `5`=wizen tree top, `6`=again broken tree top.

stem Stem quality. `0`=typical, `1`=crooked, `2`=abiotic damaged, `3`=biotic damaged, `4`=forked stem without damage, `5`=forked stem with damage, `6`=up to 1/3 of the girth is peeled, `7`=more than 1/3 of the girth is peeled, `8`=broken stem, `9`=other stem damages.

defoliation crown defoliation. `1`=low, `2`=medium, `3`=much.

Source

The Austrian Research Center for Forests established a spacing experiment with Norway spruce (*Picea abies*) in the Vienna Woods. In the "Hauersteig" experiment, several tree-level variables were measured within four sample plots over time. Data were retrieved from the paper cited below, where several details might be worth reading.

References

- Kindermann G. Kristofel F, Neumann M, Rossler G, Ledermann T & Schueler. 2018. 109 years of forest growth measurements from individual Norway spruce trees. Sci. Data 5:180077 doi:10.1038/sdata.2018.77

Examples

```
data(trlpsptime)
df<-trlpsptime
head(df)
tapply(df$dbh, list(df$year,df$plot), mean)
```

`trlremeasu` *Tree-level remeasurements for a sample plot in a* Pinus radiata *plantation*

Description

Temporal tree-level data from a sample plot established in a Monterey pine (*Pinus radiata*) forestry plantation in Chile. The plot size is 1600 m^2, and the plantation was established in 1990.

Usage

```
data(trlremeasu)
```

Format

Tree list data for a sample plot remeasured through time, and having the following columns

plot.id Plot code.

tree Tree number.

x.coord Cartesian position in the X-axis, in m.

y.coord Cartesian position in the Y-axis, in m.

year Measurement year.

dead Dead identificator, `0` means alive, and `1` otherwise.

dbh diameter at breast-height, in cm.

Source

Data were retrieved from the paper cited below, where several details might be worth reading.

References

- Pommerening A, Trincado G, Salas-Eljatib C, Burkhart H. 2023. Understanding and modelling the dynamics of data point clouds of relative growth rate and plant size. Forest Ecology and Management Volume 529:120652 doi:10.1016/j.foreco.2022.120652

Examples

```
data(trlremeasu)
head(trlremeasu)
df<-trlremeasu
df$fe<-10000/1600
df$garb.ha<- (pi/40000)*df$dbh^2*df$fe
gha.t<-tapply(df$garb.ha, df$year, sum)
nha.t<-tapply(df$fe, df$year, sum);
time<-as.numeric(rownames(gha.t))
plot(nha.t~time, type="b",las=1)
plot(gha.t~time, type="b",las=1)
```

`trlsmoopsp` *Smoothed tree list data from permanent sample plots*

Description

Temporal tree-level variables (smoothed-values) within four sample plots in an experimental forest in Austria. The dataframe contains all the variables for all trees, where observation gaps were filled from monotone increasing predictive functions. Plot sizes are 2500 m^2 (approx.) and the current dataframe only keeps the measurement years having a more reliable amount of records.

Usage

```
data(trlsmoopsp)
```

Format

Contains tree-level variables, as follows:

- **plot** Plot number.
- **tree** Tree identificator.
- **year** Year of measurement.
- **species** Species code as follows: PCAB=*Picea abies*, LADC=*Larix decidua*, PNSY=*Pinus sylvestris*, FASY=*Fagus Sylvatica*, QCPE=*Quercus petraea*, BTPE=*Betula pendula*.
- **obs** Observation in this year.
- **dbh** Diameter at breast-height, in cm.
- **toth** Tree height, in m.
- **hcb** Height to the crown base, in m.

Source

The Austrian Research Center for Forests established a spacing experiment with Norway spruce (*Picea abies*) in the Vienna Woods. In the “Hauersteig” experiment, several tree-level variables were measured within four sample plots over time. Data were retrieved from the paper cited below, where several details might be worth reading.

References

- Kindermann G. Kristofel F, Neumann M, Rossler G, Ledermann T & Schueler. 2018. 109 years of forest growth measurements from individual Norway spruce trees. Sci. Data 5:180077 doi:10.1038/sdata.2018.77

Examples

```
data(trlsmoopsp)
df<-trlsmoopsp
head(df)
table(df$year,df$plot)
tapply(df$dbh, list(df$year,df$plot), length)
```

`uestimator` *Function to compute the* U*-estimator for a sorted random variable, measured in a given sample plot.*

Description

Computes the U-estimator for a number of trees per-are (1 ha=100ares)

Usage

```
uestimator(sorty, n.per.are)
```

Arguments

`sorty`	a vector having the tree-level variable of interest being already sorted according to a criterion.
`n.per.are`	number of needed trees per are for the sample plot. Remember that 1 are=100 m2 or 1 ha=100 ares. If `n.per.are` is not an integer, it is rounded to the nearest integer, with a warning.

Details

Althought the original function was written by Dr Oscar García, and the corresponding reference is provided, the current function has several changes that makes it of a broader use.

Value

The main output is the U-estimator for the random variable of interest.

Author(s)

Dr Oscar García and Christian Salas-Eljatib.

References

- Garcia O, Batho A. 2005. Top height estimation in lodgepole pine sample plots. Western Journal of Applied forestry 20(1):64-68.

Examples

```
#Creates a fake dataframe
h <- c(29.1,28, 24.5, 26, 21,20.5,20.1);
sort.h<-sort(h,decreasing=FALSE);sort.h
plot.area.m2<-500;plot.area.ha<-plot.area.m2/10000;plot.area.ha
ndom.ha<-100;n.per.are<-plot.area.ha*ndom.ha;
# Using the  function
uestimator(sort.h,n.per.are)
```

`volume` *Compute volume of objects*

Description

Calculate the volume of objects, depending on their shapes or available measurements, to carry out the computation.

Usage

```
volume(
  form = "trapesoid",
  d = NA,
  h = NA,
  l = NA,
  d.u = "cm",
  h.u = "m",
  l.u = "m",
  o.u = "m3"
)
```

Arguments

`form`	`string` indicating the form of the object to be cubicated. The alternatives are the following: `cone`, `cilinder`, `trapesoid` (also know as the Smalian's cubic formula), `newton`, or `huber`.
`d`	`vector` of diameter values.
`h`	`vector` of height values.
`l`	Distance, generally the difference between two `h` values. If `l` is given, `h` must not be given.
`d.u`	`string` indicating the unit of `d`. Can be any of `cm` (default), `in`, `m` or `ft`.
`h.u`	`string` indicating the unit of `h`. Can be any of `cm`, `in`, `m` (default) or `ft`.

`l.u`	`string` indicating the unit of `l`. Can be any of `cm`, `in`, `m` (default) or `ft`.
`o.u`	`string` indicating the unit of the calculated volume. Can be any of `cm3`, `in3`, `m3` (default) or `ft3`.

Value

Value of volume.

Author(s)

Christian Salas-Eljatib and Nicolás Campos and Victor Pacheco

Examples

```
##- Data, diameters at different stem heights
df <- data.frame(hl = c(0.3, 3.9, 7), dl = c(40, 20, 10))
df

##- Cilinder, needs a single diameter and height
dst <- df$dl[1]
hst <- df$hl[1]
## output in cubic centimeters
volume(form = "cilinder", d = dst,  l = hst, o.u = "cm3")
## in meters
volume(form = "cilinder", d = dst,  l = hst, o.u = "m3")

##- Trapesoid between first and second measurement,
## thus is for a single section.
dl.a <- df$dl[c(1, 2)]
hl.a <- df$hl[c(1, 2)]

vs1<-volume(h = hl.a, d = dl.a)
vs1

##- Trapesoid, between first and third measurement
## thus is for a single section.
dl.b <- df$dl[c(1, 3)]
hl.b <- df$hl[c(1, 3)]
volume(h = hl.b, d = dl.b)


dl.b <- df$dl[c(2, 3)]
hl.b <- df$hl[c(2, 3)]
vs2<-volume(h = hl.b, d = dl.b)
vs2
vs1+vs2
##- Newton (only possible if three measurements are given)
volume(form = "newton",  h = df$hl, d = df$dl)

##- Huber, for all available measurements
volume(form = "huber", d = df$dl, h = df$hl)
```

```
##- Huber given 1 diameter and 1 distance
l.a <- diff(c(df$hl[1], df$hl[3]))
volume(form = "huber", d = df$d[2], l = l.a)
```

`weib.fx` *A function having the mathematical expression of the Weibull allometric model.*

Description

Function of the Weibull allometric model, based upon three parameters and a single predictor variable as follows

$$y_i = \alpha \left(1 - \mathrm{e}^{-\beta x_i}\right)^{\gamma},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
weib.fx(x, alpha, beta, gamma, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`gamma`	is the coefficient-parameter γ.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f(x_i, \theta)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Weibull W. 1951. A statistical distribution function of wide applicability. J. Appl. Mech.-Trans. ASME 18(3):293-297.
- Yang RC, A Kozak, JH Smith. 1978. The potential of Weibull-type functions as flexible growth curves. Can. J. For. Res. 8(2):424-431.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. https://biometriaforestal.uchile.cl

Examples

```
# Predictor variable values to be used
time<-seq(5,60,by=0.01)
# Using the function
y<-weib.fx(x=time,alpha=23.06,beta=.13,gamma=.63)
plot(time,y,type="l")
```

`wykoff.fx` *A function having the mathematical expression of the Wykoff model.*

Description

Function of the Wykoff model, based upon two parameters and a single predictor variable as follows

$$y_i = \mathrm{e}^{\left(\alpha+\frac{\beta}{x_i+1}\right)},$$

where: y_i and x_i are the response and predictor variable, respectively, for the *i*-th observation; and the rest are parameters (i.e., coefficients).

Usage

```
wykoff.fx(x, alpha, beta, upsilon = 0)
```

Arguments

`x`	is the predictor variable.
`alpha`	is the coefficient-parameter α.
`beta`	is the coefficient-parameter β.
`upsilon`	is an optional constant term that force the prediction of *y* when *x=0*. Thus, the new model becomes $y_i = \Upsilon + f\left(x_i, \theta\right)$, where θ is the vector of coefficients of the above described function represented by $f(\cdot)$. The default value for Υ is 0.

Value

Returns the response variable based upon the predictor variable and the coefficients.

Author(s)

Christian Salas-Eljatib.

References

- Wykoff WR, NL Crookston, AR Stage. 1982. User's guide to the Stand Prognosis Model. USDA For. Serv. Gen. Tech. Rep. INT-133, USA. 112 p.
- Salas-Eljatib C. 2025. Funciones alométricas: reparametrizaciones y características matemáticas. Documento de trabajo No. 1, Serie: Cuadernos de biometría, Laboratorio de Biometría y Modelación Forestal, Universidad de Chile. Santiago, Chile. 51 p. `https://biometriaforestal.uchile.cl`

Examples

```
# Predictor variable values to be used
d<-seq(5,60,by=0.01)
# Using the function
h<-wykoff.fx(x=d,alpha=3.87,beta=4.38,upsilon=1.3)
plot(d,h,type="l")
```

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