

Package ‘seedreg’

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Type Package

Title Regression Analysis for Seed Germination as a Function of Temperature

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Description Regression analysis using common models in seed temperature studies, such as the Gaussian model (Martins, JF, Barroso, AAM, & Alves, PLCA (2017) <[doi:10.1590/s0100-83582017350100039](https://doi.org/10.1590/s0100-83582017350100039)>), quadratic (Nunes, AL, Sossmeier, S, Gotz, AP, & Bispo, NB (2018) <[doi:10.17265/2161-6264/2018.06.002](https://doi.org/10.17265/2161-6264/2018.06.002)>) and others with potential for use, such as those implemented in the 'drc' package (Ritz, C, Baty, F, Streibig, JC, & Gerhard, D (2015). <[doi:10.1371/journal.pone.0146021](https://doi.org/10.1371/journal.pone.0146021)>), in the estimation of the ideal and cardinal temperature for the occurrence of plant seed germination. The functions return graphs with the equations automatically.

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Imports drc, ggplot2, car, crayon, emmeans, multcomp, hnp, boot, multcompView, stringr, sf, gridExtra, dplyr

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aac	<i>Param: Area below the curve</i>
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Description

Calculates the area under the germination or emergence curve. A parameter that can replace the traditional emergence or germination speed index.

Usage

```
aac(dados, trat, nrep, time)
```

Arguments

dados	data.frame containing the responses of the evaluations in separate columns side by side and without the columns with the identification of the factors
trat	vector of treatments with n repetitions
nrep	Number of repetitions
time	vector containing time

Value

Returns a vector with the index

Examples

```
data("substrate")
aac(substrate[,c(3:18)],
     trat = substrate$Trat,
     nrep = 4,
     time = 1:16)
```

aristolochia

dataset: aristolochia

Description

The data come from an experiment conducted at the Seed Analysis Laboratory of the Agricultural Sciences Center of the State University of Londrina, in which five temperatures (15, 20, 25, 30 and 35C) were evaluated in the germination of *Aristolochia elegans*. The experiment was conducted in a completely randomized design with four replications of 25 seeds each.

Usage

```
data("aristolochia")
```

Format

data.frame containing data set

trat numeric vector with factor 1

germ Numeric vector with germination percentage

vel numerical vector with germination speed

Author(s)

Hugo Roldi Guariz

Examples

```
data(aristolochia)
```

Description

The 'BC.4' and 'BC.5' logistical models provide Brain-Cousens' modified logistical models to describe u-shaped hormesis. This model was extracted from the 'drc' package and adapted for temperature analysis in seed germination

Usage

```
BC_model(
  trat,
  resp,
  npar = "BC.4",
  error = "SE",
  ylab = "Germination (%)",
  xlab = expression("Temperature ("^"o" * "C)"),
  theme = theme_classic(),
  legend.position = "top",
  cardinal = 0,
  r2 = "all",
  width.bar = NA,
  scale = "none",
  textsize = 12,
  pointsize = 4.5,
  linesize = 0.8,
  pointshape = 21,
  font.family = "sans"
)
```

Arguments

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
npar	Number of model parameters (<i>default</i> is BC.4)
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme (<i>default</i> is theme_bw())
legend.position	Legend position (<i>default</i> is c(0.3,0.8))
cardinal	Defines the value of y considered extreme (<i>default</i> considers 0 germination)
r2	Coefficient of determination of the mean or all values (<i>default</i> is all)

width.bar	bar width
scale	Sets x scale (<i>default</i> is none, can be "log")
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is sans)

Details

The model function for the Brain-Cousens model (Brain and Cousens, 1989) is

$$f(x, b, c, d, e, f) = c + \frac{d - c + fx}{1 + \exp(b(\log(x) - \log(e)))}$$

and it is a five-parameter model, obtained by extending the four-parameter log-logistic model (LL.4 to take into account inverse u-shaped hormesis effects. Fixing the lower limit at 0 yields the four-parameter model

$$f(x) = 0 + \frac{d - 0 + fx}{1 + \exp(b(\log(x) - \log(e)))}$$

used by van Ewijk and Hoekstra (1993).

Value

Coefficients	Coefficients and their p values
Optimum temperature	Optimum temperature (equivalent to the maximum point)
Optimum temperature response	Response at the optimal temperature (equivalent to the maximum point)
Minimal temperature	Temperature that has the lowest response
Minimal temperature response	Lowest predicted response
Predicted maximum basal value	Lower basal limit temperature based on the value set by the user (default is 0)
Predicted minimum basal value	Upper basal limit temperature based on the value set by the user (default is 0)
AIC	Akaike information criterion
BIC	Bayesian Inference Criterion
r-squared	Determination coefficient
RMSE	Root mean square error
grafico	Graph in ggplot2 with equation

Note

if the maximum predicted value is equal to the maximum x, the curve does not have a maximum point within the studied range. If the minimum value is less than the lowest point studied, disregard the value.

Author(s)

Model imported from the drc package (Ritz et al., 2016)

Gabriel Danilo Shimizu

Leandro Simoes Azeredo Goncalves

References

Seber, G. A. F. and Wild, C. J (1989) Nonlinear Regression, New York: Wiley and Sons (p. 330).

Ritz, C.; STREBIG, J.C. and RITZ, M.C. Package 'drc'. Creative Commons: Mountain View, CA, USA, 2016.

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)

#=====
# Germination
#=====
BC_model(trat,germ)

#=====
# Germination speed
#=====
BC_model(trat, vel, ylab=expression("v"~(dias^-1)))
```

CD_model

Analysis: Logistic regression Cedergreen-Ritz-Streibig model

Description

The 'CRS.4' and 'CRS.5' logistical models provide Brain-Cousens modified logistical models to describe u-shaped hormesis. This model was extracted from the 'drc' package and adapted for temperature analysis in seed germination

Usage

```
CD_model(
  trat,
  resp,
  npar = "CRS.4",
  error = "SE",
  ylab = "Germination (%)",
  xlab = expression("Temperature ("^"o" * "C)"),
  theme = theme_classic(),
  legend.position = "top",
```

```

cardinal = 0,
r2 = "all",
width.bar = NA,
scale = "none",
textsize = 12,
pointsize = 4.5,
linesize = 0.8,
pointshape = 21,
font.family = "sans"
)

```

Arguments

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
npar	Number of model parameters
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	treatments name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme (<i>default</i> is theme_classic())
legend.position	legend position (<i>default</i> is c(0.3,0.8))
cardinal	defines the value of y considered extreme (<i>default</i> considers 0 germination)
r2	coefficient of determination of the mean or all values (<i>default</i> is all)
width.bar	bar width
scale	Sets x scale (<i>default</i> is none, can be "log")
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is sans)

Details

The four-parameter model is given by the expression:

$$f(x) = 0 + \frac{d - 0 + f \exp(-1/x)}{1 + \exp(b(\log(x) - \log(e)))}$$

while the five-parameter is:

$$f(x) = c + \frac{d - c + f \exp(-1/x)}{1 + \exp(b(\log(x) - \log(e)))}$$

Value

Coefficients Coefficients and their p values
 Optimum temperature Optimum temperature (equivalent to the maximum point)
 Optimum temperature response Response at the optimal temperature (equivalent to the maximum point)
 Minimal temperature Temperature that has the lowest response
 Minimal temperature response Lowest predicted response
 Predicted maximum basal value Lower basal limit temperature based on the value set by the user (default is 0)
 Predicted minimum basal value Upper basal limit temperature based on the value set by the user (default is 0)
 AIC Akaike information criterion
 BIC Bayesian Inference Criterion
 r-squared Determination coefficient
 RMSE Root mean square error
 grafico Graph in ggplot2 with equation

Note

If the maximum predicted value is equal to the maximum x, the curve does not have a maximum point within the studied range. If the minimum value is less than the lowest point studied, disregard the value.

Author(s)

Model imported from the drc package (Ritz et al., 2016)
 Gabriel Danilo Shimizu
 Leandro Simoes Azeredo Goncalves

References

Seber, G. A. F. and Wild, C. J (1989) Nonlinear Regression, New York: Wiley and Sons (p. 330).
 Ritz, C.; Strebbig, J.C.; Ritz, M.C. Package 'drc'. Creative Commons: Mountain View, CA, USA, 2016.

Examples

```

library(seedreg)
data("aristolochia")
attach(aristolochia)

#=====
# Germination
#=====
CD_model(trat,germ)

```



```

#=====
# Germination speed
#=====
CD_model(trat, vel, ylab=expression("v"~(dias^-1)))

```

correl	<i>Comparison: correlation between parameters</i>
--------	---

Description

Correlation between the logistical model and the traditional model

Usage

```
correl(seeds)
```

Arguments

seeds Object returned in the seeds function

Value

Returns correlation graphs between parameters calculated by traditional methods and by logistic regression

Examples

```

data("substrate")
a=seeds(substrate[,c(3:18)],
        trat = substrate$Trat,
        nrep = 4,
        time = 1:16)
correl(a)

```

curve	<i>Analysis: Logistic regression by treatment over time</i>
-------	---

Description

Performs the construction of a logistic regression graph by treatment over time

Usage

```
curve(  
  dados,  
  trat,  
  nrep,  
  time,  
  n,  
  model = LL.3(),  
  ylab = "Emergence (%)",  
  xlab = "Time (days)",  
  legend.position = c(0.2, 0.8)  
)
```

Arguments

<code>dados</code>	data.frame containing the responses of the evaluations in separate columns side by side and without the columns with the identification of the factors
<code>trat</code>	vector of treatments with n repetitions
<code>nrep</code>	Number of repetitions
<code>time</code>	vector containing time
<code>n</code>	total seeds per repetition
<code>model</code>	logistic model according to drc package
<code>ylab</code>	y-axis name
<code>xlab</code>	x-axis name
<code>legend.position</code>	Legend position

Value

Returns a logistic regression graph by treatment over time.

Examples

```
data("substrate")  
curve(substrate[,c(3:18)],  
  trat = substrate$Trat,  
  nrep = 4,  
  n=10,  
  time = 1:16)
```

iv *Param: Index for germination speed*

Description

Calculates the emergence or germination speed index according to Maguire (1962)

Usage

```
iv(data, trat, nrep, time)
```

Arguments

data	Data.frame containing the responses of the evaluations in separate columns side by side and without the columns with the identification of the factors
trat	Vector of treatments with n repetitions
nrep	Number of repetitions
time	Vector containing time

Value

Returns the vector with the index

References

Maguire JD (1962). Seed of germination - aid in selection and evaluation for seedling emergence and vigour. J Crop Sci 2:176-177.

Examples

```
data("substrate")
iv(substrate[,c(3:18)],
  trat = substrate$Trat,
  nrep = 4,
  time = 1:16)
```

`lineplot`*Graph: line chart*

Description

Returns a graph with the frequencies of germinated or emerged seeds

Usage

```
lineplot(  
  dados,  
  trat,  
  nrep,  
  time,  
  ylab = "Emergence",  
  xlab = "Time (days)",  
  nt = NA,  
  percentage = FALSE,  
  legend.position = c(0.2, 0.8)  
)
```

Arguments

<code>dados</code>	data.frame containing the responses of the evaluations in separate columns side by side and without the columns with the identification of the factors
<code>trat</code>	vector of treatments with n repetitions
<code>nrep</code>	Number of repetitions
<code>time</code>	vector containing time
<code>ylab</code>	y-axis name
<code>xlab</code>	x-axis name
<code>nt</code>	total seeds per repetition
<code>percentage</code>	y scale in percentage
<code>legend.position</code>	Legend position

Value

Returns a graph with the frequencies of germinated or emerged seeds.

Examples

```
data("substrate")  
lineplot(substrate[,c(3:18)],  
  trat = substrate$Trat,  
  nrep = 4,  
  time = 1:16)
```

Description

Logistic models with three (LL.3) or four (LL.4) continuous data parameters. This model was extracted from the drc package and adapted for temperature analysis in seed germination.

Usage

```
LL_model(
  trat,
  resp,
  npar = "LL.3",
  error = "SE",
  ylab = "Germination (%)",
  xlab = expression("Temperature ("^"o" * "C)"),
  theme = theme_classic(),
  legend.position = "top",
  cardinal = 0,
  r2 = "all",
  width.bar = NA,
  scale = "none",
  textsize = 12,
  pointsize = 4.5,
  linesize = 0.8,
  pointshape = 21,
  font.family = "sans"
)
```

Arguments

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
npar	Number of model parameters
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme (<i>default</i> is theme_bw())
legend.position	Legend position (<i>default</i> is c(0.3,0.8))
cardinal	Defines the value of y considered extreme (<i>default</i> considers 0 germination)
r2	Coefficient of determination of the mean or all values (<i>default</i> is all)
width.bar	Bar width

scale	Sets x scale (<i>default</i> is none, can be "log")
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is sans)

Details

The three-parameter log-logistic function with lower limit 0 is

$$f(x) = 0 + \frac{d}{1 + \exp(b(\log(x) - \log(e)))}$$

The four-parameter log-logistic function is given by the expression

$$f(x) = c + \frac{d - c}{1 + \exp(b(\log(x) - \log(e)))}$$

The function is symmetric about the inflection point (e).

Value

Coefficients	Coefficients and their p values
Optimum temperature	Optimum temperature (equivalent to the maximum point)
Optimum temperature response	Response at the optimal temperature (equivalent to the maximum point)
Minimal temperature	Temperature that has the lowest response
Minimal temperature response	Lowest predicted response
Predicted maximum basal value	Lower basal limit temperature based on the value set by the user (default is 0)
Predicted minimum basal value	Upper basal limit temperature based on the value set by the user (default is 0)
AIC	Akaike information criterion
BIC	Bayesian Inference Criterion
r-squared	Determination coefficient
RMSE	Root mean square error
grafico	Graph in ggplot2 with equation

Note

if the maximum predicted value is equal to the maximum x, the curve does not have a maximum point within the studied range. If the minimum value is less than the lowest point studied, disregard the value.

Author(s)

Model imported from the drc package (Ritz et al., 2016)

Gabriel Danilo Shimizu

Leandro Simoes Azeredo Goncalves

References

Seber, G. A. F. and Wild, C. J (1989) Nonlinear Regression, New York: Wiley and Sons (p. 330).

Ritz, C.; Strebig, J.C.; Ritz, M.C. Package ‘drc’. Creative Commons: Mountain View, CA, USA, 2016.

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)

#=====
# Germination
#=====
LL_model(trat,germ)

#=====
# Germination speed
#=====
LL_model(trat, vel, ylab=expression("v"~(dias^-1)))
```

LM_model

Analysis: Linear regression graph

Description

Linear regression analysis of an experiment with a quantitative factor or isolated effect of a quantitative factor

Usage

```
LM_model(
  trat,
  resp,
  ylab = "Germination (%)",
  error = "SE",
  xlab = expression("Temperature ("^"o" * "C)"),
  grau = NA,
  theme = theme_classic(),
  cardinal = 0,
  legend.position = "top",
```

```

width.bar = NA,
scale = "none",
textsize = 12,
pointsize = 4.5,
linesize = 0.8,
pointshape = 21,
font.family = "sans"
)

```

Arguments

trat	Numerical vector with treatments (Declare as numeric)
resp	Numerical vector containing the response of the experiment.
ylab	Dependent variable name (Accepts the <i>expression()</i> function)
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
xlab	Independent variable name (Accepts the <i>expression()</i> function)
grau	Degree of the polynomial (1,2 or 3)
theme	ggplot2 theme (<i>default</i> is theme_classic())
cardinal	Defines the value of y considered extreme (<i>default</i> considers 0 germination)
legend.position	Legend position (<i>default</i> is "top")
width.bar	Bar width
scale	Sets x scale (<i>default</i> is none, can be "log")
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is sans)

Value

Coefficients	Coefficients and their p values
Optimum temperature	Optimum temperature (equivalent to the maximum point)
Optimum temperature response	Response at the optimal temperature (equivalent to the maximum point)
Minimal temperature	Temperature that has the lowest response
Minimal temperature response	Lowest predicted response
Predicted maximum basal value	Lower basal limit temperature based on the value set by the user (default is 0)
Predicted minimum basal value	Upper basal limit temperature based on the value set by the user (default is 0)
AIC	Akaike information criterion

BIC Bayesian Inference Criterion
 VIF Variance inflation factor (multicollinearity)
 r-squared Determination coefficient
 RMSE Root mean square error
 grafico Graph in ggplot2 with equation

Note

If the maximum predicted value is equal to the maximum x, the curve does not have a maximum point within the studied range. If the minimum value is less than the lowest point studied, disregard the value.

Author(s)

Gabriel Danilo Shimizu
 Leandro Simoes Azeredo Goncalves

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)

#=====
# Germination
#=====
LM_model(trat,germ, grau=3)

#=====
# Germination speed
#=====
LM_model(trat, vel, grau=3,
ylab=expression("v"~(dias^-1)))
```

loess_model

Analysis: loess regression

Description

Fit a polynomial surface determined by one or more numerical predictors, using local fitting.

Usage

```
loess_model(
  trat,
  resp,
  ylab = "Germination (%)",
  xlab = expression("Temperature (\"^\"o\" * \"C)"),
  theme = theme_classic(),
  error = "SE",
  cardinal = 0,
  width.bar = NA,
  legend.position = "top",
  scale = "none",
  textsize = 12,
  pointsize = 4.5,
  linesize = 0.8,
  pointshape = 21,
  font.family = "sans"
)
```

Arguments

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	treatments name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme (<i>default</i> is <i>theme_bw()</i>)
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
cardinal	defines the value of y considered extreme (<i>default</i> considers 0 germination)
width.bar	bar width
legend.position	legend position (<i>default</i> is <i>c(0.3,0.8)</i>)
scale	Sets x scale (<i>default</i> is <i>none</i> , can be "log")
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is <i>sans</i>)

Value

Optimum temperature Optimum temperature (equivalent to the maximum point)

Optimum temperature response Response at the optimal temperature (equivalent to the maximum point)

Minimal temperature Temperature that has the lowest response

Minimal temperature response Lowest predicted response
 Predicted maximum basal value Lower basal limit temperature based on the value set by the user
 (default is 0)
 Predicted minimum basal value Upper basal limit temperature based on the value set by the user
 (default is 0)
 grafico Graph in ggplot2 with equation

Note

if the maximum predicted value is equal to the maximum x, the curve does not have a maximum point within the studied range. If the minimum value is less than the lowest point studied, disregard the value.

Author(s)

Gabriel Danilo Shimizu
 Leandro Simoes Azeredo Goncalves

See Also

[loess](#)

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)

#=====
# Germination
#=====
loess_model(trat, germ)

#=====
# Germination speed
#=====
loess_model(trat, vel, ylab=expression("v"~(dias^-1)))
```

multicurve

Graph: Merge multiple curves into a single graph

Description

Graph: Merge multiple curves into a single graph

Usage

```

multicurve(
  plots,
  theme = theme_classic(),
  legend.title = NULL,
  legend.position = "top",
  trat = NA,
  method = "shape_color",
  fill = "gray90",
  ylab = "Germination (%)",
  xlab = expression("Temperature ("^"o" * "C)"),
  width.bar = NA,
  pointsize = 4.5,
  linesize = 0.8,
  textsize = 12,
  font.family = "sans"
)

```

Arguments

plots	list with objects of type LM_model, BC_model, CD_model, LL_model or normal_model
theme	ggplot2 theme (<i>default</i> is theme_classic())
legend.title	caption title
legend.position	legend position (<i>default</i> is c(0.3,0.8))
trat	name of the curves
method	marking method
fill	dot fill color in case gray=F
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	treatments name (Accepts the <i>expression()</i> function)
width.bar	bar width
pointsize	shape size
linesize	line size
textsize	Font size
font.family	Font family (<i>default</i> is sans)

Details

The method argument defines the type of markup desired by the user. By default, method="shape_color" is used, which differentiates by color and dot shape. For gray scale, use method="shape_gray". To use only color, use method="color", in this case, the dot shape is 16 (filled circle). You can change the stitch pattern by setting the fill color in quotes followed by a space and the stitch number (eg "gray 21"). Still starting from this last method, if the user uses the change to point format without filling, such as 15, 16, 17 or 18, the function will ignore the first argument (ex. "gray 16"), however, of either way the user must define a color.

Value

The function returns a graph joining the outputs of the functions LM_model, LL_model, BC_model, CD_model, loess_model, normal_model, piecewise_model and N_model

Author(s)

Gabriel Danilo Shimizu

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)
a=LM_model(trat,germ)
b=LL_model(trat,germ,npar = "LL.3")
c=BC_model(trat,germ, npar = "BC.4")
d=CD_model(trat,germ, npar = "CRS.4")
multicurve(list(a,b,c,d))
```

normal_model

Analysis: Normal model

Description

Analysis: Normal model

Usage

```
normal_model(  
  trat,  
  resp,  
  ylab = "Germination (%)",  
  xlab = expression("Temperature ("^"o" * "C)"),  
  theme = theme_classic(),  
  error = "SE",  
  legend.position = "top",  
  cardinal = 0,  
  r2 = "all",  
  width.bar = NA,  
  scale = "none",  
  textsize = 12,  
  pointsize = 4.5,  
  linesize = 0.8,  
  pointshape = 21,  
  font.family = "sans"  
)
```

Arguments

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	treatments name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme (<i>default</i> is theme_classic())
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
legend.position	legend position (<i>default</i> is c(0.3,0.8))
cardinal	defines the value of y considered extreme (<i>default</i> considers 0 germination)
r2	coefficient of determination of the mean or all values (<i>default</i> is all)
width.bar	bar width
scale	Sets x scale (<i>default</i> is none, can be "log")
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is sans)

Details

The model function for the normal model is:

$$f(x) = a e^{-\frac{(x-b)^2}{c^2}}$$

Value

Coefficients	Coefficients and their p values
Optimum temperature	Optimum temperature (equivalent to the maximum point)
Optimum temperature response	Response at the optimal temperature (equivalent to the maximum point)
Minimal temperature	Temperature that has the lowest response
Minimal temperature response	Lowest predicted response
Predicted maximum basal value	Lower basal limit temperature based on the value set by the user (default is 0)
Predicted minimum basal value	Upper basal limit temperature based on the value set by the user (default is 0)
AIC	Akaike information criterion
BIC	Bayesian Inference Criterion
r-squared	Determination coefficient
RMSE	Root mean square error
grafico	Graph in ggplot2 with equation

Note

if the maximum predicted value is equal to the maximum x, the curve does not have a maximum point within the studied range. If the minimum value is less than the lowest point studied, disregard the value.

Author(s)

Gabriel Danilo Shimizu
Leandro Simoes Azeredo Goncalves

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)

#=====
# Germination
#=====
normal_model(trat,germ)

#=====
# Germination speed
#=====
normal_model(trat, vel, ylab=expression("v"~"(dias^-1)))
```

N_model

Analysis: Graph for not significant trend

Description

Graph for non-significant trend. Can be used within the multicurve command

Usage

```
N_model(
  trat,
  resp,
  ylab = "Germination (%)",
  error = "SE",
  legend = "not~significant",
  xlab = expression("Temperature ("^"o" * "C)"),
  theme = theme_classic(),
  width.bar = NA,
  legend.position = "top",
  textsize = 12,
  pointsize = 4.5,
  linesize = 0.8,
```

```

    pointshape = 21,
    font.family = "sans"
  )

```

Arguments

trat	Numerical vector with treatments (Declare as numeric)
resp	Numerical vector containing the response of the experiment.
ylab	Dependent variable name (Accepts the <i>expression()</i> function)
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
legend	Add the legend
xlab	Independent variable name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme (<i>default</i> is theme_classic())
width.bar	Bar width
legend.position	Legend position (<i>default</i> is "top")
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is sans)

Value

The function returns an exploratory graph of segments

Author(s)

Gabriel Danilo Shimizu
Leandro Simoes Azeredo Goncalves

Examples

```

library(seedreg)
data("aristolochia")
attach(aristolochia)

#####
# Germination
#####
N_model(trat, germ)

#####
# Germination speed
#####
N_model(trat, vel, ylab=expression("v"~(dias^-1)))

```

piecewise_model *Analysis: Piecewise regression*

Description

Fit a degree 1 spline with 1 knot point where the location of the knot point is unknown.

Usage

```
piecewise_model(
  trat,
  resp,
  middle = 1,
  CI = FALSE,
  bootstrap.samples = 1000,
  sig.level = 0.05,
  error = "SE",
  ylab = "Germination (%)",
  xlab = expression("Temperature ("^"o" * "C)"),
  theme = theme_classic(),
  cardinal = 0,
  width.bar = NA,
  legend.position = "top",
  textsize = 12,
  pointsize = 4.5,
  linesize = 0.8,
  pointshape = 21,
  font.family = "sans"
)
```

Arguments

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
middle	A scalar in [0,1]. This represents the range that the change-point can occur in. 0 means the change-point must occur at the middle of the range of x-values. 1 means that the change-point can occur anywhere along the range of the x-values.
CI	Whether or not a bootstrap confidence interval should be calculated. Defaults to FALSE because the interval takes a non-trivial amount of time to calculate
bootstrap.samples	The number of bootstrap samples to take when calculating the CI.
sig.level	What significance level to use for the confidence intervals.
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	treatments name (Accepts the <i>expression()</i> function)

theme	ggplot2 theme (<i>default</i> is theme_classic())
cardinal	defines the value of y considered extreme (<i>default</i> considers 0 germination)
width.bar	bar width
legend.position	legend position (<i>default</i> is c(0.3,0.8))
textsize	Font size
pointsize	shape size
linesize	line size
pointshape	format point (<i>default</i> is 21)
font.family	Font family (<i>default</i> is sans)

Value

Coefficients	Coefficients and their p values
Optimum temperature	Optimum temperature (equivalent to the maximum point)
Optimum temperature response	Response at the optimal temperature (equivalent to the maximum point)
Minimal temperature	Temperature that has the lowest response
Minimal temperature response	Lowest predicted response
Predicted maximum basal value	Lower basal limit temperature based on the value set by the user (default is 0)
Predicted minimum basal value	Upper basal limit temperature based on the value set by the user (default is 0)
AIC	Akaike information criterion
BIC	Bayesian Inference Criterion
r-squared	Determination coefficient
RMSE	Root mean square error
grafico	Graph in ggplot2 with equation

Note

if the maximum predicted value is equal to the maximum x, the curve does not have a maximum point within the studied range. If the minimum value is less than the lowest point studied, disregard the value.

Author(s)

Model imported from the SiZer package
 Gabriel Danilo Shimizu
 Leandro Simoes Azeredo Goncalves

References

Chiu, G. S., R. Lockhart, and R. Routledge. 2006. Bent-cable regression theory and applications. *Journal of the American Statistical Association* 101:542-553.

Toms, J. D., and M. L. Lesperance. 2003. Piecewise regression: a tool for identifying ecological thresholds. *Ecology* 84:2034-2041.

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)

#=====
# Germination
#=====
piecewise_model(trat,germ)

#=====
# Germination speed
#=====
piecewise_model(trat, vel, ylab=expression("v"~(dias^-1)))
```

quali_model

Analysis: generalized linear models for factor qualitative

Description

Performs the deviance analysis for the generalized linear model using binomial or quasibinomial family. The function also returns multiple comparison test with tukey adjustment

Usage

```
quali_model(
  trat,
  resp,
  method = "glm",
  n = 50,
  family = "binomial",
  ylab = "Germination (%)",
  xlab = expression("Temperature ("^"o" * "C)"),
  reversed = TRUE,
  angle = 0,
  sup = NA,
  theme = theme_classic(),
  font.family = "sans",
  geom = "bar"
)
```

Arguments

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response in percentage of the experiment.
method	method for analysis (analysis of variance - aov or analysis by generalized linear model - glm)
n	Number of seeds per repetition
family	a description of the error distribution and link function to be used in the model. For glm this can be a character string naming a family function, a family function or the result of a call to a family function.
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	treatments name (Accepts the <i>expression()</i> function)
reversed	Letter order (<i>default</i> is FALSE)
angle	x-axis scale text rotation
sup	Number of units above the standard deviation or average bar on the graph
theme	ggplot2 theme (<i>default</i> is theme_bw())
font.family	Font family (<i>default</i> is sans)
geom	type of graph ("bar" or "point")

Value

The function returns analysis by glm (binomial or quasibinomial family), post-hoc and column graph

Examples

```
library(seedreg)
data("aristolochia")
attach(aristolochia)
quali_model(trat, germ, n=25, family="quasibinomial")
```

seeds

Param: Seeds

Description

Simplification of functions: acc, iv, tm and tml.

Usage

```
seeds(data, trat, nrep, time)
```

Arguments

data	Data.frame containing the responses of the evaluations in separate columns side by side and without the columns with the identification of the factors
trat	Vector of treatments with n repetitions
nrep	Number of repetitions
time	Vector containing time

Value

Returns a data.frame with the indices

Examples

```
data("substrate")
seeds(substrate[,c(3:18)],
      trat = substrate$Trat,
      nrep = 4,
      time = 1:16)
```

substrate

dataset: substrate

Description

The data come from an experiment carried out at the Universidade Estadual de Londrina, in which four types of substrates were tested in the emergence of sour passion fruit seeds. The experiment was carried out in a completely randomized design with four replications of 10 seeds each.

Usage

```
data("substrate")
```

Format

data.frame containing data set

Trat Vector with factor 1

bloco Vector with block

1, 2, 3... Numerical vector with germination

Examples

```
data(substrate)
```

tm	<i>Param: Average time</i>
----	----------------------------

Description

Calculates the average germination/emergence time according to Silva and Nakagawa (1995)

Usage

```
tm(data, trat, nrep, time)
```

Arguments

data	data.frame containing the responses of the evaluations in separate columns side by side and without the columns with the identification of the factors
trat	vector of treatments with n repetitions
nrep	Number of repetitions
time	vector containing time

Value

Returns the vector with the average time.

References

SILVA, J. B. C.; NAKAGAWA, J. Estudos de formulas para calculo de germinacao. Informativo ABRATES, Londrina, v. 5, n. 1, p. 62-73, 1995.

Examples

```
data("substrate")
tm(substrate[,c(3:18)],
  trat = substrate$Trat,
  nrep = 4,
  time = 1:16)
```

tml *Param: Logistic average time*

Description

Param: Logistic average time

Usage

```
tml(dados, trat, nrep, time)
```

Arguments

dados	Data.frame containing the responses of the evaluations in separate columns side by side and without the columns with the identification of the factors
trat	Vector of treatments with n repetitions
nrep	Number of repetitions
time	Vector containing time

Value

Returns the vector with the average time.

Examples

```
data("substrate")
tml(substrate[,c(3:18)],
     trat = substrate$Trat,
     nrep = 4,
     time = 1:16)
```

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