Package ‘seedreg’

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>), quadratic (Nunes, AL, Sossmeier, S, Gotz, AP, & Bispo, NB (2018) <doi: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>), 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 .......................... Param: Area below the curve

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
aristolochia

Examples

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

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 35°C) 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)
Analysis: Logistic regression Brain-Cousens hormesis models

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 (default is BC.4)
  error Error bar (It can be SE - default, SD or FALSE)
  ylab  Variable response name (Accepts the expression() function)
  xlab  Treatments name (Accepts the expression() function)
  theme ggplot2 theme (default is theme_bw())
  legend.position Legend position (default is c(0.3,0.8))
  cardinal Defines the value of y considered extreme (default considers 0 germination)
  r2 Coefficient of determination of the mean or all values (default is all)
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 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.
CD_model

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

References

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 ("^"\circ" * 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 - default, SD or FALSE)
ylab  Variable response name (Accepts the expression() function)
xlab  treatments name (Accepts the expression() function)
theme ggplot2 theme (default is theme_classic())
legend.position legend position (default is c(0.3,0.8))
cardinal defines the value of y considered extreme (default considers 0 germination)
r2    coefficient of determination of the mean or all values (default is all)
width.bar bar width
scale  Sets x scale (default is none, can be "log")
textsize Font size
pointsize shape size
linesize line size
pointshape format point (default is 21)
font.family Font family (default 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
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
#==============================
CD_model(trat,germ)
Germination speed

Comparison: correlation between parameters

correl

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)

Analysis: Logistic regression by treatment over time

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

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

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
- **n**: total seeds per repetition
- **model**: logistic model according to drc package
- **ylab**: y-axis name
- **xlab**: x-axis name
- **legend.position**: Legend position

Value

Returns a logistic regression graph by treatment over time.

Examples

```r
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


Examples

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

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

Usage

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

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.
- `ylab`: y-axis name.
- `xlab`: x-axis name.
- `nt`: total seeds per repetition.
- `percentage`: y scale in percentage.
- `legend.position`: Legend position.

Value

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

Examples

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

**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**

```r
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 - *default*, SD or FALSE)
- `ylab` Variable response name (Accepts the `expression()` function)
- `xlab` Treatments name (Accepts the `expression()` function)
- `theme` ggplot2 theme (*default* is theme_bw())
- `legend.position` Legend position (*default* is c(0.3,0.8))
- `cardinal` Defines the value of y considered extreme (*default* considers 0 germination)
- `r2` Coefficient of determination of the mean or all values (*default* is all)
- `width.bar` Bar width
scale  Sets x scale (default is none, can be "log")
textsize  Font size
pointsize  shape size
linesize  line size
pointshape  format point (default is 21)
font.family  Font family (default 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.
**LM_model**

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

**References**

**Examples**
```r
library(seedreg)
data("aristolochia")attach(aristolochia)

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

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

---

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

**Usage**
```r
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 expression() function)
error Error bar (It can be SE - default, SD or FALSE)
xlab  Independent variable name (Accepts the expression() function)
grau  Degree of the polynomial (1, 2 or 3)
theme ggplot2 theme (default is theme_classic())
cardinal Defines the value of y considered extreme (default considers 0 germination)
legend.position Legend position (default is "top")
width.bar Bar width
scale  Sets x scale (default is none, can be "log")
textsize Font size
pointsize shape size
linesize line size
pointshape format point (default is 21)
font.family Font family (default 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

```r
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 expression() function)  
xlab   treatments name (Accepts the expression() function)  
theme  ggplot2 theme (default is theme_bw())  
error  Error bar (It can be SE - default, SD or FALSE)  
cardinal defines the value of y considered extreme (default considers 0 germination)  
width.bar bar width  
legend.position legend position (default is c(0.3,0.8))  
scale  Sets x scale (default is none, can be "log")  
textsize Font size  
pointsize shape size  
linesize line size  
pointshape format point (default is 21)  
font.family Font family (default is sans)

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,
  fontsize = 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 (default is `theme_classic()`)
- `legend.title` : caption title
- `legend.position` : legend position (default is `c(0.3,0.8)`) (default 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 `expression()` function)
- `xlab` : treatments name (Accepts the `expression()` function)
- `width.bar` : bar width
- `pointsize` : shape size
- `linesize` : line size
- `fontsize` : Font size
- `font.family` : Font family (default 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

```r
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))
```

Analysis: Normal model

Usage

```r
normal_model(
    trat,
    resp,
    ylab = "Germination (%)",
    xlab = expression("Temperature (^"^\circ" * "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"
)
```
normal_model

Arguments

- **trat**: Numerical or complex vector with treatments
- **resp**: Numerical vector containing the response of the experiment.
- **ylab**: Variable response name (Accepts the `expression()` function)
- **xlab**: Treatments name (Accepts the `expression()` function)
- **theme**: ggplot2 theme (*default* is `theme_classic()`)
- **error**: Error bar (It can be SE - *default*, SD or FALSE)
- **legend.position**: Legend position (*default* is c(0.3,0.8))
- **cardinal**: Defines the value of y considered extreme (*default* considers 0 germination)
- **r2**: Coefficient of determination of the mean or all values (*default* is all)
- **width.bar**: Bar width
- **scale**: Sets x scale (*default* is none, can be "log")
- **textsize**: Font size
- **pointsize**: Shape size
- **linesize**: Line size
- **pointshape**: Format point (*default* is 21)
- **font.family**: Font family (*default* is sans)

Details

The model function for the normal model is:

\[ f(x) = ae^{-\frac{(x-b)^2}{c^2}} \]

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**

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

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

#================================
# Germination speed
#================================
normal_model(trat, vel, ylab=expression("v" inverse(dias)))
```

**Description**

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

**Usage**

```r
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 `expression()` function))
- **error** (Error bar (It can be SE - `default`, SD or FALSE))
- **legend** (Add the legend)
- **xlab** (Independent variable name (Accepts the `expression()` function))
- **theme** (ggplot2 theme (default is `theme_classic()`))
- **width.bar** (Bar width)
- **legend.position** (Legend position (default is "top"))
- **textsize** (Font size)
- **pointsize** (shape size)
- **linesize** (line size)
- **pointshape** (format point (default is 21))
- **font.family** (Font family (default is sans))

Value

The function returns an exploratory graph of segments

Author(s)

Gabriel Danilo Shimizu
Leandro Simoes Azeredo Goncalves

Examples

```r
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
```r
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 - default, SD or FALSE)
- **ylab**: Variable response name (Accepts the `expression()` function)
- **xlab**: treatments name (Accepts the `expression()` function)
theme ggplot2 theme (default is theme_classic())
cardinal defines the value of y considered extreme (default considers 0 germination)
width.bar bar width
legend.position legend position (default is c(0.3,0.8))
textsize Font size
pointsize shape size
linesize line size
pointshape format point (default is 21)
font.family Font family (default 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


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 expression() function)
- **xlab**: treatments name (Accepts the expression() function)
- **reversed**: Letter order (default 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 (default is theme_bw())
- **font.family**: Font family (default 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

```r
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

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

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)

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**  
*Param: Average time*

**Description**

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

**Usage**

```r
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**


**Examples**

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