# Package ‘seedreg’

October 14, 2022

**Type** Package

**Title** Regression Analysis for Seed Germination as a Function of Temperature

**Version** 1.0.3

**Date** 2022-07-07

**Maintainer** Gabriel Danilo Shimizu <shimizu@uel.br>

**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.

**License** GPL (>= 2)

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

**Depends** R (>= 3.6)

**Suggests** DT, knitr, rmarkdown, roxygen2

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.0

**NeedsCompilation** no

**Author** Gabriel Danilo Shimizu [aut, cre]
(<https://orcid.org/0000-0001-8524-508X>),
Hugo Roldi Guariz [aut, ctb] (<https://orcid.org/0000-0003-4343-379X>),
Leandro Simoes Azeredo Goncalves [aut, ctb]
(<https://orcid.org/0000-0001-9700-9375>)

**Repository** CRAN

**Date/Publication** 2022-07-07 21:20:02 UTC

# R topics documented:

---

## `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

## 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)
```

---

## `BC_model` *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) |

| | |
|---|---|
| `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 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 - *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

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

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

---

## `correl` *Comparison: correlation between parameters*

### 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` *Analysis: Logistic regression by treatment over time*

### 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

| | |
|---|---|
| `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

```
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

| | |
|---|---|
| `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

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

## `LL_model` *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

```
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.

### 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 *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

```
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,
  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 (*default* is theme_classi()) |
| `legend.title` | caption title |
| `legend.position` | legend position (*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 |
| `textsize` | 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

```
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 *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:

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

### 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~signifcant",
  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

```
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 - *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

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 *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

```
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` *Param: Average time*

---

### 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)
```

# Index