

# Package ‘sars’

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**Type** Package

**Title** Fit and Compare Species-Area Relationship Models Using  
Multimodel Inference

**Version** 1.3.0

**Description** Implements the basic elements of the multi-model  
inference paradigm for up to twenty species-area relationship models (SAR), using simple  
R list-objects and functions, as in Triantis et al. 2012 <DOI:10.1111/j.1365-2699.2011.02652.x>.  
The package is scalable and users can easily create their own model and data objects. Additional  
SAR related functions are provided.

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**URL** <https://github.com/txm676/sars>, <https://txm676.github.io/sars/>

**BugReports** <https://github.com/txm676/sars/issues>

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sars-package

*sars: Fit and compare species-area relationship models using multi-model inference*

---

## Description

This package provides functions to fit twenty models to species-area relationship (SAR) data (see Triantis et al. 2012), plot the model fits, and to construct a multimodel SAR curve using information criterion weights. A number of additional SAR functions are provided, e.g. to fit the log-log power model, the general dynamic model of island biogeography (GDM), and Coleman's Random Placement model.

## Details

Functions are provided to fit 20 individual SAR models. Nineteen are fitted using non-linear regression, whilst a single model (the linear model) is fitted using linear regression. Each model has its own function (e.g. `sar_power`). A set of multiple model fits can be combined into a fit collection (`sar_multi`). Plotting functions (`plot.sars`) are provided that enable individual model fits to be plotted on their own, or the fits of multiple models to be overlaid on the same plot. Model fits are validated using a number of checks, e.g. the normality and homogeneity of the model residuals can be assessed.

A multimodel SAR curve can be constructed using the `sar_average` function. This fits up to twenty SAR models and constructs the multimodel curve (with confidence intervals) using information criterion weights (see `summary.sars` to calculate a table of models ranked by information criterion weight). The `plot_multi` functions enables the multimodel SAR curve to be plotted with or without the fits of the individual models.

Other SAR related functions include: (i) `lin_pow`, which fits the log-log power model and enables comparison of the model parameters with those calculated using the non-linear power model, (ii) `gdm`, which fits the general dynamic model of island biogeography (Whittaker et al. 2008) using several different functions, and (iii) `coleman`, which fits Coleman's (1981) random placement model to a species-site abundance matrix.

## Author(s)

Thomas J. Matthews and Francois Guilhaumon

## References

- Coleman, B. D. (1981). On random placement and species-area relations. *Mathematical Biosciences*, 54, 191-215.
- Guilhaumon, F., Mouillot, D., & Gimenez, O. (2010). mmSAR: an R-package for multimodel species-area relationship inference. *Ecography*, 33, 420-424.
- Matthews, T.J., Guilhaumon, F., Triantis, K.A., Borregaard, M.K., & Whittaker, R.J. (2015b) On the form of species-area relationships in habitat islands and true islands. *Global Ecology & Biogeography*. DOI: 10.1111/geb.12269.

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species–area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

Whittaker, R.J., Triantis, K.A. & Ladle, R.J. (2008) A general dynamic theory of oceanic island biogeography. *Journal of Biogeography*, 35, 977-994.

### See Also

<https://github.com/txm676/sars>

### Examples

```
data(galap, package = "sars")
#fit the power model
fit <- sar_power(galap)
summary(fit)
plot(fit)

#Construct a multimodel averaged SAR curve
fit_multi <- sar_average(data = galap)
summary(fit_multi)
plot(fit_multi)
```

---

aegean	<i>A SAR dataset describing invertebrates on islands in the Aegean Sea, Greece</i>
--------	--

---

### Description

A sample dataset in the correct sars format: contains the areas of a number of islands in the Aegean Sea, Greece, and the number of invertebrate species recorded on each island.

### Usage

```
data(aegean)
```

### Format

A data frame with 2 columns and 90 rows. Each row contains the area of an island in the Aegean (1st column) and the number of inverts on that island (2nd column).

### Source

Sfenthourakis, S. & Triantis K.A. (2009). Habitat diversity, ecological requirements of species and the Small Island Effect. *Diversity Distrib.*, 15, 131–140.

### Examples

```
data(aegean)
```

---

`aegean2`*A SAR dataset describing plants on islands in the Aegean Sea, Greece*

---

**Description**

A sample dataset in the correct sars format: contains the areas of a number of islands in the Aegean Sea, Greece, and the number of plant species recorded on each island.

**Usage**

```
data(aegean2)
```

**Format**

A data frame with 2 columns and 173 rows. Each row contains the area of an island in the Aegean (1st column) and the number of plants on that island (2nd column).

**Source**

Matthews, T.J. et al. (In review) Unravelling the small-island effect through phylogenetic community ecology

**Examples**

```
data(aegean2)
```

---

`coleman`*Fit Coleman's Random Placement Model*

---

**Description**

Fit Coleman's (1981) random placement model to a species-site abundance matrix: rows are species and columns are sites. Note that the data must be abundance data and not presence-absence data. According to this model, the number of species occurring on an island depends on the relative area of the island and the regional relative species abundances. The fit of the random placement model can be determined through use of a diagnostic plot (see [plot.coleman](#)) of island area (log transformed) against species richness, alongside the model's predicted values (see Wang et al., 2010). Following Wang et al. (2010), the model is rejected if more than a third of the observed data points fall beyond one standard deviation from the expected curve.

**Usage**

```
coleman(data, area)
```

**Arguments**

data	A dataframe or matrix in which rows are species and columns are sites. Each element/value in the matrix is the abundance of a given species in a given site.
area	A vector of site (island) area values. The order of the vector must match the order of the columns in data.

**Value**

A list of class "coleman" with four elements. The first element contains the fitted values of the model. The second element contains the standard deviations of the fitted values, and the third and fourth contain the relative island areas and observed richness values, respectively. `plot.coleman` plots the model.

**References**

- Coleman, B. D. (1981). On random placement and species-area relations. *Mathematical Biosciences*, 54, 191-215.
- Matthews, T. J., Cottee-Jones, H. E. W., & Whittaker, R. J. (2015). Quantifying and interpreting nestedness in habitat islands: a synthetic analysis of multiple datasets. *Diversity and Distributions*, 21, 392-404.
- Wang, Y., Bao, Y., Yu, M., Xu, G., & Ding, P. (2010). Nestedness for different reasons: the distributions of birds, lizards and small mammals on islands of an inundated lake. *Diversity and Distributions*, 16, 862-873.

**Examples**

```
data(cole_sim)
fit <- coleman(cole_sim[[1]], cole_sim[[2]])
plot(fit, ModTitle = "Hetfield")
```

---

cole\_sim

*A simulated species-site abundance matrix with site areas*

---

**Description**

A dataset in the correct sars format:

**Usage**

```
data(cole_sim)
```

**Format**

A list with two elements. The first element contains a species-site abundance matrix in which the rows are species, and the columns are sites/islands. Each value in the matrix is the abundance of a species at a given site. The second element contains a vector of the areas of each site.

**Source**

Matthews et al. 2015.

**Examples**

```
data(cole_sim)
```

---

```
display_sars_models
```

*Display the model information table*

---

**Description**

Display Table 1 of Matthews et al. (2019). See [sar\\_multi](#) for further information.

**Usage**

```
display_sars_models()
```

**Value**

A table of model information for the twenty SAR models, including the model function, number of parameters and general model shape.

**References**

Matthews et al. (2019) sars: an R package for fitting, evaluating and comparing species–area relationship models. *Ecography*, In Review.

---

```
galap
```

*A SAR dataset describing the plants of the Galapagos Islands*

---

**Description**

A sample dataset in the correct sars format: contains the areas of a number of islands in the Galapagos, and the number of plant species recorded on each island.

**Usage**

```
data(galap)
```

**Format**

A data frame with 2 columns and 16 rows. Each row contains the area of an island (km<sup>2</sup>) in the Galapagos (1st column) and the number of plants on that island (2nd column). Preston (1962) also includes the island of Albemarle, but we have excluded this as it is almost six times larger than the second largest island.

**Source**

Preston FW 1962. The Canonical Distribution of Commonness and Rarity: Part I. – Ecology 43:185-215.

**Examples**

```
data(galap)
```

---

gdm

---

*Fit the General Dynamic Model of Island Biogeography*


---

**Description**

Fit the general dynamic model (GDM) of island biogeography using a variety of SAR models. Functions are provided to compare the GDM fitted using different SAR models, and also, for a given SAR model, to compare the GDM with alternative nested candidate models (e.g.  $S \sim A + T$ ).

**Usage**

```
gdm(data, model = "linear", mod_sel = FALSE, AST = c(1, 2, 3))
```

**Arguments**

data	A dataframe or matrix with at least three columns, where one column should include island area values, one island richness values and one island age values.
model	Name of the SAR model to be used to fit the GDM. Can be any of 'logo', 'linear', 'power', or 'all'.
mod_sel	Logical argument specifying whether, for a given SAR model, a model comparison of the GDM with other nested candidate models should be undertaken.
AST	The column locations in data for the area, richness and time values (in that order).

**Details**

The GDM models island species richness as a function of island area and island age, and takes the general form:  $S \sim A + T + T^2$ , where  $S$  = richness,  $A$  = area, and  $T$  = island age. The  $T^2$  term is included as the GDM predicts a hump-shaped relationship between island richness and island age. However, a variety of different SAR models have been used to fit the GDM and three options are available here: the logarithmic, linear and power SAR model. Model fitting follows the procedure in Cardoso et al. (2015). For example, when the linear SAR model is used, the GDM can be fitted using the expression:  $S \sim c + z \cdot \text{Area} + k \cdot T + j \cdot T^2$ , where  $c, z, k, j$  are free parameters to be estimated.

For all three SAR models, the GDM is fitted using non-linear regression and the `nls` function. For ease of fitting, the logarithmic and power SAR models are included in their logarithmic form, e.g. the logarithmic model is fitted using:  $S \sim c + x \cdot \log(A)$ , where  $c$  and  $x$  are parameters to be estimated.



For each model fit, the residual standard error (RSE) and AIC values are reported. However, as the model fit object is returned, it is possible to calculate or extract various other measures of goodness of fit (see [nls](#)).

If `mod_sel == TRUE`, the GDM (using a particular SAR model) is fitted and compared with three other (nested) candidate models: area and time (i.e. no  $\text{time}^2$  term), just area, and an intercept only model. The intercept only model is fitted using `lm` rather than `nls`. If `model == "all"`, the GDM is fitted three times (using the power, loga and linear SAR models), and the fits compared using AIC.

### Value

An object of class `'gdm'`. If `model` is one of "loga", "linear" or "power" the returned object is a `nls` model fit object. If `model == "all"`, the returned object is a list with three elements; each element being a `nls` fit object.

If `mod_sel == TRUE` and `model != "all"`, a list with four elements is returned; each element being a `lm` or `nls` fit object. When `model == "all"`, a list with three elements is returned; each element being a list of the four model fits for a particular SAR model.

### Note

AIC is calculated using the [AIC](#) function, which is based on the log-likelihood and not the residual sum of squares (the latter is used in the main functions of the `sars` package).

A plot generic function enabling 3-d plotting of the GDM fit will be provided in a future version of the package.

### References

Whittaker, R. J., Triantis, K. A., & Ladle, R. J. (2008). A general dynamic theory of oceanic island biogeography. *Journal of Biogeography*, 35, 977-994.

Borregaard, M. K. et al. (2017). Oceanic island biogeography through the lens of the general dynamic model: assessment and prospect. *Biological Reviews*, 92, 830-853.

Cardoso, P., Rigal, F., & Carvalho, J. C. (2015). BAT—Biodiversity Assessment Tools, an R package for the measurement and estimation of alpha and beta taxon, phylogenetic and functional diversity. *Methods in Ecology and Evolution*, 6, 232-236.

### Examples

```
#create an example dataset and fit the GDM using the logarithmic SAR model
data(galap)
galap$t <- rgamma(16, 5, scale = 2)
g <- gdm(galap, model = "loga", mod_sel = FALSE)

#Compare the GDM (using the logarithmic model) with other nested candidate
#models
g2 <- gdm(galap, model = "loga", mod_sel = TRUE)

#compare the GDM fitted using the linear, logarithmic and power SAR models
g3 <- gdm(galap, model = "all", mod_sel = FALSE)
```

---

get_coef	<i>Calculate the intercepts and slopes of the different segments</i>
----------	--

---

### Description

Calculate the intercepts and slopes of the different segments in any of the fitted breakpoint regression models available in the package.

### Usage

```
get_coef(fit)
```

### Arguments

`fit` An object of class 'thresholds', generated using the [sar\\_threshold](#) function.

### Details

The coefficients in the fitted breakpoint regression models do not all represent the intercepts and slopes of the different segments; to get these it is necessary to add different coefficients together.

### Value

A dataframe with the intercepts (`ci`) and slopes (`zi`) of all segments in each fitted model. The numbers attached to `c` and `z` relate to the segment, e.g. `c1` and `z1` are the intercept and slope of the first segment. For the left-horizontal models, the slope of the first segment (i.e. the horizontal segment) is not returned. NA values represent cases where a given parameter is not present in a particular model.

### Examples

```
data(aegean2)
a2 <- aegean2[1:168,]
fitT <- sar_threshold(data = a2, mod = c("ContOne", "DiscOne", "ZslopeOne"),
  interval = 0.1, non_th_models = TRUE, logAxes = "area", logT = log10)
#get the slopes and intercepts for these three models
coefs <- get_coef(fitT)
coefs
```

---

lin_pow	<i>Fit the log-log version of the power model</i>
---------	---

---

### Description

Fit the log-log version of the power model to SAR data and return parameter values, summary statistics and the fitted values.

### Usage

```
lin_pow(data, con = 1, logT = log, compare = FALSE, normaTest =
  "lillie", homoTest = "cor.fitted")
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
con	The constant to add to the species richness values in cases where one of the islands has zero species.
logT	The log-transformation to apply to the area and richness values. Can be any of log(default), log2 or log10.
compare	Fit the standard (non-linear) power model and return the z-value for comparison (default: compare = FALSE).
normaTest	The test used to test the normality of the residuals of the model. Can be any of "lillie" (Lilliefors Kolmogorov-Smirnov test; the default), "shapiro" (Shapiro-Wilk test of normality), "kolmo" (Kolmogorov-Smirnov test), or "none" (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of "cor.fitted" (a correlation of the residuals with the model fitted values; the default), "cor.area" (a correlation of the residuals with the area values), or "none" (no residuals homogeneity test is undertaken).

### Details

A check is made for any islands with zero species. If any zero species islands are found, a constant (default: con = 1) is added to each species richness value to enable log transformation. Natural logarithms are used as default, but log2 and log10 can be used instead using the logT argument.

The compare argument can be used to compare the c and z values calculated using the log-log power model with that calculated using the non-linear power model. Note that the log-log function returns log(c).

**Value**

A list of class "sars" with up to seven elements. The first element is an object of class 'summary.lm'. This is the summary of the linear model fit using the `lm` function and the user's data. The second element is a numeric vector of the model's fitted values, and the third contains the log-transformed observed data. The remaining elements depend on the function arguments selected and can include the results of the non-linear power model fit, the log-transformation function used (i.e. `logT`) and the results of the residuals normality and heterogeneity tests.

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model.

**Examples**

```
data(galap)
fit <- lin_pow(galap, con = 1)
summary(fit)
plot(fit)
```

---

niering

*A SAR dataset describing the plants of the Kapingamarangi Atoll*

---

**Description**

A sample dataset in the correct sars format: contains the areas of a number of islands in the Kapingamarangi Atoll, and the number of plant species recorded on each island.

**Usage**

```
data(niering)
```

**Format**

A data frame with 2 columns and 32 rows. Each row contains the area of an island (km<sup>2</sup>) in the Kapingamarangi Atoll (1st column) and the number of plants on that island (2nd column).

**Source**

Niering, W.A. (1963). Terrestrial ecology of Kapingamarangi Atoll, Caroline Islands. *Ecol. Monogr.*, 33, 131–160.

**Examples**

```
data(niering)
```

---

plot.coleman

*Plot Model Fits for a 'coleman' Object*


---

**Description**

S3 method for class 'coleman'. plot.coleman creates a plot for objects of class coleman, using the R base plotting framework.

**Usage**

```
## S3 method for class 'coleman'
plot(
  x,
  xlab = "Relative area (log transformed)",
  ylab = "Species richness",
  pch = 16,
  cex = 1.2,
  pcol = "black",
  cex.lab = 1.3,
  cex.axis = 1,
  lwd = 2,
  lcol1 = "black",
  lcol2 = "darkgrey",
  ModTitle = NULL,
  TiAdj = 0,
  TiLine = 0.5,
  cex.main = 1.5,
  ...
)
```

**Arguments**

x	An object of class 'coleman'.
xlab	Title for the x-axis.
ylab	Title for the y-axis.
pch	Plotting character (for points).
cex	A numerical vector giving the amount by which plotting symbols (points) should be scaled relative to the default.
pcol	Colour of the points.
cex.lab	The amount by which the the axis titles should be scaled relative to the default.
cex.axis	The amount by which the the axis labels should be scaled relative to the default.
lwd	Line width.
lcol1	Line colour of the fitted model curve.
lcol2	Line colour of the model standard deviation curves.

ModTitle	Plot title (default is null, which equates to no main title).
TiAdj	Which way the plot title (if included) is justified.
TiLine	Places the plot title (if included) this many lines outwards from the plot edge.
cex.main	The amount by which the the plot title (if included) should be scaled relative to the default.
...	Further graphical parameters (see <a href="#">par</a> , <a href="#">plot.default</a> , <a href="#">title</a> , <a href="#">lines</a> ) may be supplied as arguments.

### Details

The resultant plot contains the observed richness values with the model fit and confidence intervals. Following Wang et al. (2010), the model is rejected if more than a third of the observed data points fall beyond one standard deviation from the expected curve.

### Examples

```
data(cole_sim)
fit <- coleman(cole_sim[[1]], cole_sim[[2]])
plot(fit, ModTitle = "Hetfield")
```

---

plot.multi

*Plot Model Fits for a 'multi' Object*

---

### Description

S3 method for class 'multi'. plot.multi creates plots for objects of class multi, using the R base plotting framework. Plots of all model fits, the multimodel SAR curve (with confidence intervals) and a barplot of the information criterion weights of the different models can be constructed.

### Usage

```
## S3 method for class 'multi'
plot(
  x,
  type = "multi",
  allCurves = TRUE,
  xlab = NULL,
  ylab = NULL,
  pch = 16,
  cex = 1.2,
  pcol = "dodgerblue2",
  ModTitle = NULL,
  TiAdj = 0,
  TiLine = 0.5,
  cex.main = 1.5,
  cex.lab = 1.3,
```

```

    cex.axis = 1,
    yRange = NULL,
    lwd = 2,
    lcol = "dodgerblue2",
    mmSep = FALSE,
    lwd.Sep = 6,
    col.Sep = "black",
    pLeg = TRUE,
    modNames = NULL,
    cex.names = 0.88,
    subset_weights = NULL,
    confInt = FALSE,
    ...
)

```

### Arguments

x	An object of class 'multi'.
type	The type of plot to be constructed: either <code>type = multi</code> for a plot of the multimodel SAR curve, or <code>type = bar</code> for a barplot of the information criterion weights of each model.
allCurves	A logical argument for use with <code>type = multi</code> that specifies whether all the model fits should be plotted with the multimodel SAR curve ( <code>allCurves = TRUE</code> ; the default) or that only the multimodel SAR curve should be plotted ( <code>allCurves = FALSE</code> ).
xlab	Title for the x-axis. Only for use with <code>type = multi</code> .
ylab	Title for the y-axis.
pch	Plotting character (for points). Only for use with <code>type = multi</code> .
cex	A numerical vector giving the amount by which plotting symbols (points) should be scaled relative to the default.
pcol	Colour of the points. Only for use with <code>type = multi</code> .
ModTitle	Plot title (default is <code>ModTitle = NULL</code> , which reverts to "Multimodel SAR" for <code>type = multi</code> and to "Model weights" for <code>type = bar</code> ). For no title, use <code>ModTitle = ""</code> .
TiAdj	Which way the plot title is justified.
TiLine	Places the plot title this many lines outwards from the plot edge.
cex.main	The amount by which the plot title should be scaled relative to the default.
cex.lab	The amount by which the axis titles should be scaled relative to the default.
cex.axis	The amount by which the axis labels should be scaled relative to the default.
yRange	The range of the y-axis. Only for use with <code>type = multi</code> .
lwd	Line width. Only for use with <code>type = multi</code> .
lcol	Line colour. Only for use with <code>type = multi</code> .

<code>mmSep</code>	Logical argument of whether the multimodel curve should be plotted as a separate line (default = FALSE) on top of the others, giving the user more control over line width and colour. Only for use with <code>type = multi</code> and <code>allCurves = TRUE</code> .
<code>lwd.Sep</code>	If <code>mmSep = TRUE</code> , the line width of the multimodel curve.
<code>col.Sep</code>	If <code>mmSep = TRUE</code> , the colour of the multimodel curve.
<code>pLeg</code>	Logical argument specifying whether or not the legend should be plotted (when <code>type = multi</code> and <code>allCurves = TRUE</code> ).
<code>modNames</code>	A vector of model names for the barplot of weights (when <code>type = bar</code> ). The default ( <code>modNames = NULL</code> ) uses abbreviated versions (see below) of the names from the <code>sar_average</code> function.
<code>cex.names</code>	The amount by which the axis labels (model names) should be scaled relative to the default. Only for use with <code>type = bar</code> .
<code>subset_weights</code>	Only create a barplot of the model weights for models with a weight value above a given threshold ( <code>subset_weights</code> ). Only for use with <code>type = bar</code> .
<code>confInt</code>	A logical argument specifying whether confidence intervals should be plotted around the multimodel curve. Can only be used if confidence intervals have been generated in the <code>sar_average</code> function.
<code>...</code>	Further graphical parameters (see <code>par</code> , <code>plot.default</code> , <code>title</code> , <code>lines</code> ) may be supplied as arguments.

### Note

In some versions of R and R studio, when plotting all model fits on the same plot with a legend it is necessary to manually extend your plotting window (height and width; e.g. the 'Plots' window of R studio) before plotting to ensure the legend fits in the plot. Extending the plotting window after plotting sometimes just stretches the legend.

Occasionally a model fit will converge and pass the model fitting checks (e.g. residual normality) but the resulting fit is nonsensical (e.g. a horizontal line with intercept at zero). Thus, it can be useful to plot the resultant 'multi' object to check the individual model fits. To re-run the `sar_average` function without a particular model, simply remove it from the `obj` argument.

For visual interpretation of the model weights barplot it is necessary to abbreviate the model names when plotting the weights of several models. To plot fewer bars, use the `subset_weights` argument to filter out models with lower weights than a threshold value. To provide a different set of names use the `modNames` argument. The model abbreviations used as the default are:

- Pow = Power
- PowR = PowerR
- E1 = Extended\_Power\_model\_1
- E2 = Extended\_Power\_model\_2
- P1 = Persistence\_function\_1
- P2 = Persistence\_function\_2
- Loga = Logarithmic
- Kob = Kobayashi



- MMF = MMF
- Mon = Monod
- NegE = Negative\_exponential
- CR = Chapman\_Richards
- CW3 = Cumulative\_Weibull\_3\_par.
- AR = Asymptotic\_regression
- RF = Rational\_function
- Gom = Gompertz
- CW4 = Cumulative\_Weibull\_4\_par.
- BP = Beta-P\_cumulative
- Hel = Heleg(Logistic)
- Lin = Linear\_model

### Examples

```

data(galap)
#plot a multimodel SAR curve with all model fits included
fit <- sar_average(data = galap)
plot(fit)

#remove the legend
plot(fit, pLeg = FALSE)

#plot just the multimodel curve
plot(fit, allCurves = FALSE, ModTitle = "", lcol = "black")

#plot all model fits and the multimodel curve on top as a thicker line
plot(fit, allCurves = TRUE, mmSep = TRUE, lwd.Sep = 6, col.Sep = "orange")

#Plot a barplot of the model weights
plot(fit, type = "bar")
#subset to plot only models with weight > 0.05
plot(fit, type = "bar", subset_weights = 0.05)

```

---

plot.sars

*Plot Model Fits for a 'sars' Object*

---

### Description

S3 method for class 'sars'. `plot.sars` creates plots for objects of class 'sars' (type = 'fit', 'lin\_pow' and 'fit\_collection'), using the R base plotting framework. The exact plot(s) constructed depends on the 'Type' attribute of the 'sars' object. For example, for a 'sars' object of Type 'fit', the `plot.sars` function returns a plot of the model fit (line) and the observed richness values (points). For a 'sars' object of Type 'fit\_collection' the `plot.sars` function returns either a grid with n individual plots (corresponding to the n model fits in the fit\_collection), or a single plot with all n model fits included.

For plotting a 'sar\_average' object, see [plot.multi](#).

**Usage**

```
## S3 method for class 'sars'
plot(
  x,
  mfplot = FALSE,
  xlab = NULL,
  ylab = NULL,
  pch = 16,
  cex = 1.2,
  pcol = "dodgerblue2",
  ModTitle = NULL,
  TiAdj = 0,
  TiLine = 0.5,
  cex.main = 1.5,
  cex.lab = 1.3,
  cex.axis = 1,
  yRange = NULL,
  lwd = 2,
  lcol = "dodgerblue2",
  di = NULL,
  pLeg = FALSE,
  ...
)
```

**Arguments**

<code>x</code>	An object of class 'sars'.
<code>mfplot</code>	Logical argument specifying whether the model fits in a <code>fit_collection</code> should be plotted on one single plot ( <code>mfplot = TRUE</code> ) or separate plots ( <code>mfplot = FALSE</code> ; the default).
<code>xlab</code>	Title for the x-axis (default depends on the <code>Type</code> attribute).
<code>ylab</code>	Title for the y-axis (default depends on the <code>Type</code> attribute).
<code>pch</code>	Plotting character (for points).
<code>cex</code>	A numerical vector giving the amount by which plotting symbols (points) should be scaled relative to the default.
<code>pcol</code>	Colour of the points.
<code>ModTitle</code>	Plot title (default is <code>ModTitle = NULL</code> , which reverts to a default name depending on the type of plot). For no title, use <code>ModTitle = ""</code> . For a <code>sars</code> object of type <code>fit_collection</code> , a vector of names can be provided (e.g. <code>letters[1:3]</code> ).
<code>TiAdj</code>	Which way the plot title is justified.
<code>TiLine</code>	Places the plot title this many lines outwards from the plot edge.
<code>cex.main</code>	The amount by which the plot title should be scaled relative to the default.
<code>cex.lab</code>	The amount by which the axis titles should be scaled relative to the default.
<code>cex.axis</code>	The amount by which the axis labels should be scaled relative to the default.

yRange	The range of the y-axis.
lwd	Line width.
lcol	Line colour.
di	Dimensions to be passed to <code>par(mfrow=())</code> to specify the size of the plotting window, when plotting multiple plots from a sars object of Type <code>fit_collection</code> . For example, <code>di = c(1, 3)</code> creates a plotting window with 1 row and 3 columns. The default (null) creates a square plotting window of the correct size.
pLeg	Logical argument specifying whether or not the legend should be plotted for <code>fit_collection</code> plots (when <code>mfplot = TRUE</code> ) or. When a large number of model fits are plotted the legend takes up a lot of space, and thus the default is <code>pLeg = FALSE</code> .
...	Further graphical parameters (see <code>par</code> , <code>plot.default</code> , <code>title</code> , <code>lines</code> ) may be supplied as arguments.

### Examples

```
data(galap)
#fit and plot a sars object of Type fit.
fit <- sar_power(galap)
plot(fit, ModTitle = "A", lcol = "blue")

#fit and plot a sars object of Type fit_collection.
fc <- sar_multi(data = galap, obj = c("power", "loga", "epm1"))
plot(fc, ModTitle = letters[1:3], xlab = "Size of island")
```

---

plot.threshold                      *Plot Model Fits for a 'threshold' Object*

---

### Description

S3 method for class 'threshold'. `plot.threshold` creates plots for objects of class `threshold`, using the R base plotting framework. Plots of single or multiple threshold models can be constructed.

### Usage

```
## S3 method for class 'threshold'
plot(
  x,
  xlab = NULL,
  ylab = NULL,
  pch = 16,
  cex = 1.2,
  pcol = "black",
  ModTitle = NULL,
  TiAdj = 0,
  TiLine = 0.5,
```

```

    cex.main = 1.5,
    cex.lab = 1.3,
    cex.axis = 1,
    yRange = NULL,
    lwd = 2,
    lcol = "red",
    di = NULL,
    ...
)

```

### Arguments

<code>x</code>	An object of class 'threshold'.
<code>xlab</code>	Title for the x-axis. Defaults will depend on any axes log-transformations.
<code>ylab</code>	Title for the y-axis. Defaults will depend on any axes log-transformations.
<code>pch</code>	Plotting character (for points).
<code>cex</code>	A numerical vector giving the amount by which plotting symbols (points) should be scaled relative to the default.
<code>pcol</code>	Colour of the points.
<code>ModTitle</code>	Plot title (default is <code>ModTitle = NULL</code> ), which reverts to the model names. For no title, use <code>ModTitle = ""</code> .
<code>TiAdj</code>	Which way the plot title is justified.
<code>TiLine</code>	Places the plot title this many lines outwards from the plot edge.
<code>cex.main</code>	The amount by which the plot title should be scaled relative to the default.
<code>cex.lab</code>	The amount by which the axis titles should be scaled relative to the default.
<code>cex.axis</code>	The amount by which the axis labels should be scaled relative to the default.
<code>yRange</code>	The range of the y-axis. Default taken as the largest value bacross the observed and fitted values.
<code>lwd</code>	Line width.
<code>lcol</code>	Line colour.
<code>di</code>	Dimensions to be passed to <code>par(mfrow=())</code> to specify the size of the plotting window, when plotting multiple plots. For example, <code>di = c(1, 3)</code> creates a plotting window with 1 row and 3 columns. The default ( <code>NULL</code> ) creates a plotting window large enough to fit all plots in.
<code>...</code>	Further graphical parameters (see <code>par</code> , <code>plot.default</code> , <code>title</code> , <code>lines</code> ) may be supplied as arguments.

### Note

The raw `lm` model fit objects are returned with the `sar_threshold` function if the user wishes to construct their own plots.

Use `par(mai = c())` prior to calling `plot`, to set the graph margins, which can be useful when plotting multiple models in a single plot to ensure space within the plot taken up by the individual model fit plots is maximised.

**Examples**

```

data(aegean)

#fit two threshold models (in logA-S space) and the linear and
#intercept only models
fct <- sar_threshold(aegean, mod = c("ContOne", "DiscOne"),
                    non_th_models = TRUE, interval = 5,
                    parallel = FALSE, logAxes = "area")

#plot using default settings
plot(fct)

#change various plotting settings, and set the graph margins prior to
#plotting
par(mai = c(0.7,0.7, 0.4, 0.3))
plot(fct, pcol = "blue", pch = 18, lcol = "green",
     ModTitle = c("A", "B", "C", "D"), TiAdj = 0.5, xlab = "Yorke")

```

---

sars_models	<i>Display the 20 SAR model names</i>
-------------	---------------------------------------

---

**Description**

Display the 20 SAR model names as a vector. See [sar\\_multi](#) for further information.

**Usage**

```
sars_models()
```

**Value**

A vector of model names.

---

sar_asymp	<i>Fit the Asymptotic regression model</i>
-----------	--

---

**Description**

Fit the Asymptotic regression model to SAR data.

**Usage**

```

sar_asymp(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
          homoTest = 'cor.fitted')

```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation

- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_asymp(galap)
summary(fit)
plot(fit)
```

---

sar\_average

*Fit a multimodel averaged SAR curve*

---

## Description

Construct a multimodel averaged species-area relationship curve using information criterion weights and up to twenty SAR models.

**Usage**

```
sar_average(obj = c("power",
  "powerR", "epm1", "epm2", "p1", "p2", "loga", "koba",
  "mmf", "monod", "negexpo", "chapman", "weibull3", "asyp",
  "ratio", "gompertz", "weibull4", "betap", "heleg", "linear"), data = NULL, crit
= "Info", normaTest = "lillie", homoTest = "cor.fitted", neg_check = FALSE,
alpha_normtest = 0.05, alpha_homotest = 0.05, grid_start = FALSE,
grid_n = NULL, confInt = FALSE, ciN = 100, verb = TRUE)
```

**Arguments**

obj	Either a vector of model names or a fit_collection object created using <code>sar_multi</code> . If a vector of names is provided, <code>sar_average</code> first calls <code>sar_multi</code> before generating the averaged multimodel curve.
data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site. If obj is a fit_collection object, data should be NULL.
crit	The criterion used to compare models and compute the model weights. The default <code>crit = "Info"</code> switches to AIC or AICc depending on the number of data points in the dataset. AIC ( <code>crit = "AIC"</code> ) or AICc ( <code>crit = "AICc"</code> ) can be chosen regardless of the sample size. For BIC, use <code>crit = "Bayes"</code> .
normaTest	The test used to test the normality of the residuals of each model. Can be any of "lillie" (Lilliefors Kolmogorov-Smirnov test; the default), "shapiro" (Shapiro-Wilk test of normality), "kolmo" (Kolmogorov-Smirnov test), or "none" (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of each model. Can be any of "cor.fitted" (a correlation of the residuals with the model fitted values; the default), "cor.area" (a correlation of the residuals with the area values), or "none" (no residuals homogeneity test is undertaken).
neg_check	Whether or not a check should be undertaken to flag any models that predict negative richness values.
alpha_normtest	The alpha value used in the residual normality test (default = 0.05, i.e. any test with a P value < 0.05 is flagged as failing the test).
alpha_homotest	The alpha value used in the residual homogeneity test (default = 0.05, i.e. any test with a P value < 0.05 is flagged as failing the test).
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but we would recommend using it to ensure the fits of certain models (e.g. Gompertz, Chapman Richards) are optimal.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
confInt	A logical argument specifying whether confidence intervals should be calculated for the multimodel curve using bootstrapping.
ciN	The number of bootstrap samples to be drawn to calculate the confidence intervals (if <code>confInt == TRUE</code> ).
verb	verbose (default: <code>verb == TRUE</code> ).



## Details

The multimodel SAR curve is constructed using information criterion weights (see Burnham & Anderson, 2002; Guilhaumon et al. 2010). If `obj` is a vector of `n` model names the function fits the `n` models to the dataset provided using the `sar_multi` function. A dataset must have four or more datapoints to fit the multimodel curve. If any models cannot be fitted they are removed from the multimodel SAR. If `obj` is a `fit_collection` object (created using the `sar_multi` function), any model fits in the collection which are NA are removed. In addition, if any other model checks have been selected (i.e. residual normality and heterogeneity tests, and checks for negative predicted richness values), these are undertaken and any model that fails the selected test(s) is removed from the multimodel SAR. The order of the additional checks inside the function is: normality of residuals, homogeneity of residuals, and a check for negative fitted values. Once a model fails one test it is removed and thus is not available for further tests. Thus, a model may fail multiple tests but the returned warning will only provide information on a single test.

The resultant models are then used to construct the multimodel SAR curve. For each model in turn, the model fitted values are multiplied by the information criterion weight of that model, and the resultant values are summed across all models (Burnham & Anderson, 2002). Confidence intervals can be calculated (using `confInt`) around the multimodel averaged curve using the bootstrap procedure outlined in Guilhaumon et al (2010). The procedure transforms the residuals from the individual model fits and occasionally NAs / Inf values can be produced - in these cases, the model is removed from the confidence interval calculation (but not the multimodel curve itself). When several SAR models are used and the number of bootstraps (`ciN`) is large, generating the confidence intervals can take a long time.

The `sar_models()` function can be used to bring up a list of the 20 model names. `display_sars_models()` generates a table of the 20 models with model information.

## Value

A list of class "multi" and class "sars" with two elements. The first element ('`mml`') contains the fitted values of the multimodel sar curve. The second element ('`details`') is a list with the following components:

- `mod_names` Names of the models that were successfully fitted and passed any model check
- `fits` A `fit_collection` object containing the successful model fits
- `ic` The information criterion selected
- `norm_test` The residual normality test selected
- `homo_test` The residual homogeneity test selected
- `alpha_norm_test` The alpha value used in the residual normality test
- `alpha_homo_test` The alpha value used in the residual homogeneity test
- `ics` The information criterion values (e.g. AIC values) of the model fits
- `delta_ics` The delta information criterion values
- `weights_ics` The information criterion weights of each model fit
- `n_points` Number of data points
- `n_mods` The number of successfully fitted models
- `no_fit` Names of the models which could not be fitted or did not pass model checks

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.multi` plots the multimodel curve.

**Note**

Occasionally a model fit will converge and pass the model fitting checks (e.g. residual normality) but the resulting fit is nonsensical (e.g. a horizontal line with intercept at zero). Thus, it can be useful to plot the resultant 'multi' object to check the individual model fits. To re-run the `sar_multi` function without a particular model, simply remove it from the `obj` argument.

Choosing starting parameter values for non-linear regression optimisation algorithms is not always straight forward, depending on the data at hand. In the package, we use various approaches to choose default starting parameters. However, if any of the resultant model fits does not converge, returns a singular gradient at parameter estimates, or the plot of the model fit does not look optimum, try using the `grid_start` argument to undertake a more extensive selection of starting values, or provide your own starting values (`start`). While using `grid_start` is more time consuming, it will often provide (much) better fits for certain models, and so we recommend its use where possible. Note, that `grid_start` has been disabled for a small number of models (e.g. Weibull 3 par.). See the vignette for more information.

The generation of confidence intervals around the multimodel curve (using `confInt == TRUE`), may throw up errors that we have yet to come across. Please report any issues to the package maintainer.

There are different formulas for calculating the various information criteria (IC) used for model comparison (e.g. AIC, BIC). For example, some formulas use the residual sum of squares (rss) and others the log-likelihood (ll). Both are valid approaches and will give the same parameter estimates, but it is important to only compare IC values that have been calculated using the same approach. For example, the 'sars' package used to use formulas based on the rss, while the `nls` function in the stats package uses formulas based on the ll. To increase the compatability between `nls` and `sars`, we have changed our formulas such that now our IC formulas are the same as those used in the `nls` function. See the "On the calculation of information criteria" section in the package vignette for more information.

**References**

Burnham, K. P., & Anderson, D. R. (2002). Model selection and multi-model inference: a practical information-theoretic approach (2nd ed.). New-York: Springer.

Guilhaumon, F., Mouillot, D., & Gimenez, O. (2010). mmSAR: an R-package for multimodel species-area relationship inference. *Ecography*, 33, 420-424.

**Examples**

```
data(galap)
#attempt to construct a multimodel SAR curve using all twenty sar models
fit <- sar_average(data = galap)
summary(fit)
plot(fit)

# construct a multimodel SAR curve using a fit_collection object
ff <- sar_multi(galap, obj = c("power", "loga", "monod", "weibull3"))
fit2 <- sar_average(obj = ff, data = NULL)
summary(fit2)
```

---

sar_betap	<i>Fit the Beta-P cumulative model</i>
-----------	--

---

## Description

Fit the Beta-P cumulative model to SAR data.

## Usage

```
sar_betap(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
          homoTest = 'cor.fitted')
```

## Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

## Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The [summary.sars](#) function returns a more useful summary of the model fit results, and the [plot.sars](#) plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_betap(galap)
summary(fit)
plot(fit)
```

---

sar_chapman	<i>Fit the Chapman Richards model</i>
-------------	---------------------------------------

---

## Description

Fit the Chapman Richards model to SAR data.

## Usage

```
sar_chapman(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
             homoTest = 'cor.fitted')
```

## Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

## Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The [summary.sars](#) function returns a more useful summary of the model fit results, and the [plot.sars](#) plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_chapman(galap)
summary(fit)
plot(fit)
```

sar\_epm1

*Fit the Extended Power model 1 model***Description**

Fit the Extended Power model 1 model to SAR data.

**Usage**

```
sar_epm1(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
         homoTest = 'cor.fitted')
```

**Arguments**

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If grid_start = TRUE, the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

**Details**

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_epm1(galap)
summary(fit)
plot(fit)
```



sar\_epm2

*Fit the Extended Power model 2 model***Description**

Fit the Extended Power model 2 model to SAR data.

**Usage**

```
sar_epm2(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
         homoTest = 'cor.fitted')
```

**Arguments**

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

**Details**

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_epm2(galap)
summary(fit)
plot(fit)
```

---

sar_gompertz	<i>Fit the Gompertz model</i>
--------------	-------------------------------

---

## Description

Fit the Gompertz model to SAR data.

## Usage

```
sar_gompertz(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
             homoTest = 'cor.fitted')
```

## Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

## Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The [summary.sars](#) function returns a more useful summary of the model fit results, and the [plot.sars](#) plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_gompertz(galap)
summary(fit)
plot(fit)
```

---

sar_heleg	<i>Fit the Heleg(Logistic) model</i>
-----------	--------------------------------------

---

## Description

Fit the Heleg(Logistic) model to SAR data.

## Usage

```
sar_heleg(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
          homoTest = 'cor.fitted')
```

## Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If grid_start = TRUE, the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

## Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_heleg(galap)
summary(fit)
plot(fit)
```

---

sar_koba	<i>Fit the Kobayashi model</i>
----------	--------------------------------

---

### Description

Fit the Kobayashi model to SAR data.

### Usage

```
sar_koba(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
         homoTest = 'cor.fitted')
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If grid_start = TRUE, the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The [summary.sars](#) function returns a more useful summary of the model fit results, and the [plot.sars](#) plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_koba(galap)
summary(fit)
plot(fit)
```



---

 sar\_linear

*Fit the linear model*


---

### Description

Fit the linear model to SAR data.

### Usage

```
sar_linear(data, normaTest = 'lillie', homoTest = 'cor.fitted')
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using linear regression and the `lm` function. Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed.

A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`).

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `verge` Logical code indicating model convergence
- `data` Observed data
- `model` A list of model information (e.g. the model name and formula)
- `calculated` The fitted values of the model
- `residuals` The model residuals
- `AIC` The AIC value of the model

- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

### Examples

```
data(galap)
fit <- sar_linear(galap)
summary(fit)
plot(fit)
```

---

sar\_loga

*Fit the Logarithmic model*

---

### Description

Fit the Logarithmic model to SAR data.

### Usage

```
sar_loga(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
  homoTest = 'cor.fitted')
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.

normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation
- `data` Observed data
- `model` A list of model information (e.g. the model name and formula)
- `calculated` The fitted values of the model
- `residuals` The model residuals
- `AIC` The AIC value of the model
- `AICc` The AICc value of the model
- `BIC` The BIC value of the model
- `R2` The R2 value of the model
- `R2a` The adjusted R2 value of the model

- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_loga(galap)
summary(fit)
plot(fit)
```

---

sar\_mmf

*Fit the MMF model*

---

## Description

Fit the MMF model to SAR data.

## Usage

```
sar_mmf(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
        homoTest = 'cor.fitted')
```

## Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.

normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation
- `data` Observed data
- `model` A list of model information (e.g. the model name and formula)
- `calculated` The fitted values of the model
- `residuals` The model residuals
- `AIC` The AIC value of the model
- `AICc` The AICc value of the model
- `BIC` The BIC value of the model
- `R2` The R2 value of the model
- `R2a` The adjusted R2 value of the model

- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_mmf(galap)
summary(fit)
plot(fit)
```

---

sar\_monod

*Fit the Monod model*

---

## Description

Fit the Monod model to SAR data.

## Usage

```
sar_monod(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
  homoTest = 'cor.fitted')
```

## Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.

normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation
- `data` Observed data
- `model` A list of model information (e.g. the model name and formula)
- `calculated` The fitted values of the model
- `residuals` The model residuals
- `AIC` The AIC value of the model
- `AICc` The AICc value of the model
- `BIC` The BIC value of the model
- `R2` The R2 value of the model
- `R2a` The adjusted R2 value of the model

- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_monod(galap)
summary(fit)
plot(fit)
```

---

sar\_multi

*Create a Collection of SAR Model Fits*

---

## Description

Creates a fit collection of SAR model fits, which can then be plotted using `plot.sars`.

## Usage

```
sar_multi(data, obj = c("power",
  "powerR", "epm1", "epm2", "p1", "p2", "loga", "koba",
  "mmf", "monod", "negexpo", "chapman", "weibull3", "asympt",
  "ratio", "gompertz", "weibull4", "betap", "heleg", "linear"), normaTest =
  "lillie", homoTest = "cor.fitted", grid_start = FALSE, grid_n = NULL,
  verb = TRUE)
```

## Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
obj	A vector of model names.
normaTest	The test used to test the normality of the residuals of each model. Can be any of "lillie" (Lilliefors Kolmogorov-Smirnov test; the default), "shapiro" (Shapiro-Wilk test of normality), "kolmo" (Kolmogorov-Smirnov test), or "none" (no residuals normality test is undertaken).



homoTest	The test used to check for homogeneity of the residuals of each model. Can be any of "cor.fitted" (a correlation of the residuals with the model fitted values; the default), "cor.area" (a correlation of the residuals with the area values), or "none" (no residuals homogeneity test is undertaken).
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values (default: grid_start = FALSE).
grid_n	If grid_start = TRUE, the number of points sampled in the model parameter space.
verb	verbose (default: verb == TRUE).

### Details

The `sar_models()` function can be used to bring up a list of the 20 model names. `display_sars_models()` generates a table of the 20 models with model information.

### Value

A list of class 'sars' with n elements, corresponding to the n individual SAR model fits.

### Examples

```
data(galap)
# construct a fit_collection object of 3 SAR model fits
fit2 <- sar_multi(galap, obj = c("power", "loga", "linear"))
plot(fit2)

# construct a fit_collection object of all 20 SAR model fits
fit3 <- sar_multi(galap)
```

---

sar\_negexpo

*Fit the Negative exponential model*

---

### Description

Fit the Negative exponential model to SAR data.

### Usage

```
sar_negexpo(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
  homoTest = 'cor.fitted')
```

## Arguments

<code>data</code>	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
<code>start</code>	NULL or custom parameter start values for the optimisation algorithm.
<code>grid_start</code>	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
<code>grid_n</code>	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
<code>normaTest</code>	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
<code>homoTest</code>	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

## Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

## Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation

- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_negexpo(galap)
summary(fit)
plot(fit)
```

---

sar\_p1

*Fit the Persistence function 1 model*

---

## Description

Fit the Persistence function 1 model to SAR data.

## Usage

```
sar_p1(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
        homoTest = 'cor.fitted')
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation

- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_p1(galap)
summary(fit)
plot(fit)
```

---

sar\_p2

*Fit the Persistence function 2 model*

---

## Description

Fit the Persistence function 2 model to SAR data.

## Usage

```
sar_p2(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
        homoTest = 'cor.fitted')
```

## Arguments

<code>data</code>	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
<code>start</code>	NULL or custom parameter start values for the optimisation algorithm.
<code>grid_start</code>	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
<code>grid_n</code>	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
<code>normaTest</code>	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
<code>homoTest</code>	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

## Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

## Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation

- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_p2(galap)
summary(fit)
plot(fit)
```

---

sar\_power

*Fit the Power model*

---

## Description

Fit the Power model to SAR data.

## Usage

```
sar_power(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
  homoTest = 'cor.fitted')
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation



- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_power(galap)
summary(fit)
plot(fit)
```

---

sar\_powerR

*Fit the PowerR model*

---

## Description

Fit the PowerR model to SAR data.

## Usage

```
sar_powerR(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
  homoTest = 'cor.fitted')
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation

- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_powerR(galap)
summary(fit)
plot(fit)
```

---

sar\_pred

*Use SAR model fits to predict richness on islands of a given size*

---

## Description

Predict the richness on an island of a given size using either individual SAR model fits, a `fit_collection` of model fits, or a multi-model SAR curve.

## Usage

```
sar_pred(fit, area)
```

**Arguments**

fit	Either a model fit object, a fit_collection object (generated using <code>sar_multi</code> ), or a sar_multi object (generated using <code>sar_average</code> ).
area	A numeric vector of area values (length $\geq 1$ ).

**Details**

Extrapolation (e.g. predicting the richness of areas too large to be sampled) is one of the primary uses of the SAR. The `sar_pred` function provides an easy method for undertaking such an exercise. The function works by taking an already fitted SAR model, extracting the parameter values and then using these values and the model function to predict the richness for any value of area provided.

If a multi-model SAR curve is used for prediction (i.e. using `sar_average`), the model information criterion weight (i.e. the conditional probabilities for each of the  $n$  models) for each of the individual model fits that were used to generate the curve are stored. The  $n$  models are then each used to predict the richness of a larger area and these predictions are multiplied by the respective model weights and summed to provide a multi-model averaged prediction.

**Value**

A data.frame of class 'sars' with three columns: 1) the name of the model, 2) the area value for which a prediction has been generated, and 3) the prediction from the model extrapolation.

**Note**

This function is used in the ISAR extrapolation paper of Matthews & Aspin (2019).

Code to calculate confidence intervals around the predictions using bootstrapping will be added in a later version of the package.

**References**

Matthews, T.J. & Aspin, T.W.H. (2019) ....

**Examples**

```
data(galap)
#fit the power model and predict richness on an island of area = 5000
fit <- sar_power(data = galap)
p <- sar_pred(fit, area = 5000)

#fit three SAR models and predict richness on islands of area = 5000 & 10000
fit2 <- sar_multi(galap, obj = c("power", "loga", "koba"))
p2 <- sar_pred(fit2, area = c(5000, 10000))

#calculate a multi-model curve and predict richness on islands of area = 5000 & 10000
fit3 <- sar_average(data = galap)
p3 <- sar_pred(fit3, area = c(5000, 10000))
```

---

sar_ratio	<i>Fit the Rational function model</i>
-----------	--

---

### Description

Fit the Rational function model to SAR data.

### Usage

```
sar_ratio(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
          homoTest = 'cor.fitted')
```

### Arguments

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If <code>grid_start = TRUE</code> , the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

**Value**

A list of class 'sars' with the following components:

- par The model parameters
- value Residual sum of squares
- counts The number of iterations for the convergence of the fitting algorithm
- convergence Numeric code indicating model convergence (0 = converged)
- message Any message from the model fit algorithm
- hessian A symmetric matrix giving an estimate of the Hessian at the solution found
- verge Logical code indicating model convergence
- startValues The start values for the model parameters used in the optimisation
- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The [summary.sars](#) function returns a more useful summary of the model fit results, and the [plot.sars](#) plots the model fit.

**References**

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

**Examples**

```
data(galap)
fit <- sar_ratio(galap)
summary(fit)
plot(fit)
```

---

sar_threshold	<i>Fit threshold SAR models</i>
---------------	---------------------------------

---

### Description

Fit up to six piecewise (threshold) regression models to SAR data.

### Usage

```
sar_threshold(data, mod = "All", interval = NULL, nisl = NULL,
  non_th_models = TRUE, logAxes = "area", con = 1, logT = log, parallel =
  FALSE, cores = NULL)
```

### Arguments

data	A dataset in the form of a dataframe with at least two columns: the first with island/site areas, and the second with the species richness of each island/site.
mod	A vector of model names: an individual model, a set of models, or all models. Can be any of 'All' (fit all models), 'ContOne' (continuous one-threshold), 'ZslopeOne' (left-horizontal one-threshold), 'DiscOne' (discontinuous one-threshold), 'ContTwo' (continuous two-threshold), 'ZslopeTwo' (left-horizontal two-threshold), or 'DiscTwo' (discontinuous two-threshold).
interval	The amount to increment the threshold value by in the iterative model fitting process (not applicable for the discontinuous models). The default for non-transformed area reverts to 1, while for log-transformed area it is 0.01. However, these values may not be suitable depending on the range of area values in a dataset, and thus users are advised to manually set this argument.
nisl	Set the minimum number of islands to be contained within each of the two segments (in the case of one-threshold models), or the first and last segments (in the case of two-threshold models). It needs to be less than than half of the total number of islands in the dataset. Default = NULL.
non_th_models	Logical argument (default = TRUE) of whether two non-threshold models (i.e. a simple linear regression: $y \sim x$ ; and an intercept only model: $y \sim 1$ ) should also be fitted.
logAxes	What log-transformation (if any) should be applied to the area and richness values. Should be one of "none" (no transformation), "area" (only area is log-transformed; default) or "both" (both area and richness log-transformed).
con	The constant to add to the species richness values in cases where one of the islands has zero species.
logT	The log-transformation to apply to the area and richness values. Can be any of log(default), log2 or log10.
parallel	Logical argument for whether parallel processing should be used. Only applicable when the continuous two-threshold and left-horizontal two-threshold models are being fitted.
cores	Number of cores to use. Only applicable when parallel = TRUE.

## Details

This function is described in more detail in the accompanying paper (Matthews & Rigal, 2020).

Fitting the continuous and left-horizontal piecewise models (particularly the two-threshold models) can be time consuming if the range in area is large and/or the interval argument is small. For the two-threshold continuous slope and left-horizontal models, the use of parallel processing (using the `parallel` argument) is recommended. The number of cores (`cores`) must be provided.

Note that the interval argument is not used to fit discontinuous models, as, in these cases, the breakpoint must be at a datapoint.

There has been considerable debate regarding the number of parameters that are included in different piecewise models. Here (and thus in our calculation of AIC, AICc, BIC etc) we consider `ContOne` to have five parameters, `ZslopeOne` - 4, `DiscOne` - 6, `ContTwo` - 7, `ZslopeTwo` - 6, `DiscTwo` - 8. The standard linear model and the intercept model are considered to have 3 and 2 parameters, respectively. The raw `lm` model fits are provided in the output, however, if users want to calculate information criteria using different numbers of parameters.

The raw `lm` model fits can also be used to explore classic diagnostic plots for linear regression analysis in R using the function `plot` or other diagnostic tests such `outlierTest`, `leveragePlots` or `influencePlot`, available in the `car` package. This is advised as currently there are no model validation checks undertaken automatically, unlike elsewhere in the `sars` package.

Confidence intervals around the breakpoints in the one-threshold continuous and left- horizontal models can be calculated using the `threshold_ci` function. The intercepts and slopes of the different segments in the fitted breakpoint models can be calculated using the `get_coef` function.

Rarely, multiple breakpoint values can return the same minimum rss (for a given model fit). In these cases, we just randomly choose and return one and also produce a warning. If this occurs it is worth checking the data and model fits carefully.

The `nis1` argument can be useful to avoid situations where a segment contains only one island, for example. However, setting strict criteria on the number of data points to be included in segments could be seen as "forcing" the fit of the model, and arguably if a model fit is not interpretable, it is simply that the model does not provide a good representation of the data. Thus, it should not be used without careful thought.

## Value

A list of class "threshold" and "sars" with five elements. The first element contains the different model fits (lm objects). The second element contains the names of the fitted models, the third contains the threshold values, the fourth element the dataset (i.e. a dataframe with area and richness values), and the fifth contains details of any axes log-transformations undertaken. `summary.sars` provides a more user-friendly output (including a model summary table) and `plot.threshold` plots the model fits.

## Note

Due to the increased number of parameters, fitting piecewise regression models to datasets with few islands is not recommended. In particular, we would advise against fitting the two-threshold models to small SAR datasets (e.g. fewer than 10 islands for the one threshold models, and 20 islands for the two threshold models).



**Author(s)**

Francois Rigal and Thomas J. Matthews

**References**

Lomolino, M.V. & Weiser, M.D. (2001) Towards a more general species-area relationship: diversity on all islands, great and small. *Journal of Biogeography*, 28, 431-445.

Gao, D., Cao, Z., Xu, P. & Perry, G. (2019) On piecewise models and species-area patterns. *Ecology and Evolution*, 9, 8351-8361.

Matthews, T.J. et al. (2020) Unravelling the small-island effect through phylogenetic community ecology. *Journal of Biogeography*.

Matthews, T.J. & Rigal, F. (In Review) Thresholds and the species–area relationship: a set of functions for fitting, evaluating and plotting a range of commonly used piecewise models. *Frontiers of Biogeography*.

**Examples**

```
data(aegean2)
a2 <- aegean2[1:168,]
fitT <- sar_threshold(data = a2, mod = c("ContOne", "DiscOne"),
interval = 0.1, non_th_models = TRUE, logAxes = "area", logT = log10)
summary(fitT)
plot(fitT)
#diagnostic plots for the ContOne model
par(mfrow=c(2, 2))
plot(fitT[[1]][[1]])
```

---

sar\_weibull3

*Fit the Cumulative Weibull 3 par. model*


---

**Description**

Fit the Cumulative Weibull 3 par. model to SAR data.

**Usage**

```
sar_weibull3(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
homoTest = 'cor.fitted')
```

**Arguments**

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.

grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If grid_start = TRUE, the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

### Details

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the `optim` function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in `summary.sars` if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also `sar_average`)

### Value

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation
- `data` Observed data
- `model` A list of model information (e.g. the model name and formula)
- `calculated` The fitted values of the model
- `residuals` The model residuals

- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_weibull3(galap)
summary(fit)
plot(fit)
```

---

sar\_weibull4

*Fit the Cumulative Weibull 4 par. model*

---

## Description

Fit the Cumulative Weibull 4 par. model to SAR data.

## Usage

```
sar_weibull4(data, start = NULL, grid_start = FALSE, grid_n = NULL, normaTest = 'lillie',
             homoTest = 'cor.fitted')
```

**Arguments**

data	A dataset in the form of a dataframe with two columns: the first with island/site areas, and the second with the species richness of each island/site.
start	NULL or custom parameter start values for the optimisation algorithm.
grid_start	Logical argument specifying whether a grid search procedure should be implemented to test multiple starting parameter values. The default is set to FALSE, but for certain models (e.g. Gompertz, Chapman Richards), we advice using it to ensure an optimal fit.
grid_n	If grid_start = TRUE, the number of points sampled in the model parameter space.
normaTest	The test used to test the normality of the residuals of the model. Can be any of 'lillie' (Lilliefors Kolmogorov-Smirnov test; the default), 'shapiro' (Shapiro-Wilk test of normality), 'kolmo' (Kolmogorov-Smirnov test), or 'none' (no residuals normality test is undertaken).
homoTest	The test used to check for homogeneity of the residuals of the model. Can be any of 'cor.fitted' (a correlation of the residuals with the model fitted values; the default), 'cor.area' (a correlation of the residuals with the area values), or 'none' (no residuals homogeneity test is undertaken).

**Details**

The model is fitted using non-linear regression. The model parameters are estimated by minimizing the residual sum of squares with an unconstrained Nelder-Mead optimization algorithm and the [optim](#) function. To avoid numerical problems and speed up the convergence process, the starting values used to run the optimization algorithm are carefully chosen. However, if this does not work, custom values can be provided (using the `start` argument), or a more comprehensive search can be undertaken using the `grid_start` argument. See the vignette for more information. The fitting process also determines the observed shape of the model fit, and whether or not the observed fit is asymptotic (see Triantis et al. 2012 for further details). Model validation is undertaken by assessing the normality (`normaTest`) and homogeneity (`homoTest`) of the residuals and a warning is provided in [summary.sars](#) if either test is failed. A selection of information criteria (e.g. AIC, BIC) are returned and can be used to compare models (see also [sar\\_average](#))

**Value**

A list of class 'sars' with the following components:

- `par` The model parameters
- `value` Residual sum of squares
- `counts` The number of iterations for the convergence of the fitting algorithm
- `convergence` Numeric code indicating model convergence (0 = converged)
- `message` Any message from the model fit algorithm
- `hessian` A symmetric matrix giving an estimate of the Hessian at the solution found
- `verge` Logical code indicating model convergence
- `startValues` The start values for the model parameters used in the optimisation

- data Observed data
- model A list of model information (e.g. the model name and formula)
- calculated The fitted values of the model
- residuals The model residuals
- AIC The AIC value of the model
- AICc The AICc value of the model
- BIC The BIC value of the model
- R2 The R2 value of the model
- R2a The adjusted R2 value of the model
- sigConf The model coefficients table
- normaTest The results of the residuals normality test
- homoTest The results of the residuals homogeneity test
- observed\_shape The observed shape of the model fit
- asymptote A logical value indicating whether the observed fit is asymptotic
- neg\_check A logical value indicating whether negative fitted values have been returned

The `summary.sars` function returns a more useful summary of the model fit results, and the `plot.sars` plots the model fit.

## References

Triantis, K.A., Guilhaumon, F. & Whittaker, R.J. (2012) The island species-area relationship: biology and statistics. *Journal of Biogeography*, 39, 215-231.

## Examples

```
data(galap)
fit <- sar_weibull4(galap)
summary(fit)
plot(fit)
```

---

summary.sars

*Summarising the results of the model fitting functions*

---

## Description

S3 method for class 'sars'. `summary.sars` creates summary statistics for objects of class 'sars'. The exact summary statistics computed depends on the 'Type' attribute (e.g. 'multi') of the 'sars' object. The summary method generates more useful information for the user than the standard model fitting functions. Another S3 method (`print.summary.sars`; not documented) is used to print the output.

## Usage

```
## S3 method for class 'sars'
summary(object, order = "BIC", ...)
```

## Arguments

object	An object of class 'sars'.
order	The information criterion used to order the model summary table for objects of Type 'threshold' (Default = "BIC").
...	Further arguments.

## Value

The `summary.sars` function returns an object of class "summary.sars". A print function is used to obtain and print a summary of the model fit results.

For a 'sars' object of Type 'fit', a list with 16 elements is returned that contains useful information from the model fit, including the model parameter table (with t-values, p-values and confidence intervals), model fit statistics (e.g. R2, AIC), the observed shape of the model and whether or not the fit is asymptotic, and the results of any additional model checks undertaken (e.g. normality of the residuals).

For a 'sars' object of Type 'multi', a list with 4 elements is returned: (i) a vector of the names of the models that were successfully fitted and passed any additional checks, (ii) a character string containing the name of the criterion used to rank models, (iii) a data frame of the ranked models, and (iv) a vector of the names of any models that were not fitted or did not pass any additional checks. In regards to (iii; `Model_table`), the dataframe contains the fit summaries for each successfully fitted model (including the value of the model criterion used to compare models, the R2 and adjusted R2, and the observed shape of the fit); the models are ranked in decreasing order of information criterion weight.

For a 'sars' object of Type 'lin\_pow', a list with up to 7 elements is returned: (i) the model fit output from the `lm` function, (ii) the fitted values of the model, (iii) the observed data, (iv and v) the results of the residuals normality and heterogeneity tests, and (vi) the log-transformation function used. If the argument `compare = TRUE` is used in `lin_pow`, a 7th element is returned that contains the parameter values from the non-linear power model.

For a 'sars' object of Type 'threshold', a list with three elements is returned: (i) the information criterion used to order the ranked model summary table ('order'), (ii) a model summary table (models are ranked using the 'order' argument), and (iii) details of any axes log-transformations undertaken. Note that in the model summary table, if log-area is used as the predictor, the threshold values will be on the log scale used. Thus it may be preferable to back-transform them (e.g. using `exp(th)` if natural logarithms are used) so that they are on the scale of untransformed area. `Th1` and `Th2` in the table are the threshold value(s), and `seg1`, `seg2`, `seg3` provide the number of datapoints within each segment (for the threshold models); one-threshold models have two segments, and two-threshold models have three segments.

## Examples

```
data(galap)
#fit a multimodel SAR and get the model table
mf <- sar_average(data = galap)
summary(mf)
summary(mf)$Model_table
#Get a summary of the fit of the linear power model
fit <- lin_pow(galap, con = 1, compare = TRUE)
summary(fit)
```

---

threshold_ci	<i>Calculate confidence intervals around breakpoints</i>
--------------	--

---

### Description

Generate confidence intervals around the breakpoints of the one-threshold continuous and left-horizontal models. Two types of confidence interval can be implemented: a confidence interval derived from an inverted F test and an empirical bootstrap confidence interval.

### Usage

```
threshold_ci(object, cl = 0.95, method = "boot", interval = NULL,
             Nboot = 100, verb = TRUE)
```

### Arguments

object	An object of class 'thresholds', generated using the <a href="#">sar_threshold</a> function. The object must contain fits of either (or both) of the one-threshold continuous or the one-threshold left-horizontal model.
cl	The confidence level. Default value is 0.95 (95 percent).
method	Either bootstrapping (boot) or inverted F test (F).
interval	The amount to increment the threshold value by in the iterative model fitting process used in both the F and boot methods. The default for non-transformed area reverts to 1, while for log-transformed area it is 0.01. It is advised that the same interval value used when running <a href="#">sar_threshold</a> is used here.
Nboot	Number of bootstrap samples (for use with method = "boot").
verb	Should progress be reported. If TRUE, every 50th bootstrap sample is reported (for use with method = "boot").

### Details

Full details of the two approaches can be found in Toms and Lesperance (2003). If the number of bootstrap samples is large, the function can take a while to run. Following Toms and Lesperance (2003), we therefore recommend the use of the inverted F test confidence interval when sample size is large, and bootstrapped confidence intervals when sample size is smaller.

Currently only available for the one-threshold continuous and left- horizontal threshold models.

### Value

A list of class "sars" with two elements. If method "F" is used, the list contains only the confidence interval values. If method "boot" is used, the list contains two elements. The first element is the full set of bootstrapped breakpoint estimates for each model and the second contains the confidence interval values.

**Author(s)**

Francois Rigal and Christian Paroissin

**References**

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

**Examples**

```
data(aegean2)
a2 <- aegean2[1:168,]
fitT <- sar_threshold(data = a2, mod = "ContOne",
  interval = 0.1, non_th_models = TRUE, logAxes = "area", logT = log10)
#calculate confidence intervals using bootstrapping
#(very low Nboot just as an example)
CI <- threshold_ci(fitT, method = "boot", interval = NULL, Nboot = 3)
CI
#Use the F method instead, with 90% confidence interval
CI2 <- threshold_ci(fitT, cl = 0.90, method = "F", interval = NULL)
CI2
```



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