Package 'sars'

January 7, 2020

Type Package

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

Version 1.2.1

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

Imports dplyr, graphics, nortest, stats, utils, crayon, cli, numDeriv

Depends R(>= 3.0.0)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

Author Thomas J. Matthews [aut, cre] (<https://orcid.org/0000-0002-7624-244X>), Francois Guilhaumon [aut] (<https://orcid.org/0000-0003-4707-8932>), Kevin Cazelles [rev] (<https://orcid.org/0000-0001-6619-9874>)

Maintainer Thomas J. Matthews <txm676@gmail.com>

Repository CRAN

Date/Publication 2020-01-07 19:20:02 UTC

R topics documented:

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 overlayed 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 *A SAR dataset describing invertebrates on islands in the Aegean Sea, Greece*

Description

A sample dataset in the correct mmSAR2 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 list with two elements. The first element contains the name of the dataset. The second element contains a data frame with 2 columns and 16 rows. Each row contains the area of an island in the Galapagos (1st column) and the number of plants 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)
```

`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 mmSAR2 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 mmSAR2 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 list with two elements. The first element contains the name of the dataset. The second element contains a data frame with 2 columns and 16 rows. Each row contains the area of an island (km2) 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 ~ 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 ~ 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 ~ c + z*Area + k*T + j*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 ~ c + x*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 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)
```

---

lin_pow *Fit the log-log version of the power model*

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 mmSAR2 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 list with two elements. The first element contains the name of the dataset. The second element contains a data frame with 2 columns and 32 rows. Each row contains the area of an island (km2) 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 par, plot,title, lines) 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 type = multi for a plot of the multimodel SAR curve, or type = bar for a barplot of the information criterion weights of each model.
allCurves	A logical argument for use with type = multi that specifies whether all the model fits should be plotted with the multimodel SAR curve (allCurves = TRUE; the default) or that only the multimodel SAR curve should be plotted (allCurves = FALSE).
xlab	Title for the x-axis. Only for use with type = multi.
ylab	Title for the y-axis.
pch	Plotting character (for points). Only for use with type = multi.
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 type = multi.
ModTitle	Plot title (default is ModTitle = NULL, which reverts to "Multimodel SAR" for type = multi and to "Model weights" for type = bar). For no title, use ModTitle = "".
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 type = multi.
lwd	Line width. Only for use with type = multi.
lcol	Line colour. Only for use with type = multi.
mmSep	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 type = multi and allCurves = TRUE.
lwd.Sep	If mmSep = TRUE, the line width of the multimodel curve.
col.Sep	If mmSep = TRUE, the colour of the multimodel curve.
pLeg	Logical argument specifying whether or not the legend should be plotted (when type = multi and allCurves = TRUE).
modNames	A vector of model names for the barplot of weights (when type = bar). The default (modNames = NULL) uses abbreviated versions (see below) of the names from the sar_average function.
cex.names	The amount by which the axis labels (model names) should be scaled relative to the default. Only for use with type = bar.
subset_weights	Only create a barplot of the model weights for models with a weight value above a given threshold (subset_weights). Only for use with type = bar.

confInt	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 sar_average function.
...	Further graphical parameters (see par, plot,title, lines) 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

x	An object of class 'sars'.

mfplot	Logical argument specifying whether the model fits in a fit_collection should be plotted on one single plot (mfplot = TRUE) or separate plots (mfplot = FALSE; the default).
xlab	Title for the x-axis (default depends on the Type attribute).
ylab	Title for the y-axis (default depends on the Type attribute).
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.
ModTitle	Plot title (default is ModTitle = NULL, which reverts to a default name depending on the type of plot). For no title, use ModTitle = "". For a sars object of type fit_collection, a vector of names can be provided (e.g. letters[1:3]).
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.
lwd	Line width.
lcol	Line colour.
di	Dimensions to be passed to par(mfrow=()) to specify the size of the plotting window, when plotting multiple plots from a sars object of Type fit_collection. For example, di = c(1,3) 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 fit_collection plots (when mfplot = TRUE) or. When a large number of model fits are plotted the legend takes up a lot of space, and thus the default is pLeg = FALSE.
...	Further graphical parameters (see par, plot,title, lines) 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")
```

sars_models *Display the 20 SAR model names*

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 *Fit the Asymptotic regression model*

Description

Fit the Asymptotic regression model to SAR data.

Usage

```
sar_asymp(data, start = NULL, grid_start = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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","asymp",
  "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, confInt = FALSE, ciN = 100,
  verb = TRUE)
```

Arguments

`obj`	Either a vector of model names or a fit_collection object created using `sar_multi`. If a vector of names is provided, `sar_average` first calls `sar_multi` 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 `crit = "Info"` switches to AIC or AICc depending on the number of data points in the dataset. AIC (`crit = "AIC"`) or AICc (`crit = "AICc"`) can be chosen regardless of the sample size. For BIC, use `crit ="Bayes"`.
`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).
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 confInt == TRUE).
verb	verbose (default: verb == TRUE).

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 ('mmi') 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.

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.

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` *Fit the Beta-P cumulative model*

Description

Fit the Beta-P cumulative model to SAR data.

Usage

```
sar_betap(data, start = NULL, grid_start = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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` *Fit the Chapman Richards model*

Description

Fit the Chapman Richards model to SAR data.

Usage

```
sar_chapman(data, start = NULL, grid_start = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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 = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument start. 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 = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument start. 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` *Fit the Gompertz model*

Description

Fit the Gompertz model to SAR data.

Usage

```
sar_gompertz(data, start = NULL, grid_start = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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` *Fit the Heleg(Logistic) model*

Description

Fit the Heleg(Logistic) model to SAR data.

Usage

```
sar_heleg(data, start = NULL, grid_start = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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 *Fit the Kobayashi model*

Description

Fit the Kobayashi model to SAR data.

Usage

```
sar_koba(data, start = NULL, grid_start = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument `start`. 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 = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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 = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument `start`. 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 = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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","asymp",
  "ratio","gompertz","weibull4","betap","heleg","linear"), normaTest =
  "lillie", homoTest = "cor.fitted",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).
`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 = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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 = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument start. 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 = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument start. 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 = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument start. 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 = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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 sar_multi), or a sar_multi object (generated using sar_average).
area	A numeric vector of area values (length >= 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, extacting 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 *Fit the Rational function model*

Description

Fit the Rational function model to SAR data.

Usage

```
sar_ratio(data, start = NULL, grid_start = 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	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
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, or custom values can be provided using the argument `start`. 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_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 = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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 = 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`	NULL or the number of points sampled in the model parameter space or FALSE to prevent any grid start after a fail in initial optimization to run a grid search.
`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, or custom values can be provided using the argument `start`. 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, ...)
```

Arguments

`object`	An object of class 'sars'.
`...`	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.

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)
```

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