Package ‘mappestRisk’

November 19, 2025

Title Create Maps Forecasting Risk of Pest Occurrence

Version 0.1.2

Description There are three different modules: (1) model fitting and selection using a set of the most commonly used equations describing developmental responses to temperature helped by already existing R packages ('rTPC') and nonlinear regression model functions from 'nls.multstart' (Padfield et al. 2021, <doi:10.1111/2041-210X.13585>), with visualization of model predictions to guide ecological criteria for model selection; (2) calculation of suitability thermal limits, which consist on a temperature interval delimiting the optimal performance zone or suitability; and (3) climatic data extraction and visualization inspired on previous research (Taylor et al. 2019, <doi:10.1111/1365-2664.13455>), with either exportable rasters, static map images or html, interactive maps.

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.3

URL `https://github.com/EcologyR/mappestRisk`, `https://ecologyr.github.io/mappestRisk/`

BugReports `https://github.com/EcologyR/mappestRisk/issues`

Depends R (>= 4.3.0)

LazyData true

Suggests covr, leaflet, testthat (>= 3.0.0)

Config/testthat/edition 3

Imports dplyr, geodata, ggplot2, khroma, nls.multstart, progress, purrr, rTPC, terra, tidyr

Config/Needs/website rmarkdown

NeedsCompilation no

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Contents

`aphid` *Brachycaudus schwartzi whole life cycle development rate across temperatures*

Description

A modified data set from Table 1 in Satar and Yokomi (2002) on days of development for *Brachycaudus schwartzi* across different constant temperatures and life stages

Usage

```
data(aphid)
```

Format

`aphid`**:**

A data frame with 7 rows and 5 columns. The workflow is reproducible and available in `/data-raw` folder of the mappestRisk GitHub repository, which includes both the original summarized data set `-satar_data.xlsx-` and the R script with the dev. days to dev. rate conversion in `prepare_aphid.R`.

reference "Satar2002" refers to the source paper as cited below in section `Source`.

temperature Temperature treatments (ºC).

dev_days Development days (i.e., days to fulfill development requirements from a life-stage to the following)

rate_value Rate of Development (1/days), the reciprocal of Development days, see `dev_days`

stage Life stage or instar evaluated. In this case, only data of the whole immature stages (i.e., nymphs) were used

Source

Satar, S. and Yokomi, R. (2002). Effect of temperature and host on development of *Brachycaudus schwartzi* (Homoptera: Aphididae). Ann. Entomol. Soc. Am. 95: 597-602. doi:10.1603/0013-8746(2002)095[0597:EOTAHO]2.0.CO;2.

Licence: CC BY-NC 3.0 (modified material).

`available_models` *Available Models Table*

Description

Table containing the available models to be fit using `fit_devmodels()`. These models come from two other packages: `devRate` and `rTPC` .

Usage

```
data("available_models")
```

Format

`available_models`**:**

A data.frame/tibble with 13 rows and 6 columns:

model_name Model name to be used within `fit_devmodels()`.

package names of the packages used by `fit_devmodels()` to obtain appropriate start values for the user-provided data. When the package is rTPC package, start values are automatically computed with `rTPC::get_start_vals()`, which in turn relies on `nls.multstart::nls_multstart()`. When the package is devRate package, iterative starting values are computed using `nls.multstart::nls_multstart(` using the parameters published in `devRate::devRateEqStartVal()` as first attempts to iterate. As an exception, if `model_name == "briere1"`, generic starting values are provided and advised to the user due to the unrealistic value of some parameters in the `devRate` data set.

source_model_name name of the function in the source packages `rTPC` and `devRate`.

formula, working_formula, n_params formulas used for model fitting.

Source

Rebaudo, F., Struelens, Q., and Dangles, O. (2018). Modelling temperature-dependent development rate and phenology in arthropods: The `devRate` package for R. Methods Ecol Evol. 9: 1144-1150. doi:10.1111/2041210X.12935.

Padfield, D., O´Sullivan, H., and Pawar, S., (2021). `rTPC` and `nls.multstart`: a new pipeline to fit thermal performance curves in R. Methods Ecol Evol. 12: 1138-1143. doi:10.1111/2041-210X.13585.

`country_names` *Country names*

Description

Country names

Usage

```
country_names
```

Format

`country_names`**:**
A character vector of country names (length = 231 countries)

Source

https://gadm.org

`fit_devmodels` *Fit Thermal Performance Curves*

Description

Fit nonlinear regression models to data representing how development rate changes with temperature (known as Thermal Performance Curves), based on `nls.multstart::nls_multstart()` approach to development rate data across temperatures. The fitting procedure is built upon previous packages for starting values estimation, namely `rTPC` and `devRate`.

Usage

```
fit_devmodels(temp = NULL, dev_rate = NULL, model_name = NULL)
```

Arguments

`temp`	a vector of temperatures used in the experiment. It should have at least four different temperatures and must contain only numbers without any missing values.
`dev_rate`	a vector of estimated development rates corresponding to each temperature. These rates are calculated as the inverse of the number of days to complete the transition from the beginning of a certain life stage to the beginning of the following at each temperature. It must be numeric and of the same length as `temp`.
`model_name`	a string or a vector that specifies the model(s) to use for fitting the Thermal Performance Curves. Options include "all" or specific models listed in available_models. These models typically exhibit a common unimodal, left-skewed shape.

Value

A table in `tibble` format with estimates and standard errors for each parameter of the models specified by the user that have adequately converged. Models are sorted based on their Akaike Information Criterion (AIC) values, with the best fitting models shown first. Fitted models are also provided in list format in the `model_list` column and can be accessed using `get_fitted_model()` for for further inspection. It is important to consider ecological criteria alongside statistical information. For additional help in model selection, we recommend using `plot_devmodels()` and consulting relevant literature.

Source

The dataset used in the example was originally published in Satar & Yokomi (2022) under the CC-BY-NC license. The start values and equations for the 'briere1', 'lactin1', 'mod_polynomial' and 'wang' models have been obtained from the devRate package.

References

Angilletta, M.J., (2006). Estimating and comparing thermal performance curves. J. Therm. Biol. 31: 541-545. (for model selection in TPC framework)

Padfield, D., O'Sullivan, H. and Pawar, S. (2021). rTPC and nls.multstart: A new pipeline to fit thermal performance curves in `R`. Methods Ecol Evol. 12: 1138-1143.

Rebaudo, F., Struelens, Q. and Dangles, O. (2018). Modelling temperature-dependent development rate and phenology in arthropods: The `devRate` package for `R`. Methods Ecol Evol. 9: 1144-1150.

Satar, S. and Yokomi, R. (2002). Effect of temperature and host on development of Brachycaudus schwartzi (Homoptera: Aphididae). Ann. Entomol. Soc. Am. 95: 597-602.

See Also

`nls.multstart::nls_multstart()` for structure of model fitting approach

`browseVignettes("rTPC")` for model names, start values searching workflows and bootstrapping procedures using both `rTPC` and `nls.multstart` packages.

Examples

```
data("aphid")

fitted_tpcs <- fit_devmodels(temp = aphid$temperature,
                             dev_rate = aphid$rate_value,
                             model_name = c("lactin2", "briere2",
                                            "mod_weibull")
                             )
head(fitted_tpcs)
```

`get_fitted_model` *Get fitted model object*

Description

Get fitted model object

Usage

```
get_fitted_model(fitted_df = NULL, model_name = NULL)
```

Arguments

`fitted_df`	A table with fitted models, as produced by `fit_devmodels()`.
`model_name`	Character. Name of a fitted model, see available_models.

Value

A model object

Examples

```
data("aphid")

fitted_tpcs_aphid <- fit_devmodels(temp = aphid$temperature,
                                   dev_rate = aphid$rate_value,
                                   model_name = c("lactin2", "briere2", "ratkowsky")
                                   )
get_fitted_model(fitted_tpcs_aphid, "briere2")
```

`map_risk` *Map pest risk*

Description

This function produces a raster map where each pixel shows the number of months per year in which temperature is within a given set of bounds. If the input has several pairs of minimum and maximum temperatures (as produced by `therm_suit_bounds()`), the output raster has two layers: mean and standard deviation.

Usage

```
map_risk(
  t_vals = NULL,
  t_rast = NULL,
  region = NULL,
  res = 2.5,
  path = NULL,
  mask = TRUE,
  verbose = FALSE,
  plot = TRUE,
  interactive = FALSE
)
```

Arguments

`t_vals`	a `data.frame` or `dplyr::tibble()` as produced by `therm_suit_bounds()`. `t_vals` must contain results derived from a single model. It must contain at least one row of numeric values. Additionally, the minimum ("left") thermal boundary or `tval_left` must be lower than the maximum ("right") one, or `tval_right` for all rows. Nominative columns must be present in the input (i.e., `model_name`, `suitability`, `pred_suit` and `iter`).
`t_rast`	Optional 12-layer `terra::SpatRaster()` with monthly mean temperatures for the region of interest. If not provided, global WorldClim raster layers will be automatically (down)loaded using `geodata::worldclim_global()`, and cropped to `region` (if provided). Note that the download can be slow the first time you use the function in a new `path`. If you get a download error, consider running e.g `options(timeout = 500)` (or more).
`region`	Optional object specifying the region to map. Must overlap the extent of `t_rast` if both are provided. Can be a `terra::SpatVector()` polygon (obtained with `terra::vect()`); or an `sf` polygon, in which case it will be coerced with `terra::vect()`) to a `terra::SpatVector()`; or a character vector of country name(s) in English (see country_names), in which case climate maps will be downloaded for those countries; or a `terra::SpatExtent()` object (obtained with `terra::ext()`); or a numeric vector of length 4 specifying the region coordinates as follows: `c(xmin, xmax, ymin, ymax)`. The latter two must be in the same CRS as`t_rast` if `t_rast` is provided, or in unprojected lon-lat coordinates (WGS84, EPSG:4326) otherwise. If NULL, the output maps will cover the entire `t_rast` if provided, or the entire world otherwise.
`res`	Argument to pass to `geodata::worldclim_global()` specifying the spatial resolution for the raster maps to download, if `t_rast` is not provided. The default is 2.5 arc-minutes. Beware that lower values (e.g., 0.5) may lead to extremely heavy data sets and large computation times.
`path`	Argument to pass to `geodata::worldclim_global()` (if `t_rast` is not provided) and/or to `geodata::world()` (if `region` is a vector of country names) specifying the folder path for the downloaded maps.
`mask`	Logical value to pass to `terra::mask()` specifying whether the output raster maps should be masked with the borders of the target 'region', if this is a polygon

	map or a vector of country names. The default is TRUE. If FALSE, the entire rectangular extent of 'region' will be used.
`verbose`	Logical value specifying whether to display messages about what the function is doing at possibly slow steps. The default is FALSE. Setting it to TRUE can be useful for checking progress when maps are large.
`plot`	Logical value specifying whether to plot the results in a map. Defaults to TRUE. Note that the function will always return a `terra::SpatRaster()` object even if `plot = TRUE`.
`interactive`	Logical value specifying whether the plotted map should be interactive (if plot=TRUE). The default is TRUE if the 'leaflet' package is installed.

Value

This function returns a `terra::SpatRaster()` with up to 2 layers: the (`mean()`) number of months with temperature within the species' thermal bounds; and (if `t_vals` has >1 rows) the standard deviation (`stats::sd()`) around that mean.

Examples

```
data("aphid")

fitted_tpcs <- fit_devmodels(temp = aphid$temperature,
                             dev_rate = aphid$rate_value,
                             model_name = "all")

plot_devmodels(temp = aphid$temperature,
               dev_rate = aphid$rate_value,
               fitted_parameters = fitted_tpcs,
               species = "Brachycaudus schwartzi",
               life_stage = "Nymphs")

boot_tpcs <- predict_curves(temp = aphid$temperature,
                            dev_rate = aphid$rate_value,
                            fitted_parameters = fitted_tpcs,
                            model_name_2boot = c("lactin2", "briere2", "beta"),
                            propagate_uncertainty = TRUE,
                            n_boots_samples = 10)

print(boot_tpcs)

plot_uncertainties(temp = aphid$temperature,
                   dev_rate = aphid$rate_value,
                   bootstrap_tpcs = boot_tpcs,
                   species = "Brachycaudus schwartzi",
                   life_stage = "Nymphs")


boundaries <- therm_suit_bounds(preds_tbl = boot_tpcs,
                                model_name = "lactin2",
                                suitability_threshold = 80)
```

```
risk_map_reunion <- map_risk(t_vals = boundaries,
                             path = tempdir(),
                             region = "Réunion",
                             mask = TRUE,
                             plot = TRUE,
                             interactive = FALSE,
                             verbose = TRUE)
```

`plot_devmodels` *Plot fitted thermal performance curves*

Description

Plot the predicted development rates across temperatures based on fitted Thermal Performance Curves (TPCs) for one or several models displayed in facets.

Usage

```
plot_devmodels(
  temp = NULL,
  dev_rate = NULL,
  fitted_parameters = NULL,
  species = NULL,
  life_stage = NULL
)
```

Arguments

`temp`	a vector of temperatures used in the experiment. It should have at least four different temperatures and must contain only numbers without any missing values.
`dev_rate`	a vector of estimated development rates corresponding to each temperature. These rates are calculated as the inverse of the number of days to complete the transition from the beginning of a certain life stage to the beginning of the following at each temperature. It must be numeric and of the same length as `temp`.
`fitted_parameters`	a `tibble` obtained with `fit_devmodels()`, including parameter names, estimates, standard errors, AICs, and nls objects (fitted_models) using the `nls.multstart::nls_multstart` approach.
`species`	optional a string of the target species that will constitute the plot title. Must be of type "character".
`life_stage`	optional a string of the target life stage that will constitute the plot subtitle. Must be of type "character".

Value

A plot with predicted values (development rate) across temperatures for models that have adequately converged using `fit_devmodels()` function. It's a ggplot object, which can be assigned to a user-defined object.

References

Angilletta, M.J., (2006). Estimating and comparing thermal performance curves. J. Therm. Biol. 31: 541-545. (for model selection in TPC framework)

Padfield, D., O'Sullivan, H. and Pawar, S. (2021). rTPC and nls.multstart: A new pipeline to fit thermal performance curves in `R`. Methods Ecol Evol. 12: 1138-1143.

Rebaudo, F., Struelens, Q. and Dangles, O. (2018). Modelling temperature-dependent development rate and phenology in arthropods: The `devRate` package for `R`. Methods Ecol Evol. 9: 1144-1150.

Satar, S. and Yokomi, R. (2002). Effect of temperature and host on development of Brachycaudus schwartzi (Homoptera: Aphididae). Ann. Entomol. Soc. Am. 95: 597-602.

See Also

`fit_devmodels()` for fitting Thermal Performance Curves to development rate data, which is in turn based on `nls.multstart::nls_multstart()`.

Examples

```
data("aphid")

fitted_tpcs <- fit_devmodels(temp = aphid$temperature,
                             dev_rate = aphid$rate_value,
                             model_name = c("lactin2", "briere2", "mod_weibull"))

plot_devmodels(temp = aphid$temperature,
               dev_rate = aphid$rate_value,
               fitted_parameters = fitted_tpcs,
               species = "Brachycaudus schwartzi",
               life_stage = "Nymphs")
```

`plot_uncertainties` *Draw bootstrapped Thermal Performance Curves (TPCs) to visualize uncertainty in parameter estimation of TPC fitting*

Description

Draw bootstrapped Thermal Performance Curves (TPCs) to visualize uncertainty in parameter estimation of TPC fitting

Usage

```
plot_uncertainties(
  temp = NULL,
  dev_rate = NULL,
  bootstrap_tpcs = NULL,
  species = NULL,
  life_stage = NULL,
  alpha = 0.2
)
```

Arguments

`temp`	a vector of temperatures used in the experiment. It should have at least four different temperatures and must contain only numbers without any missing values.
`dev_rate`	a vector of estimated development rates corresponding to each temperature. These rates are calculated as the inverse of the number of days to complete the transition from the beginning of a certain life stage to the beginning of the following at each temperature. It must be numeric and of the same length as `temp`.
`bootstrap_tpcs`	a `tibble` A tibble object as produced by `predict_curves()`, containing bootstrapped TPCs to propagate uncertainty.
`species`	optional a string of the target species that will constitute the plot title. Must be of type "character".
`life_stage`	optional a string of the target life stage that will constitute the plot subtitle. Must be of type "character".
`alpha`	a number between 0 and 1 to choose transparency of the bootstrapped curves (0 = complete transparency, 1 = solid line).

Value

A ggplot object containing the visual representation of the estimate TPC and the bootstrapped uncertainty curves as a ribbon. Each model is represented in a facet, and data points are also explicit.

References

Angilletta, M.J., (2006). Estimating and comparing thermal performance curves. J. Therm. Biol. 31: 541-545. (for model selection in TPC framework)

Padfield, D., O'Sullivan, H. and Pawar, S. (2021). rTPC and nls.multstart: A new pipeline to fit thermal performance curves in `R`. Methods Ecol Evol. 12: 1138-1143.

Rebaudo, F., Struelens, Q. and Dangles, O. (2018). Modelling temperature-dependent development rate and phenology in arthropods: The `devRate` package for `R`. Methods Ecol Evol. 9: 1144-1150.

Satar, S. and Yokomi, R. (2002). Effect of temperature and host on development of Brachycaudus schwartzi (Homoptera: Aphididae). Ann. Entomol. Soc. Am. 95: 597-602.

See Also

`browseVignettes("rTPC")` for model names, start values searching workflows, and bootstrapping procedures using both `rTPC::get_start_vals()` and `nls.multstart::nls_multstart()`

`fit_devmodels()` for fitting Thermal Performance Curves to development rate data, which is in turn based on `nls.multstart::nls_multstart()`. `predict_curves()` for bootstrapping procedure based on the above-mentioned `rTPC` vignettes.

Examples

```
data("aphid")

fitted_tpcs <- fit_devmodels(temp = aphid$temperature,
                             dev_rate = aphid$rate_value,
                             model_name = "all")

plot_devmodels(temp = aphid$temperature,
               dev_rate = aphid$rate_value,
               fitted_parameters = fitted_tpcs,
               species = "Brachycaudus swartzi",
               life_stage = "Nymphs")

boot_tpcs <- predict_curves(temp = aphid$temperature,
                            dev_rate = aphid$rate_value,
                            fitted_parameters = fitted_tpcs,
                            model_name_2boot = c("lactin2", "briere2", "beta"),
                            propagate_uncertainty = TRUE,
                            n_boots_samples = 10)

print(boot_tpcs)


plot_uncertainties(temp = aphid$temperature,
                   dev_rate = aphid$rate_value,
                   bootstrap_tpcs = boot_tpcs,
                   species = "Brachycaudus schwartzi",
                   life_stage = "Nymphs")
```

`predict_curves` *Propagate parameter uncertainty of TPC fits using bootstrap with residual resampling*

Description

Propagate parameter uncertainty of TPC fits using bootstrap with residual resampling

Usage

```
predict_curves(
  temp = NULL,
  dev_rate = NULL,
  fitted_parameters = NULL,
  model_name_2boot = NULL,
  propagate_uncertainty = TRUE,
  n_boots_samples = 100
)
```

Arguments

`temp`	a vector of temperatures used in the experiment. It should have at least four different temperatures and must contain only numbers without any missing values.
`dev_rate`	a vector of estimated development rates corresponding to each temperature. These rates are calculated as the inverse of the number of days to complete the transition from the beginning of a certain life stage to the beginning of the following at each temperature. It must be numeric and of the same length as `temp`.
`fitted_parameters`	a `tibble` obtained with `fit_devmodels()` function, including parameter names, estimates, standard errors, AICs, and nls objects (fitted_models) using the `nls.multstart::nls_multsta` approach.
`model_name_2boot`	A vector of strings including one or several TPC models fitted by `fit_devmodels()`. Contrarily to that function, `model_name_2boot = "all"` is not allowed in this function due to the slow bootstrapping procedure. We recommend applying this function only to a small pre-selection of models (e.g., one to four) based on statistical and ecological criteria with the help of `plot_devmodels()` function.
`propagate_uncertainty`	A logical argument that specifies whether to propagate parameter uncertainty by bootstrap with residual resampling. If `FALSE`, the function returns predictions from the fitted TPCs for the selected model(s). If `TRUE`, bootstrap is applied using residual resampling to obtain multiple TPCs as detailed in vignettes of the `rTPC` package. Defaults to `TRUE`.
`n_boots_samples`	Number of bootstrap resampling iterations (default is 100). A larger number of iterations makes the resampling procedure more robust, but typically 100 is sufficient for propagating parameter uncertainty, as increasing `n_boots_samples` will increase computation time for predicting resampled TPCs.

Value

A tibble object with as many curves (TPCs) as the number of iterations provided in the `n_boots_samples` argument if `propagate_uncertainty = TRUE` minus the bootstrap samples that could not be fitted (i.e., new nonlinear regression models did not converge for them). Otherwise, it returns just one prediction TPC from model fit estimates. Each resampled TPC consists of a collection of predictions for a set of temperatures from `temp - 20` to `temp + 15` with a resolution of 0.1°C and a unique identifier called `boots_iter`. In addition to the uncertainty TPCs, the estimated TPC is also explicit in the output tibble.

References

Angilletta, M.J., (2006). Estimating and comparing thermal performance curves. J. Therm. Biol. 31: 541-545. (for model selection in TPC framework)

Padfield, D., O'Sullivan, H. and Pawar, S. (2021). rTPC and nls.multstart: A new pipeline to fit thermal performance curves in `R`. Methods Ecol Evol. 12: 1138-1143.

Rebaudo, F., Struelens, Q. and Dangles, O. (2018). Modelling temperature-dependent development rate and phenology in arthropods: The `devRate` package for `R`. Methods Ecol Evol. 9: 1144-1150.

Satar, S. and Yokomi, R. (2002). Effect of temperature and host on development of Brachycaudus schwartzi (Homoptera: Aphididae). Ann. Entomol. Soc. Am. 95: 597-602.

See Also

`browseVignettes("rTPC")` for model names, start values searching workflows, and bootstrapping procedures using both `rTPC::get_start_vals()` and `nls.multstart::nls_multstart()`

`fit_devmodels()` for fitting Thermal Performance Curves to development rate data, which is in turn based on `nls.multstart::nls_multstart()`.

Examples

```
data("aphid")

fitted_tpcs <- fit_devmodels(temp = aphid$temperature,
                             dev_rate = aphid$rate_value,
                             model_name = "all")

plot_devmodels(temp = aphid$temperature,
               dev_rate = aphid$rate_value,
               fitted_parameters = fitted_tpcs,
               species = "Brachycaudus schwartzi",
               life_stage = "Nymphs")

boot_tpcs <- predict_curves(temp = aphid$temperature,
                            dev_rate = aphid$rate_value,
                            fitted_parameters = fitted_tpcs,
                            model_name_2boot = c("lactin2", "briere2", "beta"),
                            propagate_uncertainty = TRUE,
                            n_boots_samples = 10)

head(boot_tpcs)
```

`therm_suit_bounds` *Determine Thermal Boundaries for Optimal Performance Level*

Description

Calculate thermal boundaries that define the suitable region of a Thermal Performance Curve (TPC) corresponding to a user-defined optimal performance level.

Usage

```
therm_suit_bounds(
  preds_tbl = NULL,
  model_name = NULL,
  suitability_threshold = NULL
)
```

Arguments

`preds_tbl`	a `tibble` object as produced by `predict_curves()`.
`model_name`	character. Name of one or several of the TPC models fitted first in `fit_devmodels()` and predicted next in `predict_curves()`. If using `model_name = "all"` all models contained in `preds_tbl` will be used. Please, note that some models (most typically, `briere`, `mod_poly`, `wang` and `ratkowsky`) may calculate unrealistic thermal boundaries. We recommend to double-check it and compare among several models.
`suitability_threshold`	A numeric value from 50 to 100 representing the quantile of the curve that provides the user-defined optimal performance. For instance, setting `suitability_threshold` to 80 identifies the top 20% (or quantile 80) of the maximum values of the development rate predicted by the chosen TPC model. If `suitability_threshold` equals 100, the function returns the optimum temperature for development rate.

Value

A tibble with six columns:

- `model_name`: A string indicating the selected TPC model used for projections.
- `suitability`: A string indicating the suitability threshold in percentage (see `suitability_threshold`).
- `tval_left`: A number representing the lower thermal boundary delimiting the suitable region of the TPC.
- `tval_right`: A number representing the upper thermal boundary delimiting the suitable region of the TPC.
- `pred_suit`: A number corresponding to the predicted development rate value determining the chosen quantile threshold of the maximum rate (i.e., suitability percentage of maximum rate).
- `iter`: A string determining the TPC identity from the bootstrapping procedure in `predict_curves()` function, or `estimate` when it represents the estimated TPC fitted in `fit_devmodels()`.

References

Angilletta, M.J., (2006). Estimating and comparing thermal performance curves. J. Therm. Biol. 31: 541-545. (for model selection in TPC framework)

Padfield, D., O'Sullivan, H. and Pawar, S. (2021). rTPC and nls.multstart: A new pipeline to fit thermal performance curves in `R`. Methods Ecol Evol. 12: 1138-1143.

Rebaudo, F., Struelens, Q. and Dangles, O. (2018). Modelling temperature-dependent development rate and phenology in arthropods: The `devRate` package for `R`. Methods Ecol Evol. 9: 1144-1150.

Satar, S. and Yokomi, R. (2002). Effect of temperature and host on development of Brachycaudus schwartzi (Homoptera: Aphididae). Ann. Entomol. Soc. Am. 95: 597-602.

See Also

`browseVignettes("rTPC")` for model names, start values searching workflows, and bootstrapping procedures using both `rTPC::get_start_vals()` and `nls.multstart::nls_multstart()`

`fit_devmodels()` for fitting Thermal Performance Curves to development rate data, which is in turn based on `nls.multstart::nls_multstart()`. `predict_curves()` for bootstrapping procedure based on the above-mentioned `rTPC` vignettes.

Examples

```
data("aphid")

fitted_tpcs <- fit_devmodels(temp = aphid$temperature,
                             dev_rate = aphid$rate_value,
                             model_name = "all")

plot_devmodels(temp = aphid$temperature,
               dev_rate = aphid$rate_value,
               fitted_parameters = fitted_tpcs,
               species = "Brachycaudus schwartzi",
               life_stage = "Nymphs")

boot_tpcs <- predict_curves(temp = aphid$temperature,
                            dev_rate = aphid$rate_value,
                            fitted_parameters = fitted_tpcs,
                            model_name_2boot = c("lactin2", "briere2", "beta"),
                            propagate_uncertainty = TRUE,
                            n_boots_samples = 10)

print(boot_tpcs)


plot_uncertainties(temp = aphid$temperature,
                   dev_rate = aphid$rate_value,
                   bootstrap_tpcs = boot_tpcs,
                   species = "Brachycaudus schwartzi",
                   life_stage = "Nymphs")


boundaries <- therm_suit_bounds(preds_tbl = boot_tpcs,
```

```
                                    model_name = "lactin2",
                                    suitability_threshold = 80)
head(boundaries)
```

Index