Models available in rTPC

November 17, 2022

`beta_2012` *Beta model for fitting thermal performance curves*

Description

Beta model for fitting thermal performance curves

Usage

```
beta_2012(temp, a, b, c, d, e)
```

Arguments

`temp`	temperature in degrees centigrade
`a`	dimensionless parameter
`b`	dimensionless parameter
`c`	dimensionless parameter
`d`	dimensionless parameter
`e`	dimensionless parameter

Details

Equation:

$$rate = \frac{a \left(\frac{temp - b + \frac{c(d-1)}{d+e-2}}{c} \right)^{d-1} \cdot \left(1 - \frac{temp - b + \frac{c(d-1)}{d+e-2}}{c} \right)^{e-1}}{\left(\frac{d-1}{d+e-2} \right)^{d-1} \cdot \left(\frac{e-1}{d+e-2} \right)^{e-1}}$$

Start values in `get_start_vals` are derived from the data or sensible values from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model difficult to fit.

Author(s)

Daniel Padfield

References

Niehaus, Amanda C., et al. Predicting the physiological performance of ectotherms in fluctuating thermal environments. Journal of Experimental Biology 215.4: 694-701 (2012)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'beta_2012')
# fit model
mod <- nls.multstart::nls_multstart(rate~beta_2012(temp = temp, a, b, c, d, e),
data = d,
iter = c(7,7,7,7,7),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'beta_2012'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'beta_2012'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

boatman_2017 *Boatman model for fitting thermal performance curves*

Description

Boatman model for fitting thermal performance curves

Usage

```
boatman_2017(temp, rmax, tmin, tmax, a, b)
```

Arguments

temp	temperature in degrees centigrade
rmax	the rate at optimum temperature
tmin	low temperature (ºC) at which rates become negative
tmax	high temperature (ºC) at which rates become negative
a	shape parameter to adjust the skewness of the curve
b	shape parameter to adjust the kurtosis of the curve

Details

Equation:

$$rate = r_{max} \cdot \left(sin\left(\pi\left(\frac{temp - t_{min}}{t_{max} - t_{min}}\right)^{a}\right)\right)^{b}$$

Start values in `get_start_vals` are derived from the data or sensible values from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Boatman, T. G., Lawson, T., & Geider, R. J. A key marine diazotroph in a changing ocean: The interacting effects of temperature, CO2 and light on the growth of Trichodesmium erythraeum IMS101. PLoS ONE, 12, e0168796 (2017)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'boatman_2017')
# fit model
mod <- nls.multstart::nls_multstart(rate~boatman_2017(temp = temp, rmax, tmin, tmax, a, b),
data = d,
iter = c(4,4,4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'boatman_2017'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'boatman_2017'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

briere2_1999 *Briere2 model for fitting thermal performance curves*

Description

Briere2 model for fitting thermal performance curves

Usage

```
briere2_1999(temp, tmin, tmax, a, b)
```

Arguments

temp	temperature in degrees centigrade
tmin	low temperature (ºC) at which rates become negative

`tmax`	high temperature (ºC) at which rates become negative
`a`	scale parameter to adjust maximum rate of the curve
`b`	shape parameter to adjust the asymmetry of the curve

Details

Equation:

$$rate = a \cdot temp \cdot (temp - t_{min}) \cdot (t_{max} - temp)^{\frac{1}{b}}$$

Start values in `get_start_vals` are derived from the data or sensible values from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Brière, J.F., Pracros, P., Le Roux, A.Y., Pierre, J.S., A novel rate model of temperature-dependent development for arthropods. Environmental Entomololgy, 28, 22–29 (1999)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'briere2_1999')
# fit model
mod <- nls.multstart::nls_multstart(rate~briere2_1999(temp = temp, tmin, tmax, a, b),
data = d,
iter = c(4,4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'briere2_1999'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'briere2_1999'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)
```

```
# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`chlorella_tpc` *Example metabolic thermal performance curves*

Description

A dataset containing example data of rates of photosynthesis and respiration of the phytoplankton Chlorella vulgaris. Instantaneous rates of metabolism were made across a range of assay temperatures to incorporate the entire thermal performance of the populations. The dataset is the cleaned version so some datapoints have been omitted.

Usage

```
data("chlorella_tpc")
```

Format

A data frame with 649 rows and 7 variables:

curve_id a unique value for each separate curve

growth_temp the growth temperature that the culture was maintained at before measurements were taken (degrees centigrade)

process whether the cultures had been kept for a long time at their growth temperature (adaptation/~100 generations) or a short time (a measure of acclimation/~10 generations)

flux whether the curve depicts respiration or gross photosynthesis

temp the assay temperature at which the metabolic rate was measured (degrees centigrade)

rate the metabolic rate measured (micro mol O2 micro gram C-1 hr-1)

Source

Daniel Padfield

References

Padfield, D., Yvon-durocher, G., Buckling, A., Jennings, S. & Yvon-durocher, G. (2015). Rapid evolution of metabolic traits explains thermal adaptation in phytoplankton, Ecology Letters, 19, 133-142.

Examples

```
data("chlorella_tpc")
library(ggplot2)
ggplot(chlorella_tpc) +
 geom_point(aes(temp, rate, col = process)) +
 facet_wrap(~ growth_temp + flux)
```

`delong_2017` *DeLong enzyme-assisted Arrhenius model for fitting thermal performance curves*

Description

DeLong enzyme-assisted Arrhenius model for fitting thermal performance curves

Usage

```
delong_2017(temp, c, eb, ef, tm, ehc)
```

Arguments

`temp`	temperature in degrees centigrade
`c`	potential reaction rate
`eb`	baseline energy needed for the reaction to occur (eV)
`ef`	temperature dependence of folding the enzymes used in the metabolic reaction, relative to the melting temperature (eV)
`tm`	melting temperature in degrees centigrade
`ehc`	temperature dependence of the heat capacity between the folded and unfolded state of the enzymes, relative to the melting temperature (eV)

Details

Equation:

$$rate = c{\cdot}exp\frac{-(e_b - (e_f(1 - \frac{temp+273.15}{t_m}) + e_{hc} \cdot ((temp + 273.15) - t_m - (temp + 273.15) \cdot ln(\frac{temp+273.15}{t_m}))))}{k \cdot (temp + 273.15)}$$

where `k` is Boltzmann's constant with a value of 8.62e-05 and `tm` is actually `tm - 273.15`

Start values in `get_start_vals` are derived from the data or sensible values from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

DeLong, John P., et al. The combined effects of reactant kinetics and enzyme stability explain the temperature dependence of metabolic rates. Ecology and evolution 7.11 (2017): 3940-3950.

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'delong_2017')
# fit model
mod <- nls.multstart::nls_multstart(rate~delong_2017(temp = temp, c, eb, ef, tm,ehc),
data = d,
iter = c(4,4,4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'delong_2017'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'delong_2017'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`flinn_1991` *Flinn model for fitting thermal performance curves*

Description

Flinn model for fitting thermal performance curves

Usage

```
flinn_1991(temp, a, b, c)
```

Arguments

`temp`	temperature in degrees centigrade
`a`	parameter that controls the height of the curve
`b`	parameter that controls the slope of the initial increase of the curve
`c`	parameter that controls the position and steepness of the decline of the curve

Details

Equation:

$$rate = \frac{1}{1 + a + b \cdot temp + c \cdot temp^2}$$

Start values in `get_start_vals` are derived from previous methods from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Flinn PW Temperature-dependent functional response of the parasitoid Cephalonomia waterstoni (Gahan) (Hymenoptera, Bethylidae) attacking rusty grain beetle larvae (Coleoptera, Cucujidae). Environmental Entomology, 20, 872–876, (1991)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'flinn_1991')
# fit model
mod <- nls.multstart::nls_multstart(rate~flinn_1991(temp = temp, a, b, c),
data = d,
iter = c(4,4,4),
start_lower = start_vals - 1,
start_upper = start_vals + 1,
lower = get_lower_lims(d$temp, d$rate, model_name = 'flinn_1991'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'flinn_1991'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)
```

```
# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`gaussian_1987` *Gaussian model for fitting thermal performance curves*

Description

Gaussian model for fitting thermal performance curves

Usage

```
gaussian_1987(temp, rmax, topt, a)
```

Arguments

`temp`	temperature in degrees centigrade
`rmax`	maximum rate at optimum temperature
`topt`	optimum temperature (ºC)
`a`	related to the full curve width

Details

Equation:

$$rate = r_{max} \cdot exp^{\left(-0.5\left(\frac{|temp - t_{opt}|}{a}\right)^2\right)}$$

Start values in `get_start_vals` are derived from the data

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Lynch, M., Gabriel, W., Environmental tolerance. The American Naturalist. 129, 283–303. (1987)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'gaussian_1987')
# fit model
mod <- nls.multstart::nls_multstart(rate~gaussian_1987(temp = temp,rmax, topt,a),
data = d,
iter = c(4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'gaussian_1987'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'gaussian_1987'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

hinshelwood_1947 *Hinshelwood model for fitting thermal performance curves*

Description

Hinshelwood model for fitting thermal performance curves

Usage

```
hinshelwood_1947(temp, a, e, b, eh)
```

Arguments

temp	temperature in degrees centigrade
a	pre-exponential constant for the activation energy
e	activation energy (eV)
b	pre-exponential constant for the deactivation energy
eh	de-activation energy (eV)

Details

Equation:

$$rate = a \cdot exp^{\frac{-e}{k \cdot (temp + 273.15)}} - b \cdot exp^{\frac{-e_h}{k \cdot (temp + 273.15)}}$$

where k is Boltzmann's constant with a value of 8.62e-05

Start values in `get_start_vals` are taken from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model difficult to fit.

References

Hinshelwood C.N. The Chemical Kinetics of the Bacterial Cell. Oxford University Press. (1947)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'hinshelwood_1947')
# fit model
mod <- nls.multstart::nls_multstart(rate~hinshelwood_1947(temp = temp,a, e, b, eh),
data = d,
iter = c(5,5,5,5),
start_lower = start_vals - 1,
start_upper = start_vals + 1,
lower = get_lower_lims(d$temp, d$rate, model_name = 'hinshelwood_1947'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'hinshelwood_1947'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`joehnk_2008` *Jöhnk model for fitting thermal performance curves*

Description

Jöhnk model for fitting thermal performance curves

Usage

```
joehnk_2008(temp, rmax, topt, a, b, c)
```

Arguments

`temp`	temperature in degrees centigrade
`rmax`	the rate at optimum temperature
`topt`	optimum temperatute (ºC)
`a`	parameter with no biological meaning
`b`	parameter with no biological meaning
`c`	parameter with no biological meaning

Details

Equation:

$$rate = r_{max}\left(1 + a\left(\left(b^{temp-t_{opt}} - 1\right) - \frac{ln(b)}{ln(c)}(c^{temp-t_{opt}} - 1)\right)\right)$$

Start values in `get_start_vals` are derived from the data or sensible values from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Joehnk, Klaus D., et al. Summer heatwaves promote blooms of harmful cyanobacteria. Global change biology 14.3: 495-512 (2008)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'joehnk_2008')
# fit model
mod <- nls.multstart::nls_multstart(rate~joehnk_2008(temp = temp, rmax, topt, a, b, c),
data = d,
iter = c(3,3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'joehnk_2008'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'joehnk_2008'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`johnsonlewin_1946` *Johnson-Lewin model for fitting thermal performance curves*

Description

Johnson-Lewin model for fitting thermal performance curves

Usage

```
johnsonlewin_1946(temp, r0, e, eh, topt)
```

Arguments

`temp`	temperature in degrees centigrade

`r0`	scaling parameter
`e`	activation energy (eV)
`eh`	high temperature de-activation energy (eV)
`topt`	optimum temperature (ºC)

Details

Equation:

$$rate = \frac{r_0 \cdot exp^{\frac{-e}{k \cdot (temp+273.15)}}}{1 + exp^{-\frac{e_h - \left(\frac{e_h}{(t_{opt}+273.15)} + k \cdot ln\left(\frac{e}{e_h - e}\right)\right) \cdot (temp+273.15)}{k \cdot (temp+273.15)}}}$$

where k is Boltzmann’s constant with a value of 8.62e-05.

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model difficult to fit.

References

Johnson, Frank H., and Isaac Lewin. The growth rate of E. coli in relation to temperature, quinine and coenzyme. Journal of Cellular and Comparative Physiology 28.1 (1946): 47-75.

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'johnsonlewin_1946')
# fit model
mod <- suppressWarnings(
nls.multstart::nls_multstart(rate~johnsonlewin_1946(temp = temp, r0, e, eh, topt),
data = d,
iter = c(5,5,5,5),
start_lower = start_vals - 1,
start_upper = start_vals + 1,
lower = get_lower_lims(d$temp, d$rate, model_name = 'johnsonlewin_1946'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'johnsonlewin_1946'),
supp_errors = 'Y',
convergence_count = FALSE)
)
```

```
# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`kamykowski_1985` *Kamykowski model for fitting thermal performance curves*

Description

Kamykowski model for fitting thermal performance curves

Usage

```
kamykowski_1985(temp, tmin, tmax, a, b, c)
```

Arguments

`temp`	temperature in degrees centigrade
`tmin`	low temperature (ºC) at which rates become negative
`tmax`	high temperature (ºC) at which rates become negative
`a`	parameter with no biological meaning
`b`	parameter with no biological meaning
`c`	parameter with no biological meaning

Details

Equation:

$$rate = a \cdot \left(1 - exp^{-b \cdot \left(temp - t_{min}\right)}\right) \cdot \left(1 - exp^{-c \cdot \left(t_{max} - temp\right)}\right)$$

Start values in `get_start_vals` are derived from the data or sensible values from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Kamykowski, Daniel. A survey of protozoan laboratory temperature studies applied to marine dinoflagellate behaviour from a field perspective. Contributions in Marine Science. (1985).

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'kamykowski_1985')
# fit model
mod <- nls.multstart::nls_multstart(rate~kamykowski_1985(temp = temp, tmin, tmax, a, b, c),
data = d,
iter = c(3,3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'kamykowski_1985'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'kamykowski_1985'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`lactin2_1995` *Lactin2 model for fitting thermal performance curves*

Description

Lactin2 model for fitting thermal performance curves

Usage

```
lactin2_1995(temp, a, b, tmax, delta_t)
```

Arguments

`temp` temperature in degrees centigrade

`a` constant that determines the steepness of the rising portion of the curve

`b` constant that determines the height of the overall curve

`tmax` the temperature at which the curve begins to decelerate beyond the optimum (ºC)

`delta_t` thermal safety margin (ºC)

Details

Equation:

$$rate == exp^{a \cdot temp} - exp^{a \cdot t_{max} - \left(\frac{t_{max} - temp}{\delta_t} \right)} + b$$

Start values in `get_start_vals` are derived from the data or sensible values from the literature.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Lactin, D.J., Holliday, N.J., Johnson, D.L. & Craigen, R. Improved rate models of temperature-dependent development by arthropods. Environmental Entomology 24, 69-75 (1995)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'lactin2_1995')
# fit model
mod <- nls.multstart::nls_multstart(rate~lactin2_1995(temp = temp, a, b, tmax, delta_t),
data = d,
iter = c(3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'lactin2_1995'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'lactin2_1995'),
supp_errors = 'Y',
convergence_count = FALSE)
```

```
# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`lrf_1991` *Lobry-Rosso-Flandros (LRF) model for fitting thermal performance curves*

Description

Lobry-Rosso-Flandros (LRF) model for fitting thermal performance curves

Usage

```
lrf_1991(temp, rmax, topt, tmin, tmax)
```

Arguments

`temp`	temperature in degrees centigrade
`rmax`	maximum rate at optimum temperature
`topt`	optimum temperature (ºC)
`tmin`	low temperature (ºC) at which rates become negative
`tmax`	high temperature (ºC) at which rates become negative

Details

Equation:

$$rate = rmax \cdot \frac{(temp - t_{max}) \cdot (temp - t_{min})^2}{(t_{opt} - t_{min}) \cdot ((t_{opt} - t_{min}) \cdot (temp - t_{opt}) - (t_{opt} - t_{max}) \cdot (t_{opt} + t_{min} - 2 \cdot temp))}$$

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

Author(s)

Daniel Padfield

References

Rosso, L., Lobry, J. R., & Flandrois, J. P. An unexpected correlation between cardinal temperatures of microbial growth highlighted by a new model. Journal of Theoretical Biology, 162(4), 447-463. (1993)

Examples

```
# load in ggplot
library(ggplot2)
library(nls.multstart)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'sharpeschoolhigh_1981')
# fit model
mod <- nls_multstart(rate~lrf_1991(temp = temp, rmax, topt, tmin, tmax),
data = d,
iter = c(3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'lrf_1991'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'lrf_1991'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`modifiedgaussian_2006` *Modified gaussian model for fitting thermal performance curves*

Description

Modified gaussian model for fitting thermal performance curves

Usage

```
modifiedgaussian_2006(temp, rmax, topt, a, b)
```

Arguments

`temp`	temperature in degrees centigrade
`rmax`	maximum rate at optimum temperature
`topt`	optimum temperature
`a`	related to full curve width
`b`	allows for asymmetry in the curve fit

Details

Equation:

$$rate = r_{max} \cdot exp^{\left[-0.5\left(\frac{|temp - t_{opt}|}{a}\right)^{b}\right]}$$

Start values in `get_start_vals` are derived from the data and `gaussian_1987`

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model difficult to fit.

References

Angilletta Jr, M. J. (2006). Estimating and comparing thermal performance curves. Journal of Thermal Biology, 31(7), 541-545.

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'modifiedgaussian_2006')
# fit model
mod <- nls.multstart::nls_multstart(rate~modifiedgaussian_2006(temp = temp, rmax, topt, a, b),
data = d,
iter = c(3,3,3,3),
```

```
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'modifiedgaussian_2006'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'modifiedgaussian_2006'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`oneill_1972` *O'Neill model for fitting thermal performance curves*

Description

O'Neill model for fitting thermal performance curves

Usage

```
oneill_1972(temp, rmax, ctmax, topt, q10)
```

Arguments

`temp`	temperature in degrees centigrade
`rmax`	maximum rate at optimum temperature
`ctmax`	high temperature (ºC) at which rates become negative
`topt`	optimum temperature (ºC)
`q10`	defines the fold change in performance as a result of increasing the temperature by 10 ºC

Details

Equation:

$$rate = r_{max} \cdot \left(\frac{ct_{max} - temp}{ct_{max} - t_{opt}}\right)^{x} \cdot exp^{x \cdot \frac{temp - t_{opt}}{ct_{max} - t_{opt}}}$$

$$where : x = \frac{w^2}{400} \cdot \left(1 + \sqrt{1 + \frac{40}{w}}\right)^2$$

$$and: \ w = (q_{10} - 1) \cdot (ct_{max} - t_{opt})$$

Start values in `get_start_vals` are derived from the data and previous values in the literature

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

O'Neill, R.V., Goldstein, R.A., Shugart, H.H., Mankin, J.B. Terrestrial Ecosystem Energy Model. Eastern Deciduous Forest Biome Memo Report Oak Ridge. The Environmental Sciences Division of the Oak Ridge National Laboratory. (1972)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'oneill_1972')
# fit model
mod <- nls.multstart::nls_multstart(rate~oneill_1972(temp = temp, rmax, ctmax, topt, q10),
data = d,
iter = c(4,4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'oneill_1972'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'oneill_1972'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`pawar_2018` *Pawar model for fitting thermal performance curves*

Description

Pawar model for fitting thermal performance curves

Usage

```
pawar_2018(temp, r_tref, e, eh, topt, tref)
```

Arguments

`temp`	temperature in degrees centigrade
`r_tref`	rate at the standardised temperature, tref
`e`	activation energy (eV)
`eh`	high temperature de-activation energy (eV)
`topt`	optimum temperature (ºC)
`tref`	standardisation temperature in degrees centigrade. Temperature at which rates are not inactivated by high temperatures

Details

This model is a modified version of `sharpeschoolhigh_1981` that explicitly models the optimum temperature. Equation:

$$rate = \frac{r_{tref} \cdot exp^{\frac{-e}{k}(\frac{1}{temp+273.15} - \frac{1}{t_{ref}+273.15})}}{1 + (\frac{e}{eh-e}) \cdot exp^{\frac{e_h}{k}(\frac{1}{t_opt+273.15} - \frac{1}{temp+273.15})}}$$

where `k` is Boltzmann's constant with a value of 8.62e-05.

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

Author(s)

Daniel Padfield

References

Kontopoulos, Dimitrios - Georgios, Bernardo García-Carreras, Sofía Sal, Thomas P. Smith, and Samraat Pawar. Use and Misuse of Temperature Normalisation in Meta-Analyses of Thermal Responses of Biological Traits. PeerJ. 6 (2018),

Examples

```
# load in ggplot
library(ggplot2)
library(nls.multstart)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'pawar_2018')
# fit model
mod <- nls_multstart(rate~pawar_2018(temp = temp, r_tref, e, eh, topt, tref = 20),
data = d,
iter = c(3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'pawar_2018'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'pawar_2018'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`quadratic_2008` *Quadratic model for fitting thermal performance curves*

Description

Quadratic model for fitting thermal performance curves

Usage

```
quadratic_2008(temp, a, b, c)
```

Arguments

`temp`	temperature in degrees centigrade
`a`	parameter that defines the rate at 0 ºC
`b`	parameter with no biological meaning
`c`	parameter with no biological meaning

Details

Equation:

$$rate = a + b \cdot temp + c \cdot temp^2$$

Start values in `get_start_vals` are derived from the data using previous methods in the literature

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Montagnes, David JS, et al. Short-term temperature change may impact freshwater carbon flux: a microbial perspective. Global Change Biology 14.12: 2823-2838. (2008)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'quadratic_2008')
# fit model
mod <- nls.multstart::nls_multstart(rate~quadratic_2008(temp = temp, a, b, c),
data = d,
iter = c(4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'quadratic_2008'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'quadratic_2008'),
supp_errors = 'Y',
convergence_count = FALSE)
```

```
# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

ratkowsky_1983 *Ratkowsky model for fitting thermal performance curves*

Description

Ratkowsky model for fitting thermal performance curves

Usage

```
ratkowsky_1983(temp, tmin, tmax, a, b)
```

Arguments

temp	temperature in degrees centigrade
tmin	low temperature (ºC) at which rates become negative
tmax	high temperature (ºC) at which rates become negative
a	parameter defined as sqrt(rate)/(temp - tmin)
b	empirical parameter needed to fit the data for temperatures beyond the optimum temperature

Details

Equation:

$$rate = (a \cdot (temp - t_{min}))^2 \cdot (1 - exp(b \cdot (temp - t_{max})))^2$$

Start values in `get_start_vals` are derived from the data and previous values in the literature.

Limits in `get_lower_lims` and `get_upper_lims` are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Ratkowsky, D.A., Lowry, R.K., McMeekin, T.A., Stokes, A.N., Chandler, R.E., Model for bacterial growth rate throughout the entire biokinetic temperature range. J. Bacteriol. 154: 1222–1226 (1983)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'ratkowsky_1983')
# fit model
mod <- nls.multstart::nls_multstart(rate~ratkowsky_1983(temp = temp, tmin, tmax, a, b),
data = d,
iter = c(4,4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'ratkowsky_1983'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'ratkowsky_1983'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

rezende_2019 *Rezende model for fitting thermal performance curves*

Description

Rezende model for fitting thermal performance curves

Usage

```
rezende_2019(temp, q10, a, b, c)
```

Arguments

temp	temperature in degrees centigrade
q10	defines the fold change in performance as a result of increasing the temperature by 10 ºC
a	parameter describing shifts in rate
b	parameter threshold temperature (ºC) beyond which the downward curve starts
c	parameter controlling the rate of decline beyond the threshold temperature, b

Details

Equation:

$$\text{if} \quad temp < b : rate = a \cdot 10^{\frac{\log_{10}(q_{10})}{(\frac{10}{temp})}}$$

$$\text{if} \quad temp > b : rate = a \cdot 10^{\frac{\log_{10}(q_{10})}{(\frac{10}{temp})}} \cdot \left(1 - c \cdot (b - temp)^2\right)$$

Start values in get_start_vals are derived from the data and previous values in the literature.

Limits in get_lower_lims and get_upper_lims are based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Rezende, Enrico L., and Francisco Bozinovic. Thermal performance across levels of biological organization. Philosophical Transactions of the Royal Society B 374.1778 (2019): 20180549.

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'rezende_2019')
# fit model
mod <- nls.multstart::nls_multstart(rate~rezende_2019(temp = temp, q10, a, b, c),
data = d,
iter = c(4,4,4,4),
start_lower = start_vals - 10,
```

```
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'rezende_2019'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'rezende_2019'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

sharpeschoolfull_1981 *Full Sharpe-Schoolfield model for fitting thermal performance curves*

Description

Full Sharpe-Schoolfield model for fitting thermal performance curves

Usage

```
sharpeschoolfull_1981(temp, r_tref, e, el, tl, eh, th, tref)
```

Arguments

temp	temperature in degrees centigrade
r_tref	rate at the standardised temperature, tref
e	activation energy (eV)
el	low temperature de-activation energy (eV)
tl	temperature (ºC) at which enzyme is 1/2 active and 1/2 suppressed due to low temperatures
eh	high temperature de-activation energy (eV)
th	temperature (ºC) at which enzyme is 1/2 active and 1/2 suppressed due to high temperatures
tref	standardisation temperature in degrees centigrade. Temperature at which rates are not inactivated by either high or low temperatures

Details

Equation:

$$rate = \frac{r_{tref} \cdot exp^{\frac{-e}{k}(\frac{1}{temp+273.15} - \frac{1}{t_{ref}+273.15})}}{1 + exp^{\frac{e_l}{k}(\frac{1}{t_l} - \frac{1}{temp+273.15})} + exp^{\frac{e_h}{k}(\frac{1}{t_h} - \frac{1}{temp+273.15})}}$$

where k is Boltzmann's constant with a value of 8.62e-05.

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

Author(s)

Daniel Padfield

References

Schoolfield, R. M., Sharpe, P. J. & Magnuson, C. E. Non-linear regression of biological temperature-dependent rate models based on absolute reaction-rate theory. Journal of Theoretical Biology 88, 719-731 (1981)

Examples

```
# load in ggplot
library(ggplot2)
library(nls.multstart)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'sharpeschoolfull_1981')
# fit model
mod <- nls_multstart(rate~sharpeschoolfull_1981(temp = temp, r_tref, e, el, tl, eh, th, tref = 20),
data = d,
iter = c(3,3,3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'sharpeschoolfull_1981'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'sharpeschoolfull_1981'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)
```

```
# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`sharpeschoolhigh_1981` *Sharpe-Schoolfield model (high temperature inactivation only) for fitting thermal performance curves*

Description

Sharpe-Schoolfield model (high temperature inactivation only) for fitting thermal performance curves

Usage

```
sharpeschoolhigh_1981(temp, r_tref, e, eh, th, tref)
```

Arguments

`temp`	temperature in degrees centigrade
`r_tref`	rate at the standardised temperature, tref
`e`	activation energy (eV)
`eh`	high temperature de-activation energy (eV)
`th`	temperature (ºC) at which enzyme is 1/2 active and 1/2 suppressed due to high temperatures
`tref`	standardisation temperature in degrees centigrade. Temperature at which rates are not inactivated by high temperatures

Details

Equation:

$$rate = \frac{r_{tref} \cdot exp^{\frac{-e}{k}(\frac{1}{temp+273.15} - \frac{1}{t_{ref}+273.15})}}{1 + exp^{\frac{e_h}{k}(\frac{1}{t_h} - \frac{1}{temp+273.15})}}$$

where k is Boltzmann's constant with a value of 8.62e-05.

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

Author(s)

Daniel Padfield

References

Schoolfield, R. M., Sharpe, P. J. & Magnuson, C. E. Non-linear regression of biological temperature-dependent rate models based on absolute reaction-rate theory. J. Theor. Biol. 88, 719-731 (1981)

Examples

```
# load in ggplot
library(ggplot2)
library(nls.multstart)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'sharpeschoolhigh_1981')
# fit model
mod <- nls_multstart(rate~sharpeschoolhigh_1981(temp = temp, r_tref, e, eh, th, tref = 20),
data = d,
iter = c(3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'sharpeschoolhigh_1981'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'sharpeschoolhigh_1981'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

sharpeschoollow_1981 *Sharpe-Schoolfield model (low temperature inactivation only) for fitting thermal performance curves*

Description

Sharpe-Schoolfield model (low temperature inactivation only) for fitting thermal performance curves

Usage

```
sharpeschoollow_1981(temp, r_tref, e, el, tl, tref)
```

Arguments

`temp`	temperature in degrees centigrade
`r_tref`	rate at the standardised temperature, tref
`e`	activation energy (eV)
`el`	low temperature de-activation energy (eV)
`tl`	temperature (ºC) at which enzyme is 1/2 active and 1/2 suppressed due to low temperatures
`tref`	standardisation temperature in degrees centigrade. Temperature at which rates are not inactivated by high temperatures

Details

Equation:

$$rate = \frac{r_{tref} \cdot exp^{\frac{-e}{k}(\frac{1}{temp+273.15} - \frac{1}{t_{ref}+273.15})}}{1 + exp^{\frac{e_l}{k}(\frac{1}{t_l} - \frac{1}{temp+273.15})}}$$

where k is Boltzmann's constant with a value of 8.62e-05.

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

Author(s)

Daniel Padfield

References

Schoolfield, R. M., Sharpe, P. J. & Magnuson, C. E. Non-linear regression of biological temperature-dependent rate models based on absolute reaction-rate theory. J. Theor. Biol. 88, 719-731 (1981)

Examples

```
# load in ggplot
library(ggplot2)
library(nls.multstart)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'sharpeschoollow_1981')
# fit model
mod <- nls_multstart(rate~sharpeschoollow_1981(temp = temp, r_tref, e, el, tl, tref = 20),
data = d,
iter = c(3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'sharpeschoollow_1981'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'sharpeschoollow_1981'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`spain_1982` *Spain model for fitting thermal performance curves*

Description

Spain model for fitting thermal performance curves

Usage

```
spain_1982(temp, a, b, c, r0)
```

Arguments

`temp`	temperature in degrees centigrade
`a`	constant that determines the steepness of the rising portion of the curve
`b`	constant that determines the position of topt
`c`	constant that determines the steepness of the decreasing part of the curve
`r0`	the apparent rate at 0 ºC

Details

Equation:

$$rate = r_0 \cdot exp^{a \cdot temp} \cdot (1 - b \cdot exp^{c \cdot temp})$$

Start values in `get_start_vals` are derived from the data or plucked from thin air.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or plucked from thin air.

Note

Generally we found this model easy to fit.

References

BASIC Microcomputer Models in Biology. Addison-Wesley, Reading, MA. 1982

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'spain_1982')
# fit model
mod <- nls.multstart::nls_multstart(rate~spain_1982(temp = temp, a, b, c, r0),
data = d,
iter = c(3,3,3,3),
start_lower = start_vals - 1,
start_upper = start_vals + 1,
lower = get_lower_lims(d$temp, d$rate, model_name = 'spain_1982'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'spain_1982'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)
```

```
# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

thomas_2012 *Thomas model (2012) for fitting thermal performance curves*

Description

Thomas model (2012) for fitting thermal performance curves

Usage

```
thomas_2012(temp, a, b, c, topt)
```

Arguments

temp temperature in degrees centigrade

a arbitrary constant

b arbitrary constant

c the range of temperatures over which growth rate is positive, or the thermal niche width (ºC)

topt determines the location of the maximum of the quadratic portion of this function. When b = 0, tref would equal topt

Details

Equation:

$$rate = a \cdot exp^{b \cdot temp}\left(1 - \left(\frac{temp - t_{opt}}{c}\right)^2\right)$$

Start values in get_start_vals are derived from the data.

Limits in get_lower_lims and get_upper_lims are derived from the data or based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Thomas, Mridul K., et al. A global pattern of thermal adaptation in marine phytoplankton. Science 338.6110, 1085-1088 (2012)

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'thomas_2012')
# fit model
mod <- nls.multstart::nls_multstart(rate~thomas_2012(temp = temp, a, b, c, topt),
data = d,
iter = c(4,4,4,4),
start_lower = start_vals - 1,
start_upper = start_vals + 2,
lower = get_lower_lims(d$temp, d$rate, model_name = 'thomas_2012'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'thomas_2012'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

thomas_2017 *Thomas model (2017) for fitting thermal performance curves*

Description

Thomas model (2017) for fitting thermal performance curves

Usage

```
thomas_2017(temp, a, b, c, d, e)
```

Arguments

`temp`	temperature in degrees centigrade
`a`	birth rate at 0 ºC
`b`	describes the exponential increase in birth rate with increasing temperature
`c`	temperature-independent mortality term
`d`	along with e controls the exponential increase in mortality rates with temperature
`e`	along with d controls the exponential increase in mortality rates with temperature

Details

Equation:

$$rate = a \cdot exp^{b \cdot temp} - (c + d \cdot exp^{e \cdot temp})$$

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based on extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Thomas, Mridul K., et al. Temperature–nutrient interactions exacerbate sensitivity to warming in phytoplankton. Global change biology 23.8 (2017): 3269-3280.

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'thomas_2017')
# fit model
mod <- nls.multstart::nls_multstart(rate~thomas_2017(temp = temp, a, b, c, d, e),
data = d,
iter = c(3,3,3,3,3),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'thomas_2017'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'thomas_2017'),
supp_errors = 'Y',
convergence_count = FALSE)
```

```
# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

`weibull_1995` *Weibull model for fitting thermal performance curves*

Description

Weibull model for fitting thermal performance curves

Usage

```
weibull_1995(temp, a, topt, b, c)
```

Arguments

`temp`	temperature in degrees centigrade
`a`	scale the height of the curve
`topt`	optimum temperature
`b`	defines the breadth of the curve
`c`	defines the curve shape

Details

Equation:

$$rate = a \cdot \left(\frac{c-1}{c}\right)^{\frac{1-c}{c}} \left(\frac{temp - t_{opt}}{b} + \left(\frac{c-1}{c}\right)^{\frac{1}{c}}\right)^{c-1} exp^{-\left(\frac{temp - t_{opt}}{b} + \left(\frac{c-1}{c}\right)^{\frac{1}{c}}\right)^{c}} + \frac{c-1}{c}$$

Start values in `get_start_vals` are derived from the data.

Limits in `get_lower_lims` and `get_upper_lims` are derived from the data or based extreme values that are unlikely to occur in ecological settings.

Note

Generally we found this model easy to fit.

References

Angilletta Jr, Michael J. Estimating and comparing thermal performance curves. Journal of Thermal Biology 31.7 (2006): 541-545.

Examples

```
# load in ggplot
library(ggplot2)

# subset for the first TPC curve
data('chlorella_tpc')
d <- subset(chlorella_tpc, curve_id == 1)

# get start values and fit model
start_vals <- get_start_vals(d$temp, d$rate, model_name = 'weibull_1995')
# fit model
mod <- nls.multstart::nls_multstart(rate~weibull_1995(temp = temp, a, topt, b, c),
data = d,
iter = c(4,4,4,4),
start_lower = start_vals - 10,
start_upper = start_vals + 10,
lower = get_lower_lims(d$temp, d$rate, model_name = 'weibull_1995'),
upper = get_upper_lims(d$temp, d$rate, model_name = 'weibull_1995'),
supp_errors = 'Y',
convergence_count = FALSE)

# look at model fit
summary(mod)

# get predictions
preds <- data.frame(temp = seq(min(d$temp), max(d$temp), length.out = 100))
preds <- broom::augment(mod, newdata = preds)

# plot
ggplot(preds) +
geom_point(aes(temp, rate), d) +
geom_line(aes(temp, .fitted), col = 'blue') +
theme_bw()
```

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