Package ‘hatchR’

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Type Package

Title Predict Fish Hatch and Emergence Timing

Version 0.3.2

Maintainer Bryan M. Maitland `<bryan.maitland@usda.gov>`

Description Predict hatch and emergence timing for a wide range of wild fishes using the effective value framework (Sparks et al., (2019) <DOI:10.1139/cjfas-2017-0468>). 'hatchR' offers users access to established phenological models and the flexibility to incorporate custom parameterizations using external datasets.

License GPL-3

Encoding UTF-8

LazyData true

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URL `https://bmait101.github.io/hatchR/`, `https://github.com/bmait101/hatchR`

BugReports `https://github.com/bmait101/hatchR/issues`

Depends R (>= 4.1.0)

Imports dplyr (>= 1.1.4), ggplot2 (>= 3.5.1), ggtext (>= 0.1.2), lifecycle (>= 1.0.4), lubridate (>= 1.9.4), rlang (>= 1.1.4), stats, tibble (>= 3.2.1), utils

Suggests knitr (>= 1.49), readr (>= 2.1.5), purrr (>= 1.0.2), rmarkdown (>= 2.29), nycflights13 (>= 1.0.2), tidyr (>= 1.3.1), stringr (>= 1.5.1), ggridges (>= 0.5.6), patchwork (>= 1.3.0), testthat (>= 3.0.0), cli (>= 3.6.1)

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Author Bryan M. Maitland [aut, cre] (<`https://orcid.org/0000-0002-4491-5064`>), Morgan M. Sparks [aut, cph] (<`https://orcid.org/0000-0003-0787-2218`>), Eli Felts [ctb] (<`https://orcid.org/0000-0002-5888-9266`>)

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Contents

`check_continuous` *Check if the dates in a data frame are continuous.*

Description

Check if the dates in a data frame are continuous.

Usage

```
check_continuous(data, dates)
```

Arguments

`data`	A data.frame, or data frame extension (e.g. a tibble).
`dates`	Column representing the date of the temperature measurements.

Value

A message indicating if the dates are continuous or if there are breaks. If there are breaks, a vector of row numbers where the breaks occur is returned.

Examples

```
library(hatchR)
check_continuous(crooked_river, date)
```

`crooked_river` *Example dataset: Crooked River, Idaho*

Description

Daily stream temperature data from Crooked River, a tributary to the North Fork Boise River, Idaho.

Usage

```
crooked_river
```

Format

Data frame with columns

date	Date and time measurement was taken.
temperture	Temperature in degrees Celsius.

Source

Dan Isaak, US Forest Service Rocky Mountain Research Station.

Examples

```
crooked_river
```

`fit_model` *Fit B&M model 2 to new data using* `stats::nls()`

Description

Generate your own custom parameterized models for predicting hatching and emergence phenology.

Usage

```
fit_model(temp, days, species = NULL, development_type = NULL)
```

Arguments

`temp`	Numeric vector of temperatures
`days`	Numeric vector of days to hatch or emerge
`species`	Character string of species name (e.g., "sockeye")
`development_type`	Character string of development type: "hatch" or "emerge"

Details

hatchR also includes functionality to generate your own custom parameterized models for predicting hatching and emergence phenology. Importantly, the custom parameterization relies on the model format developed from model 2 of Beacham and Murray (1990), which we chose because of its overall simplicity and negligible loss of accuracy. See Beacham and Murray (1990) and Sparks et al. (2019) for more specific discussion regarding model 2 and the development of the effective value approach.

Value

List with fit model object, model coefficients, model specifications data.frame, and plot of observations and model fit.

Examples

```
library(hatchR)
# vector of temperatures
temperature <- c(2, 5, 8, 11, 14)
# vector of days to hatch
days_to_hatch <- c(194, 87, 54, 35, 28)
bt_hatch_mod <- fit_model(
  temp = temperature,
  days = days_to_hatch, species = "sockeye", development_type = "hatch"
)
```

`idaho` *Central Idaho Water Temperature Data*

Description

Water temperature data from Isaak et al. (2018). Generally covers the Boise, Payette, Clearwater, and upper Salmon River watersheds.

Usage

`idaho`

Format

Data frame

date Date measurement was taken.

site Site ID.

temp_c Temperature in degrees Celsius.

Source

https://hess.copernicus.org/articles/22/6225/2018/

References

Isaak, D.J., Luce, C.H., Chandler, G.L., Horan, D.L., Wollrab, S.P. (1990). Principal components of thermal regimes in mountain river networks. *Hydrology and Earth System Sciences*, **22(12)**, 6225–6240.

Examples

```
idaho
```

`model_select` *Select a development model structure*

Description

The function calls a model table with the parameterizations for different species from different studies built in. Refer to the table (`model_table`) before using function to find inputs for the different function arguments. It pulls the model format as a string and parses it to be usable in **hatchR** model.

Usage

```
model_select(author, species, model_id, development_type = "hatch")
```

Arguments

`author`	Character string of author name.
`species`	Character string of species name.
`model_id`	Either model number from Beacham and Murray (1990) or specific to other paper (e.g., Sparks et al. 2017 = AK).
`development_type`	The phenology type. A vector with possible values "hatch" or "emerge". The default is "hatch".

Value

A data.frame giving model specifications to be passed to `predict_phenology()`.

Examples

```
library(hatchR)
# access the parameterization for sockeye hatching using
# model #2 from Beacham and Murray (1990)
sockeye_hatch_mod <- model_select(
  author = "Beacham and Murray 1990",
  species = "sockeye",
  model_id = 2,
  development_type = "hatch"
```

```
)
# print
sockeye_hatch_mod
```

`model_table` *Table of phenology models*

Description

Table providing the model parameterizations for the phenology models.

Usage

```
model_table
```

Format

Data frame with 5 columns:

author Author-year short citation

species Species name

model_id Identification number for a model parameterization

development_type Hatch or emergence

expression character string of parameterized function expression

Source

Beacham & Murray (1990), Sparks et al. (2017), Austin et al. (2019).

References

Beacham, T.D., Murray, C.B. (1990). Temperature, egg size, and development of embryos and alevins of five species of Pacific salmon: a comparative analysis. *Canadian Journal of Zoology*, **68**, 1931–1940.

Sparks, M.M., Westley, P.A.H., Falke, J.A., Quinn, T.A. (2017). Thermal adaptation and phenotypic plasticity in a warming world: Insights from common garden experiments on Alaskan sockeye salmon. *Canadian Journal of Fisheries and Aquatic Sciences*, **76(1)**, 123–135.

Austin, C.C., Essington, T.E., Quinn, T.A. (2019). Spawning and emergence phenology of bull trout *Salvelinus confluentus* under differing thermal regimes. *Canadian Journal of Fisheries and Aquatic Sciences*, **94(1)**, 191–195.

Examples

```
model_table
```

`plot_check_temp` *Visual check of imported temperature data*

Description

The `plot_check_temp` function is used to plot imported data to check temperature values. The function takes a data frame with dates and temperature values, and plots the temperature values over time. The function also allows users to specify the visual thresholds for minimum and maximum temperature values to be plotted.

Usage

```
plot_check_temp(data, dates, temperature, temp_min = 0, temp_max = 25)
```

Arguments

`data`	A data.frame, or data frame extension (e.g. a tibble).
`dates`	Vector of dates for temperature measurements. Must be date or date-time class.
`temperature`	Vector of temperature values.
`temp_min`	Threshold for lower range of expected temperature. Default is 0.
`temp_max`	Threshold for upper range of expected temperature. Default is 25.

Value

A object of class "gg" and "ggplot" that can be printed to the console or saved as an image.

Examples

```
library(hatchR)
plot_check_temp(
  data = crooked_river,
  dates = date,
  temperature = temp_c
)
```

`plot_phenology` *Visualize fish phenology*

Description

The function takes the output from `predict_phenology()` and creates a basic ggplot2 plot object to visualize the predicted phenology.

Usage

```
plot_phenology(plot, style = "all", labels = TRUE)
```

Arguments

`plot`	A list containing the output from `predict_phenology()`
`style`	The style of the plot. A vector with possible values "all", "ef_cumsum", "ef_daily". The default is "all".
`labels`	Logical. If TRUE (default), labels are added to the plot.

Value

A object of class "gg" and "ggplot".

Examples

```
library(hatchR)
# get model parameterization
sockeye_hatch_mod <- model_select(
  author = "Beacham and Murray 1990",
  species = "sockeye",
  model = 2,
  development_type = "hatch"
)
# predict phenology
sockeye_hatch <- predict_phenology(
  data = woody_island,
  dates = date,
  temperature = temp_c,
  spawn.date = "1990-08-18",
  model = sockeye_hatch_mod
)
plot_phenology(sockeye_hatch)
plot_phenology(sockeye_hatch, style = "ef_cumsum")
plot_phenology(sockeye_hatch, style = "ef_daily")
plot_phenology(sockeye_hatch, labels = FALSE)
```

`predict_phenology` *Predict phenology of fish*

Description

Predict the phenology of fish using the effective value framework.

Usage

```
predict_phenology(data, dates, temperature, spawn.date, model)
```

Arguments

`data`	Data frame with dates and temperature.
`dates`	Date of temperature measurements.
`temperature`	Temperature measurements.
`spawn.date`	Date of spawning, given as a character string (e.g., "1990-08-18"). Must be year-month-day in format shown.
`model`	A data.frame with a column named "expression" or a character vector giving model specifications. Can be obtained using `model_select()` or using you own data to obtain a model expression (see `fit_model`).

Value

A list with the following elements:

- `days_to_develop`: A numeric vector of length 1; number of predicted days to hatch or emerge.
- `ef_table`: An n x 4 tibble (n = number of days to hatch or emerge) with the dates, temperature, effective values, and cumulative sum of the effective values.
- `dev.period`: a 1x2 dataframe with the dates corresponding to when your fish's parent spawned (input with `predict_phenology(spawn.date = ...)`) and the date when the fish is predicted to hatch or emerge.
- `model_specs`: A data.frame with the model specifications.

References

Sparks, M.M., Falke, J.A., Quinn, T.A., Adkinson, M.D., Schindler, D.E. (2019). Influences of spawning timing, water temperature, and climatic warming on early life history phenology in western Alaska sockeye salmon. *Canadian Journal of Fisheries and Aquatic Sciences*, **76(1)**, 123–135.

Examples

```
library(hatchR)
# get model parameterization
sockeye_hatch_mod <- model_select(
  author = "Beacham and Murray 1990",
  species = "sockeye",
  model_id = 2,
  development_type = "hatch"
)

# predict phenology
sockeye_hatch <- predict_phenology(
  data = woody_island,
  dates = date,
  temperature = temp_c,
  spawn.date = "1990-08-18",
  model = sockeye_hatch_mod
)
```

`summarize_temp` *Summarize temperature data to daily values*

Description

The `summarize_temp` function is used to summarize sub-daily temperature measurements to obtain mean daily temperature.

Usage

```
summarize_temp(data, dates, temperature)
```

Arguments

`data`	A data.frame, or data frame extension (e.g. a tibble).
`dates`	Column representing the date of temperature measurements.
`temperature`	Column representing temperature values.

Value

A data.frame with summarized daily temperature values.

Examples

```
library(hatchR)
summarize_temp(
  data = idaho,
  dates = date,
  temperature = temp_c
)
```

`woody_island` *Example dataset: Woody Island, Lake Iliamna, Alaska*

Description

Temperature Data from Woody Island in Lake Iliamna, Alaska

Usage

```
woody_island
```

Format

Data frame with columns:

date Date measurement was taken.

temp_c Temperature in degrees Celsius.

Source

Sparks et al. (2019)

References

Sparks, M.M., Falke, J.A., Quinn, T.A., Adkinson, M.D., Schindler, D.E., Bartz, K., Young, D., Westley, P.A.H. (2019). Influences of spawning timing, water temperature, and climatic warming on early life history phenology in western Alaska sockeye salmon. *Canadian Journal of Fisheries and Aquatic Sciences*, **76(1)**, 123–135.

Examples

```
woody_island
```

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