Package ‘phenesse’

December 22, 2019

Title Estimate Phenological Metrics using Presence-Only Data

Version 0.1.0

Description Generates Weibull-parameterized estimates of phenology for any percentile of a distribution using the framework established in Cooke (1979) <doi.org/10.1093/biomet/66.2.367>. Non-parametric bootstrapping can be used to generate confidence intervals around those estimates. Additionally, this package offers an easy way to perform non-parametric bootstrapping to generate confidence intervals for quantile estimates or mean estimates.

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Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Depends R (>= 3.5)

Imports boot, fitdistrplus, stats

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URL https://github.com/mbelitz/phenesse

BugReports https://github.com/mbelitz/phenesse/issues

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

NeedsCompilation no

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Repository CRAN

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Example iNaturalist-sourced data

Example data downloaded from iNaturalist.org for the Washington, DC area using the bounding box bounds = c(38, -77, 39, -76). Data was downloaded on 10/30/2019 for four species: Speyeria cybele, Danaus plexippus, Rudbeckia hirta, and Asclepias syriaca. These data were not scored to mark phenology, so all life stages/reproductive stages are included in the download. The download only includes 2019 observations and the doy (day of year) column was added post data download by MW Belitz using the lubridate package.

Usage

```r
data(inat_examples)
```

Format

A data frame with 252 rows and 6 variables:

- **scientific_name** binomial of species
- **latitude** latitude where observations occurred
- **longitude** longitude where observations occurred
- **common_name** common name related to species
- **observed_on** original date listed of observation
- **doy** day of year when the observation occurred, variable created by MW Belitz using the package lubridate

References

https://inaturalist.org

Examples

```r
data(inat_examples)
## Not run:
View(inat_examples)
## End(Not run)
```
**Description**

mean_ci Function estimates CIs using nonparametric bootstrapping around a mean estimate.

**Usage**

```r
mean_ci(observations, bootstraps = 1e+05, conf = 0.95, type = "bca")
```

**Arguments**

- `observations`: A vector of observations given as numeric values
- `bootstraps`: The number of bootstraps you want to run to create the CIs, defaults to 100000
- `conf`: The confidence level wanted. Defaults to 95% CI.
- `type`: A vector of character strings representing the type of intervals required to calculate the CI. Defaults to "bca". See `?boot.ci` for more information.

**Value**

The estimated CIs around a mean estimate.

**Functions**

- `mean_ci`: Estimates CIs around a mean percentile estimate using non-parameteric bootstrapping from the boot package

**Examples**

```r
# Estimate when the mean observation of Rudbeckia hirta for the year 2019 up
# to October

r_hirta <- subset(inat_examples, scientific_name == "Rudbeckia hirta")
mean_ci(observations = r_hirta$doy, bootstraps = 100)

# note low number of bootstraps for quick processing speed
```
Calculating the confidence intervals (CIs) of a quantile estimate of a vector of observations using non-parametric bootstrapping.

**Description**

`quantile_ci` Estimates CIs around a quantile percentile estimate using non-parametric bootstrapping from the boot package.

**Usage**

```r
quantile_ci(
  observations,
  percentile,
  bootstraps = 1e+05,
  conf = 0.95,
  type = "bca"
)
```

**Arguments**

- `observations` A vector of observations given as numeric values
- `percentile` The percentile of interest
- `bootstraps` The number of bootstraps you want to run to create the CIs, defaults to 100000
- `conf` The confidence level wanted. Defaults to 95% CI.
- `type` A vector of character strings representing the type of intervals required to calculate the CI. Defaults to "bca". See `boot.ci` for more information.

**Value**

The quantile estimate and confidence intervals.

**Examples**

```r
# Gather sightings of iNaturalist observations for four species: # Danaus plexippus, Speyeria cybele, Rudbeckia hirta, and Asclepias syriaca
# Estimate when the first 10 percent of individuals of the butterfly species # Speyeria cybele are in flight.

data(inat_examples)
s_cybele <- subset(inat_examples, scientific_name == "Speyeria cybele")
quantile_ci(observations = s_cybele$doy, percentile = 0.1, bootstraps = 100)
```
weib_percentile

Calculating a percentile estimate of a seasonal abundance distribution from incidental observations.

Description

weib_percentile uses empirical bootstrapping to estimate a percentile of the Weibull distribution, given random variables.

Usage

weib_percentile(observations, percentile = 0.9, iterations = 500)

Arguments

- **observations** is a vector of dates/time of observations given as integers
- **percentile** is the percentile of the cumulative distribution function of interest
- **iterations** is the number of iterations you want to use to bootstrap an estimate of bias of the original CDF. The bias is used to calculate a Weibull-corrected estimate of the percentile bound.

Value

The Weibull-corrected estimate of the percentile of interest.

Examples

# Gather sightings of iNaturalist observations for four species:
# Danaus plexippus, Speyeria cybele, Rudbeckia hirta, and Asclepias syriaca

# Estimate when the first 50 percent of individuals of the milkweed species
# Asclepias syriaca have been observed.

data(inat_examples)
a_syriaca <- subset(inat_examples, scientific_name == "Asclepias syriaca")
weib_percentile(a_syriaca$doy, percentile = 0.5, iterations = 10)

# Estimate when 90 percent of individuals of the milkweed species A. syriaca
# have been observed, using only 100 iterations for quicker processing

weib_percentile(a_syriaca$doy, percentile = 0.5, iterations = 10)
weib_percentile_ci  Calculating the CIs of a percentile estimate of a seasonal abundance distribution using the non-parametric bootstrapping.

Description

weib_percentile_ci uses non-parametric bootstrapping from the boot package to estimate 95

Usage

weib_percentile_ci(
  observations,
  iterations,
  percentile,
  bootstraps,
  type = "bca",
  conf = 0.95,
  parallelize = "no",
  ncpus = getOption("boot.ncpus", 1L),
  cl = NULL
)

Arguments

observations is a vector of dates/time of observations given as numeric values
iterations is the number of iterations you want to run to create empirical bootstrapping to estimate bias of original CDF. The bias is used to calculate a bias corrected estimate of the percentile bound.
percentile is the percentile of the cumulative distribution function of interest
bootstraps is the number of bootstraps you want to run to create the CIs
type A vector of character strings representing the type of intervals required to calculate the CI. Defaults to "bca". See ??boot.ci for more information.
conf The confidence level wanted. Defaults to 95% CI.
parallelize The type of parallel operation to be used (if any). If missing, the default is that no parallelization will occur. Parallelization options are "multicore" and "snow"
ncpus An integer that represents the number of processes to be used in parallel operation.
cl An optional parallel or snow cluster for use if parallel = "snow". If not supplied, a cluster on the local machine is created for the duration of the boot call.

Value

The Weibull-corrected estimate of the percentile of interest and CIs.
weib_percentile_ci

Examples

# Gather sightings of iNaturalist observations for four species:
# Danaus plexippus, Speyeria cybele, Rudbeckia hirta, and Asclepias syriaca

# Estimate when the first 50 percent of individuals of the butterfly species
# Speyeria cybele are in flight.

data(inat_examples)
s_cybele <- subset(inat_examples, scientific_name == "Speyeria cybele")
weib_percentile_ci(observations = s_cybele$doy, iterations = 10,
                   percentile = 0.5, bootstraps = 10)
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