

Package ‘fishboot’

July 22, 2025

Type Package

Title Bootstrap-Based Methods for the Study of Fish Stocks and Aquatic Populations

Version 1.0.2

Date 2025-07-02

Description A suite of bootstrap-based models and tools for analyzing fish stocks and aquatic populations. Designed for ecologists and fisheries scientists, it supports data from length-frequency distributions, tag-and-recapture studies, and hard structure readings (e.g., otoliths). See Schwamborn et al., 2019 <[doi:10.1016/j.ecolmodel.2018.12.001](https://doi.org/10.1016/j.ecolmodel.2018.12.001)> for background. The package includes functions for bootstrapped fitting of growth curves and plotting.

Depends R (>= 4.1.0)

Imports doParallel, parallel, foreach, grDevices, graphics, stats, utils, ks, TropFishR, fishmethods

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BugReports <https://github.com/rschwamborn/fishboot/issues>

URL <https://github.com/rschwamborn/fishboot>

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-07-02 16:20:07 UTC

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alba_boot	<i>Bootstrapped VBGF estimates for the alba data set</i>
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Description

Bootstrapped VBGF estimates for the alba length frequency data set as estimated by [ELEFAN_GA](#).

Usage

alba_boot

Format

alba_boot:
A lfqBoot object with two levels:
\$bootRaw A data.frame of fitted VBGF parameters (columns) by resampling (rows).
\$seed A numeric vector of seed values set prior to each resampling call to [lfqResample](#).

bonito_boot	<i>Bootstrapped growth estimates for the bonito data set</i>
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Description

Bootstrapped growth estimates for the [bonito](#) age-growth data calculated using the [grotag_boot](#) as this:

```
data("bonito", package = "fishmethods")

grotag_boot(input.data = bonito,
            alpha = 35, beta = 55,
            design = list(nu = 1, m = 1,p = 1, sea = 1),
```

```

stvalue = list(sigma = 0.9, nu = 0.4, m = -1,
               p = 0.2, u = 0.4, w = 0.4),
upper    = list(sigma = 5, nu = 1, m = 2,
               p = 0.5, u = 1, w = 1),
lower    = list(sigma = 0, nu = 0, m = -2,
               p = 0.0, u = 0, w = 0),
control  = list(maxiter = 1e4),
seed     = 1234, nresamp = 100, cc.only = TRUE)

```

Usage

```
bonito_boot
```

Format

bonito_boot:

A grotagBoot object with four columns: Linf, K, PhiL, u, w and seed.

ELEFAN_GA_boot

Bootstrapped ELEFAN_GA

Description

This function performs a bootstrapped fitting of a von Bertalanffy growth function (VBGF) via the [ELEFAN_GA](#) function. Most of the arguments are simply passed to the function within many permutations (resampling) of the original lfq data. As the original function, ELEFAN_GA also conducts Electronic Length Frequency Analysis using a genetic algorithm (GA) to estimate growth parameters. Partial (repeated fitting on original data) and full bootstrap (with resampling) routines are possible, depending on resample.

Usage

```

ELEFAN_GA_boot(
  lfq,
  seasonalised = FALSE,
  low_par = NULL,
  up_par = NULL,
  popSize = 50,
  maxiter = 100,
  run = maxiter,
  parallel = FALSE,
  pmutation = 0.1,
  pcrossover = 0.8,
  elitism = base::max(1, round(popSize * 0.05)),
  MA = 5,
  addl.sqrt = FALSE,
  agemax = NULL,

```

```

    ...,
    seed = NULL,
    nresamp = 10,
    resample = TRUE,
    outfile = NA
)

```

Arguments

lfq	a length frequency object of the class lfq (see lfqCreate).
seasonalised	logical; indicating if the seasonalised von Bertalanffy growth function should be applied (default: FALSE).
low_par	a list providing the minimum of the search space in case of real-valued or permutation encoded optimizations. When set to NULL the following default values are used: • Linf length infinity in cm (default is calculated from maximum length class in the data), • K curving coefficient (default: 0.01), • t_anchor time point anchoring growth curves in year-length coordinate system, corresponds to peak spawning month (range: 0 to 1, default: 0), • C amplitude of growth oscillation (range: 0 to 1, default: 0), • ts summer point ($ts = WP - 0.5$) (range: 0 to 1, default: 0);
up_par	a list providing the maximum of the search space in case of real-valued or permutation encoded optimizations. When set to NULL the following default values are used: • Linf length infinity in cm (default is calculated from maximum length class in the data), • K curving coefficient (default: 1), • t_anchor time point anchoring growth curves in year-length coordinate system, corresponds to peak spawning month (range: 0 to 1, default: 1), • C amplitude of growth oscillation (range: 0 to 1, default: 1), • ts summer point ($ts = WP - 0.5$) (range: 0 to 1, default: 1);
popSize	the population size. Default: 50
maxiter	the maximum number of iterations to run before the GA search is halted. default: 100
run	the number of consecutive generations without any improvement in the best fitness value before the GA is stopped. Default: equals maxiter.
parallel	Whether a logical or integer argument specifying the configuration of parallel computing. See ga for details.
pmutation	the probability of mutation in a parent chromosome. Usually mutation occurs with a small probability, and by default is set to 0.1.
pcrossover	the probability of crossover between pairs of chromosomes. Typically this is a large value and by default is set to 0.8.

elitism	the number of best fitness individuals to survive at each generation. By default the top 5% individuals will survive at each iteration.
MA	number indicating over how many length classes the moving average should be performed (default: 5, for more information see lfqRestructure)
addl.sqrt	additional square root transformation of positive values according to Brey et al. (1988) (default: FALSE, for more information see lfqRestructure)
agemax	maximum age of species; default NULL, then estimated from L_{inf} .
...	additional parameters to pass to ga .
seed	seed value for random number reproducibility.
nresamp	numeric, the number of permutations to run (by default nresamp = 10).
resample	logical. Do you want that lfq object be resampled (TRUE by default).
outfile	character; path of the file which will register the progress of the permutation completions. If it is set as false, NA or NULL, no file will be created.

Details

If resample = TRUE, a **full non-parametric bootstrap** is performed with resampling from the original length-frequencies by using the function [lfqResample](#). Otherwise, if resample = FALSE, a partial bootstrap is performed, reflecting solution variation due only to the search algorithm, with repeated fitting to the original data (no resampling is performed).

Value

An object of class lfqBoot containing 2 levels:

`$bootRaw` A data.frame of fitted VBGF parameters (columns) by resampling (rows).

`$seed` A numeric vector of seed values set prior to each resampling call to [lfqResample](#).

References

- Brey, T., Soriano, M., and Pauly, D. 1988. Electronic length frequency analysis: a revised and expanded user's guide to ELEFAN 0, 1 and 2.
- Efron, B., & Tibshirani, R. (1986). Bootstrap methods for standard errors, confidence intervals, and other measures of statistical accuracy. *Statistical Science*, 54-75.
- Mildenerger, T., Taylor, M. H., & Wolff, A. M., 2017. TropFishR: an R package for fisheries analysis with length-frequency data. *Methods in Ecology and Evolution*, 8(11), 1520-1527.
- Pauly, D. 1981. The relationship between gill surface area and growth performance in fish: a generalization of von Bertalanffy's theory of growth. *Meeresforsch.* 28:205-211.
- Pauly, D. and N. David, 1981. ELEFAN I, a BASIC program for the objective extraction of growth parameters from length-frequency data. *Meeresforschung*, 28(4):205-211.
- Schwamborn, R., Mildenerger, T. K., & Taylor, M. H., 2019. Assessing sources of uncertainty in length-based estimates of body growth in populations of fishes and macroinvertebrates with bootstrapped ELEFAN. *Ecological Modelling*, 393, 37-51.

- Schwamborn, R., Freitas, M. O., Moura, R. L., & Aschenbrenner, A. 2023. Comparing the accuracy and precision of novel bootstrapped length-frequency and length-at-age (otolith) analyses, with a case study of lane snapper (*Lutjanus synagris*) in the SW Atlantic. Fisheries Research, 264, 106735.
- Scrucca, L., 2013. GA: a package for genetic algorithms in R. Journal of Statistical Software, 53(4), 1-37.
- von Bertalanffy, L., 1938. A quantitative theory of organic growth. Human Biology 10, 181-213.

```
# load data
data("alba", package = "TropFishR")

# Define settings (for demo only, fast settings)
MA <- 7
low_par <- list(Linf = 9, K = 0.4, t_anchor = 0.5, C = 0, ts = 0)
up_par <- list(Linf = 11, K = 0.6, t_anchor = 0.8, C = 1, ts = 1)
popSize <- 12
maxiter <- 5
run <- 4
pmutation <- 0.1
nresamp <- 2

# Non-parallel version
res <- ELEFAN_GA_boot(lfq = alba, MA = MA, seasonalised = FALSE,
  up_par = up_par, low_par = low_par,
  parallel = FALSE,
  popSize = popSize, maxiter = maxiter,
  run = run, pmuation = pmuation,
  nresamp = nresamp)

res

# Define settings (for demo only)
MA <- 7
low_par <- list(Linf = 8, K = 0.2, t_anchor = 0, C = 0, ts = 0)
up_par <- list(Linf = 12, K = 0.9, t_anchor = 1, C = 1, ts = 1)
popSize <- 40
maxiter <- 30
run <- 10
pmutation <- 0.2
nresamp <- 3

# Parallel version
res <- ELEFAN_GA_boot(lfq = alba, MA = MA, seasonalised = FALSE,
  up_par = up_par, low_par = low_par,
  parallel = TRUE,
  popSize = popSize, maxiter = maxiter,
  run = run, pmuation = pmuation,
```

```

nresamp = nresamp)

res

```

ELEFAN_SA_boot

Bootstrapped ELEFAN_SA

Description

This function performs a bootstrapped fitting of a von Bertalanffy growth function (VBGF) via the [ELEFAN_SA](#) function. Most of the arguments are simply passed to the function within many permutations (resampling) of the original lfq data. Partial (repeated fitting on original data) and full bootstrap (with resampling) routines are possible, depending on resample.

Usage

```

ELEFAN_SA_boot(
  lfq,
  seasonalised = FALSE,
  init_par = list(Linf = 50, K = 0.5, t_anchor = 0.5, C = 0, ts = 0),
  low_par = NULL,
  up_par = NULL,
  SA_time = 60 * 1,
  maxit = NULL,
  nb.stop.improvement = NULL,
  SA_temp = 1e+05,
  MA = 5,
  addl.sqrt = FALSE,
  agemax = NULL,
  seed = NULL,
  nresamp = 10,
  resample = TRUE,
  parallel = FALSE,
  outfile = NA
)

```

Arguments

- | | |
|--------------|--|
| lfq | a length frequency object of the class lfq (see lfqCreate). |
| seasonalised | logical; indicating if the seasonalised von Bertalanffy growth function should be applied (default: FALSE). |
| init_par | a list providing the Initial values for the components to be optimized. When set to NULL the following default values are used: <ul style="list-style-type: none"> • Linf length infinity in cm (default is the maximum length class in the data), • K curving coefficient (default: 0.5), |

	• t_anchor time point anchoring growth curves in year-length coordinate system, corresponds to peak spawning month (range: 0 to 1, default: 0.5), • C amplitude of growth oscillation (range: 0 to 1, default: 0), • ts summer point ($ts = WP - 0.5$) (range: 0 to 1, default: 0);
low_par	a list providing the lower bounds for components. When set to NULL the following default values are used: • Linf length infinity in cm (default is calculated from maximum length class in the data), • K curving coefficient (default: 0.01), • t_anchor time point anchoring growth curves in year-length coordinate system, corresponds to peak spawning month (range: 0 to 1, default: 0), • C amplitude of growth oscillation (range: 0 to 1, default: 0), • ts summer point ($ts = WP - 0.5$) (range: 0 to 1, default: 0);
up_par	a list providing the upper bounds for components. When set to NULL the following default values are used: • Linf length infinity in cm (default is calculated from maximum length class in the data), • K curving coefficient (default: 0.01), • t_anchor time point anchoring growth curves in year-length coordinate system, corresponds to peak spawning month (range: 0 to 1, default: 0), • C amplitude of growth oscillation (range: 0 to 1, default: 0), • ts summer point ($ts = WP - 0.5$) (range: 0 to 1, default: 0);
SA_time	numeric; Maximum running time in seconds (default : 60 * 1).
maxit	Integer. Maximum number of iterations of the algorithm. Default is NULL.
nb.stop.improvement	Integer. The program will stop when there is no any improvement in 'nb.stop.improvement' steps. Default is NULL
SA_temp	numeric; Initial value for temperature (default : 1e5).
MA	number indicating over how many length classes the moving average should be performed (default: 5, for more information see lfqRestructure).
addl.sqrt	Passed to lfqRestructure . Applied an additional square-root transformation of positive values according to Brey et al. (1988). (default: FALSE, for more information see lfqRestructure).
agemax	maximum age of species; default NULL, then estimated from L_{inf} .
seed	seed value for random number reproducibility.
nresamp	numeric, the number of permutations to run (by default nresamp = 10).
resample	logical. Do you want that lfq object be resampled (TRUE by default).
parallel	Whether a logical or integer argument specifying the configuration of parallel computing. If parallel = TRUE, the number of threads will be defined as <code>parallel::detectCores() - 2</code> .
outfile	character; path of the file which will register the progress of the permutation completions. If it is set as false, NA or NULL, no file will be created.

Details

If `resample = TRUE`, a **full non-parametric bootstrap** is performed with resampling from the original length-frequencies by using the function [lfqResample](#). Otherwise, if `resample = FALSE`, a partial bootstrap is performed, reflecting solution variation due only to the search algorithm, with repeated fitting to the original data (no resampling is performed).

Value

An object of class `lfqBoot` containing 2 levels:

`$bootRaw` A data.frame of fitted VBGF parameters (columns) by resampling (rows).

`$seed` A numeric vector of seed values set prior to each resampling call to [lfqResample](#).

References

- Brey, T., Soriano, M., and Pauly, D. 1988. Electronic length frequency analysis: a revised and expanded user's guide to ELEFAN 0, 1 and 2.
- Efron, B., & Tibshirani, R. (1986). Bootstrap methods for standard errors, confidence intervals, and other measures of statistical accuracy. *Statistical Science*, 54-75.
- Mildenerger, T., Taylor, M. H., & Wolff, A. M., 2017. TropFishR: an R package for fisheries analysis with length-frequency data. *Methods in Ecology and Evolution*, 8(11), 1520-1527.
- Pauly, D. 1981. The relationship between gill surface area and growth performance in fish: a generalization of von Bertalanffy's theory of growth. *Meeresforsch.* 28:205-211.
- Pauly, D. and N. David, 1981. ELEFAN I, a BASIC program for the objective extraction of growth parameters from length-frequency data. *Meeresforschung*, 28(4):205-211.
- Schwamborn, R., Mildenerger, T. K., & Taylor, M. H., 2019. Assessing sources of uncertainty in length-based estimates of body growth in populations of fishes and macroinvertebrates with bootstrapped ELEFAN. *Ecological Modelling*, 393, 37-51.
- Schwamborn, R., Freitas, M. O., Moura, R. L., & Aschenbrenner, A. 2023. Comparing the accuracy and precision of novel bootstrapped length-frequency and length-at-age (otolith) analyses, with a case study of lane snapper (*Lutjanus synagris*) in the SW Atlantic. *Fisheries Research*, 264, 106735.
- Scrucca, L., 2013. GA: a package for genetic algorithms in R. *Journal of Statistical Software*, 53(4), 1-37.
- von Bertalanffy, L., 1938. A quantitative theory of organic growth. *Human Biology* 10, 181-213.

Examples

```
# load data
data("alba", package = "TropFishR")

# Define settings (for demo only, fast settings)
MA      <- 7
low_par  <- list(Linf = 9, K = 0.4, t_anchor = 0.5, C = 0, ts = 0)
up_par   <- list(Linf = 11, K = 0.6, t_anchor = 0.8, C = 1, ts = 1)
init_par <- list(Linf = 10, K = 0.5, t_anchor = 0.6, C = 0.5, ts = 0.5)
```

```

SA_time <- 1.5
SA_temp <- 1e5
nresamp <- 2

# Non-parallel bootstrapped curve fitting
res <- ELEFAN_SA_boot(lfq = alba, MA = MA, seasonalised = FALSE,
                     init_par = init_par, up_par = up_par, low_par = low_par,
                     SA_time = SA_time, SA_temp = SA_temp,
                     nresamp = nresamp)

res

# Define settings (for demo only)
MA <- 7
low_par <- list(Linf = 8, K = 0.1, t_anchor = 0, C = 0, ts = 0)
init_par <- list(Linf = 12, K = 0.5, t_anchor = 0.5, C = 0.5, ts = 0.5)
up_par <- list(Linf = 15, K = 5, t_anchor = 1, C = 1, ts = 1)
SA_time <- 10
SA_temp <- 1e5
nresamp <- 12

# parallel version
res <- ELEFAN_SA_boot(lfq = alba, MA = MA, seasonalised = FALSE,
                     init_par = init_par, up_par = up_par, low_par = low_par,
                     SA_time = SA_time, SA_temp = SA_temp,
                     nresamp = nresamp,
                     parallel = TRUE)

res

```

grolenage_boot

Bootstrapped length-at-age analysis

Description

This function obtains growth parameter estimates from length-at-age data. Since it internally uses the function [growth_length_age](#), this function allows to perform different methods: Gulland and Holt, Ford Walford, Chapman, Bertalanffy, or non linear least squares method (LSM).

This function performs bootstrapped fitting of the von Bertalanffy growth function with estimated growth parameters (L_{inf} , K and t_0) from length-at-age data, based on the function [growth_length_age](#). The output is an object containing the parameters L_{inf} , K and t_0 (named here `t_anchor`) as well as the growth performance index Φ'_{iL} (named `PhiL`).

Usage

```

grolenage_boot(
  param,

```

```

method = "LSM",
Linf_est = NA,
Linf_init = 100,
K_init = 0.1,
t0_init = 0,
seed = NULL,
nresamp = 200,
nan_action = c("nothing", "nanrm", "narm", "force"),
time_lim = 5 * 60
)

```

Arguments

param	a list (or data.frame) consisting of following parameters (levels/columns): • age: age measurements (e.g. from otoliths), • length: corresponding length measurements.
method	indicating which of following methods should be applied: "GullandHolt", "FordWalford", "Chapman", "BertalanffyPlot", or "LSM" (it corresponds to the non-linear least squares fitting method, and is the default, which is recommended for bootstrapping growth).
Linf_est	BertalanffyPlot requires an estimate for L_{inf} to derive K and t_0 (for more information see Details).
Linf_init	initial parameter of L_{inf} for non-linear squares fitting (default 100).
K_init	initial parameter of K for non-linear squares fitting (default 0.1).
t0_init	initial parameter of L_0 for non-linear squares fitting (default 0).
seed	seed value for random number reproducibility (if it NULL by default, it will set internally as <code>seed = as.numeric(Sys.time())</code>).
nresamp	numeric; the number of permutations to run (Default: <code>nresamp = 200</code>).
nan_action	character that defines the action that the function will execute if there is a row with NaN (growth rate parameters inestimable for that resample): • nothing: the function will return the results including the NaNs (default). • nanrm or narm: after having the results, it will only returns the rows without NaNs. For this case narm and nanrm are equivalent, but it should be noted that the function will look for and omit the NaNs (and not the NAs). See Details. • force: The function will start an iterative process changing the internal seed values until it fulfills the <code>nresamp</code>. It only works together with the <code>time_lim</code> argument. See Details.
time_lim	If <code>nan_action = "force"</code> , it defines the maximum time (in seconds) that the function will last resampling until it achieves a result output with no-NaN rows.

Details

It is important to take into account the particular considerations of each method regarding the required parameters, so it is recommended to read the Details of the documentation of [growth_length_age](#).


```

rnorm(n = 15, mean = 57, sd = 3)))

# Perform bootstrapped curve fitting with grolenage_boot
res <- grolenage_boot(param = dat, nresamp = 70)

# Plot scatter histograms of Linf and K
LinfK_scatterhist(res = res)

# Plot univariate density plots of all parameters
univariate_density(res = res)

# Plot swarm plots of all n bootstraps
vbgfCI_time(res = res)

# Extract data.frame with all parameter estimates
# for comparisons of posterior distributions
print(res$bootRaw)

```

grotag_boot

Bootstrapped tag-and-recapture growth analysis

Description

This function performs bootstrapped fitting of the von Bertalanffy growth function (VBGF) with estimated growth parameters (L_{inf} , K and t_0) from tag-and-recapture data, based on the function [grotag](#), that estimates VBGF parameters according to Francis (1988). The output is an object containing the parameters L_{inf} and K , as well as the growth performance index Φ' (named `PhiL`).

This function resamples the input `data` by rows (i.e., by recapture date) several times (`nresamp` times, default: `nresamp = 200`). Then, a VBGF curve is fitted to each resampled data set. The output (a list of class `lfqBoot`) will store results (e.g., VBGF function parameters K and L_{inf}) in a `data.frame` accessible through `$bootRaw`. The `$bootRaw` table also includes the growth performance index **Phi'**, seasonal parameters **u** and **w** (sensu Francis, 1988), which are equal to **C** (sensu Pauly and Gaschütz, 1979) and **ts** (sensu Mildenerger et al., 2017). The `$bootRaw` table also includes seed values and system time.

Usage

```

grotag_boot(
  L1 = NULL,
  L2 = NULL,
  T1 = NULL,
  T2 = NULL,
  alpha = NULL,
  beta = NULL,
  design = list(nu = 0, m = 0, p = 0, sea = 0),
  stvalue = list(sigma = 0.9, nu = 0.4, m = -1, p = 0.1, u = 0.4, w = 0.4),
  upper = list(sigma = 5, nu = 1, m = 2, p = 1, u = 1, w = 1),
  lower = list(sigma = 0, nu = 0, m = -2, p = 0, u = 0, w = 0),

```

```

gestimate = TRUE,
st.ga = NULL,
st.gb = NULL,
st.galow = NULL,
st.gaup = NULL,
st.gblow = NULL,
st.gbup = NULL,
control = list(maxit = 10000),
input.data = NULL,
seed = NULL,
nresamp = 200,
na_action = c("nothing", "narm", "force"),
time_lim = 5 * 60
)

```

Arguments

L1, L2, T1, T2	Name of the columns to be extracted from <code>input.data</code> and used by the grotag function for the arguments L1, L2, T1 and T2, respectively. See Details.
alpha	numeric value giving an arbitrary length alpha.
beta	numeric value giving an arbitrary length beta (beta > alpha).
design	list specifying the design of the model to estimate. Use 1 to designate whether a parameter(s) should be estimated. Type of parameters are: • nu: growth variability (1 parameter). • m: bias parameter of measurement error (1 parameter). • p: outlier probability (1 parameter). • sea: seasonal variation (2 parameters: u and w). Model 1 of Francis is the default settings of 0 for nu, m, p and sea.
stvalue	Starting values of sigma(s) and depending on the design argument, nu, m, p, u, and w used as input in the nonlinear estimation (function optim) routine.
upper, lower	Upper and lower limits of the model parameters' (nu, m, p, u, and w) region to be investigated.
gestimate	logical specifying whether starting values of ga and gb (growth increments of alpha and beta) should be estimated automatically. TRUE by default.
st.ga, st.gb	If gestimate=FALSE, user-specified starting value for ga and gb respectively.
st.galow, st.gaup	If gestimate=FALSE, user-specified lower and upper limits for st.ga used in optimization.
st.gblow, st.gbup	If gestimate=FALSE, user-specified lower and upper limits for st.gb used in optimization.
control	Additional controls passed to the optimization function optim .
input.data	A growth increment object of the class <code>data.frame</code> .
seed	seed value for random number reproducibility (if it NULL by default, it will set internally as <code>seed = as.numeric(Sys.time())</code>).

nresamp	numeric; the number of permutations to run (Default: nresamp = 200).
na_action	character that defines the action that the function will execute if there is a row with NA: • nothing: the function will return the results including the NAs (default). • narm: after having the results, it will only returns the rows without NAs. See Details. • force: The function will start an iterative process changing the internal seed values until it fulfills the nresamp. It works just together time_lim argument. See Details.
time_lim	If na_action = "force", it defines the maximum time (in seconds) that the function will last resampling until it achieves a result output with no-NaN rows.

Details

There are 2 ways to specify the main input arguments (related to the size and timing of the mark-recapture): (1) in the classical way, i.e. by defining L1, L2, T1 and T2 as numeric vectors as indicated in the [grotag](#) documentation or (2) through a data.frame indicated in the input.data argument. In the latter case, the arguments L1, L2, T1 and T2 must be 1-length character vectors and they will serve to indicate the column names of the corresponding variables. If only one value is specified for input.data and any of the other arguments is NULL, a default name equal to the variable name will be assigned (e.g. L1 <- "L1").

na_action = "force" should be used carefully, as it is not always due to bootstrap data selection factors, but also to an inadequate selection of the estimation parameters that the NA values are obtained. Also, the search time may depend on the size of the input set, if you have many thousands of individuals or if (in addition) the value of nresamp is high, it is possible that the function will take a long time before obtaining complete results. time_lim avoids falling into an infinite loop by limiting the time used by this process to 5 minutes, but this value is referential and may be insufficient due to the factors mentioned above.

Value

A data.frame of fitted VBGF parameters (columns) by resampling (rows). It includes a column (seed) with seed values set prior to each resampling call.

References

- Efron, B., & Tibshirani, R., 1986. Bootstrap methods for standard errors, confidence intervals, and other measures of statistical accuracy. *Statistical Science*, 54-75.
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- Schwamborn, R., Mildenerberger, T. K., & Taylor, M. H., 2019. Assessing sources of uncertainty in length-based estimates of body growth in populations of fishes and macroinvertebrates with bootstrapped ELEFAN. *Ecological Modelling*, 393, 37-51.

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- von Bertalanffy, L., 1938. A quantitative theory of organic growth. Human Biology 10, 181-213.

Examples

```
# Load example DB from fishmethods package
data(bonito, package = "fishmethods")

## Run the example cited on ?grotag
# fishmethods::grotag(L1 = bonito$L1,
#                     L2 = bonito$L2,
#                     T1 = bonito$T1,
#                     T2 = bonito$T2,
#                     alpha = 35, beta = 55,
#                     design = list(nu = 1, m = 1, p = 1, sea = 1),
#                     stvalue = list(sigma = 0.9, nu = 0.4, m = -1, p = 0.2, u = 0.4, w = 0.4),
#                     upper = list(sigma = 5, nu = 1, m = 2, p = 0.5, u = 1, w = 1),
#                     lower = list(sigma = 0, nu = 0, m = -2, p = 0.0, u = 0, w = 0),
#                     control = list(maxit = 1e4))

# Run the example using grotag_boot
res <- grotag_boot(L1 = bonito$L1,
                  L2 = bonito$L2,
                  T1 = bonito$T1,
                  T2 = bonito$T2,
                  alpha = 35, beta = 55,
                  design = list(nu = 1, m = 1, p = 1, sea = 1),
                  stvalue = list(sigma = 0.9, nu = 0.4, m = -1, p = 0.2, u = 0.4, w = 0.4),
                  upper = list(sigma = 5, nu = 1, m = 2, p = 0.5, u = 1, w = 1),
                  lower = list(sigma = 0, nu = 0, m = -2, p = 0.0, u = 0, w = 0),
                  control = list(maxit = 1e4), seed = 18,
                  nresamp = 3, na_action = "nothing")

res
```

1fqResample

Resampling of length-frequency data

Description

This function resamples the 1fq data by sampling dates. Sampling is done in a non-parametric way following the relative frequencies of the original data, allowing for individual counts to be selected more than once (i.e. `replace = TRUE` in [sample](#)), and resulting in total counts (by sample) equal to the original data.

Usage

```
lfqResample(lfq)
```

Arguments

lfq A length frequency object of the class lfq.

Value

A resampled version of the lfq class dataset.

Examples

```
# Load data
data("alba", package = "TropFishR")

# Resample lfq data
alba_p <- lfqResample(lfq = alba)

# Side-by-side plot
op <- par(no.readonly = TRUE)
par(mfcol = c(2, 1), mar = c(4, 4, 2, 1))

# Original
plot(x = TropFishR::lfqRestructure(alba), Fname = "rcounts")
mtext("original", side=3, line=0.25)

# Resampled
plot(TropFishR::lfqRestructure(alba_p), Fname = "rcounts")
mtext("resampled", side=3, line=0.25)

par(op)
```

LinfK_scatterhist

Linf/K scatterplot of bootstrapping results

Description

This function plots a scatterplot of von Bertalanffy growth function parameters K vs L_{inf} (“Kimura plot”) with histograms.

Usage

```
LinfK_scatterhist(
  res,
  Linf.breaks = "Sturges",
  K.breaks = "Sturges",
  gridsize = rep(151, 2),
  H = NULL,
```

```

    shading = TRUE,
    shading.cols = NULL,
    dens.contour = TRUE,
    probs = c(25, 50, 75, 95),
    phi.contour = TRUE,
    phi.levels = NULL,
    phi.contour.col = 8,
    phi.contour.lty = 2,
    phi.contour.lwd = 1,
    phi.contour.labcex = 0.75,
    pt.pch = 16,
    pt.col = adjustcolor(1, 0.25),
    pt.cex = 0.5,
    pt.bg = 4,
    xlab = expression(italic("L")[infinity]),
    ylab = expression(italic("K")),
    ...
  )

```

Arguments

<code>res</code>	Object of class <code>data.frame</code> , <code>tbl_df</code> , <code>lfqBoot</code> or <code>grotagBoot</code> .
<code>Linf.breaks</code> , <code>K.breaks</code>	Arguments passed to hist function to compute the breakpoints (argument <code>breaks</code>) for Linf and K histograms respectively.
<code>gridsize</code>	numeric 2-length vector specifying the resolution of the grid.
<code>H</code>	Plug-in bandwidth object from Hpi (Default: <code>H = ks::Hpi(res[,c("Linf", "K")])</code>)
<code>shading</code>	logical. Do you want to colour 2D field of density estimates? (Default TRUE)
<code>shading.cols</code>	Colors or color palette used for background shading of 2D field of density estimates. No considered if <code>shading = FALSE</code> .
<code>dens.contour</code>	logical. Do you want to add contour lines? (TRUE by default).
<code>probs</code>	numeric Density probability cutoffs (in by contours. By default <code>probs = c(25, 50, 75, 95)</code> and not considered if <code>dens.contour = FALSE</code> .
<code>phi.contour</code>	logical. Do you want to display phi prime isolines? (FALSE by default)
<code>phi.levels</code>	numeric vector that controls Phi prime values. Omitted if <code>phi.contour = FALSE</code> and if NULL values will be chosen automatically by the contour function.
<code>phi.contour.col</code> , <code>phi.contour.lty</code> , <code>phi.contour.lwd</code> , <code>phi.contour.labcex</code>	Extra arguments used to control the color, line type, line width and labels size of the phi prime contour isolines.
<code>pt.pch</code> , <code>pt.col</code> , <code>pt.cex</code> , <code>pt.bg</code>	Extra arguments to control type, color, size and background color of resampling points.
<code>xlab</code> , <code>ylab</code>	Labels for X and Y axis respectively.
<code>...</code>	Extra arguments passed to main plot function.

Details

Isolines of growth performance (Φ') can be plotted, as well as bivariate 95 used for plotting is usually the result of a bootstrapped growth analysis (i.e. a `lfqBoot` object generated by **fishboot** functions such as `ELEFAN_SA_boot`, `ELEFAN_GA_boot`, `grotag_boot`, or `grolenage_boot`).

If NULL, it will be defined as `colorRampPalette(c("white", blues9))(1e3)`.

Value

This function returns just the described plot.

Examples

```
data(alba_boot) # lfqBoot object
LinfK_scatterhist(res = alba_boot)

data(bonito_boot) # grotagBoot object
LinfK_scatterhist(res = bonito_boot)
```

<code>univariate_density</code>	<i>Univariate kernel density estimate plot of VBGF parameter from bootstrapping results</i>
---------------------------------	---

Description

This function plots a set of vertical plots with kernel density distributions for univariate posterior distributions of the VBGF growth parameters L_{inf} , K , and Φ' . The 95 interval and the most likely optimum fit estimate are shown for each parameter.

Usage

```
univariate_density(
  res,
  CI = 95,
  use_hist = FALSE,
  nbreaks = 10,
  mar = c(1.5, 2, 2, 0),
  oma = c(1.5, 0, 0, 0.5),
  mgp = c(2, 0.5, 0),
  tcl = -0.25,
  cex = 1,
  ...
)
```

Arguments

res Object of class `lfqBoot`.
CI numeric. Confidence interval in % (default: 95).
use_hist logical Plot histogram in addition to smoothed kernel density.
nbreaks numeric vector specifying the number of breaks in the histogram.
mar, oma, mgp, tcl, cex, ...
 Additional arguments passed to [par](#).

Details

This function used the function [kde](#) to obtain kernel density estimates for the VBGF growth parameters L_{inf} , K , and Φ' . The 95 posterior distribution) and the most likely optimum fit estimate (i.e., the mode of each posterior distribution) are then plotted inside each vertical plot. The input used for plotting is usually the result of a bootstrapped growth analysis (i.e. a `lfqBoot` object generated by **fishboot** functions such as [ELEFAN_SA_boot](#), [ELEFAN_GA_boot](#), [grotag_boot](#), or [grolenage_boot](#)).

Value

This function returns just the described plot.

Examples

```
data(alba_boot)
univariate_density(alba_boot)
```

vbgfCI_time	<i>VBGF plot and CI</i>
-------------	-------------------------

Description

This function plots a swarm of von Bertalanffy growth functions (VBGF), as length vs time (age) curves, based on the results of bootstrap runs, with confidence intervals (CI).

Usage

```
vbgfCI_time(
  res,
  CI = 95,
  agemax = NULL,
  plot = TRUE,
  add_legend = TRUE,
  add_max_dens_legend = TRUE,
  xlab = "Relative time",
  ylab = "Length",
  perm.col = adjustcolor("grey50", 0.1),
```

```

    perm.lwd = 1,
    ci.col = "black",
    ci.lty = 2,
    ci.lwd = 1,
    maxd.col = "black",
    maxd.lty = 1,
    maxd.lwd = 2,
    ...
  )

```

Arguments

<code>res</code>	Object with L_{inf} , K and t_0 , it could be a <code>data.frame</code> , a <code>tbl_df</code> , a list, <code>grotagBoot</code> or a <code>lfqBoot</code> object. See Details.
<code>CI</code>	numeric. Confidence interval in % (default: 95).
<code>agemax</code>	numeric values indicating the maximum number of years to project.
<code>plot</code>	logical. If TRUE (default), a plot is returned, otherwise just a list with levels <code>limCI</code> , <code>inCI</code> , <code>density</code> and <code>max_dens</code> . See Value for a detailed description of each one.
<code>add_legend</code>	logical. Should CI and max. density legend be added (Default: 'add_legend = TRUE').
<code>add_max_dens_legend</code>	logical. Should maximum density line be added (Default: 'add_max_dens_legend = TRUE').
<code>xlab</code>	Label for x-axis
<code>ylab</code>	Label for y-axis
<code>perm.col, perm.lwd</code>	Color and width for each resample estimate line.
<code>ci.col, ci.lty, ci.lwd</code>	Color, type and width for CI line.
<code>maxd.col, maxd.lty, maxd.lwd</code>	Color, type and width for maximum density line.
<code>...</code>	Extra arguments passed to the main plot function.

Details

Each thin grey line represents the output of a single bootstrap run. The most likely optimum (i.e., the mode of the posterior distribution) is shown as a thick black line. The dashed lines show the upper and lower limits of the 95 confidence envelope. The input used for plotting is usually the result of a bootstrapped growth analysis (i.e. a `lfqBoot` object generated by **fishboot** functions such as [ELEFAN_SA_boot](#), [ELEFAN_GA_boot](#), [grotag_boot](#), or [grolenage_boot](#)).

Value

A list containing:

`$limCI` A `data.frame` with CI limits by time.

`$inCI` A `data.frame` with logical values defining whether bootstrapping samples are within each of the defined CIs.

`$density` The multivariate kernel density estimates for each sample.

`$max_dens` A list with the VBGf parameter combination having the maximum density estimate.

Examples

```
data(alba_boot) # lfqBoot object
vbgfCI_time(res = alba_boot)

vbgfCI_time(res = alba_boot, CI = c(50, 95),
            ci.col = c("red", "orange"))

data(bonito_boot) # grotagBoot object
LinfK_scatterhist(res = bonito_boot)
```

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