

Package: LHsampling (via r-universe)

September 20, 2024

Type Package

Title Functions For Simulating Fish Populations And Estimating Life History Parameters

Version 0.1.0

URL <https://github.com/NOAA-LHP/LHsampling/>

BugReports <https://github.com/NOAA-LHP/LHsampling/issues>

Reference Eva Schemmel, Erin C Bohaboy, Michael J Kinney, Joseph M O'Malley, An assessment of sampling approaches for estimating growth from fishery-dependent biological samples, ICES Journal of Marine Science, Volume 79, Issue 5, July 2022, Pages 1497–1514, <https://doi.org/10.1093/icesjms/fsac075>

Description An individual-based model (IBM) incorporating within-population variability in von Bertalanffy growth, size-dependent natural mortality, and a size-selective fishery to simulate an exploited fish population and catch (harvest). A bootstrap algorithm allows the user to investigate various sampling approaches including sampling strategy (proportional or fixed otolith sampling, POS or FOS, respectively), sample size, supplementation with fishery-independent sampling, and assumptions regarding von Bertalanffy t_0 and the relationship between variance of length at age and age. A function to produce plots of the bootstrap sampling results is also provided.

Depends reshape, dplyr, ggplot2, magrittr, assertthat

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

Repository <https://noaa-fisheries-integrated-toolbox.r-universe.dev>

RemoteUrl <https://github.com/NOAA-LHP/LHsampling>

RemoteRef HEAD

RemoteSha 9f3e21da53e3903d248245c352e4b1717e27b593

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LH_plot	<i>LH_plot</i>
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Description

A function that produces plots from the output of `LH_sample()`.

Usage

```
LH_plot <- function(sample_output, output_type = 'none')
```

Arguments

`sample_output` Output from `LH_sample()`

`output_type` How plots are written and saved: 'none' displays in R graphics device only, 'pdf' produces a single .pdf with all plots, and 'png' produces a separate .png for each plot.

LH_sample	<i>LH_sample</i>
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Description

A bootstrap sampling routine to estimate life history parameters from fishery catches simulated by `simulate_population_harvest()`. This function will take `n_boots` samples (without replacement) from the harvested individuals following either a fixed otolith sampling (FOS) or proportional otolith sampling (POS) strategy. The function then parameterizes the von Bertalanffy growth function and estimates the population coefficient of variation of length at age for each bootstrap sample.

Usage

```
LH_sample <- function(sim_output, n_boots, samp_size, sample_type, supp_large = FALSE, supp_la
```

Arguments

<code>sim_output</code>	output from <code>simulate_population_harvest()</code>
<code>n_boots</code>	number of bootstraps for von Bertalanffy growth function
<code>sample_type</code>	The sampling strategy to be used, either proportional otolith sampling ('POS') or fixed otolith sampling ('FOS')
<code>supp_large</code>	TRUE / FALSE specifying whether supplemental samples will be collected from large length bins
<code>supp_large_n_per_bin</code>	The number of samples per length bin to be collected from large bins (ignored if <code>supp_large = FALSE</code>)
<code>supp_small</code>	TRUE / FALSE specifying whether supplemental samples will be collected from small length bins
<code>supp_small_n_per_bin</code>	The number of samples per length bin to be collected from small bins (ignored if <code>supp_small = FALSE</code>)
<code>supp_min_length</code>	The minimum length fish that could be collected from the wild fish population
<code>constrained</code>	TRUE / FALSE specifying whether theoretical time at length zero (t_0) should be estimated
<code>t0</code>	If <code>constrained = TRUE</code> , the fixed value for t_0 (typically 0)
<code>SD_L_const</code>	TRUE / FALSE describing assumptions of population variance in length at age. If TRUE, then standard deviation ($\sqrt{2}$) of length at age is assumed a linear function of age. If FALSE, then the coefficient of variation of length at age is assumed a linear function of age.
<code>save_bootstraps</code>	TRUE / FALSE specifying whether all bootstrap samples will be included in the function output
<code>Amax</code>	Maximum longevity (years). If not specified, this value is taken from <code>sim_output</code> .
<code>age_max</code>	An arbitrary age selected to represent "old" fish (years). If not specified, this value is taken from <code>sim_output</code> .
<code>Lbin_width</code>	The width of each length bin (cm).

S1

*Simulated population and harvest for Prisitpomoides auricilla***Description**

Simulated population for Prisitpomoides auricilla under low fishing mortality (half of natural mortality) using life history parameters from O'Malley et al. 2019 (S1_Auric_lowF).

- \$population (dataframe: \$age, \$length): the simulated population
- \$harvest (dataframe: \$age, \$length): the simulated harvest
- \$Avg_age (dataframe: \$Ages, \$L_age, \$M_age, and \$Sex): characteristics of the simulated population at age
- \$parameters named list of 19 elements including all input parameters used in the simulation and the simulated population coefficient of variation of length at age_max and age_0

Usage

```
data(S1)
```

Format

```
list
```

References

Schemmel E., Bohaboy E., Kinney M., O'Malley J. (2022) An assessment of sampling strategies for estimating fish growth from fishery-dependent samples. ICES 79(5):1497-1514

```
simulate_population_harvest
```

```
Simulate Population Harvest
```

Description

This is a IBM to generate a population and catch from the population

Usage

```
simulate_population_harvest(  
  Linf,  
  Linf_sd,  
  M,  
  Lorenzen,  
  F,
```

```

    mincat,
    catsd,
    maxcat,
    maxcatsd,
    L0,
    L0_sd,
    k,
    k_sd,
    Amax,
    age_max,
    N
)

```

Arguments

<code>Linf</code>	Von Bertalanffy theoretical asymptotic length (cm)
<code>Linf_sd</code>	Population standard deviation of asymptotic length (cm)
<code>M</code>	Instantaneous natural mortality rate (yr-1)
<code>Lorenzen</code>	TRUE / FALSE specifying whether natural mortality is a function of individual length following Lorenzen (Lorenzen, 2000; Lorenzen, 2005)
<code>F</code>	Apical (fully selected) instantaneous fishing mortality rate (yr-1)
<code>mincat</code>	Minimum length at 50% fishery selectivity (cm)
<code>catsd</code>	Slope of the ascending region of selectivity at length (cm), see details
<code>maxcat</code>	Maximum length at 50% fishery selectivity (cm)
<code>maxcatsd</code>	Slope of the descending region of selectivity at length (cm), see details
<code>L0</code>	Von Bertalanffy length at age 0 (cm)
<code>L0_sd</code>	Population standard deviation of length at age 0 (cm)
<code>k</code>	Von Bertalanffy growth coefficient
<code>k_sd</code>	Population standard deviation of Von Bertalanffy growth coefficient
<code>Amax</code>	Maximum longevity (years)
<code>age_max</code>	An arbitrary age selected to represent “old” fish (years)
<code>N</code>	The number of age 0 fish in each simulated cohort, typical value =100,000

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