Package ‘gnomonicM’

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Title Estimate Natural Mortality for Different Life Stages
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Description Estimate natural mortality (M) throughout the life history for organisms, mainly fish and invertebrates, based on gnomonic interval approach proposed by Caddy (1996) <doi:10.1051/alr:1996023> and Martinez-Aguilar et al. (2005) <doi:10.1016/j.fishres.2004.04.008>. It includes estimation of duration of each gnomonic interval (life stage), the constant probability of death (G), and some basic plots.
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**Estimate Natural Mortality for Different Life Stages.**

**Description**

Estimate natural mortality (M) throughout the life history for organisms, mainly fish and invertebrates, based on gnomonic interval approach. It includes estimation of duration of each gnomonic interval (life stage) and the constant probability of death (G).

**Details**

Package: gnomonicM  
Type: Package  

The natural mortality (M) estimation throughout different life stages is based on the gnomonic approach (Caddy, 1991, 1996), including new features in this package-version.

In the gnomonic model, the estimation of $M_i$ for each gnomonic interval $\Delta_i$ requires at least information about: (i) the number of development stages throughout the life cycle $i$ in $1, 2, 3, \ldots n$. (ii) the duration of the first life stage corresponding to first gnomonic interval ($\Delta_1$, egg stage), (iii) the mean lifetime fecundity $MLF$, and (iv) the longevity of the species. As additional information, the duration of the other developments stages or gnomonic intervals (larval, juvenile, adults) could be provided.

According to Caddy (1996) and Martinez-Aguilar (2005), the gnomonic method is supported by a negative exponential function, where the independent variable is $\Delta_i$ representing the number of gnomonic intervals from $i$ in $1, 2, 3, \ldots n$, the equation is expressed as follows:

\[
N_i = MLF \cdot e^{-(M_i \cdot \Delta_i)}; \text{ for } i = 1 
\]

\[
N_i = N_{i-1} \cdot e^{-(M_i \cdot \Delta_i)}; \text{ for } i > 1 
\]

where:

$M_i$ is the average value for natural mortality rate, that integrates the declining death rate through the short time interval duration $\Delta_i$. The $N_i$ is the survivors from previous interval, only for the first interval ($\Delta_1$) is assumed that the numbers of hatching eggs (initial population) is equivalent to the mean lifetime fecundity ($MLF$).

The duration of first gnomonic interval $\Delta_1$ is equal to the time elapsed after the moment of hatching $t_1$. The duration of the subsequent gnomonic intervals ($i > 1$) are estimated following:

\[
\Delta_i = \Delta_1 \cdot \alpha (\alpha + 1)^{i-2}
\]
where,
\[ \Delta_i: \text{Duration of the gnomonic interval when } i > 1. \]
\[ \Delta_1: \text{Duration of the first gnomonic interval } t_1. \]
\[ \alpha: \text{Proportionality constant.} \]
\[ i: \text{ith gnomonic interval.} \]

The \( M_i \) is estimated as follows:

\[ M_i = \frac{G}{\Delta_{i, i-1}} \]

where \( G \) is the constant proportion of the overall natural death rate. The \( G \) value is calculated so that the number of individuals surviving to the last gnomonic time-interval is \( N_n = 2 \) following the assumption of stable population replacement (Caddy, 1996; Martínez-Aguilar, 2005). The new equation for \( G \) is expressed:

\[ G = -\ln\left(\left(\frac{2}{MLF}\right)^{\frac{1}{i}}\right) \]

The final solution is to estimate the proportionality constant (\( \alpha \)) parameter by iterative solution via univariate (1-dim.) minimization.

**Author(s)**

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**References**


**Examples**

#See examples for functions gnomonic() and gnomonicStochastic().
Description

Estimate natural mortality based on gnomonic interval approach.

Usage

gnomonic(
  nInterval,  
  eggDuration,  
  addInfo = NULL,  
  longevity,  
  fecundity,  
  a_init = 2  
)

Arguments

nInterval    a numeric value that represents the number of gnomonic intervals.
eggDuration  a numeric value with the egg stage (first gnomonic interval) duration in days.
addInfo      a numeric vector with additional information related to the observed duration of the other gnomonic intervals different than the first interval (egg stage duration). Write addInfo = NULL if you do not provide additional information.
longevity    a numeric value indicating the lifespan of the species in days.
fecundity    a numeric value indicating the mean lifetime fecundity (MLF) as the number of eggs produced for a female.
a_init       a numeric value indicating the initial parameter related to the proportionality optimized by iterative solution via univariate (1-dim.) minimization. a_init = 2 as default value.

Details

Estimate natural mortality (M) based on gnomonic interval approach.

The argument nInterval is NULL by default. If you have -at least- one observed value for the duration of the other gnomonic intervals you should provide this as a vector which length must be nInterval - 1, for example addInfo = c(3,NA,NA,NA,NA,NA)) for a nInterval = 7.

Value

A list of class 'gnomos'.
a the proportionality constant.
G the constant proportion of the overall natural death rate.
results a dataframe with the duration ("interval_duration_day") and natural mortality ("M_day" and "M_year") for each gnomonic interval.
References


Examples

#The values are based on Caddy (1996).
model <- gnomonic(nInterval = 7, eggDuration = 2, addInfo = NULL,
longevity = 365, fecundity = 200000, a_init = 2)

model
model$a
model$G
model$results

#Additional information for the duration of the second gnomonic intervals.
model <- gnomonic(nInterval = 7, eggDuration = 2, addInfo = c(3, NA, NA, NA, NA, NA),
longevity = 365, fecundity = 200000, a_init = 2)

model
model$a
model$G
model$results

gnomonicStochastic  Gnomonic stochastic

Description

Estimate natural mortality based on gnomonic interval approach with different distribution in fecundity.

Usage

gnomonicStochastic(
  nInterval,
  eggDuration,
  addInfo = NULL,
  longevity,
  fecundity = NULL,
  sd_fecundity = NULL,
  min_fecundity = NULL,
  max_fecundity = NULL,
  distr = "uniform",
  a_init = 2,
  niter = 999,
  seed = 7388
)
Arguments

nInterval a numeric value that represents the number of gnomonic intervals.
eggDuration a numeric value with the egg stage (first gnomonic interval) duration in days.
addInfo a numeric vector with additional information related to the observed duration of
the other gnomonic intervals different than the first interval (egg stage duration).
Write addInfo = NULL if you do not provide additional information.
longevity a numeric value indicating the lifespan of the species in days.
fecundity a numeric value indicating the mean or the mode of the fecundity as the number
of eggs produced for a female if a normal or triangular distribution is assumed,
respectively.

Details

Estimate natural mortality (M) based on gnomonic interval approach.
The argument nInterval is NULL by default. If you have -at least- one observed value for the
duration of the other gnomonic intervals you should provide this as a vector which length must be
nInterval - 1, for example addInfo = c(3,NA,NA,NA,NA,NA)) for a nInterval = 7.
The argument fecundity requires a character string indicating the name of the distribution of fec-
undity values to be used in the analysis (i.e. fecundity = "uniform").
The argument niter requires a number which is related with the number of observations. If
length(n) > 1, the length is taken to be the number required. can be calculated from each boot-
strap sample (median and confidence intervals).

Value

A list of class 'gnomosBoot'.
a the proportionality constant.
G the 'n' iter values of constant proportion of the overall natural death rate.
mean_G the mean of constant proportion of the overall natural death rate,
M a dataframe with the M values for each gnomonic intervals for each 'n' iteration.
fecundity the 'n' iter values of fecundity based on the distribution assumed.
results a dataframe with the duration ("interval_duration_day"), mean, confidence interval and
standard deviation of natural mortality ("M_lower", "M", "M_upper", "M_sd") for each gnomonic
interval.

Examples

#The values are based on Caddy (1996).
modelBoot <- gnomonicStochastic(nInterval = 7, eggDuration = 2, addInfo = NULL, longevity = 365,
distr = "uniform", min_fecundity = 100000, max_fecundity = 300000, niter = 999, a_init = 2)

# 'niter' parameters:
modelBoot$a
modelBoot$G
modelBoot$mean_G
modelBoot$M
modelBoot$fecundity
modelBoot$results

[plot.gnomos]

Plot method for gnomos class

Description

Plot method for gnomos class

Usage

## S3 method for class 'gnomos'
plot(
x,
xlab = "Gnomonic intervals",
ylab = NULL,
bg = "lightgrey",
cex = 1.75,
pch = 21,
dayUnits = TRUE,
...)

Arguments

x an object class 'gnomos'.
xlab a title for the x axis.
ylab a title for the y axis.
bg a background color for the points.
cex character expansion in the regression.
plot.gnomosBoot

### Description

Plot method for gnomosBoot class

### Usage

```r
## S3 method for class 'gnomosBoot'
plot(
  x,
  xlab = "Gnomonic intervals",
  ylab = NULL,
  col = "lightgrey",
  boxwex = 0.25,
  dayUnits = TRUE,
  ...
)
```

### Arguments

- **x**: an object class 'gnomosBoot'.
- **xlab**: a title for the x axis.
- **ylab**: a title for the y axis.
- **col**: color for the boxplot of M value for each gnomonic intervals.
- **boxwex**: a scale factor to be applied to all boxes in order to make the boxes narrower or wider.
- **dayUnits**: TRUE by default, to show the M values in 1/day unit. FALSE to show the M values in 1/year units.
- **...**: Additional arguments to the plot method.

### Examples

```r
model <- gnomonics(nInterval = 7, eggDuration = 2, addInfo = NULL,
longevity = 365, fecundity = 200000, a_init = 2)

plot(model)
```
Examples

```r
modelBoot <- gnomonicStochastic(nInterval = 7, eggDuration = 2, addInfo = NULL, longevity = 365,
                                   distr = "uniform", min_fecundity = 100000, max_fecundity = 300000, niter = 1000, a_init = 2)

plot(modelBoot)
```

## Description

Print method for gnomos class

### Usage

```r
## S3 method for class 'gnomos'
print(x, ...)
```

### Arguments

- `x`: an object class ‘gnomos’.
- `...`: Additional arguments to the print method.

### Value

The values of the proportionality constant (a), constant proportion of the overall natural death rate (G) and a data.frame with the duration and natural mortality for each gnomonic interval.

```r
model <- gnomonic(nInterval = 7, eggDuration = 2, addInfo = NULL, longevity = 365,
                   fecundity = 200000, a_init = 2)

print(model)
```

## Description

Print method for gnomosBoot class

### Usage

```r
## S3 method for class 'gnomosBoot'
print(x, ...)
```
Arguments

- `x`: an object class 'gnomosBoot'.
- `...`: Additional arguments to the print method.

Value

The values of the proportionality constant (a), constant proportion of the overall natural death rate (G) and a data.frame with the duration and natural mortality for each gnomonic interval.

Examples

```r
# The values are based on Caddy (1996).
modelBoot <- gnomonicStochastic(nInterval = 7, eggDuration = 2, addInfo = NULL, longevity = 365, distr = "uniform", min_fecundity = 100000, max_fecundity = 300000, niter = 50, a_init = 2)

print(modelBoot)
```
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