

Package ‘gnomonicM’

May 8, 2026

Type Package

Title Estimate Natural Mortality for Different Life Stages

Version 1.0.1

Date 2021-02-15

Maintainer Josymar Torrejon-Magallanes <ejosymart@gmail.com>

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](https://doi.org/10.1051/alr:1996023)> and Martinez-Aguilar et al. (2005) <[doi:10.1016/j.fishres.2004.04.008](https://doi.org/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.

Depends R (>= 3.6)

Imports minqa, triangle, grDevices, graphics, stats, utils, kableExtra

Suggests rmarkdown, knitr

VignetteBuilder knitr

License GPL-2

LazyData TRUE

Encoding UTF-8

RoxygenNote 7.1.1

NeedsCompilation no

Author Josymar Torrejon-Magallanes [cre, aut]

Repository CRAN

Date/Publication 2021-02-16 22:20:02 UTC

Contents

gnomonicM-package	2
gnomonic	4
gnomonicStochastic	5
plot.gnomos	7

plot.gnomosBoot	8
print.gnomos	9
print.gnomosBoot	9

Index	11
--------------	-----------

gnomonicM-package	<i>Estimate Natural Mortality for Different Life Stages.</i>
-------------------	--

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 Δ_i requires -at least- information about: (i) the number of development stages throughout the life cycle i in $1, 2, 3, \dots n$. (ii) the duration of the first life stage corresponding to first gnomonic interval (Δ_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 Δ_i representing the number of gnomonic intervals from i in $1, 2, 3, \dots n$, 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 Δ_i . The N_i is the survivors from previous interval, only for the first interval (Δ_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 Δ_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,

Δ_i : Duration of the gnomonic interval when $i > 1$.

Δ_1 : Duration of the first gnomonic interval t_1 .

α : Proportionality constant.

i : i^{th} 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; Martinez-Aguilar, 2005). The new equation for G is expressed:

$$G = -\ln\left(\left(\frac{2}{MLF}\right)^{\frac{1}{n}}\right)$$

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

Author(s)

Josymar Torrejon-Magallanes <ejosymart@gmail.com>

References

Caddy JF (1991). Death rates and time intervals: is there an alternative to the constant natural mortality axiom? *Rev Fish Biol Fish* 1:109–138. doi:10.1007/BF00157581.

Caddy JF (1996). Modelling natural mortality with age in short-lived invertebrate populations: definition of a strategy of gnomonic time division. *Aquat Living Resour* 9:197–207. doi:10.1051/alr:1996023.

Martínez-Aguilar S, Arreguín-Sánchez F, Morales-Bojórquez E (2005). Natural mortality and life history stage duration of Pacific sardine (*Sardinops caeruleus*) based on gnomonic time divisions. *Fish Res* 71:103–114. doi:10.1016/j.fishres.2004.04.008.

Examples

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

gnomonic

*Gnomonic deterministic***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

Caddy JF (1996). Modelling natural mortality with age in short-lived invertebrate populations: definition of a strategy of gnomonic time division. *Aquat Living Resour* 9:197–207. doi: 10.1051/alr:1996023.

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.
sd_fecundity	a numeric value indicating the standard deviation of fecundity if a normal distribution is assumed.
min_fecundity	a numeric value indicating the minimum range of fecundity if a uniform or triangle distribution is assumed.
max_fecundity	a numeric value indicating the maximum range of fecundity if a uniform or triangle distribution is assumed.
distr	a character string indicating the distribution to be applied: "uniform", "triangle" or "normal"
a_init	a numeric value indicating the initial parameter related to the proportionality constant optimized by iterative solution via univariate (1-dim.) minimization. a_init = 2 as default value.
niter	a single numeric value representing the number of iterations.
seed	a single value, interpreted as an integer.

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)) for a nInterval = 7.

The argument fecundity requires a character string indicating the name of the distribution of fecundity 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 bootstrap 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.

pch	the character indicating the type of plotting.
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

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

plot(model)
```

plot.gnomosBoot	<i>Plot method for gnomosBoot class</i>
-----------------	---

Description

Plot method for gnomosBoot class

Usage

```
## 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

```
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)
```

print.gnomos	<i>Print method for gnomos class</i>
--------------	--------------------------------------

Description

Print method for gnomos class

Usage

```
## 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. #' @examples model <- gnomonic(nInterval = 7, eggDuration = 2, addInfo = NULL, longevity = 365, fecundity = 200000, a_init = 2)

```
print(model)
```

print.gnomosBoot	<i>Print method for gnomosBoot class</i>
------------------	--

Description

Print method for gnomosBoot class

Usage

```
## 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

```
#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)
```

Index

- * **fecundity**
 - gnomonicM-package, [2](#)
- * **gnomonic**
 - gnomonicM-package, [2](#)
- * **lifespan**
 - gnomonicM-package, [2](#)
- * **natural mortality**
 - gnomonicM-package, [2](#)

- gnomonic, [4](#)
- gnomonicM (gnomonicM-package), [2](#)
- gnomonicM-package, [2](#)
- gnomonicStochastic, [5](#)

- plot.gnomos, [7](#)
- plot.gnomosBoot, [8](#)
- print.gnomos, [9](#)
- print.gnomosBoot, [9](#)