Package 'IncAAM'

November 12, 2026

Type Package

Title Bayesian Age-at-Maturity Analysis from Increment-Width Growth Series

Version 1.9

Description Bayesian hierarchical nonlinear mixed-effects analysis for estimating age at sexual maturity from annual increment-width growth series. The method estimates age at maturity using tangent-ratio and jerk approaches, including the hierarchical population-median tangent-ratio estimate and an analytical posterior crossing ogive with Bayesian credible intervals and estimated A50. Methodological details and applications are described in Campana, Smoliński, Morrongiello and Black (2027, in press).

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.3

Imports dplyr, purrr, tibble, ggplot2, posterior, minpack.lm, brms

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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Depends R (>= 4.1.0)

LazyData true

Repository CRAN

Date/Publication 2026-11-12 17:50:08 UTC

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`IncAAM` *IncAAM (Version 1.9): Bayesian age-at-maturity analysis from increment-width growth series*

Description

Fits a Bayesian hierarchical nonlinear mixed-effects model to annual increment-width data and estimates age at maturity using posterior threshold-ratio (TR) and jerk approaches. The model uses a negative exponential curve with fish-level varying parameters.

Usage

```
IncAAM(
  data,
  FishID = "FishID",
  Inc_num = "Inc_num",
  Inc_width = "Inc_width_mm",
  sex = "female",
  female_threshold = 0.16,
  male_threshold = 0.25,
  custom_threshold = NULL,
  known_A50 = NULL,
  min_Inc_num = 2,
  min_increments = 3,
  min_fish = 3,
  min_max_incnum = NULL,
  max_incnum_fit = Inf,
  jerk_step = 0.01,
  chains = 4,
  cores = 4,
  n_iter = 1500,
  n_warmup = 750,
  n_keepdraws = 500,
  seed = 123,
  backend = "cmdstanr",
  n_adapt_delta = 0.995,
  n_logc_sd = 0.1,
  max_treedepth = 15,
  make_plots = TRUE,
  save_plots = FALSE,
  output_dir = NULL
)
```

Arguments

data	A data frame containing annual increment-width measurements, with one row per increment width. Data should be filtered to the desired analysis group before calling IncAAM().
FishID	Character string giving the column name identifying individual fish.
Inc_num	Character string giving the column name containing increment number (used as the age-like predictor).
Inc_width	Character string giving the column name containing increment width.
sex	Character string selecting the sex-specific TR threshold: "female", "male", or "custom". When "custom" is selected, the value supplied to custom_threshold is used.
female_threshold	Numeric TR threshold used when sex = "female". Default is 0.16.
male_threshold	Numeric TR threshold used when sex = "male". Default is 0.25.
custom_threshold	Numeric TR threshold used when sex = "custom".
known_A50	Optional numeric value giving a known or published A50 to display as a reference in plots.
min_Inc_num	Minimum increment number retained for analysis. Default is 2.
min_increments	Minimum number of increment observations required per fish. Default is 3.
min_fish	Minimum number of fish required for the hierarchical model. Default is 3.
min_max_incnum	Optional minimum ORIGINAL maximum observed increment number needed to retain a fish, evaluated before fitting truncation. NULL (default) retains the version 1.8 selection rule.
max_incnum_fit	Maximum increment number used to fit each fish's exponential curve. Default Inf uses every eligible increment. A finite integer cap truncates increment records, NOT original fish ages. The original maximum remains available for threshold-reach diagnostics and observed increment-level probabilities. min_increments is applied AFTER the fitting cap; use min_increments = 1 to include fish with one increment within the cap (these rely heavily on partial pooling).
jerk_step	Step size used when numerically locating the jerk maximum. Default is 0.01.
chains	Number of MCMC chains. Default is 4.
cores	Number of CPU cores used for model fitting. Default is 4.
n_iter	Total number of MCMC iterations per chain. Default is 1500.
n_warmup	Number of warm-up iterations per chain. Default is 750.
n_keepdraws	Number of posterior draws retained for fish-level diagnostics and hierarchical reference-curve Jerk. Hierarchical median TR and ogive probabilities always use ALL post-warmup MCMC draws.
seed	Random-number seed. Default is 123.
backend	Backend passed to brms::brm(). Default is "cmdstanr".
n_adapt_delta	Target acceptance probability for Stan adaptation. Default is 0.995.

n_logc_sd	Prior standard deviation for the fish-level random effect of logc. Default is 0.1.
max_treedepth	Maximum NUTS tree depth. Default is 15.
make_plots	Logical; if TRUE, create the posterior distribution and threshold-crossing ogive plots. Default is TRUE.
save_plots	Logical; if TRUE, save generated plots as PDF files. Default is FALSE.
output_dir	Directory used when save_plots = TRUE. Must be supplied by the user when plots are to be saved. Default is NULL.

Details

The input data should represent one analysis group. IncAAM() does not perform grouping by species, sex, axis, stock, or other variables; users should filter the data before calling the function.

The model describes increment width using a negative exponential function,

$$Increment = a + bexp(-cInc_num),$$

with fish-level varying parameters a, b, and c. The parameters are estimated in log space in a Bayesian hierarchical model using brms.

Individual fish TR is calculated analytically from every selected fish-level posterior draw of c, without censoring at the last observed increment. The primary group-level estimator is the **hierarchical population median TR**, calculated for every post-warmup draw from the population intercept of log(c). Its uncertainty is a 95% Bayesian credible interval across these full posterior draws, not an SE across fish. Jerk remains the numerically calculated index; its group-level value is the jerk of the **hierarchical reference growth curve**, not a population median jerk.

The threshold-crossing ogive is computed analytically from the joint posterior of the population log(c) intercept and between-fish SD. The ogive displays posterior-median crossing probability and 90% Bayesian credible shading; both 90% and 95% credible limits are included in tables. The ogive A50 equals the hierarchical median TR with its own posterior 95% credible interval. No logistic regression is fitted. TR_reached_prob is a diagnostic probability of crossing by the LAST originally observed increment, not a criterion for excluding posterior TR. The TR threshold must be strictly between 0 and 1.

The TR index estimates the age at 50% maturity when the selected TR threshold has been calibrated to that criterion. The jerk index indicates the age of maximum jerk and is not currently assigned to a defined proportion or stage of sexual maturity.

Details of the model, method, outputs and applications are provided in Campana, Smoliński, Morrongiello and Black (2027, in press). Users should consult this publication for the methodological background and interpretation of IncAAM outputs.

The function returns the fitted Bayesian model together with fish-level estimates, increment-level threshold-crossing probabilities, posterior group distributions, ogive results, fitted curves, diagnostics, settings, and optional plots.

Value

An object of class IncAAM (a list) containing:

summary Hierarchical population median TR and reference-curve jerk, with 95% credible intervals; excludes redundant p5, p95, n_posterior_draws and note columns.

fish Diagnostic fish-level posterior summaries of model parameters, uncensored TR, and Jerk.

increment Fish- and increment-level posterior threshold-crossing probabilities.

posterior Posterior draws of hierarchical population median TR and reference-curve jerk.

crossing_ogive Analytical hierarchical crossing probability and credible intervals at observed increment numbers.

crossing_ogive_prediction Analytical hierarchical crossing probabilities and credible intervals over a fine age grid.

ogive_summary Hierarchical ogive A50, its 95% credible interval, and model metadata.

ogive_plot Threshold-crossing ogive plot, when plots are enabled.

fitted_curves Fish-level fitted negative-exponential curves.

model The fitted `brms` model object.

diagnostics MCMC and sampling diagnostics.

settings Analysis settings used by the function.

data Basic information on the analyzed data, including original maximum increment numbers.

plot Posterior TR/Jerk density plot, when plots are enabled.

Examples

```
## Not run:
# Example based on the current IncAAM test workflow:
library(IncAAM)
library(dplyr)

data(plaice)
head(plaice)
plaice_female <- plaice |>
dplyr::filter(Sex == "female")

fit <- IncAAM(
  data = plaice_female,
  FishID = "FishID",
  Inc_num = "Inc_num",
  Inc_width = "Inc_width_mm",
  sex = "female",
  known_A50 = 7.6,
  n_iter = 1500,
  n_warmup = 750,
  n_keepdraws = 500,
  n_adapt_delta = 0.995,
  n_logc_sd = 0.1
)

#Users can display the complete set of model outputs with `print(fit)`,
#or inspect individual output components directly (e.g. `fit$summary`).

print(fit)

fit$summary
```

```
fit$crossing_ogive
fit$ogive_summary

## End(Not run)
```

`plaice` *Example plaice otolith increment data*

Description

A small example dataset containing otolith increment-width measurements from 28 plaice (*Pleuronectes platessa*) of both sexes. The dataset is provided for demonstrating the IncAAM workflow, including data filtering, preparation, and age-at-maturity modelling.

Usage

```
data(plaice)
```

Format

A data frame with 347 rows and 7 variables:

Species Species name.

FishID Unique fish identifier.

Sex Sex of the fish (`male` or `female`).

Axis Otolith axis used for increment measurements (`section`).

Inc_num Sequential increment number.

Inc_width_mm Width of the otolith increment in millimetres.

Fishlen_cm Fish length in centimetres.

Details

The dataset contains complete increment-width series for 28 individual fish and is intentionally composed of both males and females. In the example workflow, the data are first loaded with `data(plaice)` and subsequently filtered to retain female fish before fitting the age-at-maturity model.

Source

Example data prepared for the IncAAM package.

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