

Package ‘lhmixr’

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Title Fit Sex-Specific Life History Models with Missing Classifications

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Description Fits sex-specific life-history models for fish and other taxa where some of the individuals have unknown sex.

Depends R (>= 3.2.0)

License GPL (>= 3)

URL <https://github.com/mintoc/lhmixr>

BugReports <https://github.com/mintoc/lhmixr/issues>

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Epusillus	<i>Etmopterus pusillus data</i>
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Description

Growth data for deepwater smooth lantern shark *Etmopterus pusillus* from Coelho and Erzini (2007). Data are cross-sectional with one observation (row) per individual.

Usage

Epusillus

Format

A data frame with five variables:

species Full species name

sex Sex of the animal: Female (F) or Male (M)

age Age in years

length Total length in centimetres

maturity Maturation status: immature or mature

Source

Coelho, R. and Erzini, K. (2007). Population parameters of the smooth lantern shark, *Etmopterus pusillus*, in southern Portugal (NE Atlantic). *Fisheries Research*, 86, 42–57.

Espinax	<i>Etmopterus spinax data</i>
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Description

Growth data for deepwater velvet belly lantern shark *Etmopterus spinax* from Coelho and Erzini (2008). Data are cross-sectional with one observation (row) per individual.

Usage

Espinax

Format

A data frame with five variables:

species Full species name

sex Sex of the animal: Female (F) or Male (M)

age Age in years

length Total length in centimetres

maturity Maturation status: immature or mature

Source

Coelho, R. and Erzini, K. (2008). Life history of a wide-ranging deepwater lantern shark in the north-east Atlantic, *Etmopterus spinax* (Chondrichthyes: Etmopteridae), with implications for conservation. *Journal of Fish Biology*, 73, 1419–1443.

get_growth_post_prob *Posterior probability of sex being female based on growth*

Description

get_growth_post_prob returns the probability of the observation(s) arising from the female component given a set of growth parameters and an assumed distribution (normal or lognormal). The component probability is given by Bayes' theorem. Used internally.

Usage

```
get_growth_post_prob(mixprop, muF, muM, sigmaF, sigmaM, data, distribution)
```

Arguments

mixprop	Numeric scalar of mixing proportion (overall sex ratio)
muF	Numeric vector with predicted female lengths
muM	Numeric vector with predicted male lengths
sigmaF	Numeric scalar for female residual standard deviation
sigmaM	Numeric scalar for male residual standard deviation
data	A data.frame with column "length". Note predicted means "muF" and "muM" must come from corresponding ages.
distribution	Character with options: "normal" or "lognormal".

Value

Numeric vector of the posterior probability of being female.

Source

Minto, C., Hinde, J. and Coelho, R. (2017). Including unsexed individuals in sex-specific growth models. *Canadian Journal of Fisheries and Aquatic Sciences*. DOI: 10.1139/cjfas-2016-0450.

Examples

```
get_growth_post_prob(mixprop = 0.5, muF = 4, muM = 6, sigmaF = 1,
                     sigmaM = 1, data = data.frame(length = 4.5), distribution = "normal")
```

sim_vb_data	<i>Simulate sex-specific von Bertalanffy data with missing classifications.</i>
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Description

sim_vb_data simulates sex-specific growth data according to the von Bertalanffy growth model and a logistic model governing maturity.

Usage

```
sim_vb_data(nfemale, nmale, mean_ageF, mean_ageM, growth_parF, growth_parM,
            mat_parF, mat_parM, distribution)
```

Arguments

nfemale	Numeric scalar for number of female observations.
nmale	Numeric scalar for number of male observations.
mean_ageF	Numeric scalar for female mean age - used to generate ages from <code>rnbinom(, mu = mean_ageF)</code>
mean_ageM	Numeric scalar for male mean age - used to generate ages from <code>rnbinom(, mu = mean_ageM)</code>
growth_parF	Named ("linf", "k", "t0", "sigma") numeric vector with female growth parameters
growth_parM	Named ("linf", "k", "t0", "sigma") numeric vector with male growth parameters
mat_parF	Named ("A50", "MR") numeric vector with female maturation parameters A50 is the age at 50% maturity, MR is age range between 25% and 75% mature.
mat_parM	Named ("A50", "MR") numeric vector with male maturation parameters.
distribution	Character with options: "normal" or "lognormal" for simulated length-at-age distributon.

Value

data.frame with columns "age", "length", "true.sex", "obs.sex" (observed sex assuming immature animals are unclassified), "maturity" (binary: 1 if mature; 0 if immature).

Examples

```
sim.dat <- sim_vb_data(nfemale = 30, nmale = 30, mean_ageF = 3, mean_ageM = 3,
  growth_parF = c(linf = 30, k = 0.2, t0 = -1, sigma = 0.1),
  growth_parM = c(linf = 25, k = 0.2, t0 = -1, sigma = 0.1),
  mat_parF = c(A50 = 3, MR = 1), mat_parM = c(A50 = 2, MR = 1),
  distribution = "lognormal")

plot(jitter(sim.dat$age), sim.dat$length,
  xlim=c(0, max(sim.dat$age)), ylim = c(0, max(sim.dat$length)),
  col = c("red", "blue", "grey")[match(sim.dat$obs.sex, c("female", "male", "unclassified"))],
  pch = 19, xlab = "age", ylab = "Length")
```

vb_bind_gr	<i>Gradient of the negative log-likelihood for potentially constrained von Bertalanffy growth model (typically used internally).</i>
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Description

vb_bind_gr returns the parameter gradients of negative log-likelihood for the von Bertalanffy model. Equality constraints across sexes can be implemented for any combination of parameters using the binding argument.

Usage

```
vb_bind_gr(theta, binding, data, distribution)
```

Arguments

theta	A parameter vector of the same length as the maximum of binding. Unconstrained parameters take the order: lnlinfF, lnlinfM, lnkF, lnkM, lnnt0F, lnnt0M, lnsigmaF, lnsigmaM.
binding	A (4x2) parameter index matrix with rows named (in order): "lnlinf", "lnk", "lnnt0", "lnsigma" and the left column for the female parameter index and right column for male parameter index. Used to impose arbitrary equality constraints across the sexes (see Examples).
data	A data.frame with columns: "age", "length" and "weights". "weights" are set to 1 or 0 for known females or males, respectively; proportions otherwise.
distribution	Character with options: "normal" or "lognormal".

Value

Vector of parameter gradients:

Examples

```
## Unconstrained model
binding <- matrix(c(1:8), ncol = 2, byrow = TRUE)
rownames(binding) <- c("lnlnf", "lnk", "lnnt0", "lnsigma")
colnames(binding) <- c("female", "male")
## starting values
start.par <- c(rep(log(25), 2), rep(log(0.2), 2), rep(log(3), 2), rep(log(1), 2))
vb_bind_gr(theta = start.par, binding = binding,
            data = data.frame(age = rep(1, 2), length = rep(10, 2), weights = c(1, 0)),
            distribution = "lognormal")
```

vb_bind_nll	<i>Negative log-likelihood for potentially constrained von Bertalanffy growth model (typically used internally).</i>
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Description

vb_bind_nll returns the negative log-likelihood for the von Bertalanffy model. Equality constraints across sexes can be implemented for any combination of parameters using the binding argument.

Usage

```
vb_bind_nll(theta, binding, data, distribution)
```

Arguments

theta	A parameter vector of the same length as the maximum of binding. Unconstrained parameters take the order: lnlnfF, lnlnfM, lnkF, lnkM, lnnt0F, lnnt0M, lnsigmaF, lnsigmaM.
binding	A (4x2) parameter index matrix with rows named (in order): "lnlnf", "lnk", "lnnt0", "lnsigma" and the left column for the female parameter index and right column for male parameter index. Used to impose arbitrary equality constraints across the sexes (see Examples).
data	data.frame with columns: "age", "length" and "weights". "weights" are set to 1 or 0 for known females or males, respectively; proportions otherwise.
distribution	Character with options: "normal" or "lognormal"

Value

Complete data negative log-likelihood:

Examples

```
## Unconstrained model
binding <- matrix(c(1:8), ncol = 2, byrow = TRUE)
rownames(binding) <- c("lnlinf", "lnk", "lnnt0", "lnsigma")
colnames(binding) <- c("female", "male")
## starting values
start.par <- c(rep(log(25), 2), rep(log(0.2), 2), rep(log(3), 2), rep(log(1), 2))
vb_bind_nll(theta = start.par, binding = binding,
             data = data.frame(age = rep(1, 2), length = rep(10, 2), weights = c(1, 0)),
             distribution = "normal")
```

vb_growth_mix

Fit finite mixture von Bertalanffy growth model.

Description

vb_growth_mix fits sex-specific growth models where some of the animals are of unknown sex. Optimisation is via the Expectation-Maximisation algorithm. Equality constraints across sexes can be implemented for any combination of parameters using the binding argument.

Usage

```
vb_growth_mix(start.list, data, binding, maxiter.em = 1000, reltol = 1e-08,
              plot.fit = FALSE, verbose = TRUE, optim.method = "BFGS",
              estimate.mixprop = TRUE, distribution)
```

Arguments

start.list	A list with a list called par containing starting values for: "mixprop", "growth.par" (see Examples).
data	A data.frame with columns: "age", "length" and "obs.sex". "obs.sex" must have values "female", "male", "unclassified".
binding	A (4x2) parameter index matrix with rows named (in order): "lnlinf", "lnk", "lnnt0", "lnsigma" and the left column for the female parameter index and right column for male parameter index. Used to impose arbitrary equality constraints across the sexes (see Examples).
maxiter.em	Integer for maximum number of EM iterations (1e3 default).
reltol	Relative tolerance for EM observed data log likelihood convergence (1e-8 default).
plot.fit	Logical, if TRUE fit plotted per iteration. Red and blue circles are used for known females and males, respectively. Unclassified animals are plotted as triangle with the colour indicating the expected probability of being female or male (FALSE default).
verbose	Logical, if TRUE iteration and observed data log-likelihood printed.
optim.method	Character, complete data optimisation method to use in optim.

`estimate.mixprop` Logical, if TRUE the mixing proportion is estimated, otherwise fixed at the starting value.

`distribution` Character with options: "normal" or "lognormal".

Value

List containing the components:

`logLik.vec` Observed data log-likelihood at each iteration.

`logLik` Observed data log-likelihood on the last EM iteration.

`complete_data` Data frame of the data (re-ordered) with component probabilities (tau).

`coefficients` Parameter estimates (on the real line) and associated standard errors on the real line.

`vcov` Estimated variance covariance matrix of the parameters estimated on the real line. Can be used to obtain parameter standard errors on the natural scale.

`convergence` Binary with a "0" denoting convergence of the EM algorithm.

Source

Minto, C., Hinde, J. and Coelho, R. (2017). Including unsexed individuals in sex-specific growth models. *Canadian Journal of Fisheries and Aquatic Sciences*. DOI: 10.1139/cjfas-2016-0450.

Examples

```
set.seed(1010)
sim.dat <- sim_vb_data(nfemale = 50, nmale = 50, mean_ageF = 4, mean_ageM = 4,
  growth_parF = c(linf = 30, k = 0.5, t0 = -1, sigma = 0.1),
  growth_parM = c(linf = 25, k = 0.5, t0 = -1, sigma = 0.1),
  mat_parF = c(A50 = 5, MR = 2), mat_parM = c(A50 = 3, MR = 2),
  distribution = "lognormal")

## Model fit with constrained Brody's growth coefficient
## Set up the constraint
binding <- matrix(c(1:2, rep(3, 2), 4:7), ncol = 2, byrow = TRUE)
rownames(binding) <- c("lnlinf", "lnk", "lnnt0", "lnsigma")
colnames(binding) <- c("female", "male")
## note: lnnt0 is the natural logarithm of the negative of t0 (t0 < 0)
## starting values
start.par <- c(c(log(30), log(25)), rep(log(0.3), 1), rep(log(1), 2), rep(log(.1), 2))
start.list <- list(par = list(mixprop = 0.5, growth.par = start.par))
vb.bind.fit <- vb_growth_mix(data = sim.dat, start.list = start.list,
  binding = binding, distribution = "lognormal",
  reltol = 1e-6)
```

vb_lengths	<i>von Bertalanffy growth function.</i>
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Description

vb_lengths returns the predicted length-at-age for given named set of parameters for the von Bertalanffy growth function:

$$l = L_{\infty}(1 - e^{-k(a-t_0)})$$

Usage

```
vb_lengths(theta, age)
```

Arguments

theta	A numeric vector with named values "linf", "k", "t0".
age	A numeric vector of ages.

Value

Predicted length-at-age.

Examples

```
vb_lengths(theta = c("linf" = 30, "k" = 0.2, "t0" = -1), age = 0:10)
```

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