Package ‘sizeMat’

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Title Estimate Size at Sexual Maturity

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Description Estimate morphometric and gonadal size at sexual maturity for organisms, usually fish and invertebrates. It includes methods for classification based on relative growth (using principal components analysis, hierarchical clustering, discriminant analysis), logistic regression (Frequentist or Bayes), parameters estimation and some basic plots. Optional ggplot-style graphics are available for selected plot methods.

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`classify_mature` *Classify mature*

Description

Classify the individuals in two groups (0: juveniles, 1: adults) based on relative growth.

Usage

```
classify_mature(
  data,
  varNames = c("x", "y"),
  varSex = "sex",
  selectSex = NULL,
  method = "ld"
)
```

Arguments

`data`	data.frame with allometric variables and sex category (male, female). If sex category contains NA's, that row will be filtered.
`varNames`	the name of two allometric variables to be used for analysis.
`varSex`	the name of the variable containing sex information.
`selectSex`	sex category to be used for analysis. If `selectSex = NULL` all the individuals will be used in the analysis.
`method`	a character string indicating the discriminant analysis method, linear discriminant analysis `"ld"`, quadratic discriminant analysis `"qd"`. We suggest begin the analysis using the `method = "ld"`.

Details

Classify the individuals in two groups (juveniles = 0 and adult = 1).

A Principal Components Analysis was conducted with two allometric variables (x: independent variable, y: dependent variable) in log base, allowing to distinguish two groups that would represent juveniles and adult. The individuals are assigned to each group using a hierarchical classification procedure (hierarchical cluster with agglomeration method: "Ward.D" and the distance measure:

"euclidean"). This method is based on establishing a predetermined number of groups (in this case, two) and assigning individuals to one of the groups according to their loads on the two axes of the PCA (Corgos and Freire, 2006).

Using the results of the classification (PCA + cluster), a discriminant analysis (linear or quadratic) is conducted to obtain a discriminating function that permitted any individuals to be classified as a juvenile or an adult on the basis of the X and Y allometric variables.

Value

A data.frame of class 'classify', with x (independent), y (dependent) and classification of maturity (juveniles = 0, adult = 1) variables.

Examples

```
data(crabdata)

classify_data = classify_mature(crabdata, varNames = c("carapace_width", "chela_height"),
varSex = "sex_category", selectSex = NULL, method = "ld")

classify_data
```

`Crab data` *Crab data*

Description

A database containing allometric measures and other attributes of 223 crabs of the specie $Chionectes$ $tanneri$. The variables carapace width and chela height were published in Somerton & Donaldson (1996).

Usage

```
data(crabdata)
```

Format

A data frame with different variables:

`year`

`month`

`carapace_width` (mm.)

`carapace_length` (mm.)

`chela_height` (mm.)

`chela_width` (mm.)

`sex_category` (m: male, f: female).

Source

Somerton, D. A., & Donaldson, W. (1996). Contribution of the biology of the grooved and triangle Tanner crabs, Chionectes tanneri and C. angulatus, in the eastern Bering Sea. Fishery Bulletin, 94(2), 348-357.

References

Watters, G., & Hobday, A. J. (1998). A new method for estimating the morphometric size at maturity of crabs. Canadian Journal of Fisheries and Aquatic Sciences, 55(3), 704-714.

`Fish maturity` *Fish gonadal maturity data*

Description

A data set containing the total length and the stages of sexual maturity of 1733 fishes.

Usage

```
data(matFish)
```

Format

A data frame with two variables:

`total_length` the total length in cm.

`stage_mat` the stages of sexual maturity (gonadal maturation stages, I: immature, II-III-IV: mature)

`gonad_mature` *Estimate gonadal maturity*

Description

Estimate size at gonad maturity.

Usage

```
gonad_mature(
  data,
  varNames = c("allometric", "stage"),
  immName = "imm",
  matName = "mad",
  method = "fq",
  niter = 999,
  seed = 70388
)
```

Arguments

`data`	data.frame with allometric variables and stage of sexual maturity (gonad maturation stages).
`varNames`	a character string indicating the name of the allometric and the stage of sexual maturity variables to be used for analysis.
`immName`	a character string indicating the name or names of the immaturity stage.
`matName`	a character string indicating the name or names of the maturity stage.
`method`	a character string indicating the method to be applied, `"fq"` frequentist GLM, or `"bayes"` Bayes GLM (MCMClogit function).
`niter`	number of iterations (bootstrap resampling).
`seed`	a single value, interpreted as an integer.

Details

Estimate the size at gonad maturity using a logistic regression with X variable and stages of sexual maturity (two categories: immature and mature).

The function requires a data.frame with the X (allometric variable) and the stage of sexual maturity (gonad maturation stage).

The argument `varNames` requires a character string indicating the name of one allometric and the stage of sexual maturity variable to be used for analysis (i.e. `varNames = c("total_length", "stage_mat")`). So the argument `varNames` must contain two character strings only, the first is the allometric variable and the second is the stage of sexual maturity.

The arguments `immName` and `matName` require a character string indicating the name of the stages of sexual maturity in the data.frame. The argument could contain one character string or should be a vector (i.e. `immName = "I"`, `matName = c("II", "III", "IV")`).

The argument `method` requires a character string indicating which regression will be used for the test. If `method = "fq"` the logistic regression is based on GLM (frequentist), if `method = "bayes"` a sample from the posterior distribution of a logistic regression model using a random walk Metropolis algorithm is generated (see MCMClogit function).

The argument `niter` requires a number. For the GLM regression (`method = "fq"`), a non-parametric bootstrap method consists in generate B bootstrap samples, by resampling with replacement the original data. Then all statistics for each parameter can be calculated from each bootstrap sample (median and confidence intervals). For the `method = "bayes"`, the argument `niter` is related to the number of Metropolis iterations for the sampler.

Value

An object of class 'gonadMat'.

`model` the summary statistics of the model.

`A_boot` the 'n iter' values of parameter A.

`B_boot` the 'n iter' values of parameter B.

`L50` the 'n iter' values of parameter L50 (size at gonad maturity).

`out` a dataframe with the allometric variable "X", stage of sexual maturity, the fitted values for logistic regression and confidence intervals (95%). Also the summary statistics of the model is provided.

Examples

```
data(matFish)

gonad_mat = gonad_mature(matFish, varNames = c("total_length", "stage_mat"), immName = "I",
matName = c("II", "III", "IV"), method = "fq", niter = 50)

# 'niter' parameters:
gonad_mat$A_boot
gonad_mat$B_boot
gonad_mat$L50_boot
gonad_mat$out
```

`morph_mature` *Estimate morphometric mature*

Description

Estimate size at morphometric maturity.

Usage

```
morph_mature(data, method = "fq", niter = 999, seed = 70388)
```

Arguments

`data`	an object of class 'classify' with the allometric variables ("X", "Y") and classification of maturity (juveniles = 0, adults = 1).
`method`	a character string indicating the method to be applied, `"fq"` frequentist GLM, or `"bayes"` Bayes GLM (MCMClogit function).
`niter`	number of iterations (bootstrap resampling).
`seed`	a single value, interpreted as an integer.

Details

Estimate the size at morphometric maturity using a logistic regression with X variable and maturity classification (two categories: juveniles and adults).

The function requires an object of class "classify" with the X, Y (allometric variables) and classification of maturity (juveniles = 0, adults = 1).

The argument `method` requires a character string indicating which regression will be used for the test. If `method = "fq"` the logistic regression is based on GLM (frequentist) and if `method = "bayes"` a sample from the posterior distribution of a logistic regression model using a random walk Metropolis algorithm is generated (see MCMClogit function).

The argument `niter` requires a number. For the GLM regression (`method = "fq"`), a non-parametric bootstrap method consists in generate B bootstrap samples, by resampling with replacement the original data. Then all statistics for each parameter can be calculated from each bootstrap sample (median and confidence intervals). For the `method = "bayes"`, the argument 'niter' is related to the number of Metropolis iterations for the sampler.

Value

An object of class 'morphMat'.

`model` the summary statistics of the model.

`A_boot` the 'n iter' values of parameter A.

`B_boot` the 'n iter' values of parameter B.

`L50` the 'n iter' values of parameter L50 (size at morphometric maturity).

`out` a dataframe with the allometric variables "X" and "Y", classification of maturity, the fitted values for logistic regression and confidence intervals (95%). Also the summary statistics of the model is provided.

Examples

```
data(crabdata)

classify_data = classify_mature(crabdata, varNames = c("carapace_width", "chela_height"),
varSex = "sex_category", selectSex = NULL, method = "ld")

my_mature = morph_mature(classify_data, method = "fq", niter = 50)

# 'niter' parameters:
my_mature$A_boot
my_mature$B_boot
my_mature$L50_boot
my_mature$out
```

`nagelkerkeR2` *Nagelkerme method R-square*

Description

Estimate Nagelkerke's R squared from the result of glm(). Evaluate the goodness of fit for logistic regression.

Usage

```
nagelkerkeR2(x)
```

Arguments

`x`	An object of class 'glm'.

Value

Rsquare Nagelkerke's R squared.

Examples

```
set.seed(7388)
n <- 300
x <- rnorm(n)
a <- 1
b <- -2
p <- 1/(1+exp(a+b*x))
y <- factor(ifelse(runif(n) < p, 1, 0), levels = 0:1)
mod1 <- glm(y ~ x, family=binomial)
nagelkerkeR2(mod1)
```

`plot.classify` *Plot method for classify class*

Description

Plot method for classify class

Usage

```
## S3 method for class 'classify'
plot(
  x,
  xlab = "X",
  ylab = "Y",
  col = c(1, 2),
  pch = c(4, 5),
  cex = c(1, 1),
  lty_lines = c(1, 1),
  lwd_lines = c(1, 1),
  legendPlot = TRUE,
  cex_label = 0.8,
  gg_style = FALSE,
  point_alpha = 0.8,
  base_size = 13,
  ...
)
```

Arguments

`x`	an object of class ’classify’ with the allometric variables ("X", "Y") and classification of maturity (juveniles = 0, adults = 1).
`xlab`	title for the x axis.
`ylab`	title for the y axis.
`col`	colors for juveniles and adults group.
`pch`	plotting characters for juveniles and adults.

`cex`	character expansion for points.
`lty_lines`	line types for the regression lines.
`lwd_lines`	line widths for the regression lines.
`legendPlot`	legend in the plot (FALSE or TRUE).
`cex_label`	size of the legend text in base graphics.
`gg_style`	logical. If TRUE, return a ggplot2 object.
`point_alpha`	transparency level of points, used only when gg_style = TRUE.
`base_size`	base font size, used only when gg_style = TRUE.
`...`	additional arguments passed to the base plot method.

Examples

```
data(crabdata)

classify_data = classify_mature(crabdata, varNames = c("carapace_width", "chela_height"),
varSex = "sex_category", selectSex = NULL, method = "ld")

## Showing different plots
plot(classify_data, xlab = "X")

plot(classify_data, xlab = "X", ylab = "Y", col = c(1, 2), pch = c(4, 5), cex = c(1, 3))

plot(classify_data, xlab = "Carapace width (mm.)", ylab = "Y", col = c(1, 2),
pch = c(4, 5), cex = c(1, 3), lwd_lines = c(1, 3))

plot(classify_data, xlab = "Carapace width (mm.)", ylab = "Y", col = c(1, 2),
pch = c(4, 5), cex = c(1, 3), lwd_lines = c(1, 3), main = "Classification")
```

`plot.gonadMat` *Plot method for gonadMat class (size at gonadal maturity)*

Description

Plot method for gonadMat class (size at gonadal maturity)

Usage

```
## S3 method for class 'gonadMat'
plot(
  x,
  xlab = "X",
  ylab = "Proportion mature",
  col = c("blue", "red"),
  lwd = 2,
  lty = 2,
  vline_hist = "black",
```

```
  lwd_hist = 2,
  lty_hist = 2,
  onlyOgive = FALSE,
  showLegend = TRUE,
  legendPosition = "topleft",
  gg_style = FALSE,
  pch = 19,
  cex = 2.5,
  point_alpha = 0.8,
  base_size = 13,
  label_size = 5,
  ...
)
```

Arguments

`x`	object of class 'gonadMat' with mature parameters and fitted values from the logistic regression.
`xlab`	title for the x axis.
`ylab`	title for the y axis.
`col`	colors for the logistic curve and the L50 reference lines.
`lwd`	line width for fitted values and confidence intervals.
`lty`	line type for fitted values and confidence intervals.
`vline_hist`	color of the vertical lines in the histograms.
`lwd_hist`	line width for vertical lines in the histograms.
`lty_hist`	line type for vertical lines in the histograms.
`onlyOgive`	logical. If TRUE, plot only the maturity ogive.
`showLegend`	logical. If TRUE, show L50 and R2 labels.
`legendPosition`	position of the legend in base graphics and ggplot2 style. Options are "topleft", "topright", "bottomleft", and "bottomright".
`gg_style`	logical. If TRUE, return ggplot2-style plots.
`pch`	plotting character for observed maturity proportions.
`cex`	point size in base graphics and ggplot2 style.
`point_alpha`	transparency level for points, used only when gg_style = TRUE.
`base_size`	base font size, used only when gg_style = TRUE.
`label_size`	size of L50 and R2 labels, used only when gg_style = TRUE.
`...`	additional arguments passed to base graphics.

Examples

```
data(matFish)

gonad_mat = gonad_mature(matFish, varNames = c("total_length", "stage_mat"), immName = "I",
matName = c("II", "III", "IV"), method = "fq", niter = 50)

plot(gonad_mat, xlab = "Total length (cm.)", ylab = "Proportion mature", col = c("blue", "red"))
```

`plot.morphMat` *Plot method for morphMat class (size at morphometric maturity)*

Description

Plot method for morphMat class (size at morphometric maturity)

Usage

```
## S3 method for class 'morphMat'
plot(
  x,
  xlab = "X",
  ylab = "Proportion mature",
  col = c("blue", "red"),
  lwd = 2,
  lty = 2,
  vline_hist = "black",
  lwd_hist = 2,
  lty_hist = 2,
  onlyOgive = FALSE,
  gg_style = FALSE,
  point_alpha = 0.8,
  base_size = 13,
  label_size = 5,
  ...
)
```

Arguments

`x`	object of class 'morphMat' with the mature parameters and a data.frame with the allometric variables ("X", "Y") and classification of maturity. Also the fitted values for the logistic regression and confidence intervals (95%).
`xlab`	a title for the x axis.
`ylab`	a title for the y axis.
`col`	color for the logistic curve and for the L50% size at morphometric maturity.
`lwd`	line width for drawing fitted values and confidence intervals.
`lty`	line type for drawing fitted values and confidence intervals.
`vline_hist`	color of the vertical lines in the histogram. The lines represent the median and the confidence intervals.
`lwd_hist`	line width for the vertical line in the histogram.
`lty_hist`	line type for the vertical line in the histogram.
`onlyOgive`	plot only the ogive.
`gg_style`	ggplot style (FALSE or TRUE).

`point_alpha`	transparency level of points, used only when gg_style = TRUE.
`base_size`	base font size, used only when gg_style = TRUE.
`label_size`	size of L50 and R2 labels, used only when gg_style = TRUE.
`...`	Additional arguments to the plot method.

Examples

```
data(crabdata)

classify_data = classify_mature(crabdata, varNames = c("carapace_width", "chela_height"),
varSex = "sex_category", selectSex = NULL, method = "ld")

my_mature = morph_mature(classify_data, method = "fq", niter = 50)

plot(my_mature, xlab = "Carapace width (mm.)", ylab = "Proportion mature", col = c("blue", "red"))
```

`print.classify` *Print method for classify class*

Description

Print method for classify class

Usage

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

Arguments

`x`	an object of class ’classify’ with the allometric variables ("X", "Y") and classification of maturity (juveniles = 0, adults = 1).
`...`	Additional arguments to the print method.

Value

The number of juveniles and adults. Also shows the regression analysis for juveniles and adults and an ANCOVA analysis to compare slopes.

Examples

```
data(crabdata)

classify_data = classify_mature(crabdata, varNames = c("carapace_width", "chela_height"),
varSex = "sex_category", selectSex = NULL, method = "ld")

print(classify_data)
```

`print.gonadMat` *Print method for gonadMat class (size at gonad maturity)*

Description

Print method for gonadMat class (size at gonad maturity)

Usage

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

Arguments

`x`	object of class 'gonadMat' with the parameters of the logistic regression and a data.frame with the X and stage of sexual maturity. variables. Also the fitted values for the logistic regression and confidence intervals (95%).
`...`	Additional arguments to the print method.

Value

The median of the size at gonad maturity estimation, parameters and the Nagelkerke's R squared.

Examples

```
data(matFish)

gonad_mat = gonad_mature(matFish, varNames = c("total_length", "stage_mat"), immName = "I",
matName = c("II", "III", "IV"), method = "fq", niter = 50)

print(gonad_mat)
```

`print.morphMat` *Print method for morphMat class (size at morphometric maturity)*

Description

Print method for morphMat class (size at morphometric maturity)

Usage

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

Arguments

`x`	object of class 'morphMat' with the parameters of the logistic regression and a data.frame with the allometric variables ("X", "Y") and classification of maturity. Also the fitted values for the logistic regression and confidence intervals (95%).
`...`	Additional arguments to the print method.

Value

The median of the size at morphometric maturity estimation, parameters and the Nagelkerke's R square.

Examples

```
data(crabdata)

classify_data = classify_mature(crabdata, varNames = c("carapace_width", "chela_height"),
varSex = "sex_category", selectSex = NULL, method = "ld")

my_mature = morph_mature(classify_data, method = "fq", niter = 50)

print(my_mature)
```

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