Package ‘MLZ’

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Title Mean Length-Based Estimators of Mortality using TMB

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`bin_length` *Bin length data*

Description

A tool to bin raw length observations into a length frequency matrix.

Usage

```
bin_length(df, breaks = NULL)
```

Arguments

`df`	A data frame or matrix of length observations. The first column should be named 'Year' and the second column should be named 'Length'.
`breaks`	An optional vector for breaks for `hist`.

Details

Length frequencies from `Len_df` are created by using `hist` function.

Value

A list with length bins, years, and frequency matrix.

Examples

```
## Not run:
data(SilkSnapper)
Silk.matrix <- bin_length(SilkSnapper, breaks = seq(80, 830, 10))
Silk.matrix <- bin_length(SilkSnapper)
new.dataset <- new("MLZ_data", Year = Silk.matrix$Year, Len_bins = Silk.matrix$Len_bins,
Len_matrix = Silk.matrix$Len_matrix)

## End(Not run)
```

`calc_ML` *Calculate mean lengths >= Lc*

Description

Calculates mean lengths from length data and Lc for class `MLZ_data`.

Usage

```
calc_ML(MLZ_data, length.slot = c("Len_df", "Len_matrix"),
  sample.size = TRUE)
```

Arguments

`MLZ_data`	An object of class `MLZ_data`.
`length.slot`	Name of slot in `MLZ_data` from which to calculate mean lengths, either: `Len_df` or `Len_matrix`. Only used if there are data in both slots.
`sample.size`	If `TRUE`, then the annual sample sizes will be calculated by summing the cells in slot `Len_matrix`. Otherwise, sample sizes are set to 0 or 1 (whether mean lengths are calculated).

Value

An object of class `MLZ_data` to fill slots `MeanLength`, `ss`.

Examples

```
## Not run:
data(Nephrops)
Nephrops <- calc_ML(Nephrops, sample.size = FALSE)
Nephrops@MeanLength
plot(Nephrops)

## End(Not run)
```

compare_models *Model selection*

Description

Produces a matrix of AIC for model selection.

Usage

```
compare_models(..., figure = TRUE, color = NULL)
```

Arguments

...	Multiple objects of class MLZ_model, all from the same mortality estimator and same data set.
figure	If TRUE, produces a figure of model fits to the observed data.
color	Optional vector of colors for the figure each representing a separate model in MLZ_model.list. If NULL, colors from rich.colors will be used.

Examples

```
## Not run:
data(Goosefish)
goose <- ML(Goosefish, ncp = 0)
goose1 <- ML(Goosefish, ncp = 1)
goose2 <- ML(Goosefish, ncp = 2, grid.search = TRUE, figure = FALSE)

compare_models(goose, goose1, goose2)

data(PRSnapper)
ssm <- MLmulti(PRSnapper, ncp = 1, model = "SSM")
msm1 <- MLmulti(PRSnapper, ncp = 1, model = "MSM1")
msm2 <- MLmulti(PRSnapper, ncp = 1, model = "MSM2")
msm3 <- MLmulti(PRSnapper, ncp = 1, model = "MSM3")

compare_models(ssm, msm1, msm2, msm3)

## End(Not run)
```

Goosefish *Goosefish: Northern Management Region (for ML)*

Description

Mean lengths and life history for goosefish.

Usage

```
Goosefish
```

Format

An object of class MLZ_data.

References

Gedamke, T. and Hoenig, J.M. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosefish. Transactions of the American Fisheries Society 135:476-487.

Examples

```
data(Goosefish); Goosefish
```

ML — *Mean length-based mortality estimator*

Description

Estimator of instantaneous total mortality (Z) from a time series of mean length data.

Usage

```
ML(MLZ_data, ncp, start = NULL, grid.search = TRUE,
  parallel = ifelse(ncp > 2, TRUE, FALSE), min.time = 3, Z.max = 5,
  figure = TRUE)
```

Arguments

MLZ_data	An object of class MLZ_data containing mean lengths and life history data of stock.
ncp	The number of change points in total mortality in the time series. ncp + 1 total mortality rates will be estimated.
start	An optional list of starting values. See details.
grid.search	If TRUE, a grid search will be performed using the profile_ML function to find the best starting values for the change points (the years when mortality changes). Ignored if ncp = 0 or if start is provided.
parallel	Whether grid search is performed with parallel processing. Ignored if grid.search = FALSE.
min.time	The minimum number of years between each change point for the grid search, passed to profile_ML. Not used if grid.search = FALSE.
Z.max	The upper boundary for Z estimates.
figure	If TRUE, a call to plot of observed and predicted mean lengths will be produced.

Details

For a model with `I` change points, the starting values in `start` is a list with the following entries: Z a vector of `length = I+1`. yearZ a vector of `length = I`.

`start` can be `NULL`, in which case, the supplied starting values depend on the value of `grid.search`. If `grid.search = TRUE`, starting values will use the values for `yearZ` which minimize the negative log-likelihood from the grid search. Otherwise, the starting values for `yearZ` evenly divide the time series.

Value

An object of class `MLZ_model`.

References

Gedamke, T. and Hoenig, J.M. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosefish. Transactions of the American Fisheries Society 135:476-487.

See Also

`profile_ML`

Examples

```
## Not run:
data(Goosefish)
res <- ML(Goosefish, ncp = 2)
res <- ML(Goosefish, ncp = 2, start = list(Z = c(0.1, 0.3, 0.5), yearZ = c(1978, 1988)))
res <- ML(Goosefish, ncp = 2, grid.search = TRUE)

## End(Not run)
```

MLCR — *Mean length with catch rate mortality estimator*

Description

Estimator of instantaneous total mortality (Z) from a time series of mean length data.

Usage

```
MLCR(MLZ_data, ncp, CPUE.type = c(NA, "WPUE", "NPUE"),
  loglikeCPUE = c("lognormal", "normal"), start = NULL,
  grid.search = TRUE, parallel = ifelse(ncp > 2, TRUE, FALSE),
  min.time = 3, Z.max = 5, figure = TRUE)
```

Arguments

MLZ_data	An object of class MLZ_data containing mean lengths and life history data of stock.
ncp	The number of change points in total mortality in the time series. ncp + 1 total mortality rates will be estimated.
CPUE.type	Indicates whether CPUE time series is abundance or biomass based.
loglikeCPUE	Indicates whether the log-likelihood for the CPUE will be lognormally or normally distributed.
start	An optional list of starting values. See details.
grid.search	If TRUE, a grid search will be performed using the profile_MLCR function to find the best starting values for the change points (the years when mortality changes). Ignored if ncp = 0 or if start is provided.
parallel	Whether grid search is performed with parallel processing. Ignored if grid.search = FALSE.
min.time	The minimum number of years between each change point for the grid search, passed to profile_MLCR. Not used if grid.search = FALSE.
Z.max	The upper boundary for Z estimates.
figure	If TRUE, a call to plot of observed and predicted mean lengths will be produced.

Details

For a model with I change points, the starting values in start is a list with the following entries: Z a vector of length = I+1. yearZ a vector of length = I.

start can be NULL, in which case, the supplied starting values depend on the value of grid.search. If grid.search = TRUE, starting values will use the values for yearZ which minimize the negative log-likelihood from the grid search. Otherwise, the starting values for yearZ evenly divide the time series.

Value

An object of class MLZ_model.

References

Huynh, Q.C., Gedamke, T., Porch, C.E., Hoenig, J.M., Walter, J.F, Bryan, M., and Brodziak, J. In revision. Estimating Total Mortality Rates from Mean Lengths and Catch Rates in Non-equilibrium Situations. Transactions of the American Fisheries Society.

See Also

profile_MLCR

Examples

```
## Not run:
data(MuttonSnapper)
MLCR(MuttonSnapper, ncp = 2, CPUE.type = "WPUE", grid.search = TRUE)

## End(Not run)
```

MLeffort *Mean length with effort mortality estimator*

Description

Estimator of fishing and natural mortality from a time series of mean length and effort data.

Usage

```
MLeffort(MLZ_data, start, n_age, estimate.M = TRUE, log.par = FALSE,
  eff_init = 0, n_season = 1L, obs_season = 1L, timing = 0,
  figure = TRUE)
```

Arguments

MLZ_data	An object of class MLZ_data containing mean lengths and life history data of stock.
start	A list of starting values. Names of start list must contain q and M.
n_age	The number of ages above age tc in the model.
estimate.M	If TRUE, natural mortality (M) will be estimated. Otherwise, the value of M is obtained from slot MLZ_data@M.
log.par	Whether parameters are estimated in logspace (TRUE) or untransformed space (FALSE).
eff_init	The assumed equilibrium effort prior to the first year of the model (0 = virgin conditions).
n_season	The number of seasons modeled in a year.
obs_season	The season corresponding to the observed mean lengths.
timing	The fraction of time (i.e., between 0 - 1) within obs_season that mean lengths are observed.
figure	If TRUE, a call to plot of observed and predicted mean lengths will be produced.

Value

An object of class MLZ_model.

References

Then, A.Y, Hoenig, J.M, and Huynh, Q.C. In revision. Estimating fishing and natural mortality rates, and catchability coefficient, from a series of observations on mean length and fishing effort. ICES Journal of Marine Science.

Examples

```
## Not run:
data(Nephrops)
Nephrops <- calc_ML(Nephrops, sample.size = FALSE)
res <- MLeffort(Nephrops, start = list(q = 0.1, M = 0.2),
                n_age = 24, eff_init = Nephrops@Effort[1])

## End(Not run)
```

MLmulti *Multispecies mean length mortality estimator*

Description

Estimator of instantaneous total mortality (Z) from a time series of mean length data for a suite of stocks that are fished together.

Usage

```
MLmulti(MLZ.list, ncp, model = c("SSM", "MSM1", "MSM2", "MSM3"),
  start = NULL, grid.search = TRUE, parallel = ifelse(ncp > 2, TRUE,
  FALSE), min.time = 3, Z.max = 5, figure = TRUE)
```

Arguments

`MLZ.list`	A list containing objects of class `MLZ_data`.
`ncp`	The number of change points in total mortality in the time series. `ncp + 1` total mortality rates will be estimated.
`model`	The multispecies model to be used.
`start`	An optional list of starting values. See details.
`grid.search`	If `TRUE`, a grid search will be performed using the `profile_MLmulti` function to find the best starting values for the change points (the years when mortality changes). Ignored if `start` is provided.
`parallel`	Whether grid search is performed in parallel. Ignored if `grid.search = FALSE`.
`min.time`	The minimum number of years between each change point for the grid search, passed to `profile_MLmulti`. Not used if `grid.search = FALSE`.
`Z.max`	The upper boundary for Z estimates.
`figure`	If `TRUE`, a call to `plot` of observed and predicted mean lengths will be produced.

Details

For a model with `I` change points and `N` species, the starting values in `start` is a list with the following entries:

Single Species Model (SSM, independent trends in mortality among species):

`Z`	a matrix with `nrow = I+1` and `ncol = N`.
`yearZ`	a matrix with `nrow = I` and `ncol = N`.

Multispecies Model 1 (MSM1, common mortality change points but changes in Z are independent):

`Z`	a matrix with `nrow = I+1` and `ncol = N`.
`yearZ`	a vector with `length = I`.

Multispecies Model 2 (MSM2, common mortality change points. Changes in F vary by estimated relative catchabilities among species):

`Z1`	a vector with `length = N`.
`yearZ`	a vector with `length = I`.
`delta`	a vector with `length = I`.
`epsilon`	a vector with `length = N-1`.

Multispecies Model 3 (MSM3, common mortality change points and common proportional changes in F):

`Z1`	a vector with `length = N`.
`yearZ`	a vector with `length = I`.
`delta`	a vector with `length = I`.

If `ncp = 0` change points is specified, then the method simplifies to the Single Species Model. The `start` list should contain a single entry:

`Z`	a vector with `length = N`.

`start` can be `NULL`, in which case, the supplied starting values depend on the value of `grid.search`. If `grid.search = TRUE`, starting values will use the values for `yearZ` which minimize the negative log-likelihood from the grid search. Otherwise, the starting values for `yearZ` evenly divide the time series.

Value

An object of class `MLZ_model`.

References

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. 2017. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries 9:68-78.

See Also

profile_MLmulti

Examples

```
## Not run:
data(PRSnapper)
res_eq <- MLmulti(PRSnapper, ncp = 0, start = list(Z = matrix(0.5, nrow = 1, ncol = 3)))
res_SSM <- MLmulti(PRSnapper, ncp = 1, model = "SSM")

MSM1.start.Z <- matrix(0.5, nrow = 2, ncol = 3)
MSM1.start.yearZ <- 1990
start.list <- list(Z = MSM1.start.Z, yearZ = MSM1.start.yearZ)
res_MSM1 <- MLmulti(PRSnapper, ncp = 1, model = "MSM1", start = start.list, grid.search = FALSE)

res_MSM2 <- MLmulti(PRSnapper, ncp = 1, model = "MSM2")

st.Z1 <- rep(0.5, 3)
st.yearZ <- 1990
st.delta <- 1
start.list <- list(Z1 = st.Z1, yearZ = st.yearZ, delta = st.delta)
resMSM3 <- MLmulti(PRSnapper, ncp = 1, model = "MSM3", start = start.list)

## End(Not run)
```

MLZ_data-class *MLZ_data*

Description

An S4 class for storing data and life history parameters for a single stock. Method functions summary and plot are available for this class (see examples).

Slots

Stock Name of stock.

Year A vector of years to be considered in the model. Missing years are permitted.

Len_bins A vector of midpoints of length bins for Len_matrix.

Len_matrix A matrix of size data. The i-th row corresponds to the i-th year in MLZ_data@Year. The j-th column indexes the j-th length in MLZ_data@Len_bins.

Len_df A data frame containing individual length observations. The first column should be the Year and the second column should be the length.

`vbLinf` L-infinity from the von Bertalanffy growth function.

`vbK` Parameter K from the von Bertalanffy growth function.

`vbt0` Parameter t0 from the von Bertalanffy growth function.

`Lc` Length of full selectivity.

`M` Natural mortality rate. If specified, this is also the lower limit for Z.

`lwb` Exponent b from the allometric length-weight function $W = aL^b$.

`MeanLength` Vector of mean lengths of animals larger than Lc. The i-th entry corresponds to the i-th year in `MLZ_data@Year`.

`ss` Vector of annual sample sizes for MeanLength. The i-th entry corresponds to the i-th year in `MLZ_data@Year`.

`CPUE` Vector of catch-per-unit-effort data. The i-th entry corresponds to the i-th year in `MLZ_data@Year`.

`Effort` Vector of effort data. The i-th entry corresponds to the i-th year in `MLZ_data@Year`.

`length.units` Unit of measurement for lengths, i.e. "cm" or "mm".

Examples

```
data(Goosefish); Goosefish
summary(Goosefish)
plot(Goosefish)

new("MLZ_data")
```

`MLZ_model-class` *MLZ_model*

Description

An S4 class for storing model results. Method functions `summary` and `plot` are available for this class (see examples).

Slots

`Stock` Name of stock (obtained from an object of class `MLZ_data`).

`Model` Name of model used for mortality estimation.

`time.series` A data frame summarizing observed time series data and predicted values from model.

`estimates` A matrix of parameter estimates and derived values and their standard errors, from `sdreport`.

`negLL` The negative log-likelihood from the model.

`n.changepoint` The number of change points in the model.

`n.species` The number of species/stocks in the model.

`grid.search` A data frame reporting the log-likelihood values from a grid search over change points. See `profile_ML`, `profile_MLCR`, and `profile_MLmulti`.

`obj` A list with components from `MakeADFun`.

`opt` A list with components from calling `optim` to `obj`.

`sdrep` A class `sdreport` list with components from calling `sdreport` to `obj`.

`length.units` Unit of measurement for lengths, i.e. "cm" or "mm".

Examples

```
## Not run:
data(Goosefish)
goose.model <- ML(Goosefish, ncp = 2, grid.search = FALSE, figure = FALSE)
class(goose.model)

summary(goose.model)
plot(goose.model, residuals = FALSE)

## End(Not run)
```

`modal_length` *Modal length from length data*

Description

Calculates the annual modal length from the length data, which can be used to select Lc. Note: Modal length can change over time for many reasons, including a change in mortality (Hordyk et al. 2015), recruitment, or selectivity (Huynh et al. 2017).

Usage

```
modal_length(MLZ_data, length.slot = c("Len_df", "Len_matrix"),
  breaks = NULL, figure = TRUE)
```

Arguments

`MLZ_data`	An object of class `MLZ_data`.
`length.slot`	Name of slot in `MLZ_data` from which to calculate modal lengths, either: `Len_df` or `Len_matrix`. Only used if there are data in both slots.
`breaks`	Only used for `Len_df`. An optional vector for breaks for `bin_length`.
`figure`	If TRUE, a plot is also drawn.

Details

Length frequency matrix from `Len_df` are created by using `hist` function.

Value

A data frame of plotted values.

References

Hordyk, A. Ono, K., Sainsbury, K., Loneragan, N., and Prince, J. 2015. Some explorations of the life history ratios to describe length composition, spawning-per-recruit, and the spawning potential ratio. ICES Journal of Marine Science 72:204-216.

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. 2017. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries 9:68-78.

Examples

```
## Not run:
data(Nephrops)
modal_length(Nephrops)

data(SilkSnapper)
new.dataset <- new("MLZ_data", Year = 1983:2013, Len_df = SilkSnapper)
modal_length(new.dataset)
modal_length(new.dataset, breaks = seq(80, 830, 10))

## End(Not run)
```

MuttonSnapper *Puerto Rico Mutton Snapper (for ML, MLCR)*

Description

Mean lengths, CPUE, and life history for Puerto Rico mutton snapper.

Usage

```
MuttonSnapper
```

Format

An object of class `MLZ_data`.

References

Huynh, Q.C., Gedamke, T., Porch, C.E., Hoenig, J.M., Walter, J.F, Bryan, M, and Brodziak, J. In revision. Estimating Total Mortality Rates from Mean Lengths and Catch Rates in Non-equilibrium Situations. Transactions of the American Fisheries Society.

Examples

```
data(MuttonSnapper)
```

Nephrops — *Male Nephrops FU 28-29 (for MLeffort)*

Description

An S4 object containing length and effort time series and life history parameters of male Nephrops in FU 28-29.

Usage

```
Nephrops
```

Format

An object of class MLZ_data.

References

Then, A.Y, Hoenig, J.M, and Huynh, Q.C. In revision. Estimating fishing and natural mortality rates, and catchability coefficient, from a series of observations on mean length and fishing effort. ICES Journal of Marine Science.

Examples

```
data(Nephrops)
```

plot,MLZ_data-method — plot *method for S4 class* MLZ_data

Description

Plots annual length frequencies from slot Len_matrix or Len_df. If there are data in both slots, Len_matrix is preferentially plotted.

Usage

```
## S4 method for signature 'MLZ_data'
plot(x, type = c("ML", "comp"),
  ggplot_layer = NULL)
```

Arguments

x	An object of class MLZ_data.
type	Character. "comp" produces a annual length frequencies from ggplot2, while "ML" plots mean lengths from slot MLZ_data@ML, as well as data from MLZ_data@CPUE and MLZ_data@Effort if available..
ggplot_layer	Optional layers to add to ggplot2 plot for type = "comp".

Examples

```
## Not run:
data(Nephrops)
plot(Nephrops)
plot(Nephrops, type = "ML")

## End(Not run)
```

---

plot,MLZ_model-method plot *method for S4 class* MLZ_model

Description

Plots time series of observed and predicted data from an object of class MLZ_model.

Usage

```
## S4 method for signature 'MLZ_model'
plot(x, residuals = TRUE)
```

Arguments

x	An object of class MLZ_model.
residuals	logical; whether a plot of residuals will also be produced.

Examples

```
## Not run:
data(Goosefish)
goose.model <- ML(Goosefish, ncp = 2, grid.search = FALSE, figure = FALSE)
plot(goose.model)

## End(Not run)
```

---

profile_ML *Grid search for the mean length estimator*

Description

A grid search is performed over the time series, which can be used to identify local and global minima. A plot of the likelihood surface is also created similar to Figure 6 of Gedamke and Hoenig (2006) or Figure 3 of Huynh et al. (2017).

Usage

```
profile_ML(MLZ_data, ncp, startZ = rep(0.5, ncp + 1), min.time = 3,
  parallel = ifelse(ncp > 2, TRUE, FALSE), figure = TRUE,
  color = TRUE)
```

Arguments

MLZ_data	An object of class MLZ_data.
ncp	The number of change points.
startZ	A vector of length ncp+1 as the starting value of total mortality rate used in the grid search.
min.time	The minimum number of years between change points. Only used if ncp > 1.
parallel	Whether grid search is performed using parallel processing.
figure	If TRUE, creates a plot of the likelihood over the grid search. Only used if ncp = 1 or 2.
color	If TRUE, creates a color plot for the likelihood surface. Only used if ncp = 2.

Value

A matrix of change points with the negative log-likelihood values.

References

Gedamke, T. and Hoenig, J.M. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosefish. Transactions of the American Fisheries Society 135:476-487.

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. 2017. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries 9:68-78.

Examples

```
## Not run:
data(Goosefish)
profile_ML(Goosefish, ncp = 1)
profile_ML(Goosefish, ncp = 2)

## End(Not run)
```

profile_MLCR *Grid search for the mean length with catch rate estimator*

Description

A grid search is performed over the time series, which can be used to identify local and global minima. A plot of the likelihood surface is also created similar to Figure 6 of Gedamke and Hoenig (2006) or Figure 3 of Huynh et al. (2017).

Usage

```
profile_MLCR(MLZ_data, ncp, CPUE.type = c(NA, "NPUE", "WPUE"),
  loglikeCPUE = c("normal", "lognormal"), startZ = rep(0.5, ncp + 1),
  min.time = 3, parallel = ifelse(ncp > 2, TRUE, FALSE),
  figure = TRUE, color = TRUE)
```

Arguments

MLZ_data	An object of class MLZ_data.
ncp	The number of change points.
CPUE.type	Indicates whether CPUE time series is abundance or biomass based.
loglikeCPUE	Indicates whether the log-likelihood for the CPUE will be lognormally or normally distributed.
startZ	A vector of length ncp+1 as the starting value of total mortality rate used in the grid search.
min.time	The minimum number of years between change points. Only used if ncp > 1.
parallel	Whether the grid search is performed with parallel processing.
figure	If TRUE, creates a plot of the likelihood over the grid search. Only used if ncp = 1 or 2.
color	If TRUE, creates a color plot for the likelihood surface. Only used if ncp = 2.

Value

A matrix of change points with the total negative log-likelihood values and values from the mean lengths and catch rates.

References

Gedamke, T. and Hoenig, J.M. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosefish. Transactions of the American Fisheries Society 135:476-487.

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. 2017. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries 9:68-78.

Examples

```
## Not run:
data(MuttonSnapper)
profile_MLCR(MuttonSnapper, ncp = 1, CPUE.type = 'WPUE')

## End(Not run)
```

`profile_MLmulti` *Grid search for the multispecies mean length estimator*

Description

A grid search is performed over the time series, which can be used to identify local and global minima. A plot of the likelihood surface is also created similar to Figure 6 of Gedamke and Hoenig (2006) or Figure 3 of Huynh et al. (2017).

Usage

```
profile_MLmulti(MLZ.list, ncp, model = c("SSM", "MSM1", "MSM2", "MSM3"),
  startZ1 = rep(0.5, length(MLZ.list)), parallel = ifelse(ncp > 2,
  TRUE, FALSE), min.time = 3, figure = TRUE, color = TRUE)
```

Arguments

`MLZ.list`	A list containing an object of class `MLZ_data` for each species or stock.
`ncp`	The number of change points.
`model`	The name of the multispecies model for the grid search.
`startZ1`	A vector of length `ncp+1` as the starting value of total mortality rate used in the grid search.
`parallel`	Whether the grid search is performed with parallel processing.
`min.time`	The minimum number of years between change points. Only used if `ncp > 1`.
`figure`	If `TRUE`, creates a plot of the likelihood over the grid search. Only used if `ncp = 1` or `2`.
`color`	If `TRUE`, creates a color plot for the likelihood surface. Only used if `ncp = 2`.

Value

A matrix of change points with the total negative log-likelihood values and values from the each species.

References

Gedamke, T. and Hoenig, J.M. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosefish. Transactions of the American Fisheries Society 135:476-487.

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. 2017. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries 9:68-78.

Examples

```
## Not run:
data(PRSnapper)
profile_MLmulti(PRSnapper, ncp = 1, model = "MSM1")

## End(Not run)
```

PRSnapper *Puerto Rico Snapper (for MLmulti)*

Description

Mean lengths and life history for 3 species in the Puerto Rico Deepwater Snapper Complex (Unit 1): silk snapper, blackfin snapper, and vermilion snapper.

Usage

```
PRSnapper
```

Format

A list containing objects of class MLZ_data.

References

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. In press. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries.

Examples

```
data(PRSnapper)
```

---

sensitivity_Lc *Sensitivity to Lc*

Description

The function re-calculates mean lengths for each alternative value of Lc and re-estimates mortality. Currently supports only the ML estimator.

Usage

```
sensitivity_Lc(MLZ_data, MLZ_model, Lc.vec, grid.search = FALSE,
  figure = TRUE)
```

Arguments

MLZ_data	An object of class MLZ_data containing mean lengths and life history data of stock. Must contain length composition data.
MLZ_model	An object of class MLZ_model with base value of Lc.
Lc.vec	A vector of alternative Lc values.
grid.search	Whether a grid search is performed or not. By default, the starting values in the sensitivity analysis are the estimates from object MLZ_model.
figure	Whether a figure will be produced, similar to Figure 6 of Huynh et al. (2017).

Value

A matrix of mortality and change point estimates with each value Lc.

References

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. 2017. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries 9:68-78.

See Also

ML

Examples

```
## Not run:
data(SilkSnapper)
new.dataset <- new("MLZ_data", Year = 1983:2013, Len_df = SilkSnapper, length.units = "mm",
vbLinf = 794, vbK = 0.1)

new.dataset@Lc <- 310
new.dataset <- calc_ML(new.dataset)

first.MLZmodel <- ML(new.dataset, 1)
Lc.vec <- seq(240, 340, 5)

sensitivity_Lc(new.dataset, first.MLZmodel, Lc.vec)

## End(Not run)
```

SilkSnapper *Silk Snapper*

Description

Length observed from the Puerto Rico Silk Snapper handline fishery.

Usage

```
SilkSnapper
```

Format

A data frame.

References

Huynh, Q.C, Gedamke, T., Hoenig, J.M, and Porch C. In press. Multispecies Extensions to a Nonequilibrium Length-Based Mortality Estimator. Marine and Coastal Fisheries.

Examples

```
## Not run:
data(SilkSnapper)
new("MLZ_data", Len_df = SilkSnapper)

## End(Not run)
```

---

summary,MLZ_data-method

summary *method for S4 class* MLZ_data

Description

summary method for S4 class MLZ_data

Usage

```
## S4 method for signature 'MLZ_data'
summary(object)
```

Arguments

object	An object of class MLZ_data.

Examples

```
data(MuttonSnapper)
summary(MuttonSnapper)
```

summary,MLZ_model-method

summary *method for S4 class* MLZ_model

Description

summary method for S4 class MLZ_model

Usage

```
## S4 method for signature 'MLZ_model'
summary(object)
```

Arguments

object	An object of class MLZ_model.

Examples

```
## Not run:
data(Goosefish)
goose.model <- ML(Goosefish, ncp = 2, grid.search = FALSE)
summary(goose.model)

## End(Not run)
```

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