Package ‘MEDIT’

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Type Package

Title Analysis of MEDITS-Like Survey Data

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Description Set of functions working with survey data in the format of the MEDITS project <https://www.sibm.it/SITO%20MEDITS/principaleprogramme.htm>. In this version, functions use TA, TB and TC tables respectively containing haul, catch and aggregated biological data.

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Plot of abundance indices

Description

The function, using TA (table A, hauls data), TB (table B, catches data), and TC (table C, biological data) tables estimates the abundance indices per hauls for recruits and spawners specimens or for all the caught specimens together. Recruits and spawners specimens are selected using the body length cutoff parameter defined by the user. Bathymetrical lines (class: "SpatialLinesDataFrame", "sp") refers respectively to 50m, 200m, and 800m of depth.

Usage

```r
bubble.rs(TA, TB, TC, GSA=NA, sspp =NA, stage ="recruits",
cutoff=NA, buffer =NA, country=NA,wm=wmap,
land=countries, d1=depth_1, d2=depth_2, d3=depth_3)
```
Arguments

- **TA**: data frame containing the hauls data (TA, table A).
- **TB**: data frame containing the catches data (TB, table B).
- **TC**: data frame containing the aggregated biological data (TC, table C).
- **GSA**: reference Geographical Sub-Area (GSA) for the analysis.
- **country**: string value the country selected for the analysis in case the latter should be performed by country.
- **sspp**: string of the species code (MEDIT format). The default value is NA and, in case in the data there is only one species, the species code is determined by the merge data frame. If there are more than one species, the species code is mandatory.
- **stage**: fraction of the population that is selected for the analysis: "recruits", "spawners" or "all.stages". "all.stages" allows to plot the abundance index by haul, considering all the specimens.
- **cutoff**: numeric value (threshold) of maturity length to be used for selecting the fraction of the population for the analysis.
- **buffer**: numeric value to define the extension (in meters) of the buffer around the study area (haul positions range) in the map.
- **wm**: shapefile of the land’s contours of the world map.
- **land**: shapefile of the world’s land.
- **d1**: shapefile of the 50m bathymetrical line.
- **d2**: shapefile of the 200m bathymetrical line.
- **d3**: shapefile of the 800m bathymetrical line.

Details

The function performs the analysis for one stage at time. The abundance indices per haul are estimated selecting either the total number of specimens with Total Length (TL) >= cutoff value for spawners or with TL <= cutoff for recruits.

Value

The function returns the bubble plot of the abundance indices of the selected life stage.

Author(s)

Walter Zupa

Examples

```r
library(MEDIT)
bubble.rs(TA, TB, TC, GSA=10, sspp ="ARISFOL", stage ="recruits", cutoff=29, buffer =5000, country ="ITA")
```
bubbleplot

Description

The function allows to generate a bubble plot of a given variable. If the parameter range is not provided, the function estimates the coordinate range of the plot using the points’ coordinates extension.

Usage

```r
bubbleplot(x, y, data, variable, range = NA, inches = 0.1, interval = "equal", land = countries, d1 = depth_1, d2 = depth_2, d3 = depth_3)
```

Arguments

- **x**: the x coordinates (longitude) of points in the plot.
- **y**: the y coordinates (latitude) of points in the plot.
- **data**: data frame containing the variable to be plotted.
- **variable**: character value of the variable name in `data`.
- **range**: vector of the coordinates limits of the plot in the form of `c(xmin, xmax, ymin, ymax)`.
- **inches**: maximum dimension of the circles expressed in inches.
- **interval**: character variable indicating the type of breaks to be computed for the five value levels. Allowed values: "equal" and "quantiles".
- **land**: shapefile of the world’s land.
- **d1**: shapefile of the 50m bathymetrical line.
- **d2**: shapefile of the 200m bathymetrical line.
- **d3**: shapefile of the 800m bathymetrical line.

Value

The function returns the bubble plot map of a given variable in a selected range of coordinates.

Author(s)

Walter Zupa

Examples

```r
library(MEDITS)
m <- MEDITS.to.dd(TA)
bubbleplot(x = m$SHOOTING_LONGITUDE, y = m$SHOOTING_LATITUDE, m, "SHOOTING_DEPTH", interval = "quantiles", range = c(12, 17, 38, 42))
```
Description

shapefile of the statistical grid

check.format

Check of TA (table A, hauls data), TB (table B, catches data), and TC (table C, biological data) tables’ fields format

Description

The function checks whether TA (table A, hauls data), TB (table B, catches data), and TC (table C, biological data) tables have the correct fields. Missing columns or not expected fields could generate errors in the merging functions. check.format helps to identify the presence of unexpected or missing columns generating warnings.

Usage

check.format(TA, TB, TC)

Arguments

TA data frame of hauls data (TA, table A)
TB data frame of the catches data (TB, table B)
TC data frame of the biological data (TC, table C)

Value

The function returns messages of the inconsistencies detected in the names and in the order of the columns of the TA (table A, hauls data), TB (table B, catches data) and TC (table C, biological data) tables. In case no message is generated by the function the format of the data frames is assumed to be correct.

Author(s)

Walter Zupa

Examples

check.format(TA, TB, TC)
Description

shapefile of countries. Made with Natural Earth. Free vector and raster map data @ naturalearth-data.com.

**dd.distance**

Estimation of haul distance

Description

Function to estimate the hauls length using TA (table A, hauls data) with coordinates in the decimal degrees format (dd.ddd). The distances could be returned expressed in meters, kilometers and nautical miles.

Usage

`dd.distance(data, unit = "m", verbose=TRUE)`

Arguments

- `data` data frame of the hauls data (TA, table A)
- `unit` string value indicating the measure unit of the distance. Allowed values: "m" for meters, "km" for kilometers and "NM" for nautical miles.
- `verbose` give verbose output reporting in the output the selected measure unit of the distance.

Details

The TA file should be populated with coordinates in decimal degrees format.

Value

The function returns the vector of the distances expressed in the selected measure unit.

Author(s)

Walter Zupa

Examples

```r
TA.dd <- MEDITS.to.dd(TA)
dd.distance(TA.dd, unit="km", verbose=FALSE)
```
dd.to.MEDITS  

Conversion of decimal degrees coordinates in MEDITS format

Description
Conversion of decimal degrees coordinates in MEDITS format

Usage
dd.to.MEDITS(data)

Arguments
data

data frame of the hauls data (TA, table A) in MEDITS format

Value
The function returns the data frame of the TA (table A) reporting the coordinates in MEDITS format.

Author(s)
Walter Zupa

Examples
TA.dd <- MEDITS.to.dd(TA)
dd.to.MEDITS(TA.dd)

depth_1  depth_1

Description
shapefile of bathymetrical line of 50m

depth_2  depth_2

Description
shapefile of bathymetrical line of 200m
haul.plot

Description

shapefile of bathymetrical line of 800m

haul.plot

Plot of hauls position

Description

The function plots the haul positions starting from table A file (TA, hauls data).

Usage

haul.plot(TA, GSA = NA, country=NA, year = NA, type = "m", labels = FALSE, land = countries, format="MEDITS")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TA</td>
<td>data frame containing the hauls data (TA, table A).</td>
</tr>
<tr>
<td>GSA</td>
<td>numeric value of the GSA code. The default value is NA.</td>
</tr>
<tr>
<td>country</td>
<td>string value indicating the selected country for the analysis in case the analysis should be performed by country</td>
</tr>
<tr>
<td>year</td>
<td>numeric value or vector containing the years to be selected for coordinate plotting. The default value is NA.</td>
</tr>
<tr>
<td>type</td>
<td>string value used to indicate whether (&quot;b&quot;) both shooting and hauling coordinates or (&quot;m&quot;) the mean coordinate values should be plotted.</td>
</tr>
<tr>
<td>labels</td>
<td>logic value used to indicate whether (T) haul’s code should be used as labels or not (F).</td>
</tr>
<tr>
<td>land</td>
<td>shapefile of countries. Made with Natural Earth. Free vector and raster map data @ naturalearthdata.com.</td>
</tr>
<tr>
<td>format</td>
<td>character value that define the format of the used cordinates. The two allowed values are: &quot;MEDITS&quot; for for MEDITS coordinates format; &quot;degrees&quot; for coordinates reported in decimal degrees format (dd,ddd). The default value is &quot;MEDITS&quot;</td>
</tr>
</tbody>
</table>

Value

The function returns the plot whith the positions of the selected hauls.
Author(s)
Walter Zupa

Examples

haul.plot(TA, GSA = 10, year = c(2007, 2008), type = "b", labels = TRUE)

Description

Estimation of the time series of aggregated indices for recruits or spawners. The standard deviations are also estimated. The analysis is performed by GSA.

Usage

index.rs(TA, TB, TC, GSA = NA, sspp, stage="recruits", cutoff, depth_range, str.scheme=strata_scheme, surf=stratification, country=NA, plot=TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TA</td>
<td>data frame containing the hauls data (TA, table A).</td>
</tr>
<tr>
<td>TB</td>
<td>data frame containing the catches data (TB, table B).</td>
</tr>
<tr>
<td>TC</td>
<td>data frame containing the biological data (TC, table C).</td>
</tr>
<tr>
<td>GSA</td>
<td>reference GSA for the analysis</td>
</tr>
<tr>
<td>sspp</td>
<td>string of the species code (MEDIT format). The default value is NA and the species is determined by the merge data frame.</td>
</tr>
<tr>
<td>stage</td>
<td>fraction of the population that is selected for the analysis: &quot;recruits&quot; or &quot;spawners&quot;.</td>
</tr>
<tr>
<td>cutoff</td>
<td>threshold value of the maturity length (expressed in mm) to be used for selecting the fraction of the population for the analysis (&lt;= for recruits; &gt;= for spawners).</td>
</tr>
<tr>
<td>depth_range</td>
<td>numeric vector of the extreme values of the depth range.</td>
</tr>
<tr>
<td>str.scheme</td>
<td>...</td>
</tr>
<tr>
<td>surf</td>
<td>...</td>
</tr>
<tr>
<td>country</td>
<td>string value indicating the selected country for the analysis in case the analysis should be performed by country</td>
</tr>
<tr>
<td>plot</td>
<td>boolean variable to indicate if a plot should be generated.</td>
</tr>
</tbody>
</table>
Details

**Index of recruits (number/km\(^2\))**. Recruits are often measured as the individuals belonging to the first component of the length frequency distributions, or as the individuals of the first age class, according to the recruitment mode, population structure and species. Thresholds to split the recruits from the whole population index can be also obtained from different areas or from literature. For the indices calculation see mean biomass in function index.ts.

**Index of spawners (number/km\(^2\))**. As individuals in spawning phase are not always intercepted by surveys, spawners can be approximated using the indices of adult individuals, i.e. those larger than the size at first maturity. For the indices calculation see mean biomass in function index.ts.

Value

the function returns a data frame with the time series of the abundance indices for the selected life stage:

- **year**: reference years of the estimated abundance indices
- **abundance**: time series of the estimated abundance indices
- **sd**: standard deviation of the estimated abundance indices

Author(s)

Walter Zupa

Examples

```r
library(MEDITS)
sp <- "ARISFOL"
depth <- c(500, 800)
st <- strata_scheme
st.sch <- stratification_scheme
index.rs (TA, TB, TC, GSA=10, sspp=sp, stage = "recruits", cutoff=45,
depth_range=depth, str.scheme=st, surf=st.sch, plot=TRUE)
```

---

**index.ts**

*Estimation of the time series of aggregated indices.*

Description

Estimation of the time series of the aggregated indices of abundance (n/km\(^2\)), biomass (kg/km\(^2\)) and mean individual weight (kg). The standard deviation and the standard error are also estimated.

Usage

```r
index.ts(merge, GSA = NA, sspp = NA, index = "abundance", depth_range, sex="c",
str.scheme=strata_scheme, surf=stratification_scheme, sampling="RSS",
country=NA, plot=TRUE,verbose=FALSE)
```
Arguments

merge data frame containing the merge between table A (TA, hauls data) and table B (TB, catches data) tables.

GSA integer value corresponding to the GSA number

sspp string of the species code (MEDITS format). The default value is NA and the species is determined by the merge data frame.

index string with the selected index with which the time series would be estimated. The permitted values are: "abundance", "biomass", and "MIW".

depth_range numeric vector of the extreme values of the depth range.

sex string variable used to define the sex of the specimens to be selected for the analysis. The sex selection is allowed only for the estimation of abundance indices, in the other cases the default value is "c". Allowed values are: "c" for combined sexes, "f" for females and "m" for males.

str.scheme ...

surf ...

sampling string identifying the type of sampling strategy used in the survey

country string value indicating the selected country for the analysis in case the analysis should be performed by country

plot boolean variable to indicate if a plot should be generated.

verbose boolean parameter, if TRUE returns messages about the progress of the elaboration

Details

**Number of positive hauls to the species.**

It is assumed that the size of the spreading area of a stock is mainly dependent on its abundance. A trend analysis can provide insight into the evolution of the occupied area in the medium term. This indicator can be also affected by environmental changes. It is computed as: \((\text{Positive hauls}/\text{Total hauls}) \times 100\)

**Mean biomass index (kg/km<sup>2</sup>).**

This index measures the total biomass of a species per unit area. Changes (decrease) in this index can be caused by an excessive fishing pressure. The index is calculated as (Souplet, 1996):
where $I$ is the index, $W_i$ is the weight of the stratum $i$, and $x_i$ is given by:

$$x_i = \frac{\sum_{j=1}^{n_i} x_{i,j}}{\sum_{j=1}^{n_i} A_{i,j}}$$

where $x_{i,j}$ is the weight of the individuals in the haul $j$ of the stratum $i$ and $A_{i,j}$ is the area trawled in the haul $j$ of the stratum $i$; $n_i$ is the number of hauls in the stratum $i$. Within stratum variance is calculated as:

$$S^2_{x_i} = \frac{1}{n_i - 1} \sum_{j=1}^{n_i} A_{i,j} \left( \frac{x_{i,j}}{A_{i,j}} - \bar{x}_i \right)^2$$

and the variance in the survey area as:

$$var(I) = \sum_{i=1}^{N} \frac{W_i^2 S^2_i}{\sum_{j=1}^{n_i} A_{i,j}} (1 - f_i)$$

where $f_i$ is the ratio between the area trawled in the stratum $i$ and the stratum area.
(finite population correction factor, generally negligible).

**Mean abundance index (number/km\(^2\)).** Abundance indices, like the biomass ones, can change (decrease) for the effect of an excessive fishing pressure, however more than the biomass ones, are likely to be substantially affected by large recruitment pulses in the stock, particularly if numbers of adults are low. For the analysis of time series of such index the ln transformation of the variable \(ln(x) + 1\) is usually applied. For computation see mean biomass index.

**Inverse of mean abundance Coefficient of Variation (CV).** The reciprocal of the coefficient of variation could be seen as a descriptor of the stability of the variable under investigation (higher is the metrics, more stable is the variable). It is the square root of the variance, as obtained for the biomass index, divided by the mean abundance index.

**Mean individual weight (MIW).** Mean Individual Weight (MIW) is generally considered an indicator that synthesizes the structure of the population (Piet and Jennings, 2005) and its changes in time are likely linked to changes in fishing pressure, though it can be also influenced by the recruitment peaks. This influence is expected to be less pronounced if older individuals in the population are well represented. Mean weight is particularly useful for those species caught in the trawl surveys for which no data on individual size is collected. It is computed as the ratio between overall biomass by haul \(i\) and overall number of individuals by haul \(i\): \(B_{i}/N_{i}\).

**Value**

the function returns a data frame with the time series of the selected index:

<table>
<thead>
<tr>
<th>year</th>
<th>reference years of the estimated indices</th>
</tr>
</thead>
<tbody>
<tr>
<td>abundance</td>
<td>time series of the estimated abundance indices</td>
</tr>
<tr>
<td>biomass</td>
<td>time series of the estimated biomass indices</td>
</tr>
<tr>
<td>MIW</td>
<td>time series of the estimated mean individual weight (MIW) indices</td>
</tr>
<tr>
<td>sd</td>
<td>standard deviation of the estimated indices</td>
</tr>
<tr>
<td>se</td>
<td>standard error of the estimated indices</td>
</tr>
<tr>
<td>CV</td>
<td>coefficient of variation</td>
</tr>
<tr>
<td>invCV</td>
<td>inverse value of the coefficient of variation</td>
</tr>
<tr>
<td>positive_hauls_perc</td>
<td>percentage of the hauls positive to the species caught</td>
</tr>
</tbody>
</table>

**Author(s)**

Walter Zupa

**References**

Examples

```
library(MEDITS)
merge_TATB <- m.TATB(TA,TB,"ARISFOL")
ind <- index.ts(merge_TATB, index="abundance", depth_range = c(500,800), sex="c",
str.scheme=strata_scheme, surf=stratification_scheme)
```

---

**Description**

The function checks whether the hauls coordinates is erroneously on the land.

**Usage**

```
land.points(TA, land=countries, verbose=TRUE)
```

**Arguments**

- **TA**: data frame of the hauls data (TA, table A)
- **land**: shapefile of countries. Made with Natural Earth. Free vector and raster map data @ naturalearthdata.com.
- **verbose**: boolean parameter, if TRUE returns messages about the progress of the elaboration

**Details**

The function uses a polygon shapefile of lands as reference to assess whether the points of the hauls fall either on the land or on the sea.

**Value**

The function returns the data frame of the hauls coordinates that fall on the land

**Author(s)**

Walter Zupa

**Examples**

```
land.points(TA, land=countries, verbose=FALSE)
```
**Description**

The function estimates for the selected sex the time series of the length frequency distribution (LFD)

**Usage**

`LFD(merge_TATC, indices, sex, LC, depth_range, type)`

**Arguments**

- `merge_TATC` data frame containing the hauls data (TA, table A) and the biological data (TC, table C) merged together
- `indices` data frame with the time series of the abundance indices as estimated by the function `index.ts()`
- `sex` string code of the selected sex. Permitted values: "c" (sex combined), "f" (females), and "m" (males).
- `LC` numerical value of the minimum length class interval (expressed in mm)
- `depth_range` vector of the depth range for the analysis
- `type` string value to select the type of graph to be plotted. Allowed values: "indices", "density" and "boxplot"

**Value**

the function returns a data frame in which the first column is the list of the length classes reported in the TC file and in the other columns are reported the abundance indices (n/km²) for each year of the time series by length class.

**Author(s)**

Walter Zupa

**Examples**

```r
library(MEDITS)
merge_TATB <- m.TATB(TA,TB,"ARISFOL")
merge_TATC <- m.TATC(TA,TC,"ARISFOL")
GSA <- unique(TA$AREA)
indices <- index.ts(merge_TATB,GSA,"ARISFOL",index = "abundance",
                  depth_range=c(200,800),sex="f", sampling = "RSS",plot=FALSE)
LFD(merge_TATC,indices,sex="f",LC=1,depth_range=c(200,800), type = "indices")
```
**m.TATB**

*merge of TA and TB tables*

**Description**

The function merges the hauls data (TA, table A) and catches data (TB, table B) for a selected species. The abundance, and biomass indices standardized per km$^2$ and hour are also estimated.

**Usage**

```r
m.TATB(TA, TB, sspp, str.scheme=strata_scheme, verbose=FALSE)
```

**Arguments**

- **TA**: data frame containing the hauls data (TA, table A).
- **TB**: data frame containing the catches data (TB, table B).
- **sspp**: string value of the selected species in the MEDITS format.
- **str.scheme**: data frame of the strata_scheme.
- **verbose**: boolean parameter, if TRUE returns messages about the progress of the elaboration.

**Details**

Using TA (table A) and TB (table B) table as input, the function returns a data frame containing the merge table for the selected species (sspp).

**Value**

The function returns the data frame of the resulting merge between TA table and TB table.

**Author(s)**

Walter Zupa

**Examples**

```r
m.TATB(TA, TB, "ARISFOL")
```
merge of TA and TC tables

Description

The function merges the hauls data (TA, table A) and biological data (TC, table C) for a selected species. The abundance, and biomass indices standardized per km$^2$ and hour are also estimated.

Usage

m.TATC(TA, TC, sspp, str.scheme=strata_scheme, verbose = FALSE)

Arguments

- **TA**: data frame containing the hauls data (TA, table A).
- **TC**: data frame containing the biological data (TC, table C).
- **sspp**: string value of the selected species in the MEDITS format.
- **str.scheme**: data frame of the strata_scheme
- **verbose**: boolean parameter, if TRUE returns messages about the progress of the elaboration

Details

Using TA and TC table as input, the function returns a data frame containing the merge table for the selected species (sspp)

Value

the function returns the data frame of the resulting merge between TA (table A) and TC (table C).

Author(s)

Walter Zupa

Examples

m.TATC(TA,TC,"ARISFOL")
MEDITS.distance

Estimation of haul distance

Description

Function to estimate the hauls length in meters, kilometers and nautical miles, using hauls data (TA, table A) with coordinates in the MEDITS format

Usage

MEDITS.distance(data, unit = "m", verbose=TRUE)

Arguments

data: data frame containing the hauls data (TA, table A).
unit: string value indicating the measure unit of the distance. Allowed values: "m" for meters, "km" for kilometers and "NM" for nautical miles.
verbose: give verbose output reporting in the output the selected measure unit of the distance.

Details

Use data frame containing coordinates in MEDITS format

Value

The function returns the vector of the distances expressed in the selected measure unit.

Author(s)

Walter Zupa

Examples

MEDITS.distance(TA, unit="km", verbose=TRUE)
**MEDITS.to.dd**

*Conversion of MEDITS format coordinates in decimal degrees format*

**Description**

Conversion of MEDITS format coordinates in decimal degrees format

**Usage**

MEDITS.to.dd(data)

**Arguments**

- **data**  
  data frame of the hauls data (TA, table A) in MEDITS format

**Value**

The function returns the data frame of the TA table with the coordinates expressed as decimal degrees.

**Author(s)**

Walter Zupa

**Examples**

MEDITS.to.dd(TA)

---

**quant**

$q^{th}$ percentile of LFD (Length Frequency Distribution)

**Description**

The quant function estimates the length class corresponding to the selected percentile of the annual length frequency distribution (LFD) of a time series.

**Usage**

quant(freq, quantile)

**Arguments**

- **freq**  
  data frame of the time series of the LFD, as estimated by LFD function

- **quantile**  
  percentile value
Details

**Length at the q<sup>th</sup> percentile (Lq)**

The different percentiles of a length frequency distribution (LFD) are expected to respond differently to fishing, recruitment pulses, and loss of spawning stock. It is computed from the standardised LFD that is:

\[ F_{q,j,l} = \frac{f_{q,j,l}}{A_j}, \forall j, \forall l \]

where \( f_{q,j,l} \) is the number of individuals in the length class \( l \) from the haul \( j \) standardised to the \( km^2 \), and \( A_j \) is the surface trawled in the haul \( j \). The length at the \( q \)th percentile (Lq) is computed as:

\[ L_{q,i} = l_{q,i} \mid \sum_{l=1}^{l_q} \frac{y_{l,i}}{y_i} = q \]

Where \( l \) is the length class corresponding to the \( q \)th percentile \((0 < q < 1)\) for the species \( i \), and \( y_{l,i} \) is the value of the catch for the length class \( l \). The variance of the length at the 95th percentile is computed as:

\[ \text{var} \left[ L_{q,i} \right] = \frac{q(1-q)}{y_i (y_{lq,i}/y_i)^2} \]

**Value**

The function returns a data frame containing the time series of the selected percentiles and the relative variance values.

**Author(s)**

Walter Zupa
sexratio.ts

Examples

library(MEDITS)
merge_TATB <- m.TATB(TA,TB,"ARISFOL")
merge_TATC <- m.TATC(TA,TC,"ARISFOL")
GSA <- unique(TA$AREA)
indices <- index.ts(merge_TATB,GSA,"ARISFOL",index = "abundance", depth_range=c(500,800), sampling = "RSS",plot=FALSE)
freq <- LFD(merge_TATC,indices,sex="m",LC=1,depth_range=c(500,800))
quant(freq,0.95)

sexratio.ts

Sex ratio time series

Description

Estimation of the time series of the sex ration annual indices.

Usage

sexratio.ts(merge, GSA = NA, sspp = NA, depth_range,
strata_scheme, stratification, country=NA, plot=TRUE )

Arguments

merge       data frame cantaining the hauls data (TA, table A) and the catches data (TB, table B) merged together
GSA         integer value corresponding to the GSA number. If not provided is determined by the merge file. Use merge file with only one GSA.
sspp        string of the species code (MEDITS format). The default value is NA and the species is determined by the merge data frame. If the merge file contains more than one species, the species should be indicated.
depth_range numeric vector of the extreme values of the depth range.
strata_scheme data frame containing the schema of the strata used in the survey.
stratification data frame containing the specification of the strata surface area.
country     string value indicating the selected country for the analysis in case the analysis should be performed by country
plot        boolean variable to indicate if a plot should be generated.
Details

**Sex-ratio.** Sex ratio provides information on the distribution of female and male individuals present in a population. It represents the proportion of females in a population and indicates the level of sex dominance (Adebiyi, 2013). Generally this is a peculiar trait of the population. The sex-ratio, as the proportion of the females on the overall number of individuals, can be considered correlated with the stock productivity and renewal. It is computed as:

\[
Sr = \frac{\sum_{i=1}^{n} FE_i}{\sum_{i=1}^{n} (FE_i + MA_i)}
\]

where FE are females, MA males, i is the haul and n the total number of hauls. Variance is estimated as:

\[
var(Sr) = \sqrt{\frac{Sr \ast (1 - Sr)}{\sum_{i=1}^{n} (FE_i + MA_i)}}
\]

**Value**

the function returns a data frame with the sex ratio time series:

<table>
<thead>
<tr>
<th>year</th>
<th>reference years of the estimated indices</th>
</tr>
</thead>
<tbody>
<tr>
<td>Indices_F</td>
<td>time series of the abundance indices of females specimens</td>
</tr>
<tr>
<td>Indices_FM</td>
<td>time series of the estimated abundance indices for males and females pooled together</td>
</tr>
<tr>
<td>sex.ratio</td>
<td>time series of the estimated sex ratio</td>
</tr>
<tr>
<td>variance</td>
<td>variance of the estimated sex ratio</td>
</tr>
<tr>
<td>sd</td>
<td>standard error of the estimated sex ratio</td>
</tr>
<tr>
<td>positive_hauls_perc</td>
<td>percentage of the hauls positive to the species caught</td>
</tr>
</tbody>
</table>

**Author(s)**

Walter Zupa

**References**

sp.index

Examples

library(MEDITS)
m <- m.TATB(TA,TB,"ARISFOL")
sexratio.ts(merge =m, GSA = NA, sspp = NA, depth_range=c(500,800),
strata_scheme=strata_scheme, stratification=stratification_scheme, plot=FALSE )

sp.index

Spatial indices

Description

Estimation of abundance, biomass, mean individual weight (MIW), and sex ratio indices over a statistical grid

Usage

sp.index(TA, TB, sspp, type, range=NA, GSA=NA,
country=NA, threshold=NA, grid.sf=cgpmgrid,land=countries)

Arguments

TA   data frame containing the hauls data (TA, table A).
TB   data frame containing the catches data (TB, table B).
sspp MEDITS code of the reference species
type type of index to estimate: "abundance", "invCV", "biomass", "MIW", "sex ratio"
range coordinate range of the study area in the form of c(xmin,xmax, ymin,ymax)
GSA   integer value corresponding to the GSA number
country string value indicating the selected country for the analysis in case the analysis should be performed by country
threshold numeric value indicating the minimum number of specimens per haul to be considered in the sex ratio estimation. If the threshold parameter is not defined all the available specimens are considered in the estimation of the sex ratio
grid.sf   ...
land     ...

Details

Mean biomass and mean abundance
The mean abundance (likewise the mean biomass) in the GFCM grid cells (D<sub>cell</sub>) is calculated as the average of the standardized numbers of individuals (number/km<sup>2</sup>) over the most recent 10 years of the time series (if the time series is shorter than 10 years, all the available year data are considered):
where \( n \) is the count of the combinations year-haul in all the last 10 years. The variance of the mean abundance in the cells is calculated as:

\[
var_{cell} = \frac{1}{n-1} \sum_{y,h} (N/km_{cell}^2)^2
\]

The CV is calculated as the ratio between the standard deviation of the mean annual value by haul and year (numerator) and the mean biomass (or abundance) in the cell (denominator).

\[
CV = \frac{\sqrt{var_{cell}}}{\overline{D}_{cell}}
\]

For each GFCM cell the mean individual weight is calculated by year \( y \) and haul \( h \) as ratio between the total weight \( W \) in the haul and the total number \( N \) in the haul (from the MEDITS samples data) as follows:

\[
\overline{MIW}_{cell} = \frac{\sum_{y,h} \frac{W_{y,h}}{N_{y,h}}}{n}
\]

where \( n \) is the count of the combinations year-haul in all the last 10 years. The variance of the MIW in the cells is calculated using the following formula:
Then, the Coefficient of Variation (CV) of the MIW is calculated as:

\[ CV = \frac{\sqrt{\text{var}_{cell_i}}}{\text{MIW}_{cell_i}} \]

**Sex ratio**

The sex ratio in each GFCM cell is calculated as the ratio between the sum of the standardized number of females and the sum of the standardized number of males and females over the hauls of the last 10 years:

\[ SR_{cell_i} = \frac{\sum_{y,h} N_F/km_{y,h}^2}{\sum_{y,h} (N_F/km_{y,h}^2 + N_M/km_{y,h}^2)} \]

where NF and NM are the standardized number of the females and of males in the haul \( h \) and year \( y \). The variance of the sex ratio in the cell is calculated using the following formula:

\[ SR_{cell_i} - \frac{1}{n-1} \sum_{y,h} \left( \frac{N_F/km_{y,h}^2}{N_F/km_{y,h}^2 + N_M/km_{y,h}^2} - SR_{cell} \right)^2 \]

where \( n \) is the count of the combinations year-haul in all the last pooled 10 years. The CV is calculated as the ratio between the standard deviation of the sex ratio by haul and year to the sex ratio in the cell.

\[ CV = \frac{\sqrt{\text{var}_{cell_i}}}{SR_{cell_i}} \]
**Inverse of mean abundance Coefficient of Variation (CV)**

The inverse of the coefficient of variation of the mean abundance by GFCM cell is plotted.

**Value**

the function returns the plot of the selected indices over the GFCM (General Fisheries Commission for the Mediterranean) statistical grid. Moreover, the data frame containing the values of the estimated indices is returned

- `cgpmgridlevel1` identification number value of the corresponding grid cell.
- `GSA` the corresponding geographical sub-area (GSA) of the relative cell.
- `meanNkm2` mean value of the indices.
- `sdNkm2` standard deviation of the mean value of the indices.
- `cvNkm2` Coefficient of variation of the mean indices.
- `inverse_cvNkm2` Inverse value of the mean indices coefficient of variation.
- `nhauls` number of hauls in any given cell.
- `positive_hauls` number of positive hauls used for the estimation of the indices.
- `lon` longitude coordinate of the cell’s centroid
- `lat` latitude coordinate of the cell’s centroid

**Author(s)**

Walter Zupa

**Examples**

```r
library(MEDITS)
sp.index(TA,TB,sspp="ARISFOL",type="abundance",range = c(10, 20, 38, 42))
```

---

**spear**  
*Spearman’s test*

**Description**

Spearman test function used by the function `spearman.test`

**Usage**

`spear(x)`

**Arguments**

- `x` indices time series
spearman.test

Value

statistics of the Spearman’s test.

- \( r \) Spearman’s correlation coefficient.
- \( p \) t statistics.
- \( p \) the p-value for the test.

Author(s)

Walter Zupa

Examples

```r
library(MEDITS)
x <- c(126.12,115.46,164.32,79.85,68.43,72.94, 54.23)
spear(x)
```

Description

The function uses the non parametric Spearman test to assess the presence of significant trends in the time series

Usage

```r
spearman.test(timeseries, years)
```

Arguments

- `timeseries` data frame of the indices time series as it is estimated by the `index.ts` function
- `years` vector of the time series year range

Details

In presence of a short trawl survey time series the significance of the trend can be estimated using nonparametric statistical tests as Spearman rho (Cotter, 2009). Spearman’s rho is the product-moment correlation between the ranks of paired data. To test for trend, one member of the pair is the time of observation, the other is the observed variable. This is also known as the Hotelling-Pabst test. It appears to be sensitive to monotonic trends.

Value

The function returns the statistics of the Spearman’s test.

- \( r \) Spearman’s correlation coefficient.
- \( p \) t statistics.
- \( p \) the p-value for the test.
Author(s)
Walter Zupa

References

Examples
library(MEDITS)
merge_TATB <- m.TATB(TA,TB,"ARISFOL")
timeseries <- index.ts(merge_TATB, index="abundance", depth_range = c(500,800), str.scheme=strata_scheme,surf=stratification_scheme, plot=FALSE)
spearman.test(timeseries, years=c(2007,2016))

---

**strata_scheme** | **strata_scheme**
---|---

**Description**
data frame of the strata_scheme

---

**stratification_scheme** | **stratification_scheme**
---|---

**Description**
data frame of the stratification_scheme

---

**TA** | **TA**
---|---

**Description**
TA table
TATB.grid

Overlay of TA and TB tables merge with the statistical grid

Description

Overlay of TA and TB tables merge with the statistical grid. A data frame is produced in which to each haul is associated the code of the corresponding grid cell.

Usage

TATB.grid(TA, TB, sspp, grid.sf=cgpmgrid)

Arguments

TA  
data frame of the TA table

TB  
data frame of the TB table

sspp  
string value containing the selected species code for merging. The code should be reported in the MEDIT format (rubin code), without spaces between genus and species names.

grid.sf  
shapefile of the statistical grid used by the function. It is already loaded in the package and should not be defined by the user.

Author(s)

Walter Zupa

Examples

TATB.grid(TA,TB,"ARISFOL", grid.sf=cgpmgrid)

TATC.grid

Overlay of TA and TC tables merge with the statistical grid

Description

Overlay of TA and TC tables merge with the statistical grid. A data frame is produced in which to each haul is associated the code of the corresponding grid cell.

Usage

TATC.grid(TA, TC, sspp, grid.sf=cgpmgrid)
Arguments

- **TA**: data frame of the TA table
- **TC**: data frame of the TC table
- **sspp**: string value containing the selected species code for merging. The code should be reported in the MEDITS format (rubin code), without spaces between genus and species names.
- **grid.sf**: shapefile of the statistical grid used by the function. It is already loaded in the package and should not be defined by the user.

Author(s)

Walter Zupa

Examples

```r
TATC.grid(TA, TC, "ARISFOL", grid.sf = cgpmgrid)
```

<table>
<thead>
<tr>
<th>TA_cols</th>
<th>TA_cols</th>
</tr>
</thead>
</table>

Description

**TA_cols table**

<table>
<thead>
<tr>
<th>TB</th>
<th>TB</th>
</tr>
</thead>
</table>

Description

**TB table**

<table>
<thead>
<tr>
<th>TB_cols</th>
<th>TC_cols</th>
</tr>
</thead>
</table>

Description

**TB_cols table**
**Description**

TC table

**Description**

TC_cols table

**Description**

wmap

Polygons shapefile of world lands. Made with Natural Earth. Free vector and raster map data @ naturalearthdata.com.
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