

Package ‘MEDITS’

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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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R topics documented:

bubble.rs	2
bubbleplot	4
cgpmgrid	5
check.format	5
countries	6
dd.distance	6
dd.to.MEDITS	7
depth_1	7
depth_2	7
depth_3	8
haul.plot	8

index.rs	9
index.ts	10
land.points	14
LFD	15
m.TATB	16
m.TATC	17
MEDITS.distance	18
MEDITS.to.dd	19
quant	19
sexratio.ts	21
sp.index	23
spear	26
spearman.test	27
strata_scheme	28
stratification_scheme	28
TA	28
TATB.grid	29
TATC.grid	29
TA_cols	30
TB	30
TB_cols	30
TC	31
TC_cols	31
wmap	31
Index	32

 bubble.rs

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

```
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 (MEDITS 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) \geq cutoff value for spawners or with TL \leq cutoff for recruits.

Value

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

Author(s)

Walter Zupa

Examples

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

 bubbleplot

Bubble plot (generic)

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

```
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 <code>c(xmin, xmax, ymin, ymax)</code> .
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

```
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))
```

`cgpmgrid`*cgpmgrid*

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)
```

countries	<i>countries</i>
-----------	------------------

Description

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

dd.distance	<i>Estimation of haul distance</i>
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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

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

dd.to.MEDITS	<i>Conversion of decimal degrees coordinates in MEDITS format</i>
--------------	---

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	<i>depth_1</i>
---------	----------------

Description

shapefile of bathymetrical line of 50m

depth_2	<i>depth_2</i>
---------	----------------

Description

shapefile of bathymetrical line of 200m

depth_3	<i>depth_3</i>
---------	----------------

Description

shapefile of bathymetrical line of 800m

haul.plot	<i>Plot of hauls position</i>
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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

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

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)
```

index.rs	<i>Estimation of the time series of aggregated indices for recruits or spawners.</i>
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Description

Estimation of the time series of the aggregated indices of abundance (n/km²) for recruits specimens. 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

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 biological data (TC, table C).
GSA	reference GSA for the analysis
sspp	string of the species code (MEDITS format). The default value is NA and the species is determined by the merge data frame.
stage	fraction of the population that is selected for the analysis: "recruits" or "spawners".
cutoff	threshold value of the maturity length (expressed in mm) to be used for selecting the fraction of the population for the analysis (<= for recruits; >= for spawners).
depth_range	numeric vector of the extreme values of the depth range.
str.scheme	...
surf	...
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

Index of recruits (number/km²). 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/km²). 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

```
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/km²), biomass (kg/km²) and mean individual weight (kg). The standard deviation and the standard error are also estimated.

Usage

```
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 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: $(\text{Positive hauls}/\text{Total hauls}) * 100$

Mean biomass index (kg/km²).

This index measures the total biomass of a species per unit area. Changes (decrease) in this indices can be caused by an excessive fishing pressure. The index is calculated as (Souplet, 1996):

$$I = \sum_{i=1}^N W_i \overline{x}_i$$

where I is the index, $W_{\langle i \rangle}$ is the weight of the stratum i , and $x_{\langle i \rangle}$ is given by:

$$\overline{x}_i = \frac{\sum_{j=1}^{n_i} x_{i,j}}{\sum_{j=1}^{n_i} A_{i,j}}$$

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

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

and the variance in the survey area as:

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

where $f_{\langle i \rangle}$ 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/km²). 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:

year	reference years of the estimated indices
abundance	time series of the estimated abundance indices
biomass	time series of the estimated biomass indices
MIW	time series of the estimated mean individual weight (MIW) indices
sd	standard deviation of the estimated indices
se	standard error of the estimated indices
CV	coefficient of variation
invCV	inverse value of the coefficient of variation
positive_hauls_perc	percentage of the hauls positive to the species caught

Author(s)

Walter Zupa

References

- Piet G.J. and Jennings S. (2005). Response of potential fish community indicators to fishing, ICES Journal of Marine Science, V.62-2, 214:225. Available on line at: <http://icesjms.oxfordjournals.org/content/62/2/214.full>
- Souplet A. (1996). Calculation of abundance indices and length frequencies in the MEDITS survey. In: J. A. Bertrand et al. (eds), Campagne internationale du chalutage demersal en Mediterranee. Campagne 1995. EU Final Report, Vol. III.

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)
```

land.points

Check of hauls position

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)
```

LFD

*Length Frequency Distribution***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 <code>index.ts()</code>
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/km^2) for each year of the time series by length class.

Author(s)

Walter Zupa

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(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 km² and hour are also estimated.

Usage

```
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

```
m.TATB(TA, TB, "ARISFOL")
```

m.TATC	<i>merge of TA and TC tables</i>
--------	----------------------------------

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 km² 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	<i>Estimation of haul distance</i>
-----------------	------------------------------------

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	<i>Conversion of MEDITS format coordinates in decimal degrees format</i>
--------------	--

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	<i>q percentile of LFD (Length Frequency Distribution)</i>
-------	---

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 percentile (L_q)

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:

$$Fq_{j,l} = \frac{fq_{j,l}}{A_j}, \forall j, \forall l$$

where $fq_{j,l}$ 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 percentile (L_q) is computed as:

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

Where l is the length class corresponding to the q 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 q percentile is computed as:

$$var [L_{q,i}] = \frac{q(1 - q)}{y_i (y_{l_{q,i}}/y_i)^2}$$

Value

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

Author(s)

Walter Zupa

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 containing 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:

$$var(Sr) = \sqrt{\frac{Sr * (1 - Sr)}{\sum_{i=1}^n (FE_i + MA_i)}}$$

Value

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

year	reference years of the estimated indices
Indices_F	time series of the abundance indices of females specimens
Indices_FM	time series of the estimated abundance indices for males and females pooled together
sex.ratio	time series of the estimated sex ratio
variance	variance of the estimated sex ratio
sd	standard error of the estimated sex ratio
positive_hauls_perc	percentage of the hauls positive to the species caught

Author(s)

Walter Zupa

References

Adebiyi F.A. (2013). The sex ratio, gonadosomatic index, stages of gonadal development and fecundity of sompat grunt *Pomadasys jubelini* (Cuvier, 1830). *Pakistan J. Zool.*, vol. 45(1), pp. 41-46.

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_{cell}) is calculated as the average of the standardized numbers of individuals (number/km^2) 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):

$$\overline{D}_{cell} = \frac{\sum_{y,h} N/km^2_{y,h}}{n}$$

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:

$$var_{cell} = \frac{1}{n-1} \sum_{y,h} (N/km^2_{cell})^2$$

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).

$$CV = \frac{\sqrt{var_{cell}_i}}{\overline{D}_{cell}_i}$$

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:

$$var_{cell_i} = \frac{1}{n-1} \sum_{y,h} \left(\frac{W_{y,h}}{N_{y,h}} - \overline{MIW}_{cell} \right)^2$$

Then, the Coefficient of Variation (CV) of the MIW is calculated as:

$$CV = \frac{\sqrt{var_{cell_i}}}{\overline{MIW}_{cell_i}}$$

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 N_F and N_M 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.

$$CV = \frac{\sqrt{var_{cell_i}}}{SR_{cell_i}}$$

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

cgpmgridlevel	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

```
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

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

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

spearman.test	<i>Spearman test for time series trends</i>
---------------	---

Description

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

Usage

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

Arguments

timeseries	data frame of the indices time series as it is estimated by the <code>index.ts</code> 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

Cotter J. (2009) A selection of nonparametric statistical methods for assessing trends in trawl survey indicators as part of an ecosystem approach to fisheries management (EAFM). *Aquat. Living Resour.* 22, 173-185.

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	<i>strata_scheme</i>
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Description

data frame of the strata_scheme

stratification_scheme	<i>stratification_scheme</i>
-----------------------	------------------------------

Description

data frame of the stratification_scheme

TA	<i>TA</i>
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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 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

```
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

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

TA_cols	<i>TA_cols</i>
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Description

TA_cols table

TB	<i>TB</i>
----	-----------

Description

TB table

TB_cols	<i>TC_cols</i>
---------	----------------

Description

TB_cols table

TC	<i>TC</i>
----	-----------

Description

TC table

TC_cols	<i>TC_cols</i>
---------	----------------

Description

TC_cols table

wmap	<i>wmap</i>
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Description

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

Index

- *Topic **Bubble plot**
 - bubbleplot, 4
- *Topic **GRID**
 - TATB.grid, 29
 - TATC.grid, 29
- *Topic **LFD**
 - LFD, 15
 - quant, 19
- *Topic **Mean Individual Weight indices**
 - index.ts, 10
- *Topic **Spearman test**
 - spear, 26
- *Topic **TA**
 - dd.distance, 6
 - dd.to.MEDITS, 7
 - haul.plot, 8
 - m.TATB, 16
 - m.TATC, 17
 - MEDITS.to.dd, 19
 - TATB.grid, 29
 - TATC.grid, 29
- *Topic **TB**
 - m.TATB, 16
 - TATB.grid, 29
- *Topic **TC**
 - m.TATC, 17
 - TATC.grid, 29
- *Topic **abundance indices**
 - index.ts, 10
- *Topic **abundance**
 - bubble.rs, 2
 - index.rs, 9
- *Topic **biomass indices**
 - index.ts, 10
- *Topic **biomass**
 - index.rs, 9
- *Topic **bubble plot**
 - bubble.rs, 2
- *Topic **coordinates**
 - dd.distance, 6
 - dd.to.MEDITS, 7
 - MEDITS.distance, 18
 - MEDITS.to.dd, 19
- *Topic **distance**
 - MEDITS.distance, 18
- *Topic **error**
 - check.format, 5
- *Topic **format**
 - check.format, 5
- *Topic **grid**
 - sp.index, 23
- *Topic **land**
 - land.points, 14
- *Topic **map**
 - bubbleplot, 4
- *Topic **merge table**
 - m.TATB, 16
- *Topic **merging tables**
 - m.TATC, 17
- *Topic **percentile of the LFD**
 - quant, 19
- *Topic **plot**
 - haul.plot, 8
- *Topic **points**
 - land.points, 14
- *Topic **polygons**
 - land.points, 14
- *Topic **recruits**
 - bubble.rs, 2
- *Topic **sex ratio**
 - sexratio.ts, 21
- *Topic **sex**
 - LFD, 15
- *Topic **spatial indicators**
 - sp.index, 23
- *Topic **spawners**
 - bubble.rs, 2

- *Topic **spearman test**
 - spearman.test, 27
- *Topic **time series**
 - index.ts, 10
 - sexratio.ts, 21
- *Topic **timeseries**
 - index.rs, 9
- *Topic **trend**
 - spear, 26
 - spearman.test, 27

- bubble.rs, 2
- bubbleplot, 4

- cgpmgrid, 5
- check.format, 5
- countries, 6

- dd.distance, 6
- dd.to.MEDITS, 7
- depth_1, 7
- depth_2, 7
- depth_3, 8

- haul.plot, 8

- index.rs, 9
- index.ts, 10

- land.points, 14
- LFD, 15

- m.TATB, 16
- m.TATC, 17
- MEDITS.distance, 18
- MEDITS.to.dd, 19

- quant, 19

- sexratio.ts, 21
- sp.index, 23
- spear, 26
- spearman.test, 27
- strata_scheme, 28
- stratification_scheme, 28

- TA, 28
- TA_cols, 30
- TATB.grid, 29
- TATC.grid, 29

- TB, 30
- TB_cols, 30
- TC, 31
- TC_cols, 31

- wmap, 31