

Package ‘BioIndex’

March 26, 2026

Type Package

Title collection of functions used to perform analyses on data in MEDITS format

Version 0.6.03

Author Walter Zupa

Maintainer Walter Zupa <zupa@fondazionecoispa.org>, <walter@zupa.it>

Description The package is a collection of functions used by BioIndex software.

License GPL-3

Depends R (>= 4.1),stringr,ggplot2,tidytterra

Imports

hms,marmap,gridExtra,reshape2, dplyr, magrittr,terra,methods,zip, mgcv, RoME, shiny, shinyjs

Encoding UTF-8

LazyData TRUE

LazyDataCompression xz

RoxygenNote 7.3.3

Suggests rmarkdown,
knitr,
maps (>= 3.4.1),
mapproj

VignetteBuilder knitr

Contents

ALK	3
ALKf	3
BioIndex	4
bubbleplot_RS_by_hauls	5
bubble_plot_by_haul_indexes	6
centroidi	7
cgpmgrid	7
check_date_haul	7
check_dictionary	8
check_hauls_TBTA	8
check_numeric_range	9
continent	9
convert_coordinates	10

dd.distance	10
dd.to.MEDITS	11
hauls_position	11
index_on_grid	12
index_recr	13
index_spawn	13
index_ts_F	14
index_ts_M	15
indices_ts	16
IUT	16
LFD	17
Lquant	18
LW	19
LWf	19
MEDITS.distance	20
MEDITS.to.dd	20
med_bathy	21
merge_TATB	21
merge_TATBTC	23
merge_TATC	24
MIW	26
overlayGrid	27
quant	27
run_BioIndex_app	28
sex_ratio	28
sex_ratio_on_grid	29
spear	30
spearman	30
strata_scheme	31
strata_scheme_rapana	31
stratification	32
stratification_rapana	32
stratum_0_125	32
stratum_0_200	33
stratum_0_35	33
stratum_0_45	33
stratum_0_800	34
stratum_200_800	34
TA	34
TA_cols	35
TB	35
TB_cols	35
TC	36
TC_cols	36

ALK *ALK (Age Length Key)*

Description

ALK (Age Length Key)

Usage

ALK(*ta*, *te*, *sp*, *GSA*, *country* = "all", *nyears* = NA, *wd* = NA, *verbose* = FALSE)

Arguments

<i>ta</i>	MEDITS or MEDITS-like TA table
<i>te</i>	MEDITS or MEDITS-like TE table
<i>sp</i>	species rubin code (MEDITS format, e.g. "MERLMER")
<i>GSA</i>	reference GSA for the analysis
<i>country</i>	reference country
<i>nyears</i>	number of years of the time series to be considered in the analysis
<i>wd</i>	path of the working directory
<i>verbose</i>	boolean. If TRUE messages are prompted in the console

ALKf *Estimation of ALK*

Description

Estimation of ALK

Usage

ALKf(*te*, *sp*, *GEAR*, *GSA*, *country* = NA, *years* = 5)

Arguments

<i>te</i>	MEDITS or MEDITS-like TE table
<i>sp</i>	species rubin code (MEDITS format, e.g. "MERLMER")
<i>GEAR</i>	type of gear reported in the corresponding TA file
<i>GSA</i>	reference GSA for the analysis
<i>country</i>	reference country
<i>years</i>	number of years to be considered in the analysis

 BioIndex

BioIndex

Description

R code to perform analysis of trawl survey data using MEDITS file format

Usage

```
BioIndex(
  ta,
  tb,
  tc,
  sspp,
  rec_threshold,
  spaw_threshold,
  haul_threshold = 30,
  sexes = "all",
  depth,
  GSA,
  country = "all",
  map_lim,
  depth_lines = c(10, 200, 800),
  strata = BioIndex::strata_scheme,
  stratification_tab = BioIndex::stratification,
  resolution = NA,
  buffer = 0.1,
  wd,
  zip = TRUE,
  save = TRUE,
  verbose = TRUE
)
```

Arguments

ta	data frame of the TA table in the MEDITS format
tb	data frame of the TB table in the MEDITS format
tc	data frame of the TC table in the MEDITS format
sspp	reference species for the analysis
rec_threshold	cutoff threshold for recruits (reported in mm)
spaw_threshold	cutoff threshold for spawners (reported in mm)
haul_threshold	minimum number of individuals to be used in estimation of the spatial indicators
sexes	reference sex for the analysis
depth	reference depth range
GSA	reference GSA for the analysis
country	reference country
map_lim	coordinates limits for the maps

depth_lines	depth contours to be plotted in the maps (3 values allowed, e.g c(50,200,800))
strata	data frame of the reference strata for the study area
stratification_tab	data frame of the stratification scheme
resolution	resolution of the depth line
buffer	buffer around the map
wd	path of the working directory
zip	boolean. If TRUE the results are stored in a zip file into the working directory
save	boolean. If TRUE the results are stored in the working directory
verbose	boolean. If TRUE messages are prompted in the console

Examples

```
BioIndex(ta=TA, tb=TB, tc=TC, sspp="MERLMER",rec_threshold=200,
spaw_threshold=210,sexes="all", depth=c(10,800), GSA=10, country="all",
map_lim=c(13.3,15.2,39.9,41.3),depth_lines=c(50,200,800),
strata=BioIndex::strata_scheme, stratification_tab =
BioIndex::stratification, resolution=1, buffer=0.1, wd=tempdir(),
zip=TRUE, save=TRUE, verbose=TRUE)
```

```
bubbleplot_RS_by_hauls
```

Bubbleplot of abundance indices for recruits and spawners

Description

The function generates bubbleplots of abundance indices for recruits and spawners. If no resolution is specified (`res = NA`), the function works offline and uses an internal bathymetry dataset (`med_bathy`) covering the Mediterranean and Black Sea, reducing the computational time.

Usage

```
bubbleplot_RS_by_hauls(
  mTATC,
  map_range,
  thresh_rec,
  thresh_spaw,
  depths = c(50, 200, 800),
  res = NA,
  buffer = 0.1,
  wd,
  save = FALSE,
  verbose = FALSE
)
```

Arguments

mTATC	mTATC table
map_range	range of coordinates for the map
thresh_rec	threshold value to select recruits data from mTATC table (reported in mm)
thresh_spaw	threshold value to select spawners data from mTATC table (reported in mm)
depths	three reference bathymetric lines to be plotted in the maps
res	resolution of the depth lines
buffer	buffer around the map
wd	working directory
save	boolean. If TRUE the outputs are saved in the local folder
verbose	boolean. If TRUE messages are prompted in the console

bubble_plot_by_haul_indexes

Bubble plot of abundance and biomass indices by haul

Description

The function generates bubble plot of abundance and biomass indices by haul. If no resolution is specified (res = NA), the function works offline and uses an internal bathymetry dataset (med_bathy) covering the Mediterranean and Black Sea, reducing the computational time.

Usage

```
bubble_plot_by_haul_indexes(
  mTATB,
  map_lim,
  depth_lines,
  buffer = 0,
  res = NA,
  wd = NA,
  save = TRUE,
  verbose = TRUE
)
```

Arguments

mTATB	data frame
map_lim	coordinates limits for the plotted map
depth_lines	vector of three depth bathymetrical lines to be plotted
buffer	buffer to the coordinate limits in map units
res	resolution of the bathymetrical lines
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)
verbose	boolean. If TRUE a message is printed

centroidi	<i>centroidi</i>
-----------	------------------

Description

centroidi

Usage

centroidi

Format

An object of class PackedSpatVector of length 1.

cgpmgrid	<i>cgpmgrid</i>
----------	-----------------

Description

cgpmgrid

Usage

cgpmgrid

Format

An object of class PackedSpatVector of length 1.

check_date_haul	<i>Check date consistency</i>
-----------------	-------------------------------

Description

The function allows to check the consistency of date among the tables before merging them together.

Usage

```
check_date_haul(DataTA, Data, year, wd = NA, suffix, verbose = TRUE)
```

Arguments

DataTA	data frame of the TA table
Data	data frame of one table among TB, TC, TE and TL
year	reference year for the analysis
wd	working directory
suffix	name of the logfile
verbose	boolean. If TRUE messages are reported in the console

check_dictionary	<i>Check dictionary (RoME)</i>
------------------	--------------------------------

Description

The function checks whether the values contained in specific fields are consistent with the allowed values of the dictionaries.

Usage

```
check_dictionary(
  ResultData,
  Field,
  Values,
  year,
  wd = NA,
  suffix,
  verbose = FALSE
)
```

Arguments

ResultData	data frame in MEDITS tables
Field	field of the table to be checked
Values	vector of the allowed values
year	reference year for the analysis
wd	working directory
suffix	name of the log file
verbose	boolean. If TRUE messages are prompted in the console

check_hauls_TBTA	<i>Check presence in TB of the hauls in TA</i>
------------------	--

Description

The function check the presence of the TB (catch data table) hauls in the TA (haul data table)

Usage

```
check_hauls_TBTA(DataTA, DataTB, year, wd = NA, suffix, verbose = FALSE)
```

Arguments

DataTA	data frame of TA table
DataTB	data frame of TB table
year	reference year for the analysis
wd	working directory
suffix	name of the logfile
verbose	boolean. If TRUE messages are prompted in the console

check_numeric_range *Check consistency of numeric ranges*

Description

The function checks whether the values contained in specific fields are consistent within the allowed range of values.

Usage

```
check_numeric_range(
  Data,
  Field,
  Values,
  year,
  wd = NA,
  suffix,
  verbose = FALSE
)
```

Arguments

Data	data frame of a table in MEDITS format
Field	field of the table to be checked
Values	vector of the allowed values
year	reference year for the analysis
wd	working directory
suffix	name of the log file
verbose	boolean. If TRUE messages are prompted in the console

continent *continent*

Description

continent

Usage

```
continent
```

Format

An object of class PackedSpatVector of length 1.

convert_coordinates *MEDITS coordinates in decimal degrees*

Description

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

Usage

```
convert_coordinates(Data)
```

Arguments

Data data frame of TA table

Value

the function return the same data frame with the coordinates converted in the decimal degrees format

dd.distance *Estimate hauls distances (decimal degrees)*

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) with coordinates reported as decimal degrees

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.

Value

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

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.

hauls_position	<i>Plot of hauls time series</i>
----------------	----------------------------------

Description

This function generates a spatial plot of haul positions over time, displaying haul labels and bathymetric lines over a customizable map extent. If no resolution is specified (`res = NA`), the function works offline and uses an internal bathymetry dataset (`med_bathy`) covering the Mediterranean and Black Sea, reducing the computational time.

Usage

```
hauls_position(  
  mTATB,  
  country = "all",  
  map_lim,  
  depth_lines,  
  buffer = 0,  
  res = NA,  
  wd = NA,  
  save = TRUE,  
  verbose = TRUE  
)
```

Arguments

mTATB	data frame
country	country code as reported in MEDITS format. "all" code to perform the analysis on all the countries of the same GSA
map_lim	coordinates limits for the plotted map
depth_lines	vactor of three depth bathymetrical lines to be plotted
buffer	buffer to the coordinate limits in map units
res	resolution of the bathymetrical lines
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)
verbose	boolean. If TRUE a message is printed

index_on_grid	<i>Generating maps of indexes</i>
---------------	-----------------------------------

Description

Generating maps of indexes

Usage

```
index_on_grid(
  mTATBsp,
  stratum,
  wd,
  map_range,
  threshold = 30,
  verbose = FALSE,
  save = FALSE
)
```

Arguments

mTATBsp	spatial mTATB
stratum	reference stratum range (allowed values: "10,200", "10,800", "200,800", "5,35", "5,45")
wd	working directory
map_range	range of coordinates for the map
threshold	minimum number of individuals per haul
verbose	boolean. If TRUE messages are prompted in the console
save	boolean. If TRUE the results are stored in the working directory

index_recr	<i>Estimation of abundance indices for recruits</i>
------------	---

Description

Estimation of abundance indices for recruits

Usage

```
index_recr(
  mTATB,
  mTATC,
  GSA,
  country,
  depth_range,
  cutoff,
  stratification,
  wd = NA,
  save = TRUE
)
```

Arguments

mTATB	data frame
mTATC	data frame
GSA	reference GSA for the analysis
country	vector of reference countries for the analysis
depth_range	range of depth strata to perform the analysis (min, max)
cutoff	cutoff value for splitting recruits portion of population (reported in mm)
stratification	data frame of strata surface area
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)

index_spawn	<i>Estimation of abundance indices for spawners (females)</i>
-------------	---

Description

Estimation of abundance indices for spawners (females)

Usage

```

index_spawn(
  mTATB,
  mTATC,
  GSA,
  country,
  depth_range,
  cutoff,
  stratification,
  wd = NA,
  save = TRUE
)

```

Arguments

mTATB	data frame
mTATC	data frame
GSA	reference GSA for the analysis
country	vector of reference countries for the analysis
depth_range	range of depth strata to perform the analysis (min, max)
cutoff	cutoff value for splitting spawner portion of population (reported in mm)
stratification	data frame of strata surface area
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)

index_ts_F

Estimation of abundance indices for females

Description

Estimation of abundance indices for females

Usage

```

index_ts_F(
  mTATB,
  GSA,
  country_analysis,
  depth_range,
  strata_scheme,
  stratification,
  wd = NA,
  save = TRUE
)

```

Arguments

mTATB	data frame
GSA	reference GSA for the analysis
country_analysis	vector of reference countries for the analysis
depth_range	range of depth strata to perform the analysis (min, max)
strata_scheme	data frame of the stratification scheme
stratification	data frame of strata surface area
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)

index_ts_M	<i>Estimation of abundance indices for males</i>
------------	--

Description

Estimation of abundance indices for males

Usage

```
index_ts_M(
  mTATB,
  GSA,
  country_analysis,
  depth_range,
  strata_scheme,
  stratification,
  wd = NA,
  save = TRUE
)
```

Arguments

mTATB	data frame
GSA	reference GSA for the analysis
country_analysis	vector of reference countries for the analysis
depth_range	range of depth strata to perform the analysis (min, max)
strata_scheme	data frame of the stratification scheme
stratification	data frame of strata surface area
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)

indices_ts	<i>Estimation of abundance and biomass indices</i>
------------	--

Description

Estimation of abundance and biomass indices

Usage

```
indices_ts(
  mTATB,
  GSA,
  country = "all",
  depth_range,
  strata_scheme,
  stratification,
  wd = NA,
  save = TRUE
)
```

Arguments

mTATB	data frame
GSA	reference GSA for the analysis
country	reference countries in the GSA for the analysis
depth_range	range of depth strata to perform the analysis (min, max)
strata_scheme	data frame of the stratification scheme
stratification	data frame of strata surface area
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)

IUT	<i>Interception Union Tets</i>
-----	--------------------------------

Description

Interception Union Tets

Usage

```
IUT(abundance, biomass, species, lastn = 5, save = TRUE)
```

Arguments

abundance	dataframe of abundance time series as produced by indices_ts function
biomass	dataframe of biomass time series as produced by indices_ts function
species	reference species for the analysis (MEDITS code)
lastn	number of recent years for diagnosis of change
save	boolean. If TRUE results are saved in the output folder

Description

Input parameters include biological and haul data, stratification schemes, reference filters (e.g., sex, GSA, country, depth), and output control options (working directory, saving, verbosity).

Usage

```
LFD(
  mTATC,
  sex = "all",
  GSA,
  country = "all",
  depth_range,
  strata_scheme,
  stratification,
  wd = NA,
  save = TRUE,
  verbose = TRUE
)
```

Arguments

mTATC	Data frame resulting from the merge of TA and TC datasets using ‘merge_TATBTC()’. It must include raised numbers.
sex	Character. Target sex for the analysis. Allowed values: ‘F’, ‘M’, ‘I’, ‘N’, or ‘all’ (default) for combined sexes.
GSA	Numeric. The GSA (Geographical Sub-Area) code of reference for the analysis.
country	Character vector. Reference country or countries for the analysis. Use ‘all’ (default) to include all countries available in the data.
depth_range	Numeric vector of length 2, specifying the minimum and maximum depths (in meters) to filter the hauls used in the analysis.
strata_scheme	Data frame containing the stratification scheme. Must include ‘CODE’, ‘MIN_DEPTH’, ‘MAX_DEPTH’, ‘GSA’, ‘COUNTRY’.
stratification	Data frame with surface areas per stratum. Must include columns: ‘GSA’, ‘CODE’, ‘COUNTRY’, ‘SURF’.
wd	Character. Working directory used to save output plots and tables. Required if ‘save = TRUE’.
save	Logical. If ‘TRUE’ (default), the function saves output tables and plots to ‘wd/output/’. If ‘FALSE’, no files are saved.
verbose	Logical. If ‘TRUE’ (default), informative messages are printed to the console to trace the function steps.

Details

This function estimates and plots the length frequency distribution (LFD) by year and by stratum, based on merged biological and haul data from MEDITS surveys. It computes raised numbers, applies stratification weights, and generates publication-ready plots and CSV outputs. Stratification weighting is based on swept area and surface area of the strata.

The function:

- Filters hauls by depth and country.
- Computes raised numbers per haul.
- Applies stratified weights based on the area per stratum.
- Outputs and/or plots the length frequency distribution by year and stratum.
- Handles sex-specific or combined-sex analyses.

The plot outputs include:

- Combined LFD by year across all strata.
- LFD by stratum (faceted), stratified by year.

Output files are saved as CSV and high-resolution JPEGs if 'save = TRUE' and 'wd' is defined.

Value

A named list with two elements:

• **'LFD'** A data frame of total LFD by year across all strata.

• **'LFD by stratum'** A data frame of LFD by year and by stratum.

Lquant

Estimation of L50 and L95

Description

Estimation of L50 and L95

Usage

```
Lquant(lfd, wd = NA, sspp, GSA, save = TRUE, verbose = TRUE)
```

Arguments

lfd	data frame of combined LFD
wd	working directory
sspp	MEDITS code for the selected species
GSA	reference area for the analysis
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)
verbose	boolean. If TRUE messages are reported in the console

LW *LW (Length-Weight relationship)*

Description

LW (Length-Weight relationship)

Usage

LW(ta, te, sp, GSA, country = "all", nyears = NA, wd = NA, verbose = FALSE)

Arguments

ta	MEDITS or MEDITS-like TA table
te	MEDITS or MEDITS-like TE table
sp	species rubin code (MEDITS format, e.g. "MERLMER")
GSA	reference GSA for the analysis
country	reference country
nyears	number of years of the time series to be considered in the analysis
wd	path of the working directory
verbose	boolean. If TRUE messages are prompted in the console

LWf *Estimation of LW relationship*

Description

Estimation of LW relationship

Usage

LWf(TE, sp, GEAR, GSA, country = NA, n_records = 10)

Arguments

TE	MEDITS or MEDITS-like TE table
sp	species rubin code (MEDITS format, e.g. "MERLMER")
GEAR	type of gear reported in the corresponding TA file
GSA	reference GSA for the analysis
country	reference country
n_records	minimum number of records to perform the analysis

MEDITS.distance *Estimation of haul distance*

Description

Estimation of haul distance

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.

Value

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

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

`med_bathy`*Mediterranean and Black Sea bathymetry (0–1000 m, bathy object)*

Description

A precomputed bathy object containing bathymetric data for the Mediterranean Sea and the Black Sea. Depth values are restricted between 0 and -1000 meters. This dataset was downloaded using [getNOAA.bathy](#) with a resolution of 1 arc-minute, and filtered to remove deeper areas.

Usage

```
data(med_bathy)
```

Format

An object of class bathy (a matrix with longitude and latitude as axes, and depth in meters)

Details

The object can be used directly with functions from the **marmap** package, such as `plot.bathy()` and `get.depth()`.

The spatial extent includes:

- Longitude: from -6° to 42°
- Latitude: from 30° to 47°
- Depth: from 0 to -1000 meters

Only marine cells within this depth range are retained. Land and deeper areas are set to NA.

Source

NOAA ETOPO1 via `marmap::getNOAA.bathy()`

See Also

[getNOAA.bathy](#), [plot.bathy](#), [bubbleplot_RS_by_hauls](#)

`merge_TATB`*Merge TA and TB tables (haul-level catches)*

Description

Combines a MEDITS **TA** table (haul metadata) with the corresponding **TB** table (catch-per-haul by species). The function keeps only valid hauls, performs all official RoME quality checks, computes spatial means, swept area, depth stratum, biomass/density indicators, and—optionally—writes the merged data to disk.

Usage

```
merge_TATB(
  ta,
  tb,
  species,
  country = "all",
  strata = BioIndex::strata_scheme,
  wd = NA,
  save = TRUE,
  verbose = TRUE
)
```

Arguments

ta	A 'data.frame'/'data.table' containing a full TA dataset (columns listed in 'BioIndex::TA_cols').
tb	A 'data.frame'/'data.table' containing a full TB dataset (columns listed in 'BioIndex::TB_cols').
species	Character, MEDITS 7-letter code (e.g. "ARISFOL"). The first 4 characters are interpreted as *GENUS* and the last 3 as *SPECIES*.
country	Character vector of ISO-3 country codes to keep; use "all" (default) to keep every country present in 'ta'.
strata	Depth-stratum reference table; default is 'BioIndex::strata_scheme'.
wd	Working directory. If 'NA' (the default when 'save = FALSE') no files are written.
save	Logical. If 'TRUE', writes "'mergeTATB_<GENUS><SPECIES>.csv'" to 'file.path(wd, "output")'.
verbose	Logical; if 'TRUE' (default) prints progress messages.

Details

The implementation mirrors the original BioIndex routine but includes two speed-ups: (1) vectorised replacement of missing "NA NA" records, (2) a single loop over depth strata instead of a nested haul \times stratum loop. Results are identical to the reference routine.

Value

A 'data.frame' with one row per haul and the following groups of variables: * **TA** metadata (haul position, times, depths, etc.) * **TB** catch totals (numbers and weight) * Calculated fields: mean lat/lon, swept area, depth stratum, density ('N_h', 'N_km2') and biomass ('kg_h', 'kg_km2')

See Also

[BioIndex] package documentation.

Examples

```
## Not run:
m_tb <- merge_TATB(
  ta      = ta_df,
  tb      = tb_df,
```

```

    species = "ARISFOL",
    country = "ITA",
    wd      = "/path/to/project",
    save    = TRUE
  )
head(m_tb)

## End(Not run)

```

merge_TATBTC

Merge TA–TB and TA–TC tables (MEDITS protocol)

Description

Combines a MEDITS **TA** file (haul metadata) with the corresponding **TB** file (haul-level catches by species) and **TC** file (length–frequency by haul, sex and maturity). The routine:

- filters hauls by validity and by country;
- performs the full set of RoMEBS quality checks (times, positions, wing opening, haul/date consistency);
- merges TA with TB and TA with TC, respectively;
- computes swept area, mean positions, depth stratum, raising factors, densities and biomasses;
- (optionally) writes the two merged tables to `file.path(wd, "output")`.

Usage

```

merge_TATBTC(
  ta,
  tb,
  tc,
  species,
  country = "all",
  strata = BioIndex::strata_scheme,
  wd = NA,
  save = TRUE,
  verbose = TRUE
)

```

Arguments

<code>ta</code>	A MEDITS or MEDITS-like TA table (columns listed in <code>BioIndex::TA_cols</code>).
<code>tb</code>	A MEDITS or MEDITS-like TB table (columns listed in <code>BioIndex::TB_cols</code>).
<code>tc</code>	A MEDITS or MEDITS-like TC table (columns listed in <code>BioIndex::TC_cols</code>).
<code>species</code>	Character. MEDITS 7-letter RubIN code (e.g. "MERLMER"): the first 4 letters are used as <i>GENUS</i> , the last 3 as <i>SPECIES</i> .
<code>country</code>	Character vector of MEDITS country codes to keep. Use "all" (default) to include every country present in <code>ta</code> .
<code>strata</code>	A data-frame with the depth-stratification scheme adopted by the MEDITS survey. Defaults to <code>BioIndex::strata_scheme</code> .

wd	Working directory. When save = TRUE, the merged tables are written to file.path(wd, "output").
save	Logical. If TRUE (default) the function writes "mergeTATB_<GENUS><SPECIES>.csv" and "mergeTATC_<GENUS><SPECIES>.csv".
verbose	Logical (default TRUE); prints progress messages.

Details

The implementation reproduces the official BioIndex workflow. Two micro-optimisations are included:

1. vectorised replacement of missing "NA NA" entries in both merges;
2. a single loop over depth strata (instead of haul × stratum) to assign STRATUM_CODE.

Numerical outputs are identical to the reference routine.

Value

A list of two data.frames:

merge_TA_TB One row per haul with TA metadata, TB catch totals, depth stratum, densities and biomasses.

merge_TA_TC One row per haul/length-class/sex/maturity with TA metadata, TC counts, depth stratum, raising factor, densities and biomasses.

Examples

```
## Not run:
m <- merge_TATBTC(
  ta      = TA,
  tb      = TB,
  tc      = TC,
  species = "MERLMER",
  country = "all",
  wd      = tempdir(),
  verbose = TRUE
)
mTATB <- m[[1]] # TA-TB merged table
mTATC <- m[[2]] # TA-TC merged table

## End(Not run)
```

merge_TATC

Merge TA and TC tables (haul-level length–frequency data)

Description

Combines a MEDITS **TA** table (haul metadata) with the corresponding **TC** table (length-frequency sample by haul and sex/maturity). The function keeps only valid hauls, runs all relevant RoMEBS quality checks, computes swept area, depth stratum, raising factors, abundance/biomass indicators, and—optionally—writes the merged data.

Usage

```
merge_TATC(
  ta,
  tc,
  species,
  country = "all",
  strata = BioIndex::strata_scheme,
  wd = NA,
  save = TRUE,
  verbose = TRUE
)
```

Arguments

ta	A 'data.frame'/'data.table' containing a full TA dataset (columns listed in 'BioIndex::TA_cols').
tc	A 'data.frame'/'data.table' containing a full TC dataset (columns listed in 'BioIndex::TC_cols').
species	Character, MEDITS 7-letter code (e.g. "ARISFOL"). The first 4 characters are interpreted as *GENUS* and the last 3 as *SPECIES*.
country	Character vector of ISO-3 country codes to keep; use "all" (default) to keep every country present in 'ta'.
strata	Depth-stratum reference table; default is 'BioIndex::strata_scheme'.
wd	Working directory. If 'NA' (the default when 'save = FALSE') no files are written.
save	Logical. If 'TRUE', writes "mergeTATC_<GENUS><SPECIES>.csv" to 'file.path(wd, "output")'.
verbose	Logical; if 'TRUE' (default) prints progress messages.

Details

The code is identical to the official BioIndex routine except for two micro-optimisations: vectorised handling of missing "NA NA" entries and a single depth-stratum loop. Numerical results remain unchanged.

Value

A 'data.frame' in which each row represents one length-class (and sex/maturity) sampled in a haul, including: * **TA** metadata * **TC** length-frequency counts and weights * Calculated fields: mean lat/lon, swept area, depth stratum, raising factor, density ('N_h', 'N_km2') and biomass ('kg_h', 'kg_km2')

See Also

[BioIndex] package documentation.

Examples

```
## Not run:
m_tc <- merge_TATC(
  ta      = ta_df,
```

```

tc      = tc_df,
species = "ARISFOL",
country = "ESP",
wd      = "/path/to/project",
save    = FALSE
)
head(m_tc)

## End(Not run)

```

MIW

Estimation of Mean Individual Weight (MIW) time series

Description

Estimation of Mean Individual Weight (MIW) time series

Usage

```

MIW(
  mTATB,
  GSA,
  country = "all",
  depth_range,
  strata_scheme,
  stratification,
  wd = NA,
  save = TRUE,
  verbose = TRUE
)

```

Arguments

mTATB	data frame of the merged TA and TB
GSA	reference GSA for the analysis
country	reference countries in the GSA for the analysis
depth_range	range of depth strata to perform the analysis (min, max)
strata_scheme	data frame of the stratification scheme
stratification	data frame of strata surface area
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)
verbose	boolean. If TRUE messages are reported in the console

overlayGrid	<i>Overlay mTATB and mTATC on GFCM spatial grid</i>
-------------	---

Description

Overlay mTATB and mTATC on GFCM spatial grid

Usage

```
overlayGrid(
  mTATB,
  mTATC,
  GSA = NA,
  country = "all",
  wd = NA,
  save = TRUE,
  verbose = FALSE
)
```

Arguments

mTATB	data frame of the merged TA and TB
mTATC	data frame of the merged TA and TC
GSA	reference GSA for the analysis
country	reference countries for the analysis
wd	working directory used to save results
save	boolean. If TRUE the outputs are saved in the local folder
verbose	boolean. If TRUE messages are prompted in the console

quant	<i>Quantile estimation</i>
-------	----------------------------

Description

Quantile estimation

Usage

```
quant(weighted, qlin = 0.95)
```

Arguments

weighted	LFD data.frame
qlin	reference quantile for the analysis

run_BioIndex_app	<i>Run the BioIndex Shiny application</i>
------------------	---

Description

Launches the embedded Shiny application included in the package.

Usage

```
run_BioIndex_app()
```

sex_ratio	<i>Sex ratio</i>
-----------	------------------

Description

Sex ratio

Usage

```
sex_ratio(
  mTATB,
  GSA,
  country,
  depth_range,
  stratas,
  stratification,
  wd = NA,
  save = TRUE,
  verbose = FALSE
)
```

Arguments

mTATB	data frame of the merged TA and TB
GSA	reference GSA for the analysis
country	vector of reference countries for the analysis
depth_range	range of depth strata to perform the analysis (min, max)
stratas	data frame of the reference strata for the study area
stratification	data frame of strata surface area
wd	working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)
verbose	boolean. If TRUE a message is printed

sex_ratio_on_grid *Plot sex ratio spatial distribution*

Description

This function calculates and plots the spatial distribution of sex ratio ($F / (F + M)$) over the GFCM grid for a given species. It uses data from merged MEDITS datasets (TA, TB, TC), previously spatialized with `overlayGrid()`. The function filters hauls by total abundance threshold and depth range, calculates sex ratio per grid cell, and plots the output using color-coded categories based on quantiles. The result is a choropleth map of sex ratio patterns, useful to highlight spatial differences in sex structure. Raw sex ratio estimates per grid cell can also be exported.

Usage

```
sex_ratio_on_grid(  
  mTATBsp,  
  depth,  
  wd,  
  map_range,  
  threshold = 30,  
  verbose = FALSE,  
  save = FALSE  
)
```

Arguments

mTATBsp	A spatial version of the merged TA-TB dataset, processed through <code>overlay-Grid()</code> , containing sex information.
depth	Character string specifying the depth range used for filtering (e.g., "10,800"). Must correspond to available internal GFCM grid masks.
wd	Working directory. Used to save output files if <code>save = TRUE</code> .
map_range	numeric vector with coordinates defining the map extent (<code>'xmin'</code> , <code>'xmax'</code> , <code>'ymin'</code> , <code>'ymax'</code>).
threshold	Minimum number of individuals required per haul to be included in the sex ratio estimation. Default is 30.
verbose	Logical. If <code>'TRUE'</code> , informative messages are printed to the console.
save	Logical. If <code>'TRUE'</code> , the plot and sex ratio table are saved to the working directory.

Value

A `'data.frame'` containing sex ratio (`'ratio'`), standard deviation (`'sd'`), and coefficient of variation (`'CV'`) for each GFCM grid cell.

spear	<i>Spearman test for timeseries</i>
-------	-------------------------------------

Description

Spearman test for timeseries

Usage

```
spear(x)
```

Arguments

x	time series
---	-------------

spearman	<i>Spearman test</i>
----------	----------------------

Description

Spearman test

Usage

```
spearman(abundance = NA, biomass = NA, years, sspp = NA, wd = NA, save = TRUE)
```

Arguments

abundance	data frame of abundance indices
biomass	data frame of biomass indices
years	reference years for the analysis
sspp	reference species for the analysis
wd	path of working directory
save	boolean. If TRUE the plot is saved in the user defined working directory (wd)

strata_scheme	<i>stratification scheme</i>
---------------	------------------------------

Description

Stratification scheme adopted in the bottom trawl demersal survey (e.g. MEDITS survey).

Usage

strata_scheme

Format

An object of class `data.frame` with 126 rows and 5 columns.

Author(s)

Walter Zupa <zupa@fondazionecoispa.it>

strata_scheme_rapana	<i>stratification scheme (rapa whelk)</i>
----------------------	---

Description

Stratification scheme adopted in the rapa whelk survey (e.g. Black Sea beam trawl survey).

Usage

strata_scheme_rapana

Format

An object of class `data.frame` with 7 rows and 5 columns.

Author(s)

Walter Zupa <zupa@fondazionecoispa.it>

stratification	<i>stratification</i>
----------------	-----------------------

Description

Data frame containing the surface area relative to the depth strata adopted in the stratification scheme (strata_scheme) of the demersal surveys (e.g. MEDITS survey).

Usage

```
stratification
```

Format

An object of class `data.frame` with 276 rows and 6 columns.

stratification_rapana	<i>stratification (rapa whelk)</i>
-----------------------	------------------------------------

Description

Data frame containing the surface area relative to the depth strata adopted in the stratification scheme (strata_scheme) of the rapa whelk surveys (e.g. Black Sea beam trawl survey).

Usage

```
stratification_rapana
```

Format

An object of class `data.frame` with 7 rows and 6 columns.

stratum_0_125	<i>stratum_0_125</i>
---------------	----------------------

Description

```
stratum_0_125
```

Usage

```
stratum_0_125
```

Format

An object of class `PackedSpatVector` of length 1.

stratum_0_200	<i>stratum_0_200</i>
---------------	----------------------

Description

stratum_0_200

Usage

stratum_0_200

Format

An object of class PackedSpatVector of length 1.

stratum_0_35	<i>stratum_0_35</i>
--------------	---------------------

Description

stratum_0_35

Usage

stratum_0_35

Format

An object of class PackedSpatVector of length 1.

stratum_0_45	<i>stratum_0_45</i>
--------------	---------------------

Description

stratum_0_45

Usage

stratum_0_45

Format

An object of class PackedSpatVector of length 1.

stratum_0_800	<i>stratum_0_800</i>
---------------	----------------------

Description

stratum_0_800

Usage

stratum_0_800

Format

An object of class PackedSpatVector of length 1.

stratum_200_800	<i>stratum_200_800</i>
-----------------	------------------------

Description

stratum_200_800

Usage

stratum_200_800

Format

An object of class PackedSpatVector of length 1.

TA	<i>TA table example</i>
----	-------------------------

Description

TA table example

Usage

TA

Format

An object of class data.frame with 100 rows and 43 columns.

TA_cols	<i>TA table headings</i>
---------	--------------------------

Description

TA table headings

Usage

TA_cols

Format

An object of class character of length 22.

Author(s)

Walter Zupa <zupa@fondazionecoispa.it>

TB	<i>TB table example</i>
----	-------------------------

Description

TB table example

Usage

TB

Format

An object of class data.frame with 3059 rows and 19 columns.

TB_cols	<i>TB table headings</i>
---------	--------------------------

Description

TB table headings

Usage

TB_cols

Format

An object of class character of length 8.

Author(s)

Walter Zupa <zupa@fondazionecoispa.it>

TC	<i>TC table example</i>
----	-------------------------

Description

TC table example

Usage

TC

Format

An object of class `data.frame` with 11185 rows and 22 columns.

TC_cols	<i>TC table headings</i>
---------	--------------------------

Description

TC table headings

Usage

TC_cols

Format

An object of class `character` of length 11.

Author(s)

Walter Zupa <zupa@fondazionecoispa.it>

Index

- * **Black**
 - strata_scheme_rapana, 31
 - stratification_rapana, 32
 - * **MEDITS**
 - stratification, 32
 - TA, 34
 - TB, 35
 - TC, 36
 - * **Sea**
 - strata_scheme_rapana, 31
 - stratification_rapana, 32
 - * **TA**
 - TA, 34
 - TA_cols, 35
 - * **TB**
 - TB, 35
 - TB_cols, 35
 - * **TC**
 - TC, 36
 - TC_cols, 36
 - * **bathymetry**
 - med_bathy, 21
 - * **blacksea**
 - med_bathy, 21
 - * **centroidi**
 - centroidi, 7
 - * **cgpmgrid**
 - cgpmgrid, 7
 - * **continent**
 - continent, 9
 - * **datasets**
 - med_bathy, 21
 - * **mediterranean**
 - med_bathy, 21
 - * **rapa**
 - strata_scheme_rapana, 31
 - stratification_rapana, 32
 - * **stratification**
 - strata_scheme, 31
 - strata_scheme_rapana, 31
 - stratification, 32
 - stratification_rapana, 32
 - * **stratum_0_125**
 - stratum_0_125, 32
 - * **stratum_0_200**
 - stratum_0_200, 33
 - * **stratum_0_35**
 - stratum_0_35, 33
 - * **stratum_0_45**
 - stratum_0_45, 33
 - * **stratum_0_800**
 - stratum_0_800, 34
 - * **stratum_200_800**
 - stratum_200_800, 34
 - * **whelk**
 - strata_scheme_rapana, 31
 - stratification_rapana, 32
- ALK, 3
- ALKf, 3
- BioIndex, 4
- bubble_plot_by_haul_indexes, 6
- bubbleplot_RS_by_hauls, 5, 21
- centroidi, 7
- cgpmgrid, 7
- check_date_haul, 7
- check_dictionary, 8
- check_hauls_TBTA, 8
- check_numeric_range, 9
- continent, 9
- convert_coordinates, 10
- dd.distance, 10
- dd.to.MEDITS, 11
- getNOAA.bathy, 21
- hauls_position, 11
- index_on_grid, 12
- index_recr, 13
- index_spawn, 13
- index_ts_F, 14
- index_ts_M, 15
- indices_ts, 16
- IUT, 16

LFD, 17
Lquant, 18
LW, 19
LWF, 19

med_bathy, 21
MEDITS.distance, 20
MEDITS.to.dd, 20
merge_TATB, 21
merge_TATBTC, 23
merge_TATC, 24
MIW, 26

overlayGrid, 27

plot.bathy, 21

quant, 27

run_BioIndex_app, 28

sex_ratio, 28
sex_ratio_on_grid, 29
spear, 30
spearman, 30
strata_scheme, 31
strata_scheme_rapana, 31
stratification, 32
stratification_rapana, 32
stratum_0_125, 32
stratum_0_200, 33
stratum_0_35, 33
stratum_0_45, 33
stratum_0_800, 34
stratum_200_800, 34

TA, 34
TA_cols, 35
TB, 35
TB_cols, 35
TC, 36
TC_cols, 36