# Package 'BioIndex'

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**Type** Package

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

**Version** 0.5.01

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

**License** GPL-3

**Depends** R (>= 4.1),stringr,ggplot2,tidyterra

**Imports** hms,marmap,gridExtra,reshape2, dplyr, magrittr,terra,methods,zip

**Encoding** UTF-8

**LazyData** TRUE

**LazyDataCompression** xz

**RoxygenNote** 7.2.3

**Suggests** rmarkdown,
knitr

**VignetteBuilder** knitr

## R topics documented:

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| 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 = 1,
    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 |
| `spaw_threshold` | cutoff threshold for spawners |
| `haul_threshold` | minimum number of individuals to be used in estimation of the spatial indicaticators |
| `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) |
| `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 promted in the console |

## Examples

```
BioIndex(ta=TA, tb=TB, tc=TC, sspp="MERLMER",rec_threshold=200, spaw_threshold=210,sexes="all", depth=c(10,8
```

---

`bubbleplot_RS_by_hauls`
                    *Bubbleplot of abundance indices for recruits and spawners*

---

### Description

The function generates bubbleplots of abundance indices for recruits and spawners

### Usage

```
bubbleplot_RS_by_hauls(
  mTATC,
  map_range,
  thresh_rec,
  thresh_spaw,
  depths = c(50, 200, 800),
  res = 1,
  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 |
| `thresh_spaw` | threshold value to select spawners data from mTATC table |
| `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

## Usage

```
bubble_plot_by_haul_indexes(
  mTATB,
  map_lim,
  depth_lines,
  buffer = 0,
  res = 0.1,
  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 | *centroidi* |

---

## Description

centroidi

## Usage

```
centroidi
```

## Format

An object of class `PackedSpatVector` of length 1.

cgpmgrid                    *cgpmgrid*

### Description

cgpmgrid

### Usage

cgpmgrid

### Format

An object of class `PackedSpatVector` of length 1.

check_date_haul            *Check date consistency*

### Description

The function allows to check the consistency of date among the tables befor mergin 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 | *Check dictionary (RoME)* |
|---|---|

## 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 promted in the console |

| check_hauls_TBTA | *Check presence in TB of the hauls in TA* |
|---|---|

## 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 promted 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 promted 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                    *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.

---

hauls_position                  *Plot of hauls time series*

---

### Description

Plot of hauls time series

### Usage

```
hauls_position(
  mTATB,
  country = "all",
  map_lim,
  depth_lines,
  buffer = 0,
  res = 0.1,
  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                    *Generating maps of indexes*

---

### 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 promted in the console |
| save | boolean. If TRUE the results are stored in the working directory |

---

index_recr                    *Estimation of abundance indices for recruits*

---

### 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 |
| 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             *Estimation of abundance indices for spawners (females)*

---

## 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 |
| `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                    *Estimation of abundance indices for males*

---

### 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                    *Estimation of abundance and biomass indices*

---

### 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) |

---

LFD                          *Length Frequency Distribution*

---

## Description

Length Frequency Distribution

## Usage

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

## Arguments

| | |
|---|---|
| `mTATC` | data frame of the merged TA and TC |
| `sex` | reference sef for the analysis. Allowed values: F, M, I, N. "all" code for combined sex |
| `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) |
| `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 |

---

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 |

---

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

---

merge_TATBTC *Merge Ta-TB and TA-TC tables*

---

### Description

Merge Ta-TB and TA-TC tables

### Usage

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

### Arguments

| | |
|---|---|
| ta | MEDITS or MEDITS-like TA table |
| tb | MEDITS or MEDITS-like TB table |
| tc | MEDITS or MEDITS-like TC table |
| species | species rubin code (MEDITS format, e.g. "MERLMER") |
| country | country code as reported in MEDITS format. "all" code to perform the analysis on all the countries of the same GSA |

| strata | data frame of the stratification scheme adopet by the MEDITS survey |
|---|---|
| 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 |

### Value

A list of two data frames is returned. The first element contains the TA-TB merged tables, while the second element contains the TA-TC merged tables

### Examples

```
m <- merge_TATBTC(ta=TA, tb=TB, tc=TC, species="MERLMER", country="all", wd=tempdir(), verbose=TRUE)
mTATB <- m[[1]]
mTATC <- m[[2]]
```

---

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                 *Overlay mTATB and mTATC on GFCM spatial grid*

---

## 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                 *Quantile estimation*

---

## Description

Quantile estimation

## Usage

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

## Arguments

| | |
|---|---|
| weighted | LFD data.frame |
| qlin | reference quantile for the analysis |

| sex_ratio | *Sex ratio* |
|---|---|

### 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

Plot sex ratio spatial distribution

## Usage

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

## Arguments

| | |
|---|---|
| mTATBsp | spatial mTATB |
| depth | reference depth range |
| 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 outputs are saved in the local folder |

---

| spear | *Spearman test for timeseries* |
|---|---|

---

## Description

Spearman test for timeseries

## Usage

```
spear(x)
```

## Arguments

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

---

| spearman | *Spearman test* |
|---|---|

---

## 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 | *stratification scheme* |
|---|---|

---

## Description

stratification scheme

## Usage

strata_scheme

## Format

An object of class data.frame with 142 rows and 5 columns.

## Author(s)

Walter Zupa <zupa@fondazionecoispa.it>

---

| stratification | *stratification* |
|---|---|

---

## Description

stratification

## Usage

stratification

## Format

An object of class data.frame with 277 rows and 6 columns.

## stratum_0_125 *stratum_0_125*

### Description

stratum_0_125

### Usage

stratum_0_125

### Format

An object of class PackedSpatVector of length 1.

## stratum_0_200 *stratum_0_200*

### Description

stratum_0_200

### Usage

stratum_0_200

### Format

An object of class PackedSpatVector of length 1.

## stratum_0_35 *stratum_0_35*

### Description

stratum_0_35

### Usage

stratum_0_35

### Format

An object of class PackedSpatVector of length 1.

stratum_0_45                 *stratum_0_45*

### Description

stratum_0_45

### Usage

stratum_0_45

### Format

An object of class `PackedSpatVector` of length 1.

stratum_0_800                *stratum_0_800*

### Description

stratum_0_800

### Usage

stratum_0_800

### Format

An object of class `PackedSpatVector` of length 1.

stratum_200_800              *stratum_200_800*

### Description

stratum_200_800

### Usage

stratum_200_800

### Format

An object of class `PackedSpatVector` of length 1.

---

TA                              *TA table example*

---

### Description

TA table example

### Usage

TA

### Format

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

---

TA_cols                         *TA table headings*

---

### Description

TA table headings

### Usage

TA_cols

### Format

An object of class `character` of length 22.

### Author(s)

Walter Zupa `<zupa@fondazionecoispa.it>`

---

TB                              *TB table example*

---

### Description

TB table example

### Usage

TB

### Format

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

---

TB_cols                         *TB table headings*

---

### Description

TB table headings

### Usage

TB_cols

### Format

An object of class character of length 8.

### Author(s)

Walter Zupa <zupa@fondazionecoispa.it>

---

TC                              *TC table example*

---

### Description

TC table example

### Usage

TC

### Format

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

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TC_cols                         *TC table headings*

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### Description

TC table headings

### Usage

TC_cols

### Format

An object of class character of length 11.

### Author(s)

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# Index

27