Package: RoME (via r-universe)

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Type Package

Title Multiple Checks on MEDITS Trawl Survey Data

Version 0.2.3

Description Provides quality checks for MEDITS (International Bottom Trawl Survey in the Mediterranean) trawl survey exchange data tables (TA (Haul data), TB (Catch data), TC (Biological data), TE (Biological individual data), TL (Litter data)). The main function RoME() calls all check functions in a defined sequence to perform a complete quality control of TX (Generic exchange data) data, including header validation, controlled-vocabulary checks, cross-table consistency tests, and biological plausibility checks. No automatic correction is applied: the package detects errors, warns the user, and specifies the type of error to ease data correction. Checks can be run simultaneously on multi-year datasets. An embedded 'shiny' application is also provided via run_RoME_app(). References describing the methods: MEDITS Working Group (2017) <https://www.sibm.it/MEDITS%202011/principaledownload.htm>.

Depends R (>= 4.0)

License GPL-3

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Contents

`assTL` *TL association between categories and sub-categories*

Description

List of the allowed association between categories and subcategories in litter data table (TL)

Usage

```
data("assTL")
```

Format

A data frame with 42 observations on the following 2 variables.

`LITTER_CATEGORY` List of litter categories

‘`LITTER_SUB-CATEGORY`’ List of litter sub-categories

Details

The table is used to check the correctness of the categories/sub-categories associations in litter data tables (TL).

Author(s)

W. Zupa

Source

Anonymus (2017) "MEDITS-Handbook. Version n. 9. MEDITS Working Group" `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

References

Anonymus (2017) "MEDITS-Handbook. Version n. 9. MEDITS Working Group" `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(assTL)
str(assTL)
```

`check_0_fieldsTA` *Checks the presence of 0 fields in TA*

Description

The function checks the presence of 0 fields in the following haul data table (TA, according to MEDITS protocol) fields: WING_OPENING, WARP_DIAMETER and VERTICAL_OPENING

Usage

```
check_0_fieldsTA(DataTA,wd,suffix,year)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile
`year`	reference year for the analysis

Value

The function returns a boolean value. It is FALSE in case 0 values are detected in the TA table's fields

Author(s)

Isabella Bitetto [aut,cre] <bitetto@coispa.it>; Walter Zupa [aut, cre] <zupa@coispa.it>

References

Anonymus (2017) "MEDITS-Handbook. Version n. 9. MEDITS Working Group" `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_0_fieldsTA(RoME::TA,wd,suffix, year=2007)
```

`check_abundance` *Box-plots of swept-area-standardised abundance indices*

Description

This function reads matching MEDITS `TA` (haul metadata) and `TB` (catch numbers) tables for a single survey year, computes the swept area for each haul, derives haul-level abundance indices expressed as individuals per km^2, and produces one or more box-plots that summarise the distribution of those indices by species. The plots are written to the folder '`<wd>/Graphs/Abundance/`' and a logfile is produced under '`<wd>/Logfiles/`' with a summary of any quality-control issues encountered.

Usage

```
check_abundance(ResultDataTA, ResultDataTB, year, wd,
suffix = NULL, distance_unit = "km", min_hauls = 5L)
```

Arguments

`ResultDataTA`	Data frame containing at least the columns `COUNTRY`, `YEAR`, `MONTH`, `DAY`, `HAUL_NUMBER`, `DISTANCE` (towed length) and `WING_OPENING` (gear width in metres).
`ResultDataTB`	Data frame containing at least `COUNTRY`, `YEAR`, `MONTH`, `DAY`, `HAUL_NUMBER`, `GENUS`, `SPECIES`, `TOTAL_NUMBER_IN_THE_HAUL` and `FAUNISTIC_CATEGORY`.
`year`	Single numeric value identifying the survey year to analyse.
`wd`	Writable directory where the function will place '`Logfiles/`' and '`Graphs/Abundance/`'.
`suffix`	Optional text appended to the logfile name. When missing a timestamp is used.
`distance_unit`	Either `"km"` (default) or `"nmi"`. The value determines the conversion factor applied to `DISTANCE`.
`min_hauls`	Minimum number of valid hauls a species must appear in to be plotted. Defaults to `5`.

Details

A swept area is first computed for every haul from `TA`. The function then merges `TA` and `TB`. Hauls that lack swept area information or hauls whose total number of individuals is missing (or equal to zero when not allowed by the faunistic category) are discarded and reported in the logfile. Species occurring in fewer than `min_hauls` valid hauls are also removed. The remaining species are sorted alphabetically and divided into blocks of 36; one image file is produced for each block so that labels remain readable even in years with many species.

The function returns `TRUE` when no data-quality issues were found and `FALSE` otherwise.

Value

Logical scalar (`TRUE` if no errors, `FALSE` otherwise).

Author(s)

W. Zupa.

Examples

```
wd <- tempdir()
check_abundance(ResultDataTA = RoME::TA,
                ResultDataTB = RoME::TB,
                year = 2007,
                wd   = wd)
```

`check_area` *Check if TX files have the same area*

Description

The function works with data of a single year of survey and checks if TX files have the same area code.

Usage

```
check_area(DataTA, DataTB, DataTC, DataTE=NA, DataTL=NA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`DataTB`	Catch data table according to MEDITS protocol (TB)
`DataTC`	Biological data table according to MEDITS protocol (TC)
`DataTE`	Individual biological data table according to MEDITS protocol (TE)
`DataTL`	Litter data table according to MEDITS protocol (TL)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

TA, TB and TC tables are mandatory while TE and TL could be used where available.

Value

The function returns TRUE if no error occurs, while FALSE is returned when there are differences in the AREA code among the TX tables.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA = RoME::TA
DataTB = RoME::TB
DataTC = RoME::TC
DataTE = RoME::TE
DataTL = RoME::TL
check_area(DataTA, DataTB,DataTC,DataTE=NA,DataTL=NA,year=2012, wd, suffix)
```

`check_associations_category_TL` *Check correctness of TL categories*

Description

Check correctness of association between category and sub-category in TL consistent according to INSTRUCTION MANUAL VERSION 9

Usage

```
check_associations_category_TL(DataTL, assTL, year, wd, suffix)
```

Arguments

`DataTL`	Litter data table (TL) according to MEDITS protocol.
`assTL`	data frame with the association between TL (litter table) categories and sub-categories
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The package uses a table of association between TL categories and sub-categories that is resident in the data folder of the package as assTL.rda file.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The presence of inconsistencies in the data is reported in the logfile stored in the "Logfiles"" subdirectory of the "wd"" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTL = RoME::TL
check_associations_category_TL(DataTL, assTL, year=2012, wd, suffix)
```

`check_bridles_length` *check of bridles length correctness*

Description

The function performs consistency checks of the values in the "BRIDLES_LENGTH" field of the hauls data table (TA).

Usage

```
check_bridles_length(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile
`year`	reference year for the analysis

Details

The field BRIDLES_LENGTH can assume value 100 between 10-200 m of depth or 150 between 200-800 m. The function highlights also that MEDITS handbook recommends to increase the bridle length to 200 m in depths deeper than 500 m, reporting a warning in the logfile. Empty (NA) records in "BRIDLES_LENGTH" will be eliminated being the presence of empty fields already checked by `check_no_empty_fields`

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The presence of inconsistencies in the data is reported in the logfile stored in the "Logfiles"" subdirectory of the "wd"" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_bridles_length(RoME::TA, year=2012, wd, suffix)
```

`check_class` *Check of field's class*

Description

The function checks the class of the fields included in the selected table TX using the dictionary table reported in the class data frame.

Usage

```
check_class(data, tab, suffix, wd)
```

Arguments

`data`	one of the different data tables defined by the MEDITS protocol (TX)
`tab`	character string defining the type of table used in the analysis. Allowed values: "TA", "TB", "TC", "TE" and "TL".
`suffix`	Suffix string of the Logfile
`wd`	working directory path defined by the user

Value

The function returns TRUE if no error are detected, while FALSE value is returned if any of the checked fields in the selected table has a not expected class of data.

Author(s)

W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd = tempdir()
check_class(data=RoME::TA, "TA", wd=wd,suffix="test_file")
check_class(data=RoME::TB, "TB", wd=wd,suffix="test_file")
check_class(data=RoME::TC, "TC", wd=wd,suffix="test_file")
check_class(data=RoME::TE, "TE", wd=wd,suffix="test_file")
check_class(data=RoME::TL, "TL", wd=wd,suffix="test_file")
```

`check_consistencyTA_distance`
Consistency check of distance in TA

Description

The function checks whether the distances reported in the haul data (TA) are consistent with the hauls duration.

Usage

```
check_consistencyTA_distance(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

Check between duration of the haul and distance (tolerance of 15%). The function does not check the presence of NA values in the DISTANCE field that are removed from the analysis. The eventual presence of empty records in the DISTANCE field is checked by the `check_no_empty_fields` function.

Value

The function generates warning messages in the logfile and returns always TRUE.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd=tempdir()
suffix="2020-03-05_time_h17m44s55"
check_consistencyTA_distance(RoME::TA,year=2012,wd,suffix)
```

---

check_consistencyTA_duration

Consistency check of hauls duration in TA

Description

The function checks whether the durations reported in the haul data (TA) are consistent with the differences between HAULING_TIME and SHOOTING_TIME.

Usage

```
check_consistencyTA_duration(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The DURATION, SHOOTING_TIME and HAULING_TIME fields have to be consistent

Value

The function returns a boolean value. It is FALSE in case one or more durations in the TA table are not consistent with the differences between HAULING_TIME and SHOOTING_TIME.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_consistencyTA_duration(RoME::TA,year=2012,wd,suffix)
```

`check_date_haul` *Check of date consistency*

Description

Check if in TB, TC and TE the date by haul is the same of the one reported in TA

Usage

```
check_date_haul(DataTA, Data, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`Data`	Data frame of one of the following TX table: TB, TC, TE, TL
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function check whether in one of the TX file allowed in Data argument there are date consistent with the one reported in the haul data table (TA).

Value

The function returns TRUE if no error occurs, while FALSE is returned when in the Date data frame there is one or more date not included in the TA tables.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA = RoME::TA
Data = RoME::TB
year=2009
check_date_haul(DataTA, Data, year, wd, suffix)
```

`check_depth` *Check between start depth and end depth*

Description

Check if that difference between start depth and end depth is not greater than 20%

Usage

```
check_depth(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The difference between start depth and end depth should be not greater than 20%.

Value

The function returns always TRUE because the outcome of the function is a warning that does not block the execution of the 'RoME' checks. The presence of inconsistencies between start depth and end depth is reported in the logfile stored in the "Logfiles"" subdirectory of the "wd"" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_depth(RoME::TA, year=2007,wd,suffix)
```

`check_dictionary` *Check of the dictionary of specific fields*

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, suffix)
```

Arguments

`ResultData`	Haul data table according to MEDITS protocol (TA)
`Field`	Name of the specific field of the selected TX table
`Values`	Vector of the allowed values for the field to be checked
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function checks the consistence of the contained in specific fields with the relative allowed values. The check is performed on the hauls data table (TA), the catch data table (TB), the biological data table (TC) and the individual biological data (TE).

Value

The function returns TRUE if no error occurs, while FALSE is returned when there are differences between the field values and the reference dictionaries. In the logfile is reported the list of all the records in which the inconsistency is detected.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
Field = "COURSE"
Values = c("R","N")
DataTA = RoME::TA
year = 2007
check_dictionary(ResultData = DataTA, Field, Values, year, wd, suffix)
```

`check_distance` *Check of distance consistency*

Description

The function checks whether there are inconsistencies between the `DISTANCE` field values in the TA table and the distances computed from the geographical coordinates of each haul.

Usage

```
check_distance(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table formatted according to the MEDITS protocol (TA table).
`year`	Reference year for the analysis.
`wd`	Working directory path defined by the user.
`suffix`	Suffix string to uniquely identify the output logfile and plots.

Details

The comparison between the `DISTANCE` field and the distance computed from shooting and hauling coordinates is performed with a tolerance threshold of 30%.

The geographic distance is calculated using the function `distGeo()` from the `geosphere` package, which computes the shortest path (great-circle distance) between two points on the Earth's ellipsoid (WGS84) using coordinates in decimal degrees.

Coordinates in the TA table are usually expressed in degrees and decimal minutes. These are automatically converted into decimal degrees using the internal function `MEDITS.to.dd()` before the computation.

Value

The function always returns `TRUE`. Its purpose is to generate warnings for hauls where the recorded `DISTANCE` differs significantly from the computed geographic distance.

Warnings are saved in a logfile located in the `Logfiles` subdirectory of the specified working directory. Additionally, for hauls with discrepancies, graphical maps are generated and saved in the `Graphs` subdirectory to support visual inspection and correction.

Author(s)

W. Zupa, I. Bitetto

References

Anonymous. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Hijmans, R. J. (2019). *geosphere: Spherical Trigonometry*. R package version 1.5-10. https://cran.r-project.org/package=geosphere

Examples

```
wd <- tempdir()
suffix <- "2020-03-05_time_h17m44s55"
year <- 2007
check_distance(RoME::TA, year, wd, suffix)
```

`check_dm` *Check of "WING_OPENING" and "VERTICAL_OPENING" fields*

Description

The function checks the values in "WING_OPENING" and "VERTICAL_OPENING" field are in the allowed ranges (see INSTRUCTION MANUAL VERSION 9 MEDITS 2017).

Usage

```
check_dm(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The value ranges defined in the INSTRUCTION MANUAL VERSION 9 MEDITS (2017) for wing and vertical opening expressed in dm are respectively 50 - 250 and 10 - 100.

Value

The function returns an error in case wing values are out of the allowed ranges, while it returns warnings in case vertical opening values are out of the allowed ranges and in case wing opening and vertical opening values are not integer numbers.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd=tempdir()
suffix="2020-12-16_time_h10m52s55"
check_dm(RoME::TA,year=2007,wd,suffix)
```

`check_G1_G2` *Check of length measurements for G1 and G2 species*

Description

Check if for G1 and G2 species the length measurements are present in TC

Usage

```
check_G1_G2(DataTC, year, wd, suffix)
```

Arguments

`DataTC`	Biological data table according to MEDITS protocol (TC)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

This check uses a new support table (list_g1_g2) containing the list of MEDITS G1 and G2 species and verify if the length has been collected for the selected species for each haul. If the length is lacking for any species in any haul, a warning message is given in the logfile.

Value

The function returns always TRUE because the outcome of the function is a warning that does not block the execution of the 'RoME' checks. If the length is lacking for any species in any haul, a warning message is given in the logfile.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_G1_G2(RoME::TC,year=2007,wd,suffix)
```

`check_haul_species_TCTB`

Check species of TC in TB

Description

The function checks whether all the species present in TC (biological data table) must be listed in TB (catch data table)

Usage

```
check_haul_species_TCTB(DataTB, DataTC, year, wd, suffix)
```

Arguments

`DataTB`	catch data table according to MEDITS protocol (TB)
`DataTC`	Biological data table according to MEDITS protocol (TC)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function returns a warning message in the logfile.

Value

If a species present in the TC table (biological data table) is not reported in the TB (catch data table) an error message is reported in the logfile and a "Critical_errors" file is saved in the working directory reporting details on the errors.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
year=2008
check_haul_species_TCTB(RoME::TB, RoME::TC, year, wd, suffix)
```

`check_hauls_TATB` *Check of TA hauls in TB*

Description

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

Usage

```
check_hauls_TATB(DataTA,DataTB,year,wd,suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`DataTB`	Catch data table according to MEDITS protocol (TB)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

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

Value

The function returns TRUE if no error occurs, while FALSE is returned when an inconsistency is detected between haul and catch tables.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA <- RoME::TA
DataTB <- RoME::TB
year = 2008
check_hauls_TATB(DataTA,DataTB,year,wd,suffix)
```

`check_hauls_TATL` *Check presence of TA hauls in TL*

Description

Check if the hauls in TA are present in TL

Usage

```
check_hauls_TATL(DataTA, DataTL, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`DataTL`	Litter data table according to MEDITS protocol (TL)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function checks whether all the hauls present in hauls data table (TA) are included in the litter data table (TL).

Value

The function returns always TRUE because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The list of the hauls not present in the TL table is reported in the logfile stored in the "Logfiles"" subdirectory of the "wd" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA = RoME::TA
DataTL = RoME::TL
year=2008
check_hauls_TATL(DataTA,DataTL,year,wd,suffix)
```

`check_hauls_TBTA` *Check of TB 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, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`DataTB`	Catch data table according to MEDITS protocol (TB)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

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

Value

The function returns TRUE if no error occurs, while FALSE is returned when an inconsistency is detected between haul and catch tables.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA <- RoME::TA
DataTB <- RoME::TB
check_hauls_TBTA(DataTA,DataTB,year=2008,wd,suffix)
```

`check_hauls_TLTA` *Check presence of TL hauls in TA*

Description

Check if the hauls in TL are present in TA

Usage

```
check_hauls_TLTA(DataTA,DataTL,year,wd,suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`DataTL`	Litter data table according to MEDITS protocol (TL)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function checks whether all the hauls present in litter data table (TL) are included in the haul data table (TA).

Value

The function returns TRUE if no error occurs, while FALSE is returned when there are missing hauls in the TA table.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA = RoME::TA
DataTL = RoME::TL
year=2008
check_hauls_TLTA(DataTA,DataTL,year,wd,suffix)
```

`check_identical_records` *Check of identical records in TX tables*

Description

The function checks whether there is one or more identical records in the selected type of table (TX).

Usage

```
check_identical_records(Data, year, wd, suffix)
```

Arguments

`Data`	one of the different data tables defined by the MEDITS protocol (TX)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The routine uses all the table format (TX) defined by the MEDITS protocol.

Value

The function returns TRUE if no error occurs, while FALSE is returned when there is one or more identical record in the given TX table.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
Data = RoME::TA
check_identical_records(Data, year=2007, wd, suffix)
```

`check_individual_weightTC` *Check of observed and estimated total weight in the haul*

Description

The function compares the observed

Usage

```
check_individual_weightTC(DataTC,LW=NA,year,wd,suffix,verbose=FALSE)
```

Arguments

`DataTC`	Biological data table according to MEDITS protocol (TC)
`LW`	data frame of the a and b parameters by species, area and sex
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile
`verbose`	boolean parameter, if TRUE returns messages about the progress of the elaboration

Details

The warning is given when difference between the sum of estimated individual weights (by haul, species and sub-samples) and the WEIGHT_OF_THE_SAMPLE_MEASURED is greater than 50% for at least one record. This check is based on the table LW contained in package, where the length-weight relationship coefficients are reported by species, area and sex.

Value

The file Comparison_estimated_observed_weight_in_TC.csv is automatically saved in the working directory in order to easily detect the samples with this differences in total weight. For all the records the percentage difference between observed and estimated weight is reported.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
TC = RoME::TC[1:20,]
check_individual_weightTC(DataTC=TC,year=2007, wd=wd, suffix=suffix)
```

---

check_individual_weightTE

Consistency of individual weights (according to length-weight relationship)

Description

The function checks the difference between observed and estimated individual weight in percentage.

Usage

```
check_individual_weightTE(DataTE,LW,year, wd, suffix,verbose=FALSE)
```

Arguments

`DataTE`	Individual biological data table according to MEDITS protocol (TE)
`LW`	data frame of the length-weight parameters by species, area and sex
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile
`verbose`	boolean parameter, if TRUE returns messages about the progress of the elaboration

Details

For each individual is calculated the estimated weight according to length-weight relationship coefficient stored in LW table and the difference between observed and estimated individual weight in percentage. Moreover, this function checks if for G1 species has been collected the weight or if has been entered the value ND, that is not allowed.

Value

If for at least one record the difference between observed and estimated individual weight is greater than 20% a warning is given in Logfile.dat and a table named TE_with_estimated_weights.csv is automatically produced in order to allow the user to easily eventually detect the errors. For all the records the percentage difference between observed and estimated weight is reported.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTE = RoME::TE[1:6,]
check_individual_weightTE(DataTE,year=2012, wd=wd, suffix=suffix,verbose=TRUE)
```

`check_length` *Check of length classes in TC*

Description

The function checks the consistency of length classes in the TC table for the MEDITS survey. It verifies that the recorded length classes for each species fall within the expected ranges reported in a reference table of species-specific length limits. Warnings for inconsistencies are written to a CSV file for easier downstream analysis instead of being printed extensively in the log file.

Usage

```
check_length(DataTC, DataSpecies = NA, year, wd, suffix,
             DataTargetSpecies = RoME::DataTargetSpecies)
```

Arguments

`DataTC`	Biological data table (TC) formatted according to the MEDITS protocol.
`DataSpecies`	A data frame with species-specific reference length limits. If not provided, the internal `DataTargetSpecies` dataset included in the package is used by default.
`year`	Reference year for the analysis.
`wd`	Working directory path defined by the user, where log files and CSV output will be saved.
`suffix`	Suffix string for naming the log and CSV files, allowing unique identification of output files from different runs.
`DataTargetSpecies`	Reference dataset with species-specific information on length ranges, used as default if `DataSpecies` is not provided.

Details

The function filters the TC data for the selected year and checks each length class recorded against the minimum (`LMIN01`) and maximum (`LMAX99`) length values defined for the corresponding species in the reference table. It also checks for negative or missing length class values. All detected issues are collected and saved in a CSV file for clear reporting, instead of generating verbose outputs in the log file.

Species with less than 50 observations in TC are excluded from the check by default, to focus the analysis on more frequently recorded species. The function ensures robust handling of missing (`NA`) values in both the TC table and the reference datasets to avoid false warnings.

A short summary of the check results is written to the `.dat` logfile. If no inconsistencies are detected, a message indicating successful validation is saved.

Value

Returns `TRUE`, invisibly. Detected inconsistencies are written to a CSV file in the working directory; if no issues are found, the CSV file remains empty apart from the header row.

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
DataTC <- RoME::TC[1:20,]
DataSpecies <- NA
suffix <- "2020-03-05_time_h17m44s55"
check_length(DataTC, DataSpecies = NA, year = 2007, wd, suffix)
```

`check_length_class_codeTC`

Consistency check of LENGTH_CLASS

Description

The function checks the consistency of field LENGTH_CLASSES_CODE in TC

Usage

```
check_length_class_codeTC(DataTC,Specieslist=RoME::TM_list,year,wd,suffix)
```

Arguments

`DataTC`	Biological data table according to MEDITS protocol (TC)
`Specieslist`	Information related to target species as reported in the TM list
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function checks whether the LENGTH_CLASS_CODE by species are consistent with those reported in the Specieslist dataset. When Specieslist is NA the TM_list dataset (included in the package) is used by default.

Value

If the LENGTH_CLASS_CODE in TC table (biological data table) are not consistent with CODLON field in Specieslist dataset (or TM_list if Specieslist is NA) an error is returned. In case a LENGTH_CLASS_CODE is not reported for the given species no check is done and the function returns a warning message.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
DataTC <- RoME::TC
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_length_class_codeTC(DataTC,Specieslist=NA,year=2007,wd,suffix)
```

`check_mat_stages` *Consistency of maturity stages*

Description

Consistency check of maturity stages, according to the faunistic category and sex

Usage

```
check_mat_stages(Data, year, wd, suffix, stages = RoME::mat_stages)
```

Arguments

`Data`	Biological data table (TC) or individual biological data table (TE) according to MEDITS protocol
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile
`stages`	data frame with the list of allowed maturity stages for faunistic category as defined by the mat_stages dataset included in the package

Details

The check on maturity stage is performed for the species included in the new TM list, where selachians and bony fish are distinguished. The check is applied to the following faunistic categories: Ao, Ae, B, C and Bst.

Value

The function always returns TRUE generating a warning message when inconsistencies in the maturity stages are detected, being difficult to define for all GSAs the year in which occurred the switch from the "old" MEDITS maturity scale to the current MEDITS scale.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
DataTC <- RoME::TC
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_mat_stages(DataTC,year=2007, wd, suffix)
```

`check_nb_per_sexTC` *Consistency check of number of individuals*

Description

The function checks the consistency of the number of individuals by sex measured (NO_OF_INDIVIDUAL_OF_THE_ABOV field in the biological data table, TC) with the sum of the individuals by sex, length class and maturity stage (NUMBER_OF_INDIVIDUALS_IN_THE_LENGTH_CLASS_AND_MATURITY_STAGE field in TC)

Usage

```
check_nb_per_sexTC(DataTC, year, wd, suffix)
```

Arguments

`DataTC`	Biological data table according to MEDITS protocol (TC)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function checks the consistency of the number of individuals by sex measured (NO_OF_INDIVIDUAL_OF_THE_ABOV field in the biological data table, TC) with the sum of the individuals by sex, length class and maturity stage (NUMBER_OF_INDIVIDUALS_IN_THE_LENGTH_CLASS_AND_MATURITY_STAGE field in TC)

Value

The function returns TRUE if no error occurs, while FALSE is returned when there inconsistencies between the following biological data table (TC): NO_OF_INDIVIDUAL_OF_THE_ABOVE_SEX_MEASURED and NUMBER_OF_INDIVIDUALS_IN_THE_LENGTH_CLASS_AND_MATURITY_STAGE.If the field number per sex is found completely empty, the routine will stop and will produce automatically a .csv file (TC_file_with_computed_nb_per_sex.csv) with the nb per sex column filled in. The user will have to copy and paste the column in the original file and run again the code.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTC = RoME::TC
year=2007
check_nb_per_sexTC(DataTC,year,wd,suffix)
```

`check_nb_TE` *Consistency of number of individuals sampled for weight and ageing in TE*

Description

The function checks the consistency of number of individuals sampled for weight and ageing in TE

Usage

```
check_nb_TE(DataTE, year, wd, suffix)
```

Arguments

`DataTE`	Individual biological data table according to MEDITS protocol (TE)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

this function verify the consistency of the check-fields:

- NO_PER_SEX_MEASURED_IN_SUB_SAMPLE_FOR_OTOLITH
- NO_PER_SEX_MEASURED_IN_SUB_SAMPLE_FOR_WEIGHT
- NO_PER_SEX_MEASURED_IN_SUBSAMPLE_FOR_AGEING

These fields are compared to the number of records present in TE by sex, length class and haul.

Value

The function returns FALSE in case inconsistencies are detected in the individual biological data table (TE)

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTE = RoME::TE
year=2012
check_nb_TE(DataTE,year, wd, suffix)
```

`check_nbtotTB` *Check total number of individuals in TB*

Description

The function checks that the total number of individuals is consistent with the sum of the individuals per sex

Usage

```
check_nbtotTB(DataTB, year, wd, suffix)
```

Arguments

`DataTB`	Catch data table according to MEDITS protocol (TB)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function checks that the total number of individuals is consistent with the sum of the individuals per sex

Value

The function returns TRUE if no error occurs, FALSE if one or more inconsistencies in the individuals number is detected.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTB = RoME::TB
year=2007
check_nbtotTB(DataTB,year, wd, suffix)
```

`check_nm_TB` *Check of consistency in number per sex set "not mandatory" in TB*

Description

Check if in TB there are the total number, number of females, males and undetermined for species G1

Usage

```
check_nm_TB(DataTB, year, wd, suffix)
```

Arguments

`DataTB`	Catch data table according to MEDITS protocol (TB)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

for the species G1 are not allowed that the fields related to total number, number of females, number of males and number of undetermined are simultaneously null, according to MEDITS manual version 9 of 2017.

Value

The function returns TRUE if no error occurs, FALSE if one or more inconsistencies in the individuals number per sex in TB is detected.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTB = RoME::TB
year=2007
check_nm_TB(DataTB, year, wd, suffix)
```

`check_no_empty_fields` *Check empty fields in TA, TB, TC, TE and TL*

Description

All the fields, except to HYDROLOGICAL_STATION and OBSERVATIONS, must be not empty for valid hauls

Usage

```
check_no_empty_fields(Data, year, wd, suffix)
```

Arguments

`Data`	one of the different data tables defined by the MEDITS protocol (TX)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The routine uses all the table format (TX) defined by the MEDITS protocol.

Value

The function returns TRUE if no error occurs, while FALSE is returned when there is one or more empty record in the given TX table.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
Data = RoME::TA
year=2007
check_no_empty_fields(Data, year, wd, suffix)
```

`check_numeric_range` *Check of the values range in specific fields*

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, suffix)
```

Arguments

`Data`	data table according to MEDITS protocol (TX)
`Field`	Name of the specific field of the selected TX table
`Values`	Vector of the allowed values for the field to be checked. The first two values are mandatory and indicate the extreme values of the range. The other optional values are single numerical exceptions to the field allowed values.
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function checks the consistence of the values contained in specific fields with the relative allowed range of values. The function allows to include exceptions to the allowed range of values for specific values. The check is performed on any of the "TX" data tables.

Value

The function returns TRUE if no error occurs, while FALSE is returned when inconsistencies are detected. The list of all the records in which the inconsistency is detected is reported in the logfile.

Author(s)

W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
Field = "SHOOTING_DEPTH"
Values = c(10,800,0)
Data = RoME::TA
year <- unique(Data$YEAR)[1]
check_numeric_range(Data, Field, Values, year, wd, suffix)
```

`check_position` *Plot of haul positions*

Description

The function generate three different plots, haul start position, haul end position and start and end positions together.

Usage

```
check_position(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The haul position maps are saved in the Graph directory allocated in the user defined wd directory.

Value

The function generate three maps of the haul position that are stored in the Graph folder allocated in the user defined wd directory

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
year=2007
check_position(RoME::TA,year,wd,suffix)
```

`check_position_in_Med` *Check of haul position in Mediterranean Sea*

Description

The function checks whether the position of the haul is in the Mediterranean Sea area or falls on the land.

Usage

```
check_position_in_Med(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function uses the `haul_at_sea()` function to check whether the position of the haul is in the Mediterranean Sea area or falls on the land.

Value

The function returns a boolean value. It is FALSE in case one or more haul positions fall out of the Mediterranean Sea area defined by the shapefile *MedSea* included in the package.

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time h17m44s55"
DataTA = RoME::TA
year=2007
check_position_in_Med(DataTA, year, wd, suffix)
```

`check_quadrant` *Check start and end quadrant for each haul*

Description

Function checking that the shooting quadrant and the hauling quadrant are the same.

Usage

`check_quadrant(ResultDataTA,year,wd,suffix)`

Arguments

`ResultDataTA`	Haul data table according to MEDITS protocol (TA).
`year`	reference year for the analysis
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

The function returns a warning if shooting and hauling quadrant are not the same.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The presence of inconsistencies in the data is reported in the logfile stored in the "Logfiles" subdirectory of the "wd" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

For the definition of the quadrants, please refer to: Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
TA <- RoME::TA
year=2007
check_quadrant(TA,year,wd,suffix)
```

`check_quasiidentical_records` *Function checking the presence of quasi-identical records.*

Description

Two or more "quasi-identical records" occurred when all the fields are respectively equal, except: TYPE_OF_FILE, AREA, GEAR, VESSEL, YEAR, RIGGING, DOORS, for TA table; TYPE_OF_FILE, AREA, VESSEL, YEAR for TB and TC tables.These specific fields are allowed to be identical.

Usage

```
check_quasiidentical_records(Result,year,wd,suffix)
```

Arguments

`Result`	Haul data table according to MEDITS protocol (TA), or Catch data table (TB) or Biological data table (TC).
`year`	reference year for the analysis
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

The checks always returns TRUES generating warning messages in the logfile if any quasi-identical record was found. In a given survey the following fields (of TA table) should be identical: 'TYPE_OF_FILE', 'AREA', 'VESSEL', 'GEAR', 'RIGGING', 'DOORS' and 'YEAR'. The function checks whether any differences occur in these fields in each yearly survey. The same think is done for all the other tables where these fields occur.

Value

The function always returns TRUE reporting the presence of quasi-identical records in the logfile.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
year=2007
# example using TA table
TA <- RoME::TA
check_quasiidentical_records(TA,year,wd,suffix)

# example using TB table
TB <- RoME::TB
check_quasiidentical_records(TB,year,wd,suffix)

# example using TC table
TC <- RoME::TC
check_quasiidentical_records(TC,year,wd,suffix)
```

`check_raising` *Comprehensive consistency checks between MEDITS* `TB` *and* `TC` *files*

Description

`check_raising()` performs a suite of integrity checks on a pair of MEDITS survey tables – *TB* (catch-at-haul) and *TC* (biological subsamples) – for one survey year. All inconsistencies are written to a plain-text logfile; the routine never stops at the first error, so you always get the full list of issues detected.

Usage

```
check_raising(ResultDataTB, ResultDataTC, year, wd, suffix = NULL)
```

Arguments

`ResultDataTB`	A `data.frame` containing the MEDITS **TB** table for one or more years.
`ResultDataTC`	A `data.frame` containing the MEDITS **TC** table for one or more years.
`year`	Single integer. The survey year to be checked.
`wd`	Character string. A writable directory where sub-folders ‘`Logfiles/`’ (and ‘`Graphs/`’, currently unused) will be created.
`suffix`	Optional character string appended to the logfile name. When `NULL` (default) a timestamp-based suffix is generated automatically.

Details

The function executes **five** independent validations:

1. *Weight consistency* – When more than one subsample exists for a given haul/species in `TC`, the sum of `WEIGHT_OF_THE_FRACTION` must equal `TOTAL_WEIGHT_IN_THE_HAUL` recorded in `TB`.
2. *Raising factor* – For each subsample the ratio $molt$ given by `WEIGHT_OF_THE_FRACTION` / `WEIGHT_OF_THE_SAMPLE_MEASURED` must be ≥ 1.
3. *Sex-specific numbers* – For every combination haul `*` species `*` sex the raised total of individuals in `TC` must match `TB` columns `NB_OF_FEMALES`, `NB_OF_MALES` or `NB_OF_UNDETERMINED`.
4. *Total individuals (TC -> TB)* – For every haul/species the sum of raised numbers across all sexes in `TC` must equal `TOTAL_NUMBER_IN_THE_HAUL` in `TB`. This catches cases where an entire sex is missing from `TC`.
5. *Internal TB consistency* – Within `TB` the sum of the three sex-specific columns must equal `TOTAL_NUMBER_IN_THE_HAUL` for each haul/species.

If any of these checks fails, an explanatory line is appended to the logfile ‘`Logfiles/Logfile_.dat`’. The function finally returns a single logical value: `TRUE` when no errors are detected, `FALSE` otherwise.

Tidy-evaluation is used inside the **dplyr** pipelines; the following symbols are declared in globalVariables to avoid "no visible binding" notes during `R CMD check`: `COUNTRY`, `YEAR`, `HAUL_NUMBER`, `GENUS`, `SPECIES`, `WEIGHT_OF_THE_FRACTION`, `WEIGHT_OF_THE_SAMPLE_MEASURED`, `NUMBER_OF_INDIVIDUALS_IN_THE_LENGTH_CLA` `SEX`, `NB_OF_FEMALES`, `NB_OF_MALES`, `NB_OF_UNDETERMINED`, `TOTAL_WEIGHT_IN_THE_HAUL`, `TOTAL_NUMBER_IN_THE_HAUL`, `codedsex`, `N`, `molt`, `raised`, `RaisedSex`, `RaisedTotal`, `n_subsamples`, `total_fraction`, `SumSexTB`.

Value

Logical scalar: `TRUE` if the dataset passes all checks, `FALSE` otherwise.

Author(s)

W. Zupa, I. Bitetto, M. T. Spedicato

See Also

`dplyr` for the data-manipulation verbs used under the hood.

Examples

```
# The following datasets come from the 'RoME' package demo data
DataTB <- RoME::TB
DataTC <- RoME::TC

res <- check_raising(DataTB, DataTC, year = 2015, wd = tempdir())
if (res) message("All checks passed!")
```

`check_rubincode` *Function checking the correctness of species MEDITS code and faunistic category according to TM reference list*

Description

The TM list contained in the INSTRUCTION MANUAL VERSION 9 MEDITS 2017 is taken as reference to check the correctness of species code and category.The function is applied to catch data table (TB), Biological data table (TC) and Individual data table (TE).

Usage

```
check_rubincode(ResultData,year,TMlist,wd,suffix)
```

Arguments

`ResultData`	alternatively: Catch data table (TB), Biological data table (TC) and Individual data table (TE).
`year`	reference year for the analysis
`TMlist`	TM_list reference list
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

The checks execution is stopped if any mismatching record was found.

Value

The function returns always TRUE if used to check TB tables, indicating in the logfile the species codes not present in TM list. If unexpected rubin codes are detected in both TC and TE tables an error (FALSE value) is reported in the logfile, interrupting the function running.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
year=2007

# example using TB table
TB <- RoME::TB
check_rubincode(TB,year,TM_list,wd,suffix)

# example using TC table
TC <- RoME::TC
check_rubincode(TC,year,TM_list,wd,suffix)
```

`check_smallest_mature` *Check for mature individuals below literature thresholds in TC data*

Description

This function verifies the consistency of maturity information in TC data by detecting mature individuals whose lengths are smaller than the smallest mature size reported in the literature for each species and sex. Detected inconsistencies are saved in a CSV file for traceability and further review, while a concise summary is written in the log file.

Usage

```
check_smallest_mature(ResultData, year, MaturityParameters, TargetSpecies,
  wd, suffix)
```

Arguments

`ResultData`	Biological data table (TC) formatted according to the MEDITS protocol. This table should contain length-class, sex, and maturity stage information for all recorded hauls.
`year`	Reference year for the analysis. Only records from the specified year are processed.
`MaturityParameters`	Table with bibliographic parameters describing the smallest mature individual observed for each species and sex, and the related reference sources.
`TargetSpecies`	Table containing information on target species, including taxonomic codes and faunistic categories used to identify relevant maturity checks.
`wd`	Working directory where the function writes log files and CSV outputs.
`suffix`	String appended to filenames of log and CSV files to distinguish outputs from different runs.

Details

The function processes the TC data for the selected year and examines each species listed in the `MaturityParameters` table. For each mature individual (i.e.\ not coded as immature stages), it checks whether the length class is smaller than the bibliographic minimum threshold, allowing a 10% tolerance buffer to account for biological variability. If such individuals are detected, they are recorded in a CSV file including:

- GSA
- Year
- Species
- Sex
- Haul number
- Length class (mm)
- Threshold applied (mm)
- Literature threshold (mm)
- Bibliographic reference
- Type of file
- Type of warning

A concise message summarizing how many records were written to the CSV is printed to the log file (`.dat`). If no inconsistencies are found, the function logs a message indicating that all maturity stages are above bibliographic thresholds.

The check uses the updated `DataTargetSpecies` table for consistency with current species definitions and codes.

Value

The function always returns `TRUE`. Its purpose is to perform quality checks and log potential issues, but it does not interrupt the execution of other routines in the `RoME` package.

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix <- "2020-03-05_time_h17m44s55"
TC <- RoME::TC
year <- 2007
check_smallest_mature(
  TC,
```

```
    year,
    RoME::Maturity_parameters,
    RoME::DataTargetSpecies,
    wd,
    suffix
  )
```

---

check_spawning_period *Check consistency of maturity stages with respect to the spawning period*

Description

This function checks whether maturity stages reported in TC (or TE) are consistent with the reproductive period of each species. It detects three situations:

- Immature individuals caught during the spawning period but with lengths above the bibliographic threshold (maximum L50 plus 20%).
- Mature individuals caught outside the spawning period.
- Mature individuals caught outside the spawning period and with lengths smaller than the smallest mature individual reported in the literature.

The check uses bibliographic information from the `Maturity_parameters` table, including L50 values and spawning months.

Usage

```
check_spawning_period(ResultDataTA, ResultDataTC, year,
Maturity_parameters, DataTargetSpecies, wd, suffix)
```

Arguments

`ResultDataTA`	Haul data table (TA) according to MEDITS protocol.
`ResultDataTC`	Biological data table (TC) or alternatively the individual data table (TE), according to MEDITS protocol.
`year`	Reference year for the analysis.
`Maturity_parameters`	Table containing bibliographic information on L50, reproductive season, and smallest mature size for species and sexes.
`DataTargetSpecies`	Reference table for target species, including faunistic categories and other relevant data.
`wd`	Working directory selected by the user, where logfiles and CSV outputs will be saved.
`suffix`	Suffix string to append to output filenames, useful to distinguish between multiple runs.

Details

The function reads information from `Maturity_parameters` to identify the reproductive period (spawning season) of each species and sex. It then compares each record in TC or TE with these periods:

- Immature individuals (maturity codes 0, 1, 2A) are flagged if they are captured during the spawning period and have lengths exceeding the bibliographic threshold (maximum L50 + 20%).
- Mature individuals are checked to verify whether they were caught outside the defined spawning period.
- Among mature individuals outside the spawning period, those with lengths smaller than the smallest mature specimen reported in literature are additionally flagged.

Warnings are written both to a .dat logfile and to a CSV file for easier downstream analysis. The CSV output includes details on GSA, year, haul number, species, sex, length class, spawning period months, month of capture, and type of warning.

Value

The function always returns `TRUE`, as it is designed to produce warnings rather than halt execution of further routines in the `RoME` package.

Author(s)

W. Zupa, I. Bitetto

References

Anonymous. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
suffix <- "2020-03-05_time_h17m44s55"
year <- 2007
TA <- RoME::TA
TC <- RoME::TC
check_spawning_period(
  ResultDataTA = TA,
  ResultDataTC = TC,
  year = year,
  Maturity_parameters = RoME::Maturity_parameters,
  DataTargetSpecies = RoME::DataTargetSpecies,
  wd = wd,
  suffix = suffix
)
```

`check_species_TBTC` *Function checking if all the target species in the catch data table (TB) are in Biological data table (TC)*

Description

This function verifies the presence of the target species (that is a subset of the all the species caught, reported in TB), in the TC table, where additional information (apart from number and weight) are collected.

Usage

```
check_species_TBTC(ResultTB,ResultTC,year,DataSpecies,wd,suffix)
```

Arguments

`ResultTB`	Catch data table(TB).
`ResultTC`	Biological data table (TC).
`year`	reference year for the analysis
`DataSpecies`	Information related to target species.
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

This function gives a warning message, thus the execution is not stopped when some target species are lacking in TC; the user is informed in the Logfile.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd=tempdir()
suffix = "2020-03-05_time_h17m44s55"
year=2007
ResultTB=RoME::TB
ResultTC=RoME::TC
check_species_TBTC(ResultTB,ResultTC,year,RoME::DataTargetSpecies,wd,suffix)
```

`check_step_length_distr` *The function verifies that in TC the length measures are reported with the correct precision.*

Description

Fishes and cephalopods length classes must have full or half step (in case of LENGTH_CLASSES_CODE=1 only full). All the measures , must be integer numbers.

Usage

```
check_step_length_distr(ResultData,year,wd,suffix)
```

Arguments

`ResultData`	alternatively: Biological data table (TC) and Individual data table (TE).
`year`	reference year for the analysis
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

According to the MEDITS protocol, Fishes and cephalopods length measurement must collected full or half step and all the measures, must be integer numbers. Empty (NA) records in LENGHT_CLASS field are removed from the analysis being empty fields already detected by `check_no_empty_fields` function.

Value

The function returns TRUE if no error occurs, while FALSE is returned when the step is not correctly used. In the logfile is reported the list of all the records in which the inconsistency is detected.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
data <- RoME::TC
wd=tempdir()
year = 2007
suffix= "2020-03-05_time_h17m44s55"
check_step_length_distr(data,year,wd,suffix)
```

`check_stratum` *Function that checks the consistency between start and end depth according to the stratum.*

Description

Start depth and end depth of each haul should be in the same stratum.

Usage

```
check_stratum(ResultData,year,wd,suffix)
```

Arguments

`ResultData`	Haul data table according to MEDITS protocol (TA).
`year`	reference year for the analysis
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

Start depth and end depth of each haul should be in the same stratum. The strata are the ones defined according to the MEDITS protocol: 10-15 m; 50-100 m; 100-200 m; 200-500m; 500-800 m.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The presence of inconsistencies in the data is reported in the logfile stored in the "Logfiles" subdirectory of the "wd" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

For the definition of the strata, please refer to: Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd=tempdir()
year=2007
TA = RoME::TA
suffix= "2020-03-05_time_h17m44s55"
check_stratum(TA,year,wd,suffix)
```

`check_stratum_code` *Function to check the correct codification of the strata in haul data table (TA).*

Description

This function verifies the correctness of the stratum code, following the stratification scheme table in the MEDITS protocol.

Usage

```
check_stratum_code(ResultDataTA,year,Strata,wd,suffix)
```

Arguments

`ResultDataTA`	Haul data table according to MEDITS protocol (TA).
`year`	reference year for the analysis
`Strata`	Stratification scheme according to MEDITS protocol.
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

This function checks if the stratum code associated to each haul is consistent with the code reported in MEDITS manual and in the table Stratification scheme, corresponding to the associated depth range.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The presence of inconsistencies in the data is reported in the logfile stored in the "Logfiles" subdirectory of the "wd" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

For the definition of the strata, please refer to: Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TA = RoME::TA
wd=tempdir()
year = 2007
suffix= "2020-03-05_time_h17m44s55"
check_stratum_code(TA,year,Strata=RoME::stratification_scheme,wd,suffix)
```

`check_subsampling` *Function to warn the user about the presence of subsamples <0.1 of the total catch.*

Description

Check if the sub-sample is smaller than the 10 percent of the total weight in the haul.

Usage

```
check_subsampling(ResultTC,year,wd,suffix)
```

Arguments

`ResultTC`	Biological data table (TC).
`year`	reference year for the analysis.
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

This function give a warning, reported in the Logfile, if the sub-sample is unusually small respect to the total catch of the species.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The presence of inconsistencies in the data is reported in the logfile stored in the "Logfiles" subdirectory of the "wd" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

For the definition of the strata, please refer to: Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TC = RoME::TC
year=2007
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_subsampling(TC,year,wd,suffix)
```

`check_swept_area` *Check Swept Area Calculation and Plot*

Description

Performs data validation and swept area calculation for MEDITS TA-format data. The function verifies numeric consistency in key columns, computes mean depth and swept area, logs any detected issues, and generates a plot of swept area versus mean depth for visual inspection.

Usage

```
check_swept_area(ResultDataTA, year, wd, suffix)
```

Arguments

`ResultDataTA`	A data.frame containing MEDITS hauls data in TA-format. The function uses the following columns: `YEAR`, `VALIDITY`, `HAUL_NUMBER`, `WING_OPENING`, `DISTANCE`, `SHOOTING_DEPTH`, `HAULING_DEPTH`, and `TYPE_OF_FILE`.
`year`	Numeric scalar. The year to be checked in the dataset.
`wd`	Character string. Path to the working directory where log files and plots will be saved.
`suffix`	Character string. Optional suffix to append to the output filenames. If NULL, a timestamp-based suffix is automatically generated.

Details

This function performs multiple validation steps on TA-format data for MEDITS hauls. It verifies that certain key columns contain numeric values and checks for missing or empty entries in critical fields such as `WING_OPENING` and `DISTANCE`.

For each haul, it calculates the mean depth as the average of `SHOOTING_DEPTH` and `HAULING_DEPTH`, and estimates the swept area in square kilometers using the formula $(WING\_OPENING/10) \times DISTANCE/10^6$. Any inconsistencies or errors encountered during these checks are written to a logfile stored in the `Logfiles` folder. If the data contains valid entries, the function generates and saves a scatter plot showing the swept area against mean depth. The plot includes a background shading to visually separate the depth range 0-200 meters from deeper strata, assisting in the interpretation of data distribution across depth zones. All output files are organized within subfolders named `Logfiles` and `Graphs` under the specified working directory.

Value

A logical value:

- `TRUE` if no errors were detected in the data.
- `FALSE` if at least one error was found and logged.

Author(s)

W. Zupa

Examples

```
# Define working directory
wd <- tempdir()

# Load data
ResultDataTA <- RoME::TA

# Filter for specific area if needed
ResultDataTA <- ResultDataTA[ResultDataTA$AREA == 18, ]

# Run the check for year 2005
check_swept_area(ResultDataTA, year = 2005, wd = wd, suffix = NULL)
```

`check_TE_TC` *Function to verify the consistency between individual data table (TE) and biological data table (TC) respect to number of individuals.*

Description

Check if the individuals by species, length, sex and maturity stage reported in TE are less than the number reported in TC

Usage

```
check_TE_TC(ResultDataTC,ResultDataTE,year,wd,suffix)
```

Arguments

`ResultDataTC`	Biological data table(TC).
`ResultDataTE`	Individual data table (TE).
`year`	reference year for the analysis.
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

This function gives an error message, thus the execution is stopped if in TE are reported individuals not present in TC and if the number of individuals reported in TE is greater than the ones in TE; the user is informed in the Logfile.

Value

The function returns TRUE if there is no error, while FALSE if there is one or more errors.The run, in case of error, thus, is stopped.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
tc <- RoME::TC
te <- RoME::TE
year=2012
check_TE_TC(tc,te,year,wd,suffix)
```

`check_temperature` *Function to check the consistency of the temperature data stored in haul data table (TA).*

Description

This function checks if the temperature by haul is in the range 10-30 Celsius degrees; moreover, a plot depth versus temperature is produced and stored in the Graph folder.

Usage

```
check_temperature(ResultDataTA,year,wd,suffix)
```

Arguments

`ResultDataTA`	Haul data table according to MEDITS protocol (TA).
`year`	reference year for the analysis.
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

This check uses the temperature range 10-30 Celsius degrees to provide quantitative warning and a plot, automatically stored in Graphs, for a qualitative inspection of that temperature data respect to depth.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks. The presence of inconsistencies in the data is reported in the logfile stored in the "Logfiles" subdirectory of the "wd" user-defined directory.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TA = RoME::TA
year=2012
wd=tempdir()
suffix="2020-03-05_time_h17m44s55"
check_temperature(TA,year,wd,suffix)
```

`check_type` *Consistency check of TYPE_OF_FILE field*

Description

The function checks if the correct value for TYPE_OF_FILE field is reported in each data table. This is a global function that runs with the data frames not filtered by year.

Usage

```
check_type(TA, TB, TC, TE, TL, years, wd, Errors)
```

Arguments

`TA`	Haul data table according to MEDITS protocol (TA)
`TB`	Catch data table according to MEDITS protocol (TB)
`TC`	Biological data table according to MEDITS protocol (TC)
`TE`	Individual biological data table according to MEDITS protocol (TE)
`TL`	Litter data table according to MEDITS protocol (TL)
`years`	list of the unique YEAR values in haul data (TA) table
`wd`	working directory path defined by the user
`Errors`	logfile name

Details

TA, TB and TC tables are mandatory while TE and TL could be used where available (otherwise use NA value).

Value

The function returns FALSE when errors are detected in the TYPE_OF_FILE field of the data tables.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
TL = NA
years <- unique(RoME::TA$YEAR)
Errors <- file.path(wd,"Logfiles","Logfile.dat")
check_type(TA=RoME::TA,TB=RoME::TB,TC=RoME::TC,
TE=NA,TL=NA,years=years,wd=wd,Errors=Errors)
```

`check_unique_valid_haul`

Function checking that among hauls with the same code, only one must be valid.

Description

Check the presence of unique valid haul codes.

Usage

```
check_unique_valid_haul(ResultDataTA,year,wd,suffix)
```

Arguments

`ResultDataTA`	Haul data table according to MEDITS protocol (TA).
`year`	reference year for the analysis.
`wd`	Working directory selected by the user.
`suffix`	Suffix string of the Logfile.

Details

This function produce an error, stopping the check procedure to avoid cascade errors.

Value

The function returns TRUE if no error occurs, while FALSE is returned when there is more than one valid hauls. In the logfile is reported the list of all the records in which the inconsistency is detected.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TA = RoME::TA
year=2012
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_unique_valid_haul(TA,year,wd,suffix)
```

`check_weight` *Check consistency between total weight and number of individuals in MEDITS TB data.*

Description

This function performs quality checks on the consistency between the total weight and the total number of individuals recorded in the MEDITS TB table. The consistency check is carried out both quantitatively-using known reference ranges of mean weights for each species-and qualitatively-via plots displaying the observed mean weights for each species across hauls.

Usage

```
check_weight(ResultDataTB, year, DataTargetSpecies, wd, suffix)
```

Arguments

`ResultDataTB`	Catch data table formatted according to the MEDITS protocol (table TB). This data includes information on species, number of individuals, and total weight per haul.
`year`	Reference year for the analysis. Only hauls from the specified year will be analysed.
`DataTargetSpecies`	Table providing reference weight ranges for species. It contains the lower (5th percentile) and upper (95th percentile) bounds for the mean weight of individuals per species, based on historical data collected from 2012 to 2022 across all surveyed GSAs. This table should be kept updated to reflect the latest knowledge about species biology in the Mediterranean Sea.
`wd`	Working directory chosen by the user. This directory will contain subfolders where logs and plots will be saved.
`suffix`	Suffix string appended to the filenames of the log files. Useful for distinguishing outputs from multiple runs.

Details

The function operates in two phases:

1. Quantitative Check:

- For each record in the TB table, the mean individual weight is computed.

- If the species is listed in `DataTargetSpecies`, the mean weight is compared to its 5th-95th percentile reference range.
- If the mean weight falls outside this interval, a record is saved in a CSV file reporting:
  - GSA
  - Year
  - Species
  - Haul number
  - Observed mean weight
  - Reference minimum (5th percentile)
  - Reference maximum (95th percentile)
  - Type of file

2. Qualitative Check (Plots):

- For all species present in the dataset, the function generates plots of mean weight by haul, to visually check for possible outliers or abnormal variability.
- To avoid excessive plotting, only species with at least 5 observations are plotted.
- Plots display the mean weight for each haul, with haul numbers shown as labels.
- If many species qualify for plotting, the function automatically splits the plots into multiple pages, each saved as a separate JPEG file. Each JPEG file contains up to 6 plots.

Files Produced:

- *Logfile (.dat)*: Contains a short message summarising whether any outliers were detected. Detailed warnings are no longer written here but are instead stored in the CSV file.
- *CSV File*: Named as `Check_Mean_Weights_Logfile_GSA<AREA>_Year<YEAR>_<suffix>.csv`. Contains all observations where the mean weight falls outside the expected reference range.
- *Plots*: Saved in JPEG format in the `Graphs` subdirectory. Filenames include GSA, year, and a page number.

Value

This function always returns `TRUE`. The purpose of the function is to perform checks and report inconsistencies, but it does not interrupt the execution of other routines in the `RoME` package.

Author(s)

W. Zupa, I. Bitetto

References

Anonymous. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TB <- RoME::TB
year <- 2012
wd <- tempdir()
suffix <- "2020-03-05_time_h17m44s55"
check_weight(TB, year, DataTargetSpecies, wd, suffix)
```

`check_weight_tot_nb` *Function to check if, when the weight is not null, also the number is not null.*

Description

If total weight is different from 0, total number must be different from 0 (only if the category of the species is different from "E") and vice versa (for all faunistic categories).

Usage

```
check_weight_tot_nb(ResultDataTB,year,wd,suffix)
```

Arguments

`ResultDataTB`	Catch data table according to MEDITS protocol (TB)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

In this check 'RoME' verifies if for the records with total weight not null, there is a total number not null, except for categories V, G, H, D and E, as reported in MEDITS manual.

Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the 'RoME' checks.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd=tempdir()
year=2012
TB = RoME::TB
suffix= "2020-03-05_time_h17m44s55"
check_weight_tot_nb(TB,year,wd,suffix)
```

`check_year` *Consistency check of YEAR field*

Description

The function check if the correct value for YEAR field is reported in each data table. This is a global function that runs with the data frames not filtered by year.

Usage

```
check_year(TA, TB, TC, TE, TL, years, wd, Errors)
```

Arguments

`TA`	Haul data table according to MEDITS protocol (TA)
`TB`	Catch data table according to MEDITS protocol (TB)
`TC`	Biological data table according to MEDITS protocol (TC)
`TE`	Individual biological data table according to MEDITS protocol (TE)
`TL`	Litter data table according to MEDITS protocol (TL)
`years`	list of the unique YEAR values in haul data (TA) table
`wd`	working directory path defined by the user
`Errors`	logfile name

Details

TA, TB and TC tables are mandatory while TE and TL could be used where available (otherwise use NA value).

Value

The function returns FALSE when errors are detected in the YEAR field of the data tables.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
wd <- tempdir()
years <- unique(RoME::TA$YEAR)
Errors <- file.path(wd,"Logfiles","Logfile.dat")
check_year(TA=RoME::TA, TB=RoME::TB,
TC=RoME::TC, TE=NA, TL=NA, years=years,
wd=wd, Errors=Errors)
```

`checkHeader` *Function to check the correctness of the headers.*

Description

Function to check the correctness of the headers for haul data (TA), catch data (TB), biological data (TC), individual data (TE), litter data (TL) tables.

Usage

```
checkHeader(dataframe, template,wd,suffix)
```

Arguments

`dataframe`	Table to check
`template`	Template used for the check.
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

This function produce an error, stopping the check procedure to avoid cascade errors.

Value

The function returns TRUE if no error occurs, while FALSE is returned when there is more than one valid hauls. In the logfile and in the console is reported the list of all the records in which the inconsistency is detected.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
checkHeader(RoME::TA,"TA",wd,suffix)
checkHeader(RoME::TB,"TB",wd,suffix)
checkHeader(RoME::TC,"TC",wd,suffix)
```

`classes` *Class of fields*

Description

Definition of field' classes for TX tables

Usage

```
data("classes")
```

Format

A data frame with 123 observations on the following 4 variables.

`RDBFIS`	a character vector
`MEDITS`	a character vector
`table`	a character vector
`type`	a character vector

Details

See Medits handbook.

Author(s)

W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(classes)
```

`create_catch` *Function to create the R-sufi file capt.*

Description

This function report the information contained in the biological data table (TB) from the MEDITS protocol to the format required by R-sufi (Rochet et al., 2004).

Usage

```
create_catch(ResultDataTB,year,wd,save=TRUE)
```

Arguments

`ResultDataTB`	Catch data table according to MEDITS protocol (TB)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`save`	boolean value to save the results in a csv file

Value

The function saves by default in the files R-Sufi folder the table capt in.csv format, with suffix of the year and GSA. If save parameter is FALSE the function returns the data frame as output.

Author(s)

I. Bitetto, W. Zupa

References

Rochet M. J., V. M. Trenkel, J. A. Bertrand & J.-C. Poulard, 2004. R routines for survey based fisheries population and community indicators (R-SUFI). Ifremer, Nantes. Limited distribution. Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
TB = RoME::TB
year =2012
wd = tempdir()
create_catch(TB,year,wd,save=TRUE)
```

`create_haul` *Function to create R-sufi file containing haul data.*

Description

This function reports the information contained in the haul data table (TA) from the MEDITS protocol to the format required by R-sufi (Rochet et al., 2004).

Usage

```
create_haul(ResultDataTA,year,wd,save=TRUE)
```

Arguments

`ResultDataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`save`	boolean value to save the results in a csv file

Value

The function saves by default in the files R-Sufi folder the table traits in.csv format, with suffix of the year and GSA. If `save` parameter is FALSE the function returns the data frame as output.

Author(s)

I. Bitetto, W. Zupa

References

Rochet M. J., V. M. Trenkel, J. A. Bertrand & J.-C. Poulard, 2004. R routines for survey based fisheries population and community indicators (R-SUFI). Ifremer, Nantes. Limited distribution. Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TA = RoME::TA
year = 2012
wd = tempdir()
create_haul(TA,year,wd,save=FALSE)
```

`create_length` *Function to create the R-sufi file taille.*

Description

This function reports the information contained in the biological data table (TC) from the MEDITS protocol to the format required by R-sufi (Rochet et al., 2004).

Usage

```
create_length(ResultData,year,DataSpecies=RoME::TM_list,wd,save=TRUE)
```

Arguments

`ResultData`	Biological data table according to MEDITS protocol (TC)
`year`	reference year for the analysis
`DataSpecies`	TM_list reference list
`wd`	working directory path defined by the user
`save`	boolean value to save the results in a csv file

Details

For the file taille the change in maturity scale in 2006 has been taken into account: from 1994 to 2005 the males of crustaceans have stage NA, because they were not staged until 2005. From 2006 they are considered mature for the stages strictly greater than 2A as well as for females of crustaceans. Before 2006 the females of crustaceans are considered mature for stages strictly greater than 1. Bony fish and cephalopods are considered mature from stage 3 until 2005 and then they are considered mature from stage 2B. For selachians, the immature are always stage 1 and 2.

Value

The function saves by default in the files R-Sufi folder the table taille in.csv format, with suffix of the year and GSA. If `save` parameter is FALSE the function returns the data frame as output.

Author(s)

I. Bitetto, W. Zupa

References

Rochet M. J., V. M. Trenkel, J. A. Bertrand & J.-C. Poulard, 2004. R routines for survey based fisheries population and community indicators (R-SUFI). Ifremer, Nantes. Limited distribution. Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
ResultData = RoME::TC
year=2012
DataSpecies=RoME::TM_list
wd <- tempdir()
create_length(ResultData,year,DataSpecies,wd,save=FALSE)
```

`create_strata` *Function to create R-sufi file containing strata surface data.*

Description

This function reports the information contained in the stratification scheme for the selected area from the MEDITS protocol to the format required by R-sufi (Rochet et al., 2004).

Usage

```
create_strata(Stratification,AREA,wd,save=TRUE)
```

Arguments

`Stratification`	Stratification scheme according to MEDITS protocol.
`AREA`	String of the GSA.
`wd`	Working directory selected by the user.
`save`	boolean value to save the results in a csv file

Value

The function saves automatically in the files R-Sufi folder the table strata in.csv format, with suffix of the year and GSA. If `save` parameter is FALSE the function returns the data frame as output.

Author(s)

I. Bitetto, W. Zupa

References

Rochet M. J., V. M. Trenkel, J. A. Bertrand & J.-C. Poulard, 2004. R routines for survey based fisheries population and community indicators (R-SUFI). Ifremer, Nantes. Limited distribution. Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
Stratification=RoME::stratification_scheme
wd <- tempdir()
AREA = 18
create_strata(Stratification,AREA,wd,save=TRUE)
```

`DataTargetSpecies` *Length and weight ranges for relevant species*

Description

Data frame containing information about length and individual weight ranges for relevant species, including quantiles and various statistics. It also contains metadata about faunistic category and period of relevance as target species.

Usage

```
data("DataTargetSpecies")
```

Format

A data frame with 392 observations on the following 26 variables:

`SPECIES` Rubincode species identifier (character).

`WMIN` Minimum observed individual weight (numeric).

`WMIN05` 5th percentile of individual weight (numeric).

`WMIN10` 10th percentile of individual weight (numeric).

`WMIN25` 25th percentile of individual weight (numeric).

`WMAX_75` 75th percentile of individual weight (numeric).

`WMAX90` 90th percentile of individual weight (numeric).

`WMAX95` 95th percentile of individual weight (numeric).

`WMAX` Maximum observed individual weight (numeric).

`LMIN` Minimum observed length (numeric, in mm).

`LMIN01` 1st percentile of length (numeric, in mm).

`LMIN05` 5th percentile of length (numeric, in mm).

`LMIN10` 10th percentile of length (numeric, in mm).

`LMIN25` 25th percentile of length (numeric, in mm).

`LMAX75` 75th percentile of length (numeric, in mm).

`LMAN90` 90th percentile of length calculated via mean or other method (numeric, in mm).

`LMAX95` 95th percentile of length (numeric, in mm).

`LMAX99` 99th percentile of length (numeric, in mm).

`LMAX` Maximum observed length (numeric, in mm).

`obs_in_TC` Number of observations found in TC data (numeric).

`FAUNISTIC_CATEGORY` Old faunistic categories (character).

`START_YEAR` Year when the species started to be considered target (numeric).

`END_YEAR` Year when the species stopped being considered target (numeric).

`GROUP` Species group or classification (character).

Author(s)

W. Zupa

Source

Literature and other data sources.

Examples

```
data(DataTargetSpecies)
head(DataTargetSpecies)
```

`dd.distance` *Estimation of haul distance*

Description

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

Usage

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

Arguments

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

Details

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

Value

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

Author(s)

Walter Zupa

Examples

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

`error.table` *Summary table of the errors*

Description

Function generating the error summary table.

Usage

```
error.table(check.df,check_without_errors,
check_without_warnings,checkName,table,Field,yea)
```

Arguments

`check.df`	data frame of the checks
`check_without_errors`	boolean variable reporting if errors were detected
`check_without_warnings`	boolean variable reporting if warnings were detected
`checkName`	string of the check name
`table`	reference table checked by the function
`Field`	field checked by check dictionary
`yea`	reference year

Details

The function generate the summary table of the errors detected by the `RoMEcc` function.

Value

The output of the function is the data frame `check.df` updated with the result of the check.

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

`graphs_TA` *Function for qualitative checks of shooting depth, warp length and wing opening in Haul data table (TA).*

Description

Qualitative control (by means of 2 graphs) of relation between shooting depth e warp opening and between warp length e wing opening

Usage

```
graphs_TA(DataTA, year, wd, suffix)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function generate 2 graphs for qualitative controls.

Value

Two graphs are stored in the Graphs folder in the wd user defined directory

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TA = RoME::TA
year = 2012
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
graphs_TA(RoME::TA,year,wd,suffix)
```

`GSAs` *List of GFCM Geographical subareas (GSAs)*

Description

GSAs table

Usage

```
data("GSAs")
```

Format

A data frame with 31 observations on the following 3 variables.

`GSA` a numeric vector

`CODE` a character vector

`Area` a character vector

Author(s)

W. Zupa

Source

https://www.fao.org/gfcm/data/maps/gsas/en/

References

https://www.fao.org/gfcm/data/maps/gsas/en/

Examples

```
data(GSAs)
str(GSAs)
head(GSAs)
```

`haul_at_sea` *Check of haul position on sea area*

Description

The function identify the hauls that don't fall in the user defined sea area.

Usage

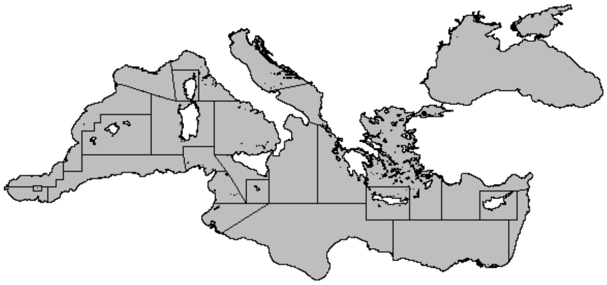
```
haul_at_sea(DataTA,year,seas=RoME::MedSea,verbose = TRUE)
```

Arguments

`DataTA`	Haul data table according to MEDITS protocol (TA)
`year`	reference year for the analysis
`seas`	polygon shapefile defining the extension of the sea area. The default `MedSea` dataset is referred to the Mediterranean and Black Sea area.
`verbose`	boolean variable returning verbose output if TRUE

Details

The function check whether the haul position falls in the polygon `seas` defining the extension of the reference sea area.



Value

The function returns the list of the hauls out of the `seas` polygon. In case only starting haul positions are out of the sea's area a data frame is returned. If both starting and end positions are out of the polygon an object of class `list` is returned.

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
TA = RoME::TA
year = 2012
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
haul_at_sea(TA,year, seas = MedSea, verbose = TRUE)
```

`headers.conversion` *Headers conversion for MEDITS tables*

Description

Headers conversion for MEDITS tables

Usage

```
headers.conversion(table, type, verbose = FALSE)
```

Arguments

`table`	data frame of the TX table
`type`	type of tables to be analysed. Allowed values: "TA","TB","TC","TE","TL"
`verbose`	boolean. If TRUE a message is printed.

Details

The functions allow to convert headers of table coming from RDBFIS data base to the MEDITS format expected from RoME package

Value

A data frame object is returned including the only allowed field

---

`list_g1_g2` *List of G1 and G2 species*

Description

List of the target species G1 and G1 as defined by the MEDITS protocol (see MEDITS-Handbook Version 9 2017)

Usage

```
data("list_g1_g2")
```

Format

A data frame with 88 observations on the following 17 variables.

`No`	a numeric vector of progressive number
`Medit_LIST_proposal_2011`	a factor with levels of the list proposed in 2011
`Species_group_DCF`	a factor with levels of the DCF species groups
`MEDITS_G1`	a numeric vector of G1 species
`MEDITS_G2`	a numeric vector of G2 species
`Group`	a factor with levels of groups
`Old_MEDITS_list`	a numeric vectorof the old MEDITS list
`Tot_No`	Tot_No
`Tot_W`	Tot_W
`Ind_Length`	Ind_Length
`Sex`	a factor with levels of sex
`Mat_stage`	a factor with levels of maturity stages
`Age`	a factor with levels of age
`Ind_weight`	a factor with levels of Ind_weight
`Date`	a factor with levels of Date
`CODE`	a factor with levels CODE
`English_common_name`	a factor with levels of common names in english language

Author(s)

W. Zupa

Source

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.https://www.sibm.it/MEDITS%202011/principaledownload.htm

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(list_g1_g2)
```

`LW` *Table of the Length-Weight parameters*

Description

Table of the length-weight relationship coefficients reported by species, area and sex.

Usage

```
data("LW")
```

Format

A data frame with 460 observations on the following 5 variables.

`AREA` vector of the reference geographic area

`SPECIES` reference species for the a and b parameters

`SEX` reference sex for the a and b parameters

`a` a parameters of the length-weight relationship function

`b` b parameters of the length-weight relationship function

Details

Table of the length-weight relationship coefficients a and b.

Author(s)

W. Zupa

Examples

```
data(LW)
str(LW)
```

`mat_stages` *Table of maturity stages*

Description

Table of maturity stages

Usage

```
data("mat_stages")
```

Format

A data frame with 132 observations on the following 4 variables.

- `TYPE_OF_FILE` a character vector
- `FAUNISTIC_CATEGORY` a character vector
- `SEX` a character vector
- `MATURITY` a character vector
- `MATSUB` a character vector
- `code` a character vector

Details

Table of maturity stages per faunistic category.The maturity scales adopted up to 2006 is also provided.

Author(s)

W. Zupa

Source

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(mat_stages)
str(mat_stages)
```

`Maturity_parameters` *Maturity parameters*

Description

Maturity parameters used for the checks: check_smallest_mature, check_spawning_period and check_sex_inversion

Usage

```
data("Maturity_parameters")
```

Format

A data frame with 64 observations on the following 12 variables.

`Species`	a factor with levels the rubincodes of the species for which the information is known.
`SEX`	a factor with levels `C` `F` `M`
`min_L50`	a numeric vector
`max_L50`	a numeric vector
`smallest_mature_individual_observed`	a numeric vector
`min_length_SEX_INVERSION`	a numeric vector
`max_length_SEX_INVERSION`	a numeric vector
`Type_of_hermaphroditism`	a factor with levels `proterandrous` `protogynous`
`Area`	a factor with levels as the area of the relevant information
`Start_reproductive_season`	a numeric vector
`End_reproductive_season`	a numeric vector
`Reference`	a factor with levels of the bibliographic references

Author(s)

W. Zupa

Source

Literature and others

Examples

```
data(Maturity_parameters)
```

`MEDITS.to.dd` *Conversion of MEDITS format coordinates in decimal degrees format*

Description

Conversion of MEDITS format coordinates in decimal degrees format

Usage

```
MEDITS.to.dd(data)
```

Arguments

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

Value

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

Author(s)

Walter Zupa

Examples

```
MEDITS.to.dd(TA)
```

`MedSea` *Shapefile of Mediterranean and Black Sea area*

Description

Polygon shapefile describing the GFCM's Geographical subareas (GSAs)

Usage

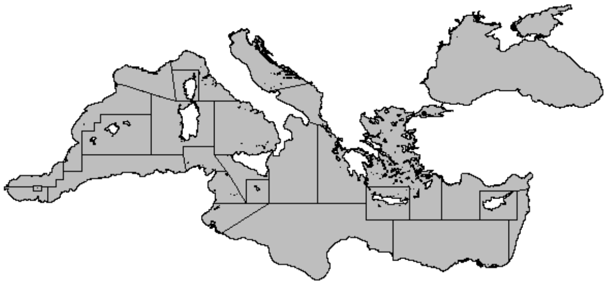
```
data("MedSea")
```

Format

The shapefile is derived from the GFCM's Geographical subareas (GSAs) shapefile

Details

Polygon shapefile describing the GFCM's Geographical subareas (GSAs) compressed with the `xz` type of compression.



Author(s)

W. Zupa

Source

https://www.fao.org/fileadmin/user_upload/faoweb/GFCM/Maps/GSAs_simplified.zip

References

https://www.fao.org/gfcm/data/maps/gsas/en/

Examples

```
library(sp)
data(MedSea)
plot(MedSea)
```

`printError` *Management of the error in logfile.*

Description

Management of the error in logfile.

Usage

```
printError(funname,check_without_errors, stop_)
```

Arguments

`funname`	name of the check function.
`check_without_errors`	TRUE if there is no error, FALSE if there is any error.
`stop_`	TRUE if the 'RoME' function has to stop, FALSE if the run should continue

Value

The function updates the 'stop_' value and returns it as a logical value.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
printError("check_abundance", FALSE, FALSE)
```

`printError_cc` *Management of the error in logfile.*

Description

Management of the error in logfile.

Usage

```
printError_cc(funname,check_without_errors, stop_)
```

Arguments

`funname`	name of the check function.
`check_without_errors`	TRUE if there is no error, FALSE if there is any error.
`stop_`	TRUE if the 'RoME' function has to stop, FALSE if the run should continue

Value

The function updates the 'stop_' value and returns it as a logical value.

Author(s)

W. Zupa, I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
printError_cc("check_abundance", FALSE, FALSE)
```

RoME *Multiple Checks on MEDITS Trawl Survey Data*

Description

The function calls all the functions built in the package in an ordered way to perform a complete quality check of TX data available. The check is performed simultaneously on the files that can contain also data of more than one year.

Usage

```
RoME(TA,TB,TC,TE=NA,TL=NA,wd,suffix=NA,
create_RSufi_files = FALSE, create_global_RSufi_files=FALSE,
Year_start=NA,Year_end=NA,verbose =TRUE,Stratification=RoME::stratification_scheme,
Ref_list=RoME::TM_list,DataTargetSpecies=RoME::DataTargetSpecies,
Maturity=RoME::Maturity_parameters,
ab_parameters=RoME::LW,
stages_list=RoME::mat_stages,assTL=assTL)
```

Arguments

`TA`	Haul data table according to MEDITS protocol (TA)
`TB`	Catch data table according to MEDITS protocol (TB)
`TC`	Biological data table according to MEDITS protocol (TC)
`TE`	Individual biological data table according to MEDITS protocol (TE) if available, if TE data are not available, use NA.
`TL`	Litter data table according to MEDITS protocol (TL) if available, if TL data are not available, use NA
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile, in case it `suffix=NA` it is automatically generated by the function using date and time of the check
`create_RSufi_files`	boolean variables used to choose if create R-sufi files. The files are saved in the R-sufi directory and named with a suffix of the year and GSA
`create_global_RSufi_files`	boolean variables used to choose if global R-sufi files should be created from an year to another year
`Year_start`	numeric value indicating the starting year for the production of R-sufi file. This parameter must to be reported in case
`Year_end`	numeric value indicating the ending year for the production of R-sufi files
`verbose`	...
`Stratification`	Stratification scheme according to MEDITS protocol.
`Ref_list`	TM_list reference list
`DataTargetSpecies`	Information related to target species.
`Maturity`	Information related to sex and maturity from literature or other sources.
`ab_parameters`	dataframe containing the a and b parameters of the length-weight relationships
`stages_list`	Table of maturity stages.
`assTL`	data frame with the association between TL (litter table) categories and sub-categories

Details

`RoME` checks can be used to integrate a list of common quality checks on survey data. This function calls all the functions built in the package in an ordered way to perform a complete quality check of TX data available. The order of the checks in `RoME` was implemented in a defined sequence to avoid cascade errors due to the correction of a previous error. No automatic correction is implemented in 'RoME'. 'RoME' stops if an error occurs; then the user has to correct the error and run again the code to continue with the other checks. The function runs on a complete time series dataset, checking year after year, until the end of the time series. After the checks of the mandatory fields and the controlled vocabulary, that are carried out for all the TX tables, the specific checks on each kind of TX table are performed. Finally, `RoME` provides a list of cross checks aimed to guarantee the consistency among the data tables.

Some functions included in the 'RoME' library and used by `RoME` function need specific dictionaries or tables. It is the case of `Stratification`, `Ref_list`, `DataTargetSpecies`, `Maturity_parameters`, `mat_stages` and `assTL` tables. All of them are provided by default in this library. Anyway, the user has the possibility to provide *ad hoc* modified versions of these tables adapting the checks to specific needs.

Value

The function does not correct data, but it detects the errors, warning the user that there is the possibility of one or more errors, specifying the type of the error and easing the data correction. If parameter `verbose=TRUE` returns a series of text output in console to let the user to trace the state of the checks. All the output of the functions are stored in the user defined working directory `wd` and in the sub-directory there resident. In the Lofile subfolder are stored the logfiles of each run of the function.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix=NA
DataTA = RoME::TA
DataTB = RoME::TB
DataTC = RoME::TC
DataTE = NA
DataTL = NA
RoME(DataTA, DataTB,DataTC,DataTE,DataTL, wd, suffix,
  Stratification=RoME::stratification_scheme,
  Ref_list=RoME::TM_list,DataTargetSpecies=RoME::DataTargetSpecies,
  Maturity=RoME::Maturity_parameters,ab_parameters=RoME::LW,
  stages_list=RoME::mat_stages,assTL=RoME::assTL)
```

`RoMEBScc` *Continuous Quality Checks on Black Sea trawl Survey Data*

Description

The function `RoMEBScc` performs a full suite of automated, non-stopping quality checks on survey data for the Black Sea. It invokes the same sequence of validation routines as `RoMEcc` (for TA, TB, TC, TE and TL tables) but uses tables and parameters tailored to Black Sea strata, species and maturity references.

Usage

```
RoMEBScc(
  TA,
  TB,
  TC,
  TE = NA,
  TL = NA,
  wd,
  suffix = NA,
  verbose = TRUE,
  Stratification = RoME::stratification_scheme,
  Ref_list = RoME::TM_list,
  DataTargetSpecies = RoME::DataTargetSpecies,
  Maturity = RoME::Maturity_parameters,
  ab_parameters = RoME::LW,
  stages_list = RoME::mat_stages,
  assTL = RoME::assTL,
  zip = TRUE
)
```

Arguments

`TA`	Haul metadata table (TA)
`TB`	Catch data table (TB)
`TC`	Biological data table (TC)
`TE`	Individual biological data table (TE), or `NA` if unused.
`TL`	Litter table (TL), or `NA` if unused.
`wd`	Working directory path where "Logfiles" and "Graphs" subfolders are written.
`suffix`	Character suffix for output filenames. If `NA`, a timestamp is auto-generated.
`verbose`	Logical; if `TRUE`, progress messages are printed to the console.
`Stratification`	Stratification scheme object; defaults to `RoME::stratification_scheme`.
`Ref_list`	Reference list for tow metadata; defaults to `RoME::TM_list`.
`DataTargetSpecies`	Species-specific reference dataset; defaults to `RoME::DataTargetSpecies`.
`Maturity`	Maturity-parameter table; defaults to `RoME::Maturity_parameters`.
`ab_parameters`	Length-weight parameter table; defaults to `RoME::LW`.
`stages_list`	Maturity-stage lookup table; defaults to `RoME::mat_stages`.
`assTL`	Category-subcategory mapping for TL; defaults to `RoME::assTL`.
`zip`	Logical; if `TRUE`, a ZIP archive of results is created at the end.

Details

`RoMEBScc` checks can be used to integrate a list of common quality checks on survey datafrom Black Sea. This function calls all the functions built in the package in an ordered way to perform a complete quality check of TX data available. The order of the checks in `RoME` was implemented in a defined sequence to avoid cascade errors due to the correction of a previous error. No automatic correction is implemented in 'RoME'. 'RoME' stops if an error occurs; then the user has to correct the error and run again the code to continue with the other checks. The function runs on a complete time series dataset, checking year after year, until the end of the time series. After the checks of the mandatory fields and the controlled vocabulary, that are carried out for all the TX tables, the specific checks on each kind of TX table are performed. Finally, `RoME` provides a list of cross checks aimed to guarantee the consistency among the data tables.

Some functions included in the 'RoME' library and used by `RoME` function need specific dictionaries or tables. It is the case of `Stratification`, `TM_list`, `DataTargetSpecies`, `Maturity_parameters`, `mat_stages` and `assTL` tables. All of them are provided by default in this library. Anyway, the user has the possibility to provide *ad hoc* modified versions of these tables adapting the checks to specific needs.

Value

The function does not correct data, but it detects the errors, warning the user that there is the possibility of one or more errors, specifying the type of the error and easing the data correction. If parameter `verbose=TRUE` returns a series of text output in console to let the user to trace the state of the checks. All the output of the functions are stored in the user defined working directory `wd` and in the sub-directory there resident. In the Lofile subfolder are stored the logfiles of each run of the function.

Author(s)

W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
# Example using TA, TB, TC slices for 2018
TA_sub <- RoME::TA[RoME::TA$YEAR == 2018, ]
TB_sub <- RoME::TB[RoME::TB$YEAR == 2018, ]
TC_sub <- RoME::TC[RoME::TC$YEAR == 2018, ]
# TE/TL not used in this example
RoMEBScc(
  TA_sub, TB_sub, TC_sub, TE = NA, TL = NA,
  wd = wd, suffix = "BS_test",
  verbose = FALSE
)
```

`RoMEcc` *Continuous Quality Checks on MEDITS Trawl Survey Data*

Description

The function calls all the functions included in the package in an ordered way to perform a complete quality check of TX data available. The check is performed simultaneously on the files that can contain also data of more than one year. Unlike the `RoME` function, `RoMEcc` does not stop at the first detected error, allowing user to correct data. Instead, it checks all the data and returns a report on the errors found, as well as compiling a detailed log file.

Usage

```
RoMEcc(TA,TB,TC,TE=NA,TL=NA,wd,suffix=NA,
verbose =TRUE,Stratification=RoME::stratification_scheme,
Ref_list=RoME::TM_list,DataTargetSpecies=RoME::DataTargetSpecies,
Maturity=RoME::Maturity_parameters,
ab_parameters=RoME::LW,
stages_list=RoME::mat_stages,assTL=RoME::assTL, zip=TRUE)
```

Arguments

`TA`	Haul data table according to MEDITS protocol (TA)
`TB`	Catch data table according to MEDITS protocol (TB)
`TC`	Biological data table according to MEDITS protocol (TC)
`TE`	Individual biological data table according to MEDITS protocol (TE) if available, if TE data are not available, use NA.
`TL`	Litter data table according to MEDITS protocol (TL) if available, if TL data are not available, use NA
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile, in case it `suffix=NA` it is automatically generated by the function using date and time of the check
`verbose`	...
`Stratification`	Stratification scheme according to MEDITS protocol.
`Ref_list`	TM_list reference list
`DataTargetSpecies`	Information related to target species.
`Maturity`	Information related to sex and maturity from literature or other sources.
`ab_parameters`	dataframe containing the a and b parameters of the length-weight relationships
`stages_list`	Table of maturity stages.
`assTL`	data frame with the association between TL (litter table) categories and subcategories
`zip`	boolean, if TRUE a zip file containing the results is generated

Details

`RoMEcc` checks can be used to integrate a list of common quality checks on survey data. This function calls all the functions built in the package in an ordered way to perform a complete quality check of TX data available. The order of the checks in `RoME` was implemented in a defined sequence to avoid cascade errors due to the correction of a previous error. No automatic correction is implemented in 'RoME'. 'RoME' stops if an error occurs; then the user has to correct the error and run again the code to continue with the other checks. The function runs on a complete time series dataset, checking year after year, until the end of the time series. After the checks of the mandatory fields and the controlled vocabulary, that are carried out for all the TX tables, the specific checks on each kind of TX table are performed. Finally, `RoME` provides a list of cross checks aimed to guarantee the consistency among the data tables.

Some functions included in the 'RoME' library and used by `RoME` function need specific dictionaries or tables. It is the case of `Stratification`, `TM_list`, `DataTargetSpecies`, `Maturity_parameters`, `mat_stages` and `assTL` tables. All of them are provided by default in this library. Anyway, the user has the possibility to provide *ad hoc* modified versions of these tables adapting the checks to specific needs.

Value

The function does not correct data, but it detects the errors, warning the user that there is the possibility of one or more errors, specifying the type of the error and easing the data correction. If parameter `verbose=TRUE` returns a series of text output in console to let the user to trace the state of the checks. All the output of the functions are stored in the user defined working directory `wd` and in the sub-directory there resident. In the Lofile subfolder are stored the logfiles of each run of the function.

Author(s)

W. Zupa,I. Bitetto

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix=NA
DataTA = data.frame(RoME::TA[RoME::TA$YEAR==2012 ,])
DataTB = data.frame(RoME::TB[RoME::TB$YEAR==2012 ,])
DataTC = data.frame(RoME::TC[RoME::TC$YEAR==2012 ,])
DataTE = NA
DataTL = NA
RoMEcc(DataTA, DataTB,DataTC,DataTE,DataTL, wd, suffix,
  Stratification=RoME::stratification_scheme,
  Ref_list=RoME::TM_list,DataTargetSpecies=RoME::DataTargetSpecies,
  Maturity=RoME::Maturity_parameters,ab_parameters=RoME::LW,
  stages_list=RoME::mat_stages,assTL=RoME::assTL, verbose=FALSE)
```

`RSufi_files` *Function to concatenate the R-sufi files of the different years.*

Description

When the check procedure is completed for a number of years, it is possible to obtain the 4 R-Sufi global files from an year to another year.

Usage

```
RSufi_files(Year_start,Year_end,AREA,wd)
```

Arguments

`Year_start`	Start year
`Year_end`	Start end
`AREA`	String of the GSA. Include only the number.
`wd`	working directory path defined by the user

Value

The function saves automatically in the files R-Sufi folder the 4 global files, with suffix of the year range and GSA.

Author(s)

I. Bitetto, W. Zupa

References

Rochet M. J., V. M. Trenkel, J. A. Bertrand & J.-C. Poulard, 2004. R routines for survey based fisheries population and community indicators (R-SUFI). Ifremer, Nantes. Limited distribution. Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
TA = RoME::TA
TB = RoME::TB
TC = RoME::TC
DataSpecies=RoME::TM_list
Stratification=RoME::stratification_scheme
year = 2012
wd <- tempdir()
create_haul(TA,year,wd,save=TRUE)
create_catch(TB,year,wd,save=TRUE)
create_length(TC,year,DataSpecies,wd,save=TRUE)
create_strata(Stratification,"10",wd,save=TRUE)
RSufi_files(2012,2012,"10",wd) # run only if you are working outside a temporary directory
```

`run_RoME_app` *Run the RoME Shiny application*

Description

Launches the embedded Shiny application included in the package.

Usage

```
run_RoME_app()
```

Value

No return value, called for side effects

`scheme_individual_data` *Summary of the individual data collected by species*

Description

Check for summarize the individual data collection (goodness of individual data sampling)

Usage

```
scheme_individual_data(DataTC, DataTE, year, wd, suffix)
```

Arguments

`DataTC`	Biological data table according to MEDITS protocol (TC)
`DataTE`	Individual biological data table according to MEDITS protocol (TE)
`year`	reference year for the analysis
`wd`	working directory path defined by the user
`suffix`	Suffix string of the Logfile

Details

The function uses biological data and individual biological data to produce a table where for each species are stored the number of length measurements, individual weights and number of otoliths taken by length class.

Value

This check has as output a table (automatically saved in the wd user defined directory) named `sampling_individual_measures.csv` where for each species are stored the number of length measurements, individual weights and number of otoliths taken by length class. This table is useful to the user to evaluate the coverage of the individual measurements collections in order to verify if the sampling is in line with the protocol and to understand how eventually improve the sampling procedure.

Author(s)

I. Bitetto, W. Zupa

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTC = RoME::TC
DataTE = RoME::TE
year=2012
scheme_individual_data(DataTC,DataTE,year, wd, suffix)
```

`stratification_scheme` *stratification_scheme*

Description

data frame of the stratification_scheme

Author(s)

W. Zupa

`stratification_scheme_rapana` *stratification_scheme_rapana*

Description

Data frame of the stratification scheme specifically used in Romania and Bulgaria in the rapa whelk beam trawl survey.

Author(s)

W. Zupa

`TA` *TA*

Description

TA table

Author(s)

W. Zupa

`TB` *TB*

Description

TB table

Author(s)

W. Zupa

`TC` *TC*

Description

TC table

Author(s)

W. Zupa

`TE` *TE*

Description

TE table

Author(s)

W. Zupa

`templateTA` *Template haul data table (TA).*

Description

Dataframe containing the headers of TA, according to the MEDITS manual.

Usage

```
data("templateTA")
```

Format

A data frame with 0 observations on the following 43 variables.

`TYPE_OF_FILE` a logical vector

`COUNTRY` a logical vector

`AREA` a logical vector

`VESSEL` a logical vector

`GEAR` a logical vector

`RIGGING` a logical vector

`DOORS` a logical vector

`YEAR` a logical vector

`MONTH` a logical vector

`DAY` a logical vector

`HAUL_NUMBER` a logical vector

`CODEND_CLOSING` a logical vector

`PART_OF_THE_CODEND` a logical vector

`SHOOTING_TIME` a logical vector

`SHOOTING_QUADRANT` a logical vector

`SHOOTING_LATITUDE` a logical vector

`SHOOTING_LONGITUDE` a logical vector

`SHOOTING_DEPTH` a logical vector

`HAULING_TIME` a logical vector

`HAULING_QUADRANT` a logical vector

`HAULING_LATITUDE` a logical vector

`HAULING_LONGITUDE` a logical vector

`HAULING_DEPTH` a logical vector

`HAUL_DURATION` a logical vector

`VALIDITY` a logical vector

`COURSE` a logical vector

`RECORDED_SPECIES` a logical vector

`DISTANCE` a logical vector

`VERTICAL_OPENING` a logical vector

`WING_OPENING` a logical vector

`GEOMETRICAL_PRECISION` a logical vector

`BRIDLES_LENGTH` a logical vector

`WARP_LENGTH` a logical vector

`WARP_DIAMETER` a logical vector

`HYDROLOGICAL_STATION` a logical vector

`OBSERVATIONS` a logical vector

`BOTTOM_TEMPERATURE_BEGINNING` a logical vector

`BOTTOM_TEMPERATURE_END` a logical vector

`MEASURING_SYSTEM` a logical vector

`NUMBER_OF_THE_STRATUM` a logical vector

`BOTTOM_SALINITY_BEGINNING` a logical vector

`BOTTOM_SALINITY_END` a logical vector

`MEASURING_SYSTEM_SALINITY` a logical vector

Details

See Medits handbook.

Author(s)

W. Zupa

Source

The dataframe is empty and it is to be used to verify the correctness of headers.

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(templateTA)
```

`templateTB` *Template catch data table (TB).*

Description

Dataframe containing the headers of TB, according to the MEDITS manual.

Usage

```
data("templateTB")
```

Format

A data frame with 0 observations on the following 43 variables.

`TYPE_OF_FILE` a logical vector

`COUNTRY` a logical vector

`AREA` a logical vector

`VESSEL` a logical vector

`YEAR` a logical vector

`MONTH` a logical vector

`DAY` a logical vector

`HAUL_NUMBER` a logical vector

`CODEND_CLOSING` a logical vector

`PART_OF_THE_CODEND` a logical vector

`FAUNISTIC_CATEGORY` a logical vector

`GENUS` a logical vector

`SPECIES` a logical vector

`NAME_OF_THE_REFERENCE_LIST` a logical vector

`TOTAL_WEIGHT_IN_THE_HAUL` a logical vector

`TOTAL_NUMBER_IN_THE_HAUL` a logical vector

`NB_OF_FEMALES` a logical vector

`NB_OF_MALES` a logical vector

`NB_OF_UNDETERMINED` a logical vector

Details

See Medits handbook.

Author(s)

W. Zupa

Source

The dataframe is empty and it is to be used to verify the correctness of headers.

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(templateTB)
```

`templateTC` *Template biological data table (TC).*

Description

Dataframe containing the headers of TC, according to the MEDITS manual.

Usage

```
data("templateTC")
```

Format

A data frame with 0 observations on the following 43 variables.

`TYPE_OF_FILE` a logical vector

`COUNTRY` a logical vector

`AREA` a logical vector

`VESSEL` a logical vector

`YEAR` a logical vector

`MONTH` a logical vector

`DAY` a logical vector

`HAUL_NUMBER` a logical vector

`CODEND_CLOSING` a logical vector

`PART_OF_THE_CODEND` a logical vector

`FAUNISTIC_CATEGORY` a logical vector

`GENUS` a logical vector

`SPECIES` a logical vector

`LENGTH_CLASSES_CODE` a logical vector

`WEIGHT_OF_THE_FRACTION` a logical vector

`WEIGHT_OF_THE_SAMPLE_MEASURED` a logical vector

`SEX` a logical vector

`NO_OF_INDIVIDUAL_OF_THE_ABOVE_SEX_MEASURED` a logical vector

`LENGTH_CLASS` a logical vector

`MATURITY` a logical vector

`MATSUB` a logical vector

`NUMBER_OF_INDIVIDUALS_IN_THE_LENGTH_CLASS_AND_MATURITY_STAGE` a logical vector

Details

See Medits handbook.

Author(s)

W. Zupa

Source

The dataframe is empty and it is to be used to verify the correctness of headers.

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. https://www.sibm.it/MEDITS%202011/principaledownload.htm

Examples

```
data(templateTC)
```

`templateTE` *Template individual data table (TE).*

Description

Dataframe containing the headers of TE, according to the MEDITS manual.

Usage

```
data("templateTE")
```

Format

A data frame with 0 observations on the following 43 variables.

`TYPE_OF_FILE` a logical vector

`COUNTRY` a logical vector

`AREA` a logical vector

`VESSEL` a logical vector

`YEAR` a logical vector

`MONTH` a logical vector

`DAY` a logical vector

`HAUL_NUMBER` a logical vector

`FAUNISTIC_CATEGORY` a logical vector

`GENUS` a logical vector

`SPECIES` a logical vector

`LENGTH_CLASSES_CODE` a logical vector

`SEX` a logical vector

`NO_PER_SEX_MEASURED_IN_SUB_SAMPLE_FOR_OTOLITH` a logical vector

`LENGTH_CLASS` a logical vector

`MATURITY` a logical vector

`MATSUB` a logical vector

`INDIVIDUAL_WEIGHT` a logical vector

`NO_PER_SEX_MEASURED_IN_SUB_SAMPLE_FOR_WEIGHT` a logical vector

`OTOLITH_SAMPLED` a logical vector

`NO_PER_SEX_MEASURED_IN_SUB_SAMPLE_FOR_AGEING` a logical vector

`OTOLITH_READ` a logical vector

`AGE` a logical vector

`OTOLITH_CODE` a logical vector

`RECORD_NUMBER` a logical vector

Details

See Medits handbook.

Author(s)

W. Zupa

Source

The dataframe is empty and it is to be used to verify the correctness of headers.

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(templateTE)
```

`templateTL` *TL table template*

Description

Template of the Litter data table (TL) as defined in the MEDITS protocol

Usage

```
data("templateTL")
```

Format

A data frame with 0 observations on the following 14 variables.

`TYPE_OF_FILE`	a logical vector
`COUNTRY`	a logical vector
`AREA`	a logical vector
`VESSEL`	a logical vector
`YEAR`	a logical vector
`MONTH`	a logical vector
`DAY`	a logical vector
`HAUL_NUMBER`	a logical vector
`LITTER_CATEGORY`	a logical vector
`‘LITTER_SUB-CATEGORY’`	a logical vector
`TOTAL_WEIGHT_IN_THE_CATEGORY_HAUL`	a logical vector
`TOTAL_NUMBER_IN_THE_CATEGORY_HAUL`	a logical vector
`‘TOTAL_WEIGHT_IN_THE_SUB-CATEGORY_HAUL’`	a logical vector
`‘TOTAL_NUMBER_IN_THE_SUB-CATEGORY_HAUL’`	a logical vector

Details

For details see MEDITS Survey - Instruction Manual - Version 9 (2017)

Author(s)

W. Zupa

Source

MEDITS Survey - Instruction Manual - Version 9 (2017)

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.`https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(templateTL)
```

`time` *allowed values for SHOOTING_TIME and HAULING_TIME*

Description

allowed values for SHOOTING_TIME and HAULING_TIME

Usage

```
data("time")
```

Format

A data frame with allowed values for SHOOTING_TIME and HAULING_TIME.

Details

The integer values vector is used to check the correctness of SHOOTING_TIME and HAULING_TIME.

Author(s)

W. Zupa

Source

Anonymus (2017) "MEDITS-Handbook. Version n. 9. MEDITS Working Group" `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

References

Anonymus (2017) "MEDITS-Handbook. Version n. 9. MEDITS Working Group" `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(time)
str(time)
```

`TL` *TL*

Description

TL table

Author(s)

W. Zupa

`TM_list` *TM list*

Description

The present list is destined to code the marine species encountered in the Mediterranean. It has been built following the principle used in the Nordic Code Centre (Stockholm). For most of the species the codes are identical to those proposed by the NCC. However some species can be coded differently. In addition numerous Mediterranean species are not included in the NCC code and have been added. So the present list is specific. It has to be referred as the TM list (Taxonomic list not only Faunistic, FM list).

Usage

```
data("TM_list")
```

Format

A data frame with 1470 observations on the following 11 variables.

`N.` a numeric vector

`MeditsCode` a factor with levels of species codes in the RUBIN format (see MEDITS manual)

`Scientific.Name..............................................valid` a factor with levels of the scientific names of the species

`Authorship` a factor with levels of the authorship of the information

`Source` a factor with levels sources of the information

`Reference` a factor with levels of the bibliographic references

`Remarks` a factor with levels the reported remarks

`CATFAU` a factor with levels of the faunistic categories of the species

`CODLON` a factor with CODLON that represents the Length classes code: m = 1 mm; 0 = 0,5 cm; 1 = 1 cm.

`GSAs` a factor with levels of the Geographic Sub-Areas (GSA) adopted in the MEDITS protocol.

`Year` a factor with levels of the years

Author(s)

W. Zupa

Source

MEDITS MEDITS-Handbook, Version n. 9 (2017)

References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. `https://www.sibm.it/MEDITS%202011/principaledownload.htm`

Examples

```
data(TM_list)
str(TM_list)
head(TM_list)
```

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