

# Package ‘RoMEBS’

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**Type** Package

**Title** R Code to Perform Multiple Checks on MEDITS Survey Data

**Version** 0.2.01

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

**Maintainer** Walter Zupa <zupa@coispa.it>

**Description** In order to unify the checks that are made independently over the MEDITS data by the 18 GSAs (Geographical Sub-Area) participating to MEDITS Survey, an R code performing all the main checks on exchange MEDITS data tables was developed. The first version of RoMEBS has been presented for the first time in the MEDITS Coordination meeting held in Nantes (March 2011). The use of RoME by experts belonging to different GSAs participating to MEDITS Programme brought to the implementation of several adjustments of the functions. The package does not correct the 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. The check is performed simultaneously on the files that can contain also data of more than one year.

**Depends** R (>= 4.0),svDialogs,MEDITS,timeDate,stringr,ggplot2,rnaturalearth,rnaturalearthdata

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Imports** maps,sp,tcltk

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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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).

**Source**

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

## References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

## Examples

```
data(assTL)
## maybe str(assTL) ; plot(assTL) ...
```

---

checkHeader	<i>Function to check the correctness of the headers.</i>
-------------	--

---

## 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)
```

## Arguments

dataframe	Table to check
template	Template used for the check.

## 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 valide 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.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
checkHeader(TA,"TA")
checkHeader(TB,"TB")
checkHeader(TC,"TC")
```

---

check_0_fieldsTA	<i>Checks the presence of 0 fields in TA</i>
------------------	--

---

**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)
```

**Arguments**

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

**Value**

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

**Author(s)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.<https://www.sibm.it/MEDITS2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
library(RoMEBS)
check_0_fieldsTA(MEDITS::TA,wd,suffix)
```

---

check_area	<i>Check if TX files have the same area</i>
------------	---

---

### 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, 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)
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/2011/principaledownload.htm>

### Examples

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

**Arguments**

<code>DataTL</code>	Litter data table (TL) according to MEDITS protocol.
<code>assTL</code>	data frame with the association between TL (litter table) categories and sub-categories
<code>wd</code>	working directory path defined by the user
<code>suffix</code>	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 RoMEBS 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. [http://www.sibm.it/MEDITS 2011/principaledownload.htm](http://www.sibm.it/MEDITS%2011/principaledownload.htm)

**Examples**

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

### Details

The field BRIDLES\_LENGTH can assume value: 100,150 and 200 according to the haul mean depth. The '-1' value was also accepted in case bridles length value is not available.

### Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the RoMEBS 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/2011/principaledownload.htm>

### Examples

```
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
library(RoMEBS)
check_bridles_length(MEDITS::TA, wd, suffix)
```



---

`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, 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

**Details**

Check between duration of the haul and distance (tolerance of 15%)

**Value**

The function returns a boolean value. It is FALSE in case one or more distances in the TA table are out the 15% of the tolerance from the expected values.

**Author(s)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.<https://www.sibm.it/MEDITS2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
wd=tempdir()
suffix="2020-03-05_time_h17m44s55"
library(RoMEBS)
check_consistencyTA_distance(MEDITS::TA,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, 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

### 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/MEDITS2011/principaledownload.htm>

### Examples

```
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
library(RoMEBS)
check_consistencyTA_duration(MEDITS::TA,wd,suffix)
```

---

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

---

**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, 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
wd	working directory path defined by the user
suffix	Suffix string of the Logfile

**Details**

The function check whethe 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.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(RoMEBS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA = MEDITS::TA
Data = MEDITS::TB
check_date_haul(DataTA, Data, wd, suffix)
```

---

check_depth	<i>Check between start depth and end depth</i>
-------------	--

---

### Description

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

### Usage

```
check_depth(DataTA, 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

### 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 lock the execution of the RoMEBS 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/MEDITS2011/principaledownload.htm>

### Examples

```
library(RoMEBS)
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_depth(MEDITS::TA,wd,suffix)
```

---

check_dictionary	<i>Check of the dictionary of specific fields</i>
------------------	---

---

### Description

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

### Usage

```
check_dictionary(ResultData, Field, Values, 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
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/MEDITS2011/principaledownload.htm>

### Examples

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

---

check_distance	<i>Check of distance consistency</i>
----------------	--------------------------------------

---

### Description

The function checks whether there are inconsistencies between the DISTANCE field values and the computed distance.

### Usage

```
check_distance(DataTA, 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

### Details

The comparison between distance in TA and computed distance is performed with a tolerance of 30%. The formula used to compute the distance from the start and end coordinates is:

$$d = \left| 60 \cdot \frac{lat_{end} - lat_{start}}{\cos(N_3)} \right| \cdot 1852$$

where:

$$N_3 = \arctan \left( \frac{\pi \cdot (long_{end} - long_{start})}{180 \cdot (\ln(\tan(N_2)) - \ln(\tan(N_1)))} \right)$$

and

$$N_1 = \frac{\left( \frac{lat_{start}}{2} + 45 \right) \cdot \pi}{180}$$

$$N_2 = \frac{\left( \frac{lat_{end}}{2} + 45 \right) \cdot \pi}{180}$$

All the coordinates involved in the formulas above are in decimal degrees; the routine converts automatically the coordinates listed in TA using the package MEDITS.

### Value

The function returns always TRUE because the outcome of the function is a warning that does not lock the execution of the RoMEBS checks. The presence of inconsistencies between DISTANCE field and computed distance is reported in the logfile stored in the "Logfiles" subdirectory of the "wd" user-defined directory. For the hauls with a computed distance quite different from the distance recorded in TA a plot is produced and stored in Graphs directory to allow an easier correction.

### Author(s)

I. Bitetto, W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. <https://www.sibm.it/MEDITS2011/principaledownload.htm>

### Examples

```
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
library(RoMEBS)
check_distance(MEDITS::TA,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, wd, suffix)
```

**Arguments**

<code>DataTA</code>	Haul data table according to MEDITS protocol (TA)
<code>wd</code>	working directory path defined by the user
<code>suffix</code>	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 decimeters (dm) are respectively 50 - 250 (30 is also accepted being it used in *Rapana venosa* beam trawl survey) and 10 - 100 ('-1' value is also accepted in case vertical opening value is not available).

**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/MEDITS2011/principaledownload.htm>

**Examples**

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

**Arguments**

<code>DataTC</code>	Biological data table according to MEDITS protocol (TC)
<code>wd</code>	working directory path defined by the user
<code>suffix</code>	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 lock the execution of the RoMEBS 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/2011/principaledownload.htm>

**Examples**

```
library(RoMEBS)
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_G1_G2(MEDITS::TC,wd,suffix)
```

---

check_hauls_TATB	<i>Check of TA hauls in TB</i>
------------------	--------------------------------

---

### 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,wd,suffix)
```

### Arguments

DataTA	Haul data table according to MEDITS protocol (TA)
DataTB	Catch data table according to MEDITS protocol (TB)
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 always TRUE and warnings are reported in logfile inconsistencies are 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/2011/principaledownload.htm>

### Examples

```
library(RoMEBS)
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA <- MEDITS::TA
DataTA <- DataTA[DataTA$YEAR ==2018 , ]
DataTB <- MEDITS::TB
DataTB <- DataTB[DataTB$YEAR ==2018 , ]
check_hauls_TATB(DataTA,DataTB,wd,suffix)
```

---

check_hauls_TATL	<i>Check presence of TA hauls in TL</i>
------------------	---

---

**Description**

Check if the hauls in TA are present in TL

**Usage**

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

**Arguments**

DataTA	Haul data table according to MEDITS protocol (TA)
DataTL	Litter data table according to MEDITS protocol (TL)
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 RoMEBS 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/2011/principaledownload.htm>

**Examples**

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

---

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

---

### Description

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

### Usage

```
check_hauls_TBTA(DataTA, DataTB, wd, suffix)
```

### Arguments

DataTA	Haul data table according to MEDITS protocol (TA)
DataTB	Catch data table according to MEDITS protocol (TB)
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/MEDITS2011/principaledownload.htm>

### Examples

```
library(RoMEBS)
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA <- MEDITS::TA
DataTA <- DataTA[DataTA$YEAR ==2018 , ]
DataTB <- MEDITS::TB
DataTB <- DataTB[DataTB$YEAR ==2018 , ]
check_hauls_TBTA(DataTA,DataTB,wd,suffix)
```

---

check_hauls_TLTA	<i>Check presence of TL hauls in TA</i>
------------------	---

---

**Description**

Check if the hauls in TL are present in TA

**Usage**

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

**Arguments**

DataTA	Haul data table according to MEDITS protocol (TA)
DataTL	Litter data table according to MEDITS protocol (TL)
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/2011/principaledownload.htm>

**Examples**

```
library(RoMEBS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTA = MEDITS::TA
DataTL = RoMEBS::TL
check_hauls_TLTA(DataTA,DataTL,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, wd, suffix)
```

### Arguments

DataTB	catch data table according to MEDITS protocol (TB)
DataTC	Biological data table according to MEDITS protocol (TC)
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

The function returns always TRUE because the outcome of the function is a warning that does not lock the execution of the RoMEBS checks. If a species present in the TC table (biological data table) is not reported in the TB (catch data table) 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/2011/principaledownload.htm>

### Examples

```
library(RoMEBS)
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_haul_species_TCTB(MEDITS::TB, MEDITS::TC, 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, wd, suffix)
```

**Arguments**

<code>Data</code>	one of the different data tables defined by the MEDITS protocol (TX)
<code>wd</code>	working directory path defined by the user
<code>suffix</code>	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/2011/principaledownload.htm>

**Examples**

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
Data = MEDITS::TA
check_identical_records(Data, 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,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
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/2011/principaledownload.htm>

### Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
TC = RoMEBS::TC[1:20,]
check_individual_weightTC(DataTC=TC, 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, 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
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/MEDITS2011/principaledownload.htm>

**Examples**

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

---

check_length	<i>Check of length classes in TC</i>
--------------	--------------------------------------

---

**Description**

The function checks the consistency of length classes in TC.

**Usage**

```
check_length(DataTC,DataSpecies=NA,wd,suffix)
```

**Arguments**

DataTC	Biological data table according to MEDITS protocol (TC)
DataSpecies	Information related to target species
wd	working directory path defined by the user
suffix	Suffix string of the Logfile

**Details**

The function checks whether the length classes by species are included in the range reported in the DataSpecies dataset. When DataSpecies is NA the DataTargetSpecies dataset (included in the package) is used by default.

**Value**

The function returns TRUE (warning message in logfile) in case of LENGTH\_CLASS value out of the allowed range. If the length classes in TC table (biological data table) are not consistent with DataSpecies dataset (or DataTargetSpecies if DataSpecies is NA) a warning message is given in the logfile. Furthermore, the function returns FALSE in case the value in the LENGTH\_CLASS field is empty, exiting with an error message.

**Author(s)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
DataTC <- RoMEBS::TC[1:20,]
DataSpecies=NA
suffix= "2020-03-05_time_h17m44s55"
check_length(DataTC,DataSpecies,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=RoMEBS::TM_list,wd,suffix)
```

**Arguments**

DataTC	Biological data table according to MEDITS protocol (TC)
Specieslist	Information related to target species as reported in the TM list
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 COD-LON 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
## Not run:
library(MEDITS)
library(RoMEBS)
DataTC <- MEDITS::TC
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_length_class_codeTC(DataTC, Specieslist=NA, wd, suffix)

## End(Not run)
```

---

check\_mat\_stages

*Consistency of maturity stages*


---

**Description**

Consistency check of maturity stages, according to the faunistic category (TM\_list included in the package), sex and species

**Usage**

```
check_mat_stages(Data, wd, suffix, DataTargetSpecies = RoMEBS::DataTargetSpecies,
DataSpecies = RoMEBS::TM_list, stages = RoMEBS::mat_stages)
```

**Arguments**

Data	Biological data table (TC) or individual biological data table (TE) according to MEDITS protocol
wd	working directory path defined by the user
suffix	Suffix string of the Logfile
DataTargetSpecies	data frame of species information as defined by the DataTargetSpecies dataset included in the package
DataSpecies	data frame with the list of the species as defined by the TM_list dataset included in the package
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 all the species using the new TM list, where selachians and bony fish are distinguished.

**Value**

The function returns TRUE if no error occurs, while FALSE is returned when inconsistencies in the maturity stages are detected. This function also gives a warning message, because it is difficult to define for all GSAs the year of passing from the "old" MEDITS maturity scale to the current MEDITS scale. Furthermore, the function returns an error (FALSE value) in case the faunistic category reported in the TC (or TE) table is present in the TM the one expected for the given species.

**Author(s)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(RoMEBS)
DataTC <- RoMEBS::TC
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_mat_stages(DataTC, 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, wd, suffix)
```

**Arguments**

DataTB	Catch data table according to MEDITS protocol (TB)
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\\_2011/principaledownload.htm](https://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTB = MEDITS::TB
check_nbtotTB(DataTB, 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\_ABOVE\_SEX\_MEASURED 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\_MATURITTY\_STAGE field in TC)

**Usage**

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

**Arguments**

DataTC	Biological data table according to MEDITS protocol (TC)
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\_ABOVE\_SEX\_MEASURED 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\_MATURITTY\_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\_MATURITTY\_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/2011/principaledownload.htm>

**Examples**

```
library(RoMEBS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTC = MEDITS::TC
check_nb_per_sexTC(DataTC,wd,suffix)
```

---

check_nb_TE	<i>Consistency of number of individuals sampled for weight and ageing in TE</i>
-------------	---

---

**Description**

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

**Usage**

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

**Arguments**

DataTE	Individual biological data table according to MEDITS protocol (TE)
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/MEDITS2011/principaledownload.htm>

**Examples**

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTE = TE
check_nb_TE(DataTE, 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, DataTC, wd, suffix)
```

**Arguments**

DataTB	Catch data table according to MEDITS protocol (TB)
DataTC	Biological data table according to MEDITS protocol (TC)
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/MEDITS2011/principaledownload.htm>



**Examples**

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTB = MEDITS::TB
DataTC = MEDITS::TC
check_nm_TB(DataTB,DataTC, 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, wd, suffix)
```

**Arguments**

Data	one of the different data tables defined by the MEDITS protocol (TX)
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/2011/principaledownload.htm>

**Examples**

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
Data = MEDITS::TA
check_no_empty_fields(Data, 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 with the allowed range of values.

### Usage

```
check_numeric_range(DataTA, Field, Values, wd, suffix)
```

### Arguments

DataTA	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.
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 check is performed on any of the "TX" data tables.

### Value

The function returns TRUE if no error occurs, while FALSE is returned when there are empty values in data (NA). Furthermore, the function returns a warning message in case a field value is out of the expected range of values. In the logfile is reported the list of all the records in which the inconsistency is detected.

### Author(s)

W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.<https://www.sibm.it/MEDITS2011/principaledownload.htm>

### Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
Field = "SHOOTING_DEPTH"
Values = c(10,800,0)
DataTA = MEDITS::TA
library(RoMEBS)
check_dictionary(ResultData = DataTA, Field, Values, wd, suffix)
```

---

check_position	<i>Plot of haul positions</i>
----------------	-------------------------------

---

### Description

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

### Usage

```
check_position(DataTA, 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

### 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)

I. Bitetto, W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.<https://www.sibm.it/MEDITS2011/principaledownload.htm>

### Examples

```
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
check_position(MEDITS::TA,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, 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

### 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 shapefileMedSea included in the package.

### Author(s)

I. Bitetto, W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.<https://www.sibm.it/MEDITS/2011/principaledownload.htm>

### Examples

```
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time h17m44s55"
c
```

---

check_quadrant	<i>Check start and end quadrant for each haul</i>
----------------	---

---

**Description**

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

**Usage**

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

**Arguments**

ResultDataTA	Haul data table according to MEDITS protocol (TA).
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 RoMEBS 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_quadrant(TA,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,wd,suffix)
```

### Arguments

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

### Details

The checks execution is stopped if any quasi-identical record was found. In a give 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 returns TRUE if no error occurs, FALSE is at least a quasi-identical record was found.

### Author(s)

I. Bitetto, W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. [http://www.sibm.it/MEDITS 2011/principaledownload.htm](http://www.sibm.it/MEDITS%2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_quasiidentical_records(TA,wd,suffix)
# check_quasiidentical_records(TB,wd,suffix)
# check_quasiidentical_records(TC,wd,suffix)
```

---

check_raising	<i>Function checking if, in case of sub-sampling in TC, the Total number and the number per sex in TB is raised correctly</i>
---------------	---

---

### Description

This function takes into account also the possibility of a "differentiated" sampling, according to the MEDITS protocol. The word "Fraction" means any sub-group of individual from the total catch of a species (males, females, large sized individuals, small individuals, juveniles, etc.) on which it could be proceed to a sub-sample. For example: total weight = 1000 g which is divided into 100g of big individuals and 900 g of small. The big individuals will be entirely measured (PFRAC = 100; PECHAN = 100). The small ones will be sub -sampled with a ratio of 1/10 (PFRAC = 900; PECHAN = 90). In the check check\_raising the comparison between the number in TB and the raised number in TC has been not taking into account decimals, but comparing the integer numbers.

### Usage

```
check_raising(ResultDataTB,ResultDataTC,wd,suffix)
```

### Arguments

ResultDataTB	Catch data table (TB) .
ResultDataTC	Biological data table (TC).
wd	Working directory selected by the user.
suffix	Suffix string of the Logfile.

### Details

The check must be executed year by year. The checks execution is stopped if any mismatching record was found.

### Value

The function returns TRUE if no error occurs, FALSE if some error record was found.

### Author(s)

I. Bitetto, W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. [http://www.sibm.it/MEDITS 2011/principaledownload.htm](http://www.sibm.it/MEDITS%2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_raising(TB,TC,wd,suffix)
```

---

check_rubincode	<i>Function checking the correctness of species MEDITS code and faunistic category according to TM reference list</i>
-----------------	---

---

### 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,species_list=RoMEBS::TM_list,wd,suffix)
```

### Arguments

ResultData	alternatively: Catch data table (TB), Biological data table (TC) and Individual data table (TE).
species_list	species 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 and 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_rubincode(TB,species_list=RoMEBS::TM_list,wd,suffix)
check_rubincode(TC,species_list=RoMEBS::TM_list,wd,suffix)
```



---

check\_sex\_inversion    *Function to verify the consistency of sex information about hermaphrodite species.*

---

### Description

The user will be informed if information about sex-inversion size for hermaphrodite species (at the moment only for Pagellus spp. and Spicara spp.) is stored in Maturity parameters dataframe.

### Usage

```
check_sex_inversion(Data,Maturity_parameters,wd,suffix)
```

### Arguments

Data	alternatively: Biological data table (TC) and Individual data table (TE).
Maturity_parameters	Information related to sex and maturity from literature or other sources.
wd	Working directory selected by the user.
suffix	Suffix string of the Logfile.

### Details

This last check is performed only for proteroginic and proterandrous target species; the user will be only informed if information about sex-inversion size for hermaphrodite species (at the moment only for Pagellus spp. and Spicara spp.) is present in Maturity parameters.csv (folder Tables) in order to be used by the user to check the sex data of these species.

### Value

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

### Author(s)

I. Bitetto, W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_sex_inversion(TC,Maturity_parameters,wd,suffix)
```

---

check\_smallest\_mature *Function to verify the consistency of maturity information respect to the smallest mature individual observed in literature.*

---

### Description

In this check mature individuals with length smaller than size of the smallest mature individuals reported in literature are detected

### Usage

```
check_smallest_mature(ResultData,Maturity_parameters,DataTargetSpecies,wd,suffix)
```

### Arguments

ResultData	alternatively: Biological data table (TC) and Individual data table (TE).
Maturity_parameters	Information related to sex and maturity from literature or other sources.
DataTargetSpecies	Information related to target species.
wd	Working directory selected by the user.
suffix	Suffix string of the Logfile.

### Details

In these checks are involved the information stored in Maturity\_parameters data frame.

### Value

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

### Author(s)

I. Bitetto, W. Zupa

### References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_smallest_mature(TC,Maturity_parameters,DataTargetSpecies,wd,suffix)
```

---

check\_spawning\_period *Function to check the consistency of the maturity stages according to the spawning period.*

---

### Description

The mature individuals caught outside the spawning are detected; moreover, the mature individuals caught outside the spawning with size smaller than the size of smallest mature individual in bibliography and the immature individuals caught during the reproductive period, but with size greater than maximum  $L50 + 0.2 * L50$  are detected.

### Usage

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

### Arguments

ResultDataTA	Haul data table(TA).
ResultDataTC	alternatively: Biological data table (TC) and Individual data table (TE).
Maturity_parameters	Information related to sex and maturity from literature or other sources.
DataTargetSpecies	Information related to reference species.
wd	Working directory selected by the user.
suffix	Suffix string of the Logfile.

### Details

In this checks are involved the information stored in Maturity\_parameters data.frame about the L50 and spawning period is used.)

### 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_spawning_period(TA,TC,Maturity_parameters,DataTargetSpecies,wd,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,DataSpecies,wd,suffix)
```

**Arguments**

ResultTB	Catch data table(TB).
ResultTC	Biological data table (TC).
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 RoMEBS checks.

**Author(s)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_species_TBTC(TB,TC,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,wd,suffix)
```

**Arguments**

ResultData	alternatively: Biological data table (TC) and Individual data table (TE).
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.

**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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_step_length_distr(TC,wd,suffix)
```

---

check_stratum	<i>Function that checks the consistency between start and end depth according to the stratum.</i>
---------------	---

---

### Description

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

### Usage

```
check_stratum(ResultData,wd,suffix,Stratification=RoMEBS::Stratification)
```

### Arguments

ResultData	Haul data table according to MEDITS protocol (TA).
wd	Working directory selected by the user.
suffix	Suffix string of the Logfile.
Stratification	Stratification scheme

### Details

Start depth and end depth of each haul should be in the same stratum. The strata are either the ones defined according to the MEDITS protocol: 10-15 m; 50-100 m; 100-200 m; 200-500m; 500-800 m or the ones defined by the given survey, in accordance with data reported in Stratification table. For the format refer to the Stratification table included in the library.

### Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the RoMEBS 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_stratum(TA,wd,suffix,Stratification=RoMEBS::Stratification)
```

---

check_stratum_code	<i>Function to check the correct codification of the strata in haul data table (TA).</i>
--------------------	--

---

### Description

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

### Usage

```
check_stratum_code(ResultDataTA, Stratification, wd, suffix)
```

### Arguments

ResultDataTA	Haul data table according to MEDITS protocol (TA).
Stratification	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 RoMEBS 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_stratum_code(RoMEBS::TA, Stratification, wd, suffix)
```

---

check_subsampling	<i>Function to warn the user about the presence of subsamples &lt;0.1 of the total catch.</i>
-------------------	---

---

### Description

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

### Usage

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

### Arguments

ResultTC	Biological data table (TC).
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 doesn't lock the execution of the RoMEBS 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_subsampling(TC,wd,suffix)
```



---

check_temperature	<i>Function to check the consistency of the temperature data stored in haul data table (TA).</i>
-------------------	--

---

### 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, wd, suffix)
```

### Arguments

ResultDataTA	Haul data table according to MEDITS protocol (TA).
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 the 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 RoMEBS 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. [http://www.sibm.it/MEDITS 2011/principaledownload.htm](http://www.sibm.it/MEDITS%202011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix="2020-03-05_time_h17m44s55"
check_temperature(TA, wd, suffix)
```

---

check_TE_TC	<i>Function to verify the consistency between individual data table (TE) and biological data table (TC) respect to number of individuals.</i>
-------------	---

---

### 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,wd,suffix)
```

### Arguments

ResultDataTC	Biological data table(TC).
ResultDataTE	Individual data table (TE).
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. [http://www.sibm.it/MEDITS 2011/principaledownload.htm](http://www.sibm.it/MEDITS%2011/principaledownload.htm)

### Examples

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
tc <- RoMEBS::TC
tc <- tc[tc$YEAR == 2012, ]
te <- RoMEBS::TE
te <- te[te$YEAR == 2012, ]
check_TE_TC(tc,te,wd,suffix)
```

---

check_type	<i>Consistency check of TYPE_OF_FILE field</i>
------------	--

---

### Description

The function check if the current value for TYPE\_OF\_FILE field is reported in each data table.

### 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/2011/principaledownload.htm>

### Examples

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

### **Arguments**

ResultDataTA	Haul data table according to MEDITS protocol (TA).
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 valide 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.  
[http://www.sibm.it/MEDITS 2011/principaledownload.htm](http://www.sibm.it/MEDITS%2011/principaledownload.htm)

### **Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_unique_valid_haul(TA,wd,suffix)
```

---

check_weight	<i>Function that checks if number of individuals and total weight collected in the haul are consistent.</i>
--------------	---

---

### Description

The total weight and total number in the haul have to be consistent. The check is quantitative if there is information related to average individual weight. Alternatively the check is qualitative (through a plot).

### Usage

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

### Arguments

ResultDataTB	Catch data table according to MEDITS protocol (TB).
DataTargetSpecies	Information related to individual weight of target and not target species.
wd	Working directory selected by the user.
suffix	Suffix string of the Logfile.

### Details

The check of the consistency of total weight and total number in TB is performed after computing the mean weight for each species in each haul; a list of the weight intervals is provided in the package (DataTargetSpecies); this list was created in on the basis of the data collected in GSA 10 and 18 from 1994 to 2014. Of course, the user should update and complete as much as possible the table in order to allow RoMEBS to detect errors on the basis of the updated weight intervals. This check is divided in a quantitative control (using the ranges mentioned above) and a qualitative control (using plots of the mean weight). The function gives a warning message. A maximum of 20 graphs will have been displayed in the R console and a maximum of 20 .tif files (6 plots per file) will have been stored in Graphs directory. The species with at least an occurrence of 10 hauls are plotted and saved.

### Value

The function returns always TRUE, because the outcome of the function is a warning that does not lock the execution of the RoMEBS 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. [http://www.sibm.it/MEDITS 2011/principaledownload.htm](http://www.sibm.it/MEDITS%202011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_weight(TB,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,wd,suffix)
```

**Arguments**

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

**Details**

In this check RoMEBS 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 RoMEBS checks.

**Author(s)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd=tempdir()
suffix= "2020-03-05_time_h17m44s55"
check_weight_tot_nb(TB,wd,suffix)
```

---

check_year	<i>Consistency check of YEAR field</i>
------------	--

---

### Description

The function check if the current value for YEAR field is reported in each data table.

### 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/2011/principaledownload.htm>

### Examples

```
wd <- tempdir()
years <- unique(RoMEBS::TA$YEAR)
Errors <- file.path(wd,"Logfiles","Logfile.dat")

check_year(TA=RoMEBS::TA, TB=RoMEBS::TB,
TC=RoMEBS::TC, TE=NA, TL=NA, years=years,
wd=wd, Errors=Errors)
```

---

`cood.conv`*Coordinates conversion tool*

---

**Description**

The function performs conversion between the coordinates' formats: decimal degrees and MEDITS formats

**Usage**

```
cood.conv(x,y,q=NA,type=1)
```

**Arguments**

<code>x</code>	vector of longitude coordinates in either decimal degrees format or in MEDITS' projects format
<code>y</code>	vector of latitude coordinates in either decimal degrees format or in MEDITS' projects format
<code>q</code>	vector of quadrant information. Default value is NA. It is used, and hence it is mandatory, in case of MEDITS' format coordinates.
<code>type</code>	type code defining the type of coordinates' conversion to be applied. Allowed values are 1 and 2: 1 should be used to convert digital degrees to MEDITS format. 2 should be used to convert MEDITS coordinates in decimal degrees

**Details**

The `cood.conv` function performs conversion between the coordinates' formats: decimal degrees and MEDITS formats. Use `type=1` to perform decimal degrees to MEDITS format conversion, otherwise use `type=2`. The `q` field has NA default value, even if it should be used in case of `type=2` conversion. `x`, `y` and `q` should have the same length.

**Value**

The function `cood.conv` returns a data.frame that is made of 3 columns (`x,y,q`) in case of `type=1` conversion, and 2 columns in case of `type=2` conversions.

**Author(s)**

Walter Zupa <zupa@coispa.it>

**Examples**

```
ta <- RoMEBS::TA
coord1 <- cood.conv(x=ta$SHOOTING_LONGITUDE, y=ta$SHOOTING_LATITUDE, q=ta$SHOOTING_QUADRANT, type=2)
coord2 <- cood.conv(coord1$x, coord1$y, NA, 1)
```



---

create_catch	<i>Function to create the R-sufi file capt.</i>
--------------	---

---

**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, wd)
```

**Arguments**

ResultDataTB	Catch data table according to MEDITS protocol (TB)
wd	working directory path defined by the user

**Value**

The function saves automatically in the files R-Sufi folder the table capt in.csv format, with suffix of the year 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/MEDITS2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd <- tempdir()
create_catch(TB, wd)
```

---

create_haul	<i>Function to create R-sufi file containing haul data.</i>
-------------	---

---

**Description**

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

**Usage**

```
create_haul(ResultDataTA, wd, suffix)
```

**Arguments**

ResultDataTA    Haul data table according to MEDITS protocol (TA)  
 wd                working directory path defined by the user  
 suffix            Suffix string of the Logfile

**Value**

The function saves automatically in the files R-Sufi folder the table traits in.csv format, with suffix of the year 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/MEDITS2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd <- tempdir()
create_haul(TA,wd)
```

---

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,DataSpecies=RoMEBS::TM_list,wd)
```

**Arguments**

ResultData        Biological data table according to MEDITS protocol (TC)  
 DataSpecies      TM\_list reference list  
 wd                working directory path defined by the user

**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 automatically in the files R-Sufi folder the table taille in.csv format, with suffix of the year 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/2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
create_length(TC, TM_list, wd)
```

---

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)
```

**Arguments**

Stratification Stratification scheme according to MEDITS protocol.  
AREA String of the GSA.  
wd Working directory selected by the user.

**Value**

The function saves automatically in the files R-Sufi folder the table strata in.csv format, with suffix of the year 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/MEDITS2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
library(ROMEBS)
wd <- tempdir()
create_strata(stratification_scheme,"18",wd)
```

---

DataTargetSpecies      *Length and weight ranges*

---

**Description**

Data related to the range for length and mean individual weight for all the relevant species. The year for which the species is target is also indicated.

**Usage**

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

**Format**

A data frame with 392 observations on the following 10 variables.

SPECIES a factor with levels the rubincode of the species for which the information is present.

FAUNISTIC\_CATEGORY a factor with levels the old faunistic categories

MIN\_WEIGHT a numeric vector

MAX\_WEIGHT a numeric vector

UNIT\_WEIGHT grams

MIN\_LEN a numeric vector, in mm

MAX\_LEN a numeric vector, in mm

UNIT\_LEN mm

TARGET\_START a value indicating the year when the species entered in the target species list

TARGET\_END a value indicating the year when the species going out the target species list

**Source**

Literature and others

**Examples**

```
data(DataTargetSpecies)
```

---

graphs_TA	<i>Function for qualitative checks of shooting depth, warp length and wing opening in Haul data table (TA).</i>
-----------	---

---

**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, 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

**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)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.<https://www.sibm.it/MEDITS/2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
graphs_TA(MEDITS::TA,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

**Source**

<http://www.fao.org/gfcm/data/maps/gsas/en/>

**References**

<http://www.fao.org/gfcm/data/maps/gsas/en/>

**Examples**

```
data(GSAs)
## maybe str(GSAs) ; plot(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, seas = RoMEBS::MedSea, verbose = TRUE)
```

**Arguments**

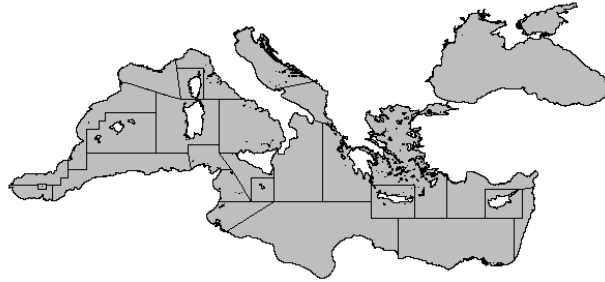
DataTA Haul data table according to MEDITS protocol (TA)

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)

I. Bitetto, W. Zupa

## References

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.<https://www.sibm.it/MEDITS/2011/principaledownload.htm>

## Examples

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

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

G1 a numeric vector of G1 species

G2 a numeric vector of G2 species

Group a factor with levels of groups

Old\_MEDITS\_list a numeric vector of 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

**Source**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. <https://www.sibm.it/MEDITS2011/principaledownload.htm>

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. <https://www.sibm.it/MEDITS2011/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.

**Examples**

```
data(LW)
## maybe str(LW) ; plot(LW) ...
```

---

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 bibliografic references

**Source**

Literature and others

**Examples**

```
data(Maturity_parameters)
```

---

mat_stages	<i>Table of maturity stages</i>
------------	---------------------------------

---

**Description**

Table of maturity stages

**Usage**

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

**Format**

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

FAUNISTIC\_CATEGORY a character vector

SEX a character vector

MEDITS\_STAGE\_from\_2012 a character vector

MEDITS\_STAGE\_up\_to\_2006 a numeric vector

**Details**

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

**Source**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
data(mat_stages)
## maybe str(mat_stages) ; plot(mat_stages) ...
```

---

MedSea

*Shapefile of Mediterranean and Black Sea area*

---

**Description**

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

**Usage**

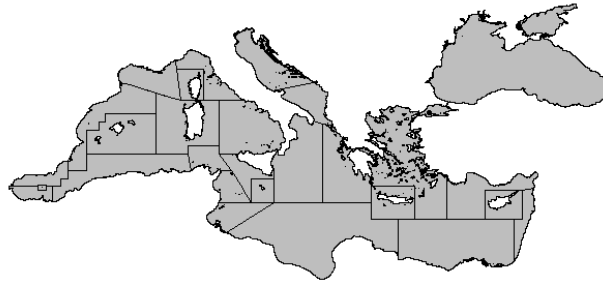
```
data("MedSea")
```

**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.

**Source**

[http://www.fao.org/fileadmin/user\\_upload/faoweb/GFCM/Maps/GSAs\\_simplified.zip](http://www.fao.org/fileadmin/user_upload/faoweb/GFCM/Maps/GSAs_simplified.zip)

**References**

<http://www.fao.org/gfcm/data/maps/gsas/en/>

**Examples**

```
data(MedSea)
## maybe str(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 RoMEBS function has to stop, FALSE if the run should continue

**Value**

Description of the error is reported in the logfile and/or in the console.

**Author(s)**

I. Bitetto, W. Zupa

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp. <https://www.sibm.it/MEDITS2011/principaledownload.htm>

**Examples**

```
## Not run:
printError(funname,check_without_errors, stop_)

## End(Not run)
```

---

RoMEBS	<i>R code to perform multiple checks on MEDITS-like Survey data (TA, TB, TC, TE and TL files)</i>
--------	---

---

**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**

```
function(TA, TB, TC, TE = NA, TL = NA, wd, suffix = NA,
         verbose= TRUE,
         Strata = RoMEBS::Stratification,
         Ref_list =RoMEBS::TM_list,
         LW_table = RoMEBS::LW,
         TargetSpecies = RoMEBS::DataTargetSpecies,
         Maturity = RoMEBS::Maturity_parameters,
         mstages =RoMEBS::mat_stages,
         ass_TL = RoMEBS::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
verbose	...
Strata	Stratification scheme according to MEDITS protocol.
Ref_list	TM_list reference list
LW_table	Table of the Length-Weight parameters
TargetSpecies	Information related to target species.
Maturity	Information related to sex and maturity from literature or other sources.
mstages	Table of maturity stages.
ass_TL	data frame with the association between TL (litter table) categories and sub-categories

### Details

RoMEBS 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 RoMEBS was implemented in a defined sequence to avoid cascade errors due to the correction of a previous error. No automatic correction is implemented in RoMEBS. RoMEBS 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, RoMEBS provides a list of cross checks aimed to guarantee the consistency among the data tables.

Some functions included in the RoMEBS library and used by RoMEBS function need specific dictionaries or tables. It is the case of Stratification, TM\_list, DataTargetSpecies, Maturity\_parameters, 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\\_2011/docs/Medits\\_Handbook\\_2017\\_version\\_9\\_5-60417r.pdf](https://www.sibm.it/MEDITS_2011/docs/Medits_Handbook_2017_version_9_5-60417r.pdf)

## Examples

```
library(RoMEBS)
wd <- tempdir()
suffix=NA
verbose= TRUE
DataTA = RoMEBS::TA
DataTB = RoMEBS::TB
DataTC = RoMEBS::TC
DataTE = NA
DataTL = NA

RoMEBS(DataTA, DataTB,DataTC,DataTE,DataTL, wd, suffix,verbose=TRUE,
        Strata=RoMEBS::Stratification,
        Ref_list=RoMEBS::TM_list, LW_table=RoMEBS::LW,
        TargetSpecies=RoMEBS::DataTargetSpecies,
        Maturity=RoMEBS::Maturity_parameters,
        mstages=RoMEBS::mat_stages,ass_TL=RoMEBS::assTL)
```

---

RoMEBS.wizard

*Wizard function for RoMEBS*

---

## Description

This function is a useful support tool to launch 'RoMEBS', especially in case the user is not familiar with R environment.

## Usage

```
RoMEBS.wizard()
```

## Details

This function is a useful support tool to launch 'RoMEBS', especially in case the user is not familiar with R environment. The function guides user in selecting working directory, where the analysis results will be saved, selecting the comma separated values files containing the TX tables. Furthermore the function helps the user in modify the reference tables.

## Value

The function returns all the results produced by RoMEBS function such as plots and logfiles.

## Author(s)

W. Zupa

## Examples

```
library(RoMEBS)
RoMEBS.wizard()
```

---

`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**

<code>Year_start</code>	Start year
<code>Year_end</code>	Start end
<code>AREA</code>	String of the GSA. Include only the number.
<code>wd</code>	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/MEDITS2011/principaledownload.htm>

**Examples**

```
library(MEDITS)
library(RoMEBS)
wd <- tempdir()

create_haul(TA,wd)
create_catch(TB,wd)
create_length(TC, TM_list,wd)
create_strata(stratification_scheme,"10",wd)
# RSufi_files(2007,2007,"10",wd) # run only if you are working outside a temporary directory
```



---

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, wd, suffix)
```

### Arguments

DataTC	Biological data table according to MEDITS protocol (TC)
DataTE	Individual biological data table according to MEDITS protocol (TE)
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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

### Examples

```
wd <- tempdir()
suffix="2020-03-05_time_h17m44s55"
DataTC = TC
DataTE = TE
check_date_haul(DataTC,DataTE, wd, suffix)
```

---

Stratification	<i>Stratification</i>
----------------	-----------------------

---

**Description**

data frame of the stratification\_scheme

---

TA	<i>TA</i>
----	-----------

---

**Description**

TA table

---

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

---

**Description**

TB table

---

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

---

**Description**

TC table

---

TE	<i>TE</i>
----	-----------

---

**Description**

TE table

---

templateTA	<i>Template haul data table (TA).</i>
------------	---------------------------------------

---

**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.

### 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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/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.

### **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.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/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

HAUL\_NUMBER a logical vector

CODEND\_CLOSING a logical vector

PART\_OF\_THE\_CODEND 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.

**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. [http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
data(templateTC)
```

---

templateTE	<i>Template individual data table (TE).</i>
------------	---

---

**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.

**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.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/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)



**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/MEDITS2011/principaledownload.htm>

**Examples**

```
data(templateTL)
```

---

TL	<i>TL</i>
----	-----------

---

**Description**

TL table

---

TM_list	<i>TM list</i>
---------	----------------

---

**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

MeditCode 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 bibliografic 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

**Source**

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

**References**

Anonymus. 2017. MEDITS-Handbook. Version n. 9. MEDITS Working Group. 106 pp.  
[http://www.sibm.it/MEDITS\\_2011/principaledownload.htm](http://www.sibm.it/MEDITS_2011/principaledownload.htm)

**Examples**

```
data(TM_list)
## maybe str(TM_list) ; plot(TM_list) ...
```

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