

Package ‘BENMMI’

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Type Package

Title Benthic Multi-Metric Index

Description Analysis tool for evaluating benthic multimetric indices (BENMMIs).

It generates reproducible reports on the analysis of benthic data, e.g., validation and correction of species names, sample pooling, automatic conversion of genus to species names, outlier detection, benthic indicator calculation, optimization of single and multimetric indicators against a pressure gradient, and spatial aggregation of benthic indicators. One of its use cases was the development of a common benthic indicator for <<https://www.ospar.org>> (publication accepted by Ecological Indicators). See Van Loon et al. (2018) <[doi:10.1016/j.ecolind.2017.09.029](https://doi.org/10.1016/j.ecolind.2017.09.029)> for details.

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Depends R (>= 3.2.0)

Imports benthos (>= 1.3-5), readr, purrr, knitr, markdown, jsonlite, xtable, dplyr (>= 0.7.0), tidyr, ggplot2 (>= 2.0.0)

Suggests DEoptim

License GPL (>= 3)

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| benmmi | <i>Perform BENMMI Analysis</i> |
|--------|--------------------------------|

Description

This function performs a complete BENMMI analysis following the settings provided in filename.

Usage

```
benmmi(filename = NULL, tmpdir = tempfile(pattern = "BENMMI"),
        browse = TRUE)
```

```
BENMMI(filename = NULL, tmpdir = tmpdir(), browse = TRUE)
```

Arguments

| | |
|----------|---|
| filename | name of the JSON file defining all analysis steps. |
| tmpdir | directory to store temporary files (for debugging only) |
| browse | load resulting report in a browser? TRUE or FALSE |

Examples

```
# This example illustrates a typical use case of the BENMMI-package.
# Note: execution may take several minutes.
# See the package vignette for more advanced examples and details.
```

```
if (interactive()) {
```

```
  # Create a work directory (in this example, a temporary
  # directory, but in real use cases a persistent directory
  # will obviously be more useful).
```

```
  my_dir <- tempfile("benmmi-example")
  dir.create(my_dir)
```

```
  # Populate this directory with simple use cases
```

```

# (see the package-vignette for details).
# Most users will probably use one of these use cases as a
# template for their own study.
BENMMI_dir(my_dir)

# Run BENMMI given the settings in "settings-S-D-lin.json". This file
# relates to one of the predefined use cases.
my_settings_file <- file.path(my_dir, "settings-S-D-lin.json")
benmmi(my_settings_file, browse = FALSE)

# The output (HTML-report and data-files) is stored in 'my_dir'
# and described in the package-vignette and resulting HTML-report itself.
# It is also possible to directly view the generated
# HTML-report by setting the browse-argument of the benmmi-function to TRUE.
}

```

benmmi-pkg

Benthic Multi-Metric Indicator Analysis

Description

Reporting tool for a benthic multimetric indicator

Author(s)

Dennis Walvoort (Wageningen University & Research) & Willem van Loon (Rijkswaterstaat-The Netherlands)

BENMMI_dir

Create BENMMI Directory Structure

Description

Creates a BENMMI-directory structure and populates it with some relevant BENMMI-files. Users may wish to modify this directory structure and add their own data.

Usage

```
BENMMI_dir(path = NULL)
```

Arguments

path name of an existing directory. This directory should be empty to prevent loss of data. If missing, a dialogue will appear.

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|---------|-------------------------------------|
| ci_mean | <i>Mean and Confidence Interval</i> |
|---------|-------------------------------------|

Description

Mean and Confidence Interval

Usage

```
ci_mean(x, level = 0.9)
```

Arguments

| | |
|-------|------------------|
| x | numeric vector |
| level | confidence level |

Note

Internal function. Not supposed to be called directly

Examples

```
stopifnot(all.equal(ci_mean(NA_real_), c(NA_real_, NA_real_, NA_real_)))
stopifnot(all.equal(ci_mean(1), c(lower = NA_real_, mean = 1, upper = NA_real_)))
stopifnot(all.equal(
  ci_mean(1:9, 0.95),
  c(lower = 2.934942, mean = 5.000000, upper = 7.065058),
  tolerance = 0.0001)
)
```

| | |
|----------|---|
| read_mmi | <i>Read and Validate BENMMI Input Files</i> |
|----------|---|

Description

This function reads and checks benthos files. The format is a superset of the BEQI2-format as specified in Van Loon (2013). In addition to the BEQI2-format, the benthos-format also includes columns latitude (LAT), longitude (LONG), and sieve mesh size (MESH).

Usage

```
read_mmi(filename)
```

Arguments

| | |
|----------|----------------------------------|
| filename | name of benthos file (character) |
|----------|----------------------------------|

References

Willem van Loon, 2013. BEQI2 INPUT FORMAT

See Also

[read_beqi2](#)

| | |
|---------------|----------------------------------|
| read_settings | <i>Read BENMMI Settings File</i> |
|---------------|----------------------------------|

Description

This function reads BENMMI settings files. See the package vignette for a description of its format. Create an example file by calling the [BENMMI_dir](#)-function.

Usage

```
read_settings(filename)
```

Arguments

filename name of BENMMI input file (character)

Details

The function performs the following tasks:

- checks the existence of filename;
- reads JSON file while ignoring C-style comments;
- checks availability of required keys in the JSON-file
- checks values in JSON-file

See Also

[BENMMI_dir](#)

| | |
|------------------|---|
| toString_weights | <i>Construct a Text Representation of a Weight Vector</i> |
|------------------|---|

Description

Construct a Text Representation of a Weight Vector

Usage

```
toString_weights(x)
```

Arguments

x numeric or character vector

Note

Internal function. Not supposed to be called directly

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