

# Package: BENMMI (via r-universe)

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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.

**Version** 4.3-7

**Date** 2020-10-12

**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

**VignetteBuilder** knitr

**License** GPL (>= 3)

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**NeedsCompilation** no

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**Additional\_repositories** <https://cranhaven.r-universe.dev>

**Repository** <https://cranhaven.r-universe.dev>

**RemoteUrl** <https://github.com/cranhaven/cranhaven.r-universe.dev>

**RemoteRef** package/BENMMI

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benmmi	<i>Perform BENMMI Analysis</i>
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## 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.
}

```

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benmmi-pkg

*Benthic Multi-Metric Indicator Analysis*


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### Description

Reporting tool for a benthic multimetric indicator

### Author(s)

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

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BENMMI\_dir

*Create BENMMI Directory Structure*


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### 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>
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**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>
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**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)
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## References

Willem van Loon, 2013. BEQI2 INPUT FORMAT

## See Also

[read\\_beqi2](#)

---

read_settings	<i>Read BENMMI Settings File</i>
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## 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](#)

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`toString_weights`*Construct a Text Representation of a Weight Vector*

---

**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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