

# Package ‘mumarinex’

October 14, 2025

**Title** Computation of the Multivariate Marine Recovery Index

**Version** 1.0

**Description** Computation of the multivariate marine recovery index, including functions for data visualization and ecological diagnostics of marine ecosystems. The computational details are described in the original publication. Reference: Chauvel, N., Grall, J., Thiébaud, E., Houbin, C., Pezy, J.P. (in press). ``A general-purpose Multivariate Marine Recovery Index for quantifying the influence of human activities on benthic habitat ecological status''. Ecological Indicators.

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Suggests** rmarkdown

**VignetteBuilder** knitr

**Imports** knitr, vegan

**Collate** 'Simulated\_data.R' 'decomplot.R' 'mumarinex.R'  
'diagnostic\_tool.R'

**NeedsCompilation** no

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**Depends** R (>= 3.5.0)

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`decomplot`*Decomposition of the MUMARINEX value into its three sub-indices and representation as boxplots*

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### Description

Generates a graphical representation (boxplot) of MUMARINEX sub-indices to assess which component(s) contribute most strongly to the overall MUMARINEX score.

### Usage

```
decomplot(  
  x,  
  g,  
  ref,  
  fill = c("lightblue", "#FFFFFF0DF", "#90F0909E"),  
  border = c("#0080AB", "#C7C700DF", "#0091009E"),  
  main = NULL  
)
```

### Arguments

<code>x</code>	A data frame organized with samples in rows and species in columns.
<code>g</code>	A vector of length <code>nrow(x)</code> indicating how the samples should be grouped (e.g., stations, treatments).
<code>ref</code>	A logical or numeric vector identifying the reference row positions.
<code>fill</code>	Fill color of the boxplots.
<code>border</code>	Border color of the boxplots.
<code>main</code>	Main title of the plot.

### Details

Decomposition of the MUMARINEX value into its three sub-indices and representation as boxplots

### Value

A boxplot of length `g` representing the variations in the different MUMARINEX sub-indices (CSR, CBCD, and CPI).

### See Also

[diagnostic\\_tool\(\)](#)

**Examples**

```
data("Simulated_data")
ref_idx<-41:50
stations<-matrix(unlist(strsplit(rownames(Simulated_data),".",fixed=TRUE)),ncol=2,byrow=TRUE)[,1]
decomplot(x=Simulated_data,g=stations,ref=ref_idx,main="Simulated data")
```

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diagnostic_tool	<i>Diagnostic tool to identify the key components that best explain the MUMARINEX sub-indices</i>
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**Description**

Identifies, for each sub-index, the species or taxa that contribute most to its variation.

**Usage**

```
diagnostic_tool(x, g, ref, signif_test = TRUE, mute = FALSE)
```

**Arguments**

x	A data frame or a matrix organized with samples in rows and species in columns.
g	A vector of length nrow(x) indicating how the samples should be grouped (e.g., stations, treatments).
ref	A logical or numeric vector identifying the reference row positions.
signif_test	Logical; if TRUE, only sub-indices significantly lower than the reference conditions (t-test, $p < 0.05$ ) are returned. Conditions that are not statistically significant are indicated by 'ns'.
mute	A logical indicating whether the results are displayed in the console.

**Details**

diagnostic\_tool

**Value**

A data frame summarizing the key information explaining variations in CSR, CBCD, and CPI.

**Note**

To reduce the risk of misleading interpretations, a one-sided significance test (t-test) is applied to sub-indices against the reference condition. Nevertheless, taxa identified as contributing to sub-index and MUMARINEX variations may not always be ecologically relevant, and the results are provided without any guarantee. This tool is not a substitute for a thorough ecological knowledge of the studied site and careful examination of the data, although it may help guide users toward potential hypotheses. The significance tests can be disabled, but the resulting outputs should then be interpreted with extreme caution.

**See Also**

[decomplot\(\)](#)

**Examples**

```
data("Simulated_data")
ref_idx<-41:50
stations<-matrix(unlist(strsplit(rownames(Simulated_data),"."),fixed=TRUE)),ncol=2,byrow=TRUE)[,1]
diagnostic_tool(x=Simulated_data,g=stations,ref=ref_idx)
```

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mumarinex

*MUMARINEX and subindices computation*

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**Description**

Computes the MUMARINEX index and its sub-indices (CSR, CBCD, and CPI), following the method described in Chauvel et al. (2025).

**Usage**

```
mumarinex(x, ref, subindices = FALSE)
```

**Arguments**

x	A data frame or a matrix organized with samples in rows and species in columns.
ref	A logical or numeric vector identifying the reference row positions.
subindices	A logical indicating whether the sub-indices (CSR, CBCD, and CPI) should be returned.

**Details**

mumarinex

**Value**

A data frame with the MUMARINEX values. When subindices = TRUE, an additional data frame is returned containing the results of the sub-indices (CSR, CBCD, and CPI).

**References**

Chauvel, N., Pezy, J.P., Grall, J., Thiébaud, E. (2025). A general-purpose Multivariate Marine Recovery Index for quantifying the influence of human activities on benthic habitat ecological status. Ecological Indicator.

**Examples**

```
data("Simulated_data")
ref_idx<-41:50
mumarinex(x=Simulated_data,ref=ref_idx)
mumarinex(x=Simulated_data,ref=ref_idx,subindices=TRUE)
```

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 Simulated\_data

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*Simulated\_data*


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**Description**

This dataset was constructed to simulate the theoretical impacts of a disturbance on the abundances of 12 hypothetical species. Stations R1 to R3 illustrate changes in community richness, represented by the loss of species C and D (station R1), the appearance of species E and F (station R2), or both simultaneously (station R3). Stations S1 to S3 represent changes in community structure, expressed as a decrease in the abundance of species G and H (station S1), an increase in the abundance of species I and J (station S2), or both (station S3). Station D1 focuses on community dominance shifts, characterized by a strong increase in the abundance of species K and L. Station M1 combines all of these effects (loss, gain, structural shifts, and dominance changes). Reference stations REF1 and REF2 represent control sites, with alternating taxa showing normally distributed abundances (means of 50 and 10, standard deviation of 10% of mean). Species A and B are insensitive to impacts and act as tolerant taxa.

**Usage**

```
data(Simulated_data)
```

**Format**

A data frame with 50 rows (samples) and 12 species:

**Sp\_A** Species tolerant to different impacts, mean abundance = 50

**Sp\_B** Species tolerant to different impacts, mean abundance = 10

**Sp\_C** Species highly sensitive to impacts at stations A1, A3, and M1, leading to their disappearance, mean abundance = 50

**Sp\_D** Species highly sensitive to impacts at stations A1, A3, and M1, leading to their disappearance, mean abundance = 10

**Sp\_E** Species favored by impacts at stations A2, A3, and M1, leading to their appearance, mean abundance = 50

**Sp\_F** Species favored by impacts at stations A2, A3, and M1, leading to their appearance, mean abundance = 10

**Sp\_G** Species sensitive to impacts at stations S1, S3, and M1, leading to decreased abundance, mean abundance = 50

**Sp\_H** Species sensitive to impacts at stations S1, S3, and M1, leading to decreased abundance, mean abundance = 10

**Sp\_I** Species stimulated by impacts at stations S2, S3, and M1, leading to increased abundance, mean abundance = 50

**Sp\_J** Species stimulated by impacts at stations S2, S3, and M1, leading to increased abundance, mean abundance = 10

**Sp\_K** Species strongly stimulated by impacts at stations D1 and M1, leading to a shift in dominance, mean abundance = 50

**Sp\_L** Species strongly stimulated by impacts at stations D1 and M1, leading to a shift in dominance, mean abundance = 10

**Author(s)**

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