Package ‘forams’

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Type Package

Title Foraminifera and Community Ecology Analyses

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Author Rodrigo Aluizio

Maintainer Rodrigo Aluizio <`r.aluizio@gmail.com`>

Description SHE, FORAM Index and ABC Method analyses and custom plot functions for community data.

License GPL (>= 2)

Depends methods

Imports vegan, stats, graphics

NeedsCompilation no

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Contents

`forams-package` *Foraminifera and Community Ecology Analyses*

Description

SHE, FORAM Index and ABC Method analyses and custom plot functions for community data.

Details

Package:	forams
Type:	Package
Version:	2.0-6
Date:	2023-08-24
License:	GLP (>=2)
Depends:	methods, vegan, permute

This package always uses data frames with *taxa* as rows and sites or variables as columns. It also provides customizable plot functions to use with the objects resulting from the analyses, and randomly generated example datasets.

The analyses performed by this package are: SHE, FORAM Index and ABC Method.

Author(s)

Rodrigo Aluizio

Maintainer: Rodrigo Aluizio <r.aluizio@gmail.com>

References

Buzas, M.A. & Hayek, L.A.C. (1998). SHE analysis for biofacies identification. *Journal of Foraminiferal Research* **28** (3), 233-239.

Hallock, P., Lidz, B.H., Cockey-Burkhard, E.M. & Donnelly, K.B. (2003). Foraminifera as bioindicators in coral reef assessment and monitoring: The foram index. *Environmental monitoring and assessment* **81**, 221-238.

Warwick, R.M. (1986). A new method for detecting pollution effects on marine macrobenthic communities. *Marine Biology* **92** (4), 557-562.

Warwick, R.M., & Clarke, K.R. (1994). Relearning the ABC: taxonomic changes and abundance/biomass relationships in disturbed benthic communities. *Marine Biology* **118** (4), 739-744.

Wilson, B., Dawe, R., Gopee, A., Grant, S., Kissoon, A., Young, T., Noon, C., McLean, A. & Singh, K. (2010). Determining Boundaries between Abundance Biozones Using Minimal Equipment. *International Journal of Ecology* **2010**, 1-14.

See Also

`abc`, `fi`, `she`

Examples

```
data(NB)
data(Factors)
data(LF)
# ABC
plot(abc(NB))
# FORAM Index
plot(fi(LF, Factors))
# SHE
plot(she(LF))
```

`abc` *Abundance and Biomass Comparison Method*

Description

This function performs the ABC and W statistic calculation.

Usage

```
abc(df, Perm, confInt)
```

Arguments

`df`	a numeric data frame containing the abundance and biomass as columns and *taxa* as rows. NAs are not allowed.
`Perm`	the number of permutations to be realized for calculating the Confidence Interval.
`confInt`	the Confidence interval range (90%, 95% or 99%, any other values will cause an error).

Details

The function generates a list of cumulative percentage values of Abundance, Biomass and Biomass - Abundance for each *taxon* (*Warwick 1986*), which are used for W statistic (*Warwick & Clarke 1994*) calculation and posterior k-dominance curve plotting.

Value

An `abc` S4 object has the fallowing elements:

An abc slot with:

`Accum.Abun`	The cumulative percentage of abundance contribution.
`Accum.Biomass`	The cumulative percentage of biomass contribution.
`BiAi`	Biomass - Abundance calculation results.

and a W.Stat slot with:

`W.Stat`	The result of the W statistic calculation and its Confidence Interval.

Note

The list elementes are ordered according to `Accum.Abun`, but the calculation is based on the contribution decreasing order, independently of any of the variables or *taxon*.

Author(s)

Rodrigo Aluizio

References

Warwick, R.M. (1986). A new method for detecting pollution effects on marine macrobenthic communities. *Marine Biology* **92** (4), 557-562.

Warwick, R.M., & Clarke, K.R. (1994). Relearning the ABC: taxonomic changes and abundance/biomass relationships in disturbed benthic communities. *Marine Biology* **118** (4), 739-744.

Examples

```
data(NB)
MyABC <- abc(NB)
plot(MyABC)
```

`abc-class` *Class* `"abc"`

Description

Class used to store `"abc"` analysis objects.

Objects from the Class

Objects can be created by calls of the form `new("abc", ...)`. This class is composed by two slots, the first one stores a table with the abc analysis results and the second one the W Statistic result and its Confidence Interval.

Slots

`abc`**:** Object of class `"data.frame"` ~~

`W.Stat`**:** Object of class `"numeric"` ~~

Methods

plot `signature(x = "abc")`: ...

Author(s)

Rodrigo Aluizio

See Also

See Also as `abc`

Examples

```
showClass("abc")
```

`Factors` *FORAM Index Factors*

Description

An example dataset defining factors levels to use with the `fi` function.

Usage

```
data(Factors)
```

Format

A data frame with 29 observations on the following variable.

FI a factor with levels: `Ph`, `Po` and `Ps`

Details

This dataset is an artificial random generated example. Unfortunately at the moment, due to authorship issues I can not present any real one. This may change in future versions.

Examples

```
data(Factors)
summary(Factors)
```

`fi` *The FORAM Index*

Description

This function implements the FORAM Index (FI) in community abundance datasets.

Usage

```
fi(df, groups)
```

Arguments

`df`	a numerical data frame with samples as columns and *taxa* as rows.
`groups`	a three level grouping factor.

Details

his analysis is directed for health evaluation and monitoring of reef environments (*Hallock et al. 2003*) and it is based in foraminiferal total fauna methodology.

The *taxa* classification that determines the groups are originally based on genera, but species data from literature or experiments will be accepted as well. The grouping factor must be composed solely by `Ps` (simbiont-bearing), `Po` (opportunistic), or `Ph` (other small heterotrophic) levels. NAs are not allowed.

The plot uses the `axis` function, so a complete customization (i.e. `side`) of the axes is not possible at this moment, and some other parameters may show improperly if changed.

Value

A `fi` object has the fallowing elements:

`PlotOrder`	a numerical vector defining the sites plot order, only used for plotting.
`FI`	a numerical vector with the sites FORAM Index values.

Note

FI > 4 indicates environment conducive to reef growth (CRG), FI varying between 3 and 5 indicates environmental change (Coefficient of Variation > 0.1), 2 < FI < 4 indicates environment marginal for reef growth (MRG) and unsuitable for recovery and FI < 2 indicates stressed conditions unsuitable for reef growth (UGR).

For more details on other graphic prameters see `plot.default` and `par`.

Author(s)

Rodrigo Aluizio

References

Hallock, P., Lidz, B.H., Cockey-Burkhard, E.M. & Donnelly, K.B. (2003). Foraminifera as bioindicators in coral reef assessment and monitoring: The foram index. *Environmental monitoring and assessment* **81**, 221-238.

Examples

```
data(LF)
data(Factors)
MyFI <- fi(LF, Factors)
plot(MyFI)
```

`fi-class` *Class* `"fi"`

Description

Class used to store `"fi"` analysis objects.

Objects from the Class

Objects can be created by calls of the form `new("fi", ...)`. Single slot classe used to store a `"data.frame"` object.

Slots

`fi`: Object of class `"data.frame"` ~~

Methods

plot `signature(x = "fi")`: ...

Author(s)

Rodrigo Aluizio

See Also

See Also as `fi`

Examples

```
showClass("fi")
```

`LF` *FORAM Index and SHE dataset*

Description

An example dataset containing some *taxa* abundances to use in exemples of the `fi` and `she` functions.

Usage

```
data(LF)
```

Format

A data frame with 29 *taxa* on 23 sites.

Details

This dataset is an artificial random generated example. Unfortunately at the moment, due to authorship issues I can not present any real one. This may change in future versions.

Examples

```
data(LF)
str(LF)
```

`NB` *ABC Method Dataset*

Description

An example dataset containing some *taxa* abundances and Biomasses to use in exemples of the `abc` function.

Usage

```
data(NB)
```

Format

A data frame with 316 *taxa* on the following 2 variables.

N a numeric vector with abundance data.

Biomass a numeric vector with biomass data.

Details

This dataset is an artificial random generated example. Unfortunately at the moment, due to authorship issues I can not present any real one. This may change in future versions.

Examples

```
data(NB)
str(NB)
```

`plot-methods` *~~ Methods for Function* `plot` *~~*

Description

~~ Methods for function `plot` ~~

Methods

`signature(x = "abc")`	An object of class `"abc"` resulting from and `abc` analysis.
`signature(x = "ANY")`	Other classes objects that will be handled by `plot.default`.
`signature(x = "fi")`	An object of class `"fi"` resulting from and `fi` analysis.
`signature(x = "she")`	An object of class `"she"` resulting from and `she` analysis.

`plot.abc` *Plot function for Abundance and Biomass Comparison Method objects.*

Description

This function is a customizable plot for the abundance and biomass lines from the ABC object.

Usage

```
## S4 method for signature 'abc'
plot(x, xlim = c(0, ceiling(log(length(x@abc$Accum.Abund)))),
     ylim = c(0, 100), yaxp = c(0, 100, 10), lty.bio = 'dotted',
     lty.abu = 'solid', lwd = 2, col.bio = 'black', col.abu = 'black',
     xlab = expression('Species Rank'~(Log[e]~Scale)),
     ylab = 'Cumulative Dominance %', leg = TRUE, W = TRUE, col.pol = '#f5f5f5',
     ...)
```

Arguments

`x`	an object of class abc.
`xlim`	the x limits (x1, x2) of the plot, defaults from 0 to the maximum value of x (in a log scale).
`ylim`	the y limits (x1, x2) of the plot, defaults to `c(0, 100)`
`yaxp`	a vector of the form c(y1, y2, n) giving the coordinates of the extreme tick marks and the number of intervals between tick-marks, defaults to `c(0, 100, 10)`.
`lty.bio`	line type of the biomass curve, defaults to `"dotted"`.
`lty.abu`	line type of the abundance curve, defaults to `"solid"`.
`lwd`	the line width, a positive number, defaulting to 2.

`col.bio`	the line color of the biomass curve, defaulting to `"black"`.
`col.abu`	the line color of the abundance curve, defaulting to `"black"`.
`xlab`	a label for the x axis, defaults to `expression('Species Rank'~(Log[e]~Scale))`.
`ylab`	a label for the y axis, defaults to `"Cumulative Dominance %"`.
`leg`	logical; if TRUE draws a legend at the `bottomright` part of the plotting area, defaults to `TRUE`.
`W`	logical; if TRUE draws the W statistics value at the `topleft` part of the plotting area, defaults to `TRUE`.
`col.pol`	the polygon filling color, defaults to `"#f5f5f5"`.
`...`	other graphical parameters, see `par` for details.

Details

The plot produces a two lines plot with a ln abscissa and uses the `axis` function, so a complete customization (i.e. `side`) of the axes is not possible at this moment.

Note

For more details on other graphic prameters such as line and box types see `par` and `plot.default`.

Author(s)

Rodrigo Aluizio

References

Warwick, R.M. (1986). A new method for detecting pollution effects on marine macrobenthic communities. *Marine Biology* **92** (4), 557-562.

Warwick, R.M., & Clarke, K.R. (1994). Relearning the ABC: taxonomic changes and abundance/biomass relationships in disturbed benthic communities. *Marine Biology* **118** (4), 739-744.

Examples

```
data(NB)
MyABC <- abc(NB)
plot(MyABC)
```

`plot.fi` *Custom plot function for FORAM Index results*

Description

This function generates custom plots for FI objects.

Usage

```
## S4 method for signature 'fi'
plot(x, ylim = c(1, 10), yaxp = c(1, 10, 9), xlab = 'Samples',
  ylab = 'FORAM Index', pch.urg = 25, pch.mrg = 21, pch.crg = 24,
  bg.urg = 'red', bg.mrg = 'yellow', bg.crg = 'green', pt.cex = 1,
  limits = TRUE, ...)
```

Arguments

`x`	an object of class `fi`.
`ylim`	the y limits (x1, x2) of the plot, defaults to `c(1, 10)`
`yaxp`	a vector of the form c(y1, y2, n) giving the coordinates of the extreme tick marks and the number of intervals between tick-marks, defaults to `c(1, 10, 9)`.
`xlab`	a label for the x axis, defaults to `"Samples"`.
`ylab`	a label for the y axis, defaults to `"FORAM Index"`.
`pch.urg`	plotting 'character', i.e., symbol to use, prefer one between 21:25, defaults to 25
`pch.mrg`	plotting 'character', i.e., symbol to use, prefer one between 21:25, defaults to 21
`pch.crg`	plotting 'character', i.e., symbol to use, prefer one between 21:25, defaults to 24
`bg.urg`	background (fill) color for the open plot symbols given by `pch=21:25`, defaults to `"red"`.
`bg.mrg`	background (fill) color for the open plot symbols given by `pch=21:25`, defaults to `"yellow"`.
`bg.crg`	background (fill) color for the open plot symbols given by `pch=21:25`, defaults to `"green"`.
`pt.cex`	character (or symbol) expansion: a numerical vector, defaults to 1.
`limits`	logical; if TRUE, draws lines limiting the three FORAM Index classes and identifies them, defaults to `TRUE`.
`...`	other graphical parameters, see `par` for details.

Details

The plot uses the `axis` function, so a complete customization (i.e. `side`) of the axes is not possible at this moment, and some other parameters may show improperly if changed.

Note

FI > 4 indicates environment conducive to reef growth (CRG), FI varying between 3 and 5 indicates environmental change (Coefficient of Variation > 0.1), 2 < FI < 4 indicates environment marginal for reef growth (MRG) and unsuitable for recovery and FI < 2 indicates stressed conditions unsuitable for reef growth (UGR).

For more details on other graphic prameters see `plot.default` and `par`.

Author(s)

Rodrigo Aluizio

References

Hallock, P., Lidz, B.H., Cockey-Burkhard, E.M. & Donnelly, K.B. (2003). Foraminifera as bioindicators in coral reef assessment and monitoring: The foram index. *Environmental monitoring and assessment* **81**, 221-238.

Examples

```
data(LF)
data(Factors)
MyFI <- fi(LF, Factors)
plot(MyFI)
```

`plot.she` *Custom plot function for SHE Analysis objects*

Description

This function generates customizable graphics for objects of the class `she`.

Usage

```
## S4 method for signature 'she'
plot(x, pch = 20, pcol = 'black', pcex = 1, pbg = 'black', lcol = 'black',
  lwd = 1, lty = 'dotted', ylab = expression('ln'~italic(E)), bty = 'l', ...)
```

Arguments

`x`	an object of class she.
`pch`	plotting 'character', i.e., symbol to use with the points, defaults to `20`.
`pcol`	color code or name for plot symbols, defaults to `"black"`.
`pcex`	character (or symbol) expansion: a numerical vector, defaults to `1`.
`pbg`	background (fill) color for the open plot symbols given by pch=21:25, defaults to `"black"`
`lcol`	a specification for the default plotting color of the line, defaults to `"black"`.

`lwd`	the line width, a positive number, defaulting to `1`.
`lty`	the line type. Line types can either be specified as an integer (0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "blank", "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash", where "blank" uses 'invisible lines' (i.e., does not draw them).
`ylab`	a label for the y axis, defaults to `expression("ln" ~ italic(E))`.
`bty`	box type drawn about the plot, defaults to `"l"`. Other types will not reproduce ideally.
`...`	other parameters to be passed to `plot.default`.

Details

The plot produces a line plot with points on a ln abscissa and uses the `axis` function, so a complete customization (i.e. `side`) of the axes is not possible at this moment.

Note

For more details on other graphic prameters see `par`.

Author(s)

Rodrigo Aluizio

References

Buzas, M.A. & Hayek, L.A.C. (1998). SHE analysis for biofacies identification. *Journal of Foraminiferal Research* **28** (3), 233-239.

Wilson, B., Dawe, R., Gopee, A., Grant, S., Kissoon, A., Young, T., Noon, C., McLean, A. & Singh, K. (2010). Determining Boundaries between Abundance Biozones Using Minimal Equipment. *International Journal of Ecology* **2010**, 1-14.

Examples

```
data(LF)
MySHE <- she(LF, "abun")
plot(MySHE)
```

`she` *SHE Analysis*

Description

This function implements the SHE method in community abundance datasets.

Usage

```
she(df, method)
```

Arguments

`df`	a numerical data frame with samples as columns and *taxa* as rows.
`method`	the method to be used, (`"abundance"` or `"frequency"`), defaults to `"abundance"`.

Details

This method is intended to determine boundaries between abundance biozones, based in raw abundance (SHEbi) or in frequency (SHEbip) (*Buzas et al. 1998*, *Wilson et al. 2010*). The custom plot produces a line plot with points on a ln abscissa and uses the `axis` function, so a complete customization (i.e. `side`) of the axes is not possible at this moment.

Value

`S`	richness values.
`H`	shannon diversity values.
`E`	equitability values.
`N or L`	number of specimens (N) or sites rank based on specimens frequency (L).

Note

This function implements great part of the process, but a small part must be caried out for the researcher when defining where to cut biozones before reruning the test. For more details on other graphic prameters see `par`.

Author(s)

Rodrigo Aluizio

References

Buzas, M.A. & Hayek, L.A.C. (1998). SHE analysis for biofacies identification. *Journal of Foraminiferal Research* **28** (3), 233-239.

Wilson, B., Dawe, R., Gopee, A., Grant, S., Kissoon, A., Young, T., Noon, C., McLean, A. & Singh, K. (2010). Determining Boundaries between Abundance Biozones Using Minimal Equipment. *International Journal of Ecology* **2010**, 1-14.

Examples

```
data(LF)
MySHE <- she(LF, "abun")
plot(MySHE)
```

`she-class` *Class* `"she"`

Description

Class used to store `"she"` analysis objects.

Objects from the Class

Objects can be created by calls of the form `new("she", ...)`. Single slot classe used to store a `"data.frame"` object.

Slots

`bi`**:** Object of class `"data.frame"` ~~

Methods

plot `signature(x = "she")`: ...

Author(s)

Rodrigo Aluizio

See Also

See Also as `she`

Examples

```
showClass("she")
```

Index