Package 'forams'

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Type Package

Title Foraminifera and Community Ecology Analyses

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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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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
Date:	2012-08-08
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

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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.

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