

# Package ‘forams’

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**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.

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**Depends** methods

**Imports** vegan, stats, graphics

**NeedsCompilation** no

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## R topics documented:

forams-package . . . . .	2
abc . . . . .	3
abc-class . . . . .	4
Factors . . . . .	5
fi . . . . .	5
fi-class . . . . .	7
LF . . . . .	7
NB . . . . .	8
plot-methods . . . . .	9
plot.abc . . . . .	9
plot.fi . . . . .	11
plot.she . . . . .	12
she . . . . .	13
she-class . . . . .	15

<b>Index</b>	<b>16</b>
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forams-package

*Foraminifera and Community Ecology Analyses*

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## 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 <i>taxa</i> 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 following 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 elements 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 (symbiont-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 following 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 parameters 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 examples 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 examples 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 <code>expression('Species Rank'~(Log[e]~Scale))</code> .
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 <a href="#">par</a> 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 parameters 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 <code>fi</code> .
ylim	the y limits (x1, x2) of the plot, defaults to <code>c(1, 10)</code>
yaxp	a vector of the form <code>c(y1, y2, n)</code> giving the coordinates of the extreme tick marks and the number of intervals between tick-marks, defaults to <code>c(1, 10, 9)</code> .
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 <code>pch=21:25</code> , defaults to "red".
bg.mrg	background (fill) color for the open plot symbols given by <code>pch=21:25</code> , defaults to "yellow".
bg.crg	background (fill) color for the open plot symbols given by <code>pch=21:25</code> , 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 <a href="#">par</a> 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 parameters 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 <code>expression("ln" ~ italic(E))</code> .
bty	box type drawn about the plot, defaults to "1". Other types will not reproduce ideally.
...	other parameters to be passed to <code>plot.default</code> .

### 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 parameters 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 carried 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

- \* **arith**
    - abc, 3
  - \* **arth**
    - fi, 5
    - she, 13
  - \* **classes**
    - abc-class, 4
    - fi-class, 7
    - she-class, 15
  - \* **datasets**
    - Factors, 5
    - LF, 7
    - NB, 8
  - \* **dplot**
    - plot.abc, 9
    - plot.fi, 11
    - plot.she, 12
  - \* **hplot**
    - plot.abc, 9
    - plot.fi, 11
    - plot.she, 12
  - \* **math**
    - abc, 3
    - fi, 5
    - she, 13
  - \* **methods**
    - plot-methods, 9
  - \* **package**
    - forams-package, 2
  - \* **plot**
    - plot-methods, 9
- abc, 2, 3, 5, 8, 9  
abc-class, 4
- Factors, 5  
fi, 2, 5, 5, 7, 9  
fi-class, 7  
forams (forams-package), 2  
forams-package, 2
- LF, 7
- NB, 8
- par, 6, 10–14  
plot, abc-method (plot.abc), 9  
plot, ANY-method (plot-methods), 9  
plot, fi-method (plot.fi), 11  
plot, she-method (plot.she), 12  
plot-methods, 9  
plot.abc, 9  
plot.default, 6, 9, 10, 12, 13  
plot.fi, 11  
plot.she, 12
- she, 2, 7, 9, 13, 15  
she-class, 15