

# Package ‘tabula’

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**Title** Analysis and Visualization of Archaeological Count Data

**Version** 1.8.0

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**Description** An easy way to examine archaeological count data. This package provides several tests and measures of diversity: heterogeneity and evenness (Brillouin, Shannon, Simpson, etc.), richness and rarefaction (Chao1, Chao2, ACE, ICE, etc.), turnover and similarity (Brainerd-Robinson, etc.). The package make it easy to visualize count data and statistical thresholds: rank vs abundance plots, heatmaps, Ford (1962) and Bertin (1977) diagrams.

**License** GPL (>= 3)

**URL** <https://packages.tesselle.org/tabula/>,  
<https://github.com/tesselle/tabula>

**BugReports** <https://github.com/tesselle/tabula/issues>

**Depends** R (>= 3.3)

**Imports** arkhe (>= 0.5.0), boot, kairos (>= 1.1.0), ggplot2, methods, rlang, stats, utils

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'index\_heterogeneity.R' 'index\_rarefaction.R'  
'index\_richness.R' 'index\_similarity.R' 'index\_test.R'  
'index\_turnover.R' 'mutators.R' 'plot\_bertin.R'  
'plot\_diversity.R' 'plot\_ford.R' 'plot\_heatmap.R' 'plot\_rank.R'  
'plot\_spot.R' 'reexport.R' 'show.R' 'statistics.R' 'subset.R'  
'tabula-package.R' 'utilities.R' 'validate.R' 'zzz.R'

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## R topics documented:

cantabria . . . . .	3
DiversityIndex-class . . . . .	3
heterogeneity . . . . .	4
independance . . . . .	8
mutator . . . . .	10
occurrence . . . . .	10
plot_bar . . . . .	11
plot_diversity . . . . .	13
plot_heatmap . . . . .	15
plot_line . . . . .	16
plot_spot . . . . .	17
rarefaction . . . . .	19
resample . . . . .	21
richness . . . . .	23
similarity . . . . .	27
simulate . . . . .	30
subset . . . . .	31
test_diversity . . . . .	32
turnover . . . . .	33

**Index**

**36**

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`cantabria`*Early Magdalenian Engraved Bones*

---

**Description**

A dataset of design elements in engraved bones from Cantabrian Spain.

**Usage**

```
cantabria
```

**Format**

A `data.frame` with 5 rows and 44 variables (designs):

**Source**

Conkey, M. W. (1980). The Identification of prehistoric hunter-gatherer aggregation sites: The case of Altamira. *Current Anthropology*, 21(5), 609-630.

Kintigh, K. W. (1989). Sample Size, Significance, and Measures of Diversity. In Leonard, R. D. and Jones, G. T., *Quantifying Diversity in Archaeology*. New Directions in Archaeology. Cambridge: Cambridge University Press, p. 25-36.

---

`DiversityIndex-class` *Diversity Index*

---

**Description**

An S4 class to represent a diversity measure.

**Slots**

`names` A `character` vector giving the sample names.

`size` A `integer` vector giving the sample sizes.

`simulation` A four columns `numeric` matrix giving the diversity measures for the simulated assemblage (sample size, mean estimate, lower and upper boundaries of the confidence interval).

`method` A `character` string specifying the method used.

**Coerce**

In the code snippets below, `x` is an `DiversityIndex` object.

```
as.data.frame(x)
```

 Coerces to a `data.frame`.

**Note**

This class inherits from base `numeric`.

**Author(s)**

N. Frerebeau

---

heterogeneity

*Heterogeneity and Evenness*

---

**Description**

- `heterogeneity()` returns an heterogeneity or dominance index.
- `evenness()` returns an evenness measure.

**Usage**

```
heterogeneity(object, ...)
```

```
evenness(object, ...)
```

```
index_berger(x, ...)
```

```
index_boone(x, ...)
```

```
index_brillouin(x, ...)
```

```
index_mcintosh(x, ...)
```

```
index_shannon(x, ...)
```

```
index_simpson(x, ...)
```

```
## S4 method for signature 'matrix'
```

```
heterogeneity(  
  object,  
  method = c("berger", "boone", "brillouin", "mcintosh", "shannon", "simpson"),  
  j = NULL  
)
```

```
## S4 method for signature 'data.frame'
```

```
heterogeneity(  
  object,  
  method = c("berger", "boone", "brillouin", "mcintosh", "shannon", "simpson"),  
  j = NULL  
)
```

```

## S4 method for signature 'matrix'
evenness(object, method = c("shannon", "brillouin", "mcintosh", "simpson"))

## S4 method for signature 'data.frame'
evenness(object, method = c("shannon", "brillouin", "mcintosh", "simpson"))

## S4 method for signature 'numeric'
index_berger(x, na.rm = FALSE, ...)

## S4 method for signature 'matrix'
index_boone(x, j = NULL, na.rm = FALSE, ...)

## S4 method for signature 'numeric'
index_brillouin(x, evenness = FALSE, na.rm = FALSE, ...)

## S4 method for signature 'numeric'
index_mcintosh(x, evenness = FALSE, na.rm = FALSE, ...)

## S4 method for signature 'numeric'
index_shannon(x, evenness = FALSE, base = exp(1), na.rm = FALSE, ...)

## S4 method for signature 'numeric'
index_simpson(x, evenness = FALSE, na.rm = FALSE, ...)

```

### Arguments

object	A $m \times p$ numeric <a href="#">matrix</a> or <a href="#">data.frame</a> of count data (absolute frequencies giving the number of individuals for each class).
...	Currently not used.
x	A <a href="#">numeric</a> vector of count data (absolute frequencies).
method	A <a href="#">character</a> string specifying the index to be computed (see details). Any unambiguous substring can be given.
j	An <a href="#">integer</a> giving the index of the reference type/taxa. If NULL (the default), the most frequent type/taxa in any assemblage will be used.
na.rm	A <a href="#">numeric</a> scalar: should missing values (including NaN) be removed?
evenness	A <a href="#">logical</a> scalar: should an evenness measure be computed instead of an heterogeneity/dominance index?
base	A positive <a href="#">numeric</a> value specifying the base with respect to which logarithms are computed.

### Details

*Diversity* measurement assumes that all individuals in a specific taxa are equivalent and that all types are equally different from each other (Peet 1974). A measure of diversity can be achieved by using indices built on the relative abundance of taxa. These indices (sometimes referred to as non-parametric indices) benefit from not making assumptions about the underlying distribution of taxa

abundance: they only take relative abundances of the species that are present and species richness into account. Peet (1974) refers to them as indices of *heterogeneity*.

Diversity indices focus on one aspect of the taxa abundance and emphasize either *richness* (weighting towards uncommon taxa) or *dominance* (weighting towards abundant taxa; Magurran 1988).

*Evenness* is a measure of how evenly individuals are distributed across the sample.

### Value

- `heterogeneity()` returns an `HeterogeneityIndex` object.
- `evenness()` returns an `EvennessIndex` object.
- `index_*` return a `numeric` vector.

### Heterogeneity and Evenness Measures

The following heterogeneity index and corresponding evenness measures are available (see Magurran 1988 for details):

`berger` Berger-Parker dominance index. The Berger-Parker index expresses the proportional importance of the most abundant type. This metric is highly biased by sample size and richness, moreover it does not make use of all the information available from sample.

`boone` Boone heterogeneity measure.

`brillouin` Brillouin diversity index. The Brillouin index describes a known collection: it does not assume random sampling in an infinite population. Pielou (1975) and Laxton (1978) argues for the use of the Brillouin index in all circumstances, especially in preference to the Shannon index.

`mcintosh` McIntosh dominance index. The McIntosh index expresses the heterogeneity of a sample in geometric terms. It describes the sample as a point of a  $S$ -dimensional hypervolume and uses the Euclidean distance of this point from the origin.

`shannon` Shannon-Wiener diversity index. The Shannon index assumes that individuals are randomly sampled from an infinite population and that all taxa are represented in the sample (it does not reflect the sample size). The main source of error arises from the failure to include all taxa in the sample: this error increases as the proportion of species discovered in the sample declines (Peet 1974, Magurran 1988). The maximum likelihood estimator (MLE) is used for the relative abundance, this is known to be negatively biased by sample size.

`simpson` Simpson dominance index for finite sample. The Simpson index expresses the probability that two individuals randomly picked from a finite sample belong to two different types. It can be interpreted as the weighted mean of the proportional abundances. This metric is a true probability value, it ranges from 0 (perfectly uneven) to 1 (perfectly even).

The `berger`, `mcintosh` and `simpson` methods return a *dominance* index, not the reciprocal or inverse form usually adopted, so that an increase in the value of the index accompanies a decrease in diversity.

### Note

Ramanujan approximation is used for  $x!$  computation if  $x > 170$ .

**Author(s)**

N. Frerebeau

**References**

- Berger, W. H. & Parker, F. L. (1970). Diversity of Planktonic Foraminifera in Deep-Sea Sediments. *Science*, 168(3937), 1345-1347. doi:10.1126/science.168.3937.1345.
- Boone, J. L. (1987). Defining and Measuring Midden Catchment. *American Antiquity*, 52(2), 336-45. doi:10.2307/281785.
- Brillouin, L. (1956). *Science and information theory*. New York: Academic Press.
- Kintigh, K. W. (1989). Sample Size, Significance, and Measures of Diversity. In Leonard, R. D. and Jones, G. T., *Quantifying Diversity in Archaeology*. New Directions in Archaeology. Cambridge: Cambridge University Press, p. 25-36.
- Laxton, R. R. (1978). The measure of diversity. *Journal of Theoretical Biology*, 70(1), 51-67. doi:10.1016/00225193(78)903028.
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- McIntosh, R. P. (1967). An Index of Diversity and the Relation of Certain Concepts to Diversity. *Ecology*, 48(3), 392-404. doi:10.2307/1932674.
- Peet, R. K. (1974). The Measurement of Species Diversity. *Annual Review of Ecology and Systematics*, 5(1), 285-307. doi:10.1146/annurev.es.05.110174.001441.
- Pielou, E. C. (1975). *Ecological Diversity*. New York: Wiley. doi:10.4319/lo.1977.22.1.0174b
- Shannon, C. E. (1948). A Mathematical Theory of Communication. *The Bell System Technical Journal*, 27, 379-423. doi:10.1002/j.15387305.1948.tb01338.x.
- Simpson, E. H. (1949). Measurement of Diversity. *Nature*, 163(4148), 688-688. doi:10.1038/163688a0.

**See Also**

Other diversity measures: [occurrence\(\)](#), [plot\\_diversity](#), [rarefaction\(\)](#), [richness\(\)](#), [similarity\(\)](#), [simulate\(\)](#), [turnover\(\)](#)

**Examples**

```
data("cantabria")

## Shannon diversity index
(h <- heterogeneity(cantabria, method = "shannon"))
(e <- evenness(cantabria, method = "shannon"))

## Bootstrap resampling (summary statistics)
bootstrap(h, f = NULL)

bootstrap(h, f = summary)

quant <- function(x) quantile(x, probs = c(0.25, 0.50))
```

```
bootstrap(h, f = quant)

## Jackknife resampling
jackknife(h)
```

---

independance

*Independance*


---

### Description

Independance

### Usage

```
eppm(object, ...)

pvi(object, ...)

## S4 method for signature 'matrix'
eppm(object)

## S4 method for signature 'data.frame'
eppm(object)

## S4 method for signature 'matrix'
pvi(object)

## S4 method for signature 'data.frame'
pvi(object)
```

### Arguments

object	A $m \times p$ numeric <a href="#">matrix</a> or <a href="#">data.frame</a> of count data (absolute frequencies giving the number of individuals for each class).
...	Currently not used.

### Details

Computes for each cell of a numeric matrix one of the following statistic.

### Value

A [numeric matrix](#).



## EPPM

This positive difference from the column mean percentage (in french "écart positif au pourcentage moyen", EPPM) represents a deviation from the situation of statistical independence. As independence can be interpreted as the absence of relationships between types and the chronological order of the assemblages, EPPM is a useful tool to explore significance of relationship between rows and columns related to seriation (Desachy 2004).

## PVI

PVI is calculated for each cell as the percentage to the column theoretical independence value: PVI greater than 1 represent positive deviations from the independence, whereas PVI smaller than 1 represent negative deviations (Desachy 2004).

The PVI matrix allows to explore deviations from independence (an intuitive approach to  $\chi^2$ ), in such a way that a high-contrast matrix has quite significant deviations, with a low risk of being due to randomness (Desachy 2004).

## Author(s)

N. Frerebeau

## References

Desachy, B. (2004). Le sériographe EPPM: un outil informatisé de sériation graphique pour tableaux de comptages. *Revue archéologique de Picardie*, 3(1), 39-56. doi:10.3406/pica.2004.2396.

## See Also

[plot\\_ford\(\)](#), [plot\\_heatmap\(\)](#), [seriate\\_rank\(\)](#)

Other statistics: [test\\_diversity\(\)](#)

## Examples

```
data("cantabria")

## Compute EPPM
counts_eppm <- eppm(cantabria)
plot_heatmap(counts_eppm) +
  khroma::scale_fill_YlOrBr(name = "EPPM")

## Compute PVI
counts_pvi <- pvi(cantabria)
plot_heatmap(counts_pvi) +
  khroma::scale_fill_BuRd(name = "PVI", midpoint = 1)
```

---

mutator

*Get or Set Parts of an Object*

---

### Description

Getters and setters to extract or replace parts of an object.

### Usage

```
get_method(x)  
  
## S4 method for signature 'DiversityIndex'  
get_method(x)
```

### Arguments

x                    An object from which to get or set element(s).

### Value

An object of the same sort as object with the new values assigned.

### Author(s)

N. Frerebeau

### See Also

Other mutator: [subset\(\)](#)

---

occurrence

*Co-Occurrence*

---

### Description

Co-Occurrence

### Usage

```
occurrence(object, ...)  
  
## S4 method for signature 'matrix'  
occurrence(object)  
  
## S4 method for signature 'data.frame'  
occurrence(object)
```

**Arguments**

object            A  $m \times p$  matrix of count data.  
 ...                Currently not used.

**Details**

A co-occurrence matrix is a symmetric matrix with zeros on its main diagonal, which works out how many times each pairs of taxa/types occur together in at least one sample.

**Value**

A `stats::dist` object.

**Author(s)**

N. Frerebeau

**See Also**

Other diversity measures: [heterogeneity\(\)](#), [plot\\_diversity](#), [rarefaction\(\)](#), [richness\(\)](#), [similarity\(\)](#), [simulate\(\)](#), [turnover\(\)](#)

**Examples**

```
data("cantabria")

## Plot spot diagram of a co-occurrence matrix
occ <- occurrence(cantabria)
plot_spot(occ)
```

---

plot\_bar

*Bar Plot*

---

**Description**

Plots a Bertin, Ford (battleship curve) or Dice-Leraas diagram.

**Usage**

```
plot_bertin(object, ...)

plot_ford(object, ...)

## S4 method for signature 'matrix'
plot_bertin(object, threshold = NULL, scale = NULL)

## S4 method for signature 'data.frame'
plot_bertin(object, threshold = NULL, scale = NULL)
```

```
## S4 method for signature 'matrix'
plot_ford(object, EPPM = FALSE)

## S4 method for signature 'data.frame'
plot_ford(object, EPPM = FALSE)
```

### Arguments

object	A $m \times p$ numeric <code>matrix</code> or <code>data.frame</code> of count data (absolute frequencies giving the number of individuals for each class).
...	Currently not used.
threshold	A <code>function</code> that takes a numeric vector as argument and returns a numeric threshold value (see below). If NULL (the default), no threshold is computed.
scale	A <code>function</code> used to scale each variable, that takes a numeric vector as argument and returns a numeric vector. If NULL (the default), no scaling is performed.
EPPM	A <code>logical</code> scalar: should the EPPM be drawn (see below)?

### Details

If EPPM is TRUE and if a relative abundance is greater than the mean percentage of the type, the exceeding part is highlighted.

### Value

A `ggplot2::ggplot` object.

### Bertin Matrix

As de Falguerolles *et al.* (1997) points out: "In abstract terms, a Bertin matrix is a matrix of displays. ... To fix ideas, think of a data matrix, variable by case, with real valued variables. For each variable, draw a bar chart of variable value by case. High-light all bars representing a value above some sample threshold for that variable."

### EPPM

This positive difference from the column mean percentage (in french "écart positif au pourcentage moyen", EPPM) represents a deviation from the situation of statistical independence. As independence can be interpreted as the absence of relationships between types and the chronological order of the assemblages, EPPM is a useful tool to explore significance of relationship between rows and columns related to seriation (Desachy 2004).

### Author(s)

N. Frerebeau

## References

Bertin, J. (1977). *La graphique et le traitement graphique de l'information*. Paris: Flammarion. Nouvelle Bibliothèque Scientifique.

de Falguerolles, A., Friedrich, F. & Sawitzki, G. (1997). A Tribute to J. Bertin's Graphical Data Analysis. In W. Badilla & F. Faulbaum (eds.), *SoftStat '97: Advances in Statistical Software 6*. Stuttgart: Lucius & Lucius, p. 11-20.

Desachy, B. (2004). Le sériographe EPPM: un outil informatisé de sériation graphique pour tableaux de comptages. *Revue archéologique de Picardie*, 3(1), 39-56. doi:10.3406/pica.2004.2396.

Ford, J. A. (1962). *A quantitative method for deriving cultural chronology*. Washington, DC: Pan American Union. Technical manual 1.

## See Also

[eppm\(\)](#)

Other plot methods: [plot\\_diversity](#), [plot\\_heatmap\(\)](#), [plot\\_line](#), [plot\\_spot\(\)](#)

## Examples

```
## Ceramic data
data("mississippi", package = "folio")

## Plot a Bertin diagram...
## ...without threshold
plot_bertin(mississippi)
## ...with variables scaled to 0-1 and the variable mean as threshold
scale_01 <- function(x) (x - min(x)) / (max(x) - min(x))
plot_bertin(mississippi, threshold = mean, scale = scale_01)

## Abundance data
## Coerce dataset to a count matrix (data from Desachy 2004)
data("compiegne", package = "folio")

## Plot a Ford diagram...
## ...without threshold
plot_ford(compiegne)
## ...with EPPM
plot_ford(compiegne, EPPM = TRUE)
```

---

plot\_diversity

*Diversity Plot*

---

## Description

Diversity Plot

**Usage**

```
## S4 method for signature 'DiversityIndex'  
autoplot(object, ...)  
  
## S4 method for signature 'DiversityIndex,missing'  
plot(x, y, ...)  
  
## S4 method for signature 'RarefactionIndex'  
autoplot(object, ...)  
  
## S4 method for signature 'RarefactionIndex,missing'  
plot(x, y, ...)
```

**Arguments**

object, x	A <a href="#">DiversityIndex</a> object to be plotted.
...	Currently not used.
y	Currently not used.

**Value**

- `autoplot()` returns a [ggplot](#) object.
- `plot()` is called it for its side-effects: it results in a graphic being displayed (invisibly returns `x`).

**Author(s)**

N. Frerebeau

**See Also**

Other diversity measures: [heterogeneity\(\)](#), [occurrence\(\)](#), [rarefaction\(\)](#), [richness\(\)](#), [similarity\(\)](#), [simulate\(\)](#), [turnover\(\)](#)

Other plot methods: [plot\\_bar](#), [plot\\_heatmap\(\)](#), [plot\\_line](#), [plot\\_spot\(\)](#)

**Examples**

```
data("cantabria")  
  
## Assemblage diversity size comparison  
## Warning: this may take a few seconds!  
h <- heterogeneity(cantabria, method = "shannon")  
h_sim <- simulate(h)  
plot(h_sim)  
  
r <- richness(cantabria, method = "count")  
r_sim <- simulate(r)  
plot(r_sim)
```

---

plot_heatmap	<i>Heatmap</i>
--------------	----------------

---

## Description

Plots a heatmap.

## Usage

```
plot_heatmap(object, ...)  
  
## S4 method for signature 'matrix'  
plot_heatmap(object, diag = TRUE, upper = TRUE, lower = TRUE, freq = FALSE)  
  
## S4 method for signature 'data.frame'  
plot_heatmap(object, diag = TRUE, upper = TRUE, lower = TRUE, freq = FALSE)  
  
## S4 method for signature 'dist'  
plot_heatmap(object, diag = FALSE, upper = FALSE, lower = !upper)
```

## Arguments

object	A $m \times p$ numeric <a href="#">matrix</a> or <a href="#">data.frame</a> of count data (absolute frequencies giving the number of individuals for each class).
...	Currently not used.
diag	A <a href="#">logical</a> scalar indicating whether the diagonal of the matrix should be plotted. Only used if object is a symmetric matrix.
upper	A <a href="#">logical</a> scalar indicating whether the upper triangle of the matrix should be plotted. Only used if object is a symmetric matrix.
lower	A <a href="#">logical</a> scalar indicating whether the lower triangle of the matrix should be plotted. Only used if object is a symmetric matrix.
freq	A <a href="#">logical</a> scalar indicating whether relative frequency should be used instead of counts (absolute frequency).

## Value

A [ggplot2::ggplot](#) object.

## Author(s)

N. Frerebeau

## References

Desachy, B. (2004). Le sériographe EPPM: un outil informatisé de sériation graphique pour tableaux de comptages. *Revue archéologique de Picardie*, 3(1), 39-56. doi:10.3406/pica.2004.2396.

## See Also

[pvi\(\)](#)

Other plot methods: [plot\\_bar](#), [plot\\_diversity](#), [plot\\_line](#), [plot\\_spot\(\)](#)

## Examples

```
data("cantabria")

## Plot matrix diagram...
plot_heatmap(cantabria)
plot_heatmap(cantabria, freq = TRUE)

## Presence/absence data
inc <- sample(0:1, size = 100, replace = TRUE)
bin <- matrix(data = as.logical(inc), nrow = 10, ncol = 10)

plot_heatmap(bin) +
  khroma::scale_fill_logical()
```

---

plot\_line

*Line Plot*

---

## Description

Plots a rank vs relative abundance diagram.

## Usage

```
plot_rank(object, ...)

## S4 method for signature 'matrix'
plot_rank(object, log = NULL, facet = FALSE)

## S4 method for signature 'data.frame'
plot_rank(object, log = NULL, facet = FALSE)
```

## Arguments

object	A $m \times p$ numeric <a href="#">matrix</a> or <a href="#">data.frame</a> of count data (absolute frequencies giving the number of individuals for each class).
...	Further arguments to be passed to internal methods.



`log` A [character](#) string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic (base 10).

`facet` A [logical](#) scalar: should a matrix of panels defined by case/sample be drawn?

**Value**

A [ggplot2::ggplot](#) object.

**Author(s)**

N. Freyrebeau

**References**

Magurran, A. E. (1988). *Ecological Diversity and its Measurement*. Princeton, NJ: Princeton University Press. [doi:10.1007/9789401573580](https://doi.org/10.1007/9789401573580).

**See Also**

Other plot methods: [plot\\_bar](#), [plot\\_diversity](#), [plot\\_heatmap\(\)](#), [plot\\_spot\(\)](#)

**Examples**

```
data("cantabria")

## Plot rank vs abundance
plot_rank(cantabria)
plot_rank(cantabria, facet = TRUE)
```

---

plot\_spot

*Spot Plot*

---

**Description**

Plots a spot matrix.

**Usage**

```
plot_spot(object, ...)

## S4 method for signature 'matrix'
plot_spot(
  object,
  type = c("ring", "plain"),
  threshold = NULL,
  diag = TRUE,
  upper = TRUE,
```

```

    lower = TRUE,
    freq = FALSE,
    ...
)

## S4 method for signature 'data.frame'
plot_spot(
  object,
  type = c("ring", "plain"),
  threshold = NULL,
  diag = TRUE,
  upper = TRUE,
  lower = TRUE,
  freq = FALSE,
  ...
)

## S4 method for signature 'dist'
plot_spot(
  object,
  type = c("ring", "plain"),
  diag = FALSE,
  upper = FALSE,
  lower = !upper,
  ...
)

```

### Arguments

object	A $m \times p$ numeric <a href="#">matrix</a> or <a href="#">data.frame</a> of count data (absolute frequencies giving the number of individuals for each class).
...	Extra parameters to be passed to threshold.
type	A <a href="#">character</a> string specifying the graph to be plotted. It must be one of "ring" (the default) or "plain". Any unambiguous substring can be given.
threshold	A <a href="#">function</a> that takes a numeric vector as argument and returns a numeric threshold value. If NULL (the default), no threshold is computed.
diag	A <a href="#">logical</a> scalar indicating whether the diagonal of the matrix should be plotted. Only used if object is a symmetric matrix.
upper	A <a href="#">logical</a> scalar indicating whether the upper triangle of the matrix should be plotted. Only used if object is a symmetric matrix.
lower	A <a href="#">logical</a> scalar indicating whether the lower triangle of the matrix should be plotted. Only used if object is a symmetric matrix.
freq	A <a href="#">logical</a> scalar indicating whether relative frequency should be used instead of counts (absolute frequency).

**Details**

The spot matrix can be considered as a variant of the [Bertin diagram](#) where the data are first transformed to relative frequencies.

**Value**

A `ggplot2::ggplot` object.

**Note**

Adapted from Dan Gopstein's original [idea](#).

**Author(s)**

N. Frerebeau

**See Also**

Other plot methods: [plot\\_bar](#), [plot\\_diversity](#), [plot\\_heatmap\(\)](#), [plot\\_line](#)

**Examples**

```
data("cantabria")

## Plot spot diagram of count data...
### ...without threshod
plot_spot(cantabria)
### ...with the column means as threshold
plot_spot(cantabria, threshold = mean)
### ...with the column medians as threshold
plot_spot(cantabria, threshold = median)
```

---

rarefaction

*Rarefaction*

---

**Description**

Rarefaction

**Usage**

```
rarefaction(object, ...)

index_baxter(x, ...)

index_hurlbert(x, ...)

## S4 method for signature 'matrix'
```

```

rarefaction(object, sample = NULL, method = c("hurlbert", "baxter"), step = 1)

## S4 method for signature 'data.frame'
rarefaction(object, sample = NULL, method = c("hurlbert", "baxter"), step = 1)

## S4 method for signature 'numeric'
index_baxter(x, sample, ...)

## S4 method for signature 'numeric'
index_hurlbert(x, sample, ...)

```

### Arguments

object	A $m \times p$ numeric <a href="#">matrix</a> or <a href="#">data.frame</a> of count data (absolute frequencies).
...	Currently not used.
x	A <a href="#">numeric</a> vector of count data (absolute frequencies).
sample	A length-one <a href="#">numeric</a> vector giving the sub-sample size. The size of sample should be smaller than total community size.
method	A <a href="#">character</a> string or vector of strings specifying the index to be computed (see details). Any unambiguous substring can be given.
step	An <a href="#">integer</a> giving the increment of the sample size.

### Value

- `rarefaction()` returns a [RarefactionIndex](#) object.
- `index_*` return a [numeric](#) vector.

### Rarefaction Measures

The following rarefaction measures are available for count data:

`baxter` Baxter's rarefaction.

`hurlbert` Hurlbert's unbiased estimate of Sander's rarefaction.

### Details

The number of different taxa, provides an instantly comprehensible expression of diversity. While the number of taxa within a sample is easy to ascertain, as a term, it makes little sense: some taxa may not have been seen, or there may not be a fixed number of taxa (e.g. in an open system; Peet 1974). As an alternative, *richness* ( $S$ ) can be used for the concept of taxa number (McIntosh 1967).

It is not always possible to ensure that all sample sizes are equal and the number of different taxa increases with sample size and sampling effort (Magurran 1988). Then, *rarefaction* ( $E(S)$ ) is the number of taxa expected if all samples were of a standard size (i.e. taxa per fixed number of individuals). Rarefaction assumes that imbalances between taxa are due to sampling and not to differences in actual abundances.

**Author(s)**

N. Frerebeau

**References**

Baxter, M. J. (2001). Methodological Issues in the Study of Assemblage Diversity. *American Antiquity*, 66(4), 715-725. doi:10.2307/2694184.

Hurlbert, S. H. (1971). The Nonconcept of Species Diversity: A Critique and Alternative Parameters. *Ecology*, 52(4), 577-586. doi:10.2307/1934145.

Sander, H. L. (1968). Marine Benthic Diversity: A Comparative Study. *The American Naturalist*, 102(925), 243-282.

**See Also**

Other diversity measures: [heterogeneity\(\)](#), [occurrence\(\)](#), [plot\\_diversity](#), [richness\(\)](#), [similarity\(\)](#), [simulate\(\)](#), [turnover\(\)](#)

**Examples**

```
data("cantabria")

## Replicate fig. 3 from Baxter 2011
rare <- rarefaction(cantabria, sample = 23, method = "baxter")
plot(rare)
```

---

resample

*Resampling Methods*

---

**Description**

- `resample()` simulate observations from a multinomial distribution.
- `bootstrap()` generate bootstrap estimations of a statistic.
- `jackknife()` generate jackknife estimations of a statistic.

**Usage**

```
resample(object, ...)
```

```
bootstrap(object, ...)
```

```
jackknife(object, ...)
```

```
## S4 method for signature 'DiversityIndex'
```

```
bootstrap(object, n = 1000, f = NULL)
```

```
## S4 method for signature 'DiversityIndex'
```

```
jackknife(object)

## S4 method for signature 'numeric'
resample(object, do, n, size = sum(object), ..., f = NULL)
```

### Arguments

object	A <b>numeric</b> vector of count data (absolute frequencies).
...	Extra arguments passed to do.
n	A non-negative <b>integer</b> specifying the number of bootstrap replications.
f	A <b>function</b> that takes a single numeric vector (the result of do) as argument.
do	A <b>function</b> that takes object as an argument and returns a single numeric value.
size	A non-negative <b>integer</b> specifying the sample size.

### Value

If f is NULL, resample() returns the n values of do. Else, returns the result of f applied to the n values of do.

If f is NULL, bootstrap() and jackknife() return a **data.frame** with the following elements (else, returns the result of f applied to the n values of do) :

**original** The observed value of do applied to object.  
**mean** The bootstrap/jackknife estimate of mean of do.  
**bias** The bootstrap/jackknife estimate of bias of do.  
**error** The bootstrap/jackknife estimate of standard error of do.

### Author(s)

N. Frerebeau

### See Also

[stats::rmultinom\(\)](#)

### Examples

```
## Sample observations from a multinomial distribution
x <- sample(1:100, 50, TRUE)
resample(x, do = median, n = 100)

## Estimate the 25th, 50th and 95th percentiles
quant <- function(x) { quantile(x, probs = c(0.25, 0.50, 0.75)) }
resample(x, n = 100, do = median, f = quant)
```

---

richness	<i>Richness</i>
----------	-----------------

---

**Description**

- richness() returns sample richness.
- composition() returns asymptotic species richness.

**Usage**

```
richness(object, ...)
```

```
composition(object, ...)
```

```
index_ace(x, ...)
```

```
index_ice(x, ...)
```

```
index_chao1(x, ...)
```

```
index_chao2(x, ...)
```

```
index_margalef(x, ...)
```

```
index_menhinick(x, ...)
```

```
## S4 method for signature 'matrix'
```

```
richness(object, method = c("count", "margalef", "menhinick"))
```

```
## S4 method for signature 'data.frame'
```

```
richness(object, method = c("count", "margalef", "menhinick"))
```

```
## S4 method for signature 'matrix'
```

```
composition(  
  object,  
  method = c("chao1", "ace", "chao2", "ice"),  
  unbiased = FALSE,  
  improved = FALSE,  
  k = 10  
)
```

```
## S4 method for signature 'data.frame'
```

```
composition(  
  object,  
  method = c("chao1", "ace", "chao2", "ice"),  
  unbiased = FALSE,  
  improved = FALSE,
```

```

    k = 10
  )

## S4 method for signature 'numeric'
index_margalef(x, na.rm = FALSE, ...)

## S4 method for signature 'numeric'
index_menhinick(x, na.rm = FALSE, ...)

## S4 method for signature 'numeric'
index_ace(x, k = 10, ...)

## S4 method for signature 'numeric'
index_chao1(x, unbiased = FALSE, improved = FALSE, ...)

## S4 method for signature 'matrix'
index_ice(x, k = 10, ...)

## S4 method for signature 'matrix'
index_chao2(x, unbiased = FALSE, improved = FALSE, ...)

```

### Arguments

object	A $m \times p$ numeric <a href="#">matrix</a> or <a href="#">data.frame</a> of count data (absolute frequencies).
...	Further arguments to be passed to internal methods.
x	A <a href="#">numeric</a> vector or matrix of count data (absolute frequencies).
method	A <a href="#">character</a> string or vector of strings specifying the index to be computed (see details). Any unambiguous substring can be given.
unbiased	A <a href="#">logical</a> scalar. Should the bias-corrected estimator be used? Only used with "chao1" or "chao2" (improved) estimator.
improved	A <a href="#">logical</a> scalar. Should the improved estimator be used? Only used with "chao1" or "chao2".
k	A length-one <a href="#">numeric</a> vector giving the threshold between rare/infrequent and abundant/frequent species. Only used if method is "ace" or "ice".
na.rm	A <a href="#">numeric</a> scalar: should missing values (including NaN) be removed?

### Value

- richness() returns a [RichnessIndex](#) object.
- composition() returns a [CompositionIndex](#) object.
- index\_\*( ) return a [numeric](#) vector.

### Details

The number of different taxa, provides an instantly comprehensible expression of diversity. While the number of taxa within a sample is easy to ascertain, as a term, it makes little sense: some taxa



may not have been seen, or there may not be a fixed number of taxa (e.g. in an open system; Peet 1974). As an alternative, *richness* ( $S$ ) can be used for the concept of taxa number (McIntosh 1967).

It is not always possible to ensure that all sample sizes are equal and the number of different taxa increases with sample size and sampling effort (Magurran 1988). Then, *rarefaction* ( $E(S)$ ) is the number of taxa expected if all samples were of a standard size (i.e. taxa per fixed number of individuals). Rarefaction assumes that imbalances between taxa are due to sampling and not to differences in actual abundances.

### Richness Measures

The following richness measures are available for count data:

count Returns the number of observed taxa/types.

margalef Margalef richness index.

menhinick Menhinick richness index.

### Asymptotic Species Richness

The following measures are available for count data:

ace Abundance-based Coverage Estimator.

chao1 (improved/unbiased) Chao1 estimator.

The following measures are available for replicated incidence data:

ice Incidence-based Coverage Estimator.

chao2 (improved/unbiased) Chao2 estimator.

### Author(s)

N. Frerebeau

### References

Chao, A. (1984). Nonparametric Estimation of the Number of Classes in a Population. *Scandinavian Journal of Statistics*, 11(4), 265-270.

Chao, A. (1987). Estimating the Population Size for Capture-Recapture Data with Unequal Catchability. *Biometrics* 43(4), 783-791. doi:10.2307/2531532.

Chao, A. & Chiu, C.-H. (2016). Species Richness: Estimation and Comparison. In Balakrishnan, N., Colton, T., Everitt, B., Piegorsch, B., Ruggeri, F. & Teugels, J. L. (Eds.), *Wiley StatsRef: Statistics Reference Online*. Chichester, UK: John Wiley & Sons, Ltd., 1-26. doi:10.1002/9781118445112.stat03432.pub2

Chao, A. & Lee, S.-M. (1992). Estimating the Number of Classes via Sample Coverage. *Journal of the American Statistical Association*, 87(417), 210-217. doi:10.1080/01621459.1992.10475194.

Chiu, C.-H., Wang, Y.-T., Walther, B. A. & Chao, A. (2014). An improved nonparametric lower bound of species richness via a modified good-turing frequency formula. *Biometrics*, 70(3), 671-682. doi:10.1111/biom.12200.

Magurran, A. E. (1988). *Ecological Diversity and its Measurement*. Princeton, NJ: Princeton University Press. doi:10.1007/9789401573580.

Kintigh, K. W. (1989). Sample Size, Significance, and Measures of Diversity. In Leonard, R. D. and Jones, G. T., *Quantifying Diversity in Archaeology*. New Directions in Archaeology. Cambridge: Cambridge University Press, p. 25-36.

Magurran, A. E. & Brian J. McGill (2011). *Biological Diversity: Frontiers in Measurement and Assessment*. Oxford: Oxford University Press.

Margalef, R. (1958). Information Theory in Ecology. *General Systems*, 3, 36-71.

Menhinick, E. F. (1964). A Comparison of Some Species-Individuals Diversity Indices Applied to Samples of Field Insects. *Ecology*, 45(4), 859-861. doi:10.2307/1934933.

McIntosh, R. P. (1967). An Index of Diversity and the Relation of Certain Concepts to Diversity. *Ecology*, 48(3), 392-404. doi:10.2307/1932674.

### See Also

[plot\\_diversity\(\)](#)

Other diversity measures: [heterogeneity\(\)](#), [occurrence\(\)](#), [plot\\_diversity](#), [rarefaction\(\)](#), [similarity\(\)](#), [simulate\(\)](#), [turnover\(\)](#)

### Examples

```
## Margalef and Menhinick index
## Data from Magurran 1988, p. 128-129
trap <- matrix(data = c(9, 3, 0, 4, 2, 1, 1, 0, 1, 0, 1, 1,
                       1, 0, 1, 0, 0, 0, 1, 2, 0, 5, 3, 0),
               nrow = 2, byrow = TRUE, dimnames = list(c("A", "B"), NULL))
richness(trap, method = "margalef") # 2.55 1.88
richness(trap, method = "menhinick") # 1.95 1.66

## Chao1-type estimators (asymptotic species richness)
## Data from Chao & Chiu 2016
brazil <- matrix(
  data = rep(x = c(1:21, 23, 25, 27, 28, 30, 32, 34:37, 41,
                  45, 46, 49, 52, 89, 110, 123, 140),
             times = c(113, 50, 39, 29, 15, 11, 13, 5, 6, 6, 3, 4,
                       3, 5, 2, 5, 2, 2, 2, 2, 1, 2, 1, 1, 1, 1, 1,
                       0, 0, 2, 1, 1, 1, 1, 1, 0, 1, 1, 0, 0)),
             nrow = 1, byrow = TRUE
)

composition(brazil, method = c("chao1"), unbiased = FALSE) # 461.625
composition(brazil, method = c("ace"), k = 10) # 445.822
```

---

similarity	<i>Similarity</i>
------------	-------------------

---

**Description**

Similarity

**Usage**

```
similarity(object, ...)  
  
index_jaccard(x, y, ...)  
  
index_sorenson(x, y, ...)  
  
index_bray(x, y, ...)  
  
index_morisita(x, y, ...)  
  
index_brainerd(x, y, ...)  
  
index_binomial(x, y, ...)  
  
## S4 method for signature 'matrix'  
similarity(  
  object,  
  method = c("brainerd", "bray", "jaccard", "morisita", "sorenson", "binomial")  
)  
  
## S4 method for signature 'data.frame'  
similarity(  
  object,  
  method = c("brainerd", "bray", "jaccard", "morisita", "sorenson", "binomial")  
)  
  
## S4 method for signature 'character,character'  
index_jaccard(x, y)  
  
## S4 method for signature 'logical,logical'  
index_jaccard(x, y)  
  
## S4 method for signature 'numeric,numeric'  
index_jaccard(x, y)  
  
## S4 method for signature 'logical,logical'  
index_sorenson(x, y)
```

```
## S4 method for signature 'numeric,numeric'
index_sorenson(x, y)

## S4 method for signature 'numeric,numeric'
index_bray(x, y)

## S4 method for signature 'numeric,numeric'
index_morisita(x, y)

## S4 method for signature 'numeric,numeric'
index_brainerd(x, y)

## S4 method for signature 'numeric,numeric'
index_binomial(x, y)
```

### Arguments

object	A $m \times p$ matrix of count data.
...	Currently not used.
x, y	A length- $p$ <code>numeric</code> vector of count data.
method	A <code>character</code> string specifying the method to be used (see details). Any unambiguous substring can be given.

### Details

$\beta$ -diversity can be measured by addressing *similarity* between pairs of samples/cases (Brainerd-Robinson, Jaccard, Morisita-Horn and Sorenson indices). Similarity between pairs of taxa/types can be measured by assessing the degree of co-occurrence (binomial co-occurrence).

Jaccard, Morisita-Horn and Sorenson indices provide a scale of similarity from 0-1 where 1 is perfect similarity and 0 is no similarity. The Brainerd-Robinson index is scaled between 0 and 200. The Binomial co-occurrence assessment approximates a Z-score.

`binomial` Binomial co-occurrence assessment. This assesses the degree of co-occurrence between taxa/types within a dataset. The strongest associations are shown by large positive numbers, the strongest segregations by large negative numbers.

`brainerd` Brainerd-Robinson quantitative index. This is a city-block metric of similarity between pairs of samples/cases.

`bray` Sorenson quantitative index (Bray and Curtis modified version of the Sorenson index).

`jaccard` Jaccard qualitative index.

`morisita` Morisita-Horn quantitative index.

`sorenson` Sorenson qualitative index.

### Value

- `similarity()` returns a `stats::dist` object.
- `index_*`() return a `numeric` vector.

**Author(s)**

N. Frerebeau

**References**

- Brainerd, G. W. (1951). The Place of Chronological Ordering in Archaeological Analysis. *American Antiquity*, 16(04), 301-313. doi:10.2307/276979.
- Bray, J. R. & Curtis, J. T. (1957). An Ordination of the Upland Forest Communities of Southern Wisconsin. *Ecological Monographs*, 27(4), 325-349. doi:10.2307/1942268.
- Kintigh, K. (2006). Ceramic Dating and Type Associations. In J. Hantman and R. Most (eds.), *Managing Archaeological Data: Essays in Honor of Sylvia W. Gaines*. Anthropological Research Paper, 57. Tempe, AZ: Arizona State University, p. 17-26.
- Magurran, A. E. (1988). *Ecological Diversity and its Measurement*. Princeton, NJ: Princeton University Press. doi:10.1007/9789401573580.
- Robinson, W. S. (1951). A Method for Chronologically Ordering Archaeological Deposits. *American Antiquity*, 16(04), 293-301. doi:10.2307/276978.

**See Also**

Other diversity measures: [heterogeneity\(\)](#), [occurrence\(\)](#), [plot\\_diversity](#), [rarefaction\(\)](#), [richness\(\)](#), [simulate\(\)](#), [turnover\(\)](#)

**Examples**

```
## Data from Huntley 2008
ceramics <- matrix(
  data = c(16, 9, 3, 0, 1,
           13, 3, 2, 0, 0,
           9, 5, 2, 5, 0,
           14, 12, 3, 0, 0,
           0, 26, 4, 0, 0,
           1, 26, 4, 0, 0,
           0, 11, 3, 13, 0,
           0, 0, 17, 0, 16,
           0, 0, 18, 0, 14),
  nrow = 9, byrow = TRUE
)
rownames(ceramics) <- c("Atsinna", "Cienega", "Mirabal", "PdMuertos",
                       "Hesh", "LowPesc", "BoxS", "Ojo Bon", "S170")
colnames(ceramics) <- c("DLH-1", "DLH-2a", "DLH-2b", "DLH-2c", "DLH-4")

## Brainerd-Robinson measure
(C <- similarity(ceramics, "brainerd"))
plot_spot(C)

## Data from Magurran 1988, p. 166
birds <- matrix(
  data = c(1.4, 4.3, 2.9, 8.6, 4.2, 15.7, 2.0, 50, 1, 11.4, 11.4, 4.3, 13.0,
           14.3, 8.6, 7.1, 10.0, 1.4, 2.9, 5.7, 1.4, 11.4, 2.9, 4.3, 1.4, 2.9,
```

```

      0, 0, 0, 2.9, 0, 0, 0, 10, 0, 0, 5.7, 2.5, 5.7, 8.6, 5.7, 2.9, 0, 0,
      2.9, 0, 0, 5.7, 0, 2.9, 0, 2.9),
  nrow = 2, byrow = TRUE
)
rownames(birds) <- c("unmanaged", "managed")

## Jaccard measure (presence/absence data)
similarity(birds, "jaccard") # 0.46

## Sorenson measure (presence/absence data)
similarity(birds, "sorenson") # 0.63

# Jaccard measure (Bray's formula ; count data)
similarity(birds, "bray") # 0.44

# Morisita-Horn measure (count data)
similarity(birds, "morisita") # 0.81

```

---

simulate

---

*Measure Diversity by Comparing to Simulated Assemblages*


---

## Description

Measure Diversity by Comparing to Simulated Assemblages

## Usage

```

## S4 method for signature 'DiversityIndex'
simulate(
  object,
  n = 1000,
  step = 1,
  interval = c("percentiles", "student", "normal"),
  level = 0.8,
  progress = getOption("tabula.progress")
)

```

## Arguments

object	A <a href="#">DiversityIndex</a> object.
n	A non-negative <a href="#">integer</a> giving the number of bootstrap replications.
step	An <a href="#">integer</a> giving the increment of the sample size.
interval	A <a href="#">character</a> string giving the type of confidence interval to be returned. It must be one "percentiles" (sample quantiles, as described in Kintigh 1984; the default), "student" or "normal". Any unambiguous substring can be given.
level	A length-one <a href="#">numeric</a> vector giving the confidence level.
progress	A <a href="#">logical</a> scalar: should a progress bar be displayed?

**Value**

Returns a [DiversityIndex](#) object.

**Author(s)**

N. Frerebeau

**References**

Baxter, M. J. (2001). Methodological Issues in the Study of Assemblage Diversity. *American Antiquity*, 66(4), 715-725. doi:10.2307/2694184.

Kintigh, K. W. (1984). Measuring Archaeological Diversity by Comparison with Simulated Assemblages. *American Antiquity*, 49(1), 44-54. doi:10.2307/280511.

**See Also**

[plot\\_diversity\(\)](#), [resample\(\)](#)

Other diversity measures: [heterogeneity\(\)](#), [occurrence\(\)](#), [plot\\_diversity](#), [rarefaction\(\)](#), [richness\(\)](#), [similarity\(\)](#), [turnover\(\)](#)

**Examples**

```
data("cantabria")

## Assemblage diversity size comparison
## Warning: this may take a few seconds!
h <- heterogeneity(cantabria, method = "shannon")
h_sim <- simulate(h)
plot(h_sim)

r <- richness(cantabria, method = "count")
r_sim <- simulate(r)
plot(r_sim)
```

---

subset

*Extract or Replace Parts of an Object*

---

**Description**

Operators acting on objects to extract or replace parts.

**Arguments**

x            An object from which to extract element(s) or in which to replace element(s).  
i            A [character](#) string specifying elements to extract. Any unambiguous substring can be given (see details).

**Value**

A subsetting object.

**Author(s)**

N. Frerebeau

**See Also**

Other mutator: [mutator](#)

---

test_diversity	<i>Diversity Test</i>
----------------	-----------------------

---

**Description**

Compares Shannon diversity between samples.

**Usage**

```
test_diversity(object, ...)  
  
## S4 method for signature 'matrix'  
test_diversity(object, adjust = "holm", ...)  
  
## S4 method for signature 'data.frame'  
test_diversity(object, adjust = "holm", ...)
```

**Arguments**

object	A $m \times p$ matrix of count data.
...	Further arguments to be passed to internal methods.
adjust	A <a href="#">character</a> string specifying the method for adjusting $p$ values (see <a href="#">stats::p.adjust()</a> ).

**Details**

This test produces two sided pairwise comparisons: it returns a matrix of adjusted  $p$  values.

**Value**

A [numeric matrix](#).

**Author(s)**

N. Frerebeau



## References

Magurran, A. E. (1988). *Ecological Diversity and its Measurement*. Princeton, NJ: Princeton University Press. doi:10.1007/9789401573580.

## See Also

Other statistics: [independance](#)

## Examples

```
data("cantabria")

## Shannon diversity test
test_diversity(cantabria)
```

---

turnover	<i>Turnover</i>
----------	-----------------

---

## Description

Returns the degree of turnover in taxa composition along a gradient or transect.

## Usage

```
turnover(object, ...)

index_whittaker(x, ...)

index_cody(x, ...)

index_routledge1(x, ...)

index_routledge2(x, ...)

index_routledge3(x, ...)

index_wilson(x, ...)

## S4 method for signature 'matrix'
turnover(
  object,
  method = c("whittaker", "cody", "routledge1", "routledge2", "routledge3", "wilson"),
  ...
)

## S4 method for signature 'data.frame'
turnover(
```

```

    object,
    method = c("whittaker", "cody", "routledge1", "routledge2", "routledge3", "wilson"),
    ...
)

## S4 method for signature 'matrix'
index_whittaker(x)

## S4 method for signature 'matrix'
index_cody(x)

## S4 method for signature 'matrix'
index_routledge1(x)

## S4 method for signature 'matrix'
index_routledge2(x)

## S4 method for signature 'matrix'
index_routledge3(x)

## S4 method for signature 'matrix'
index_wilson(x)

```

### Arguments

object, x	A $m \times p$ matrix of count data or incidence data.
...	Further arguments to be passed to internal methods.
method	A <a href="#">character</a> string specifying the method to be used (see details). Any unambiguous substring can be given.

### Details

The following methods can be used to ascertain the degree of *turnover* in taxa composition along a gradient ( $\beta$ -diversity) on qualitative (presence/absence) data. This assumes that the order of the matrix rows (from 1 to  $n$ ) follows the progression along the gradient/transect.

whittaker Whittaker measure.

cody Cody measure.

routledge1 Routledge first measure.

routledge2 Routledge second measure.

routledge3 Routledge third measure. This is the exponential form of the second measure.

wilson Wilson measure.

### Value

A [numeric](#) vector.

**Author(s)**

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**See Also**

Other diversity measures: [heterogeneity\(\)](#), [occurrence\(\)](#), [plot\\_diversity](#), [rarefaction\(\)](#), [richness\(\)](#), [similarity\(\)](#), [simulate\(\)](#)

**Examples**

```
## Data from Magurran 1988, p. 162
trees <- matrix(
  data = c(1, 1, 1, 0, 0, 0,
           1, 1, 1, 1, 1, 1,
           0, 0, 1, 0, 1, 0,
           0, 0, 0, 1, 1, 1,
           0, 0, 0, 0, 1, 1,
           0, 0, 0, 1, 0, 1),
  nrow = 6, byrow = FALSE
)
colnames(trees) <- c("Birch", "Oak", "Rowan", "Beech", "Hazel", "Holly")

## Whittaker's measure
turnover(trees, "whittaker") # 1

## Cody's measure
turnover(trees, "cody") # 3

## Routledge's measures
turnover(trees, "routledge1") # 0.29
turnover(trees, "routledge2") # 0.56
turnover(trees, "routledge3") # 1.75

## Wilson and Shmida's measure
turnover(trees, "wilson") # 1
```

# Index

- \* **classes**
  - DiversityIndex-class, 3
- \* **datasets**
  - cantabria, 3
- \* **diversity measures**
  - heterogeneity, 4
  - occurrence, 10
  - plot\_diversity, 13
  - rarefaction, 19
  - richness, 23
  - similarity, 27
  - simulate, 30
  - turnover, 33
- \* **mutator**
  - mutator, 10
  - subset, 31
- \* **plot methods**
  - plot\_bar, 11
  - plot\_diversity, 13
  - plot\_heatmap, 15
  - plot\_line, 16
  - plot\_spot, 17
- \* **resampling methods**
  - resample, 21
- \* **statistics**
  - independance, 8
  - test\_diversity, 32
- ..., 12
- .CompositionIndex
  - (DiversityIndex-class), 3
- .DiversityIndex (DiversityIndex-class), 3
- .EvennessIndex (DiversityIndex-class), 3
- .HeterogeneityIndex
  - (DiversityIndex-class), 3
- .RarefactionIndex
  - (DiversityIndex-class), 3
- .RichnessIndex (DiversityIndex-class), 3
- autoplot, DiversityIndex-method
  - (plot\_diversity), 13
- autoplot, RarefactionIndex-method
  - (plot\_diversity), 13
- Bertin (plot\_bar), 11
- Bertin diagram, 19
- bootstrap (resample), 21
- bootstrap, DiversityIndex-method
  - (resample), 21
- bootstrap-method (resample), 21
- cantabria, 3
- character, 3, 5, 17, 18, 20, 24, 28, 30–32, 34
- composition (richness), 23
- composition, data.frame-method
  - (richness), 23
- composition, matrix-method (richness), 23
- composition-method (richness), 23
- CompositionIndex, 24
- CompositionIndex-class
  - (DiversityIndex-class), 3
- data.frame, 3, 5, 8, 12, 15, 16, 18, 20, 22, 24
- DiversityIndex, 14, 30, 31
- DiversityIndex-class, 3
- eppm (independance), 8
- eppm(), 13
- eppm, data.frame-method (independance), 8
- eppm, matrix-method (independance), 8
- eppm-method (independance), 8
- evenness (heterogeneity), 4
- evenness, data.frame-method
  - (heterogeneity), 4
- evenness, matrix-method (heterogeneity), 4
- evenness-method (heterogeneity), 4
- EvennessIndex, 6
- EvennessIndex-class
  - (DiversityIndex-class), 3

- Ford (plot\_bar), 11
- function, 12, 18, 22
- get (mutator), 10
- get\_method (mutator), 10
- get\_method, DiversityIndex-method (mutator), 10
- get\_method-method (mutator), 10
- ggplot, 14
- ggplot2::ggplot, 12, 15, 17, 19
- heterogeneity, 4, 11, 14, 21, 26, 29, 31, 35
- heterogeneity, data.frame-method (heterogeneity), 4
- heterogeneity, matrix-method (heterogeneity), 4
- heterogeneity-method (heterogeneity), 4
- HeterogeneityIndex, 6
- HeterogeneityIndex-class (DiversityIndex-class), 3
- independence, 8, 33
- index\_ace (richness), 23
- index\_ace, numeric-method (richness), 23
- index\_ace-method (richness), 23
- index\_baxter (rarefaction), 19
- index\_baxter, numeric-method (rarefaction), 19
- index\_baxter-method (rarefaction), 19
- index\_berger (heterogeneity), 4
- index\_berger, numeric-method (heterogeneity), 4
- index\_berger-method (heterogeneity), 4
- index\_binomial (similarity), 27
- index\_binomial, numeric, numeric-method (similarity), 27
- index\_binomial-method (similarity), 27
- index\_boone (heterogeneity), 4
- index\_boone, matrix-method (heterogeneity), 4
- index\_boone-method (heterogeneity), 4
- index\_brainerd (similarity), 27
- index\_brainerd, numeric, numeric-method (similarity), 27
- index\_brainerd-method (similarity), 27
- index\_bray (similarity), 27
- index\_bray, numeric, numeric-method (similarity), 27
- index\_bray-method (similarity), 27
- index\_brillouin (heterogeneity), 4
- index\_brillouin, numeric-method (heterogeneity), 4
- index\_brillouin-method (heterogeneity), 4
- index\_chao1 (richness), 23
- index\_chao1, numeric-method (richness), 23
- index\_chao1-method (richness), 23
- index\_chao2 (richness), 23
- index\_chao2, matrix-method (richness), 23
- index\_chao2-method (richness), 23
- index\_cody (turnover), 33
- index\_cody, matrix-method (turnover), 33
- index\_cody-method (turnover), 33
- index\_hurlbert (rarefaction), 19
- index\_hurlbert, numeric-method (rarefaction), 19
- index\_hurlbert-method (rarefaction), 19
- index\_ice (richness), 23
- index\_ice, matrix-method (richness), 23
- index\_ice-method (richness), 23
- index\_jaccard (similarity), 27
- index\_jaccard, character, character-method (similarity), 27
- index\_jaccard, logical, logical-method (similarity), 27
- index\_jaccard, numeric, numeric-method (similarity), 27
- index\_jaccard-method (similarity), 27
- index\_margalef (richness), 23
- index\_margalef, numeric-method (richness), 23
- index\_margalef-method (richness), 23
- index\_mcintosh (heterogeneity), 4
- index\_mcintosh, numeric-method (heterogeneity), 4
- index\_mcintosh-method (heterogeneity), 4
- index\_menhinick (richness), 23
- index\_menhinick, numeric-method (richness), 23
- index\_menhinick-method (richness), 23
- index\_morisita (similarity), 27
- index\_morisita, numeric, numeric-method (similarity), 27
- index\_morisita-method (similarity), 27
- index\_routledge1 (turnover), 33
- index\_routledge1, matrix-method

- (turnover), 33
- index\_routledge1-method (turnover), 33
- index\_routledge2 (turnover), 33
- index\_routledge2,matrix-method (turnover), 33
- index\_routledge2-method (turnover), 33
- index\_routledge3 (turnover), 33
- index\_routledge3,matrix-method (turnover), 33
- index\_routledge3-method (turnover), 33
- index\_shannon (heterogeneity), 4
- index\_shannon,numeric-method (heterogeneity), 4
- index\_shannon-method (heterogeneity), 4
- index\_simpson (heterogeneity), 4
- index\_simpson,numeric-method (heterogeneity), 4
- index\_simpson-method (heterogeneity), 4
- index\_sorenson (similarity), 27
- index\_sorenson,logical,logical-method (similarity), 27
- index\_sorenson,numeric,numeric-method (similarity), 27
- index\_sorenson-method (similarity), 27
- index\_whittaker (turnover), 33
- index\_whittaker,matrix-method (turnover), 33
- index\_whittaker-method (turnover), 33
- index\_wilson (turnover), 33
- index\_wilson,matrix-method (turnover), 33
- index\_wilson-method (turnover), 33
- integer, 3, 5, 20, 22, 30
- jackknife (resample), 21
- jackknife,DiversityIndex-method (resample), 21
- jackknife-method (resample), 21
- logical, 5, 12, 15, 17, 18, 24, 30
- matrigraphe (plot\_heatmap), 15
- matrix, 5, 8, 12, 15, 16, 18, 20, 24, 32
- mutator, 10, 32
- numeric, 3–6, 8, 20, 22, 24, 28, 30, 32, 34
- occurrence, 7, 10, 14, 21, 26, 29, 31, 35
- occurrence,data.frame-method (occurrence), 10
- occurrence,matrix-method (occurrence), 10
- plot,DiversityIndex,missing-method (plot\_diversity), 13
- plot,RarefactionIndex,missing-method (plot\_diversity), 13
- plot\_bar, 11, 14, 16, 17, 19
- plot\_bertin (plot\_bar), 11
- plot\_bertin,data.frame-method (plot\_bar), 11
- plot\_bertin,matrix-method (plot\_bar), 11
- plot\_bertin-method (plot\_bar), 11
- plot\_diversity, 7, 11, 13, 13, 16, 17, 19, 21, 26, 29, 31, 35
- plot\_diversity(), 26, 31
- plot\_ford (plot\_bar), 11
- plot\_ford(), 9
- plot\_ford,data.frame-method (plot\_bar), 11
- plot\_ford,matrix-method (plot\_bar), 11
- plot\_ford-method (plot\_bar), 11
- plot\_heatmap, 13, 14, 15, 17, 19
- plot\_heatmap(), 9
- plot\_heatmap,data.frame-method (plot\_heatmap), 15
- plot\_heatmap,dist-method (plot\_heatmap), 15
- plot\_heatmap,matrix-method (plot\_heatmap), 15
- plot\_heatmap-method (plot\_heatmap), 15
- plot\_line, 13, 14, 16, 16, 19
- plot\_rank (plot\_line), 16
- plot\_rank,data.frame-method (plot\_line), 16
- plot\_rank,matrix-method (plot\_line), 16
- plot\_rank-method (plot\_line), 16
- plot\_spot, 13, 14, 16, 17, 17
- plot\_spot,data.frame-method (plot\_spot), 17
- plot\_spot,dist-method (plot\_spot), 17
- plot\_spot,matrix-method (plot\_spot), 17
- plot\_spot-method (plot\_spot), 17
- pvi (independance), 8
- pvi(), 16
- pvi,data.frame-method (independance), 8
- pvi,matrix-method (independance), 8
- pvi-method (independance), 8

- rarefaction, [7](#), [11](#), [14](#), [19](#), [26](#), [29](#), [31](#), [35](#)
- rarefaction, data.frame-method
  - (rarefaction), [19](#)
- rarefaction, matrix-method
  - (rarefaction), [19](#)
- rarefaction-method (rarefaction), [19](#)
- RarefactionIndex, [20](#)
- RarefactionIndex-class
  - (DiversityIndex-class), [3](#)
- resample, [21](#)
- resample(), [31](#)
- resample, numeric-method (resample), [21](#)
- resample-method (resample), [21](#)
- richness, [7](#), [11](#), [14](#), [21](#), [23](#), [29](#), [31](#), [35](#)
- richness, data.frame-method (richness),  
[23](#)
- richness, matrix-method (richness), [23](#)
- richness-method (richness), [23](#)
- RichnessIndex, [24](#)
- RichnessIndex-class
  - (DiversityIndex-class), [3](#)
  
- seriate\_rank(), [9](#)
- seriogramme (plot\_bar), [11](#)
- set (mutator), [10](#)
- similarity, [7](#), [11](#), [14](#), [21](#), [26](#), [27](#), [31](#), [35](#)
- similarity, data.frame-method
  - (similarity), [27](#)
- similarity, matrix-method (similarity),  
[27](#)
- similarity-method (similarity), [27](#)
- simulate, [7](#), [11](#), [14](#), [21](#), [26](#), [29](#), [30](#), [35](#)
- simulate, DiversityIndex-method
  - (simulate), [30](#)
- stats::dist, [11](#), [28](#)
- stats::p.adjust(), [32](#)
- stats::rmultinom(), [22](#)
- subset, [10](#), [31](#)
  
- test\_diversity, [9](#), [32](#)
- test\_diversity, data.frame-method
  - (test\_diversity), [32](#)
- test\_diversity, matrix-method
  - (test\_diversity), [32](#)
- test\_diversity-method (test\_diversity),  
[32](#)
- turnover, [7](#), [11](#), [14](#), [21](#), [26](#), [29](#), [31](#), [33](#)
- turnover, data.frame-method (turnover),  
[33](#)
- turnover, matrix-method (turnover), [33](#)
- turnover-method (turnover), [33](#)