Package ‘tabula’

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Title Analysis and Visualization of Archaeological Count Data

Version 3.1.0

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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.). It allows to easily visualize count data and statistical thresholds: rank vs abundance plots, heatmaps, Ford (1962) and Bertin (1977) diagrams, etc.

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URL `https://packages.tesselle.org/tabula/`,
`https://github.com/tesselle/tabula`

BugReports `https://github.com/tesselle/tabula/issues`

Depends R (>= 3.5)

Imports arkhe (>= 1.6.0), graphics, grDevices, methods, stats, utils

Suggests folio (>= 1.4.0), khroma (>= 1.12.0), knitr, markdown, rsvg, svglite, tinysnapshot, tinytest

VignetteBuilder knitr

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LazyData true

RoxygenNote 7.3.1

Collate 'AllClasses.R' 'AllGenerics.R' 'coerce.R' 'data.R' 'diversity.R' 'diversity_alpha.R' 'diversity_beta.R' 'diversity_test.R' 'matrigraph.R' 'mutators.R' 'occurrence.R' 'plot_bertin.R' 'plot_diceleraas.R' 'plot_diversity.R' 'plot_ford.R' 'plot_heatmap.R' 'plot_matrix.R' 'plot_rank.R' 'plot_spot.R' 'rarefaction.R' 'reexport.R' 'seriograph.R' 'show.R' 'similarity.R' 'statistics.R' 'subset.R' 'tabula-deprecated.R' 'tabula-internal.R' 'tabula-package.R' 'validate.R' 'zzz.R'

NeedsCompilation no

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R topics documented:

`aves` *Birds Species and Abundances*

Description

A dataset of birds species and abundances in managed and unmanaged areas along the River Wye (UK).

Usage

```
aves
```

Format

A `data.frame` with 2 rows and 26 variables (bird species).

Source

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

See Also

Other datasets: `cantabria`, `pueblo`, `woodland`

`bootstrap` *Bootstrap Estimation*

Description

Samples randomly from the elements of `object` with replacement.

Usage

```
## S4 method for signature 'DiversityIndex'
bootstrap(object, n = 1000, f = NULL)
```

Arguments

`object`	An R object (typically a DiversityIndex object).
`n`	A non-negative `integer` giving the number of bootstrap replications.
`f`	A `function` that takes a single numeric vector (the result of do) as argument.

Value

If `f` is `NULL` (the default), `bootstrap()` returns a named `numeric` vector with the following elements:

`original` The observed value of do applied to `object`.

`mean` The bootstrap estimate of mean of do.

`bias` The bootstrap estimate of bias of do.

`error` he bootstrap estimate of standard error of do.

If `f` is a `function`, `bootstrap()` returns the result of `f` applied to the `n` values of do.

Author(s)

N. Frerebeau

See Also

Other resampling methods: `jackknife()`, `resample()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

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

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

bootstrap(h, f = summary)

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

`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.

See Also

Other datasets: `aves`, `pueblo`, `woodland`

`heterogeneity` *Heterogeneity and Evenness*

Description

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

Usage

```
heterogeneity(object, ...)

evenness(object, ...)

## S4 method for signature 'matrix'
heterogeneity(
  object,
  ...,
  method = c("berger", "boone", "brillouin", "mcintosh", "shannon", "simpson")
)

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

## 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")
)
```

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.

`...`	Further arguments to be passed to internal methods (see below).
`method`	A `character` string specifying the index to be computed (see details). Any unambiguous substring can be given.
`evenness`	A `logical` scalar: should an evenness measure be computed instead of an heterogeneity/dominance index?

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.

Heterogeneity and Evenness Measures

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

`berger` Berger-Parker dominance index.

`boone` Boone heterogeneity measure.

`brillouin` Brillouin diversity index.

`mcintosh` McIntosh dominance index.

`shannon` Shannon-Wiener diversity index.

`simpson` Simpson dominance index.

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.

Author(s)

N. Frerebeau

References

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

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.

See Also

`index_berger()`, `index_boone()`, `index_brillouin()`, `index_mcintosh()`, `index_shannon()`, `index_simpson()`

Other diversity measures: `occurrence()`, `profiles()`, `rarefaction()`, `richness()`, `she()`, `similarity()`, `simulate()`, `turnover()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

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

plot(h)
```

`index_ace` *Abundance-based Coverage Estimator*

Description

Abundance-based Coverage Estimator

Usage

```
index_ace(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`k`	A length-one `numeric` vector giving the threshold between rare/infrequent and abundant/frequent species.
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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.

See Also

Other alpha diversity measures: `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_baxter` *Baxter's Rarefaction*

Description

Baxter's Rarefaction

Usage

```
index_baxter(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`sample`	A length-one `numeric` vector giving the sub-sample size. The size of sample should be smaller than total community size.

Value

A `numeric` vector.

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.

See Also

Other alpha diversity measures: `index_ace()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_berger` *Berger-Parker Dominance Index*

Description

Berger-Parker Dominance Index

Usage

```
index_berger(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Details

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.

This is a *dominance* index, so that an increase in the value of the index accompanies a decrease in diversity.

Value

A `numeric` vector.

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.

See Also

Other alpha diversity measures: `index_ace`(), `index_baxter`(), `index_boone`(), `index_brillouin`(), `index_chao1`(), `index_chao2`(), `index_hurlbert`(), `index_ice`(), `index_margalef`(), `index_mcintosh`(), `index_menhinick`(), `index_shannon`(), `index_simpson`(), `index_squares`()

`index_binomial` *Binomial Co-Occurrence Assessment*

Description

Binomial Co-Occurrence Assessment

Usage

```
index_binomial(x, y, ...)

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

Arguments

`x, y`	A `numeric` vector.
`...`	Currently not used.

Details

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.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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.

See Also

Other beta diversity measures: `index_brainerd`(), `index_bray`(), `index_cody`(), `index_jaccard`(), `index_morisita`(), `index_routledge`, `index_sorenson`(), `index_whittaker`(), `index_wilson`()

`index_boone` *Boone Heterogeneity Measure*

Description

Boone Heterogeneity Measure

Usage

```
index_boone(x, ...)

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

Arguments

`x`	A $m \times p$ `numeric` `matrix` of count data (absolute frequencies, i.e. a contingency table).
`...`	Currently not used.
`j`	An `integer` 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 `numeric` scalar: should missing values (including `NaN`) be removed?

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

Boone, J. L. (1987). Defining and Measuring Midden Catchment. *American Antiquity*, 52(2), 336-45. doi:10.2307/281785.

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.

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_brainerd` *Brainerd-Robinson Quantitative Index*

Description

Brainerd-Robinson Quantitative Index

Usage

```
index_brainerd(x, y, ...)

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

Arguments

`x, y`	A `numeric` vector.
`...`	Currently not used.

Details

A city-block metric of similarity between pairs of samples/cases.

Value

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.

Robinson, W. S. (1951). A Method for Chronologically Ordering Archaeological Deposits. *American Antiquity*, 16(04), 293-301. doi:10.2307/276978.

See Also

Other beta diversity measures: `index_binomial()`, `index_bray()`, `index_cody()`, `index_jaccard()`, `index_morisita()`, `index_routledge`, `index_sorenson()`, `index_whittaker()`, `index_wilson()`

`index_bray` *Sorenson Quantitative Index*

Description

Bray and Curtis modified version of the Sorenson index.

Usage

```
index_bray(x, y, ...)

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

Arguments

`x, y`	A `numeric` vector.
`...`	Currently not used.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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.

See Also

Other beta diversity measures: `index_binomial()`, `index_brainerd()`, `index_cody()`, `index_jaccard()`, `index_morisita()`, `index_routledge`, `index_sorenson()`, `index_whittaker()`, `index_wilson()`

`index_brillouin` *Brillouin Diversity Index.*

Description

Brillouin Diversity Index.

Usage

```
index_brillouin(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`evenness`	A `numeric` scalar: should evenness be computed?
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Details

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.

Value

A `numeric` vector.

Note

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

Author(s)

N. Frerebeau

References

Brillouin, L. (1956). *Science and information theory*. New York: Academic Press.

Laxton, R. R. (1978). The measure of diversity. *Journal of Theoretical Biology*, 70(1), 51-67. doi:10.1016/00225193(78)903028.

Pielou, E. C. (1975). *Ecological Diversity*. New York: Wiley. doi:10.4319/lo.1977.22.1.0174b

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_chao1` *Chao1 Estimator*

Description

Chao1 Estimator

Usage

```
index_chao1(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`unbiased`	A `logical` scalar: should the bias-corrected estimator be used?
`improved`	A `logical` scalar: should the improved estimator be used?
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Value

A `numeric` vector.

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.

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.

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_chao2` *Chao2 Estimator*

Description

Chao2 Estimator

Usage

```
index_chao2(x, ...)

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

Arguments

`x`	A $m \times p$ `matrix` of presence/absence data (incidence).
`...`	Currently not used.
`unbiased`	A `logical` scalar: should the bias-corrected estimator be used?
`improved`	A `logical` scalar: should the improved estimator be used?

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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

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:10.2307/2531532.

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_cody` *Cody Measure*

Description

Cody Measure

Usage

```
index_cody(x, ...)

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

Arguments

`x`	A $m \times p$ `numeric` `matrix` of count data (absolute frequencies, i.e. a contingency table).
`...`	Currently not used.

Details

This assumes that the order of the matrix rows (from 1 to n) follows the progression along the gradient/transect.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

Cody, M. L. (1975). Towards a theory of continental species diversity: Bird distributions over Mediterranean habitat gradients. *In* M. L. Cody & J. M. Diamond (Eds.), *Ecology and Evolution of Communities*. Cambridge, MA: Harvard University Press, p. 214-257.

See Also

Other beta diversity measures: `index_binomial()`, `index_brainerd()`, `index_bray()`, `index_jaccard()`, `index_morisita()`, `index_routledge`, `index_sorenson()`, `index_whittaker()`, `index_wilson()`

`index_hurlbert` *Hurlbert's Rarefaction*

Description

Hurlbert's unbiased estimate of Sander's rarefaction.

Usage

```
index_hurlbert(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`sample`	A length-one `numeric` vector giving the sub-sample size. The size of sample should be smaller than total community size.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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 alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_ice` *Incidence-based Coverage Estimator*

Description

Incidence-based Coverage Estimator

Usage

```
index_ice(x, ...)

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

Arguments

`x`	A $m \times p$ `matrix` of presence/absence data (incidence).
`...`	Currently not used.
`k`	A length-one `numeric` vector giving the threshold between rare/infrequent and abundant/frequent species.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_jaccard` *Jaccard Index*

Description

Jaccard Index

Usage

```
index_jaccard(x, y, ...)

## 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)
```

Arguments

`x, y`	A `numeric` vector.
`...`	Currently not used.

Value

A `numeric` vector.

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 beta diversity measures: `index_binomial()`, `index_brainerd()`, `index_bray()`, `index_cody()`, `index_morisita()`, `index_routledge`, `index_sorenson()`, `index_whittaker()`, `index_wilson()`

`index_margalef` *Margalef Richness Index*

Description

Margalef Richness Index

Usage

```
index_margalef(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_mcintosh` *McIntosh Dominance Index.*

Description

McIntosh Dominance Index.

Usage

```
index_mcintosh(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`evenness`	A `numeric` scalar: should evenness be computed?
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Details

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.

This is a *dominance* index, so that an increase in the value of the index accompanies a decrease in diversity.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_menhinick` *Menhinick Richness Index*

Description

Menhinick Richness Index

Usage

```
index_menhinick(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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.

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_shannon()`, `index_simpson()`, `index_squares()`

`index_morisita` *Morisita-Horn Quantitative Index*

Description

Morisita-Horn Quantitative Index

Usage

```
index_morisita(x, y, ...)

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

Arguments

`x, y`	A `numeric` vector.
`...`	Currently not used.

Value

A `numeric` vector.

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 beta diversity measures: `index_binomial`(), `index_brainerd`(), `index_bray`(), `index_cody`(), `index_jaccard`(), `index_routledge`, `index_sorenson`(), `index_whittaker`(), `index_wilson`()

`index_routledge` *Routledge Measures*

Description

Routledge Measures

Usage

```
index_routledge1(x, ...)

index_routledge2(x, ...)

index_routledge3(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)
```

Arguments

`x`	A $m \times p$ `numeric` `matrix` of count data (absolute frequencies, i.e. a contingency table).
`...`	Currently not used.

Details

This assumes that the order of the matrix rows (from 1 to n) follows the progression along the gradient/transect.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

Routledge, R. D. (1977). On Whittaker's Components of Diversity. *Ecology*, 58(5), 1120-1127. doi:10.2307/1936932.

See Also

Other beta diversity measures: `index_binomial()`, `index_brainerd()`, `index_bray()`, `index_cody()`, `index_jaccard()`, `index_morisita()`, `index_sorenson()`, `index_whittaker()`, `index_wilson()`

`index_shannon` *Shannon-Wiener Diversity Index*

Description

Shannon-Wiener Diversity Index

Usage

```
index_shannon(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`evenness`	A `numeric` scalar: should evenness be computed?
`unbiased`	A `logical` scalar: should the bias-corrected estimator be used?
`ACE`	A `logical` scalar: should the ACE species richness estimator be used in the bias correction?
`base`	A positive `numeric` value specifying the base with respect to which logarithms are computed.
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Details

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.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

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.

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

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.

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_simpson()`, `index_squares()`

`index_simpson` *Simpson Dominance Index*

Description

Simpson Dominance Index

Usage

```
index_simpson(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`evenness`	A `numeric` scalar: should evenness be computed?
`unbiased`	A `logical` scalar: should the bias-corrected estimator be used?
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Details

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 (all taxa are equally present) to 1 (one taxon dominates the community completely).

This is a *dominance* index, so that an increase in the value of the index accompanies a decrease in diversity.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

Simpson, E. H. (1949). Measurement of Diversity. *Nature*, 163(4148), 688-688. doi:10.1038/163688a0.

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_squares()`

`index_sorenson` *Sorenson Qualitative Index*

Description

Sorenson Qualitative Index

Usage

```
index_sorenson(x, y, ...)

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

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

Arguments

`x, y`	A `numeric` vector.
`...`	Currently not used.

Value

A `numeric` vector.

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 beta diversity measures: `index_binomial()`, `index_brainerd()`, `index_bray()`, `index_cody()`, `index_jaccard()`, `index_morisita()`, `index_routledge`, `index_whittaker()`, `index_wilson()`

`index_squares` *Squares Estimator*

Description

Squares Estimator

Usage

```
index_squares(x, ...)

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

Arguments

`x`	A `numeric` vector of count data (absolute frequencies).
`...`	Currently not used.
`na.rm`	A `numeric` scalar: should missing values (including `NaN`) be removed?

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

Alroy, J. (2018). Limits to Species Richness in Terrestrial Communities. *Ecology Letters*, 21(12), 1781-1789. doi:10.1111/ele.13152.

See Also

Other alpha diversity measures: `index_ace()`, `index_baxter()`, `index_berger()`, `index_boone()`, `index_brillouin()`, `index_chao1()`, `index_chao2()`, `index_hurlbert()`, `index_ice()`, `index_margalef()`, `index_mcintosh()`, `index_menhinick()`, `index_shannon()`, `index_simpson()`

`index_whittaker` *Whittaker Measure*

Description

Whittaker Measure

Usage

```
index_whittaker(x, ...)

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

Arguments

`x`	A $m \times p$ `numeric` `matrix` of count data (absolute frequencies, i.e. a contingency table).
`...`	Currently not used.

Details

This assumes that the order of the matrix rows (from 1 to n) follows the progression along the gradient/transect.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

Whittaker, R. H. (1960). Vegetation of the Siskiyou Mountains, Oregon and California. *Ecological Monographs*, 30(3), 279-338. doi:10.2307/1943563.

See Also

Other beta diversity measures: `index_binomial()`, `index_brainerd()`, `index_bray()`, `index_cody()`, `index_jaccard()`, `index_morisita()`, `index_routledge`, `index_sorenson()`, `index_wilson()`

`index_wilson` *Wilson Measure*

Description

Wilson Measure

Usage

```
index_wilson(x, ...)

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

Arguments

`x`	A $m \times p$ `numeric` `matrix` of count data (absolute frequencies, i.e. a contingency table).
`...`	Currently not used.

Details

This assumes that the order of the matrix rows (from 1 to n) follows the progression along the gradient/transect.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

References

Wilson, M. V., & Shmida, A. (1984). Measuring Beta Diversity with Presence-Absence Data. *The Journal of Ecology*, 72(3), 1055-1064. doi:10.2307/2259551.

See Also

Other beta diversity measures: `index_binomial()`, `index_brainerd()`, `index_bray()`, `index_cody()`, `index_jaccard()`, `index_morisita()`, `index_routledge`, `index_sorenson()`, `index_whittaker()`

`jackknife` *Jackknife Estimation*

Description

Jackknife Estimation

Usage

```
## S4 method for signature 'DiversityIndex'
jackknife(object, f = NULL)
```

Arguments

`object`	An R object (typically a DiversityIndex object).
`f`	A `function` that takes a single numeric vector (the leave-one-out values of do) as argument.

Value

If `f` is `NULL` (the default), `jackknife()` returns a named `numeric` vector with the following elements:

`original` The observed value of do applied to `object`.

`mean` The jackknife estimate of mean of do.

`bias` The jackknife estimate of bias of do.

`error` he jackknife estimate of standard error of do.

If `f` is a `function`, `jackknife()` returns the result of `f` applied to the leave-one-out values of do.

Author(s)

N. Frerebeau

See Also

Other resampling methods: `bootstrap()`, `resample()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

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

## Jackknife resampling
jackknife(h)
```

```
jackknife(h, f = summary)
```

`matrigraph` *Matrigraph*

Description

- `matrigraph()` produces a heatmap highlighting the deviations from independence.
- `pvi()` computes for each cell of a numeric matrix the percentage to the column theoretical independence value.

Usage

```
matrigraph(object, ...)

pvi(object, ...)

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

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

## S4 method for signature 'matrix'
matrigraph(object, reverse = FALSE, axes = TRUE, ...)

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

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table).
`...`	Currently not used.
`reverse`	A `logical` scalar: should negative deviations be centered (see details)?
`axes`	A `logical` scalar: should axes be drawn on the plot? It will omit labels where they would abut or overlap previously drawn labels.

Details

PVI (in french "pourcentages de valeur d'indépendance") 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 χ^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).

`matrigraph()` displays the deviations from independence:

- If the PVI is equal to 1 (statistical independence), the cell of the matrix is filled in grey.
- If the PVI is less than 1 (negative deviation from independence), the size of the grey square is proportional to the PVI (the white margin thus represents the fraction of negative deviation).
- If the PVI is greater than 1 (positive deviation), a black square representing the fraction of positive deviations is superimposed. For large positive deviations (PVI greater than 2), the cell in filled in black.

If `reverse` is `TRUE`, the fraction of negative deviations is displayed as a white square.

Value

- `matrigraph()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).
- `pvi()` returns a `numeric` `matrix`.

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_heatmap()`

Other plot methods: `plot_bertin()`, `plot_diceleraas()`, `plot_diversity`, `plot_ford()`, `plot_heatmap()`, `plot_rank()`, `plot_rarefaction`, `plot_spot()`, `seriograph()`

Examples

```
## Data from Desachy 2004
data("compiegne", package = "folio")

## Matrigraph
matrigraph(compiegne)
matrigraph(compiegne, reverse = TRUE)

## Compute PVI
counts_pvi <- pvi(compiegne)
plot_heatmap(counts_pvi, col = khroma::color("iridescent")(12))
```

`mutators` *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'
labels(object, ...)

## S4 method for signature 'RarefactionIndex'
labels(object, ...)

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

Arguments

`object, x`	An R object from which to get or set element(s).
`...`	Currently not used.

Value

- `labels()` returns a suitable set of labels from an object for use in printing or plotting.

Author(s)

N. Frerebeau

`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 $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	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()`, `profiles()`, `rarefaction()`, `richness()`, `she()`, `similarity()`, `simulate()`, `turnover()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

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

`plot_bertin` *Bertin Diagram*

Description

Plots a Bertin diagram.

Usage

```
plot_bertin(object, ...)

## S4 method for signature 'matrix'
plot_bertin(
  object,
  threshold = NULL,
  freq = FALSE,
  margin = 1,
  col = c("white", "black"),
  flip = TRUE,
  axes = TRUE,
  ...
)

## S4 method for signature 'data.frame'
plot_bertin(
  object,
  threshold = NULL,
  freq = FALSE,
  margin = 1,
  col = c("white", "black"),
  flip = TRUE,
  axes = TRUE,
  ...
)
```

Arguments

`object`	A $m \times p$ numeric `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table).
`...`	Currently not used.
`threshold`	A `function` that takes a numeric vector as argument and returns a numeric threshold value (see below). If `NULL` (the default), no threshold is computed. Only used if `freq` is `FALSE`.
`freq`	A `logical` scalar indicating whether conditional proportions given `margins` should be used (i.e. entries of `object`, divided by the appropriate marginal sums).

`margin`	An `integer` vector giving the margins to split by: `1` indicates individuals/rows (the default), `2` indicates variables/columns. Only used if `freq` is `TRUE`.
`col`	A vector of colors.
`flip`	A `logical` scalar: should `x` and `y` axis be flipped? Defaults to `TRUE`.
`axes`	A `logical` scalar: should axes be drawn on the plot? It will omit labels where they would abut or overlap previously drawn labels.

Value

`plot_bertin()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `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."

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.

See Also

Other plot methods: `matrigraph()`, `plot_diceleraas()`, `plot_diversity`, `plot_ford()`, `plot_heatmap()`, `plot_rank()`, `plot_rarefaction`, `plot_spot()`, `seriograph()`

Examples

```
## Data from Lipo et al. 2015
data("mississippi", package = "folio")

## Plot a Bertin diagram...
## ...without threshold
plot_bertin(mississippi)

## ...with the variable mean as threshold
plot_bertin(mississippi, threshold = mean)

## Plot conditional proportions
plot_bertin(mississippi, freq = TRUE, margin = 1)
```

```
plot_bertin(mississippi, freq = TRUE, margin = 2)
```

`plot_diceleraas` *Dice-Leraas Diagram*

Description

Plots a Dice-Leraas diagram.

Usage

```
plot_diceleraas(object, ...)

## S4 method for signature 'matrix'
plot_diceleraas(
  object,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = FALSE,
  panel.first = NULL,
  panel.last = NULL,
  ...
)

## S4 method for signature 'data.frame'
plot_diceleraas(
  object,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = FALSE,
  panel.first = NULL,
  panel.last = NULL,
  ...
)
```

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Further graphical parameters.
`main`	A `character` string giving a main title for the plot.

`sub`	A `character` string giving a subtitle for the plot.
`ann`	A `logical` scalar: should the default annotation (title and x, y and z axis labels) appear on the plot?
`axes`	A `logical` scalar: should axes be drawn on the plot?
`frame.plot`	A `logical` scalar: should a box be drawn around the plot?
`panel.first`	An an `expression` to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
`panel.last`	An `expression` to be evaluated after plotting has taken place but before the axes, title and box are added.

Details

In a Dice-Leraas diagram, the horizontal line represents the range of data (min-max) and the small vertical line indicates the mean. The black rectangle is twice the standard error on the mean, while the white rectangle is one standard deviation on either side of the mean.

Value

`plot_diceleraas()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).

Author(s)

N. Frerebeau

References

Dice, L. R., & Leraas, H. J. (1936). A Graphic Method for Comparing Several Sets of Measurements. *Contributions from the Laboratory of Vertebrate Genetics*, 3: 1-3.

Hubbs, C. L., & C. Hubbs (1953). An Improved Graphical Analysis and Comparison of Series of Samples. *Systematic Biology*, 2(2): 49-56. doi:10.2307/sysbio/2.2.49.

Simpson, G. G., Roe, A., & Lewontin, R. C. *Quantitative Zoology*. New York: Harcourt, Brace and Company, 1960.

See Also

Other plot methods: `matrigraph()`, `plot_bertin()`, `plot_diversity`, `plot_ford()`, `plot_heatmap()`, `plot_rank()`, `plot_rarefaction`, `plot_spot()`, `seriograph()`

Examples

```
## Data from Desachy 2004
data("compiegne", package = "folio")

## Plot a Dice-Leraas diagram
plot_diceleraas(compiegne)
```

plot_diversity *Diversity Plot*

Description

Diversity Plot

Usage

```
## S4 method for signature 'DiversityIndex,missing'
plot(
  x,
  log = "x",
  col.mean = "#DDAA33",
  col.interval = "#004488",
  lty.mean = "solid",
  lty.interval = "dashed",
  lwd.mean = 1,
  lwd.interval = 1,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = axes,
  panel.first = NULL,
  panel.last = NULL,
  ...
)
```

Arguments

`x`	A DiversityIndex object to be plotted.
`log`	A `character` string indicating which axes should be in log scale. Defaults to `x`.
`col.mean, col.interval`	A `character` string specifying the color of the lines.
`lty.mean, lty.interval`	A `character` string or `numeric` value specifying the line types.
`lwd.mean, lwd.interval`	A non-negative `numeric` value specifying the line widths.
`main`	A `character` string giving a main title for the plot.
`sub`	A `character` string giving a subtitle for the plot.
`ann`	A `logical` scalar: should the default annotation (title and x, y and z axis labels) appear on the plot?
`axes`	A `logical` scalar: should axes be drawn on the plot?
`frame.plot`	A `logical` scalar: should a box be drawn around the plot?

`panel.first`	An an `expression` to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
`panel.last`	An `expression` to be evaluated after plotting has taken place but before the axes, title and box are added.
`...`	Further graphical parameters to be passed to `graphics::points()`, particularly, `cex`, `col` and `pch`.

Value

`plot()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `x`).

Author(s)

N. Frerebeau

See Also

Other plot methods: `matrigraph()`, `plot_bertin()`, `plot_diceleraas()`, `plot_ford()`, `plot_heatmap()`, `plot_rank()`, `plot_rarefaction`, `plot_spot()`, `seriograph()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
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_ford` *Ford Diagram*

Description

Plots a Ford (battleship curve) diagram.

Usage

```
plot_ford(object, ...)

## S4 method for signature 'matrix'
plot_ford(
  object,
  weights = FALSE,
  EPPM = FALSE,
  fill = "darkgrey",
  border = NA,
  axes = TRUE,
  ...
)

## S4 method for signature 'data.frame'
plot_ford(
  object,
  weights = FALSE,
  EPPM = FALSE,
  fill = "darkgrey",
  border = NA,
  axes = TRUE,
  ...
)
```

Arguments

`object`	A $m \times p$ numeric `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table).
`...`	Currently not used.
`weights`	A `logical` scalar: should the row sums be displayed?
`EPPM`	A `logical` scalar: should the EPPM be drawn? See `seriograph()`.
`fill`	The color for filling the bars.
`border`	The color to draw the borders.
`axes`	A `logical` scalar: should axes be drawn on the plot? It will omit labels where they would abut or overlap previously drawn labels.

Value

`plot_ford()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).

Author(s)

N. Frerebeau

References

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

See Also

Other plot methods: `matrigraph()`, `plot_bertin()`, `plot_diceleraas()`, `plot_diversity`, `plot_heatmap()`, `plot_rank()`, `plot_rarefaction`, `plot_spot()`, `seriograph()`

Examples

```
## Data from Lipo et al. 2015
data("mississippi", package = "folio")

## Plot a Ford diagram
plot_ford(mississippi)

plot_ford(mississippi, weights = TRUE)
```

`plot_heatmap` *Heatmap*

Description

Plots a heatmap.

Usage

```
plot_heatmap(object, ...)

## S4 method for signature 'matrix'
plot_heatmap(
  object,
  col = grDevices::hcl.colors(12, "YlOrBr", rev = TRUE),
  diag = TRUE,
  upper = TRUE,
  lower = TRUE,
  freq = FALSE,
  margin = 1,
  fixed_ratio = TRUE,
  axes = TRUE,
  legend = TRUE,
  ...
)

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

```
  object,
  col = grDevices::hcl.colors(12, "YlOrBr", rev = TRUE),
  diag = TRUE,
  upper = TRUE,
  lower = TRUE,
  freq = FALSE,
  margin = 1,
  fixed_ratio = TRUE,
  axes = TRUE,
  legend = TRUE,
  ...
)

## S4 method for signature 'dist'
plot_heatmap(
  object,
  col = grDevices::hcl.colors(12, "YlOrBr", rev = TRUE),
  diag = FALSE,
  upper = FALSE,
  lower = !upper,
  axes = TRUE,
  legend = TRUE,
  ...
)
```

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table).
`...`	Currently not used.
`col`	A vector of colors.
`diag`	A `logical` scalar indicating whether the diagonal of the matrix should be plotted. Only used if `object` is a symmetric matrix.
`upper`	A `logical` scalar indicating whether the upper triangle of the matrix should be plotted. Only used if `object` is a symmetric matrix.
`lower`	A `logical` scalar indicating whether the lower triangle of the matrix should be plotted. Only used if `object` is a symmetric matrix.
`freq`	A `logical` scalar indicating whether conditional proportions given `margins` should be used (i.e. entries of `object`, divided by the appropriate marginal sums).
`margin`	An `integer` vector giving the margins to split by: `1` indicates individuals/rows (the default), `2` indicates variables/columns. Only used if `freq` is `TRUE`.
`fixed_ratio`	A `logical` scalar: should a fixed aspect ratio (1) be used?
`axes`	A `logical` scalar: should axes be drawn on the plot? It will omit labels where they would abut or overlap previously drawn labels.
`legend`	A `logical` scalar: should a legend be displayed?

Value

`plot_heatmap()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).

Author(s)

N. Frerebeau

See Also

Other plot methods: `matrigraph()`, `plot_bertin()`, `plot_diceleraas()`, `plot_diversity`, `plot_ford()`, `plot_rank()`, `plot_rarefaction`, `plot_spot()`, `seriograph()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

## Plot raw data
plot_heatmap(cantabria)

## Plot conditional proportions
plot_heatmap(cantabria, freq = TRUE, margin = 1)
plot_heatmap(cantabria, freq = TRUE, margin = 2)
```

`plot_rank` *Rank Plot*

Description

Plots a rank *vs* relative abundance diagram.

Usage

```
plot_rank(object, ...)

## S4 method for signature 'matrix'
plot_rank(
  object,
  log = NULL,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = axes,
  panel.first = NULL,
  panel.last = NULL,
  legend = list(x = "topright"),
```

```
  ...
)

## S4 method for signature 'data.frame'
plot_rank(
  object,
  log = NULL,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = axes,
  panel.first = NULL,
  panel.last = NULL,
  legend = list(x = "topright"),
  ...
)
```

Arguments

`object`	A $m \times p$ numeric `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Further graphical parameters.
`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).
`main`	A `character` string giving a main title for the plot.
`sub`	A `character` string giving a subtitle for the plot.
`ann`	A `logical` scalar: should the default annotation (title and x, y and z axis labels) appear on the plot?
`axes`	A `logical` scalar: should axes be drawn on the plot?
`frame.plot`	A `logical` scalar: should a box be drawn around the plot?
`panel.first`	An an `expression` to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
`panel.last`	An `expression` to be evaluated after plotting has taken place but before the axes, title and box are added.
`legend`	A `list` of additional arguments to be passed to `graphics::legend()`; names of the list are used as argument names. If `NULL`, no legend is displayed.

Value

`plot_rank()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).

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 plot methods: `matrigraph`(), `plot_bertin`(), `plot_diceleraas`(), `plot_diversity`, `plot_ford`(), `plot_heatmap`(), `plot_rarefaction`, `plot_spot`(), `seriograph`()

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

## Plot rank vs abundance
plot_rank(cantabria)

## Change graphical parameters
col <- khroma::color("bright")(5)
plot_rank(cantabria, col = col, pch = 15:19, lty = 2)
```

`plot_rarefaction` *Rarefaction Plot*

Description

Rarefaction Plot

Usage

```
## S4 method for signature 'RarefactionIndex,missing'
plot(
  x,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = axes,
  panel.first = NULL,
  panel.last = NULL,
  legend = list(x = "topleft"),
  ...
)
```

Arguments

`x`	A RarefactionIndex object to be plotted.
`main`	A `character` string giving a main title for the plot.
`sub`	A `character` string giving a subtitle for the plot.
`ann`	A `logical` scalar: should the default annotation (title and x, y and z axis labels) appear on the plot?
`axes`	A `logical` scalar: should axes be drawn on the plot?
`frame.plot`	A `logical` scalar: should a box be drawn around the plot?
`panel.first`	An an `expression` to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
`panel.last`	An `expression` to be evaluated after plotting has taken place but before the axes, title and box are added.
`legend`	A `list` of additional arguments to be passed to `graphics::legend()`; names of the list are used as argument names. If `NULL`, no legend is displayed.
`...`	Further graphical parameters to be passed to `graphics::lines()`.

Value

`plot()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `x`).

Author(s)

N. Frerebeau

See Also

Other plot methods: `matrigraph()`, `plot_bertin()`, `plot_diceleraas()`, `plot_diversity`, `plot_ford()`, `plot_heatmap()`, `plot_rank()`, `plot_spot()`, `seriograph()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

## Replicate fig. 3 from Baxter 2011
rare <- rarefaction(cantabria, sample = 23, method = "baxter")
plot(rare, panel.first = graphics::grid())

## Change graphical parameters
col <- khroma::color("bright")(5)
plot(rare, col = col, lty = 1:5)
```

`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"),
  col = grDevices::hcl.colors(12, "YlOrBr", rev = TRUE),
  diag = TRUE,
  upper = TRUE,
  lower = TRUE,
  freq = FALSE,
  margin = 1,
  axes = TRUE,
  legend = TRUE,
  ...
)

## S4 method for signature 'data.frame'
plot_spot(
  object,
  type = c("ring", "plain"),
  col = grDevices::hcl.colors(12, "YlOrBr", rev = TRUE),
  diag = TRUE,
  upper = TRUE,
  lower = TRUE,
  freq = FALSE,
  margin = 1,
  axes = TRUE,
  legend = TRUE,
  ...
)

## S4 method for signature 'dist'
plot_spot(
  object,
  type = c("ring", "plain"),
  col = grDevices::hcl.colors(12, "YlOrBr", rev = TRUE),
  diag = FALSE,
```

```
    upper = FALSE,
    lower = !upper,
    axes = TRUE,
    legend = TRUE,
    ...
  )
```

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table).
`...`	Currently not used.
`type`	A `character` string specifying the graph to be plotted. It must be one of "`ring`" (the default) or "`plain`". Any unambiguous substring can be given.
`col`	A vector of colors.
`diag`	A `logical` scalar indicating whether the diagonal of the matrix should be plotted. Only used if `object` is a symmetric matrix.
`upper`	A `logical` scalar indicating whether the upper triangle of the matrix should be plotted. Only used if `object` is a symmetric matrix.
`lower`	A `logical` scalar indicating whether the lower triangle of the matrix should be plotted. Only used if `object` is a symmetric matrix.
`freq`	A `logical` scalar indicating whether conditional proportions given `margins` should be used (i.e. entries of `object`, divided by the appropriate marginal sums).
`margin`	An `integer` vector giving the margins to split by: `1` indicates individuals/rows (the default), `2` indicates variables/columns. Only used if `freq` is `TRUE`.
`axes`	A `logical` scalar: should axes be drawn on the plot? It will omit labels where they would abut or overlap previously drawn labels.
`legend`	A `logical` scalar: should a legend be displayed?

Details

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

Value

`plot_spot()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).

Note

Adapted from Dan Gopstein's original idea.

Author(s)

N. Frerebeau

See Also

Other plot methods: `matrigraph()`, `plot_bertin()`, `plot_diceleraas()`, `plot_diversity`, `plot_ford()`, `plot_heatmap()`, `plot_rank()`, `plot_rarefaction`, `seriograph()`

Examples

```
## Data from Huntley 2004, 2008
data("pueblo")

## Plot spot diagram of count data
plot_spot(pueblo, type = "ring")
plot_spot(pueblo, type = "plain")

## Plot conditional proportions
plot_spot(pueblo, freq = TRUE, margin = 1)
plot_spot(pueblo, freq = TRUE, margin = 2)
```

`profiles` *Diversity Profiles*

Description

Diversity Profiles

Usage

```
profiles(object, ...)

## S4 method for signature 'matrix'
profiles(
  object,
  alpha = seq(from = 0, to = 4, by = 0.04),
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = axes,
  panel.first = NULL,
  panel.last = NULL,
  legend = list(x = "topright"),
  ...
)

## S4 method for signature 'data.frame'
profiles(
  object,
  alpha = seq(from = 0, to = 4, by = 0.04),
```

```
    main = NULL,
    sub = NULL,
    ann = graphics::par("ann"),
    axes = TRUE,
    frame.plot = axes,
    panel.first = NULL,
    panel.last = NULL,
    legend = list(x = "topright"),
    ...
)
```

Arguments

`object`	A $m \times p$ numeric `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Further graphical parameters to be passed to `graphics::lines()`
`alpha`	A `numeric` vector giving the values of the alpha parameter.
`main`	A `character` string giving a main title for the plot.
`sub`	A `character` string giving a subtitle for the plot.
`ann`	A `logical` scalar: should the default annotation (title and x, y and z axis labels) appear on the plot?
`axes`	A `logical` scalar: should axes be drawn on the plot?
`frame.plot`	A `logical` scalar: should a box be drawn around the plot?
`panel.first`	An an `expression` to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
`panel.last`	An `expression` to be evaluated after plotting has taken place but before the axes, title and box are added.
`legend`	A `list` of additional arguments to be passed to `graphics::legend()`; names of the list are used as argument names. If `NULL`, no legend is displayed.

Details

If the profiles cross, the diversities are non-comparable across samples.

Value

`profiles()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).

Author(s)

N. Frerebeau

References

Tóthmérész, B. (1995). Comparison of Different Methods for Diversity Ordering. *Journal of Vegetation Science*, 6(2), 283-290. doi:10.2307/3236223.

See Also

Other diversity measures: `heterogeneity()`, `occurrence()`, `rarefaction()`, `richness()`, `she()`, `similarity()`, `simulate()`, `turnover()`

Examples

```
## Replicate fig. 1 of Tóthmérész 1995
spc <- matrix(
  data = c(33, 29, 28, 5, 5, 0, 0, 42, 30, 10,
           8, 5, 5, 0, 32, 21, 16, 12, 9, 6, 4),
  nrow = 3, byrow = TRUE, dimnames = list(c("A", "B", "C"), NULL)
)

profiles(spc)
```

`pueblo` *Pueblo IV Period Ceramics*

Description

A dataset of ceramic counts from the Zuni region.

Usage

```
pueblo
```

Format

A `data.frame` with 9 rows and 5 variables (compositional groups).

Source

Huntley, D. L. (2004). *Interaction, Boundaries, and Identities: A Multiscalar Approach to the Organizational Scale of Pueblo IV Zuni Society*. Ph.D. Dissertation, Arizona State University.

Huntley, D. L. (2022). *Ancestral Zuni Glaze-Decorated Pottery: Viewing Pueblo IV Regional Organization through Ceramic Production and Exchange*. Anthropological Papers of the University of Arizona 72. Tucson: University of Arizona Press. doi:10.2307/j.ctv2ngx5n8.

See Also

Other datasets: `aves`, `cantabria`, `woodland`

`rarefaction` *Rarefaction*

Description

Rarefaction

Usage

```
rarefaction(object, ...)

## 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)
```

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Currently not used.
`sample`	A length-one `numeric` vector giving the sub-sample size. The size of sample should be smaller than total community size.
`method`	A `character` string or vector of strings specifying the index to be computed (see details). Any unambiguous substring can be given.
`step`	An `integer` giving the increment of the sample size.

Value

A RarefactionIndex object.

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

See Also

`index_baxter()`, `index_hurlbert()`, `plot()`

Other diversity measures: `heterogeneity()`, `occurrence()`, `profiles()`, `richness()`, `she()`, `similarity()`, `simulate()`, `turnover()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

## Replicate fig. 3 from Baxter 2011
rare <- rarefaction(cantabria, sample = 23, method = "baxter")
plot(rare, panel.first = graphics::grid())

## Change graphical parameters
col <- khroma::color("bright")(5)
plot(rare, col = col, lty = 1:5)
```

`resample` *Resample*

Description

Simulates observations from a multinomial distribution.

Usage

```
resample(object, ...)

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

Arguments

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

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`.

Author(s)

N. Frerebeau

See Also

`stats::rmultinom()`

Other resampling methods: `bootstrap()`, `jackknife()`

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` *Richness*

Description

- `richness()` computes sample richness.
- `composition()` computes asymptotic species richness.

Usage

```
richness(object, ...)

composition(object, ...)

## 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", "squares", "chao2", "ice"))

## S4 method for signature 'data.frame'
composition(object, ..., method = c("chao1", "ace", "squares", "chao2", "ice"))
```

Arguments

`object`	A $m \times p$ numeric `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Further arguments to be passed to internal methods (see below).
`method`	A `character` string or vector of strings specifying the index to be computed (see details). Any unambiguous substring can be given.

Value

- `richness()` returns a RichnessIndex object.
- `composition()` returns a CompositionIndex object.

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` 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.

`squares` Squares 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

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

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

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.

See Also

`index_margalef()`, `index_menhinick()`, `index_ace()`, `index_chao1()`, `index_squares()`, `index_ice()`, `index_chao2()`

`plot()`

Other diversity measures: `heterogeneity()`, `occurrence()`, `profiles()`, `rarefaction()`, `she()`, `similarity()`, `simulate()`, `turnover()`

Examples

```
## 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))

## Margalef and Menhinick index
richness(trap, method = "margalef") # 2.55 1.88
richness(trap, method = "menhinick") # 1.95 1.66

## 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
)

## Chao1-type estimators (asymptotic species richness)
composition(brazil, method = c("chao1"), unbiased = FALSE) # 461.625
composition(brazil, method = c("ace"), k = 10) # 445.822
```

`seriograph` *Seriograph*

Description

- `seriograph()` produces a Ford diagram highlighting the relationships between rows and columns.
- `eppm()` computes for each cell of a numeric matrix the positive difference from the column mean percentage.

Usage

```
seriograph(object, ...)

eppm(object, ...)

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

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

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

```
  object,
  weights = FALSE,
  fill = "darkgrey",
  border = NA,
  axes = TRUE,
  ...
)

## S4 method for signature 'data.frame'
seriograph(
  object,
  weights = FALSE,
  fill = "darkgrey",
  border = NA,
  axes = TRUE,
  ...
)
```

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table).
`...`	Currently not used.
`weights`	A `logical` scalar: should the row sums be displayed?
`fill`	The color for filling the bars.
`border`	The color to draw the borders.
`axes`	A `logical` scalar: should axes be drawn on the plot? It will omit labels where they would abut or overlap previously drawn labels.

Details

The 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).

`seriograph()` superimposes the frequencies (grey) and EPPM values (black) for each row-column pair in a Ford diagram.

Value

- `seriograph()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).
- `eppm()` returns a `numeric` `matrix`.

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()`

Other plot methods: `matrigraph()`, `plot_bertin()`, `plot_diceleraas()`, `plot_diversity`, `plot_ford()`, `plot_heatmap()`, `plot_rank()`, `plot_rarefaction`, `plot_spot()`

Examples

```
## Data from Desachy 2004
data("compiegne", package = "folio")

## Seriograph
seriograph(compiegne)
seriograph(compiegne, weights = TRUE)

## Compute EPPM
counts_eppm <- eppm(compiegne)
plot_heatmap(counts_eppm, col = khroma::color("YlOrBr")(12))
```

---

she *SHE Analysis*

Description

SHE Analysis

Usage

```
she(object, ...)

## S4 method for signature 'matrix'
she(
  object,
  unbiased = FALSE,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = axes,
  panel.first = NULL,
  panel.last = NULL,
  legend = list(x = "right"),
  ...
```

```
)

## S4 method for signature 'data.frame'
she(
  object,
  unbiased = FALSE,
  main = NULL,
  sub = NULL,
  ann = graphics::par("ann"),
  axes = TRUE,
  frame.plot = axes,
  panel.first = NULL,
  panel.last = NULL,
  legend = list(x = "right"),
  ...
)
```

Arguments

`object`	A $m \times p$ numeric `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Further graphical parameters to be passed to `graphics::lines()` and `graphics::points()`.
`unbiased`	A `logical` scalar: should the bias-corrected estimator be used (see `index_shannon()`)?
`main`	A `character` string giving a main title for the plot.
`sub`	A `character` string giving a subtitle for the plot.
`ann`	A `logical` scalar: should the default annotation (title and x, y and z axis labels) appear on the plot?
`axes`	A `logical` scalar: should axes be drawn on the plot?
`frame.plot`	A `logical` scalar: should a box be drawn around the plot?
`panel.first`	An an `expression` to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
`panel.last`	An `expression` to be evaluated after plotting has taken place but before the axes, title and box are added.
`legend`	A `list` of additional arguments to be passed to `graphics::legend()`; names of the list are used as argument names. If `NULL`, no legend is displayed.

Details

If samples are taken along a gradient or stratigraphic section, breaks in the curve may be used to infer discontinuities.

This assumes that the order of the matrix rows (from 1 to n) follows the progression along the gradient/transect.

Value

`she()` is called for its side-effects: it results in a graphic being displayed (invisibly returns `object`).

Author(s)

N. Frerebeau

References

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

Hayek, L.-A. C. & Buzas, M. A. (2010). *Surveying Natural Populations: Quantitative Tools for Assessing Biodiversity*. Second edition. New York: Columbia University Press.

See Also

Other diversity measures: `heterogeneity()`, `occurrence()`, `profiles()`, `rarefaction()`, `richness()`, `similarity()`, `simulate()`, `turnover()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
data("cantabria")

## SHE analysis
she(cantabria)
```

`similarity` *Similarity*

Description

Similarity

Usage

```
similarity(object, ...)

## 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")
)
```

Arguments

`object`	A $m \times p$ `numeric` `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Currently not used.
`method`	A `character` string specifying the method to be used (see details). Any unambiguous substring can be given.

Details

β-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.

`brainerd` Brainerd-Robinson quantitative index.

`bray` Sorenson quantitative index.

`jaccard` Jaccard qualitative index.

`morisita` Morisita-Horn quantitative index.

`sorenson` Sorenson qualitative index.

Value

A stats::dist object.

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

`index_binomial()`, `index_brainerd()`, `index_bray()`, `index_jaccard()`, `index_morisita()`, `index_sorenson()`

Other diversity measures: `heterogeneity()`, `occurrence()`, `profiles()`, `rarefaction()`, `richness()`, `she()`, `simulate()`, `turnover()`

Examples

```
## Data from Huntley 2004, 2008
data("pueblo")

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

## Data from Magurran 1988, p. 166
data("aves")

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

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

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

# Morisita-Horn measure (count data)
similarity(aves, "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 DiversityIndex object.
`n`	A non-negative `integer` giving the number of bootstrap replications.
`step`	An `integer` giving the increment of the sample size.

`interval`	A `character` 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 `numeric` vector giving the confidence level.
`progress`	A `logical` 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()`, `resample()`

Other diversity measures: `heterogeneity()`, `occurrence()`, `profiles()`, `rarefaction()`, `richness()`, `she()`, `similarity()`, `turnover()`

Examples

```
## Data from Conkey 1980, Kintigh 1989
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)
```

`test` *Diversity Test*

Description

Compares Shannon/Simpson diversity between samples.

Usage

```
test_shannon(x, y, ...)

test_simpson(x, y, ...)

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

## S4 method for signature 'matrix,missing'
test_shannon(x, adjust = "holm", ...)

## S4 method for signature 'data.frame,missing'
test_shannon(x, adjust = "holm", ...)

## S4 method for signature 'numeric,numeric'
test_simpson(x, y, adjust = "holm", ...)

## S4 method for signature 'matrix,missing'
test_simpson(x, adjust = "holm", ...)

## S4 method for signature 'data.frame,missing'
test_simpson(x, adjust = "holm", ...)
```

Arguments

`x, y`	A `numeric` vector, a $m \times p$ `matrix` or `data.frame` of count data (absolute frequencies giving the number of individuals for each category, i.e. a contingency table). A `data.frame` will be coerced to a `numeric` `matrix` via `data.matrix()`.
`...`	Further arguments to be passed to internal methods.
`adjust`	A `character` string specifying the method for adjusting p values (see `stats::p.adjust()`).

Value

If `x` and `y` are `numeric` vectors, returns a `list` containing the following components:

`statistic` The value of the t-statistic.

`parameter` The degrees of freedom for the t-statistic.

`p.value` The p-value for the test.

If `x` is a `matrix` or a `data.frame`, returns a table of adjusted p-values in lower triangular form.

Functions

- `test_shannon(x = matrix, y = missing)`: Produces two sided pairwise comparisons.
- `test_shannon(x = data.frame, y = missing)`: Produces two sided pairwise comparisons.
- `test_simpson(x = matrix, y = missing)`: Produces two sided pairwise comparisons.
- `test_simpson(x = data.frame, y = missing)`: Produces two sided pairwise comparisons.

Author(s)

N. Frerebeau

References

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

Examples

```
## Data from Magurran 1988, p. 145-149
oakwood <- c(35, 26, 25, 21, 16, 11, 6, 5, 3, 3,
             3, 3, 3, 2, 2, 2, 1, 1, 1, 1, 0, 0)
spruce <- c(30, 30, 3, 65, 20, 11, 0, 4, 2, 14,
            0, 3, 9, 0, 0, 5, 0, 0, 0, 0, 1, 1)

test_shannon(oakwood, spruce)
test_simpson(oakwood, spruce)

## Data from Conkey 1980, Kintigh 1989
data("cantabria")

test_shannon(cantabria)
test_simpson(cantabria)
```

`turnover` *Turnover*

Description

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

Usage

```
turnover(object, ...)

## 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")
)
```

Arguments

`object`	A $m \times p$ numeric `matrix` or `data.frame` of count data or incidence data. A `data.frame` will be coerced to a numeric matrix via `data.matrix()`.
`...`	Further arguments to be passed to internal methods.
`method`	A `character` 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 (β-diversity) on qualitative (presence/absence) data:

`cody` Cody measure.

`routledge1` Routledge first measure.

`routledge2` Routledge second measure.

`routledge3` Routledge third measure (exponential form of the second measure).

`whittaker` Whittaker measure.

`wilson` Wilson measure.

This assumes that the order of the matrix rows (from 1 to n) follows the progression along the gradient/transect.

Value

A `numeric` vector.

Author(s)

N. Frerebeau

See Also

`index_cody()`, `index_routledge1()`, `index_routledge2()`, `index_routledge3()`, `index_whittaker()`, `index_wilson()`

Other diversity measures: `heterogeneity()`, `occurrence()`, `profiles()`, `rarefaction()`, `richness()`, `she()`, `similarity()`, `simulate()`

Examples

```
## Data from Magurran 1988, p. 162
data("woodland")

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

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

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

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

`woodland` *Trees Incidences*

Description

A dataset of presence or absence of trees in six (10 x 10 m) quadarts along a transect through a deciduous woodland.

Usage

```
woodland
```

Format

A `data.frame` with 6 rows (quadarts) and 6 variables (tree species).

Source

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

See Also

Other datasets: `aves`, `cantabria`, `pueblo`

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