Package ‘rtk’

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Description Rarefy data, calculate diversity and plot the results.
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LinkingTo Rcpp
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Description

Rarefy data, calculate diversity and plot the results.

Details

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- collectors.curve
- get.diversity
- plot
- rtk
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- Rarefaction Tool Kit

This package might be used to rarefy data and compute diversity measures. Rarefied tables can be returned to R and be further processed.

Author(s)

Paul Saary, Falk Hildebrand

Maintainer: Paul Saary <rtk@paulsaary.de>

References

collectors.curve

See Also

rtk, plot.rtk, collectors.curve

Description

Collectors curves visualize the richness gained by picking more samples.

Usage

collectors.curve(x, y = NULL, col = 1, times = 10, bin = 3, add = FALSE,
                 ylim = NULL, xlim = NULL, doPlot = TRUE, rareD = NULL,
                 cls = NULL, pch = 20, col2 = NULL, accumOrder = NULL, ...)

Arguments

x Input a rarefaction object with one matrix and one depth or dataframe/matrix or the output of collectors.curve itself
y secondary input matrix for comparative plots
col fill color of the boxplots (set to c(0) for no color)
times Number of times the sampling of samples should be performed
bin Number of samples to be added each step. Useful to adjust for a quick glance.
add add the plot to an existing plot?
ylim Limits for Y-scale
xlim Limits for X-scale
doPlot should this function plot the collectors curve, or just return an object that can be plotted later with this function?
rareD Depth to which rarefy the dataset using rtk
cls vector describing the class of each input sample
pch Plotting symbols
col2 Color for the border of the boxplot, defaults to col
accumOrder accumulate successively within each class, given by cls in the order given in this vector. All classes in cls must be represented in this vector.
... Options passed to plot or boxplot

Details

The function collectors.curve can visualize the richness a dataset has, if samples are picked at random. It can handle rarefaction results as well as normal dataframes.
Author(s)
Falk Hildebrand, Paul Saary

References

See Also
Use plot.rtk for how to plot your results.

Examples
```r
require("rtk")
data <- matrix(sample(x = c(rep(0, 15000),rep(1:10, 100)), size = 10000, replace = TRUE), ncol = 80)
data.r <- rtk(data, ReturnMatrix = 1, depth = min(colSums(data)))

# collectors curve on dataframe/matrix
collectors.curve(data, xlab = "No. of samples", ylab = "richness")
# same with rarefaction results (one matrix recommended)
collectors.curve(data.r, xlab = "No. of samples (rarefied data)", ylab = "richness")

# if you want to have an accumulated order, to compare various studies to one another:
.cls <- rep_len(c("a","b","c","d"), ncol(data)) # study origin of each sample
apcumOrder <- c("b","a","d","c") # define the order, for the plot
colors <- c(1,2,3,4)
names(colors) <- accumOrder # names used for legend
collectors.curve(data, xlab = "No. of samples", ylab = "richness", col = colors, bin = 1,cls = cls, accumOrder = accumOrder)
```

Description
Collectorscurves visualize the richness gained by picking more samples.

Usage
```r
get.diversity(obj, div = "richness", multi = FALSE)
get.mean.diversity(obj, div = "richness")
get.median.diversity(obj, div = "richness")
```
plot

Arguments

<table>
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<tr>
<th>obj</th>
<th>Object of type rtk</th>
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<tr>
<td>div</td>
<td>diversity measure as string e.g &quot;richness&quot;</td>
</tr>
<tr>
<td>multi</td>
<td>Argument set to true if called recursively and class should not be checked. Should not be set in normal use case.</td>
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Details

This set of functions allows fast and easy access to calculated diversity measures by rtk. It returns a matrix, when rarefaction was only performed to one depth and a list of matrices or vectors if rarefaction was done for multiple depths.

Author(s)

Falk Hildebrand, Paul Saary

References


See Also

Use rt before calling this function.

Examples

```r
require("rtk")
data <- matrix(sample(x = c(rep(0, 15000), rep(1:10, 100)), size = 10000, replace = TRUE), ncol = 80)
data.r <- rtk(data, depth = min(colSums(data)))
get.diversity(data.r)
get.median.diversity(data.r)
get.mean.diversity(data.r)
```

plot

Plot rarefaction results

Description

Rarefy datasets in R or from a path.

Usage

```r
# S3 method for class 'rtk'
plot(x, div = c("richness"), groups = NA, col = NULL, lty = 1,
pch = NA, fit = "arrhenius", legend = TRUE, legend.pos = "topleft",
log.dim = "", boxplot = FALSE, ...)
```
Arguments

- **x**: a rare result object
- **div**: Diversity measure to plot. Can be any of c('richness', 'shannon', 'simpson', 'invsimpson', 'chao1', 'eve')
- **groups**: If grouping is desired a vector of factors corresponding to the input samples
- **col**: Colors used for plotting. Can be a vector of any length which will be recycled if it is to small. By default a rainbow is used.
- **lty**: Linetypes used for plotting. Can be a vector of any length which will be recycled if it is to small.
- **pch**: Symbols used for plotting. Can be a vector of any length which will be recycled if it is to small.
- **fit**: Fit the rarefaction curve. Possible values: c("arrhenius", "michaelis-menten", "logis")
- **legend**: Logical indicating if a legend should be created or not
- **legend.pos**: Position of the said legend
- **log.dim**: Character vector indicating which scale log log transform for plotting rarefaction curves.
- **boxplot**: If a boxplot should be added to the lineplot of the rarefaction curve.
- **...**: Other plotting input will be passed to plot or boxplot respectively

Details

To create plots from the rarefaction results you can easily just call a plot on the resulting elements. This will either produce a rarefaction curve, if more than one depth was rarefied to, or a boxplot for a single depth. Grouping of samples is possible by simply passing a vector of the length of the samples to the option `groups`.

Rarefaction curves can be fitted to either the arrhenius-equation, the michaelis-menten (SSmicmen) equation or the logis function SSlogis. To disable fitting `fit` must be set to `FALSE`.

Author(s)
Falk Hildebrand, Paul Saary

References

See Also
rtk, collectors.curve
Examples

require("rtk")
# generate semi sparse example data
data <- matrix(sample(x = c(rep(0, 1500),rep(1:10, 500),1:1000),
size = 120, replace = TRUE), 40)
# find the column with the lowest abundance
samplesize <- min(colSums(data))
# rarefy the dataset, so each column contains the same number of samples
d1 <- rtk(input = data, depth = samplesize)
# rarefy to different depths between 1 and samplesize
d2 <- rtk(input = data, depth = round(seq(1, samplesize, length.out = 10))]

# just the richness of all three samples as boxplot
plot(d1, div = "richness")
# rarefaction curve for each sample with fit
plot(d2, div = "evenness", fit = "arrhenius", pch = c(1,2,3))
# rarefaction curve with boxplot, samples pooled together (grouped)
plot(d2, div = "richness", fit = FALSE, boxplot = TRUE, col = 1, groups = rep(1, ncol(data)))
threads Number of threads to use during rarefaction
tmpdir Location to store temporary files
seed Set seed to integer > 0 to get reproducible results. default: 0

details
Function rare takes a dataset and calculates the diversity measures, namely the shannon diversity, richness, simpson index, the inverse simpson index, chaol and evenness.
If wished for the function can also return one or multiple rarefied matrices rarefied to one or multiple depths. Those can then also be used to create collectorcurves (see collectors.curve).

value
The function rare returns an object of class 'rarefaction', containing the objects divvs, raremat, skipped, div.median and depths. If more than one depth was computed the elements 1-4 are inside a list themself and can be accessed by the index of the desired depth.
The object divvs contains a list of diversity measures for each sample provided.
raremat is one or multiple rarefied matrices. Samples with not enough counts are removed, thus not all raremat-matrices for different depths might be of the same size. If and which samples where excluded is denoted in the element skipped using the names of the respective samples.
depths just contains the input variable and might be usefull for further analysis of the results.
It is possible to plot the results of the rarefaction, depending on the parameters passed to rare. See plot.rtk for examples.

author(s)
Paul Saary, Falk Hildebrand

references

see also
plot.rtk, collectors.curve

examples
```r
require("rtk")
# generate semi sparse example data
data <- matrix(sample(x = c(rep(0, 1500),rep(1:10, 500),1:1000),
size = 120, replace = TRUE), 10)
# find the column with the lowest aboundance
samplesize <- min(colSums(data))
# rarefy the dataset, so each column contains the same number of samples
data.rarefied <- rtk(input = data, depth = samplesize, ReturnMatrix = 1)
```
richness <- get.diversity(data.rarefied, div = "richness")
eveness <- get.diversity(data.rarefied, div = "eveness")
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