Package ‘rtk’

January 13, 2020

Type Package
Title Rarefaction Tool Kit
Version 0.2.5.8
Date 2020-01-13
Author Paul Saary, Falk Hildebrand
Maintainer Paul Saary <rtk@paulsaary.de>
Description Rarefy data, calculate diversity and plot the results.
License GPL (>= 2)
Imports Rcpp (>= 0.12.3),methods
LinkingTo Rcpp
SystemRequirements C++11
Suggests testthat
NeedsCompilation yes
Repository CRAN
Date/Publication 2020-01-13 14:50:02 UTC

R topics documented:

rtk-package .......................................................... 2
collectors.curve .................................................. 3
get.diversity ...................................................... 4
plot ................................................................. 5
rtk ................................................................. 7

Index 10
**rtk-package**

---

**Rarefaction Tool Kit**

**Description**

Rarefy data, calculate diversity and plot the results.

**Details**

The DESCRIPTION file:

```
Package: rtk
Type: Package
Title: Rarefaction Tool Kit
Version: 0.2.5.8
Date: 2020-01-13
Author: Paul Saary, Falk Hildebrand
Maintainer: Paul Saary <rtk@paulsaary.de>
Description: Rarefy data, calculate diversity and plot the results.
License: GPL (>= 2)
Imports: Rcpp (>= 0.12.3),methods
LinkingTo: Rcpp
SystemRequirements: C++11
Suggests: testthat
```

Index of help topics:

```
collectors.curve collectors.curve
get.diversity get.diversity
plot Plot rarfeaction results
rtk Rarefy tables
rtk-package 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

collectors.curve  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, t compare various studies to one another:
cls <- rep_len(c("a","b","c","d"), ncol(data))  # study origin of each sample
accumOrder <- c("b","a","d","c")  # define the order, for the plot

# 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

Collectors curves 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")
```
**Arguments**

- **obj**: Object of type rtk
- **div**: Diversity measure as string e.g. "richness"
- **multi**: Argument set to true if called recursively and class should not be checked. Should not be set in normal use case.

**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)
```

**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 too 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 too small.
- **pch**: Symbols used for plotting. Can be a vector of any length which will be recycled if it is too 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 either to 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

```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), 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 = "eveness", 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)))
```

### rtk

**Rarefy tables**

**Description**

Rarefy datasets in R or from a path.

**Usage**

```r
rtk(input, repeats = 10, depth = 1000, ReturnMatrix = 0, margin = 2,
    verbose = FALSE, threads = 1, tmpdir = NULL )
```

**Arguments**

- **input**
  This can be either a numeric matrix or a path to a text file in tab-delimited format on the locally available storage. The later option is for very big matrices, to avoid unnecessary memory consumption in R.

- **repeats**
  Number of times to compute diversity measures. (default: 10)

- **depth**
  Number of elements per row/column to rarefy to. The so called rarefaction depth or samplesize. Can also be a vector of ints. (default: 1000)

- **ReturnMatrix**
  Number of rarefied matrices which are returned to R. Set to zero to only measure diversity. (default: 1)

- **margin**
  Indicates which margin in the matrix represents the Samples and Species. Default is to rarefy assuming columns represent single samples (margin=2). If margin=1, rows are assumed to be samples. (default: 2 (columns))

- **verbose**
  If extra output should be printed to std::out or not to see progress of rarefaction. (default: TRUE)
threads  Number of threads to use during rarefaction
tmpdir   Location to store temporary files

Details

Function `rare` takes a dataset and calculates the diversity measures, namely the shannon diversity, richness, simpson index, the inverse simpson index, chao1 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 themselves 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 useful 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 abundance
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")
```
Index

collectors.curve, 3, 3, 6, 8
get.diversity, 4
get.mean.diversity (get.diversity), 4
get.median.diversity (get.diversity), 4
plot, 5
plot.rtk, 3, 4, 8
rarefactioncurve (plot), 5
rt, 5
rtk, 3, 6, 7
rtk-package, 2
SSlogis, 6
SSmicmen, 6