Package ‘rtk’

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Type Package

Title Rarefaction Tool Kit

Version 0.2.7

Date 2026-01-30

Description Rarefy data, calculate diversity and plot the results.

Depends R (>= 4.1.0)

License GPL (>= 2)

Imports Rcpp (>= 0.12.3),methods

LinkingTo Rcpp

Suggests testthat

NeedsCompilation yes

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`rtk-package` *Rarefaction Tool Kit*

Description

Rarefy data, calculate diversity and plot the results.

Details

The DESCRIPTION file:

Package:	rtk
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Title:	Rarefaction Tool Kit
Version:	0.2.7
Date:	2026-01-30
Authors@R:	c(person("Paul", "Saary", email = "rtk@paulsaary.de", role = c("aut", "cre")), person("Falk", "Hildebrand", ro
Description:	Rarefy data, calculate diversity and plot the results.
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LinkingTo:	Rcpp
Suggests:	testthat
Author:	Paul Saary [aut, cre], Falk Hildebrand [aut]
Maintainer:	Paul Saary <rtk@paulsaary.de>

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`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 [aut, cre], Falk Hildebrand [aut]

Maintainer: Paul Saary <rtk@paulsaary.de>

References

Saary, Paul, et al. "RTK: efficient rarefaction analysis of large datasets." Bioinformatics (2017): btx206.

See Also

`rtk`, `plot.rtk`, `collectors.curve`

`collectors.curve` *collectors.curve*

Description

Collectorscurves 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 sampeling of samples should be perfomed
`bin`	Number of samples to be added each step. Usefull 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 sampels are picked at random. It can handle rareafaction results as well as normal dataframes.

Author(s)

Falk Hildebrand, Paul Saary

References

Saary, Paul, et al. "RTK: efficient rarefaction analysis of large datasets." Bioinformatics (2017): btx206.

See Also

Use `plot.rtk` for how to plot your results.

Examples

```
require("rtk")
# Collectors Curve dataset should be broad and contain many samples (columns)
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
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)
```

`get.diversity` *get.diversity*

Description

Collectorscurves visualize the richness gained by picking more samples.

Usage

```
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 recursivly 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

Saary, Paul, et al. "RTK: efficient rarefaction analysis of large datasets." Bioinformatics (2017): btx206.

See Also

Use `rt` before calling this function.

Examples

```
require("rtk")
# Collectors Curve dataset should be broad and contain many samples (columns)
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 rarfeaction results*

Description

Rarefy datasets in R or from a path.

Usage

```
## 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 corresponting 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` repectivly

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 mor than one depth was rarefied to, or a boxplot for a single depth. Grouping of samples is possible by simply passing a vetor of the length of the samples to the option `groups`.

Rarefaction curves can be fittet 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

Saary, Paul, et al. "RTK: efficient rarefaction analysis of large datasets." Bioinformatics (2017): btx206.

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 aboundance
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, sampels 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

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

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
`seed`	Set seed to integer > 0 to get reproducible results. `default: 0`

Details

Function `rare` takes a dataset and calcualtes 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 themself and can be acessed by the index of the desired depth.

The object `divvs` contains a list of diversity measures for each sample provieded.

`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 sampels 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 [aut, cre], Falk Hildebrand [aut]

References

Saary, Paul, et al. "RTK: efficient rarefaction analysis of large datasets." Bioinformatics (2017): btx206.

See Also

`plot.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), 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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