

Package: vegetools (via r-universe)

August 17, 2024

Title Tools for vegetation analysis

Version 0.1.2

Description By now, just tools to calculate vegetation cover from field transects data.

Depends R (>= 3.3.0)

License GPL-3

Encoding UTF-8

LazyData true

Imports dplyr, gtools, plyr, tidyr

Suggests testthat

URL <https://github.com/Pakillo/vegetools>

BugReports <https://github.com/Pakillo/vegetools/issues>

RoxygenNote 5.0.1

Repository <https://pakillo.r-universe.dev>

RemoteUrl <https://github.com/Pakillo/vegetools>

RemoteRef HEAD

RemoteSha 9c3a7aea5c5692bfee13e1e10f66123a7824336f

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calculate_cover	<i>Calculate total cover per species in vegetation transects</i>
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Description

Calculate total cover per species in each transect, layer within transect, etc. Optionally, the function can also calculate length of bare ground (as ground not covered by any plant species).

Usage

```
calculate_cover(df, split.cols, first.spcol, last.spcol = ncol(df), tr.length,
  bare = FALSE, precision, check.incremental = TRUE, sort.cols = TRUE,
  prop = FALSE, long.format = FALSE, show.progress = TRUE)
```

Arguments

df	A dataframe with one column per recorded species, plus additional columns to identify transects (and possibly sections within transects, shrub or tree layers, etc). For each species, introduce initial and ending distances every time the species appears along the transect (see example).
split.cols	A character vector with the names of the variables in df that identify transects or any other structure of the data (e.g. sections within transects, shrub or tree layers, etc.)
first.spcol	Integer. Number of the first column containing species cover data.
last.spcol	Integer. Number of the last column containing species cover data (last column in df by default).
tr.length	Numeric. Total transect length (e.g. in meters).
bare	Logical. Calculate bare cover? Default is TRUE.
precision	Numeric. Precision of species cover measurements. Only used to calculate bare cover by exclusion.
check.incremental	Logical (default is TRUE). Check that cover data are sorted incrementally? Must be TRUE if calculating bare cover with this function.
sort.cols	Logical. If TRUE (default), sort species columns alphabetically (including bare as a species).
prop	Logical. If TRUE, results are expressed as proportion of tr.length covered by each species. If FALSE (the default), results represent linear absolute length covered by each species.
long.format	Logical. Produce the output dataframe in long format? Default is wide format. See gather .
show.progress	Logical. Show progress bar?

Value

A dataframe with total cover values per species and transect (plus optionally bare ground).

Author(s)

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Examples

```
df <- data.frame(transect = sort(rep(c(1,2,3), 20)),
                 section = rep(1, 60),
                 species1 = c(replicate(3, sort(round(runif(20, 0, 100), digits = 1)))),
                 species2 = c(sort(round(runif(8, 0, 100), digits = 1)), rep(NA, times = 60 - 8)))
head(df)
calculate_cover(df, split.cols = "transect", first.spcol = 3,
tr.length = 100, check.incremental = FALSE)
calculate_cover(df, split.cols = "transect", first.spcol = 3, tr.length = 100,
check.incremental = FALSE, long.format = TRUE)
```

vegetools

vegetools.

Description

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