

Package ‘stratigraph’

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Type Package

Title Toolkit for the plotting and analysis of stratigraphic and palaeontological data

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Depends R (>= 2.13.1), grid

Description A collection of tools for plotting and analyzing paleontological and geological data distributed through through time in stratigraphic cores or sections. Includes some miscellaneous functions for handling other kinds of palaeontological and paleoecological data.

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stratigraph-package *Plots stratigraphic data*

Description

A collection of tools for plotting and analyzing paleontological and geological data distributed through through time in stratigraphic cores or sections. Includes some miscellaneous functions for handling other kinds of palaeontological and paleoecological data.

Details

Package: stratigraph
 Type: Package
 Version: 0.64
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 License: GPL v. 3 or later copyleft

Package overview; still in beta.

The development of this package was supported by the Colombian Petroleum Institute, Ecopetrol S.A.

Includes functions: [writeTilia](#)

[writeGPDascii](#)
[readTilia](#)
[readGPDascii](#)
[gluesheets](#)

[a.datums](#)
[fads](#)
[lads](#)
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addpart
oe.rates

plot.strat.column
strat.column
as.strat.column
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rogerslk
mohawk
corneta
cerrejon

Author(s)

Walton A. Green, Carlos Jaramillo, Scott Wing
Maintainer: Walton A. Green <wagreen@bricol.net>

References

Shaw, A. B. (1964) Time in Stratigraphy. New York: McGraw-Hill.
Edwards, L. E. (1984) Insights on why graphic correlation (Shaw's Method) works. Journal of Geology 92:583–597.

See Also

[plot.strat.column](#)

Examples

```
cat('Put some examples here')
```

a.datums *Returns first and last appearance datums*

Description

Returns the first and last appearance datums (FADs and LADs) for taxa in a stratigraphic column.

Usage

```
a.datums(x, depths = NULL, skip = 0, increasing.down = FALSE, ...)
```

```
fads(x, depths = NULL, skip = 0, increasing.down = FALSE, ...)
```

```
lads(x, depths = NULL, skip = 0, increasing.down = FALSE, ...)
```

Arguments

x	an object of class strat.column.
depths	depths from which to calculate the datums
skip	a number of depths (levels) to skip, returning NA instead of values for FAD or LAD; defaults to 0.
increasing.down	FALSE (default) returns FADs less than or equal to LADs, as is the case when depths are measured up from the bottom of, e.g. a stratigraphic section; TRUE reverses FADs and LADs, as is the case when depths are measured from the surface in wells or cores.
...	not currently used.

Details

If depths is provided, it will clobber x\$depths, should x\$depths exist.

Value

a.datums returns a data frame with columns fads and lads, each of which is a numeric vector giving the FAD or LAD of each taxon in the stratigraphic column. fads and lads return respectively just the fads and just the lads in a single named numeric vector.

Author(s)

Walton Green

See Also

[plot.strat.column](#), [stratigraph](#)

Examples

```
data(mohawk)
fads(as.strat.column(mohawk))
# should make mohawk a strat.column without coercion
```

addpart

Calculates additive partitioning of diversity

Description

Returns or writes to a file measures of the additive partitioning of diversity according to Lande (1996).

Usage

```
addpart(x = NULL, file = 'rawcounts.txt', outfile = NULL)
```

Arguments

x	an object of class <code>strat.column</code> or a counts matrix with species in rows and sites in columns
file	ignored unless x is NULL; otherwise a file from which to read the counts matrix. Must be in tab-delimited text format with column labels in the first, header row, which must be one entry shorter than the following data rows. Row labels in the first column. [check this]
outfile	a file to which to write the output. If NULL (the default) writes to standard output.

Details

Based on an Excel spreadsheet set up by Scott Wing.

Value

returns a data frame list with components `$counttable`, `$Sstats`, and `$Saddpart`.

`$counttable` is a data frame giving the original count matrix with row and column marginals added to the right and bottom.

`$Sstats` is a data frame giving species diversity (Sobs), Simpson's Diversity Index (SimpsonsD = $1 - \text{sum of squares of proportional counts}$), and Hurlbert's PIE ($\text{PIE} = \text{SimpsonsD} * (n/(n-1))$), where n = total number of individuals found at a site) for each site.

`$Saddpart` is a data frame giving alpha and beta partitions of diversity under three different weighting scenarios: with sites weighted by n = total number of individuals found at a site, natural log of n (ln n), and assuming that all sites have equal number of individuals.

Note

Currently no other notes.

Author(s)

Scott Wing, Walton Green

References

Hurlbert (1971)

Lande, R. (1996) 'Statistics and Partitioning of Species Diversity, and Similarity among Multiple Communities'. *Oikos*. 76(1):5–13.

See Also

[plot.strat.column](#), [stratigraph](#)

Examples

```
#none yet
```

cerrejon

Cerrejon Core

Description

Pollen counts from the Cerrejon core. This is to illustrate how to read in 'raw' data in an arbitrary format, so it has been left entirely as character data.

Usage

```
data(cerrejon)
```

Format

A data frame with 189 observations (rows) of 113 variables (columns). The columns represent depths and the rows (after the first two) taxa; the data are raw counts.

Details

Levels of ENVIRONMENT

1, Ch	channel-fill deposits in fluvial settings (sandstone)
2, Ov	overbank, crevasse splays and sand sheets deposits in flood plains (mixed sandstone and siltstone, mudstone, paleosols)
2.1	coal—transgressive
2.2	coal—regressive
2.3	coal—unidentified
3, La	subaqueous coastal-lagoon, ponds (fossiliferous shale, shale)
4, Sp	supratidal flats, mud flats, tidal creeks (siltstone, mudstone, paleosols)
5, In	intertidal flats, tidal creeks (heterolithic and rhythmite sandstones and siltstones; sandstones)

Source

Carlos Jaramillo

References

Jaramillo, C., Pardo-Trujillo, A., Rueda, M., Harrington, G., Bayona, G., Torres, V., and Mora, G. Palynology of the Upper Paleocene Cerrejon Formation, Northern Colombia. Submitted to Palynology

Examples

```
data(cerrejon)
str(cerrejon)
```

compress2matrix *Converts compressed format files to flat matrices*

Description

Reads 'compressed format' text files giving the species found at particular sites and rewrite them into a sites by species matrix.

Usage

```
compress2matrix(path, skip = 3, verbose = TRUE,
                 lump.queries = FALSE,
                 exclude.taxa = NULL)
```

Arguments

path	the directory within which to process all the files that end in '.BB' (which must be capitalized).
skip	skip is the number of lines to skip at the beginning of each file, defaulting to 3.
verbose	verbose = TRUE (the default) prints diagnostic messages.
lump.queries	lump.queries = TRUE treats taxon names/codes that are followed by question marks as if they were the same as the same name/code not followed by a question mark. FALSE (the default) treats queries as separate taxa.
exclude.taxa	character vector giving taxon names to exclude.

Details

Compressed format data has a line of data for each site consisting of tab-separated records, the first two records give the site name; the remaining records are pairs separated by a single space giving species names and counts (species names can be repeated).

Value

The return value of the function is a list including a vector of site names, a vector of taxon names/codes, and a sites-by-species matrix. As a side-product, the function saves (in the directory specified by path) a matrix (tab-delimited text file ending in .MTX) for each locality (.BB file) and the overall sites-by-species matrix as a file named 'SiteBySp.MTX'.

Note

Currently no other notes.

Author(s)

Walton Green

See Also

[plot.strat.column](#), [stratigraph](#)

corneta

Corneta Outcrop

Description

Pollen counts from a stratigraphic section at the Corneta outcrop. This is to illustrate how to read in 'raw' data in an arbitrary format, so it has been left entirely as character data.

Usage

data(corneta)

Format

A data frame with 13 observations (rows) of 169 variables (columns).
The rows represent depths and the columns taxa.

Details

Not yet available.

Source

Silane da Silva

Examples

```
data(corneta)
str(corneta)
```

dloc

Draws a line of correlation between two sections

Description

Calculates and draws a line of correlation between two sections.

Usage

```
dloc(x, y, weights = NULL, pin.ends = FALSE,
     method = 'genetic', end.segs = ceiling(length(x)/3),
     pop = 100, max.gen = 200, mut = 0.01,
     recomb = 'roulette', ext = 0.5, tol = 0.005,
     start = 'lm', verbose = 2, plot = 1)
```

```
dcloc(x, y, pins, weights = NULL,
      method = 'genetic', end.segs = 3,
      pop = 100, max.gen = 200, mut = 0.01,
      recomb = 'roulette', ext = 0.5, tol = 0.005,
      start = 'lm', verbose = 2, plot = 1)
```

Arguments

x	a vector of the depths of datums in the better ('reference') section
y	a vector of the depths of datums in the worse section.
pins	a vector of fixed points (marker beds) through which the LOC is constrained to pass.

weights	a vector of weights the same length as x and y for weighted least squares.
pin.ends	whether the ends should be pinned to (fixed at) the first and last points: TRUE or 'both' fixes both top and bottom, 'top' and 'bottom' fix one or the other and FALSE (the default) allows both to float.
method	currently only 'genetic' supported.
end.segs	the maximum number of line segments in the LOC to consider.
pop	the population size of evolving LOCs.
max.gen	the maximum number of generations to evolve.
mut	mutation rate; the fraction of the the range of supplied values given to rnorm() as standard deviation of the mutation of solutions each generation.
recomb	type of recombination; in this case only 'roulette' is supported, producing 'fitness proportionate selection'.
ext	extinction rate; the proportion of solutions that go extinct each generation.
tol	a tolerance at which to stop evolving; not yet implemented.
start	the solution from which to begin: either 'lm' for a least-squares linear model or 'uniform' for a random-uniform model.
verbose	0, 1, 2; larger number gives more information.
plot	0, 1, 2; larger number provides more plots.

Value

Returns a list of three things: locs, bestloc and bestsse. locs gives the ending population of LOCs; best loc gives the best LOC; and bestsse gives the sum of squared errors for the best LOC. Each of these has a length equal to the number of different numbers of segments considered, so if 1, 2, 3, 4, and 5-segment LOCs were considered, locs, bestloc and bestsse will each have length 5.

Author(s)

Walton Green

References

- Zhang, T (2000) Artificial Intelligence Models for Quantitative Biostratigraphy. PhD. Dissertation, University of Illinois, Chicago.
- Zhang, T. and R. Plotnick (2006) 'Graphic correlation using genetic algorithms' *Mathematical Geology* 38(7):781–800.
- Miller, F.X., 1977 'The graphic correlation method in biostratigraphy' in *Concepts and Methods in Biostratigraphy* (Kauffman et al., eds.), pp. 165–186.

See Also

[plot.strat.column](#), [stratigraph](#)

Examples

```
# simplest example
#x <- c(0,1,2,3,5,7,9,17,18,20) + rnorm(10)/5
#y <- c(0,1,2,4,4,4,4,8,9,10) + rnorm(10)/5
x <- c(0.103, 1.336, 2.036, 2.928, 5.123, 6.738,
      8.998,17.145,17.960,19.753)
y <- c(0.152, 0.855, 1.784, 4.072, 4.055, 3.992,
      4.336, 7.963, 9.238,10.162)

xy.loc <- dloc(x, y, end.segs = 3, pop = 10, max.gen = 10,
              start = 'uniform', plot = 2)

## Not run:

xy.loc <- dloc(x, y, pin.ends = 'top', end.segs = 3,
              pop = 100, max.gen = 5, start = 'lm', plot = 1)

xy.loc <- dloc(x, y)

xy.cloc <- dcloc(x, y, pins = list(x = c(5,10), y = c(4,6)),
                max.gen = 10)

## End(Not run)
```

fill.ranges

Fills in missing values in the ranges of taxa

Description

Given a matrix or object of type `strat.column` with missing values (coded as NA), `fill.ranges` replaces the missing values that are between first and last occurrences of each taxon (column) with zeros.

Usage

```
fill.ranges(x, out = 'internals', ...)
```

Arguments

<code>x</code>	an object of class <code>strat.column</code> or a numerical matrix
<code>out</code>	'internals' returns an index to the counts that are internal to ranges, 'min' replaces these internals with the minimum non-zero counts in each taxon, 'pa' returns a presence/absence matrix with ranges filled
<code>...</code>	not currently used.

Details

Any missing values (NAs) are converted to zeros before filling ranges.

Value

`fill` ranges returns the type of output that it was given as input to `x`: either a `strat.column` or a numeric matrix.

Author(s)

Walton Green

See Also

[plot.strat.column](#), [stratigraph](#)

Examples

```
##Need an example of data with missing values
```

gluesheets

Glues tab-delimited spreadsheets together for further analysis

Description

Glues tab-delimited spreadsheets of species (the columns) by stratigraphic depths (the rows) together in such a way that the output is correctly formatted for analysis of ‘unitary associations’ in the PAST software package.

Usage

```
gluesheets(PATH = NULL, out.file = 'fileout.txt')
```

Arguments

<code>PATH</code>	a string giving the file path to the directory in which the sheets to be glued together are located.
<code>out.file</code>	the name of the file to which to write the output.

Details

Ask Silane da Silva....

Note

This is legacy code that will probably be removed soon....

Author(s)

Walton Green

See Also

[plot.strat.column](#)

Examples

```
## No examples
```

grid.prop.plot	<i>Plots proportions</i>
----------------	--------------------------

Description

Plots a chart of proportional data (or another continuous variable) through time.

Usage

```
grid.prop.plot(x, y = NULL,  
              increasing.down = FALSE)
```

Arguments

x the matrix of data to be plotted as proportions; each column is a variable; each row is a time (or depth).

y a vector with length equal to the number of rows in x; if NULL, it will be replaced by 1:nrow(x)

increasing.down FALSE (default) plots times (depths) increasing up from the bottom to the top of the plot.

Value

Returns invisibly.

Author(s)

Walton Green

See Also

[plot.strat.column](#), [rangechart](#)

Examples

```
xx <- matrix(sample(1:100), ncol = 4)
grid.prop.plot(xx)
grid.prop.plot(xx, c(1:10, 23, 24:35, 40, 42), increasing.down = FALSE)
```

mohawk

Mohawk Pond

Description

A pollen core from Mohawk Pond, Connecticut in the data structure produced by [readGPDascii](#)

Usage

```
data(mohawk)
```

Format

The output format is a data frame with columns:

\$counts	count matrix with species in columns, depths in rows num [1:50, 1:101] 0 0 0 0 0 0 0 0 0 1- attr(*, "dimnames")=List of 2\$: chr [1:50] "10" "50" "85" "110"\$: chr [1:101] "Abi" "Ace.ne" "Ace.ru" "Ace.sc-t" ...
\$depths	num [1:50] 10 50 85 110 140 190 210 250 290 310 ...
\$sample.names	chr [1:50] " " " " " " " " " " ...
\$absolute.ages	num [1:50] 200 365 602 814 1103 ...
\$taxa	chr [1:101] "Abies" "Acer negundo" "Acer rubrum" "Acer saccharinum-type" ...
\$short.names	chr [1:101] "Abi" "Ace.ne" "Ace.ru" "Ace.sc-t" ...
\$tax.cat	Factor w/ 8 levels "-", "A", "B", "F", ...: 2 2 2 2 2 2 2 2 2 ...
\$metadata	chr [1:75] " GPD ASCII Format" " 24 Apr 00" " Raw Counts - All Pollen Types" "" ...

Source

<ftp://ftp.ncdc.noaa.gov/pub/data/paleo/pollen/asciifiles/fossil/ascfiles/gpd/mohawk.txt>

References

- Steventon, R.L., and J.E. Kutzbach. 1983. University of Wisconsin radiocarbon dates XX. Radiocarbon 25:152-168.
- Steventon, R.L., and J.E. Kutzbach. 1986. University of Wisconsin radiocarbon dates XXIII. Radiocarbon 28:1206-1223.
- Gaudreau, D.C. 1986. Late-Quaternary vegetational history of the northeast: paleoecological implications of topographic patterns in pollen distributions. Dissertation. Yale University, New Haven,

Connecticut, USA.

Steventon, R.L., and J.E. Kutzbach. 1984. University of Wisconsin radiocarbon dates XXI. Radiocarbon 26:135-147.

Examples

```
data(mohawk)
str(mohawk)
```

nonuser	<i>Non user-level subroutines</i>
---------	-----------------------------------

Description

Subroutines called by other functions; none are intended to be called directly by the user.

Author(s)

Walton Green

See Also

[plot.strat.column](#), [stratigraph](#)

oe.rates	<i>Returns origination and extinction rates</i>
----------	---

Description

Returns the origination and extinctions rates of taxa in a stratigraphic column.

Usage

```
oe.rates(x, depths = NULL, breaks = NULL,
         per.capita = FALSE, remove.below = 1, ...)
```

Arguments

x	an object of class <code>strat.column</code> .
depths	depths, if different from those provided in x.
breaks	breaks from which to calculate interpolated rates.
per.capita	logical. Whether the origination and extinction rates should be given as fractions of the standing diversity.
remove.below	remove species that occur only this number or fewer levels.
...	not currently used.

Details

If depths is provided, it will clobber x\$depths, should x\$depths exist.

Value

oe.rates returns a list of \$basic, which is a data frame with columns stand.div, orig and ext giving standing diversity, origination and extinction rates at the sampled depths/times; \$bx, which are the boundary crossers at each sampled depth/time; \$intervals, which gives the lengths of each interval (in depth or time); and \$interpol, which gives interpolated rates per time as calculated by Foote(2000b).

Author(s)

Walton Green

References

Foote, M. (2000a) 'Origination and Extinction Components of Taxonomic Diversity: Paleozoic and Post-Paleozoic Dynamics' *Paleobiology* 26(4):578–605.

Foote, M. (2000b) 'Origination and extinction components of taxonomic diversity: general problems' *Paleobiology* 26 (supplement to No. 4):74–102.

See Also

[plot.strat.column](#), [stratigraph](#)

Examples

```
data(sI)
sc <- sI[,-1]
rownames(sc) <- sI[,1]
sc <- sc[-c(3, 6, 10, 11, 12)]
oe.rates(sc, depths = sI[,1])

data(mohawk)
oe.rates(mohawk)
oe.rates(as.strat.column(mohawk))
oe.rates(as.strat.column(mohawk), remove.below = 2)
oe.rates(as.strat.column(mohawk), breaks = seq(0, 1500, by = 50))
```

plain	<i>'plain' example section</i>
-------	--------------------------------

Description

Three very simple example sections used as examples by Edwards (1984).

Usage

```
data(plain)
```

Format

Data frames with taxa in columns (except the first column, which has the depth of each sample) and samples in rows.

Source

Edwards, L. E. (1984) Insights on why graphic correlation (Shaw's Method) works. *Journal of Geology* 92:583–597.

Examples

```
data(plain)
str(plain)
```

plot.strat.column	<i>Plots (bio)stratigraphic data</i>
-------------------	--------------------------------------

Description

Plots abundance (or range or relative abundance) diagrams of stratigraphic data, e.g. 'pollen diagrams'.

Usage

```
## S3 method for class 'strat.column'
plot(x = NULL,
     counts = NULL,
     depths = NULL,
     at.depths = NULL,
     sample.labels = NULL,
     taxa = NULL,
     short.names = NULL,
     higher.grp = NULL,
     tax.cat = NULL,
```

```

metadata = NULL,
prop.cutoff = NULL,
cols = c('depths', 'tick', 'samples', 'tick',
         'blank', 'data', 'tick', 'depths', 'totals'),
colwidths = NULL,
output.size = NULL,
output.file = NULL,
style = 'mountains',
reorder = NULL,
outer.margins = list(bottom = unit(1, "lines"),
                     left = unit(1, "lines"),
                     top = unit(1, "lines"),
                     right = unit(1, "lines")),

fontsize = 9,
width.multiplier = 2,
height.increment = 0.25, # inches per stratigraphic level
fill.cols = NULL,
line.cols = NULL,
box.pars = NULL,
proportional = FALSE,
use.color = TRUE,
bottom.axis = TRUE,
count.label = TRUE,
sample.totals = TRUE,
sample.category.totals = FALSE,
sample.nos = TRUE,
show.taxon.count.totals = TRUE,
plot.depths.increasing.down = TRUE,
debug = FALSE,
...)
```

Arguments

x	an object of class <code>strat.column</code> to be plotted.
counts	a data frame or matrix of counts or a string giving the path to a comma separated flat text file in the proper form to be read in by read.csv to a data frame and plotted.
depths	a vector of depths the same length as the number of rows in counts.
at.depths	a vector of depths at which to draw axis ticks.
sample.labels	a character vector of labels, the same length as the number of rows in counts, with which to label the samples.
taxa	taxon names.

short.names	abbreviated taxon names.
higher.grp	a higher taxonomic group for each taxon, empty by default (Factor taking levels: ???).
tax.cat	a category or label for each taxon, empty by default (Factor taking levels: ???).
metadata	a list including any or all of the following named values: SiteName, Latitude, Longitude, Country, Location, SiteType, Interval, Scale, PlotDate, Contact, Publications, Notes.
prop.cutoff	defaults to NULL (no effect); otherwise a proportion such that taxa are removed if they account for less than the given proportion of total counts.
cols	a vector of strings chosen from 'depths', 'tick', 'samples', 'totals', and 'blank' describing the columns that will be plotted to the left of the data columns in the plot.
colwidths	a vector of units the same length as cols giving the widths of the columns.
output.size	a 2-vector giving the width and height (in that order) of the final output size of the plot in inches. If NULL (the default) the size is calculated by the number of taxa in the data matrix.
output.file	a string giving the path and filename to which to save the plot. If NULL (the default), the plot is produced in the active graphics device.
style	'mountains' and 'bars' currently available.
reorder	a vector to reorder the taxa. Ignored if NULL(default). If a string of length 1, invokes special options 'fad.by.category', 'lad.by.category', and 'by.count'
outer.margins	a list of length four with the named values bottom, left, top and right, each of which is a unit and gives the appropriate outer margin.
fontsize	the basic font size of taxa names.
width.multiplier	multiplier for calculating the final width of the plot; it is the times larger than the base column width of the widest column. Ignored if output.size is specified.
height.increment	the height increment allowed for each stratigraphic level when calculating the final height of the plot. Ignored if output.size is specified.
fill.cols	a vector of colors the same length as the number of taxa with which to fill the profiles.
line.cols	a vector of colors the same length as the number of taxa with which to draw the outline of the profiles.
box.pars	a list of gpar() objects for passing graphics parameters to the various boxes in the plot.
proportional	FALSE
use.color	TRUE
bottom.axis	TRUE
count.label	TRUE
sample.totals	TRUE (default) plots total abundance of counted specimens (in each level/sample) through the section. FALSE suppresses this feature.

```

sample.category.totals
    TRUE plots total abundances of each group of taxa (as grouped by 'category');
    defaults to FALSE, in which case nothing is done.
sample.nos      TRUE (default) prints sample numbers as well as depths. FALSE suppresses
                this feature.
show.taxon.count.totals
    TRUE (default) prints total counts in each taxon; FALSE suppresses this feature.
plot.depths.increasing.down
    TRUE (default) plots depths increasing from the top to the bottom of the plot.
debug          TRUE (default) prints debugging information.
...           arguments passed through to lower level plotting functions.

```

Details

Note that the way `plot.strat.column` is now set up, it returns an error if too small a fixed `output.size` is specified for a plot of more than 30 taxa or if no fixed size is specified for a plot of fewer than 30 taxa.

Value

Returns invisibly.

Note

The output of this function will almost always need to be modified slightly in a vector drawing program like Inkscape or Adobe Illustrator before publication.

Author(s)

Walton Green

See Also

[strat.column](#)

Examples

```

## Examples

data(plain)
plot.strat.column(counts = plain[,2:4], depths = plain[,1],
                 tax.cat = as.factor(c(1,2,1)), output.size = c(4,4),
                 reorder = 'lad.by.category')
# Note there is a bug in this: the category vector needs to be reordered too

## Not run:

data(cerrejon)
cerrejon.counts <- t(cerrejon[-(1:2),])

```

```

cerrejon.counts <- apply(cerrejon.counts, 2, as.numeric)
row.names(cerrejon.counts) <- names(cerrejon)
cerrejon.depths <- names(cerrejon)
cerrejon.depths <- as.numeric(gsub('X', '', cerrejon.depths, perl = TRUE))
cerrejon.samp.names <- cerrejon[1,]
cerrejon.lith <- as.factor(as.character(cerrejon[2,]))

plot.strat.column(counts = cerrejon.counts, depths = cerrejon.depths,
                  output.file = 'cerrejon.pdf')

data(corneta)
corneta.counts <- corneta[-1,-(1:2)]
corneta.counts <- corneta.counts[-(ncol(corneta.counts))]
corneta.counts <- apply(corneta.counts, 2, as.numeric)
corneta.depths <- row.names(corneta)[-1]
corneta.samp.names <- corneta$label[-1]
corneta.tax.cat <- as.factor(as.character(corneta[1,-(1:2)]))
corneta.tax.cat <- corneta.tax.cat[1:(length(corneta.tax.cat)-1)]

plot.strat.column(counts = corneta.counts, depths = corneta.depths,
                  tax.cat = corneta.tax.cat, output.file = 'corneta.pdf',
                  reorder = 'lad.by.category')

## Coloring the different categories....
data(mohawk)
plot.strat.column(counts = mohawk$count, depths = mohawk$depths,
                  tax.cat = mohawk$tax.cat, reorder = 'lad.by.category',
                  output.file = 'mohawk.pdf',
                  fill.cols = as.numeric(mohawk$tax.cat))

## End(Not run)

```

rangechart

Plots a range chart

Description

Plots a range chart of stratigraphic data.

Usage

```

rangechart(x = NULL,
           counts = NULL,
           depths = NULL,
           sample.labels = NULL,
           taxa = NULL,
           short.names = NULL,
           higher.grp = NULL,
           tax.cat = NULL,

```

```

reorder = NULL,
plot.points = FALSE,
plot.depths.increasing.down = TRUE,
llwd = 2,
cex.xaxis = 0.5,
cex.yaxis = 1,
...)
```

Arguments

<code>x</code>	an object of class <code>strat.column</code> to be plotted.
<code>counts</code>	a data frame or matrix of counts or a string giving the path to a comma separated flat text file in the proper form to be read in by <code>read.csv()</code> to a data frame and plotted.
<code>depths</code>	a vector of depths the same length as the number of rows in <code>counts</code> .
<code>sample.labels</code>	a character vector of labels, the same length as the number of rows in <code>counts</code> , with which to label the samples.
<code>taxa</code>	taxon names.
<code>short.names</code>	abbreviated taxon names.
<code>higher.grp</code>	a higher taxonomic group for each taxon, empty by default (Factor taking levels: ???).
<code>tax.cat</code>	a category or label for each taxon, empty by default (Factor taking levels: ???).
<code>reorder</code>	a vector to reorder the taxa. Ignored if <code>NULL</code> (default). If a string of length 1, invokes special options <code>'fad.by.category'</code> , <code>'lad.by.category'</code> , and <code>'by.count'</code>
<code>plot.points</code>	<code>FALSE</code> (default) plots actual occurrences as points when <code>TRUE</code> .
<code>plot.depths.increasing.down</code>	<code>TRUE</code> (default) plots depths increasing from the top to the bottom of the plot.
<code>llwd</code>	line width of the range bars, defaulting to 2. Compare <code>par(lwd = 2)</code> ; passed to <code>segments()</code> .
<code>cex.xaxis</code>	character expansion applied to x-axis labels, defaulting to 0.5. Compare <code>par(cex.axis = 0.5)</code> ; passed to <code>axis(1, ...)</code> .
<code>cex.yaxis</code>	character expansion applied to y-axis labels, defaulting to 1. Compare <code>par(cex.axis = 1)</code> ; passed to <code>axis(2, ...)</code> .
<code>...</code>	arguments passed through to lower level plotting functions.

Value

Returns invisibly.

Author(s)

Walton Green

See Also

[strat.column](#)

Examples

```
## Examples

#data(cerrejon)
#cerrejon.counts <- t(cerrejon[-(1:2),])
#cerrejon.counts <- apply(cerrejon.counts, 2, as.numeric)
#row.names(cerrejon.counts) <- names(cerrejon)
#cerrejon.depths <- names(cerrejon)
#cerrejon.depths <- as.numeric(gsub('X', '', cerrejon.depths, perl = TRUE))
#cerrejon.samp.names <- cerrejon[1,]
#cerrejon.lith <- as.factor(as.character(cerrejon[2,]))
#rangechart(counts = cerrejon.counts, depths = cerrejon.depths)

data(corneta)
corneta.counts <- corneta[-1,-(1:2)]
corneta.counts <- corneta.counts[,-(ncol(corneta.counts))]
corneta.counts <- apply(corneta.counts, 2, as.numeric)
corneta.depths <- row.names(corneta)[-1]
corneta.samp.names <- corneta$label[-1]
corneta.tax.cat <- as.factor(as.character(corneta[1,-(1:2)]))
corneta.tax.cat <- corneta.tax.cat[1:(length(corneta.tax.cat)-1)]
rangechart(counts = corneta.counts, depths = corneta.depths,
            tax.cat = corneta.tax.cat,
            reorder = 'lad.by.category')

data(plain)
rangechart(counts = plain[,2:4], depths = plain[,1],
            tax.cat = as.factor(c(1,2,1)),
            reorder = 'lad.by.category')

data(rogerslk)
rangechart(as.strat.column(rogerslk), reorder = 'fad', pch = 20)

## Coloring the different categories...
data(mohawk)
rangechart(counts = mohawk$counts, depths = mohawk$depths,
            tax.cat = mohawk$tax.cat, reorder = 'lad.by.category')
```

readGPDascii

Reads GPD ascii files

Description

Reads ascii files written in the Global Pollen Database ascii format.

Usage

```
readGPDascii(x)
readTilia(...)
```

Arguments

x a string giving the file path and name or a URL from which to obtain the ascii (.txt) file to read.

... not currently used.

Value

Returns a list with the following elements: `counts` (count matrix of depths by taxa), `depths`, `sample.names`, `absolute.ages`, `taxa` (the full taxon names), `short.names` (8 character short names), `tax.cat` (taxonomic category, a factor to group the taxa), and `metadata` (a character vector providing commented metadata).

Author(s)

Walton Green

References

Eric Grimm?

<http://www.ncdc.noaa.gov/paleo/gpd.html> <http://www.ncdc.noaa.gov/paleo/pollen/gpdascii.html>

See Also

[plot.strat.column](#), [writeGPDascii](#)

Examples

```
## Note that this example will only work when executed on a
## computer connected to the net

## Not run:
URL <- paste('ftp://ftp.ncdc.noaa.gov/pub/data/paleo/pollen/',
             'asciifiles/fossil/ascfiles/gpd/mohawk.txt', sep = '')
mohawk <- readGPDascii(URL)

## End(Not run)
```

rogerslk

Rogers Lake

Description

A pollen core from Rogers Lake, Connecticut in the data structure produced by [readGPDascii](#)

Usage

```
data(roverslk)
```

Format

The output format is a data frame with columns:

\$counts	count matrix with species in columns, depths in rows num [1:91, 1:78] 0 0 0 0 0 0 0 0 0- attr(*, "dimnames")=List of 2\$: chr [1:91] "7.5" "17.5" "22.5" "32"\$: chr [1:78] "Abi" "Ace.ru" "Ace.sa-t" "Ace.ud" ...
\$depths	num [1:91] 7.5 17.5 22.5 32 37.5 47.4 58 68.5 79 94.6 ...
\$sample.names	chr [1:91] " " " " " " " " " ...
\$absolute.ages	num [1:91] 0 79 119 200 293 ...
\$taxa	chr [1:78] "Abies" "Acer rubrum" "Acer saccharum-type" "Acer undiff." ...
\$short.names	chr [1:78] "Abi" "Ace.ru" "Ace.sa-t" "Ace.ud" ...
\$tax.cat	Factor w/ 7 levels "A","B","F","M",...: 1 1 1 1 1 1 1 1 1 ...
\$metadata	chr [1:138] " GPD ASCII Format" " 24 Apr 00" " Raw Counts - All Pollen Types" "" ...

Source

<ftp://ftp.ncdc.noaa.gov/pub/data/paleo/pollen/asciifiles/fossil/ascfiles/gpd/roverslk.txt>

References

- Davis, M.B. 1967. Pollen accumulation rates at Rogers Lake, Connecticut, during late- and post-glacial time. *Review of Paleobotany and Palynology* 2:219-230.
- Davis, M.B., and E.S. Deevey, Jr. 1964. Pollen accumulation rates: estimates from late-glacial sediment of Rogers Lake. *Science* 145:1293-1295.
- Davis, M.B. 1969. Climatic changes in southern Connecticut recorded by pollen deposition at Rogers Lake. *Ecology* 50:409-422.

Examples

```
data(roverslk)
str(roverslk)
```

sI

Section I

Description

Six synthetic sections used as examples by Edwards (1984).

Usage

```
data(sI)
```

Format

Data frames with taxa in columns (except the first column, which has the depth of each sample) and samples in rows.

Source

Edwards, L. E. (1984) 'Insights on why graphic correlation (Shaw's Method) works' *Journal of Geology* 92:583–597.

Examples

```
data(sI)
str(sI)
```

<code>strat.column</code>	<i>Creates a strat.column object</i>
---------------------------	--------------------------------------

Description

Creates and manipulates S3 objects of class `strat.column`

Usage

```
## S3 method for class 'strat.column'
summary(object, ...)
strat.column(counts, ...)
is.strat.column(x, ...)
as.strat.column(x)
```

Arguments

<code>counts</code>	a count matrix to be converted to a <code>strat.column</code> object.
<code>x</code>	an object to be checked for class attribute or coerced to a <code>strat.column</code> .
<code>object</code>	a <code>strat.column</code> object.
<code>...</code>	other components of a <code>strat.column</code> object to be included; see below for argument names that can be assigned values.

Details

An object of class `strat.column` is a list `x` with `attr(x, 'class') == 'strat.column'`. `is.strat.column()` only checks that it has the correct class attribute and a non-empty `counts`, which is the minimum needed for plotting. `summary.strat.column` provides a longer summary of what data are available, and `str` provides a full description of the data structure.

The following names are defined elements of a `strat.column`; more can be defined by the user simply by assigning a value to `x$new.name`.

REQUIRED: `counts`

OPTIONAL: taxa, short.names, higher.grp, tax.cat, reorder, depths, sample.names, absolute.ages, envir.facies, sample.labels, sample.label.title, CaCO₃, TOC, TIC, N, S, caliper, gamma.ray, density, fe.resist, mag.sus, resistivity, lithology, porosity, taxa.clust, sample.clust, lat.ddmmss, lat.dd, long.ddmmss, long.dd, loc.descript, site.name, country, state, county, elevation, elev.units, rc.ages, contact, refs, metadata

THE BASIC COUNT MATRIX with m taxa as columns and n depths as rows

\$counts : num [1:n, 1:m]

ATTRIBUTES OF THE TAXA

\$taxa : chr [1:m]

\$short.names : chr [1:m]

\$higher.grp : Factor [1:m] w/ levels: Angiosperm, Conifer, Fern, Pteridophyte, Moss, Indet. (levels not on this list can also be used.)

\$tax.cat : Factor [1:m] w/ levels: Arborescent, Herbaceous, Wetland, Xerophyte, Phytolith, Indet., Marker (levels not on this list can also be used.)

\$reorder : num [1:m]

ATTRIBUTES OF THE SAMPLES

\$depths : num [1:n] by default, depths are measured down from a datum.

\$sample.names : chr [1:n] text for labels in addition to the depths.

\$absolute.ages: num [1:n]

\$envir.facies : factor [1:n] w/ levels: ??? (a factor giving an environmental interpretation of the sample.)

\$sample.labels: chr [1:n] other labels for each sample (e.g. numbers)

\$sample.label.title: chr [1] title for the extra sample label, e.g. 'Sample Number'.

GEOCHEMICAL DATA \$CaCO₃ : num [1:n] (wt

\$TOC : num [1:n] (wt

\$TIC : num [1:n] (wt

\$N : num [1:n] (wt

\$S : num [1:n] (wt

CORE LOG DATA

\$caliper : num [1:p]

\$gamma.ray : num [1:p]

\$density : num [1:p]

\$fe.resist : num [1:p]

\$mag.sus : num [1:p]

\$resistivity : num [1:p]

\$lithology : num [1:p]

\$porosity : num [1:p]

where p can be any integer; the complete vector fits into the same distance in the stratigraphic column as the n samples. If alignment of log and sample data is required, it is up to the user to down-sample appropriately.

CLUSTERING

\$taxa.clust : cluster object for columns

\$sample.clust : cluster object for rows

SITE INFORMATION

\$lat.ddmmss : chr [1]

\$lat.dd : chr [1]

\$long.ddmmss : chr [1]

\$long.dd : chr [1]

\$loc.descript : chr [1]

\$site.name : chr [1]

\$country : chr [1]

\$state : chr [1]

\$county : chr [1]

\$elevation : num [1]

\$elev.units : chr [1]

DATING METADATA

\$src.ages : data.frame [,]

METADATA

\$contact : chr [1:x] \# a person to contact

\$refs : chr [1:y] \# citations

\$metadata : chr [1:z] \# random other notes

Value

Returns an object of type `strat.column`

Author(s)

Walton Green

See Also

[readGPDascii](#), [plot.strat.column](#)

Examples

```
# PUT EXAMPLES HERE
```

`writeCONOP`*Writes out data in a form appropriate for input into CONOP*

Description

Takes a series of stratigraphic columns and exports them in the right format to be read into CONOP.

Usage

```
writeCONOP(x, tax.check = TRUE, out.dir = getwd(),
           sect.names = NULL, neg.depths = FALSE,
           scaling = rep('yes', length(x)),
           REGION = NULL, AGE = NULL,
           REF1 = NULL, REF2 = NULL, REF3 = NULL)
```

Arguments

<code>x</code>	not documented.
<code>tax.check</code>	not documented.
<code>out.dir</code>	not documented.
<code>sect.names</code>	not documented.
<code>neg.depths</code>	not documented.
<code>scaling</code>	not documented.
<code>REGION</code>	not documented.
<code>AGE</code>	not documented.
<code>REF1</code>	not documented.
<code>REF2</code>	not documented.
<code>REF3</code>	not documented.

Note

This is a legacy function that may be removed soon.

Author(s)

Walton Green

See Also

[strat.column](#), [stratigraph](#)

Examples

```
# examples?
```

```
writeGPDascii      Reads GPD ascii files
```

Description

Writes ascii files in the Global Pollen Database (GPD) ascii format.

Usage

```
writeGPDascii(x, counts = NULL, depths = NULL,
              sample.names = NULL,
              absolute.ages = NULL,
              taxa = NULL,
              short.names = NULL,
              tax.cat = NULL,
              metadata = NULL,
              output.file = NULL, ...)
writeTilia(...)
```

Arguments

x	an object of class strat.column.
counts	NULL
depths	NULL
sample.names	NULL
absolute.ages	NULL
taxa	NULL
short.names	NULL
tax.cat	NULL
metadata	NULL
output.file	if NULL (the default), print output to the terminal
...	not currently used.

Value

Returns invisibly.

Author(s)

Walton Green

References

Eric Grimm?

<http://www.ncdc.noaa.gov/paleo/gpd.html> <http://www.ncdc.noaa.gov/paleo/pollen/gpdascii.html>

See Also

[readGPDascii](#), [plot.strat.column](#)

Examples

```
## Note that this example will only work when executed on a
## computer connected to the net

## Not run:
URL <- paste('ftp://ftp.ncdc.noaa.gov/pub/data/paleo/pollen/',
            'asciifiles/fossil/ascfiles/gpd/rogerslk.txt', sep = '')
rogerslk <- readGPDascii(URL)
cat(writeGPDascii(rogerslk))

## End(Not run)
```

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