Package ‘StratigrapheR’

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Description Includes bases for litholog generation: graphical functions based on R base graphics, interval management functions and svg importation functions among others. Also include stereographic projection functions, and other functions made to deal with large datasets while keeping options to get into the details of the data.
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R topics documented:

as.lim ............................................................... 4
bedtext ............................................................ 6
blackSet ............................................................ 7
casing ............................................................. 9
centresvg ......................................................... 10
changejoint ....................................................... 12
changesvg ......................................................... 13
clipsvg ........................................................... 15
collection ......................................................... 16
collections ....................................................... 18
convert ............................................................ 18
convertAxis ....................................................... 19
dipfix .............................................................. 20
divisor .............................................................. 21
earinc .............................................................. 22
earnet ............................................................... 23
earplanes ........................................................ 24
earpoints ........................................................ 25
everencase ........................................................ 27
everencircle ..................................................... 28
enlarge ............................................................. 29
every_nth .......................................................... 30
flip.lim ............................................................ 31
fmean .............................................................. 32
fmod ............................................................... 33
folder ............................................................... 34
formFunction ..................................................... 34
framesvg ........................................................ 35
greySet ........................................................... 37
homogenise ....................................................... 39
ignore ............................................................. 40
in.lim ............................................................... 41
in.window ........................................................ 43
incfix .............................................................. 45
infobar ............................................................ 46
is.clockwise ..................................................... 47
is.join ............................................................. 49
leftlog ............................................................. 50
litholog .......................................................... 51
memento .......................................................... 52
merge_list ........................................................ 54
mid.lim ............................................................ 57
R topics documented:

- minorAxis .................................................. 57
- minorAxisTicks .......................................... 59
- multigons ................................................ 60
- multilines ............................................... 63
- neatPick .................................................. 64
- neatPicked .............................................. 67
- nlegend ................................................... 69
- nset .......................................................... 70
- octapos .................................................... 71
- octashift ................................................... 72
- outliner ..................................................... 73
- pdfDisplay .................................................. 74
- pkgfind ...................................................... 76
- placesvg .................................................... 76
- planepoints .............................................. 78
- pointsvg ................................................... 79
- profiler ..................................................... 80
- rebound ..................................................... 82
- repitch ..................................................... 83
- reposition .................................................. 84
- restore ...................................................... 85
- rmatrix ...................................................... 87
- rotate ....................................................... 88
- seq_log ...................................................... 89
- seq_mult .................................................... 90
- shift ........................................................ 90
- simp.lim .................................................. 92
- sinpoint ................................................... 93
- strat.mean ............................................... 94
- strat.repair .............................................. 94
- strat.var ................................................... 95
- StratigrapheR ........................................... 96
- StratigrapheR.examples ................................. 108
- symbology ................................................. 108
- tie.lim ..................................................... 110
- trace.lim .................................................. 111
- transphere ............................................... 114
- weld ......................................................... 115
- weldjoint ................................................. 116
- weldlog .................................................... 118
- weldprofile .............................................. 119
- whiteSet .................................................. 121
- ylink ........................................................ 123
- zijderveld ............................................... 124

Index ......................................................... 127
Description

Functions to create and check limits of intervals (what we define here as a ‘lim’ object), with control of specified properties. Basically we define an interval by its left and right boundaries, by an id and by a rule of boundary inclusion.

Usage

```
as.lim(lim = NULL, l = NULL, r = NULL, id = 1L, b = "[]")
```

```
is.lim(lim = NULL, l = NULL, r = NULL, id = 1L, b = "[]")
```

```
are.lim.nonunique(lim = NULL, l = NULL, r = NULL, check.lim = TRUE)
```

```
are.lim.nonadjacent(lim = NULL, l = NULL, r = NULL, b = "[]", check.lim = TRUE)
```

```
are.lim.distinct(lim = NULL, l = NULL, r = NULL, check.lim = TRUE)
```

```
are.lim.ordered(
    lim = NULL,
    l = NULL,
    r = NULL,
    id = 1L,
    decreasingly = FALSE,
    dependently = FALSE,
    check.lim = TRUE
)
```

```
order.lim(
    lim = NULL,
    l = NULL,
    r = NULL,
    id = 1L,
    b = "[]",
    decreasingly = FALSE
)
```

Arguments

- `lim`: a list of n left (1st element) and n right (2ndt element) interval limits, of n interval IDs, and of n interval boundary rules (e.g. "[]").
- `l`: the left interval limits (numerical vector of length n).
- `r`: the right interval limits (numerical vector of length n).
the interval IDs (numerical or character vector of length n, the default is 1 for each interval). They can be similar for different intervals.

b the interval boundaries rules: "[" (or "closed") to include both boundaries points, "]" (or "open") to exclude both boundary points, "[" (or "]", "right-open" and "left-closed") to include only the left boundary point, and "]" (or "[", "left-open", "right-closed") to include only the right boundary point. The notation is simplified to "]", "[", "]" and "]" only.

check.lim whether to check if the object is a lim object.
decreasingly whether the order to check for or to set is decreasing.
dependently whether the intervals themselves should be ordered relatively to the other.

Details

as.lim: creates a lim object
is.lim: checks if arguments qualify as a lim object
are.lim.nonunique: checks if there are no intervals of identical l and r
are.lim.nonadjacent: checks if there are no pairs of intervals having at least one similar boundary
are.lim.distinct: checks if the intervals are not overlapping
are.lim.ordered: checks if the intervals are ordered (in l and r, and if dependently is TRUE, relative to the other intervals of same id)
order.lim: orders l and r parts of the intervals (use simp.lim for more advanced ordering)

See Also

To find which values are in which interval: in.lim
To simplify intervals by merging overlapping parts: simp.lim
To extract the part outside of intervals: flip.lim
To make intervals with boundaries in between given values: mid.lim
To discretise intervals: tie.lim
To simplify boundary rules into "]", "[", "]" and "]": rebound
To plot interval data as lines: trace.lim and plot_lim
To plot interval data as rectangles: infobar

Examples

e <- as.lim(l = c(0,1,2), r = c(0.5,2,2.5), id = "I")

is.lim(lim = e)

are.lim.nonunique(l = c(0,1,2), r = c(0.5,1,2.5))

are.lim.nonunique(l = c(0,1,2), r = c(0.5,1.5,2.5))
are.lim.nonadjacent(l = c(0,1,2), r = c(0.5,1.5,2.5))
are.lim.nonadjacent(l = c(0,1,1.5), r = c(0.5,1.5,2))
are.lim.ordered(l = c(0,1,2), r = c(0.5,1.5,2.5))
are.lim.ordered(l = c(0,1,2), r = c(0.5,1.5,2))
are.lim.ordered(l = c(0,1,2), r = c(0.5,1.5,2.5), dependently = TRUE)
are.lim.ordered(l = c(0,2,1), r = c(0.5,2.5,1.5), dependently = TRUE)
are.lim.distinct(l = c(0,1,2), r = c(0.5,1.5,2.5))
are.lim.distinct(l = c(0,1,2), r = c(0.5,3.5,2.5))
order.lim(l = c(0,6,4,6,50), r = c(1,5,6,9,8),
          b = c("[[", "]", "]", "]", "]")

---

**bedtext**

*Writes the names of the beds in a litholog*

**Description**

Writes the names of the beds in a litholog. You can either place them at the centre of the beds or in their upper and lower part. You can also define a thickness below which the name won’t be written, to avoid excessive text crowding the plot.

**Usage**

```r
bedtext(
labels,
  l,
  r,
  x = 0.2,
  arg = list(cex = 1),
  adj = c(0.5, 0.5),
  ymin = NA,
  edge = FALSE
)
```

**Arguments**

- **labels**
  the name of each bed
- **l**
  a vector of n left y (or dt, i.e. depth or time) interval limits for each bed
- **r**
  a vector of n right y (or dt, i.e. depth or time) interval limits for each bed
- **x**
  the position where to write the text (0.2 by default)
blackSet

Sets the plot environment to draw a long vertical data set

Description

Sets the plot environment to draw a long dataset. It provides lines as supplementary scale, and axes with major and minor ticks.

Usage

blackSet(
  xlim,
  ylim,
  xtick = NA,
  ytick = NA,
  xwidth = NA,
  ywidth = NA,
  xadj = 0,
  yadj = 0,
  yline = NA,
  xline = NA,
  black = TRUE,
  arg = list()
)
Arguments

- **xlim, ylim** the x and y limits (e.g. `xlim = c(-1,1)`)
- **xtick, ytick** the interval between each major ticks for x and y
- **nx, ny** the number of intervals between major ticks to be divided by minor ticks in the x and y axes
- **xaxs, yaxs** The style of axis interval calculation to be used for the x and y axes. By default it is "i" (internal): it just finds an axis with pretty labels that fits within the original data range. You can also set it to "r" (regular): it first extends the data range by 4 percent at each end and then finds an axis with pretty labels that fits within the extended range. See `?par` for further explanation.
- **xarg, yarg** a list of arguments to feed to `minorAxis()` for the x and y axes. See the `?minorAxis` help page for the possible arguments. See `?merge_list` for further information.
- **v** whether the lines are vertical
- **abbr** text to be repeated on the lines at each major tick
- **skip** number of text redundancies to be skipped
- **targ, sarg** a list of arguments to feed to `text()` and `segments()` respectively. If set to NULL, does not add the corresponding element.

Value

A plotting environment to draw a long data set

See Also

Similar functions: `whiteSet` and `greySet`

To create axes with major and minor ticks: `minorAxis`

To print a plot in pdf: `pdfDisplay`

To automatically determine pretty interval limits: `encase`
**casing**

**Examples**

```r
y <- c(0,11,19,33)
x <- c(1,2,2.5,4)
a <- min(y)
b <- max(y)
f <- encase(a-1,b,5)
blackSet(c(0,4),f, ytick = 10, ny = 10, skip = 1)
points(x, y, pch=19)
```

---

**casing**

*Finds values in a vector directly above and below a number*

**Description**

Finds values in a vector directly above and below a number

**Usage**

```r
casing(x, into)
```

**Arguments**

- `x`  
a number  
- `into`  
a vector where to find the values directly above and below x

**Value**

a vector of the values of "into" vector directly above and below x respectively

**See Also**

Similar function: `encase`

**Examples**

```r
casing(0.21,c(0.3,0.4,0.1,0.2))
```
centresvg  

Draws a `pointsvg` object around a given point.

**Description**

Draws a svg object imported as data frame using `pointsvg` around a given point.

**Usage**

```r
centresvg(
  object,  
  x,  
  y,  
  xfac = 1,  
  yfac = 1,  
  xadj = 0,  
  yadj = 0,  
  forget = NULL,  
  front = NULL,  
  back = NULL,  
  standard = FALSE,  
  keep.ratio = FALSE,  
  col = NA,  
  border = "black",  
  density = NA,  
  angle = 45,  
  lty = par("lty"),  
  lwd = par("lwd"),  
  scl = border,  
  slty = lty,  
  slwd = lwd,  
  plot = TRUE,  
  output = FALSE
)
```

centersvg(
  object,  
  x,  
  y,  
  xfac = 1,  
  yfac = 1,  
  xadj = 0,  
  yadj = 0,  
  forget = NULL,  
  front = NULL,  
  back = NULL,  
  standard = FALSE,
centresvg

```
keep.ratio = FALSE,
col = NA,
border = "black",
density = NA,
angle = 45,
lty = par("lty"),
lwd = par("lwd"),
scol = border,
slty = lty,
slwd = lwd,
plot = TRUE,
output = FALSE
```

Arguments

- **object**: a pointsvg object (svg object imported as data frame using pointsvg).
- **x, y**: numeric vectors of coordinates where the object should be drawn.
- **xfac**: the x size factor.
- **yfac**: the y size factor.
- **xadj**: value specifying the x adjustment of the drawing.
- **yadj**: value specifying the y adjustment of the drawing.
- **forget**: the elements that should be discarded, by their id or index (i.e. name or number of appearance).
- **front, back**: the elements to be put in front and back position, by their id or index (i.e. name or number of appearance). By default the order is the one of the original .svg file.
- **standard**: whether to standardise (centre to (0,0), rescale so that extreme points are at -1 and 1) or not (T or F)
- **keep.ratio**: if the object is to be standardised, whether to keep the x/y ratio (T or F)
- **col**: the polygones background color. If density is specified with a positive value this gives the color of the shading lines.
- **border**: the lines color.
- **density**: the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn.
- **angle**: the slope of shading lines, given as an angle in degrees (counter-clockwise)
- **lty, lwd**: the border line type and width, see ?par for details.
- **scol, slty, slwd**: the colour, type and width of the shading lines.
- **plot**: whether to add to a plot
- **output**: whether to output the new object coordinates
Details

The `centresvg` and `framesvg` have a lot of similarities with the `multigons` function: the graphical parameters are mostly identical. However there is a strong distinction between the .svg functions and multigons: when providing several graphical arguments, multigons will attribute them to each polygon, whereas the .svg functions will use them for each repetition of the .svg object. Using the latter, the graphical parameters will be applied to all the elements of a drawing. If you want a finer personalisation you have to use multigons and multilines (or an hybrid of the two, yet to be coded).

See Also

Similar functions: `framesvg` and `placesvg`
Change the drawing: `changesvg` and `clipsvg`
Uses `ignore` to avoid drawing unnecessary objects

Examples

```r
object <- example.ammonite
plot(c(-10,10), c(-10,10), type = "n")
centresvg(object, 5, 5, xfac = 2, yfac = 2,lty = 1,density = 20, angle = 45)
points(5,5,pch = 19, col = "blue")
```

---

`changejoint`  
*Change the dimensions of bedding joints*

Description

Change the dimensions of bedding joints

Usage

```r
changejoint(
  joint,
  yinv = F,
  xinv = F,
  yleft = NA,
  yright = NA,
  ymin = NA,
  ymax = NA,
  xmin = NA,
  xmax = NA
)
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>joint</td>
<td>the bedding joint to be modified</td>
</tr>
<tr>
<td>yinv, xinv</td>
<td>whether to inverse the plotting for x and y values (T or F)</td>
</tr>
<tr>
<td>yleft, yright</td>
<td>the depth/height/time value for the extreme point at the right or left of the joint (yleft overruns yright, which overruns ymin and ymax)</td>
</tr>
<tr>
<td>ymin, ymax</td>
<td>the extreme values for the y axis (in case of conflict with yleft and/or yright, defaults to the smallest exaggeration)</td>
</tr>
<tr>
<td>xmin, xmax</td>
<td>the extreme values for the x axis</td>
</tr>
</tbody>
</table>

Examples

# Create an initial litholog ----

```r
l <- c(-2,-1,0,1,2)
r <- c(-1,0,1,2,3)
h <- c(4,3,4,3,4)
i <- c("B1","B2","B3","B4","B5")
log <- litholog(l, r, h, i)
```

# Get a custom bedding joint to specific dimensions using changejoint() ----

```r
liq <- changejoint(oufti99$liquefaction,
                   yleft = 0, ymax = 0.3,
                   xmin = 1, xmax = 2)
```

```r
nlog <- weldlog(log, dt = 0, seg = list(liq = liq), j = c("liq"))
```

# Plots for visualisation ----

```r
plot.new()
plot.window(xlim = c(0,5), ylim = c(-2,3))
axis(1)
axis(2)
multigons(nlog$i, nlog$xy, nlog$dt)
```

---

changesvg  \hspace{1cm} Changes a pointsvg object

Description

Changes a svg object imported as data frame using pointsvg.
Usage

```r
changesvg(
  object,
  forget = NULL,
  front = NULL,
  back = NULL,
  standard = FALSE,
  keep.ratio = F,
  round = FALSE,
  xdigits = 4,
  ydigits = 4,
  xinverse = FALSE,
  yinverse = FALSE
)
```

Arguments

- `object`: a `pointsvg` object (svg object imported as data frame using `pointsvg`).
- `forget`: the elements that should be discarded, by their id or index (i.e. name or number of appearance).
- `front`, `back`: the elements to be put in front and back position, by their id or index (i.e. name or number of appearance). By default the order is the one of the original .svg file.
- `standard`: whether to standardise (centre to (0,0), rescale so that extreme points are at -1 and 1) or not (T or F)
- `keep.ratio`: if the object is to be standardised, whether to keep the x/y ratio (T or F)
- `round`: whether to round the coordinates or not (T or F)
- `xdigits`: the number of digits after the decimal to round to for x values
- `ydigits`: the number of digits after the decimal to round to for y values
- `xinverse`: whether to inverse the plotting for x values (T or F)
- `yinverse`: whether to inverse the plotting for y values (T or F)

Value

A data.frame with x and y coordinates, ids for each object, and a type, either line (L) or polygon (P)

See Also

- Importing .svg objects: `pointsvg`
- Plot the drawing and change the coordinates: `placesvg`, `centresvg` and `framesvg`
- Clip the drawing: `clipsvg`
Examples

```r
object1 <- example.lense

opar <- par("mfrow")
par(mfrow = c(1,3))

plot(c(-1,1), c(-1,1), type = "n")
placesvg(object1)

plot(c(-1,1), c(-1,1), type = "n")
object2 <- changesvg(object1, forget = 1)
placesvg(object2)

plot(c(-1,1), c(-1,1), type = "n")
object3 <- changesvg(object1, forget = "P1", standard = TRUE)
placesvg(object3)

par(mfrow = opar)
```

---

clipsvg

Clips a standardised pointsvg object into a given frame

Description

Clips a svg object imported as data frame using `pointsvg` if outside of a given frame. In other words it removes the elements of the svg that are entirely outside a given area.

Usage

```r
clipsvg(
  object, 
  xmin = -Inf, 
  xmax = +Inf, 
  ymin = -Inf, 
  ymax = +Inf, 
  by.entity = TRUE
)
```

Arguments

- **object**: a pointsvg object (svg object imported as data frame using `pointsvg`).
- **xmin, xmax, ymin, ymax**: clipping coordinates, default to +Inf (no clipping)
- **by.entity**: whether to remove all entities having points out of the clipping zone (TRUE; default) or to only remove the points out it (FALSE, and to use on lines for better result)
collection

Create a list of symbols

Description

From a file containing SVG files, extracts all the SVGS into a list of symbols that can be used in lithogs.

Usage

collection(dir = getwd())

is.collection(collection)
```r
plot_collection(
  collection,
  col = "grey90",
  cex = 2,
  as.pdf = T,
  name = "symbols",
  ext = ".pdf",
  dir = tempdir(),
  width = 7,
  height = 0.8 * width/5.6,
  track = T,
  openfile = T
)
```

**Arguments**

- `dir` the file where the document will be saved (by default a temporary directory, `tempdir()`)
- `collection` an object similar to the output of `collection()`
- `col` the background colour of the symbols
- `cex` the size of the text in the plot
- `as.pdf` whether to output the plot as a pdf
- `name` the name of the pdf document to plot the symbols of a collection
- `ext` the extension of the document: ".pdf" by default, but ".svg" works also.
- `width` the width of the drawing area (in inches)
- `height` the height of the drawing area (in inches)
- `track` whether to generate different files for each rerun of `pdfDisplay` with identical 'name'. The name will be followed by '_(i)' where i is the version number. With this you avoid closing your pdf file at each rerun if your pdf reader is not able to deal with (to my knowledge only SumatraPDF is able)
- `openfile` should the pdf file be opened (for the moment works only in Windows). Use SumatraPDF as default pdf reader to be able to write over current file

**Value**

a collection is a list of `pointsvg`-objects (see `pointsvg`)

**Examples**

```r
# To show you how to import, we first have to have a svg file to import. The
# following lines of code will create a svg in a temporary files:

# 1. Create temporary file
svg.file.directory <- tempfile(pattern = "ammonite",
  fileext = ".svg")

# 2. Write the svg in the file
writelines(example.ammonite.svg, svg.file.directory)
```
print(paste("An example .svg file was created at ", svg.file.directory, 
sep = ","))

coll <- collection(dirname(svg.file.directory))

is.collection(coll)

## Not run:
plot_collection(coll, cex = 1.5)

plot_collection(oufti99, name = "Oufti99")
## End(Not run)

collections

Collections of symbols

Description

oufti99 First experimental symbol dataset, developed in Liege University by Anne-Christine Da Silva, Michiel Arts and Sébastien Wouters

Examples

## Not run:
plot_collection(oufti99, name = "Oufti99")
## End(Not run)

convert

Converts x values having an index into n values defined by the same y index

Description

Converts x values having an index (of y values for instance) into n values defined by the same index (but having possibly more values)

Usage

convert(x, xindex, n, nindex)

Arguments

x a vector
xindex the index for each x value (vector of same length than x)
n a vector of the values into which to convert the x values
nindex the index for each n value (vector of same length than n)
Examples

```r
x <- c(10,20)
xindex <- c(1,2)

n <- seq(0.1,1,by = 0.1)
nindex <- 1:length(n)

convert(x,xindex,n,nindex)
```

---

**convertAxis**

*Converts the axis following a given formula*

**Description**

Converts the axis following a given formula, and places ticks in the new axis value

**Usage**

```r
convertAxis(
  side,
  formula,
  at.maj,
  at.min = NULL,
  labels = at.maj,
  tick.ratio = 0.75,
  line = NA,
  pos = NA,
  font = NA,
  lty = "solid",
  lwd = 1,
  lwd.ticks = lwd,
  col = NULL,
  col.ticks = NULL,
  hadj = NA,
  padj = NA,
  tcl = NA,
  ...
)
```

**Arguments**

- `side` an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
- `formula` the formula to be converted. Should be of the form `y ~ f(x)`
- `at.maj` a vector of the position and labels of the major ticks
at.min a vector of the position of minor ticks
labels his can either be a logical value specifying whether (numerical) annotations are to be made at the major tickmarks, or a character or expression vector of labels to be placed at the major tickpoints.
tick.ratio the ratio of minor to major tick size
line, pos, font, lty, lwd, lwd.ticks, col, col.ticks, hadj, padj, tcl, ... see ?axis function help page for these parameters

See Also
minorAxis

Examples
plot(1,1,type = "n", xlim = c(0,12), axes = FALSE ,xlab = "", ylab = "")
axis(3)
l <- seq_log(10^0,10^12,divide = TRUE)
convertAxis(l,y ~ log10(x),l[[1]],l[[2]])

dipfix Fix Dip

Description
Fix dip and strike of planes so that they fall in the correct quadrant. The provided quadrant is the determining factor. If unavailable or not helpful, the sign of the dip is used as determining factor.

Usage
dipfix(strike, dip, quadrant = NA, inverted = NA)

Arguments
strike strike of the data; it is the angle from the north of the horizontal line of the plane. Corrected, its range goes from 0° to 360°.
dip dip of the data; it is the angle from the horizontal taken on the line of the plane perpendicular to the one of the strike. In other words it is the plane’s maximum angular deviation from the horizontal. It is positive downward, and ranges from +90° for straight down to -90° for straight up. Dip values in [-180,-90] or/and [90,180] indicate inversion of the plane.
quadrant the quadrant where the plane dips downward. Accepted values are NA, 'N', 'S', 'W' or 'E' (lower- or uppercase alike). Is independant of inversion
inverted whether the plane is upside down.
**divisor**

**Details**

the strike will be corrected as the orientation of the dip (i.e. downward) minus 90°; it ranges from 0 to 360°. It is determined firstly from the quadrant. If the quadrant is missing or not helpful (e.g. 'N' or 'S' for a strike of 0° or 180°, 'E' or 'W' for a strike of 90° or 270°), it is determined using the sign of the dip. Inversion will be indicated if the dip values are in [-180,-90] or/and ]90,180[, or simply if inverted = T. The inversion does not influence the calculation of the strike, dip and quadrant: whether the plane is upside down does not change these parameters output.

**Value**

a list of the corrected strike, dip and quadrant

**See Also**

fmod, incfix and transphere

**Examples**

```r
strike <- c(-60, 180, 20, 0, 20)
dip <- c(-60, 20, -45, 110, -90)
quadrant <- c("N", NA, NA, NA, "E")
inverted <- c(FALSE, TRUE, FALSE, TRUE, FALSE)

dipfix(strike, dip, quadrant, inverted)
dipfix(strike, dip, quadrant)
```

---

`divisor`  

**Greatest Common Rational Divisor**

**Description**

Compute the Greatest Common Rational Divisor or test whether a value is a common rational divisor of a suite of number

**Usage**

```r
divisor(x, tolerance = 8, relative = T, tries = 4, speak = T)
is.divisor(x, y, tolerance = 8, relative = T, use.names = T)
```

**Arguments**

- `x` a numeric or integer vector
- `tolerance` the order of tolerance for errors, i.e. the number of decimals considered as being meaningful
relative

whether to apply the tolerance to the x values divided by the smallest x value (TRUE, is the default), or to the x values themselves

tries

the amount of iterations: each iteration tests $10^n+1$ more possibilities than the previous one. This is to optimise computation while allowing all possibilities to be explored. Each try takes exponentially more time than the previous one

speak

whether to print a sentence at each try

y

a numeric or integer vector of values to be tested as divisors of x

use.names

whether to use y values as names for the output

Examples

divisor(x = c(0.03,0.75,0.3,2,100, 0.03, 100, 0), speak = FALSE)
divisor(x = c(0.02,0.75,0.3,2,100.000002, 0.03, 100, 0), speak = FALSE)
divisor(x = c(0.02,0.75,0.3,2,100.000002, 0.03, 100, 0) * 10^{-10}, speak = FALSE)

a <- c(0.02,0.75,0.3,2,100.000000002, 0.03, 100, 0)
divisor(x = a)
is.divisor(x = a, y = c(1, 0.01, 2*10^{-9}))
divisor(x = a, tolerance = 7, speak = FALSE)
divisor(x = a, relative = FALSE, speak = FALSE)

earinc

Recalculates inclination in equal area projection

Description

Recalculates the inclination in equal area projection

Usage

earinc(inc)

Arguments

inc

inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010).

Examples

earinc(20)
earnet

Draws an equal area stereonet

Description

Draws Equal Area Stereo-Net. Lambert azimuthal Equal-Area (Schmidt) from Snyder p. 185-186 (modified from RFOC package)

Usage

earnet(
  xlim = c(-1.1, 1.1),
  ylim = c(-1.1, 1.1),
  ndiv = 10,
  col = gray(0.7),
  border = "black",
  lwd = 1,
  orientation = TRUE,
  xh = "WE",
  add = FALSE
)

Arguments

xlim, ylim  the x and y minimal limits. The actual limits can change to keep a x/y ratio of 1
ndiv  the number of intervals between each line crossing
col  the colour of the net
border  the colour of the border and crosshair
lwd  the line width
orientation  logical, whether to add captions indicating the orientation of the plot.
xh  orientation of the x axis: can be 'WE' or 'SN'. Has to be provided to earplanes and earpoints
add  logical, whether to add the circle to an existing plot

References


See Also

earinc, earplanes, earpoints and zijderveld
Examples

```r
par(mfrow = c(1,2))
earnet()
earnet(xh = "SN")
par(mfrow = c(1,1))
```

Description

Draws planes on an equal area stereonet (modified from RFOC package)

Usage

```r
earplanes(
  strike,  # strike of the data; it is the angle from the north of the horizontal line of the plane. It is corrected by the `dipfix` function.
  dip,     # dip of the data; it is the angle from the horizontal taken on the line of the plane perpendicular to the one of the strike. It is corrected by the `dipfix` function.
  quadrant = NA,  # the quadrant were the plane dips downward. Accepted values are NA, 'N', 'S', 'W' or 'E' (lower- or uppercase alike) for correction by the `dipfix` function.
  hsphere = "l",  # the hemisphere onto which to project the data. Either "b" for both, "l" for lower, and "u" for upper.
  ndiv = 10,  # the number of intervals between each 10° (in declination)
  a = list(col = "black", lwd = 1),  # list of graphical parameters to feed lines() for the all lines, or for the lines of the upper (u) and lower (l) hemisphere (the two latter override a). See ?lines help page for the possible arguments. See ?merge_list for further information.
  l = list(lty = 1),
  u = list(lty = 3),
  output = FALSE,
  plot = TRUE,
  xh = "WE",
  unique = TRUE
)
```

Arguments

- **strike**: strike of the data; it is the angle from the north of the horizontal line of the plane. It is corrected by the `dipfix` function.
- **dip**: dip of the data; it is the angle from the horizontal taken on the line of the plane perpendicular to the one of the strike. It is corrected by the `dipfix` function.
- **quadrant**: the quadrant were the plane dips downward. Accepted values are NA, 'N', 'S', 'W' or 'E' (lower- or uppercase alike) for correction by the `dipfix` function.
- **hsphere**: the hemisphere onto which to project the data. Either "b" for both, "l" for lower, and "u" for upper.
- **ndiv**: the number of intervals between each 10° (in declination)
- **a, l, u**: list of graphical parameters to feed lines() for the all lines, or for the lines of the upper (u) and lower (l) hemisphere (the two latter override a). See ?lines help page for the possible arguments. See ?merge_list for further information.
**earpoints**

output: whether to return an output (position of the points making the lines in the stereographic projection)

plot: whether to plot

xh: orientation of the x axis: can be ‘WE’ or ‘SN’.

unique: whether to only plot each similar plan once.

**Value**

the x,y coordinates of each projected plane

**References**

RFOC package

**See Also**

[earnet, earpoints] and [dipfix]

**Examples**

```r
strike <- c(45, 0)
dip <- c(20, 65)

earnet()
earplanes(strike, dip, hsphere = "b")
encircle(earinc(dip))
```

---

**earpoints**  

*Draws points on an equal area stereonet*

**Description**

Draws points on an equal area stereonet (modified from RFOC package)

**Usage**

```r
earpoints(
  dec,
  inc,
  hsphere = "b",
  double = FALSE,
  a = list(pch = 21, col = "black"),
  l = list(bg = "black"),
  h = list(bg = "grey"),
  u = list(bg = "white"),
  labels = NA,
)```
Arguments

dec declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010). Values outside this range are corrected by the \texttt{incfix} function.

inc inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010). Values outside this range are corrected by the \texttt{incfix} function.

hsphere the hemisphere onto which to project the data. The default is "b" for both: this useful in the case of oriented vectors rather than lines like for paleomagnetism. Other choices are "l" and "u" for lower and upper hemisphere.

double whether to plot the equivalent point to one having an inclination of 0°(with \texttt{dec = dec +180})

a, l, h, u list of graphical parameters to feed points() for all points, or for the points of the upper (u) and lower (l) hemisphere, and of the samples having an inclination of 0° (h) (the three latter override a). See \texttt{points} help page for the possible arguments. See the example for illustration, and \texttt{merge_list} for further information.

labels labels to each point

pos position of each label (see \texttt{text()} help page)

output whether to return an output (position of the points in the stereographic projection)

plot whether to plot

xh orientation of the x axis: can be 'WE' or 'SN'.

Value

the x, y coordinates of each point in the projection

References


See Also

earnet, earplanes and incfix
Examples

```r
earnet()

h <- 17
m <- 11

if(m < 10) a <- "0" else a <- ""

title(paste("Il est ", h, "h", a, m, sep = ""))

i1 <- seq(40, 100, by = 10)
i2 <- seq(0, -100, by = -10)
d1 <- rep(h * 30 + m * 0.5, length(i1))
d2 <- rep(m * 6, length(i2))

inc <- c(i1, i2)
dec <- c(d1, d2)

earpoints(dec, inc)
```

encase

Encases two numbers between multiples of a given number

Description

Encases two numbers between multiples of a given number

Usage

```r
encase(x1, x2, n)
```

Arguments

- **x1**: the first value of the interval
- **x2**: the second value of the interval (can be higher or lower, but never equal to x1)
- **n**: the number to find the multiples from

Value

the multiples of n directly encompassing x1 and x2

See Also

Similar function: casing

Examples

```r
encase(5, 1, 5)
```
encircle  \hspace{1cm} \textit{Draws circles}

\section*{Description}

Draws circles

\section*{Usage}

\begin{verbatim}
encircle(
    r = 1,
    x = 0,
    y = 0,
    ndiv = 360,
    plot = TRUE,
    add = TRUE,
    output = FALSE,
    ...
)
\end{verbatim}

\section*{Arguments}

- \textbf{r} \hspace{1cm} \text{the radius of the circles (of length 1 or n)}
- \textbf{x} \hspace{1cm} \text{the x value of the centre of the circles (of length 1 or n)}
- \textbf{y} \hspace{1cm} \text{the y value of the centre of the circles (of length 1 or n)}
- \textbf{ndiv} \hspace{1cm} \text{the number of segments making the circles}
- \textbf{plot} \hspace{1cm} \text{whether to plot the circles}
- \textbf{add} \hspace{1cm} \text{whether to add to an existing plot}
- \textbf{output} \hspace{1cm} \text{whether to return an output}
- \ldots \hspace{1cm} \text{graphical parameters to feed to lines}

\section*{Value}

a list of x and y matrices having n rows, one for each circle

\section*{Examples}

\begin{verbatim}
plot(0, 0, xlim = c(-1,1), ylim = c(-1,1), asp = 1)
encircle(lwd = 2)
encircle(r = seq(0.1,0.9,0.1))
\end{verbatim}
enlarge

Expands the TRUE values of a T/F vector to their nth neighbours

Description

Expands the TRUE values of a T/F vector to their nth neighbours

Usage

enlarge(x, n)

Arguments

x  
a TRUE/FALSE vector (e.g. c(T,T,F,F,T,T))

n  
the proximity order of the FALSE values neighbouring the TRUE values to be converted into TRUE (can be negative, should be convertible into an integer). For instance 1 means that the F values directly next to a T will be converted into T. 2 will apply that to the neighbours neighbours, etc...

Value

a vector of T/F values, with the TRUE values expanded to their nth neighbours

Examples

# Creating a test dataset ----
y <- c(rep(c(0,1,0,-1),8),rep(-1,3),-1.5, rep(-1,2),rep(c(0,1,0,-1),8))
x <- 1:length(y)
df <- data.frame(x,y)
xclip <- c(20,48.5)
yclip <- c(-0.5,1.5)

normt <- df[conditions,]

# Plotting supporting data ----
plot(df$x, df$y, type = "l", lty = 2, ylim = c(-2,2))
rect(xclip[1], yclip[1], xclip[2], yclip[2])

# See how the function reacts ----
embiggened <- enlarge(conditions, 1)

test <- df[embiggened,]

lines(test$x, test$y, lwd = 2, col = "blue")

points(normt$x, normt$y, type = "o", pch = 19, lty = 2, lwd = 2, col = "red")

legend(10, -1.6, legend = c(paste("Points initially isolated: they were chosen", "to be the ones inside the rectangle"), paste("Extension of the points: the first neighbours", "of the points were added")), col = c("red", "blue"), pch = 19, lty = c(2, 1), lwd = 2)

every_nth

**every_nth**

Suppresses every n th element of a vector

**Description**

Suppresses every n th element of a vector

**Usage**

every_nth(x, nth, empty = TRUE, inverse = FALSE)

**Arguments**

- **x**: a vector (numbers, integers, characters, you name it)
- **nth**: the multiple of position where the elements will be suppressed (nth + 1 actually) or kept (if inverse = T)
- **empty**: whether the suppressed element should be replaced by ""
- **inverse**: opposite reaction: n th elements only will be kept

**Value**

a vector with the remaining values

**Author(s)**

Adam D. Smith

**See Also**

practical usage of this function for axes: **minorAxis**
**Examples**

```r
every_nth(numvec, 3)
every_nth(numvec, 3, empty = FALSE)
every_nth(numvec, 3, inverse = TRUE)
every_nth(numvec, 3, empty = FALSE, inverse = TRUE)
```

---

**Description**

Gives a negative of the intervals of a lim object

**Usage**

```r
flip.lim(lim = NULL, l = NULL, r = NULL, b = "[]", xlim = NA)
```

**Arguments**

- `lim` an object convertible into a lim object: either a vector of length 2 or a list of `n` left (1st element) and `n` right (2ndt element) interval limits
- `l` a vector of `n` left interval limits
- `r` a vector of `n` right interval limits
- `b` a character vector for the interval boundaries rules: "[]" (or "closed") to include both boundaries points, "[]" (or "()" and "open") to exclude both boundary points, "[]" (or "[]", "right-open" and "left-closed") to include only the left boundary point, and "[]" (or "["", "left-open", "right-closed") to include only the right boundary point. The notation is simplified to "[]", "[", "]" and "]" only.
- `xlim` the minimum and maximum of the new lim object (minimum and maximum of the old one if NA; is the default)

**Value**

a lim object of intervals in between the provided intervals

**See Also**

`as.lim`
Examples

```r
l <- c(1,3,5,7,9,10)
r <- c(3,4,7,8,9,11)
b <- "["
xlim <- c(-1,15)
res <- flip.lim(l = l, r = r, b = b, xlim = xlim)

plot(1,1,type = "n", xlim = c(-4, 20), ylim = c(0.3, 1.8))
rect(l, 1.1, r, 1.4, col = "green", border = "darkgreen", lwd = 3)
rect(res$l, 1, res$r, 0.7, col = "red", border = "darkred", lwd = 3)
abline(v = xlim)
```

---

### fmean

**Fischer mean**

#### Description

Fischer mean

#### Usage

```r
fmean(dec = NA, inc = NA, int = 1, x = NA, y = NA, z = NA, id = NULL, cart = F)
```

#### Arguments

- **dec**: declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010). Values outside this range are corrected by incfix().
- **inc**: inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010). Values outside this range are corrected by incfix().
- **int**: intensity of the data. Defaults to one (unit sphere).
- **x, y, z**: cartesian coordinates. x is the North, y the East, and z straight down. If dec and inc are not provided they are used to be converted back in dec, inc and int data. Output is corrected by incfix().
- **id**: a name for each point, identifying each group of points you would like to treat separately
- **cart**: whether to output as cartesian coordinates, defaults to F

#### Value

a list of coordinates for the fischer mean, in cartesian form or dec, inc, int form
fmod

Universal remainder function

Description

Given a [xmin,xmax[ or ]xmin,xmax] interval, this function determines the remainder of each numeric relative to this interval. In other words if the interval was repeated over the whole numeric domain, this function determines where each value would be positioned in a given repetition.

Usage

fmod(x, xmax, xmin = 0, bounds = "["")

Arguments

x vector of floating point numbers
xmax, xmin the limits of the interval
bounds how to deal with boundaries (right- or left-open; '[[' or ']']')

See Also

incfix, dipfix and transphere

Examples

fmod(c(1260.23,360),360)
fmod(c(1260.23,360),360,bounds = "]")
fmod(c(1260.23,360),360 + 180, 180)
folder

Creates a new folder where wanted if it does not exist yet

Usage

folder(dir, name)

Arguments

- dir: directory containing the folder
- name: name of the folder

Value

the directory of the folder itself

Examples

folder(tempdir(), "test")

formFunction

Converts a formula into a function

Description

Converts a formula into a function

Usage

formFunction(formula)

Arguments

- formula: the formula to be converted. Should be of the form y ~ f(x)

Examples

f <- formFunction(y ~ log10(x))
f(x=1:10)
framesvg

Draws a standardised pointsvg object into a given frame

Description

Draws a svg object imported as data frame using pointsvg into a given frame.

Usage

framesvg(
  object,  # a pointsvg object (svg object imported as data frame using pointsvg).
  xmin, xmax,  # the x value for the left and right side of the symbol
  ymin, ymax,  # the y value for the low and high side of the symbol
  forget = NULL,  # the elements that should be discarded, by their id or index (i.e. name or number of appearance).
  front = NULL,  # the elements to be put in front and back position, by their id or index (i.e. name or number of appearance). By default the order is the one of the original .svg file.
  back = NULL,  # whether to standardise (centre to (0,0), rescale so that extreme points are at -1 and 1) or not (T or F)
  standard = FALSE,  # whether to standardise (centre to (0,0), rescale so that extreme points are at -1 and 1) or not (T or F)
  keep.ratio = FALSE,  # whether to keep the ratio of the object.
  col = NA,  # whether to keep the ratio of the object.
  border = "black",  # whether to keep the ratio of the object.
  density = NA,  # whether to keep the ratio of the object.
  angle = 45,  # whether to keep the ratio of the object.
  lwd = par("lwd"),  # whether to keep the ratio of the object.
  lty = par("lty"),  # whether to keep the ratio of the object.
  scol = border,  # whether to keep the ratio of the object.
  slty = lty,  # whether to keep the ratio of the object.
  slwd = lwd,  # whether to keep the ratio of the object.
  plot = TRUE,  # whether to plot the object.
  output = FALSE  # whether to plot the object.
)

Arguments

- **object**: a pointsvg object (svg object imported as data frame using pointsvg).
- **xmin, xmax**: the x value for the left and right side of the symbol.
- **ymin, ymax**: the y value for the low and high side of the symbol.
- **forget**: the elements that should be discarded, by their id or index (i.e. name or number of appearance).
- **front, back**: the elements to be put in front and back position, by their id or index (i.e. name or number of appearance). By default the order is the one of the original .svg file.
- **standard**: whether to standardise (centre to (0,0), rescale so that extreme points are at -1 and 1) or not (T or F).
keep.ratio if the object is to be standardised, whether to keep the x/y ratio (T or F)
col the polygones background color. If density is specified with a positive value this gives the color of the shading lines.
border the lines color.
density the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn.
angle the slope of shading lines, given as an angle in degrees (counter-clockwise)
lty, lwd the border line type and width, see ?par for details.
scol, slty, slwd the colour, type and width of the shading lines.
plot whether to add to a plot
output whether to output the new object coordinates

Details

The centresvg and framesvg have a lot of similarities with the multigons function: the graphical parameters are mostly identical. However there is a strong distinction between the -svg functions and multigons: when providing several graphical arguments, multigons will attribute them to each polygon, whereas the .svg functions will use them for each repetition of the .svg object. Using the latter, the graphical parameters will be applied to all the elements of a drawing. If you want a finer personalisation you have to use multigons and multilines (or an hybrid of the two, yet to be coded).

See Also

Similar functions: centresvg and placesvg
Change the drawing: changesvg and clipsvg
Uses ignore to avoid drawing unnecessary objects

Examples

# Simple use

object <- example.ammonite
xmin <- c(8,7)
xmax <- c(10,9)
ymin <- c(7,6)
ymax <- c(9,8)

plot(c(-10,10), c(-10,10), type = "n")
abline(v = unique(c(xmax, xmin)))
abline(h = unique(c(ymax, ymin)))
framesvg(object, xmin, xmax, ymin, ymax, col = c("white", "grey80"))

# Precision positioning
greySet

Sets the plot environment to draw a long vertical data set

Description

Sets the plot environment to draw a long dataset. It provides grey bands as supplementary scale, and axes with major and minor ticks.

Usage

greySet(
xlim, ylim, xtick = NA, ytick = NA, nx = 1, ny = 1, xaxs = "i", yaxs = "i", xarg = list(tick.ratio = 0.5), yarg = list(tick.ratio = 0.5, las = 1), v = T, inverse = F, abbr = "", skip = 0, targ = list(col = "white", lwd = 2), rarg = list(border = NA, col = "grey85")
)

Arguments

xlim, ylim the x and y limits (e.g. xlim = c(-1,1))
xtick, ytick the interval between each major ticks for x and y
### greySet

- **nx, ny** the number of intervals between major ticks to be divided by minor ticks in the x and y axes
- **xaxs, yaxs** The style of axis interval calculation to be used for the x and y axes. By default it is "i" (internal): it just finds an axis with pretty labels that fits within the original data range. You can also set it to "r" (regular): it first extends the data range by 4 percent at each end and then finds an axis with pretty labels that fits within the extended range. See `?par` for further explanation.
- **xarg, yarg** a list of arguments to feed to `minorAxis()` for the x and y axes. See the `?minorAxis` help page for the possible arguments. See `?merge_list` for further information.
- **v** whether the grey bands are vertical
- **inverse** inverse the bands position
- **abbr** text to be repeated in the grey bands each major tick
- **skip** number of text redundancies to be skipped
- **targ, rarg** a list of arguments to feed to `text()` and `rect()` respectively. If set to NULL, does not add the corresponding element.

### Value

A plotting environment to draw a long data set

### See Also

Similar functions: `whiteSet` and `greySet`

To create axes with major and minor ticks: `minorAxis`

To print a plot in pdf: `pdfDisplay`

To automatically determine pretty interval limits: `encase`

### Examples

```r
y <- c(0, 11, 19, 33)
x <- c(1, 2, 2.5, 4)

a <- min(y)
b <- max(y)

f <- encase(a-1, b, 5)
greySet(c(0, 4), f, abbr="abbr", ytick = 10, ny = 10)
points(x, y, pch=19)
```
homogenise

Homogenise a list

Description
Takes each element of a list and repeats each one so they have the same length. This function is designed to be integrated in another function and clean its arguments. **IF YOU RECEIVED A WARNING FROM THIS FUNCTION IN ANOTHER FUNCTION:** Check that the length of the arguments indicated by the warning are correct.

Usage

```r
homogenise(i = NULL, n = NULL, l = list(), cycle = TRUE)
homogenize(i = NULL, n = NULL, l = list(), cycle = TRUE)
```

Arguments

- `i` reference object of length n
- `n` length to reach (is overridden by i)
- `l` list for each element to be repeated to have a length n. These elements have to be integers, numerics or characters.
- `cycle` whether to recycle the elements or to only allow elements of length 1 or n

Value
A list identical to the one initially provided, with elements length homogenized to i

See Also

`merge_list`

Examples

```r
i <- rep(1:4, 2)
l <- list(a = c(1,2,3),
         b = "R",
         d = 1:100,
         e = c("a", "b"),
         f = FALSE )

homogenise(i = i, l = l)
homogenise(n = 10, l = l)
```
Description

Ignores useless objects: this function will discard the polygons or polylines outside a certain range. This allows to avoid unnecessary work for multigons(), multilines(), centresvg() and framesvg().

Usage

ignore(
  i,
  x,
  y = NA,
  d = list(),
  j = unique(i),
  arg = list(),
  xlim = par("usr")[[1, 2]],
  ylim = par("usr")[[3, 4]],
  xlog = par("xlog"),
  ylog = par("ylog")
)

Arguments

i
   a polygon id for each x and y coordinate. If n objects are provided there should be n unique ids describing them, and the graphical parameters should be of length 1 or n.

x, y
   numeric vectors of coordinates.

d
   a list of named vectors going with i, x and y

j
   a list of the ids in the order used for the arg arguments. By default they are in their order of appearance in i

arg
   a list of arguments of length 1 or n.

xlim, ylim
   the limits in x and y; if any object has all his points past one of these limits, it will be removed.

xlog, ylog
   whether the axes have logarithmic scale

Value

a list of i, x, y, d, j and arguments.

See Also

Tributary functions: multigons, multilines, centresvg and framesvg
Examples

i <- c(rep("A1",6), rep("A2",6), rep("A3",6))
x <- c(1,2,3,3,1,4,5,6,6,5,4,7,8,9,9,8,7)
y <- c(1,2,3,4,5,6,1,2,3,4,5,6,1,2,3,4,5,6)
xlim <- c(2,5)
ylim <- c(0,1.5)

plot(c(0,10),c(0,10),type = "n")
rect(xlim[1], ylim[1], xlim[2], ylim[2])
multilines(i, x, y, lty = 3, col = "grey80")

res <- ignore(i, x, y, arg = list(lty = 1, lwd = 3,
col = c("orange", "green", "red"),
xlim = xlim, ylim = ylim)
do.call(multilines, res)

---

in.lim

Finds the intervals encompassing values

Description

This function returns the intervals encompassing x values. This works only if the intervals (as lim objects) are non-overlapping and non-adjacent (if certain boundaries are neighbouring, the boundary rule should exclude all, or all but one)

Usage

in.lim(x, lim = NULL, l = NULL, r = NULL, id = 1L, b = "][", index = FALSE)

Arguments

x a vector values
lim an object convertible into a lim object: either a vector of length 2 or a list of n left (1st element) and n right (2ndt element) interval limits. The intervals should be non-overlapping and non-adjacent.
l a vector of n left interval limits
r a vector of n right interval limits
id a vector of n interval IDs (default is 1 for each interval)
b a character vector for the interval boundaries rules: "]" (or "closed") to include both boundaries points, "[" (or ")" and "open") to exclude both boundary points, "[" (or "]", "right-open" and "left-closed") to include only the left boundary point, and "]" (or "]", "left-open", "right-closed") to include only the right boundary point.
whether the output should be a list of the initial vector and of the corresponding intervals in which they lay (index = FALSE, is the default), or simply the index of the intervals in the initial lim object (index = TRUE)

Value

a list of the intervals where the x values lay or a vector of their index

See Also

as.lim

Examples

```r
x <- c(99,1,3,5,2,4,5,6,9,4,8,20,26,52,42,24,25,12,40,10,16,17)
lim <- as.lim(l = c(100,10,20,27), r = c(99,12,27,42), b = "]")
in.lim(x, lim = lim)
in.lim(x, lim = lim, index = TRUE)

# Applications to Stratigraphy
proxy <- proxy.example # This is a data.frame with (fake) magnetic
    # susceptibility (ms) and depth (dt)

    # Each sample was taken in a specific bed (not at the boundary between two,
    # to make things easier). We will invoke the data of the beds (bed.example)
    # and identify the lithology of each sample
res <- in.lim(proxy.example$dt, # Position of each sample
    l = bed.example$l, # Left boundary of the beds
    r = bed.example$r, # Right boundary of the beds
    id = bed.example$litho) # Lithology of each bed (if you wanted
    # to know the name of the bed each
    # sample is in you would have put
    # bed.example$id)
proxy$litho <- res$id # The result provides the id (here the lithology) of
    # each interval encompassing the measurement (x, here
    # proxy.example$dt)

plot(proxy$ms, proxy$dt, type = "l", xlim = c(-2*10^-8, 8*10^-8))
shale <- subset(proxy, proxy$litho == "S")
points(shale$ms, shale$dt, pch = 4)
limestone <- subset(proxy, proxy$litho == "L")
points(limestone$ms, limestone$dt, pch = 19)
chert <- subset(proxy, proxy$litho == "C")
```
in.window

Description

Find the index of points in time-series that fall into a specific window, even with irregular sampling rate. The iterations needed in this function are equal to the maximum amount of points found in the windows, therefore it should be reasonably efficient for short windows at least.

Usage

in.window(x, w, xout = unique(x), b = "[]", warn = 100, ...)

Arguments

x
  the position values to be regrouped in windows
w
  the window length (top to bottom)
xout
  the center of each window, defaults to x
b
  the boundary rule at the top and bottom of the window: "][]" means that neither the top nor bottom are taken in, "[[]" means that top and bottom are taken in, "[]"]" and "][][" mean that only the top or the bottom are taken in, respectively. Also accepts: "]","[", "()", "open", "closed", "left-open", "right-open", "left-closed" and "right-closed": see rebound for more information
warn
  an integer of the amount of iterations after which a warning is issued: this could mean that there are too many data points in a window, and that the computation will become very inefficient. This is up to the user to see. If you want to remove the warning, set this parameter to Inf
...
  intensity values corresponding to each x position, making time-series. They will be provided window by window in the output.

Value

a list made of the center values of the windows ($xout), a matrix of the index of the original x values in each corresponding window ($x.index; the rows correspond to each $xout value), a matrix of the x values in each corresponding window ($x; the rows correspond to each $xout value), the amount of points in each window ($n.size), and additional matrices of additional intensity values provided in ... (names correspond to the names provided in ...; the rows correspond to each $xout value)
Examples

# Visual example ----

```r
set.seed(42)

n <- 600
t <- seq_len(n)
p1 <- 30
p2 <- 240

xy <- (1 + 0.6 * sin(t*2*pi/p2)) * sin(t*2*pi/p1) + 2 * sin(t*2*pi/p2) +
      rnorm(n, sd = 0.5) + t * 0.01

inter_dt <- round(runif(length(xy), min = 0.5, max = 1.5),1)
dt <- cumsum(inter_dt)

keep <- runif(length(dt)) < 0.5

xy <- xy[keep]
dt <- dt[keep]

window <- in.window(dt, w = 30, 1:590, xy = xy)

par(mfrow = c(1,2))

plot(xy, dt, type = "o", pch = 19,
     ylim = c(0,600), main = "Moving Average")

lines(rowMeans(window$xy, na.rm = TRUE), window$xout,
     col = "red", lwd = 2)

plot(window$n.size, window$xout, pch = 19,
     ylim = c(0,600), xlim = c(0,20), ylab = "dt",
     main = "Amount of Points in Average")

# Test the boundary rule ----

x <- c(1,1,2,3,4,6,8,10,15,16)
xout <- -6:22

output <- in.window(x = x, w = 10, xout = xout, b = "[]")

test <- output$x - output$xout

see <- cbind(output$xout, output$x)

colnames(see) <- c("xout", paste0("x", seq_len(ncol(see)-1)))

test # difference between x and xout: it is contained in ]-5,5]

see
Fix Inclination

Fix inclination and declination so that they fall in the correct quadrant and hemisphere (modified from RFOC package)

Usage

```r
incfix(dec, inc, hsphere = "b")
```

Arguments

dec  declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010). Values outside this range are corrected by this function.

inc  inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010). Values outside this range are corrected by this function.

hsphere  the hemisphere onto which to project the data. Either "b" for both. This is the default and useful for paleomagnetism. In this case positive and negative values of inc are permitted. Or "l" for lower, and "u" for upper, allowing only negative or positive inc values respectively.

Details

Quadrants are determined by the sine and cosine of the dip angle: co = cos(dip), si = sin(dip), quad[co>=0 & si>=0] = 1, quad[co<0 & si>=0] = 2, quad[co<0 & si<0] = 3 and quad[co>=0 & si<0] = 4. Samples at inc == 0° and inc == 90° are taken as exceptions (cf. code). Be cautious with the floating point error however, round if needed.

See Also

```r
fmod, dipfix and transphere
```

Examples

```r
incfix(591,-425,"b")
incfix(591,-425,"u")
incfix(591,-425,"l")
```
infobar

Draws rectangles with text in them

Description

Draws rectangles with text in them, typically to delimit (stratigraphical) intervals (e.g. magnetocho- 
trons, but also lithostratigraphy,...)

Usage

infobar(
  xmin, xmax, 
  ymax, ymin, 
  labels = NA, 
  m = list(), 
  t = list(), 
  srt = 90, 
  family = par("family"), 
  xpd = par("xpd") 
)

Arguments

xmin, xmax, ymin, ymax
  x and y limits for the rectangles. You can either provide 1 or n of each (if you 
  want to have always the same x limits but multiple and different y ones it is 
  possible)

labels
  a 1 or n character vector (i.e. text) specifying the text to be written in the rectan-
  gle. You can write "" for no text.

m, t
  a list graphical parameters (of length 1 or n) to feed multigons() for m and to 
  text() for t. See respective help pages ?multigons and ?text for the possible argu-
  ments. See the example for illustration, and ?merge_list for further information.

srt, family, xpd
  further graphical parameters, see ?par for information

See Also

Similar functions: multigons, bedtext, nlegend and ylink

To deal with intervals: as.lim and related functions
is.clockwise

Examples

labels <- c("High 5", "Low 5", "5")
ymin <- c(10, -10, 2.5)
ymax <- c(20, 0, 7.5)

plot(c(0,6),c(-20,20), type = "n")

infobar(xmin = 0, xmax = 1, ymin = ymin, ymax = ymax, labels,
m = list(col = c("grey","grey", "red"),
        border = "black", density = 10),
t = list(cex = 1.5, col = "white"))

is.clockwise

Identify whether the points of a polygon are ordered clockwise

Description

Identify whether the points of a polygon are ordered clockwise

Usage

is.clockwise(x, y, i = rep("A1", length(x)), get.pos = F)

Arguments

x, y the coordinates of the polygons
i the identification of the polygons if there are multiple ones
get.pos get the output as a list of the result and of the output of octapos()

Value

logical values for each polygon: TRUE for clockwise, FALSE for counterclockwise, NA for ambiguous order, typically in lines or the polygons whose lines cross each other (although sometimes such polygons are still giving T or F values, as this function only consider certain reference points, for more details see octapos).

Examples

# Generate some polygons ----

x1 <- c(0,1,0.5)
y1 <- c(3,3,4)
i1 <- rep("P1", 3)
s1 <- 1:3

x2 <- c(3,3.5,4)
y2 <- c(3,4,3)
i2 <- rep("P2", 3)
s2 <- 1:3
x3 <- c(0, 0.5, 1)
y3 <- c(1, 1.5, 2)
i3 <- rep("P3", 3)
s3 <- 1:3
x4 <- c(3, 4, 4, 3)
y4 <- c(1, 2, 1, 2)
i4 <- rep("P4", 4)
s4 <- 1:4
x5 <- c(1, 2, 3, 2, 1)
y5 <- c(-0.5, 0.4, -0.5, 0.5, -0.4, 0.5)
i5 <- rep("P5", 6)
s5 <- 1:6
x6 <- c(1, 2, 3, 2, 1)
y6 <- c(-2, -1, -2, -1, -2.5, -1)
i6 <- rep("P6", 6)
s6 <- 1:6
x <- c(x1, x2, x3, x4, x5, x6)
y <- c(y1, y2, y3, y4, y5, y6)
i <- c(i1, i2, i3, i4, i5, i6)
s <- c(s1, s2, s3, s4, s5, s6)

# Test whether they are clockwise or not ----

is.clockwise(x = x, y = y, i = i)

# Visualise the result ----

plot.new()
plot.window(xlim = c(-0.5, 5.5), ylim = c(-2.5, 4.5))
axis(1)
axis(2)
multigons(i = i, x = x, y = y)

center.x <- c(0.5, 3.5, 0.5, 3.5, 2, 2)
center.y <- c(3.4, 3.4, 2, 1.5, 0, -1.5)
center.lab <- c("P1", "P2", "P3", "P4", "P5", "P6")
text(x = center.x, y = center.y, labels = center.lab)
text(x = x, y = y, labels = s)
is.joint

Check (bedding) joint objects

Description

Check whether a data.frame complies with the criteria to be a valid bedding joint to be integrated in a litholog.

Usage

is.joint(joint, warn = F)

Arguments

joint the data.frame to test
warn whether to have a warning explaining why the candidate joint is invalid

Examples

# Plots for visualisation ----

opar <- par("mfrow")
par(mfrow = c(2,1))

plot.new()
plot.window(xlim = range(oufti99$'sin'x),
            ylim = range(oufti99$'sin'y))
title("oufti99$'sin'")
placesvg(oufti99$'sin')

plot.new()
plot.window(xlim = range(oufti99$ammonite$x),
            ylim = range(oufti99$ammonite$y), asp = 1)
title("oufti99$ammonite")
placesvg(oufti99$ammonite)

par(mfrow = opar)

# Exemplification of is.joint ----

is.joint(oufti99$'sin')

is.joint(oufti99$ammonite)
leftlog  

Finds bed intervals in a "litholog()"-like data frame

Description

Determines the interval of bed boundaries at the far left of a litholog. This is used when the welding of varying bed boundaries changes these intervals, and that you want to use bedtext() to print the name of the beds on the log.

Usage

leftlog(i, dt, xy, warn = TRUE)

Arguments

i       the id of the polygons in the "litholog()"-like data frame
dt      the depth of the polygons in the "litholog()"-like data frame
xy      the x values (i.e. hardness) of the polygons in the "litholog()"-like data frame
warn    whether you want to be annoyed

Value

a list of minima (l) and maxima (r) of boundaries corresponding to each bed (id)

See Also

litholog, weldlog and bedtext

Examples

l <- c(0,1,2,3,4)
r <- c(1,2,3,4,5)
h <- c(4,3,4,3,4)
i <- c("B1","B2","B3","B4","B5")
log <- litholog(l, r, h, i)

whiteSet(xlim = c(-1,5), ylim = c(-1,6))

title("leftlog() gets the bed names in the right position")

multigons(log$i, log$xy, log$dt, lty = 3)

seg1 <- sinpoint(4, 0, 0.25, pos = 1, phase=0)
seg2 <- sinpoint(4, 0, 0.25, pos = 1, phase=1)

welded <- weldlog(log, dt = c(2,3), seg = list(seg1, seg2), add.dt = 0.5)

multigons(welded$i, welded$xy, welded$dt, lwd = 3, lty = 2, border = "red")
litholog

Create/check lithologs

Description

Creates and checks basic coordinates of polygons to draw a simple litholog with rectangles

Usage

litholog(l, r, h, i)

is.litholog(object)

Arguments

l, r  
the height of each delimitation (upper and lower; l and r stand for left and right boundaries of the interval, their order does not matter)

h  
the hardness of each bed

i  
the id of each bed: it should be different for each bed

object  
an R object to test whether it is a litholog, as outputted by the litholog function

Value

A table of ids (i), depth (dt) and xy value (i.e. hardness, or simply the x position if your litholog is vertical) of rectangles for each bed. This order of column variable (i, dt, xy) is checked by is.litholog

See Also

For a more detailed explanation of how to make a litholog: StratigrapherR
How to prepare the plot background for the litholog: whiteSet
How to draw the litholog: multigons
How to add the names of the beds in the litholog: bedtext
How to plot in pdf: pdfDisplay
To add personalised boundaries between beds: weldlog
To have open beds at the extremities of the log. More generally to transform a polygon into a polyline and control the part that is not drawn: multilines and shift
To add details and drawings: `centresvg` and `framesvg`

Go further with interval data (between two boundaries, as there often is in stratigraphy): `as.lim` and related functions.

Complementary functions: `infobar` and `ylink`

**Examples**

```r
l <- c(1,2,3)  # left boundary of the bed interval (upper or lower)
r <- c(0,1,2)  # right boundary of the bed interval (upper or lower)
h <- c(4,3,4)  # hardness (arbitrary)
i <- c("B1","B2","B3")  # Bed name

basic.litholog <- litholog(l,r,h,i)  # Generate data frame of the polygons
                                # making the litholog

is.litholog(basic.litholog)

whiteSet(xlim = c(0,4), ylim = c(0,3), ytick = 1, ny = 10)  # Plot background
multigons(basic.litholog$i, basic.litholog$xy, basic.litholog$dt)  # Draw log
```

---

**memento**

*Remembers and outputs the result of a slow function*

**Description**

Memento mori: you do not have time to lose on unnecessary calculations. This function remembers the output of a slow function, for given arguments and, if asked politely, given files and a given random seed. If they match the previous arguments, files and seeds, the output is provided without delay, otherwise the function runs, and all the parameters are saved for next time. The trade-off is to assign a folder to store the data (see also details). The function can also be forced to rerun.

**Usage**

```r
memento(
  what,
  args,
  name,
  dir = getwd(),
  subdir = "memento",
  rerun = F,
  check.files = list(),
  files.dir = getwd(),
  check.seed = F,
  speak = T
)
```
Arguments

what  a (slow) function
args  a list of the the arguments to give to the function. If they differ from saved values, the function will run again.
name  the name of the folder where to store the info. THIS NEEDS TO BE DIFFERENT FOR EACH IMPLEMENTATION OF THE FUNCTION IN IDENTICAL DIRECTORIES.
dir  the directory. You can set it as the working directory via `getwd`.
subdir  a name for a subdirectory (useful when the function is used several time in a script)
rerun  if TRUE, the function is rerun no matter what. This is useful to update information that is not present in the R environment, for instance if you load data from external files that have been updated.
check.files  a list of files to check changes in (see details). If the list is of length 0, no file is checked.
files.dir  directory for the files to be checked.
check.seed  if TRUE, the value of the random seed in effect will be taken into account; if it changes, the function will run again.
speak  whether to signify when the (slow) function is running

Details

file data is summarized using MD5sum, which can have limitations in data size (2^{64} bits) and in cryptographic purposes.

Value

the output of the function

Examples

tf <- tempdir()
if(exists("run.number")) run.number <- run.number + 1 else run.number <- 1
name <- paste("T",run.number)

testfun <- function(a = 1, time = 3){
    Sys.sleep(time)
    return(a + 0.1 * abs(rnorm(1)))
}

# First time running; the function takes some time, memento needs the # output to be generated, and will remember for later.
set.seed(43)
memento(testfun,  args = list(a = 7), name = name, dir = tf)
merge_list

Method for merging lists by name

Description

This is a method that merges the contents of lists based on the name of the elements. In the case of identical names, the order of the lists determines which element is kept.

Usage

merge_list(l1, l2, ...)

Arguments

11 the first list.
12 the list which will supply additional elements to l1 that are not already there by name.
... additionnal lists, that bring elements if they are not existing by name in the ones before.
Details

if a name appears more than once in a list, only the first one will be kept. This is particularly useful if you want to still be able to provide whichever argument you want to a function inside another function. See the advanced use in the examples to see how to do it.

Value

A merged list of all lists provided, each element (determined by its name) appearing only once.

See Also

homogenise provides a general way of dealing with function arguments.

To get a better understanding of how to deal with function arguments, go see ?do.call and ?list.

Examples

# Simple use

a <- list(lty = c(2,4), mar = 4, plot = TRUE)
b <- list(lty = "hype", lty = "hype", pink = TRUE)
d <- list(lty = FALSE, pink = "Yikes", mar = "ldkfj", test = "Successful")

merge_list(a,b,d)

Advanced use

# We will plot points with different parameters for each lithology (see also the example in ?in.lim)

advanced.ex <- function(line.args = list(lty = 3, col = "grey"),
                          all = list(pch = 21, cex = 2),
                          chert = list(bg = "white"),
                          limestone = list(bg = "black"),
                          shale = list(bg = "red"),
                          main = "")
{

  # Preparation of plot and necessary data frames

  plot(proxy.example.litho$ms, proxy.example.litho$dt, type = "n",
       xlim = c(-2*10^-8, 8*10^-8), main = main)

  shale.df <- subset(proxy.example.litho, proxy.example.litho$litho == "S")
  limestone.df <- subset(proxy.example.litho, proxy.example.litho$litho == "L")
  chert.df <- subset(proxy.example.litho, proxy.example.litho$litho == "C")

  # Important part:

  # We use the do.call function, which calls a given function and provides
  # its arguments via a list. It is that list that is created by merge list.
  # for the lines function, we provide x and y coordinates, a personalised
merge_list

# list of arguments (line), and the default parameters. In this order the # personalised arguments override the default ones, but the latter are used # in the absence of personalised arguments

line.args <- merge_list(list(x = proxy.example.litho$ms, 
y = proxy.example.litho$dt), 
  line.args, # personalised list of arguments 
  list(lty = 3, col = "grey") # default parameters
)

do.call(lines, args = line.args)

# Same procedure for the points of each lithology, but we add an 'all' # argument that applies for each point

chert.args <- merge_list(list(x = chert.df$ms, 
y = chert.df$dt), # Coordinates 
  chert, # Personalised arguments for cherts 
  all,   # Personalised arguments for all points 
  list(bg = "red"), # Default arguments 
  list(pch = 21, cex = 2) # Default arguments
)

limestone.args <- merge_list(list(x = limestone.df$ms, 
y = limestone.df$dt), 
  limestone, all, 
  list(bg = "red"), list(pch = 21, cex = 2))

shale.args <- merge_list(list(x = shale.df$ms, y = shale.df$dt), 
  shale, all, 
  list(bg = "red"), list(pch = 21, cex = 2))

do.call(points, args = chert.args)
do.call(points, args = limestone.args)
do.call(points, args = shale.args)

)

omfrow <- par()$mfrow

par(mfrow = c(1,3))

advanced.ex(main = "Default")

advanced.ex(main = "Change line and all", 
  line.args = list(lty = 1), 
  all = list(pch = 22))

advanced.ex(main = "Personalise more", 
  line.args = list(lty = 1, col = "black"), 
  all = list(pch = 22), 
  shale = list(pch = 4))
mid.lim

Par(mfrow = omfrow)

mid.lim

Provides mid-points intervals in an ordered vector

Description

Provides mid-points intervals in an ordered vector

Usage

mid.lim(x, id = 1L, b = "[]")

Arguments

x an ordered vector
id a vector of n interval IDs (default is 1 for each interval)
b a character vector for the interval boundaries rules, see as.lim help page for
details

Value

a lim object of intervals with boundaries at midway between the x values

See Also

as.lim

Examples

mid.lim(c(1,3,7,20,45,63))

minorAxis

Adds an axis with minor ticks to a plot

Description

Adds an axis with minor ticks to a plot, but with the possibility to have no superposition of minor
ticks on major ticks, allowing to export a clean plot in vector format. It is based on the minor.tick
function in the Hmisc package.
Usage

\[ \text{minorAxis}( \]
\[ \text{side,} \]
\[ n = \text{NULL}, \]
\[ \text{at.maj = NULL,} \]
\[ \text{at.min = NULL,} \]
\[ \text{range = NULL,} \]
\[ \text{tick.ratio = 0.5,} \]
\[ \text{labels.maj = TRUE,} \]
\[ \text{line = NA,} \]
\[ \text{pos = NA,} \]
\[ \text{outer = FALSE,} \]
\[ \text{font = NA,} \]
\[ \text{lty = "solid",} \]
\[ \text{lwd = 1,} \]
\[ \text{lwd.ticks = lwd,} \]
\[ \text{col = NULL,} \]
\[ \text{col.ticks = NULL,} \]
\[ \text{hadj = NA,} \]
\[ \text{padj = NA,} \]
\[ \text{extend = FALSE,} \]
\[ \text{tcl = NA,} \]
\[ \ldots \]
\[ ) \]

Arguments

\text{side} \quad \text{an integer (here 1,2,3 or 4) specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and, 4=right.}

\text{n} \quad \text{the number of intervals defined by the minor ticks}

\text{at.maj} \quad \text{the positions at which major tick-marks are to be drawn. By default (when NULL) tickmark locations are computed, see the "Details" part in the ?axis help page.}

\text{at.min} \quad \text{the positions at which minor tick-marks are to be drawn. This parameter overrides n.}

\text{range} \quad \text{the range of the axis}

\text{tick.ratio} \quad \text{ratio of lengths of minor tick marks to major tick marks. The length of major tick marks is retrieved from par("tcl") unless specified otherwise.}

\text{labels.maj} \quad \text{this can either be a logical value specifying whether (numerical) annotations are to be made at the major tickmarks, or a character or expression vector of labels to be placed at the major tickpoints.}

\text{line, pos, outer, font, lty, lwd, lwd.ticks, col, col.ticks, hadj, padj, tcl, ...} \quad \text{see the ?axis function help page for the other parameters}

\text{extend} \quad \text{whether to add minor ticks even outside the major ticks (T) or not (F)
See Also

Set a plot environment with minorAxis: whiteSet, blackSet and greySet

The ticks repartition is computed using minorAxisTicks

Examples

```r
plot.new()
plot.window(xlim = c(0,1), ylim = c(0,1))
minorAxis(1, n = 10, range = c(0.12,0.61))
minorAxis(3, n = 10, extend=FALSE)
```

---

**Description**

Compute pretty mark locations for minor ticks, based on the way that traditional R graphics do it.

**Usage**

```r
minorAxisTicks(usr, n = NULL, at.maj = NULL, extend = T)
```

**Arguments**

- `usr`: the user coordinates of the minimum and maximum limits of the axis
- `n`: the number of intervals defined by the minor ticks
- `at.maj`: the positions at which major tick-marks are to be drawn. By default (when `NULL`) tickmark locations are computed buy the `axisTicks` function
- `extend`: whether to add minor ticks even outside the major ticks (`T`) or not (`F`)

**See Also**

minorAxis, seq_log

This function is based on `every_nth`, which suppresses values every multiple of a given number.

**Examples**

```r
minorAxisTicks(usr = c(-20, 620), n = 10)
```
multigons  

Draws several polygons.

Description

Draws several polygons. This function expands on the polygon() function from base R graphics. The difference is that several polygons can be drawn in one line by providing a polygon id: i. To each polygon you can provide different graphical parameters (i.e. colour, shading, etc). On the contrary of the polygon() function the graphical parameters of the shading lines can be independent of the border lines.

Usage

multigons(
  i,
  x,
  y,
  j = unique(i),
  forgot = NULL,
  front = NULL,
  back = NULL,
  density = 0,
  angle = 45,
  border = "black",
  col = NA,
  lty = par("lty"),
  lwd = par("lwd"),
  scol = border,
  slty = lty,
  slwd = lwd,
  lend = 0,
  ljoin = 0,
  lmitre = 10
)

Arguments

i  

A polygon id for each x and y coordinate, i.e. the name of each polygon. If you want to give each polygon a different aspect you should provide a vector of n elements (if you have three polygons "A1", "A2" and "A3" with "A2" that should be blue you should provide the colours of all three: e.g. col = c("white", "blue", "white"))

x, y  

Numeric vectors of x and y coordinates

j  

A list of the ids (names) in the order used for the graphical parameters (e.g. colour, shading, etc...). By default they are in their order of appearance in i
The `multigons` function in R allows for the drawing of polygons with advanced control over their appearance. This function shares similarities with `centresvg` and `framesvg`, but offers more advanced control for each element.

**Parameters**

- **forget**: the polygons that should not be drawn, by their id or index (i.e. name or number of appearance).
- **front, back**: the polygons to be put in front and back position, by their id or index (i.e. name or number of appearance). By default the order is the one defined by `j`, and if `j` is absent by the order in `i`.
- **density**: the density of shading lines, in lines per inch. The default value of 0 means that no shading lines are drawn.
- **angle**: the slope of shading lines, given as an angle in degrees (counter-clockwise).
- **border**: the colour to draw the border. The default is black. Use `border = NA` to omit borders.
- **col**: the colour for filling the polygon. The default, NA, is to leave polygons unfilled.
- **lty, lwd**: the border line type and width, see `?par` for details.
- **scol, slty, slwd**: the colour, type and width of the shading lines.
- **lend, ljoin, lmitre**: additional graphical parameters, see `?par` for details.

**Details**

In the case you want shading this function will draw three overlapping polygons: one for the background, one for the shading lines and one for the border. `multigons` shares similarities with `centresvg` and `framesvg`, but allows more advanced control of each element.

**See Also**

Similar functions: `multilines`, `infobar`

Complementary function: `shift`

Uses `ignore` to avoid drawing unnecessary objects

**Examples**

```r
# Simple use:
i <- c(rep("A1",6), rep("A2",6), rep("A3",6)) # Polygon ids
x <- c(1,2,3,2,1,2,3,4,3,2,3,4,5,5,4,3) # x coordinates
y <- c(1,2,3,4,5,6,1,2,3,4,5,6,1,2,3,4,5,6) # y coordinates
plot(c(-1,7), c(-2,9), type = "n", xlab = "", ylab = "", main = "Simple use")
multigons(i, x, y,
   front = "A2", # This gets the polygon A2 in front of all others
density = c(NA, 5, 10), # Different shading density
   scol = "darkred", # Same shading colour
col = c("black", "grey", "white"), # Different background colour
   lwd = 2, # Width of border lines for all polygons
   slty = 2, # Shading lines type, same for all polygons
   slwd = 1) # Shading lines width, same for all polygons
```
# Advanced use:
# Lets first create more polygons

```r
i2 <- c(i, rep("A4", 6), rep("A5", 6), rep("A6", 6))
x2 <- rep(x, 2)
y2 <- c(y, y - 4)
```

# Then lets attribute a group to each of them: lets say blue and red polygons

```r
                     group = c("blue", "red", "blue", "red", "red", "blue"),
                     stringsAsFactors = FALSE)
```

# Then lets attribute different graphical parameters for each group

```r
legend <- data.frame(group = c("red", "blue"),
                      col = c("red", "blue"),
                      density = c(10, 20),
                      scol = c("darkred", "darkblue"),
                      stringsAsFactors = FALSE)
```

# Now that you have a data frame saying which polygon is in which group,
# and one providing distinct graphical parameters for each group, you can
# join the two with help of the dplyr package:

```r
library(dplyr)
parameters <- left_join(groups, legend, by = "group")
```

# Then simply apply them to multigons:

```r
plot(c(0, 12), c(-3, 7), type = "n", xlab = "", ylab = "",
     main = "Advanced use")
multigons(i2, x2, y2,
         forget = c("A1"),  # If you want to avoid drawing one polygon
         front = c("A2", "A3"),  # Puts A2 in front and A3 right behind
         col = parameters$col,
         density = parameters$density,
         scol = parameters$scol,
         lwd = 2)
```

# Another way (more advanced, but with interesting programming applications)
# to code this:

```r
all.parameters <- merge_list(list(i = i2, x = x2 + 6, y = y2),
                            as.list(parameters),
                            list(lwd = 3, slwd = 2, slty = 2))
all.parameters <- all.parameters[!names(all.parameters) == "group"]
do.call(multigons, all.parameters)
```
multilines

Description

Draws several polylines or group of points. This function expands on the lines() and points functions from base R graphics. The difference is that several lines and group of points can be drawn in one line by providing an id: i. To each line and group of point you can provide different graphical parameters (i.e. colour, type, etc).

Usage

multilines(i, x, y, j = unique(i), forget = NULL, front = NULL, back = NULL, type = "l", col = "black", bg = NA, pch = 19, lty = par("lty"), lwd = par("lwd"), cex = par("cex"), lend = 0, ljoin = 0, lmitre = 10)

Arguments

i a line id for each x and y coordinate, i.e. the name of each polyline. If you want to give each line a different aspect you should provide a vector of n elements (if you have three lines "A1", "A2" and "A3" with "A2" that should be blue you should provide the colours of all three: e.g. col = c("white", "blue", "white"))

x, y numeric vectors of x and y coordinates

j a list of the ids (names) in the order used for the graphical parameters (e.g. colour, shading, etc...). By default they are in their order of appearance in i

forget the lines that should not be drawn, by their id or index (i.e. name or number of appearance).

front, back the lines to be put in front and back position, by their id or index (i.e. name or number of appearance). By default the order is the one defined by j, and if j is absent by the order in i.
type character indicating the type of plotting. For this function it is limited to "l" (lines, is the default), "p" (points) and "o" (points overplotting lines).

col the color to draw the line. The default is black.

bg background (fill) color for the open plot symbols given by pch = 21:25.

pch plotting 'character', i.e., symbol to use. See ?points for further details

lty, lwd the line type and width, see ?par for details.

cex character (or symbol) expansion: a numerical vector. This works as a multiple of par("cex")

lend, ljoin, lmitre additional graphical parameters, see ?par for details.

See Also

multigons

Complementary function: shift

Uses ignore to avoid drawing unnecessary objects

Examples

i <- c(rep("A1",6), rep("A2",6), rep("A3",6))
x <- c(1,2,3,3,2,1,4,5,6,5,4,7,8,9,9,8,7)
y <- c(1,2,3,4,5,6,1,2,3,4,5,6,1,2,3,4,5,6)

plot(c(0,10),c(0,7),type = "n")

multiline(i, x, y, j = c("A3", "A1", "A2"), lty = c(1,2,3), lwd = 2,
          type = c("l", "o", "o"), pch = c(NA,21,24), cex = 2)

neatPick( fun,
          n,
          args = list(),
          class.args = list(),
          pick = NA,
          fix = NA,
          lend, ljoin, lmitre
          cex
          )

Interactive user modification of the arguments of a repeated function

Description

This opens a shiny app that will allow to manipulate the arguments of a function interactively, with different conditions that the user can provide a priori and modify at will

Usage

neatPick( fun,
          n,
          args = list(),
          class.args = list(),
          pick = NA,
          fix = NA,
          lend, ljoin, lmitre
          cex
          )
buttonswidth = 2,
text = "output",
textwidth = 4,
plotwidth = 800,
plotheight = 600,
args.only = F,
width = 10,
height = 10,
name = "fig",
dir = tempdir(),
gfile = "onePDF",
openfile = TRUE,
folder = "Rfig",
gfun = "jpeg",
ext = ".jpeg",
gargs = list(units = "in", res = 300),
pargs = list(ps = 12, cex = 1.5)
)

Arguments

fun
the function to be applied n times.
n
number of runs.
args
the arguments to be supplied to fun. Should be a list of each argument to be supplied to fun, having n elements stored indiscriminately in list or in vector form.
class.args
the class of the arguments, in a list. This is useful when the starting arguments are NA
pick
which arguments to be able to adapt interactively
fix
which arguments that cannot be chosen interactively (if pick is NA)
buttonswidth
the width of the buttons panel (integer from 1 to 12)
text
which information to send to the text panel. The default is the output of the current element (ni); "output". Can be the whole dataset of arguments; "all". Otherwise the panel does not show.
textwidth
the width of the text panel (integer from 1 to 12)
plotwidth
the width of the plot panel (arbitrary units)
plotheight
the height of the plot panel (arbitrary units)
args.only
whether to be only allowed to download and return the arguments (this simplifies things and makes the workflow more efficient)
width, height, name, dir, gfile, openfile, folder, gfun, ext, gargs
arguments to be supplied to neatPicked, the equivalent of neatPick without interactivity: it runs the function for each ni and saves the output (normal and graphical). In neatPick this happens when the button 'Run and Download Output' is clicked. See ?neatPicked function help page for details.
pargs
the arguments to transmit to par(), in neatPick and neatPicked
Details

This is a complicated function. A few basics:

neatPick works using the formals() function. It evaluates the arguments and their default values of any function that you provide without parentheses, like this for instance: formals(multigons).

neatPick is capable of providing interaction with arguments of class integer or numeric (e.g. 10, or 13,58745), character (e.g. "BlipBlapBLoup") and logical (T or F), as long as for each iteration (n) the length of the argument is one (you cannot use arguments like xlim = c(0,1), however you can use xmin = 0 and xmax = 1 for instance). But you can provide a different value for each iteration n (if n = 3, you can provide col = c("red", "blue", "green") in the args list of arguments)

You can chose which arguments are interactive or not using the 'pick' and 'fix' arguments.

To return the arguments or the output, you have to click on 'End & Return Arguments' or 'End & Return Output', respectively.

You can also save the obtained output and arguments via the download buttons: you get a .RData file where the arguments are in the object saved.args and the output is in the saved.output object. The arguments can also be found at saved.output$args. The arguments can be provided to the args argument of the same neatPick function to rework the changes you made.

Examples

```r
## Not run:
# You create a simple function. The one below creates sinusoidal waves between
# x0 = 0 and x1 = 1. You want to personalise the amplitude (delta), the y
# offset (pos, see ?sinpoint for more details), the phase (phase, expressed
# in multiples of pi), the number of waves between x0 and x1, and the number
# of intervals between each discrete point (nint).
# So you set all these as arguments of the function. This function can also
# have a graphical output of one plot (which can be subdivided if necessary
# using par(mfrow)). And the function can return output.

fun <- function(delta = 1, pos = 1, phase = 1.5, nwave = 1, nint = 50)
{
  res <- sinpoint(1, 0, delta = delta, pos = pos, phase = phase,
                   nwave = nwave, nint = nint)

  plot(res$x, res$y)

  return(res)
}

# Once this simple function is coded, it can be integrated to neatPick(). The
# argument n defines to number of different realisations of the function.

# WHEN YOU ARE HAPPY WITH THE OUTPUTS, click on 'END & RETURN ARGUMENTS'
a <- neatPick(fun, n = 10, args.only = TRUE)

# If you have clicked right (on the 'END & RETURN ARGUMENTS' button), the
```
# arguments will be returned and stored in a;

a

# These arguments can then serve for a more efficient function:

seg <- sinpoint(1, 0, delta = a$delta, pos = a$pos, phase = a$phase,
    nwave = a$nwave, nint = a$nint)

# Basically neatPick applies a for loop to fun, but if you work on a large
# dataset, you can also create a function that can handle the arguments more
# efficiently. This is what sinpoint does here

# Now you can see the results imported in R and do whatever you want with:

plot(seg$x, seg$y, type = "n")

multilines(seg$i, seg$x, seg$y)

# You can even rework your initial changes:

b <- neatPick(fun, n = 10, args.only = TRUE, args = a)

## End(Not run)

---

**neatPicked** 

*Runs neatPick without user input*

**Description**

Is the user input free version of neatPick. Runs a function n times, with its arguments n times different. The graphical output is stored into a n pages pdf or a n files folder. The output of the function is accumulated in a list.

**Usage**

```r
neatPicked(
    fun,
    n,
    args = NA,
    width = 10,
    height = 10,
    output = "all",
    name = "Fig",
    dir = tempdir(),
    gfile = "onePDF",
    openfile = TRUE,
    track = TRUE,
    folder = "My file",
```
 Arguments

 fun the function to be applied \( n \) times.

 n number of runs.

 args the arguments to be supplied to fun. Should be a list of each argument to be supplied to fun, having \( n \) elements stored indiscriminately in list or in vector form.

 width, height the width and height of the graphics region. In inches by default, can be adapted if onePDFfile = FALSE

 output the kind of output : "function" for the accumulated outputs of the function (list of \( n \) elements), "all" to add args, and everything else to output nothing

 name the names of the graphic file(s)

 dir the directory of the file or of the folder of files, by default a temporary file

 gfile whether to create a single pdf with \( n \) pages ("onePDF"; default) or a folder of \( n \) graphical files ("gfun"). If anything else is given ("none for instance"), it won’t produce graphical files. This reduces computation speed by a little more than 15 percents (one try of 1000 samples with simple graphs).

 openfile, track parameters for pdfDisplay()

 folder the name of the folder containing the \( n \) graphical files

 gfun a non-empty character string naming the graphical function to be called to create the \( n \) graphical files

 ext the extension of the \( n \) graphical files

 gargs list of arguments transmitted to the graphical function

 pargs list of arguments transmitted to the par() function

 Value

 the accumulated outputs of fun (and arguments if asked) if asked

 Examples

```r
## Not run:
fun <- function(x, y, xlim = c(-1,1),...)
{
  plot(x, y, xlim = xlim,...)

  return(paste(x, y, paste(xlim, collapse = "; "), sep = "; "))
}
```
args <- list(x = list(-0.5, 1), y = c(0.8, 0.8), pch = c(2,4),
             xlim = list(c(-1,1), c(-20,20)))

temp <- tempfile()
dir.create(temp)

neatPicked(fun, 2, args = args, width = 5, height = 5, dir = temp)
## End(Not run)

---

**nlegend**  
*New legend element*

**Description**

Prepares a plotting environment for a new element of a multfigure legend

**Usage**

```r
nlegend(
  t = "Text",
  xt = 1.3,
  xmax = 5,
  xmin = -1.2,
  ymax = 1.5,
  ymin = -ymax,
  asp = NA,
  temp = FALSE,
  ...
)
```

**Arguments**

- `t`  
  text to provide the legend
- `xt`  
  the x position of the text
- `xmin, xmax, ymin, ymax`  
  the x and y limits for the plotting area
- `asp`  
  numeric, giving the aspect ratio y/x, see ‘Details’ of `plot.window`.
- `temp`  
  whether to plot a template for visualisation
- `...`  
  parameters to be fed to the text function, such as `cex` for the size of the text

**See Also**

`multigons`, `bedtext`, `infobar` and `ylink`
Examples

```r
opar <- par("mar")
par(mar = c(0,0,0,0))
layout(matrix(1:6, 6, 1, byrow = TRUE))

nlegend(t = paste("Shaded stuff. By the way you can\nwrite",
"text in several lines if needed"), cex = 1.2)
rect(-1,-1,1,1, density = 10)

nlegend(t = paste0("Text: left side at x = 1.3 (default xt value)
",";\nsize adapted with cex argument"),
temp = TRUE, cex = 1.4)
par(mar = opar)
```

---

**nset**

*Find indexes for n identical elements*

**Description**

For a given vector, this function gives the indexes of identical sets for a given number of repetitions

**Usage**

```r
nset(x, n, first = T, warn = T)
```

**Arguments**

- `x`: a vector, normally with repeated values
- `n`: the amount of repetitions that needs to be identified
- `first`: whether to take the first repetitions (T; is the default), or the last ones (F)
- `warn`: whether to warn if NA values are generated due to the lack of right amount of repetitions

**Examples**

```r
ids <- c(rep("A", 4), rep("B", 6), rep("C", 2))
val <- paste(ids, c(1:4, 1:6, 1:2), sep = "")
nset(ids, 3, warn = FALSE)
matrix(val[nset(ids, 3, warn = FALSE)], ncol = 3)
matrix(val[nset(ids, 3, first = FALSE, warn = FALSE)], ncol = 3)
```
octapos

Identify points in a polygon in reference to an octagon

Description

Identify points in a polygon as if they were constituting a reference octagon, having two sides horizontal and two sides vertical: there are eight points, starting from the right side of the upper horizontal side, and following each other in a clockwise order.

Usage

octapos(x, y, i = "I1", pos = 1:8)

Arguments

x, y the coordinates of the polygons
i the identification of the polygons if there are multiple ones
pos which reference points to compute

Value

a data frame with as much columns as positions, labelled from pos1 to pos8, or a vector if only one position is required

Examples

# Define polygons (in this case, two octagons) ----
dt1 <- c(0, 0, 0.33, 0.67, 1, 1, 0.67, 0.33) - 0.5
xy1 <- c(0.33, 0.67, 1, 1, 0.67, 0.33, 0, 0) - 0.5
dt2 <- rev(0.5 * (c(0, 0, 0.33, 0.67, 1, 1, 0.67, 0.33) - 0.5))
xy2 <- rev(0.5 * (c(0.33, 0.67, 1, 1, 0.67, 0.33, 0, 0) - 0.5))
dt <- c(dt1, dt2)
xy <- c(xy1, xy2)
gr <- rep(c("B2", "A3"), each = 8)

# Compute the position to the octagon reference ----
octa <- octapos(x = xy, y = dt, i = gr)

# Plot base----
plot.new()
plot.window(xlim = c(-0.5, 0.5), ylim = c(-0.5, 0.5))
axis(1)
axis(2, las = 1)
title(xlab = "x", ylab = "y")
octashift

Shifts the order of polygon points

Description
Shifts the order of polygon points based on octagon-like reference

Usage
octashift(x, y, i, pos, clockwise = NA)

Arguments
x, y the coordinates of the polygons
i the identification of the polygons if there are multiple ones
pos an integer from 1 to 8 identifying a points, based on the formalism of the octapos function
clockwise whether to have the points in the polygon be ordered clockwise (T), counterclockwise (F). If NA (which is the default), this will not be addressed

Value
a data frame with $x, $y and $i of the polygons as columns
Examples

```r
xy <- c(-3,-4,-3,0,-1,-2,-1,0,2,1,3,4,5,4,3)
dt <- c(1,1.5,2,1,1.5,2,2,1.5,2,1,1.5,2,2)

out <- octashift(xy, dt, id, pos = 3, clockwise = TRUE)

par(mfrow = c(2,1))
plot.new()
plot.window(xlim = range(xy) + c(-1, 1), ylim = range(dt) + 0.5 * c(-1, 1))
axis(1)
axis(2)
multilines(i = id, x = xy, y = dt)

plot.new()
plot.window(xlim = range(xy) + c(-1, 1), ylim = range(dt) + 0.5 * c(-1, 1))
axis(1)
axis(2)
multilines(i = out$i, x = out$x, y = out$y)
```

outliner

Find the points of a litholog that are along a given vertical line

Description

Through interpolation, this function identifies all the points of a litholog that are at a given intensity value, along a vertical line.

Usage

```r
outliner(log, xy, add = F)
```

Arguments

- `log`: a "litholog()-like data frame
- `xy`: the intensity value for the vertical line
- `add`: whether to have the interpolated points added to the litholog

Value

A data frame of the extracted vertical line or the litholog with points along this line wherever the log intersects the vertical line, with its `i` (bed identification), `dt` (depth/time), and `xy` (intensity).
Examples

l <- c(1,2,3,4,5)  # left boundary of the bed interval (upper or lower)
r <- c(0,1,2,3,4)  # right boundary of the bed interval (upper or lower)
h <- c(4,3,5,3,4)  # hardness (arbitrary)
i <- c("B1","B2","B3","B4","B5")  # Bed name

olog <- litholog(l,r,h,i)  # Generate data frame of the polygons
# making the litholog

log <- weldjoint(olog, c(1 ,4, 5), oufti99,
   sym = c("1sin", "liquefaction", "1sin"),
   ymax = c(NA, 0.2, 0.2),
   xmin = c(0, 1, 0),
   xmax = c(4, 1.5, 3))

log_line <- outliner(log, 2)

plot.new()
plot.window(xlim = c(0,5), ylim = c(0,5))
axis(1)
axis(2)
multigons(log$i, log$xy, log$d)
points(log_line$xy, log_line$dt, pch = 19, col = "red")

pdfDisplay

Generates PDF and SVG figures

Description

Takes an ensemble of figures, represented by a function g(), and generates a PDF (or SVG if specified). The PDF can be visualised immediately on the default PDF reader.

Usage

pdfDisplay(
  g,
  name,
  ext = ".pdf",
  dir = tempdir(),
  width = 10,
  height = 10,
  parg = list(),
  track = T,
  openfile = T,
  output = F,
pdfDisplay

    warn = F

Arguments

g                           the plot function to be exported and looked at
ame                           the name of the document
ext                          the extension of the document: ".pdf" by default, but ".svg" works also.
dir                          the file where the document will be saved (by default a temporary directory, tempdir())
width                       the width of the drawing area (in inches)
height                      the height of the drawing area (in inches)
parg                        list of arguments transmitted to the par() function
track                       whether to generate different files for each rerun of pdfDisplay with identical 'name'. The name will be followed by '_(i)' where i is the version number. With this you avoid closing your pdf file at each rerun if your pdf reader is not able to deal with (to my knowledge only SumatraPDF is able)
openfile                    should the pdf file be opened (for the moment works only in Windows). Use SumatraPDF as default pdf reader to be able to write over current file
output                      whether to output the output of g() or not
warn                        useless vestigial parameter, kept for compatibility with StratigrapheR 0.0.1

Details

The width and height you provide will not exactly be respected. I could not find a pdf printing function that respects dimensions scrupulously for R base graphics.

Value

the output of the g() function if output = TRUE

Examples

## Not run:
temp <- tempfile()
dir.create(temp)

g1 <- function() plot(1,1)
pdfDisplay(g1(),"TestGraph", dir = temp,
           parg = list(mar = c(6,6,6,6), ps = 24,lwd = 4))

g1 <- function() plot(1,1, col = "red")
pdfDisplay(g1(), "TestGraph", dir = temp,
           parg = list(mar = c(6,6,6,6), ps = 24,lwd = 4))
## End(Not run)
pkgfind

*Find a specific pattern in the code of functions in a package*

**Description**

This function names all the functions in a package that contain a specific character pattern, typically the name of a function.

**Usage**

`pkgfind(pkg, pattern)`

**Arguments**

- `pkg`: a character string of the package to search in
- `pattern`: the pattern to search in the codes of the functions in the package

**Value**

a vector of the names of the functions in which the pattern is identified

**Examples**

`pkgfind("StratigrapheR", "every_nth")`

placesvg

*Draws a pointsvg object*

**Description**

Draws a svg object imported as data frame using `pointsvg`, with its importation coordinates (or with standardisation).

**Usage**

`placesvg(
    object,
    forget = NULL,
    front = NULL,
    back = NULL,
    standard = FALSE,
    keep.ratio = FALSE,
    col = NA,
    border = "black",
    density = NULL,
placesvg

angle = 45,
lwd = par("lwd"),
lty = par("lty"),
scol = border,
slty = lty,
slwd = lwd

Arguments

object a pointsvg object (svg object imported as data frame using pointsvg).

forget the elements that should be discarded, by their id or index (i.e. name or number of appearance).

front, back the elements to be put in front and back position, by their id or index (i.e. name or number of appearance). By default the order is the one of the original .svg file.

standard whether to standardise (centre to (0,0), rescale so that extreme points are at -1 and 1) or not (T or F)

keep.ratio if the object is to be standardised, whether to keep the x/y ratio (T or F)

col the polygons background color. If density is specified with a positive value this gives the color of the shading lines.

border the lines color.

density the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn.

angle the slope of shading lines, given as an angle in degrees (counter-clockwise)

lty, lwd the border line type and width, see ?par for details.

scol, slty, slwd the colour, type and width of the shading lines.

See Also
centresvg and framesvg

Examples

object <- example.ammonite

plot(c(-2,2), c(-2,2), type = "n")

placesvg(object, lty = 1, density = 20, angle = 45)
planepoints

Describes planes by points

Description

Gives the coordinates (dec and inc) of three perpendicular directions to describe planes.

Usage

planepoints(strike, dip, quadrant = NA, inverted = NA)

Arguments

strike  strike of the data; it is the angle from the north of the horizontal line of the plane. It is corrected by dipfix().
dip     dip of the data; it is the angle from the horizontal taken on the line of the plane perpendicular to the one of the strike. It is corrected by dipfix().
quadrant the quadrant where the plane dips downward. Accepted values are NA, 'N', 'S', 'W' or 'E' (lower- or uppercase alike) for correction by dipfix().
inverted whether the plane is inverted or not. The default is NA, it assumes that no bed is inverted.

Details

The directions are x for dip-direction line (direction of maximum downward dip), y for the horizontal line, z for the upper pole; additionally a magnitude is given to use y as a rotation axis to get the plane back at the horizontal. If the plane is inverted, y, z and mag will be changed, accordingly, with a rotation of 180° around x for y and z.

Value

a list of x, y and z declinations and inclinations (dec and inc), and a rotation magnitude

Examples

strike <- c(-60, 180, 20)
dip <- c(-60, 20, -45)
quadrant <- c("N","W",NA)
inverted <- c(FALSE,FALSE,TRUE)
res <- planepoints(strike,dip,quadrant,inverted)
deci <- c(res$x$dec, res$y$dec, res$z$dec)
inci <- c(res$x$inc, res$y$inc, res$z$inc)
earnet()
Converts line, rect, polygon and polyline class SVG objects into data frames.

**Description**

Converts 'line', 'rect', 'polygon' and 'polyline' class SVG objects into data frames. **ONLY THESE CLASSES OF OBJECTS CAN BE IMPORTED.** If you have bezier or spline curves, they will be stored as 'path' class objects that cannot be imported here. The same goes for 'rect' objects that are transformed (rotation, etc...).

**Usage**

```r
pointsvg(
  file,
  standard = TRUE,
  keep.ratio = FALSE,
  round = TRUE,
  xdigits = 4,
  ydigits = 4,
  xinverse = FALSE,
  yinverse = TRUE,
  warn = T
)
```

`is.pointsvg(object)`

**Arguments**

- **file**: a .svg file
- **standard**: whether to standardise (centre to (0,0), rescale so that extreme points are at -1 and 1) (T or F)
- **keep.ratio**: if the object is to be standardised, whether to keep the x/y ratio (T or F)
- **round**: whether to round the coordinates (T or F)
- **xdigits**: the number of digits after the decimal to round to for x values
- **ydigits**: the number of digits after the decimal to round to for y values
- **xinverse**: whether to inverse the plotting for x values (T or F)
- **yinverse**: whether to inverse the plotting for y values (T or F)
- **warn**: whether you want to be annoyed
- **object**: for is.pointsvg, the R object to be checked if it can be considered similarly to a svg outputted by pointsvg
Details

This function is quite empirical. There is no guarantee it is bug free. If you have .svg files that should work but do not, you can email me: <wouterseb@gmail.com>

Value

A data.frame with x and y coordinates, ids for each object, and a type, either line (L) or polygon (P)

See Also

Plot the drawing: `placesvg`.
Plot the drawing and change the coordinates: `centresvg` and `framesvg`.
Change the drawing: `changesvg` and `clipsvg`.

Examples

```r
# To show you how to import, we first have to have a svg file to import. The following lines of code will create a svg in a temporary files:

svg.file.directory <- tempfile(fileext = "svg") # Creates temporary file
writelines(example.ammonite.svg, svg.file.directory) # Writes svg in the file

print(paste("An example .svg file was created at ", svg.file.directory, sep = ""))

# The pointsvg function allows to import simple svg drawings into R
ammonite.drawing <- pointsvg(file = svg.file.directory) # Provide file
is.pointsvg(ammonite.drawing)
plot(c(-2,2), c(-2,2), type = "n")
placesvg(ammonite.drawing)

# If you want to import your own .svg file uncomment the following line:
# pointsvg(file.choose())
```

profiler  

Extract the profile of a litholog

Description

Extract the induration, grain-size, lithology, facies, or any other information coded in the profile variations of a litholog.
profiler

Usage

profiler(log, gap, ext = Inf, down.xy = NA, up.xy = NA)

Arguments

log  a "litholog()-like data frame

gap  the most inward values of the profile, i.e. the minimum values expected in the signal

ext  the most outward values of the profile; defaults to infinity Inf, for "left-side" profiles, set to -Inf

down.xy, up.xy  the xy values to give the the lower and upper parts of the signal.

Value

a data frame of the extracted profile, with its i (bed identification), dt (depth/time), and xy (intensity).

Examples

l <- c(1,2,3,4,5)  # left boundary of the bed interval (upper or lower)
r <- c(0,1,2,3,4)  # right boundary of the bed interval (upper or lower)
h <- c(4,3,4,2,3)  # hardness (arbitrary)
i <- c("B1","B2","B3","B4","B5")  # Bed name

log <- litholog(l,r,h,i)  # Generate data frame of the polygons

# making the litholog

# Extract the profile of the litholog, with the upper and lower values set # at a value of 2 ----

pro <- profiler(log, gap = 2, up.xy = 2, down.xy = 2)

opar <- par()$mfrow

par(mfrow = c(1,2))

# Draw the litholog ----

plot.new()
plot.window(xlim = c(0,4), ylim = c(0,5))

axis(1)
axis(2)

multigons(log$i, log$xy, log$dt,
  col = c("grey80","grey20","grey80","grey80","grey80"))  # Draw log

# Draw the profile ----

plot(pro$xy, pro$dt, type = "l", xlab = "hardness", ylab = "", axes = FALSE)
rebound

Simplifies boundary indicators for lim objects

Description

Simplifies boundary indicators for lim objects: from the wide range supported by R ("[]", "[)", "[", "()", "[", "[", "[]", "[" open", "closed", "left-open", "right-open", "left-closed", "right-closed") to "[", "[", "[" and "[" only

Usage

rebound(b, na.errors = F)

Arguments

b a vector of boundary indicators
na.errors whether to replace all other values by NA (rather than simply stopping the function)

Value

a simplified vector of boundary indicators ("[]", "[]", "[]" and "[]" only)

See Also

as.lim

Examples

bounds <- c("[]", "[]", "()", "[", "[", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]", "[]")

rebound(bounds)
**Description**

Finds the declination and inclination of a line defined by a pitch on a plane

**Usage**

```r
repitch(pitch, strike, dip, quadrant = NA)
```

**Arguments**

- **pitch**: pitch (or rake) of the data; it is the angle between the strike of the plane and a line. It is taken from the left side going downward along the dip, and is positive downward.
- **strike**: strike of the data; it is the angle from the north of the horizontal line of the plane. It is corrected by the `dipfix` function.
- **dip**: dip of the data; it is the angle from the horizontal taken on the line of the plane perpendicular to the one of the strike. It is corrected by the `dipfix` function.
- **quadrant**: the quadrant were the plane dips downward. Accepted values are NA, 'N', 'S', 'W' or 'E' (lower- or uppercase alike) for correction by the `dipfix` function.

**Value**

a list of declination and inclination of the defined lines

**References**

Eric Carlson of the Colorado School of Mines is acknowledged for his rake to plunge calculator on which this function is based.

**See Also**

dipfix, incfix and transphere

**Examples**

```r
strike <- c(90, 135, 135, 135)
dip <- c(0, 65, 65, 65)
pitch <- c(40, 40, 140, -40)

earnet()
earplanes(strike,dip,hsphere = "b", a = list(col = "red", lwd = 2))

res <- repitch(pitch = pitch, strike = strike, dip = dip)
earpoints(dec = res$dec, inc = res$inc)
```
Description
Core correction: declination and inclination are corrected for cores of given declination, inclination and rotation

Usage
reposition(dec, inc, cdec = 0, cinc = 90, crot = 0)

Arguments

\begin{itemize}
\item \texttt{dec} \hspace{1cm} \text{declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010).}
\item \texttt{inc} \hspace{1cm} \text{inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010).}
\item \texttt{cdec} \hspace{1cm} \text{declination of the core.}
\item \texttt{cinc} \hspace{1cm} \text{inclination of the core.}
\item \texttt{crot} \hspace{1cm} \text{rotation of the core; it is the angle of rotation around the core direction clockwise between the measurement and the actual core orientation. In others words it is the magnitude of the rotation to apply clockwise to the measured data using the core direction as an axis.}
\end{itemize}

See Also
rotate and restore

Examples

\begin{verbatim}
# ----

d <- zeq_example
dec <- d$Dec
ing <- d$Inc
cdec <- 75
cinc <- 45
crot <- 90

par(mfrow = c(2,2))
earnet()
earpoints(dec,inc)
\end{verbatim}
Plane correction

Description

Plane correction: declination and inclination are corrected for planes of given strike, dip, quadrant and inversion
Usage

```r
restore(dec, inc, strike, dip, quadrant = NA, inverted = NA, percent = 100)
```

Arguments

dec declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010).

inc inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010).

strike strike of the plane used for correction; it is the angle from the north of the horizontal line of the plane. It is corrected by dipfix().

dip dip of the plane used for correction; it is the angle from the horizontal taken on the line of the plane perpendicular to the one of the strike. It is corrected by dipfix().

quadrant the quadrant were the plane dips downward. Accepted values are NA, 'N', 'S', 'W' or 'E' (lower- or uppercase alike) for correction by dipfix().

inverted whether the plane is inverted or not. The default is NA, it assumes that no bed is inverted.

percent the percentage of correction (can be of length >= 1), by default it is 100 (%), bringing the plane to the horizontal.

See Also

`rotate` and `reposition`

Examples

```r
dec <- c(90,210)
inc <- c(20,60)
strike <- c(0,120)
dip <- c(20,60)
inverted <- c(FALSE,TRUE)
res <- restore(dec = dec, inc = inc, strike = strike, dip = dip,
quadrant = NA, inverted = inverted,
percent = seq(20,100, by = 20))

earnet()
earplanes(strike, dip)
earpoints(dec,inc)
earpoints(round(res$dec,2), round(res$inc,2), a = list(pch = 22))
```
**rmatrix**

**Rotation matrix**

**Description**
Computes a rotation matrix for a given rotation axis and angle based on Tauxe et al. (2010).

**Usage**

```r
rmatrix(dec, inc, mag, as.data.frame = FALSE)
```

**Arguments**

- `dec` declination of the rotation axis; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010).
- `inc` inclination of the rotation axis; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010).
- `mag` magnitude of rotation (following the notation of the Stereonet software) a positive rotation is clockwise looking in the direction of the given declination and inclination.
- `as.data.frame` logical, whether to output the matrix as a data frame. This is used when multiple arguments are provided to simplify and boost calculations.

**References**


**Examples**

```r
rmatrix(135,20,60)
rmatrix(c(135,0),c(20,90),c(60,90), as.data.frame = TRUE)
```
rotate

*Spherical rotation around fixed axes*

**Description**

Spherical rotation around given rotation axes

**Usage**

rotate(dec, inc, rdec, rinc, rmag)

**Arguments**

- **dec**: declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010).
- **inc**: inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010).
- **rdec**: declination of the rotation axes (of length 1 or n).
- **rinc**: inclination of the rotation axes (of length 1 or n).
- **rmag**: magnitude of rotation (following the notation of the Stereonet software): a positive rotation is clockwise looking in the direction of the given declination and inclination; of length 1 or n).

**References**


**See Also**

rmatrix, restore and reposition

**Examples**

```r
earnet()
inc <- seq(0,85,5)
dec <- rep(0,length(inc))
earpoints(dec,inc)
rdec <- rep(0, length(inc))
```
seq_log

seq_log <- rep(90, length(inc))

mag <- 90
rmag <- seq(mag, 0, by = -mag/(length(inc)-1))

rot <- rotate(dec, inc, rdec, rinc, rmag)

earpoints(dec = round(rot$dec, digits = 2), inc = round(rot$inc, digits = 2),
           l = list(bg = "green"),
           u = list(bg = "blue"),
           h = list(bg = "yellow"))

earpoints(dec = 0, inc = 90, l = list(bg = "red"))

seq_log

Gives the repartition of values for a log 10 scale between a given interval

Description

Gives the repartition of values for a log 10 scale between a given interval

Usage

seq_log(x1, x2, divide = FALSE)

Arguments

x1 the first value of the interval
x2 the second value of the interval (can be higher or lower, but never equal to x1)
divide whether to divide the result for major values (1, 10, 100) and minor values (2, 3, ..., 20, 30, ...)

Value

the repartition of values for a log 10 scale between x1 and x2

See Also

convertAxis

Examples

x1 <- 101
x2 <- 0.29

seq_log(x1, x2)
seq_log(x1, x2, divide = TRUE)
**seq_mult**  
*Sequence ordered by multiple*

**Description**
Sequence ordered by multiple

**Usage**
```r
describe = seq_mult(l, mult, inv = FALSE)
```

**Arguments**
- `l`: the length of the sequence, or an object convertible into a vector from which to determine the length from
- `mult`: the multiple to order by
- `inv`: whether to change mult into l/mult

**Examples**
```r
seq_mult(10, 2)
seq_mult(15, 3)
seq_mult(24, 8)
seq_mult(seq(0.5, 12, 0.5), 8)
seq_mult(10, 2)[seq_mult(10, 5)]
seq_mult(10, 2)[seq_mult(10, 2, inv = TRUE)]
```

---

**shift**  
*Circular shift*

**Description**
Circular shift; the order of points will be lagged as if the beginning is preceded by the end.

**Usage**
```r
shift(x, n = 1L, p = -n + 1L, i = NA, names = T)
```
Arguments

- **x**: a vector (characters, numerics, integers,...), data.frame or list
- **n**: a positive integer of length 1, giving the number of positions to shift by (positive values generate lag)
- **p**: the index position or row that will become the first one (overrides n)
- **i**: a vector of ids to divide x in various groups; the shift will occur on the subgroups defined by identical i ids.
- **names**: whether the names of the elements or rows should also shift

Value

the same object than the input, but with a shifted order

Examples

```r
# Simple use ----------------------------------------------------------------
shift(x = c(6,8,10,12,2,4), n = 2)
#> [1] 2 4 6 8 10 12

vector <- rep(1:4, 3)
names(vector) <- rep(c("P1", "P2", "P3"), each = 4)
split(vector, f = names(vector))

#> $P1
#> P1 P1 P1 P1
#> 1 2 3 4
#>
#> $P2
#> P2 P2 P2 P2
#> 1 2 3 4
#>
#> $P3
#> P3 P3 P3 P3
#> 1 2 3 4

sh <- shift(x = vector, i = names(vector), p = c(1,2,3))
split(sh, f = names(sh))

#> $P1
#> P1 P1 P1 P1
#> 1 2 3 4
#>
#> $P2
#> P2 P2 P2 P2
#> 2 3 4 1
#>
#> $P3
#> P3 P3 P3 P3
```
# Applications to litholog generation ---------------------------------------

```r
l <- c(1, 2, 3)
r <- c(0, 1, 2)
h <- c(4, 3, 4)
i <- c("B1", "B2", "B3")

basic.litholog <- litholog(l, r, h, i)

whiteSet(xlim = c(0, 4), ylim = c(0, 3),
         xaxs = "r", yaxs = "r",  # This gives a little room to the graph
         ytick = 1, ny = 10)

multigons(basic.litholog$i, basic.litholog$xy, basic.litholog$dt,
          forget = "B1", lwd = 2)

openbed <- subset(basic.litholog, basic.litholog == "B1")

openbed <- shift(openbed, -1)

lines(openbed$xy, openbed$dt, lwd = 2)
```

---

**simp.lim**

Joins and orders adjacent or overlapping lim objects of same ID

### Description

Joins and orders adjacent or overlapping lim objects of same ID

### Usage

```r
simp.lim(lim = NULL, l = NULL, r = NULL, id = 1L, b = "[]")
```

### Arguments

- **lim**: an object convertible into a lim object: either a vector of length 2 or a list of n left (1st element) and n right (2ndt element) interval limits
- **l**: a vector of n left interval limits
- **r**: a vector of n right interval limits
- **id**: a vector of n interval IDs (default is 1 for each interval)
- **b**: a character vector for the interval boundaries rules: "[" (or "closed") to include both boundaries points, "]" (or "()" and "open") to exclude both boundary points, "[" (or "]", "right-open" and "left-closed") to include only the left boundary point, and "]" (or "[", "left-open", "right-closed") to include only the right boundary point. The notation is simplified to "[", "[", "]" and "]" only.
Value

a lim object of the joined intervals

See Also

as.lim

Examples

l <- c(50,2,4,6,50,8,50,51,50,80)
r <- c(50,5,9,8,2,51,50,51,50,80)
id <- c("i1", "i1", "i1", "i2", "i2", "i2", "i2", "i2", "i2")
b <- c("[", "]", "[", "]", "[", "]", "]", "]", "]", "]")
simp.lim(l = l, r = r, id = id, b = b)

sinpoint

Gives a table of equally sampled points following a sinusoidal function

Description

Gives a table of equally sampled points following a sinusoidal function

Usage

sinpoint(x, y, delta, x0 = 0, pos = 1, phase = 1.5, nwave = 1, nint = 50)

Arguments

x
the x value of the end of the interval

y
the y offset (see next parameter)

delta
the difference between the min- and maxima in y

x0
the x value of the beginning of the interval (0 as default)

pos
an integer specifying the kind of vertical offset; should the sinusoidal function be shifted so that y is the first value (pos = 1, is the default), the last value (2), the minimum (3) or the maximum (4) of the function

phase
the phase of the function at x0 in multiples of pi (1.5 as default; begins at its lowest)

nwave
number of complete sinuses waves (1 as default)

nint
number of intervals for the sampling (50 as default)

Value

a table of points following a sinusoidal function
Examples

```r
res <- sinpoint(c(4,5), 5, 1, x0 = c(0,1), pos = 3)
plot(res$x, res$y)
multilines(res$i, res$x, res$y, col = c("black","red"), type = "o")
```

---

**strat.mean**

*Extrapolate and intrapolate tie points*

**Description**

Extrapolate and intrapolate of stratigraphical tie points or events, based on their position in different sections.

**Usage**

```r
strat.mean(dt, events = NULL, sections = NULL)
```

**Arguments**

- `dt`: a matrix of depth (or time) of the different tie points. Columns are for the sections, rows for each tie point.
- `events`: the name of the tie points.
- `sections`: the name of the sections.

**Examples**

```r
dt <- tie.points.example[,2:6]
events <- tie.points.example[,1]
strat.mean(dt = dt, events = events)
```

---

**strat.repair**

*Remove instantaneous deposits and add thickness in hiatuses*

**Description**

Remove instantaneous deposits, or 'fills', (e.g. turbidites) and add thickness estimated to be lost, or 'gaps' (i.e. hiatuses).
strat.var

Usage

strat.repair(
  
  dt,
  gap = list(),
  fill = list(),
  clean = F,
  left.side = T,
  left.norm = T
)

Arguments

dt depth or time
gap list
fill list

clean whether to set the points in fills as NA
left.side l
left.norm l

Examples

dt <- as.list(tie.points.example[,2:6])

gap <- list()
fill <- list()

gap$Charce <- data.frame(dt = c(370,400), span = c(50,10))
gap$El.Porton <- data.frame(dt = -400, span = 30)

fill$Charce <- data.frame(l = 63, r = 65)
fill$El.Porton <- data.frame(l = c(-530), r = c(-630))
fill$Frielingen <- data.frame(l = 20, r = 30)

strat.repair(dt, gap, fill)

strat.var

Compute the relative thickness variations of sections

Description

Based on tie-points, this function computes the relative thickness variations of different sections compared to a reference section or composite sections

Usage

strat.var(dt, initial = NULL, ref = 1, events = NULL, sections = NULL)
Arguments

dt      a matrix of depth (or time) of the different tie points. Columns are for the sections, rows for each tie point. No NA values are accepted, if necessary, tie-points have to be estimated, using for instance the strat.mean function
initial which tie-points are originally present in the sections (if NULL, by default all the values are considered as originally present)
ref      the column index for the section which acts as a reference (by default, it is set to 1, for the first columns)
events   the name of the tie points
sections the name of the sections

Examples

dt <- tie.points.example[,2:6]
events <- tie.points.example[,1]

extended <- strat.mean(dt = dt, events = events)

strat.var(extended$dt, extended$initial)

StratigrapheR: integrated stratigraphy for R

Description

This package includes bases for litholog generation: graphical functions based on R base graphics (e.g. multigons()), interval gestion functions (with the as.lim() function, and other related .lim functions) and simple svg importation functions (e.g. pointsvg()) among others. It also includes stereographic projection functions (e.g. the earnet(), earpoints() and earplanes() functions; ear standing for equal area), and other functions made to deal with large datasets while keeping options to get into the details of the data. **IF YOU WANT TO START LEARNING HOW TO CREATE LITHOLOGS WITH STRATIGRAPHER GO SEE THE EXAMPLE BELOW.**

A StratigrapheR() function is provided: it generates organisational charts for common use of the functions in the package

Usage

StratigrapheR(i = 1:3)

Arguments

i      the index(es) of the organisational charts of the functions in the StratigrapheR package
Details

Package: StratigrapheR
Type: R package
Version: 1.3.0 (End 2022)
License: GPL-3

Note


Author(s)

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Examples

# This is an example of litholog generation script, along with some
# explanations: if you want to start somewhere, start here. You may run the
# whole thing and follow the explanations.

library(StratigrapheR)
library(dplyr) # very useful package, used here for joining data frames

# You may want to change your working directory for this, the example will
# generate .pdf and .txt files;
# setwd()

# If you want to have an organisational chart of the functions:
## Not run:
pdfDisplay(StratigrapheR(), "Organisational Chart StratigrapheR",
           width = 9, height = 7.5, track = FALSE)
## End(Not run)

# Bed dataset ----

bed.example

# this dataset should include the description of each bed with :
# - l - the position of the base of each bed (in cm or m) - l stands for the
#   left side or boundary of an interval-
# - r - the position of the top of each bed (in cm or m) - r stands for the
#   right side or boundary of an interval-
# - litho - the lithology, basics are for instance C for chert, S for shale, L
#   for limestone... but you can include anything you want in any way you want
# - h - relief or hardness of each bed
# - id - is the bed identification, number (e.g. B1, B2, ...)
# you can also include other columns with anything else you find useful for
# each bed such as color or lithofacies

# Ponctual elements datasets ----

fossil.example
boundary.example
chron.example

# These dataset(s) should include any ponctual information you want in the log,
# such as the position of particular fossils, bioturbations, minerals, tectonic
# features, etc...

# We will also see how to add proxy information with:

proxy.example

# Work the datasets ----

# Basic litholog (rectangles) --
# it will take the basic data (l, r, h, id)

basic.log <- litholog(l = bed.example$l, r = bed.example$r,
                       h = bed.example$h, i = bed.example$id)

# Define the legend for each lithology ----
# for each lithology you can provide a color (col), a density of shading
# (density) and orientation for the lines (angle)

legend <- data.frame(litho = c("S", "L", "C"),
                      col = c("grey30", "grey90", "white"),
                      density = c(30, 0, 10),
                      angle = c(180, 0, 45), stringsAsFactors = FALSE)

bed.legend <- left_join(bed.example, legend, by = "litho")

# Plot a basic litholog ----

# Be warned that the most efficient way to generate a litholog is to put it
# in a function. We will see this lower in the explanasion. The three first
# lithologs generated in the R plot window are simply an example to help you
# understand the functions in StratigrapherR

# First prepare the plot using whiteSet(): this provides a clean drawing area

whiteSet(xlim = c(0, 10), ylim = c(-1, 77), ytick = 5, ny = 5) # Prepare plot
title("Using litholog() and bedtext()")
# Then add the polygons making the litholog. This is done with a single function
# identifying each polygon by the id of points. The graphical parameters of the
# polygons can be adapted to fit the legend, polygon by polygon.

multigons(basic.log$i, x = basic.log$xy, y = basic.log$dt,
          col = bed.legend$col,
          density = bed.legend$density,
          angle = bed.legend$angle)

# You can further add the name of each bed on each corresponding polygon

bedtext(labels = bed.example$id, l = bed.example$l, r = bed.example$r,
         x = 0.5, # x position where to centre the text
         ymin = 3) # ymin defines the minimum thickness for the beds where text
# will be added, making for a clean litholog

# Vectorised drawing: example of importation ----

# This creates a svg in one of your temporary files, to show how to import svg
# files
svg.file.directory <- tempfile(fileext = ".svg")
writeLines(example.ammonite.svg, svg.file.directory)
print(paste("An example .svg file was created at ", svg.file.directory,
         sep = "\n"))

# The pointsvg function allows to import simple svg drawings into R
ammonite.drawing <- pointsvg(file = svg.file.directory)

# If you want to import your own .svg file uncomment the following line:
# pointsvg(file.choose())

# Other data frames of vectorised drawings are imbedded into the
# Stratigrapher package for this example : example.ammonite.svg (to see how to
# use pointsvg), example.ammonite, example.belemnite and example.liquefaction

# Now that ammonite.drawing is available, lets see what it looks like

whiteSet(ylim = c(-1,1), xlim = c(-1,1)) # Plot
box()

title("ammonite.drawing")

placesvg(ammonite.drawing)

# The placesvg() function plots any pointsvg-like dataset, which is a data frame
# with a column x, y, id (for each polygon or polyline) and type (polygone or
# line). Note that only polygons and polylines drawings can be imported by
# pointsvg()

# You can see that the ammonite drawing is centred on 0,0, and has its maxima
# and minima at 1 and -1 respectively, for x and y alike. To plot a drawing
# at the right position and ratio, you can use the centresvg and framesvg
# functions

# For that you have to provide information about the position, for instance:

y.ammonite <- fossil.example$dt[fossil.example$type == "ammonite"]
y.ammonite

# y.ammonite is the y position (or depth) where each ammonite should be drawn.
# It is provided via a vector of any length (i.e. you can have any number of y
# positions and of corresponding ammonites), as long as all the other parameters
# are of length 1 or of same length (i.e. you could provide two values for x if
# you want the two ammonite drawings to have a different x position)

# First build the log

whiteSet(xlim = c(0,10), ylim = c(-1,77), ytick = 5, ny = 5)
title("Using pointsvg() and centresvg()")

multigons(basic.log$i, x = basic.log$xy, y = basic.log$dt,
col = bed.legend$col,
density = bed.legend$density,
angle = bed.legend$angle)

bedtext(labels = bed.example$id, l = bed.example$l, r = bed.example$r,
x = 0.5, ymin = 3)

# Then add the drawings

centresvg(ammonite.drawing,
  x = 7, # this is an arbitrary x position for each ammonite drawing
  y = y.ammonite,
  xfac = 0.75, # Correction factor for the ratio in x
  yfac = c(3,5)) # Correction factor for the ratio in y. As the other
# parameters it can be adapted for each drawing
# individually

# The centresvg() function will take a data frame outputted by pointsvg() - or
# from changesvg(), and even centresvg() and framesvg() if the output is TRUE as
# these two functions can output drawings with modified coordinates -.

# Dealing with bed thickness changes ----

# You can also weld changes of bed thickness at bed boundaries to the basic log

# For instance we can define here two types of sinuosidal boundaries. If you
# want you can even design a different type of 'wiggle' for each boundary.

s1 <- sinpoint(5,0,0.5,nwave = 1.5)
s2 <- sinpoint(5,0,1,nwave = 3, phase = 0)
# You can also weld lines you have drawn in svg and imported with pointsvg().
# However there are a few rules to use them as boundaries in StratigrapheR:
# you have to think about their coordinates. The function welding the 'wiggles'
# of the boundaries to the rectangles of the log, weldlog(), will require to set
# what you consider to be the beginning of the wiggle (at the left of the
# litholog) at 0,0 (if you run with the default parameters of weldlog, which is
# advised if you start), and define their coordinates to suit the scale of the
# litholog

# You can use centresvg() or framesvg() to change the coordinates, setting the
# output argument to TRUE (and the plot argument to FALSE if you don’t want to
# plot)

s3 <- framesvg(example.liquefaction, 1, 4, 0, 2, plot = FALSE, output = TRUE)

# In framesvg(), rather than providing the point to center the drawing on, and
# correction in x and y (as centresvg does), you provide the maxima and minima
# in x and y

# With the function wedlog, we combine the lithological log we created
# (basic.log) with the wavy bed boundaries we created. We provide the log
# -parameter log-, the position of the joints we would lie to change -dt-, the
# segments that are going to be welded to the basic log -seg, as a list of
# data frames, by default having the first column for the xy coordinates and
# second for dt coordinates- and j making the link between the boundaries
# position -dt- and the segments -seg-.

# For each j corresponds a respective dt of same index (for each dt corresponds
# a j at the same position), and each j refers to the index or the name of a
# segment in the list of segments.

# with the function wedlog, we combine the lithological log we created
# (basic.log) with the wavy bed boundaries we created. So you can use any
# wiggle you define on your own and weld it to the log

final.log <- weldlog(log = basic.log, dt = boundary.example$dt,
                     seg = list(s1 = s1, s2 = s2, s3 = s3),
                     j = c("s1","s1","s1","s3","s2","s2","s1"))

# Lets see the result of the welding

whiteSet(xlim = c(-3,8), ylim = c(-1,77), ytick = 5, ny = 5) # Prepare plot

# This plot is going to serve to explain other functions;
title("Using weldlog(), infobar(), simp.lim() and minorAxis()")

multigons(final.log$i, x = final.log$xy, y = final.log$dt,
          col = bed.legend$col,
          density = bed.legend$density,
          angle = bed.legend$angle)
### Defining and drawing specific intervals

Let's say we would like to plot the position of magnetochrons. For that we first define a legend for each type of interval, here for normal and reverse polarity.

```r
legend.chron <- data.frame(polarity = c("N", "R"),
                           bg.col = c("black", "white"),
                           text.col = c("white", "black"),
                           stringsAsFactors = FALSE)
```

Then we set the legend for each chron.

```r
chron.legend <- left_join(chron.example, legend.chron, by = "polarity")
```

There are three chrons, but what we did can be applied to any number of them, as long as they are identified by a column (or more, `left_join` can merge using more than one column).

Using this legend we can draw rectangles with text in it using the `infobar()` function. In this function we define the coordinates of each rectangle (linked to `dt` for `y`, and different for each rectangle, but constant in `x`), the text to be in the rectangles with the `labels` parameter, and graphical parameters to be used by the `multigons()` and `text()` functions embedded in the `infobar()` function. The number of rectangles is `n`, and the length of the `y`, `x`, and `labels` elements can be `1` or `n` (i.e. the same `n` for each parameter).

You can provide a list of graphical parameters such as the colour for the rectangles and the text, as long as the length of each parameter in that list is `1` or `n`.

Notice that this function shares a lot in common with `litholog()` and `multigons()` in functionality and arguments. Note that you could obtain a similar result using `litholog()`, `multigons()` and `bedtext()`. You would simply need to code more :-)

```r
infobar(-2.5, -2, chron.legend$l, chron.legend$r,
        labels = chron.legend$polarity,
        m = list(col = chron.legend$bg.col),
        t = list(col = chron.legend$text.col),
        srt = 0)
```

### Treat data sets made of intervals (as happens a lot in geology)

As you have seen with `litholog`, intervals are dealt with by defining `lim` objects having a left and right boundary (`l` and `r`), an `id` and a boundary rule. Whichever of `l` and `r` is the maxima or minima usually does not
# matter. StratigrapheR offers a few functions to treat lim objectss. Here
# we will see the simp.lim() function, but if you want more info go see the
# ?as.lim help page, and the functions in its See Also part.

# simp.lim: this functions merges intervals of same id (if adjacent or
# overlapping)

# Basically, the lim objects are boundaries, for instance in the form [0,1[
# which would indicate an interval going from 0 to 1, zero included but 1 not.
# simp.lim takes the left and right boundaries, assumes that each boundary
# is included in the interval (by default b = "[]"), and simplifies the interval
# by merging them by id, which gives the lithological information in merged
# rectangles (with S, C and L indicating shales, cherts and limestones in this
# case).

litho.intervals <- simp.lim(l = bed.legend$l, r = bed.legend$r,
                           id = bed.legend$litho)

# The resulting list needs to be transformed into a data frame to merge with the
# legend.

litho.intervals <- data.frame(litho.intervals, stringsAsFactors = FALSE)

# Note the parameter stringsAsFactors that is set to FALSE, which is usually
# required when you create data frames to avoid problems, for instance using
# left_join()

colnames(litho.intervals)[3] <- "litho"  # Change a column name to be able to merge
# legend and data

litho.intervals.legend <- left_join(litho.intervals, legend, by = "litho")

infobar(-1.25, -0.75, litho.intervals.legend$l, litho.intervals.legend$r,
        m = list(col = litho.intervals.legend$col,
                 density = litho.intervals.legend$density,
                 angle = litho.intervals.legend$angle))

# As you can see if you look closely at the "Using weldlog(), infobar() and
# simp.lim()" plot, the subdivisions between beds of same lithology is gone.
# This is the result of the simp.lim() function by interval manipulation

# Add sample position with axis ----

# If you want you can also show where every sample is using the minorAxis()
# function, which allows distinction between major and minor ticks

at.min <- every_nth(proxy.example$dt, 5, empty = FALSE)
at.maj <- every_nth(proxy.example$dt, 5, inverse = TRUE, empty = FALSE)
labels.maj <- every_nth(proxy.example$name, 5, inverse = TRUE, empty = FALSE)

# The every_nth function allows here to skip samples regularly (to avoid having
\texttt{minorAxis(side = 4, at.min = at.min, at.maj = at.maj, labels.maj = labels.maj, tick.ratio = 0.5, pos = 6, las = 1, lwd = 0, lwd.ticks = 1)}

# Final litholog generation: getting it in a convenient function ----

# Once the final design for the lithology is established, it can be integrated into a graphical function which will draw every component of the final litholog with each desired feature.

# The most efficient way to generate the litholog is to directly put it in a reusable function so that you do not do all the work twice. However you need some of the data sets we've prepared, in this case \texttt{bed.example}, \texttt{fossil.example}, \texttt{boundary.example}, \texttt{chron.example} (that are already imbedded in StratigrapheR), \texttt{final.log}, \texttt{bed.legend}, \texttt{chron.legend} and \texttt{litholeg} (that are created in this script)

# If you do not want to run all unnecessary functions whenever you want to draw your log, a good trick is to save all the necessary data.frames needed in the litholog drawing function (here \texttt{one.log}) and load them in it. You just need to have the saving file (here \texttt{one.log.txt}) in a file (here a temporary file, see \texttt{?setwd} and \texttt{?getwd} help pages to manage files in your working directory)

\texttt{save(final.log, bed.legend, chron.legend, litho.intervals.legend, file = file)}

\texttt{one.log <- function(xlim = c(-2.5,7), ylim = c(-1,77), xarg = NULL, yarg = list(tick.ratio = 0.5, las = 1), main = "Final litholog")

\{
    load(file) # Load the saved data frames

    whiteSet(xlim = xlim, ylim = ylim, ytick = 5, ny = 5, xarg = xarg, yarg = yarg)

    title(main = main)

    multigons(final.log$i, x = final.log$xy, y = final.log$dt,}
col = bed.legend$col,
density = bed.legend$density,
angle = bed.legend$angle)

bedtext(labels = bed.example$id, l = bed.example$l, r = bed.example$r,
         x = 0.5, edge = TRUE)

centresvg(example.ammonite, 6,
         fossil.example$dt[fossil.example$type == "ammonite"],
         xfac = 0.5)

centresvg(example.belemnite, 6,
         fossil.example$dt[fossil.example$type == "belemnite"],
         xfac = 0.5)

infobar(-2, -1.5, chron.legend$l, chron.legend$r,
         labels = chron.legend$id,
         m = list(col = chron.legend$bg.col),
         t = list(col = chron.legend$text.col))

infobar(-1, -0.5, litho.intervals.legend$l, litho.intervals.legend$r,
         labels = litho.intervals.legend$litho, srt = 0)

}

# This graphical function can then be used as a standalone function, or
# integrated in a for loop to draw the entirety in a succession of panels
# (typically in pdf form)

# Indeed, if you go back to the definition of the one.log() function, you can
# see that we gave it a parameter, ylim. That parameter defines the range of dt
# that is covered in the plot. So you can plot a smaller part of the log:

one.log(ylim = c(18, 53), main = "Final litholog from dt 18 to 53")

# Or you can create a second function that creates a loop of the log if you want
# to generate an ensemble of sheets that placed end to end would create a
# complete litholog

# Basically can want to set up the scale (i.e. the y-or dt- interval of the
# litholog seen for each plot -or pdf page-: if you want to see each time an
# interval of 30 y-units of the litholog on each plot/pdf page, can set the
# parameter 'interval' of the following function to 30)

repeated.log <- function(start = 0, interval = 20)
{
    omar <- par("mar")

    par(mar = c(1, 4, 3, 2)) # This allows to define the margins as you wish

    l1 <- seq(start, max(final.log$dt), interval)
    l2 <- seq(start, max(final.log$dt), interval) + interval

    for(i in length(l1):1)
    {
\{ one.log(ylim = c(l1[i],l2[i]),
                main = paste("Repeated litholog, part from dt", l1[i], "to", l2[i]))
    
par(mar = omar)
\}

repeated.log()

# Printing and seeing you litholog in pdf ----

# The next function, pdfDisplay, generates a pdf of a graphical function.
# Any function producing plots such as repeated.log() can be inserted into it to
# generate plots. These plots will all be of the same size. I believe this
# function might not work on every computer. And its openfile argument, which
# causes the pdf to open, only works in Windows. If You are working with
# Windows, I recommend using SumatraPDF as your default pdf reader: this will
# allow pdfs to be changed while they are being visualised.
## Not run:
pdfDisplay(repeated.log(), width = 10, height = 15,
              name = "StratigrapheR_Example_a", track = FALSE)
## End(Not run)

# Plotting data -e.g. time-series data of a proxy - along the litholog ----

# Now lets say you want to plot information along the litholog. For that we will
# work in a graphical function that we will provide to pdfDisplay. Note that
# it is not possible to base yourself on the repeated.log() function, because
# it will print all the plots sucessively without allowing modification or
# addition

# One way of working is to create two plots next to each other and provide
# identical y axis parameters

graphical.function.1 <- function()
{
  opar <- par("mar","mrow")

  par(mar = c(3,4,3,2),
          mrow = c(1,2)) # This creates two windows where to plot sucessively

  # Plot the litholog on the left
  one.log(main = "")

  # Plot the other data on the right
  blackSet(xlim = c(-2*10^-8,8*10^-8),
          ylim = c(l1[i],l2[i]),
          main = paste("Repeated litholog, part from dt", l1[i], "to", l2[i]))
  
par(mar = omar)
}
ylim = c(-1,77), # It is important to define identical y limits # between the litholog and the proxy
ytick = 5, ny = 1,
targ = NULL)

lines(proxy.example$ms, proxy.example$dt, type = "o", pch = 19)

par(mar = opar$mar, mfrow = opar$mrow)

} ## Not run:
pdfDisplay(graphical.function.1(), width = 10, height = 15,
name = "StratigrapheR_Example_b", track = FALSE)
## End(Not run)

# If you want to put that repeated litholog in A4 format, the best way is to # use LaTeX. The following lines of code will create a TeX file that would # do that, test it if you want (the file will be in a temporary directory, # but you can change tempdir(), to getwd() for instance):
## Not run:
writeLines(log.loop.tex, paste(tempdir(),"log.loop.tex", sep = "/"))
## End(Not run)

# Another way to work this out is to create more space than needed on the # litholog plot and to add elements

graphical.function.2 <- function()
{
  omar <- par("mar")

  par(mar = c(3,4,3,2))

  # Plot the litholog with room for the rest

  one.log(main = "", xlim = c(-3,16), xarg = list())

  par(fig = c(0.5,1, 0, 1), # 'fig' defines the overlapping plotting window # dimensions x1, x2, y1 and y2
    new = TRUE) # 'new' allows addition to a preexisting plot

  # The graphical parameter 'fig' that you can set using the par() function # allows you to define a new plotting region overlapping the original one. # This allows you to redefine x axes values. But again using this you have to # be careful to provide the right y limits between the litholog and the proxy. # Be aware that the functions white-, black- and greySet() set the xaxis and # yaxis to "i", which means that the limits you provide in x and y are the # actual limits of the plot (while the default setting of xaxis and yaxis are # "r", which extends the data range by 4 percent at each end)

  blackSet(xlim = c(-2*10^-8,8*10^-8),
    ylim = c(-1,77),
    ytick = 5, ny = 1,
    targ = NULL,
```r
xarg = list(side = 3))

lines(proxy.example$ms, proxy.example$dt, type = "o", pch = 19)

par(mar = omar)

}

## Not run:
pdfDisplay(graphical.function.2(), width = 8, height = 15,
            name = "StratigrapheR_Example_c", track = FALSE)
## End(Not run)
```

---

**StratigrapheR.examples**

*Data for examples*

---

**Description**

Supporting data sets to use in the examples. Some will be used in the examples. `example.ammonite.svg` and `log.loop.tex` are meant to generate their respective .svg and .tex files. Others are used in the article (to be published soon).

**Details**

- **Litholog drawing data** `bed.example`, `boundary.example`, `example.ammonite`, `example.ammonite.svg`, `example.belemnite`, `example.breccia`, `example.HB2000.svg`, `example.lense`, `example.liquefaction`, `fossil.example`, `proxy.example`, `proxy.example.litho`
- **Time-Series** `irreg.example`
- **Magnetostratigraphical data** `chron.example`
- **Litholog exportation script** `log.loop.tex`
- **Oriented data** `zeq.example`
- **Stratigraphical tie points** `tie.points.example`

---

**symbology**

*Draws the symbols of a collection*

---

**Description**

Draws all the required symbols from a collection of them
Usage

symbology(
  collection,
  sym,
  x,
  y,
  xfac = 1,
  yfac = 1,
  xadj = 0,
  yadj = 0,
  col = NA,
  border = "black",
  density = NA,
  angle = 45,
  lty = par("lty"),
  lwd = par("lwd"),
  scol = border,
  slty = lty,
  slwd = lwd
)

Arguments

collection       a collection object (e.g. oufti)
sym               the name of the symbols in the collection
x, y              numeric vectors of coordinates where the object should be drawn.
xfac              the x size factor.
yfac              the y size factor.
xadj              value specifying the x adjustment of the drawing.
yadj              value specifying the y adjustment of the drawing.
col               the polygons background color. If density is specified with a positive value this
gives the color of the shading lines.
border            the lines color.
density           the density of shading lines, in lines per inch. The default value of NULL means
                  that no shading lines are drawn.
angle             the slope of shading lines, given as an angle in degrees (counter-clockwise)
lty, lwd           the border line type and width, see ?par for details.
scol, slty, slwd   the colour, type and width of the shading lines.

See Also

Similar functions: centresvg, framesvg and placesvg
Collections available in StratigrapheR: oufti99
Examples

# Create a data frame for all the required information ----

```r
a <- data.frame(name = c("ammonite", "marcassite", "nodule.point", "ammonite"),
                 x = c(1,3,5,1),
                 y = c(1,3,5,5),
                 col = c(NA, "grey90", "grey50", "grey90"))
```

# Draw them all in a single line of code ----

```r
plot.new()
plot.window(xlim = c(0,6), ylim = c(0, 6))
axis(1)
axis(2, las = 1)
symbology(oufti99, a$name, a$x, a$y, col = a$col)
```

tie.lim

Discretises lim objects

Description

Discretises continuous lim objects by constant interpolation

Usage

```r
tie.lim(
  lim = NULL,
  l = NULL,
  r = NULL,
  y = NULL,
  xout = NULL,
  id = 1L,
  to.lower = T,
  warn = T
)
```

Arguments

- **lim**: an object convertible into a lim object: either a vector of length 2 or a list of n left (1st element) and n right (2ndt element) interval limits, and of n interval IDs. In this case the lim objects have to be ordered, by ids, dependently to each other, and from left to right. For each id the lim objects have to cover the entire interval from the lowest to the highest value, without overlap.
trace.lim

1  a vector of n left interval limits
r  a vector of n right interval limits
y  a vector of n values to discretise
xout  a vector of numeric values specifying where interpolation is to take place. It will be identical for each id. If NULL the result will be continuous (points of a continuous line).
id  a vector of n interval IDs (default is 1 for each interval)
to.lower  whether to take the left (lower) or right point for interpolation at adjacent points
warn  whether to warn if the sampling interval is prone to miss the smallest intervals.

See Also

as.lim

Examples

l <- matrix(1:30, ncol = 3, byrow = FALSE)
r <- matrix(2:31, ncol = 3, byrow = FALSE)
id <- matrix(rep(c("C1", "C2", "C3"),10), ncol = 3, byrow = TRUE)
y <- matrix(rep(1:10,3), ncol = 3, byrow = FALSE)
xout <- seq(-2,32,0.5)

res <- tie.lim(l = l, r = r, y = y, xout = xout, id = id)

cont <- tie.lim(l = l, r = r, y = y, id = id)

plot(res$x, res$y, pch = 19, col = "red")
lines(cont$x[,1], cont$y[,1])
lines(cont$x[,2], cont$y[,2])
lines(cont$x[,3], cont$y[,3])

---

trace.lim

Visualize lim objects

Description

Visualize lim objects as lines for each interval. The lines are time series with the dt (depth/time) being the boundaries of the interval, and an xy intensity is defined as values attributed to the interval.

Usage

trace.lim(
  lim = NULL,
  l = NULL,
  r = NULL,
id = 1L,
b = "[]",
xy = 0,
order = F,
decreasingly = F,
output = T,
plot = T,
link = F,
point = T,
style = list(),
close = list(pch = 19),
open = list(pch = 21, bg = "white"),
add = F,
gen = list(xlab = "dt", ylab = "xy")
)

plot_lim(
dt,
xy,
int,
include,
link = F,
point = T,
style = list(),
close = list(pch = 19),
open = list(pch = 21, bg = "white"),
add = F,
gen = list(xlab = "dt", ylab = "xy")
)

**Arguments**

- **lim**
  - a list of n left (1st element) and n right (2nd element) interval limits, of n interval IDs, and of n interval boundary rules (e.g. "[]").

- **l**
  - the left interval limits (numerical vector of length n).

- **r**
  - the right interval limits (numerical vector of length n).

- **id**
  - the interval IDs (numerical or character vector of length n, the default is 1 for each interval). They can be similar for different intervals.

- **b**
  - the interval boundaries rules: "[]" (or "closed") to include both boundaries points, "[]" (or "()" and "open") to exclude both boundary points, "[]" (or "[]"), "right-open" and "left-closed") to include only the left boundary point, and "[]" (or "[]", "left-open", "right-closed") to include only the right boundary point. The notation is simplified to "[]", "[]", "[]" and "[]" only.

- **xy**
  - the intensity attributed to each interval.

- **order**
  - whether to order the intervals.

- **decreasingly**
  - whether the order to set is decreasing.
The `trace.lim` function is used to output, plot, link, and add points to the boundaries of intervals. The function has the following arguments:

- `output`: whether to output the results.
- `plot`: whether to plot the results.
- `link`: whether to link all the intervals into one line.
- `point`: whether to add points to the boundaries of each interval.
- `style`: the style of the lines.
- `close`: the style of the points for closed boundaries.
- `open`: the style of the points for open boundaries.
- `add`: whether to add the plot to an existing plot.
- `gen`: parameters for `plot`.
- `dt`: the boundaries of the intervals as provided by `trace.lim`.
- `int`: the id of each interval as provided by `trace.lim`.
- `include`: whether the boundaries of the intervals are included in them, as provided by `trace.lim`.

The `Value` section explains that `trace.lim` returns a list of `dt` values (dt stands for depth/time, which corresponds to the boundaries of intervals), `xy` values (the "intensity" of each interval), `int` which is an id for each interval, `id` which is the ids defined in the lim objects (these ids can be similar for different intervals, and therefore define groups of intervals), and `include` which are boolean (T/F) values whether a boundary of the interval is included in the interval.

The `See Also` section refers to generalities on lim data: `as.lim`.

The `Examples` section provides an example of how to use the function:

```r
lim <- as.lim(l = c(0,6,4,6,50), r = c(1,5,6,9,8), b = c("[[", "]", "]", "]", "]")
xy <- c(1,2,3,4,5)
trace <- trace.lim(lim = lim, xy = xy, plot = FALSE)
trace
plot_lim(dt = trace$dt, xy = trace$xy,
         int = trace$int, include = trace$include)
```
transphere

Conversion between declinaison/inclination/intensity and cartesian coordinates

Description

Conversion between declinaison/inclination/intensity and cartesian coordinates (modified from RFOC package)

Usage

transphere(dec = NA, inc = NA, int = 1, x = NA, y = NA, z = NA, into = "other")

Arguments

dec  declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010). Values outside this range are corrected by incfix().

inc  inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010). Values outside this range are corrected by incfix().

int  intensity of the data. Defaults to one (unit sphere).

x, y, z  cartesian coordinates. x is the North, y the East, and z straight down. If dec and inc are not provided they are used to be converted back in dec, inc and int data. Output is corrected by incfix().

into  overriding parameter for generalisation: if "dii" dec, inc and int will remain as they are, and if "xyz" cartesian coordinates will remain as they are

Value

a list of coordinates, in cartesian form or dec, inc, int form following the input

See Also

fmod, dipfix and incfix

Examples

transphere(dec = c(65,135), inc = c(32,74))

l <- transphere(dec = c(65,135), inc = c(32,74))
transphere(x = l$x, y = l$y, z = l$z)
weld

Combines segments with "litholog()"-like data frame

Description

Adds segments to the polygon forming the bed of a log in a "litholog()"-like data frame.

Usage

weld(log, dt, xy, begin, end, erase = "none", order = "current")

Arguments

log a "litholog()"-like data frame on which the new segment needs to be welded.
dt the dt value for each point of the added segment.
xy the xy value for each point of the added segment.
begin the row of log after which the segment will be added.
end the row of log before which the segment will be added (end should be superior to begin).
erase erase the begin point ('begin'), end point ('end'), both ('both') or only the points in between ('none').
order the order of the added points : can be the current order ('current'), the current order inversed ('inverse'), or ordered by xy ('xy' or '-xy') or dt ('dt' or '-dt').

Value

a "litholog()"-like data frame with the bed that comprises the begin and end row having the segment welded to it.

See Also

litholog and weldlog

Examples

l <- c(1)
r <- c(2)
h <- c(4)
i <- c("B1")
log <- litholog(l, r, h, i)

seg <- sinpoint(4, 1, 0.25, pos = 2, phase = 0.5)
welded <- weld(log, seg$y, seg$x, 3, 4, order = "inverse", erase = "both")

plot(c(-1,5),c(0,3),type = "n")
multigons(log$i,log$xy,log$dt)
weldjoint

Changes boundaries segments in basic lithologs

Description

Adds personalised segments to bed boundaries of lithologs from "litholog()"-like data frames

Usage

weldjoint(
  log,  
dt,  
collection,  
sym,  
yinv = F,  
xinv = F,  
yleft = 0,  
yright = NA,  
ymin = NA,  
ymax = NA,  
xmin = 0,  
xmax = max(log$xy),  
add.dt = 0,  
tolerance = 8
)

Arguments

log a "litholog()"-like data frame on which the new segments need to be welded.
dt the position of the n boundaries to change.
collection a collection object (e.g. oufti)
sym the name of the symbols in the collection. This should be a symbol that can be considered as a bedding joint; see is.joint.
yinv, xinv whether to inverse the plotting for x and y values (T or F)
yleft, yright the depth/height/time value for the extreme point at the right or left of the joint (yleft overruns yright, which overruns ymin and ymax)
ymin, ymax the extreme values for the y axis (in case of conflict with yleft and/or yright, defaults to the smallest exaggeration)xmin, xmax the extreme values for the x axis
whether to automatically add the dt value to the dt of the segments (with the add.dt value when it is not zero)

tolerance the order of tolerance for errors, i.e. the number of decimals considered as being meaningful for matching dt to log

Value

a "litholog()"-like data frame, with new bed boundaries

Examples

# Generate litholog ----

l <- c(0,1,2,3,4)
    r <- c(1,2,3,4,5)
    h <- c(4,3,4,3,4)
i <- c("B1","B2","B3","B4","B5")
    log <- litholog(l, r, h, i)

# Modify the boundaries of the litholog ----

nlog <- weldjoint(log, c(1,2,3,4), oufti99,
    sym = c("1sin", "stylolith", "3sin", "liquefaction"),
    ymax = c(NA, NA, NA, 0.2),
    xmin = c(0,0,0,1),
    xmax = c(4,4,4,1.5))

# Visualise

par(mfrow = c(1,2))

plot.new()
plot.window(xlim = c(0,5), ylim = c(0,5))
axis(1)
axis(2)
multigons(log$i, log$xy, log$dt)

plot.new()
plot.window(xlim = c(0,5), ylim = c(0,5))
axis(1)
axis(2)
multigons(nlog$i, nlog$xy, nlog$dt)
Description

Adds personalised segments to bed boundaries of lithologs from "litholog()-like data frames

Usage

\[
weldlog(\log, \ dt, \ seg, j = 1: length(dt), \ col.xy = 1, \ col.dt = 2, \ auto.dt = T, \ add.dt = 0, \ omit1 = NULL, \ omit2 = NULL, \ warn = T, \ tolerance = 8 )
\]

Arguments

- **log**: a "litholog()-like data frame on which the new segments need to be welded.
- **dt**: the position of the n boundaries to change.
- **seg**: a list of n dataframes having xy and dt coordinates for the segments that are going to be welded to the log.
- **j**: the indexes of the segments attributed to each boundary or the names of these segments. Should be of same length than dt.
- **col.xy**: the number of the column for the xy coordinates in the seg dataframes.
- **col.dt**: the number of the column for the dt coordinates in the seg dataframes.
- **auto.dt**: whether to automatically add the dt value to the dt of the segments (with the add.dt value when it is not zero)
- **add.dt**: a value to add to the dt of the segments for each boundary (in addition of the value of the dt parameter). Should be of length 1 or of same length than dt.
- **omit1, omit2**: the dt of the boundary for which either the upper or lower bed should not be welded to (1 and 2 depending on the order of the beds in the original log)
- **warn**: whether you want to be annoyed (beginners should find it useful to be annoyed)
- **tolerance**: the order of tolerance for errors, i.e. the number of decimals considered as being meaningful for matching dt to log
weldprofile

Value

a "litholog()"-like data frame, with new bed boundaries

See Also

Complementary function litholog

Underlying function: weld

To generate sinuousidal segments: sinpoint To generate a lot of different sinuousidal segments: see the example in neatPick

To import and adapt .svg files as segments: pointsvg, framesvg, centresvg and changesvg

Examples

```r
l <- c(0,1,2,3,4)
r <- c(1,2,3,4,5)
h <- c(4,3,4,3,4)
i <- c("B1", "B2", "B3", "B4", "B5")
log <- litholog(l, r, h, i)

whiteSet(xlim = c(-1,5), ylim = c(-1,6))
multigons(log$i, log$xy, log$dt, lty = 3)

seg1 <- sinpoint(4, 0, 0.25, phase=0.5)
seg2 <- sinpoint(4, 0, 0.25, phase=1.5)
welded <- weldlog(log, dt = c(2,3,4), seg = list(seg1 = seg1, seg2 = seg2),
                 j = c("seg1", "seg2", "seg2"))
multigons(welded$i, welded$xy, welded$dt, lwd = 3, lty = 2, border = "red")
```
Arguments

log
a "litholog()-like data frame on which the new profile needs to be welded.

gap
The xy value delimiting the litholog in the parts that will remain, and the parts
that will be replaced by the profile. This should be comparable to the most
inward values of the profile. What side of the litholog will remain depends on
the ext parameter.

dt, xy
the depth and intensity values for the profile

i
the beds ids for the points of the profile (is optional; this is useful for complex
profiles, which can go back and forth in depth).

ext
the most outward values of the profile; defaults to infinity Inf, for "left-side"
profiles, set to -Inf.

tolerance
the order of tolerance for errors, i.e. the number of decimals considered as being
meaningful for matching dt to log

correct
this parameter applies in a very specific case, when i is provided, and when the
order of points is not straightforward (going from low to high values, or vice
versa). If correct is TRUE, the ambiguous parts (in ambiguous beds) of the
profile will be reversed.

Value

A litholog object, i.e., a table of bed id (i), depth (dt) and xy values (the x position if your litholog
is vertical).

Examples

# Make an initial log ----

r <- c(1,2,3,4,5)  # left boundary of the bed interval (upper or lower)
l <- c(0,1,2,3,4)  # right boundary of the bed interval (upper or lower)
h <- c(4,3,5,3,4)  # hardness (arbitrary)
i <- c("B1","B2","B3","B4","B5")  # Bed name

log <- litholog(l,r,h,i)  # Generate data frame of the polygons
# making the litholog

# Define the profile ----

# Depths (dt), intensity (xy), and ids (id) of profile points
dt <- c(0,1,1,2,2,2,3,3,4,4,5)
xy <- c(5,4,3,4,3,3,6,5,3,4,3,5,4)
id <- c("B1","B1","B1","B2","B2","B3","B3","B3","B4","B4","B4","B5","B5")

# Weld profile to litholog ----

nlog <- weldprofile(log = log, gap = 3, dt = dt, xy = xy, i = id, ext = Inf)

# Visualisation ----

opar <- par()$mfrow
whiteSet

Sets the plot environment to draw a long data set.

Description

Sets the plot environment to draw a long dataset. It is without background, and with only axes with major and minor ticks.

Usage

whiteSet(
  xlim,
  ylim,
  xtick = NA,
  ytick = NA,
  nx = 1,
  ny = 1,
  xaxs = "i",
  yaxs = "i",
  xarg = list(tick.ratio = 0.5),
)
whiteSet

```r
yarg = list(tick.ratio = 0.5, las = 1),
add = FALSE
```

**Arguments**

- `xlim, ylim`: the x and y limits (e.g. `xlim = c(-1,1)`)
- `xtick, ytick`: the interval between each major ticks for x and y
- `nx, ny`: the number of intervals between major ticks to be divided by minor ticks in the x and y axes
- `xaxs, yaxs`: The style of axis interval calculation to be used for the x and y axes. By default it is "i" (internal): it just finds an axis with pretty labels that fits within the original data range. You can also set it to "r" (regular): it first extends the data range by 4 percent at each end and then finds an axis with pretty labels that fits within the extended range. See ?par for further explanation
- `xarg, yarg`: a list of arguments to feed to minorAxis() for the x and y axes. See the ?minorAxis help page for the possible arguments. See ?merge_list for further information.
- `add`: whether to add to an existing plot

**See Also**

- Similar functions: `greySet` and `blackSet`
- To create axes with major and minor ticks: `minorAxis`
- To print a plot in pdf: `pdfDisplay`
- To automatically determine pretty interval limits: `encase`

**Examples**

```r
y <- c(0,11,19,33)
x <- c(1,2,2.5,4)
a <- min(y)
b <- max(y)
f <- encase(a-1,b,5)
whiteSet(c(0,4), f, ytick = 5, ny = 5, xaxs = "r")
points(x, y, pch=19)
```
**ylink**

*Draws connection lines to connect two points in y*

**Description**

Draws connection lines to connect two points in y

**Usage**

```r
ylink(y1, y2, x1, x2, ratio = 0.1, xi1 = NA, xi2 = NA, l = list(lty = 3))
```

**Arguments**

- `y1, y2`: y positions (you can provide several ones at once)
- `x1, x2`: x positions (you can provide several ones at once)
- `ratio`: the ratio of the breaking points of the lines (from the start or end to the centre)
- `xi1, xi2`: x positions of the breaking points of the lines.
- `l`: a list of arguments to feed `lines()`. Go see ?lines to know which arguments can be provided. See ?merge.list for further information.

**See Also**

`multilines`, `bedtext`, `infobar` and `nlegend`

**Examples**

```r
plot(c(0,6),c(-20,20), type = "n")
infobar(ymin = c(-20,0), ymax = c(0,20), xmin = 1, xmax = 0,
       m = list(col = c("black", "white")))
infobar(ymin = c(-20,10), ymax = c(10,20), xmin = 5, xmax = 6,
       m = list(col = c("black", "white")))
ylink(c(0,12),c(10,20), x1 = 1, x2 = 5, ratio = 0.2,
     l = list(lty = c(1,3), lwd = 2))
```
**zijderveld**  
*Draws a Zijderveld plot*

**Description**

Draws a Zijderveld plot: it projects 3D points (having declination, inclination and intensity) in 2D, horizontally and vertically.

**Usage**

```r
zijderveld(
  dec,
  inc,
  int,
  xh = "WE",
  xv = xh,
  centre = F,
  xlim = NA,
  ylim = NA,
  unit = NA,
  xlab = "",
  ylab = "",
  labels = NA,
  nlabels = 1,
  h = list(pch = 19),
  v = list(pch = 21, bg = "white"),
  f = list(pch = 21, bg = "white", cex = 1.5),
  t = list(pos = 3, offset = 0.5),
  l = list(),
  anchored = T,
  style = "branches",
  tcl = 0.2,
  orientation = TRUE,
  scientific = NA,
  decimals = 10,
  add = FALSE
)
```

**Arguments**

- **dec**: declination of the data; it is the angle from the north taken on an horizontal plane. It is measured clockwise from North and ranges from 0 to 360° (Tauxe 2010). Values outside this range are corrected by incfix().

- **inc**: inclination of the data; it is the angle from the horizontal, is positive downward, and ranges from +90° for straight down to -90° for straight up (Tauxe, 2010). Values outside this range are corrected by incfix().
int
orientation of the x axis for the horizontal points: can be 'SN' or 'WE'.

xh
orientation of the x axis for the horizontal points: can be 'SN', 'WE' or 'modified' (for the latter the horizontal projection of the vector given by the square root of the addition of the squared horizontal components).

xv
orientation of the x axis for the horizontal points: can be 'SN', 'WE' or 'modified' (for the latter the horizontal projection of the vector given by the square root of the addition of the squared horizontal components).

centre
logical, whether the [0,0] point should be in the centre of the plot. Is ignored if xlim and/or ylim are defined.

xlim, ylim
the x and y minimal limits. The actual limits can change to keep a x/y ratio of 1.

unit
the tick interval.

xlab, ylab
the titles for the axes.

labels
a character vector of labels to add to each point.

nlabels
the number of labels to skip (for clarity).

h, v, f, t, l
list of graphical parameters to feed the graphical functions: h, v and f are fed to points() for the horizontal, vertical and first points respectively; t is fed to the text() for the labels and l is fed to lines() for the lines joining each horizontal and vertical points. See ?points, ?text and ?lines help page for the possible arguments. See ?merge_list for further information.

anchored
logical, whether the lines should be anchored to the [0,0] point.

style
the style of the plot: 'branches', 'box0', 'box1', or 'box2'. The boxes are advised when zooming using xlim and/or ylim.

tcl
The length of tick marks (see par() help page).

orientation
logical, whether to add captions indicating the orientation of the plot.

scientific
logical or NA, whether have scientific notation (e.g. -1.0E-06) or not (e.g. 0.00015). If NA, R will be left only judge.

decimals
the number of decimals if scientific is T or F. Having not enough decimals can lead to override the unit parameter, but the tick labels will be correctly aligned.

add
logical, whether to add the plot to an existing plot.

Details
By default horizontal projection is made of black points, vertical of white points.

References

See Also
earnert
Examples

zd <- zeq_example
ori <- par()$mfrow
par(mfrow = c(1,2))

zijderveld(dec = zd$Dec, inc = zd$Inc, int = zd$Int,
           xh = "WE", unit = 10^-5)

zijderveld(dec = zd$Dec, inc = zd$Inc, int = zd$Int,
           style = "box1", scientific = FALSE, decimals = 5,
           labels = zd$Treat, nlabels = 2)

par(mfrow = ori)
Index

are.lim.distinct (as.lim), 4
are.lim.nonadjacent (as.lim), 4
are.lim.unique (as.lim), 4
are.lim.ordered (as.lim), 4
as.lim, 4, 31, 42, 46, 52, 57, 82, 93, 111, 113
bed.example (StratigrapheR.examples), 108
bedtext, 6, 46, 50, 51, 69, 123
blackSet, 7, 59, 122
boundary.example
  (StratigrapheR.examples), 108
casing, 9, 27
centresvg (centresvg), 10
centresvg, 10, 12, 14, 16, 36, 40, 52, 61, 77, 80, 109, 119
changejoint, 12
changesvg, 12, 13, 16, 36, 80, 119
chron.example (StratigrapheR.examples), 108
clipsvg, 12, 14, 15, 36, 80
collection, 16
collections, 18
convert, 18
convertAxis, 19, 89
dipfix, 20, 24, 25, 33, 45, 83, 114
divisor, 21
earinc, 22, 23
earnet, 23, 25, 26, 125
earplanes, 23, 24, 26
earpoints, 23, 25, 25
encase, 8, 9, 27, 38, 122
encircle, 28
enlarge, 29
every_nth, 30, 59
example.ammonite
  (StratigrapheR.examples), 108
eexample.belemnite
  (StratigrapheR.examples), 108
eexample.breccia
  (StratigrapheR.examples), 108
eexample.HB2000.svg
  (StratigrapheR.examples), 108
eexample.lense (StratigrapheR.examples), 108
eexample.liquefaction
  (StratigrapheR.examples), 108
flip.lim, 5, 31
fmean, 32
fmod, 21, 33, 33, 45, 114
folder, 34
formFunction, 34
fossil.example
  (StratigrapheR.examples), 108
framesvg, 12, 14, 16, 35, 36, 40, 52, 61, 77, 80, 109, 119
getwd, 53
greySet, 8, 37, 38, 59, 122
homogenise, 39, 55
homogenize (homogenise), 39
ignore, 12, 16, 36, 40, 61, 64
in.lim, 5, 41
in.window, 43
incfix, 21, 26, 33, 45, 83, 114
infobar, 5, 7, 46, 52, 61, 69, 123
irreg.example (StratigrapheR.examples), 108
is.clockwise, 47
is.collection (collection), 16
is.divisor (divisor), 21
is.joint, 49, 116
is.lim (as.lim), 4
is.litholog (litholog), 51
is.pointsvg (pointsvg), 79
leftlog, 7, 50
litholog, 7, 50, 51, 115, 119
log.loop.tex (StratigrapheR.examples), 108
memento, 52
merge_list, 39, 54
mid.lim, 5, 57
minorAxis, 8, 20, 30, 38, 57, 59, 122
minorAxisTicks, 59, 59
multigons, 12, 36, 40, 46, 51, 60, 64, 69
multilines, 40, 51, 61, 63, 123
neatPick, 64, 119
neatPicked, 67
nlegend, 46, 69, 123
noise_emd (StratigrapheR.examples), 108
nset, 70
octapos, 47, 71, 72
octashift, 72
order.lim (as.lim), 4
oufti99, 109
oufti99 (collections), 18
outliner, 73
pdfDisplay, 8, 38, 51, 74, 122
pkgfind, 76
placesvg, 12, 14, 36, 76, 80, 109
planepoints, 78
plot, 113
plot.window, 69
plot_collection (collection), 16
plot_lim, 5
plot_lim (trace.lim), 111
pointsvg, 10, 11, 13–17, 35, 76, 77, 79, 119
profiler, 80
proxy.example (StratigrapheR.examples), 108
rebound, 5, 43, 82
repitch, 83
reposition, 84, 86, 88
restore, 84, 85, 88
rmatrix, 87, 88
rotate, 84, 86, 88
seq_log, 59, 89
seq_mult, 90
shift, 51, 61, 64, 90
simp.lim, 5, 92
sinpoint, 93, 119
strat.mean, 94, 96
strat.repair, 94
strat.var, 95
StratigrapheR, 51, 96
StratigrapheR.examples, 108
symbology, 108
tie.lim, 5, 110
tie.points.example
   (StratigrapheR.examples), 108
trace.lim, 5, 111
transphere, 21, 33, 45, 83, 114
weld, 115, 119
weldjoint, 116
weldlog, 50, 51, 115, 118
weldprofile, 119
whiteSet, 8, 38, 51, 59, 121
ylink, 7, 46, 52, 69, 123
zeq_example (StratigrapheR.examples), 108
zijderveld, 23, 124