Package 'sclero'

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Title Measure Growth Patterns and Align Sampling Spots in Photographs

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Description Provides functions to measure growth patterns and align sampling spots in chronologically deposited materials. The package is intended for the fields of sclerochronology, dendrochronology and geology.

Depends R (>= 3.0), RImageJROI, spatstat, plyr

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R topics documented:

assign.size 2
assign.value 3
barium 4
coln 5
convert.ijdata 5
create.rawDist 6
order.ijdata 8
plot.rawDist 9
plot.spotDist 11
print.spotDist 13
read.ijdata 13
samplemap 16

sclero 17
shellsizes 17
shellspots 18
spot.dist 18

Index **21**

`assign.size` *Assign spot sizes to 'rawDist' objects for estimating spatial extent of sample averaging error.*

Description

Assigns spot sizes to `rawDist` objects for estimating averaging error.

Usage

```
assign.size(rawDist, file = NULL, path = NULL, names = "generate.invalid",
  types = c("oval", "freehand", "rect"))
```

Arguments

`rawDist`	`rawDist` object to which the values should be assigned.
`file`	optional. ImageJ .zip file containing the spot size information. If `NULL` (default), the file name is assumed to be the same than from where `rawDist` data was read from.
`path`	optional. A character argument specifying the location of the `file`. If `NULL` (default), the `file` is assumed to be located in the working directory. See `dir` for further information.
`names`	optional. A character argument specifying how the names of `spots` should be generated. See `read.ijdata` for details. Defaults to "generate.invalid".
`types`	optional. A character vector specifying the `strType` of ROI objects to be considered as sample spots (see `plot.ijroi` for possible pattern types). Defaults to `c("oval", "freehand", "rect")` meaning that oval and freehand selections, as well as rectangle tool selections will be used to calculate the spatial extent of sample spots.

Details

If the .zip file containing spot size information is the same than from which the `rawDist` object was derived from and located in your working directory, assignment of spot sizes is simply specified by `assign.size(rawDist)`. Otherwise, use the `path` argument to specify the folder where the `file` is located.

Value

Returns a list of class 'rawDist' with a list of `ppp` objects containing locations of sample spot centroids and a list of `hyperframe`s containing spot size information.

Author(s)

Mikko Vihtakari

See Also

read.ijdata spot.dist assign.value plot.spotDist

Examples

```
data(shellspots)
shell <- convert.ijdata(shellspots)
path <- file.path(system.file("extdata", package = "sclero"))
sizes <- assign.size(shell, path = path)
sizes$spot.area
```

---

assign.value *Assign values to 'rawDist' objects for plotting.*

Description

Assigns values to rawDist objects for spatial density plotting.

Usage

```
assign.value(rawDist, value, value.name = NULL)
```

Arguments

rawDist	rawDist object to which the values should be assigned.
value	a data.frame or list of data.frames of the same length than spot spequences (spots). Each data.frame has to have identical length to spots. First column specifies the order. Second column containing the values (see Details).
value.name	a character or function defining the name for the assigned value. Can be expression

Details

This function can be used to plot values as color-densities on sample maps. The function is useful e.g. for examining the spatial distribution of geochemical data, such as element ratios or isotope ratios, along sample materials. If the rawDist object contains only one sample spot sequence, the value parameter should be expressed as a data.frame with two columns. If the rawDist object consists of several sample spot sequences, the value parameter should be a list of data.frames with length equivalent to number of spot sequences. The first column in all value data.frames represents spot number and should be equivalent to $spots marks in the rawDist object. The second column represents the values to be assigned. Column names are ignored.

Value

Returns a list of class rawDist containing spot value information.

Author(s)

Mikko Vihtakari

See Also

read.ijdata spot.dist assign.size plot.rawDist

Examples

```
data(barium)
data(shellsizes)

## rawDist
shellvalues <- assign.value(shellsizes, barium, value.name = "Ba/Ca")
plot(shellvalues, spot.size = "actual", spot.type = "value", main.type = "none")

## spotDist
shellvalues.aligned <- spot.dist(shellvalues)
plot(shellvalues.aligned, spot.size = "actual", spot.type = "idvalue",
spot.color = "darkgrey", highlight.gbs = c("WG_start", "WG_end"))
```

---

barium *Barium to calcium ratios for sample spots in shellspots dataset*

Description

Barium to calcium ratios for sample spots in shellspots dataset

Usage

```
data(barium)
```

Format

A dataframe containing Ba/Ca information for shellspots. The object is ready for assign.size function.

coln — *Print the order and names of columns in a data frame*

Description

Prints the order and names of columns in a data.frame.

Usage

```
coln(X)
```

Arguments

X	a data.frame for which the column names should be printed.

Value

A list containing the column names and their numeric order.

Author(s)

Mikko Vihtakari

See Also

data.frame, colnames

Examples

```
dat <- data.frame(a = 1:10, b = 10:1)
coln(dat)
```

convert.ijdata — *Convert IJDATA object to a list of spatstat objects*

Description

Converts an IJDATA to a list of spatstat patterns ready for plotting or sample spot alignment.

Usage

```
convert.ijdata(X)
```

Arguments

X	an IJDATA object to be converted.

Value

Returns a list of class `rawDist`, which contains spatstat point patterns. The returned `rawDist` can be plotted using the generic plotting command.

Author(s)

Mikko Vihtakari

See Also

`read.ijdata` for generating `IJDATA` objects.

`plot.rawDist` for plotting.

`spot.dist` for aligning sample spots.

Examples

```
data(shellspots)
shell_map <- convert.ijdata(shellspots)
plot(shell_map)
```

`create.rawDist` *Create rawDist data from arbitary coordinates*

Description

Creates a `rawDist` data object from arbitary coordinates ready for plotting or sample spot alignment.

Usage

```
create.rawDist(spots, gbs, main, spot.seq.names = NULL, sample.name = NULL,
  scaling.factor = 1, unit = NULL)
```

Arguments

`spots`	A list of `ppp` objects or a single ppp object defining the sample spot sequences. If `marks` are not specified, sequencial names will be used.
`gbs`	`psp` object defining the growth lines. If `marks` are not specified, sequencial names will be used.
`main`	`psp` object defining the measurement axis. If `marks` are not specified, sequencial 'main' will assigned as the marks. Only on 'main' axis is allowed per 'rawDist' object.
`spot.seq.names`	optional. A character vector of equal length to number of sample `spots` sequences defining the name for each sequence. If left empty sequencial names will be generated.
`sample.name`	optional. A character vector (`length == 1`) defining the name of the sample.

`scaling.factor` optional. A numeric value defining the scale of photograph in pixels / `unit`. Defaults to 1.

`unit` optional. A charater vector (`length == 1`) defining the unit of measurements. See `scale`.

Details

This function can be used to create arbitary test data, which can be passed further on in `sclero` package function hierarchy.

Value

Returns a list of class `rawDist`, which contains spatstat point patterns. The returned `rawDist` can be plotted using the generic plotting command.

Author(s)

Mikko Vihtakari

See Also

`read.ijdata` for generating `IJDATA` objects.

`convert.ijdata` for converting `IJDATA` objects to `rawDist` objects.

`plot.rawDist` for plotting.

`spot.dist` for aligning sample spots.

Examples

```
dev.off()
W <- square(10)
S <- ppp(x = c(7, 5, 3), y = rep(5,3), window = W)
G <- psp(x0 = c(8,6,4,2), y0 = rep(2,4), x1 = c(8,6,4,2), y1 = rep(8,4), window = W)
M <- psp(x0 = 0, x1 = 8, y0 = 5, y1 = 5, window = W)
x <- create.rawDist(spots = S, gbs = G, main = M)
plot(x)

## Generate random points for alignment
set.seed(1)
S <- rpoint(n = 5, win = owin(xrange = c(2,7), yrange = c(5,7)))
S$window <- W
G <- psp(x0 = c(7,5,3,1), y0 = rep(2,4), x1 = c(9,7,5,3), y1 = rep(8,4), window = W)
M <- psp(x0 = 0, x1 = 8, y0 = 1, y1 = 1, window = W)
x <- create.rawDist(spots = S, gbs = G, main = M)
plot(x)
y <- spot.dist(x)
plot(y)
```

order.ijdata *Order IJDATA spot sequences and growth lines*

Description

Reorders spot sequences and growth lines within object of class IJDATA.

Usage

```
order.ijdata(IJDATA, spots = "", gbs = "", print.order = FALSE)
```

Arguments

IJDATA	an IJDATA object.
spots	a character or numeric vector specifying the desired order of sample spot sequences.
gbs	a character or numeric vector specifying the desired order of growth lines.
print.order	logical. Should the current order of spot sequences and growth lines be printed instead of changing the order?

Details

Reorders IJDATA spot.x and spot.y and/or gbs.x and gbs.y coordinate data.frames. Useful when order of ROIs does not correspond with the desired order of convert.ijdata or spot.dist output. Can also be used to print the order of spot sequences and growth lines within IJDATA object (see 'print.order'). In addition the function can also be used to drop spot sequences or growth lines from the data set by leaving out ROI names. In this case a warning is produced to confirm that the user has not forgotten something.

Author(s)

Mikko Vihtakari

See Also

read.ijdata for reading zip files containing ImageJ ROIs.

convert.ijdata for converting the coordinate information to spatstat point patterns.

Examples

```
data(shellspots)
order.ijdata(shellspots, print.order = TRUE) # Prints the current order. Does not change anything
dat <- order.ijdata(shellspots, gbs = c(1,3,6:14,4,5,2)) # Changes order of growth bands
order.ijdata(dat, print.order = TRUE)

## Subset the first sample spot sequence
dat2 <- order.ijdata(shellspots, gbs = 1:13)
```

```
## Warning message:
## In order.ijdata(shellspots, gbs = 1:13) :
## Length of gbs does not correspond the number of columns. Data removed.
order.ijdata(dat2, print.order = TRUE)
```

`plot.rawDist` *Plot rawDist object*

Description

Plots a map of `rawDist` object.

Usage

```
## S3 method for class 'rawDist'
plot(x, ..., sample.name = "keep", spot.type = "id",
  spot.size = 2, spot.color = NULL, main.type = "all",
  color.palette = colorRampPalette(c("blue", "cyan", "yellow", "red"), bias =
  1)(100), highlight.gbs = NULL, highlight.col = "red")
```

Arguments

`x`	`rawDist` object
`...`	Arguments to be passed to other methods, such as graphical parameters.
`sample.name`	A character argument specifying the sample name to be plotted as an overall title for the plot (`main`). Defaults to `"keep"` meaning that the sample name will be extracted from the `rawDist` object. The plot title can be omitted by specifying `sample.name = NULL`.
`spot.type`	A character argument with three possible levels (`"id"`, `"value"`, and `"idvalue"`) indicating how sample spots should be plotted. Defaults to `"id"`, which plots sample spot numbers within open circles. The size of the circles can be controlled using the `spot.size` argument. The option `"value"` results to a sample map where the color of circles is related to a value through `assign.value` function. The color scale can be set using the `color.palette` argument, and size of the symbols (pch = 21) and through the `spot.size` argument. The option `"idvalue"` combines `"id"` and `"value"` leading to a sample map with sample spot numbers.
`spot.size`	An integer or a character argument with value `"actual"` indicating the size (`cex`) of points. If `"actual"`, the actual size and shape of sample spots will be plotted. In this case, sample spot size information is required. Defaults to 2 meaning that sample spots are plotted as points with pch = 21 and cex = 2.
`spot.color`	A vector with equal length to number of spot sequences defining the color of sample spot labels. If `NULL` (default) a preset set of colors will be used.

`main.type` A character argument with four possible levels (`"all"`, `"axis"`, `"ends"`, and `"none"`) indicating how the distance / main axis should be plotted. Defaults to `"all"` indicating that both the main axis and end points should be plotted. If `"axis"` only the main axis will be plotted. If `"ends"` only the end points will be plotted, and if `"none"` the main axis intormation will not be plotted.

`color.palette` color palette used for "value" and "idvalue" `spot.type` options. Passed to `colorRampPalette`.

`highlight.gbs` A character vector specifying the names of growth bands to be highlighted (i.e. colored with a different color than "darkgrey"). If `NULL` (default) all growth bands will be drawn using the standard color.

`highlight.col` A character argument specifying the color to be used in growth band highlighting (`highlight.gbs`).

Details

The **sclero** package currently uses the **graphics** package distributed with R for plotting (see `plot`). Plotting sample maps is carried out by the `sclero:::samplemap` function, which works as an internal function and therefore has not been exported. Users willing to modify **sclero** plots beyond the flexibility allowed by the `plot.rawDist` function are instructed to modify the `samplemap` function, which consists of standard R graphics syntax. It should be noted that the `samplemap` (and therefore also the `plot.rawDist`) function calls for the `layout` function every time the arguments `spot.type = "value"` or `spot.type = "idvalue"` are used. Consequently, the graphics window is divided into two regions that might cause issues when combining **sclero** plots with other graphics. The users are adviced to consider the graphics window resetting procedure specified in `layout` examples.

Because the function plots a sample map, the **aspect ratio** is forced to 1 and cannot be changed. If this causes troubles when trying to set the axis limits (`ylim` and `xlim`), try resizing the graphics window.

Author(s)

Mikko Vihtakari

See Also

`convert.ijdata` for converting the coordinate information to spatstat point patterns.

`read.ijdata` for reading zip files containing ImageJ ROIs.

`plot.spotDist` for plotting `spotDist` objects.

`plot.default` and other methods; `points`, `lines`, `par`.

Examples

```
data(shellspots)
shell_map <- convert.ijdata(shellspots)
plot(shell_map)
```

plot.spotDist *Plot spotDist object*

Description

Plots a map of spotDist object.

Usage

```
## S3 method for class 'spotDist'
plot(x, ..., sample.name = "keep", spot.type = "id",
  spot.size = 2, spot.color = NULL, main.type = "all",
  color.palette = colorRampPalette(c("blue", "cyan", "yellow", "red"), bias =
  1)(100), highlight.gbs = NULL, highlight.col = "red",
  crossing.points = FALSE)
```

Arguments

x	spotDist object
...	Arguments to be passed to other methods, such as graphical parameters.
sample.name	A character argument specifying the sample name to be plotted as an overall title for the plot (main). Defaults to "keep" meaning that the sample name will be extracted from the rawDist object. The plot title can be omitted by specifying sample.name = NULL.
spot.type	A character argument with three possible levels ("id", "value", and "idvalue") indicating how sample spots should be plotted. Defaults to "id", which plots sample spot numbers within open circles. The size of the circles can be controlled using the spot.size argument. The option "value" results to a sample map where the color of circles is related to a value through assign.value function. The color scale can be set using the color.palette argument, and size of the symbols (pch = 21) and through the spot.size argument. The option "idvalue" combines "id" and "value" leading to a sample map with sample spot numbers.
spot.size	An integer or a character argument with value "actual" indicating the size (cex) of points. If "actual", the actual size and shape of sample spots will be plotted. In this case, sample spot size information is required. Defaults to 2 meaning that sample spots are plotted as points with pch = 21 and cex = 2.
spot.color	A vector with equal length to number of spot sequences defining the color of sample spot labels. If NULL (default) a preset set of colors will be used.
main.type	A character argument with four possible levels ("all", "axis", "ends", and "none") indicating how the distance / main axis should be plotted. Defaults to "all" indicating that both the main axis and end points should be plotted. If "axis" only the main axis will be plotted. If "ends" only the end points will be plotted, and if "none" the main axis intormation will not be plotted.

`color.palette` color palette used for "value" and "idvalue" `spot.type` options. Passed to `colorRampPalette`.

`highlight.gbs` A character vector specifying the names of growth bands to be highlighted (i.e. colored with a different color than "darkgrey"). If `NULL` (default) all growth bands will be drawn using the standard color.

`highlight.col` A character argument specifying the color to be used in growth band highlighting (`highlight.gbs`).

`crossing.points`
Indicates whether the crossing points between sampling spot sequence traverses and growth lines should be plotted. Defaults to FALSE.

Details

The **sclero** package currently uses the **graphics** package distributed with R for plotting (see `plot`). Plotting sample maps is carried out by the `sclero:::samplemap` function, which works as an internal function and therefore has not been exported. Users willing to modify **sclero** plots beyond the flexibility allowed by the `plot.spotDist` function are instructed to modify the `samplemap` function, which consists of standard R graphics syntax. It should be noted that the `samplemap` (and therefore also the `plot.spotDist`) function calls for the `layout` function every time the arguments `spot.type = "value"` or `spot.type = "idvalue"` are used. Consequently, the graphics window is divided into two regions that might cause issues when combining **sclero** plots with other graphics. The users are adviced to consider the graphics window resetting procedure specified in `layout` examples.

Because the function plots a sample map, the **aspect ratio** is forced to 1 and cannot be changed. If this causes troubles when trying to set the axis limits (`ylim` and `xlim`), try resizing the graphics window.

Author(s)

Mikko Vihtakari

See Also

`spot.dist` for aligning sample spots.

`convert.ijdata` for converting the coordinate information to spatstat point patterns.

`read.ijdata` for reading zip files containing ImageJ ROIs.

`plot.rawDist` for plotting `rawDist` objects.

`plot.default` and other methods; `points`, `lines`, `par`.

Examples

```
data(shellspots)
shell_map <- convert.ijdata(shellspots)
x <- spot.dist(shell_map)
plot(x)
```

print.spotDist *Print* spotDist *objects*

Description

print function for spotDist objects

Usage

```
## S3 method for class 'spotDist'
print(x, ...)
```

Arguments

x	spotDist object to be printed.
...	further arguments passed to print.

Author(s)

Mikko Vihtakari

See Also

spot.dist

read.ijdata *Read ImageJ zip file containing several ROI files and extract coordinate information.*

Description

A wrapper function, which reads an ImageJ zip file containing a collection of ROI files and outputs a list of data frames ready for convert.ijdata function.

Usage

```
read.ijdata(X, spots = "point", gbs = "polyline", main = "line",
  names = "generate.invalid", spot.names = NULL, gbs.names = NULL,
  main.name = "main", sample.name = "file", scale = 1, unit = NULL)
```

Arguments

X	character string defining the name (including extension) or file path of an ImageJ zip file. Alternatively an ijzip object.
spots	optional. A character argument specifying the type of ROI objects that should be considered as sample spot sequences. Alternatively a numeric vector specifying the order of elements or a character vector specifying the names of ROI objects that should be assigned as sampling spot sequences. Defaults to "point" (See "Details" for further information).
gbs	optional. A character argument, numeric vector or character vector specifying the type of ROI objects that should be considered as growth bands. Defauls to "polyline". f left empty the remaining elements that are not defined in holes and main are assumed to be growth lines. For further information see spots and "Details". At the moment spots must be specified for this option to work.
main	optional. A character argument specifying the type of ROI object that should be considered as the measurement axis. Only one measurement axis per ImageJ .zip file is allowed. Defaults to "line". At the moment spots must be specified for this option to work.
names	optional. A character argument specifying how the names of spots and gbs should be generated. These names will be used in further functions (convert.ijdata, spot.dist). In general, it is adviced to use simple ROI names without special characters (for example - is not allowed in a ROI name; see 'Details'). Possible names options are: • "generate.invalid" (default). Uses the ROI object names, except when they are not valid data.frame column names. In the latter case sequential names will be generated. • "generate". Generates sequential names for all elements. • "keep". Uses the ROI object names, except when they are not valid data.frame column names. In the latter case make.names function will be used to generate data.frame combatible column names. • "force.keep". Uses the ROI object names as they are in the .zip file. Using this option might cause problems in consequent functions and is not recommended. • "manual". Names for both spots and gbs are searched from spot.names and gbs.names arguments, respectively. • "manual.spots". Names for spots are searched from spot.names argument. Names for gbs are generated following "generate.invalid". • "manual.gbs". Names for gbs are searched from gbs.names argument. Names for spots are generated following "generate.invalid".
spot.names	optional. A character vector of equal length to spots defining the names of sample spot sequences. Required if names = "manual" or "manual.spots". Ignored otherwise.
gbs.names	optional. A character vector of equal length to gbs defining the names of growth bands. Required if names = "manual" or "manual.gbs". Ignored otherwise.
main.name	optional. A character vector of lenght 1 defining the name of the measurement axis (main). If main.name = "keep", the ROI object name will be used (not

recommended, see "Details"). Otherwise the name will be taken from the argument. Defaults to `"main"`.

`sample.name` optional. A character vector of length 1 defining the name of the sample. File name without the extension or alternatively `ijzip` object name is used as a default (`sample.name = "file"`).

`scale` optional. A numeric value defining the scale of photograph in pixels / `unit`. Defaults to 1.

`unit` optional. A charater vector of length 1 defining the unit of measurements. See `scale`.

Details

In order to minimize the amount of text to be typed by a user, ROI objects of type "point" (this includes the "Multi-point Tool" points) are considered as sample spot sequences (`spots`) by default. Further, all "polyline" objects are assumed as growth bands (`gbs`) and "line" objects as the measurement axis (`main`) resulting to that only one "line" object is allowed per .zip file using the default settings. Alternatively, the user can specify the `spots`, `gbs`, and `main` objects manually using the order of the ImageJ .zip file with the exception that **only one measurement axis is allowed** per `rawDist` or `spotDist` object.

Punctuation characters other than `_` or `.` should not be used as names of `spots` or `gbs`, because they tend to confuse the internal `grep` functions in `spot.dist` function. Hence it is adviced to use one of the options renaming invalid names of `spots` and `gbs` (`"generate.invalid"`, `"generate"`, `"keep"`).

Value

Returns an "IJDATA" object, which is a list of data frames containing the x and y coordinates for sampling spot sequences (`spots.x` and `spots.y`), growth bands (`gbs.x` and `gbs.y`), and measurement axis (`main.x` and `main.y`) together with sample name, scaling factor and unit of measurement.

Author(s)

Mikko Vihtakari

See Also

`order.ijdata` for ordering and subsetting `read.ijdata` output.

`convert.ijdata` for converting the coordinate information to spatstat point patterns.

`spot.dist` for aligning sample spot sequences.

`read.ijroi` and `read.ijzip` for reading ImageJ ROI and .zip files.

Examples

```
# Locate the example zip file
path <- file.path(system.file("extdata", package = "sclero"), "shellspots.zip")

# You can replace 'path' by 'Your_file_name.zip'
dat <- read.ijdata(path)
```

```
summary(dat)

## Works also for IJZIP objects
dat2 <- read.ijzip(path)
dat2 <- read.ijdata(dat2)
dat[!(dat %in% dat2)] # Only the sample name differs
```

---

samplemap *Common plotting function for plot.rawDist and plot.spotDist functions*

Description

Used as an internal function to make the code more comprehensible. See plot.rawDist and plot.spotDist for plotting rawDist and spotDist objects, respectively.

Usage

```
samplemap(x, ..., sname, sptype, size, scol, mtype, colpalette, hlight, hlcol)
```

Arguments

x	rawDistor spotDist object.
...	Arguments to be passed to other methods, such as graphical parameters.
sname	equals to sample.name
sptype	equals to sample.type
size	equals to spot.size
scol	equals to spot.color
mtype	equals to main.type
colpalette	equals to color.palette
hlight	equals to highlight.gbs
hlcol	equals to highlight.col

Author(s)

Mikko Vihtakari

See Also

plot.rawDist, plot.spotDist

sclero — *Measure Growth Patterns and Align Sampling Spots in Photographs*

Description

Provides functions to measure growth patterns and align sampling spots in chronologically deposited materials. The package is intended for the fields of geology, sclerochronology, and dendrochronology.

Author(s)

Mikko Vihtakari <mikko.vihtakari@gmail.com>

References

M. Vihtakari, P. E. Renaud, L. J. Clarke, M. J. Whitehouse, H. Hop, M. L. Carroll, and W. G. Ambrose Jr. Decoding the oxygen isotope signal for seasonal growth patterns in Arctic bivalves. Palaeogeogr Palaeoclimatol Palaeoecol, 2016. http://dx.doi.org/10.1016/j.palaeo.2016.01.008.

M. Vihtakari. Bivalves as indicators of environmental perturbations related to climate and ocean acidification. Phd thesis, UiT The Arctic University of Norway, 2014. http://hdl.handle.net/10037/7152.

shellsizes — *Coordinates of sample spots together with spot size information and growth lines along a bivalve mollusk shell section*

Description

Coordinates of sample spots together with spot size information and growth lines along a bivalve mollusk shell section

Usage

```
data(shellsizes)
```

Format

`rawDist` object. A list containing spatstat point and line patterns as well as owin objects defining the sample spot, growth line, distance axis and sample spot size coordinates.

shellspots — *Coordinates of sample spots and growth lines along a bivalve mollusk shell section*

Description

Coordinates of sample spots and growth lines along a bivalve mollusk shell section

Usage

```
data(shellspots)
```

Format

`IJDATA` object. A list containing ImageJ ROI information about sample spots and growth lines along a bivalve mollusk shell section. The information is acquired by running "shellspots.zip" dataset through the `read.ijdata` function (see Examples). The list contains following data frames / vectors:

- spots.x. A data frame containing x-coordinates for sample spots with each sample spot sequence in its own column.
- spots.y. A data frame containing y-coordinates for sample spots.
- gbs.x. A data frame containing x-coordinates for growth lines with each growth line in its own column.
- gbs.y. A data frame containing y-coordinates for growth lines
- main.x. A data frame containing x-coordinates for the measurement axis
- main.y. A data frame containing y-coordinates for the measurement axis
- sample.name. A vector containing the sample name
- scaling.factor. A numeric value defining the scale of photograph in pixels / `unit`.
- unit. A charater vector defining the unit of measurements.

spot.dist — *Distance of sampling spots from margin along a measurement axis*

Description

Scale the location of sampling spots to visible growth bands, project the sampling spots along a measurement axis (`main`) and calculate the distance from margin. Useful for locating high-resolution LA-ICP-MS or SIMS sample spots in samples with non-linear growth bands.

Usage

```
spot.dist(rawDist, sample.name = NULL, run.ae = TRUE,
  use.centroids = TRUE)
```

Arguments

rawDist	a rawDist object for which the alignment should be done.
sample.name	An optional parameter over-riding the sample name. If NULL (default), the sample name will be passed from the previous steps (read.ijdata, convert.ijdata)
run.ae	a logical indicating whether to run averaging error estimation, if rawDist contains spot size information. Defaults to TRUE.
use.centroids	a logical indicating whether to use centroids of spot.owins instead of spots, if rawDist contains spot size information. Defaults to TRUE.

Details

The alignment information with sample spot numbers is stored as a sublist called output and can be extracted to a data.frame. Otherwise the object behaves like any list in R. Relevant data can be subsetted as needed. Detailed data containing information of the alignment process is stored in a sublist called det.dat.

The function can either project growth lines on the distance (main) axis or use the crossing points between growth lines and the main axis. These two types of the main axis can be used for different applications. The main axis type is automatically selected by the following criteria:

along Approperiate for samples with cut-off growth lines such as bivalve margin cross-sections and tree, sediment or ice-cores. This option is selected by placing the measurement axis such that **it does not cross any of the marked growth lines**. The location of each growth line is projected along the measurement axis from the beginning of the growth line (the point where you started marking the growth line in ImageJ).

cross Approperiate for approximately round cross-sections: samples where the growth lines continue through the entire width of the sample (such as tree, coral or calcareous algae cross-sections and umbo-regions of bivalves). This type is selected by making the **main axis to cross each individual marked growth line**. The location of each growth line along the main axis is considered as a crossing point.

These criteria are set due to the need of defining a location for each marked growth line along the distance (main) axis. The choice is rigid, to simplify calculations, and to avoid bias in results by allowing two different methods for growth line locations. The easiest way to test which type suits a particular sample best is to save two sets of ImageJ zip files by moving the measurement axis.

Value

Returns a list of class spotDist containing information of the aligned sample spots and the digitized representation of the shell cross-section, which was already included in the rawDist object.

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See Also

`read.ijdata` for reading zip files containing ImageJ ROIs.

`order.ijdata` for ordering and subsetting `read.ijdata` output.

`convert.ijdata` for converting the coordinate information to spatstat point patterns.

`plot.spotDist` for plotting.

`print.spotDist` for printing.

Examples

```
data(shellspots)
shell_map <- convert.ijdata(shellspots)
x <- spot.dist(shell_map)
plot(x)
```

Index

∗Topic **datasets**
barium, 4
shellsizes, 17
shellspots, 18

assign.size, 2, *4*
assign.value, *3*, 3, *9*, *11*

barium, 4

cex, *9*, *11*
coln, 5
colnames, *5*
color.palette, *16*
colorRampPalette, *10*, *12*
convert.ijdata, 5, *7, 8*, *10*, *12–15*, *19, 20*
create.rawDist, 6

data was read from, *2*
data.frame, *3*, *5*, *14*
dir, *2*

estimating averaging error, *2*
expression, *3*

graphical parameters, *9*, *11*, *16*
grep, *15*

highlight.col, *16*
highlight.gbs, *16*
hyperframe, *2*

IJDATA, *5*, *8*
ijzip, *14*

layout, *10*, *12*
lines, *10*, *12*

main, *9*, *11*
main.type, *16*
make.names, *14*

marks, *6*

order.ijdata, 8, *15*, *20*

par, *10*, *12*
plot, *10*, *12*
plot.default, *10*, *12*
plot.ijroi, *2*
plot.rawDist, *4*, *6, 7*, 9, *10*, *12*, *16*
plot.spotDist, *3*, *10*, 11, *12*, *16*, *20*
plotting, *5, 6*
points, *10*, *12*
ppp, *2*, *6*
print, *13*
print.spotDist, 13, *20*
psp, *6*

rawDist, *2, 3*, *9*, *11, 12*, *15, 16*, *19*
rawDist contains spot size information, *19*
read.ijdata, *2–4*, *6–8*, *10*, *12*, 13, *18–20*
read.ijroi, *15*
read.ijzip, *15*

sample maps, *3*
sample spot alignment, *5, 6*
sample spot size information, *9*, *11*
sample.name, *16*
sample.type, *16*
samplemap, *10*, *12*, 16
sclero, 17
sclero-package *(*sclero*)*, 17
shellsizes, 17
shellspots, *4*, 18
spatial density plotting, *3*
spatstat, *5–8*, *10*, *12*, *15*, *17*, *20*
spot.color, *16*
spot.dist, *3, 4*, *6, 7*, *12–15*, 18
spot.size, *16*
spotDist, *10, 11*, *13*, *15, 16*

spots, *3*

working directory, *2*