Package ‘tgram’

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Type Package

Title Compute and Plot Tracheidograms

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Description
Functions to compute and plot tracheidograms, as in De Soto et al. (2011) <doi:10.1139/x11-045>.

Depends zoo

License GPL (>= 2)

LazyLoad yes

NeedsCompilation no

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Contents

juniperus 2
standz.all 2
tgram 4
traq.profile 6

Index **7**

`juniperus` *Traqueid Measurements in Juniperus thurifera*

Description

An example of traqueid measurements to standarize with function `tgram`.

Usage

```
data(juniperus)
```

Format

A data frame with 77 observations on the following 4 variables.

`traqueidogram`	Numeric vector indicating the traqueidogram to which each measurement belongs
`lumen.wall`	A factor indicating if the measurement is lumen (`l`)or wall (`w`)
`order`	Position of the measurement in the ordered sequence within each traqueidogram
`width.um`	Width (micrometres) of each measurement

Examples

```
data(juniperus)
cosa <- with(juniperus,
                 standz.all(traq=width.um, series=traqueidogram,
                                 wl=lumen.wall, w.char="w", G=20)
                 )

plot(cosa, type="l")
```

`standz.all` *Vaganov Normalized Tracheidogram*

Description

The function produces a normalized tracheidogram, i.e. a curve showing variations in cell parameters as a function of the cell position within an annual ring, following the procedure of Vaganov (1990).

Usage

```
standz.all(traq, series, wl = NULL, w.char = NULL, order = NULL, G = 30)
standz(tgl1, G=30)

## S3 method for class 'standz.all'
plot(x, which=NULL,...)
```

Arguments

`traq`	A vector with the ordered sequences of measurements for each tracheidogram.
`series`	A vector of indicator values (i.e. a factor) with each level indicating each unique tracheidogram.
`wl`	A vector indicating if the measurement is wall or lumen.
`w.char`	Character used in `wl` to indicate "wall".
`order`	Vector indicating the ordering of each measurement in each lumen or wall series within a tracheidogram.
`G`	Number of cells to get the original measurements normalized to.
`tgl1`	Vector with the ordered sequences of measurements of a single tracheidogram.
`x`	An object of class `standz.all` resulting from applying the standz.all function.
`which`	One of NULL, "w", or any other character. This produces the plot function to draw all the tracheidograms together, only the "wall" traqueidograms or only the "lumen" ones, respectively.
`...`	Additional graphical parameters passed to `link{plot}`.

Value

`standz` returns a vector of length *G* with the normalized values. `standz.all` returns an object of class `standz.all`. Basically a list with the following elements:

`data.stdz`	A matrix with *G* columns and as many rows as unique wall and lumen tracheidograms were in the original data, each with the normalized values of each tracheidogram.
`which.w`	Vector indicating which rows in `data.stdz` are "wall" tracheidograms.
`which.l`	Vector indicating which rows in `data.stdz` are "lumen" tracheidograms.

Author(s)

Marcelino de la Cruz Rot and Lucia DeSoto

References

Vaganov, E.A. 1990. The tracheidogram method in tree-ring analysis and its application. In: Cook E.R., Kairiukstis L.A., eds. *Methods of dendrochronology: applications in the environmental sciences* . Kluwer Academic Publishers. Dordrecht, the Netherlands. pp. 63-76.

Examples

```
data(juniperus)

cosa <- with(juniperus,
                  standz.all(traq=width.um, series=traqueidogram,
                             wl=lumen.wall, w.char=”w”, G=20)
                 )
```

```
plot(cosa, type="l")
plot(cosa, type="l", which="w")
plot(cosa, type="l", which="l", add=TRUE)

standz(with(juniperus,width.um[traqueidogram==1 & lumen.wall =="l"]), G=20)

lines(1:20,
      standz(with(juniperus,width.um[traqueidogram==1 & lumen.wall =="l"]), G=20),
      lwd=3)
```

`tgram` *Compute Tracheidograms*

Description

Function to compute tracheidograms from microscopic measurements.

Usage

```
tgram(traq, val50 = 50, xlim = NULL, ylim = NULL, mw = 1, plotit = TRUE)

## S3 method for class 'tgram'
plot(x, xlim = NULL, ylim = NULL, colores = c("red", "green"),
      leyenda = c("lumen", "double wall"), lwd = 2,
      add = FALSE,traq.0 = TRUE, bg.legend = NULL, ...)
```

Arguments

`traq`	microscopic light profile. A vector with the light measurements or a `data.frame` or `matrix` with two columns. In this case, the first column contains pixel order (i.e. position along the x axis) and the second one contains the light (i.e. "y") lectures.
`val50`	"y-value" at wich measurements should be made.
`mw`	integer. Width of the rolling window to smooth the original data.
`plotit`	logical. should the original data and the computed tracheidogram be drawn?
`xlim`	extent of the x-axis. A vector of length 2.
`ylim`	extent of the y-axis. A vector of length 2.
`x`	an object of class tgram, resulting from `tgram` function.
`colores`	a vector of length 2, with the colors to draw the lumen and wall measurements, respectively.
`leyenda`	a vector of length 2 with the legend to appear in the plot. By default leyenda =c("lumen","double wall").
`lwd`	width of the lines in the legend.
`add`	logical. If TRUE, add to a current plot.

`traq.0`	logical. If TRUE, draw the original measurements.
`bg.legend`	background color for the legend.
`...`	additional graphical parameters.

Details

The purpouse of this fucntion is obtaining cell anatomical data from microscopic light measurements (see DeSoto et al. for details of data adquisition). The microscopic lectures are first smoothed with a rolling window (using function `rollmean` of package `zoo`, using the selected width `mw`. Then, the smoothed curve is "cut" at the treshold value `val50` and the distances among the intersection points are computed. This provides an ordered sequence of lumen diameters (LD) and double wall thikness (DWT) measurements. From this sequence some other anatomical measurements are computed. Radial cell wall thickness is computed as $CWT[t] = 1/2 * (DWT[t]/2 + DWT[t+1]/2)$. Tracheid diameter is computed as $TD[t] = DWT[t]/2 + LD[t] + DWT[t+1]/2$.

Value

tgram returns an object of class *tgram*, bassically a list with

`traq`	original data.
`traq0`	if `traq` was a 2 column matrix, then `traq0` returns the same object. If `traq` was a vector, `traq0` returns a two column matrix (first column with pixel position and second with ligh lectures).
`cut.points`	two column matrix with the coordinates of the intersection of $y = val50$ and the smoothed curve.
`what`	vector indicating if the computed distances are of lumen (1) or double wall (2) .
`distances`	ordered sequence of the computed distances (both of lumen and double wall).
`LD`	ordered sequence of lumen diameters.
`DWT`	ordered sequence of double wall thickness.
`mw`	width of the rolling window employed to smooth the data.
`CWT`	ordered sequence of radial cell wall thikness'.
`TD`	ordered sequence of tracheid diameters.
`LD_CWT_ratio`	ordered sequence of LD/CWT ratio.

Author(s)

Marcelino de la Cruz Rot and Lucia DeSoto

References

DeSoto, L., De la Cruz, M. & Fonti, P. 2011. Intra-annual pattern of tracheid size in the Mediterranean Juniperus thurifera as indicator for seasonal water stress. *Canadian Journal of Forest Research* 41: 1280-1294.

Examples

```
data(traq.profile)

plot(tgram(traq.profile, mw=10),leyenda=c("lumen","double wall"),
        xlab="distance pixel", ylab="grey value",ylim=c(0,250),
        bg.legend="white")
```

`traq.profile` *Light Throughout a Microscopic Section of Juniperus Wood*

Description

A measurement of light intensity troughout a sequence of pixels in a microscopic section of *Juniperus thurifera* wood.

Usage

```
data(traq.profile)
```

Format

A data frame with 883 observations on the following 2 variables.

`X1` Pixel position in the sequence

`Y1` Light intensity

Examples

```
data(traq.profile)
tgram(traq.profile, mw=10)
```

Index

∗ **datasets**
    juniperus, 2
    traq.profile, 6
∗ **manip**
    standz.all, 2
    tgram, 4
∗ **smooth**
    standz.all, 2
    tgram, 4

juniperus, 2

plot.standz.all *(*standz.all*)*, 2
plot.tgram *(*tgram*)*, 4

rollmean, *5*

standz *(*standz.all*)*, 2
standz.all, 2

tgram, 4
traq.profile, 6