

Package ‘tgram’

November 25, 2017

Type Package

Title Compute and Plot Tracheidograms

Version 0.2-3

Date 2017-11-24

Author Marcelino de la Cruz and Lucia DeSoto

Maintainer Marcelino de la Cruz <marcelino.delacruz@urjc.es>

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

Repository CRAN

Date/Publication 2017-11-24 23:31:50 UTC

R topics documented:

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.
tg11	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" tracheidograms 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 purpose of this function is obtaining cell anatomical data from microscopic light measurements (see DeSoto et al. for details of data acquisition). 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 threshold value `val50` and the distances among the intersection points are computed. This provides an ordered sequence of lumen diameters (LD) and double wall thickness (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`, basically 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 light 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 thickness'.
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 throughout 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

*Topic **datasets**

juniperus, 2

traq.profile, 6

*Topic **manip**

standz.all, 2

tgram, 4

*Topic **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