Package ‘tgram’

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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

```r
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

```r
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 traqueidogram.
- **series**: A vector of indicator values (i.e. a factor) with each level indicating each unique traqueidogram.
- **wl**: A vector indicating if the measurement is wall or lumen.
`standz.all` 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)

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### References


### Examples

```r
## Not run:
data(juniperus)

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

plot(cosa, type="1")
plot(cosa, type="1", which="w")
plot(cosa, type="1", which="l", add=T)

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

*Compute tracheidograms*

**Description**

Function to compute tracheidograms from microscopic measurements.

**Usage**

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

## S3 method for class 'tgram'

```r
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 which 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.
- `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 `valU0` 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 \( CWT[t] = 1/2 \times (DWT[t]/2 + DWT[t+1]/2) \). 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 \( y = valU0 \) 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 <marcelino.delacruz@upm.es> and Lucia DeSoto

References


Examples

```r
## Not run:
data(tgram.profile)
plot(tgram(tgram.profile, mw=10), leyenda=c("lumen","double wall"),
     xlab="distance pixel", ylab="grey value", ylim=c(0,255),
     bg.legend="white")
```
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)
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