Package 'dyntaper'

October 13, 2022

Title Dynamic Stem Profile Models, AKA Tree Taper Equations

Version 1.1

Description Performs calculations with tree taper (or stem
profile) equations, including model fitting. The package
implements the methods from García, O. (2015) ``Dynamic
modelling of tree form''
<http://mcfns.net/index.php/Journal/article/view/MCFNS7.1_2>.
The models are parsimonious, describe well the tree bole shape
over its full length, and are consistent with wood formation
mechanisms through time.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Depends R (>= 2.10)

VignetteBuilder knitr

Suggests knitr, lattice

URL https://github.com/ogarciav/dyntaper

BugReports https://github.com/ogarciav/dyntaper/issues

NeedsCompilation no

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Repository CRAN

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R topics documented:

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brink   *Small taper dataset from Brink and von Gadow (1986).*

Description

Taper measurements on 10 *Eucalyptus cloeziana* trees.

Usage

    brink

Format

A data frame with 108 rows and 5 variables:

Tree tree identification number (factor)

h height level, meters

dib diameter inside bark, centimeters

Dob dbh outside bark, cm (breast height is 1.35 m)

H total height, meters

Source

Brink, C. and von Gadow, K. (1986) "On the use of growth and decay functions for modelling stem profiles". *EDV in Medizin und Biologi 17*, 20-27

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decay   *Decay function delta*

Description

Calculates $(1 - p * x)_+^{1/p}$, or its limit $exp(-x)$ when p tends to 0.

Usage

    decay(x, p)

Arguments

x	Input value(s), possibly a vector.
p	Parameter.

Details

Perhaps overkill, but uses `log1p()` function for better accuracy than the more obvious formula.

Value

Decay function value(s).

Examples

```
decay(2, 0) == exp(-2)
decay(1.5, 0.5)
decay(2.5, 0.5)
decay(2.5, -0.5)
for(p in seq(1, -1, -0.5)) curve(decay(x, p), 0, 3, add=(p != 1))
```

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hlevel	*Height level for given diameter or area.*

Description

Find the height level at which the tree reaches a given diameter (if `area == FALSE`, default) or a given cross-sectional area (if `area == TRUE`). That is, the inverse of `taper()`, except that a vector argument is not allowed.

Usage

```
hlevel(ds, H, D, b, bh, area = FALSE)
```

Arguments

ds	The given diameter or area.
H	Tree total height.
D	Tree diameter at breast height.
b	Vector with the 5 parameters.
bh	Breast height. Typically 1.2, 1.3 or 1.4 m, or 4.5 ft.
area	If TRUE, 'ds' is a cross-sectional area, otherwise a diameter. Default is FALSE.

Value

Height level corresponding to 'ds' if any, otherwise `NA`.

Examples

```
b <- c(2.569, 0, 1.042, 0.3012, -1)  # parameters
Dib <- 0.956 * 24  # convert dbh outside bark to inside bark
hlevel(15, 32, Dib, b, 1.3)  # height where the diameter is 15
hlevel(24, 32, Dib, b, 1.3)  # breast height
hlevel(35, 32, Dib, b, 1.3)  # height where the diameter is 35
```

Id   *Integral of decay function.*

Description

Integral of decay function.

Usage

```
Id(x, p)
```

Arguments

x   Input value(s), possibly a vector.

p   Parameter.

Value

Integral of the decay function between 0 and x.

Examples

```
Id(2, 0)
Id(1.5,0.5)
Id(2.5, 0.5)
Id(2.5, -0.5)
for(p in seq(1, -1, -0.5)) curve(Id(x, p), 0, 3, add=(p != 1))
```

Idd *Double integral of decay function.*

Description

Double integral of decay function.

Usage

```
Idd(x, p)
```

Arguments

x   Input value(s), possibly a vector.

p   Parameter.

Value

Iterated integral of the decay function between 0 and x, that is, the integral of Id(x, p).

Examples

```
Idd(2, 0)
Idd(1.5,0.5)
Idd(2.5, -1)
Idd(2.5, -0.5)
for(p in seq(1, -1, -0.5)) curve(Idd(x, p), 0, 3, add=(p != 1))
```

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taper *Tree taper (or profile) equation.*

Description

Returns the diameter or cross-sectional area at one or more hight levels.

Usage

```
taper(h, H, D, b, bh, area = FALSE)
```

Arguments

h	Height level(s), possibly a vector.
H	Tree total height.
D	Tree diameter at breast height (dbh).
b	Vector with the 5 parameters.
bh	Breast height. Typically 1.2, 1.3 or 1.4 m, or 4.5 ft.
area	If TRUE, returns cross-sectional areas, otherwise returns diameters. Default is FALSE.

Value

Diameter(s) at level(s) 'h' if 'area' is FALSE, otherwise cross-sectional area(s).

Note

Diameters or areas are either all outside bark, or all inside bark. A dbh outside bark can be used with an inside-bark taper equation through a substitution D -> k * D, where k is an outside to inside bark conversion factor.

Examples

```
curve(taper(x, 32, 0.956*24, c(2.569, 0, 1.042, 0.3012, -1), 1.3), 0, 32)
```

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tbase	*Unscaled base taper curve of cross-sectional area vs height level.*

Description

Unscaled base taper curve of cross-sectional area vs height level.

Usage

```
tbase(h, H, b)
```

Arguments

h	Height level(s), possibly a vector.
H	Tree total height.
b	Vector with the 5 parameters.

Value

Value(s) proportional to the area(s) at the level(s) h.

Examples

```
tbase(16, 32, c(2.569, 0, 1.042, 0.3012, -1))
```

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volume   *Volume between two height levels.*

Description

Volume between two height levels.

Usage

```
volume(h1, h2, H, D, b, bh, rhd)
```

Arguments

h1, h2	The two height levels.
H	Tree total height.
D	Tree diameter at breast height.
b	Vector with the 5 parameters.
bh	Breast height. Typically 1.2, 1.3 or 1.4 m, or 4.5 ft.
rhd	Ratio between the height and diameter units. E.g., 100 for m and cm, or 12 for feet and inches.

Value

Volume between h1 and h2.

Examples

```
b <- c(2.569, 0, 1.042, 0.3012, -1)  # parameters
Dib <- 0.956 * 24  # convert dbh outside bark to inside bark
volume(0, 32, 32, Dib, b, 1.3, 100)  # total volume
h15 <- hlevel(15, 32, Dib, b, 1.3)  # height for diameter 15
volume(0.3, h15, 32, Dib, b, 1.3, 100)  # volume between stump and h15
```

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