

# Package ‘dyntaper’

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**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](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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decay	<i>Decay function delta</i>
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**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  $\log_1 p()$  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	<i>Height level for given diameter or area.</i>
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**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
```

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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))
```

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Idd                                      *Double integral of decay function.*

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**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.*

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**Description**

Returns the diameter or cross-sectional area at one or more high 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  $D \rightarrow k * D$ , 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.*


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**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))
```

---

volume	<i>Volume between two height levels.</i>
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**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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