



# Theoretical concept for initialization of forest stands

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## 1. Initialization using averaged stand data

### 1.1. Data requirement

The initialization requires per stand

- *species type*
- *averaged diameter at breast height  $D_g$*
- *averaged height  $H_g$*
- *age and*
- *basal area  $G$  of the stand.*

Species specific parameters of various functions are necessary:

- $p_0 - p_4$  for Weibull distribution function, equation (1.2)
- $c_1, c_2$  for bole height function, equation (1.9)
- $a_0 - a_2$  for height function, equation (1.4)
- $b_0 - b_2$  for height function, equation (1.4)
- $kc_0 - kc_2$  for height function, equation (1.4)
- $wk_1, wk_2$  for height function, equation (1.6)

### 1.2. Method

#### 1.2.1. Generating of single tree data

A capping limit parameter  $L = 7$  is defined. If  $(D_g - L) < 3$  then  $L = D_g - 4$ . A maximum diameter  $d_{max}$  is estimated from  $D_g$  by a function of (Gerold, 1990):

$$D_{max} = 8.2 + 1.8D_g - 0.1D_g^2 \quad (1.1)$$

Two parameters  $b$  and  $c$  of a Weibull distribution are calculated:

$$\begin{aligned} b &= p_0 + p_1 \cdot D_g \\ c &= p_2 + p_3 \cdot D_g + p_4 \cdot D_{max} \end{aligned} \quad (1.2)$$

The generation of a single tree with the diameter  $d_{bh}$  is realized by a number  $x$  equally distributed between 0 and 1 and the following function (Weibull distribution):

$$d_{bh} = b \cdot \left( \left( \frac{L}{b} \right)^c - \log(1-x) \right)^{\frac{1}{c}} \quad (1.3)$$

The height of the tree with diameter  $d_{bh}$  is estimated by different height functions.

For pine and birch the height function the height function from Kuleschis (see (Gerold, 1990)) is used with the parameters  $ka, kb, kc$ :



$$\begin{aligned}
 ka &= 1 - (a_0 + a_1 D_g + a_2 D_g^2) \\
 kb &= 1 - (b_0 + b_1 D_g + b_2 D_g^2) \\
 kc &= 1 - (kc_0 + kc_1 D_g + kc_2 D_g^2)
 \end{aligned} \tag{1.4}$$

and the function:

$$H = H_g \cdot \left( ka + \left( \frac{kb}{\left( d_{bh} + \frac{D_g}{2} \right)} \right) D_g + \left( \frac{kc}{\left( d_{bh} + \frac{D_g}{2} \right)} \right)^2 D_g^2 \right) \tag{1.5}$$

For other species (beech, spruce, oak) the height function of (Weimann, 1980) is applied with the parameter wf:

$$wf = wk_1 + wk_2 \cdot H_g \tag{1.6}$$

For the case  $d_{bh}$  is greater or equal  $D_g - H_g/2$  the following function is used:

$$H = H_g + wf \cdot (\log(H_g - D_g + d_{bh}) - \log(H_g)) \tag{1.7}$$

Otherwise:

$$= \left( H_g + wf \cdot \left( \log\left(\frac{H_g}{2}\right) - \log(H_g) \right) - 1.3 \right) \left( \frac{d_{bh}}{\left( D_g - \frac{H_g}{2} \right)} \right)^{0.5} + 1.3 \tag{1.8}$$

For Douglas fir (Nagel, 2002) and Eucalyptus (Medhurst et al., 1999; Ranatunga et al., 2008) specific height functions are implemented .

The bole height  $H_b$  of the tree is estimated according to a function of (Nagel, 1995):

$$H_b = H \cdot \left( 1 - e^{\left( -1 \left( c_1 + c_2 \frac{H}{d_{bh}} \right)^2 \right)} \right) \tag{1.9}$$

Trees are generated by this method until the basal area G is reached. For Eucalyptus the bole height is estimated by a function of (Nutto et al., 2006):



$$H_b = -5.12 - 0.407 \cdot d_{bh} + 1.193 \cdot H \quad (1.10)$$

### 1.2.2. Building cohorts

The generated trees are classified into tree cohorts. The maximum number of classes is 60. The class width is calculated from the maximum and minimum DBH.

The further initial data of the cohorts are estimated as follows.

#### a) Parameter rsap

A parameter rsap is estimated, rsap describes the fraction of wood which is sapwood.

#### b) The height of sapwood pipes $H_s$ and stem wood

$H_s$  is calculated as

$$H_s = \frac{2H_{bc}}{3} + \frac{H}{3} \quad (1.11)$$

#### c) The stem volume VD

VD is calculated with different function per species.

For Douglas fir (Nagel, 2002) the following functions are used:

$$HFD = \frac{-200.31914}{H \cdot d_{bh}^2} + \frac{0.8734}{d_{bh}} - 0.0052 \cdot \log(d_{bh}^2) + \frac{7.3594}{H \cdot d_{bh}} + 0.46155 \quad (1.12)$$

and for other species (SILVA, (Pretzsch et al., 2002)):

$$\begin{aligned} k1 &= s1 + s2 \cdot \log(DBH) + s3 \cdot \log(DBH)^2 \\ k2 &= s4 + s5 \cdot \log(DBH) + s6 \cdot \log(DBH)^2 \\ k3 &= s7 + s8 \cdot \log(DBH) + s9 \cdot \log(DBH)^2 \end{aligned} \quad (1.13)$$

with s1-s9 species-specific parameters

$$HFD = e^{k1 + k2 \cdot \log(H) + k3 \cdot \log(H)^2} \quad (1.14)$$

The resulting stem volume is:

$$VD = \frac{HFD \cdot \pi \cdot d_{bh}^2}{4000} \quad (1.15)$$

For pine stem volume is calculated as follows:



$$VD = e^{(p_1 + p_2 \log(d_{bh}) + p_3 \log(H))} \quad (1.16)$$

For Eucalyptus a function of (Binkley et al., 2002) is used:

$$VD = 0.00005447 \cdot d_{bh}^{1.921157} \cdot \left(\frac{H}{100}\right)^{0.950581} \quad (1.17)$$

or a function of (Stape et al., 2010) depending on the site is used:

$$VD = \frac{p_1 d_{bh}^{p_2} \cdot \left(\frac{H}{100}\right)^{p_3}}{500} \quad (1.18)$$

$p_1, p_2, p_3$  – site depending parameters

d) *Sapwood area  $A_s$*

If  $H_b$  less than 137 the diameter at base of the crown  $d_{cb}$  is calculated:

$$d_{cb} = \frac{d_{bh}}{H} (137 - H_b) + d_{bh} \quad (1.19)$$

and the sapwood area  $A_s$

$$A_s = \frac{\pi}{4} \cdot d_{cb}^2 \cdot rsap \quad (1.20)$$

If  $H_b$  is greater than 137 cm

$$A_s = \frac{\pi}{4} d_{bh}^2 \cdot rsap \quad (1.21)$$

$$rsap = \frac{A_s}{\frac{\pi}{4} \cdot d_{bh}^2}$$

e) *Sapwood biomass  $M_s$*

$$M_s = \rho_s \cdot A_s \cdot H_s \quad (1.22)$$

$\rho_s$  - sapwood density

f) *cross sectional area of heart wood at crown base  $A_{hc}$  and cross sectional area of heart wood at stem base  $A_{hb}$*

If  $H_b$  is less than 137 cm then



$$A_{hc} = \frac{\pi}{4} d_{cb}^2 - A_s \quad (1.23)$$

$$A_{hb} = \frac{\pi}{4} \left( \frac{d_{cb} \cdot a}{\tau_{max}} \right)^2 - A_s \quad (1.24)$$

$\tau_{max}$  – parameter

$a$  - age

If  $H_b$  is greater than 137 cm then

$$A_{hc} = \frac{\pi}{4} d_{bh}^2 (1 - rsap) \cdot 0.04 \quad (1.25)$$

as initial value for the calculation of  $A_{hc}$  with a Newton algorithm. This algorithm uses a function  $F$  (in SR fdfahc):

$$F = M_{bio} - \rho_s \cdot VD \quad (1.26)$$

$VD$ – estimation of stem mass by yield table functions

$M_{bio}$  –total stem biomass

Stem biomass is considered as truncated cone with base area  $A_{bs}$  and the diameter  $d_{cb}$  and the height  $H_b$  and a cone with height  $H-H_b$  and ground base  $A_s + A_{hc}$  ( $A_{bs}$ ). The ground base of heartwood  $A_{hb}$  is:

$$A_{hb} = A_{bs} - A_s \quad (1.27)$$

The heartwood area at crown base  $A_{hc}$  (x) has to calculate.

The biomass of stem is calculated as sum of sapwood and heartwood biomass, which is calculated from the truncated cone with the ground base area  $A_{hb}$ , the upper area  $A_{hc}$  and the height  $H_b$  and the cone with the height  $H-H_b$  and the base area  $A_{hc}$ .

Sapwood biomass is calculated:

$$M_s = A_s \frac{1}{3} (2H_b + H) \quad (1.28)$$

Heartwood biomass:

$$M_{hw} = \frac{1}{3} x (H - H_b) + \frac{1}{3} H_b \left( x + \left( \frac{\pi}{4} d_{bs}^2 - A_s + \sqrt{x \left( \frac{\pi}{4} d_{bs}^2 - A_s \right)} \right) \right) \quad (1.29)$$

The total stem biomass is:



$$\begin{aligned}
 M_{bio} &= M_s + M_{hw} \\
 &= A_s \frac{1}{3} (2H_b + H) + \frac{1}{3} x (H - H_b) + \frac{1}{3} H_b \left( x + \left( \frac{\pi}{4} d_{bs}^2 - A_s + \sqrt{x \left( \frac{\pi}{4} d_{bs}^2 - A_s \right)} \right) \right) \\
 &= \frac{1}{3} \left( H(A_s + x) + H_b \left( 2A_s - x + x - A_s + \frac{\pi}{4} d_{bs}^2 + \sqrt{x \left( \frac{\pi}{4} d_{bs}^2 - A_s \right)} \right) \right) \\
 &= \frac{1}{3} \left( H(A_s + x) + H_b \left( A_s + \frac{\pi}{4} d_{bs}^2 + \sqrt{x \left( \frac{\pi}{4} d_{bs}^2 - A_s \right)} \right) \right)
 \end{aligned} \tag{1.30}$$

The diameter  $d_{bs}$  of the area  $A_{bs}$  is calculated as follows.

The diameter of the upper base area of the truncated cone with height  $H_b$  of the total biomass is  $d_{cb}$ :

$$d_{cb} = \sqrt{\frac{4}{\pi} (A_s + x)} \tag{1.31}$$

According to the Strahlensatz the relations between  $d_{bs}$  und  $d_{bh}$  are:

$$\frac{D_{bh} - d_{cb}}{d_{bs} - d_{cb}} = \frac{H_b - H_d}{H_b} \tag{1.32}$$

$H_d$  - Höhe des DBH (137 cm)

$$\begin{aligned}
 \frac{d_{bh} - d_{cb}}{d_{bs} - d_{cb}} &= \left( 1 - \frac{H_d}{H_b} \right) \\
 d_{bs} - d_{cb} &= \frac{d_{bh} - d_{cb}}{\left( 1 - \frac{H_d}{H_b} \right)} \\
 d_{bs} &= \frac{d_{bh} - d_{cb}}{\left( 1 - \frac{H_d}{H_b} \right)} + d_{cb} \\
 &= \frac{d_{bh} - d_{cb} + d_{cb} \left( 1 - \frac{H_d}{H_b} \right)}{\left( 1 - \frac{H_d}{H_b} \right)} = \frac{d_{bh} - d_{cb} \frac{H_d}{H_b}}{\left( 1 - \frac{H_d}{H_b} \right)}
 \end{aligned} \tag{1.33}$$

Together with equation (1.32) it yields:



$$d_{bs} = \frac{d_{bh} - \sqrt{\frac{4}{\pi} (A_s + x) \frac{H_d}{H_b}}}{\left(1 - \frac{H_d}{H_b}\right)} \quad (1.34)$$

and

$$\frac{dd_{bs}}{dx} = \frac{-H_d}{H_b \pi \left(1 - \frac{H_d}{H_b}\right) \sqrt{\frac{1}{\pi} (A_s + x)}} \quad (1.35)$$

A solution for x is found by assuming F(x)=0 with the Newton algorithm.

g) *Stem biomass*

Calculated as heartwood cone above  $H_b$  and a truncated cone below  $H_b$  (first term) plus a coat of sapwood (second term):

$$\begin{aligned} M_{bio} &= \rho_s \frac{1}{3} \left( A_{hc} H + H_b \left( A_{hb} + \sqrt{A_{hb} A_{hc}} \right) \right) + \rho_s A_{sap} \left( \frac{2}{3} H + \frac{1}{3} H_b \right) \\ &= \rho_s \left( \frac{1}{3} H (A_s + A_{hc}) + \frac{1}{3} H_b (2A_s + A_{hb} + \sqrt{A_{hb} A_{hc}}) \right) \\ &= \rho_s \frac{1}{3} \left( H (A_s + A_{hc}) + H_b (2A_s + A_{hc} + \sqrt{A_{hb} A_{hc}}) \right) \end{aligned} \quad (1.36)$$

h) *Heart wood biomass  $M_{hw}$*

$$M_{hw} = M_{bio} - M_s \quad (1.37)$$

i) *Foliage biomass  $M_f$  and foliage area  $A_{fol}$*

$$M_f = \eta_s \cdot A_s \quad (1.38)$$

$$A_{fol} = M_f \cdot s_{min} + 0.5 \cdot s_{a,c} \quad (1.39)$$

$\eta_s$ — species-specific foliage to sapwood area relationship

$s_{min}$ — minimum specific one-side leaf area

$s_{a,c}$ — light depended specific one-side leaf area

j) *Fine root biomass  $M_r$*





$$M_r = M_f \quad (1.40)$$

as rough estimate.

## 2. Initialization using single tree data

### 2.1. Data requirements

The initialization requires per tree the following data:

- *Patch size*
- *species type*
- $d_{bh}$  (mm)
- $H$  (m)
- $H_b$  (mandatory)
- *age*

### 2.2. Method

The given data are classified into diameter classes to build cohorts. The class width is 1cm, but could be changed. If  $H_b$  is not available, the functions (1.9) and (1.10) are used to calculate  $H_b$ . For each diameter class an averaged  $d_{bh}$ ,  $H$  and  $H_b$  and the number of trees are calculated as values of the cohort. Further on, all cohort variables, described in chapter 1.2.2, are calculated.

## 3. Initialization of saplings

### 3.1. Data requirements

If the height of planted trees are less than a specific limit (e.g. 200 cm) the DBH is not available. In this case a more simple way of initialization of cohorts is realised. It requires:

- *Species type*
- *Age*
- *Number of trees  $N_p$*
- *Mean height  $H$*
- *Minimum height  $H_{min}$*
- *Standard deviation of height  $\sigma_H$*

### 3.2. Method

#### 3.2.1. Height and number of trees per cohort

A number of saplings is generated, standard values of plants per hectare are given in the model, as well as the other required data. A number of cohorts  $N_{class}$  is calculated in different way, e.g. the integer of  $H$  is used or a number is fixed ( $N_{class} = 20$ ). For each sapling class/ cohort  $c_i$  the height  $H_i$  is calculated:



$$H_i = H_{min} + (i - 1)$$

3-1

The number of trees per cohort I  $NH_i$  is calculated:

$$NH_i = \frac{1}{\sqrt{2 \cdot \pi \cdot \sigma_H}} \cdot e^{\frac{-(H_i - H)^2}{2 \cdot \sigma_H^2}} \quad 3-2$$

The the total number  $N_{tot}$  is

$$N_{tot} = \sum_{i=1}^{N_{class}} NH_i \quad 3-3$$

And following the number of trees per class/ cohort  $N_i$  is recalculated:

$$N_i = NH_i \cdot \frac{N_p}{N_{tot}} \quad 3-4$$

### 3.2.2. Further initialization of cohorts

For the calculation of sapwood biomass  $X_{sap,i}$  per sapling cohort I the roots of the following equation has to solve

$$XH_{sap,i} = p_3 \cdot x^2 + p_2 \cdot x + p_1 - \log(H_i) \quad 3-5$$

$$X_{sap,i} = \frac{10^{XH_{sap,i}}}{100000} \quad 3-6$$

$p_1, p_2, p_3$  – species specific parameters

The foliage biomass  $X_{fol,i}$  is calculated as follows:

$$X_{fol,i} = p_a \cdot X_{sap,i}^{p_b} \quad 3-7$$

$p_a, p_b$  – species-specific parameters

and the fine root biomass  $X_{frt,i}$  is estimated:

$$X_{frt,i} = X_{fol,i} \quad 3-8$$

The parametrization of saplings of the main tree species in 4C is based on data found in (Barigah et al., 1994; Bond-Lamberty et al., 2002; Dohrenbusch, 1997; Hauskeller-Bullerjahn, 1997; Mailly and Kimmins, 1997; Ter-Mikaelian and Korzukhin, 1997; Van Hees, 1997).

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