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ENBIOCAL: An application to estimate the amount of biomass for bioenergy production in fast-growing species plantations and fallow lands

User's Guide Version 1.0

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Table of Contents

1. Introduction	5
2. Theory	5
2.1 Random sampling	5
2.1.1 Suggested field sampling procedures	5
2.1.2 Simple random sampling method	6
2.1.3 Stratified random sampling method	7
2.2 Field measurements	7
2.3 Calculations	8
2.3.1 Sample size	8
2.3.2 Biomass	8
3. Application Guide	11
3.1 Language of the application	11
3.2 Selection of the computation type	11
3.2.1 Useful information	12
3.3 Selection of sampling method and computation of sample size (n)	12
3.3.1 Useful information	12
3.3.2 Simple random sampling	13
3.3.2.1 Useful information	13
3.3.2.2 Input window entries	15
3.3.2.3 Results	16
3.3.3 Stratified random sampling	16
3.3.3.1 Useful information	16
3.3.3.2 Input window entries	17
3.3.3.3 Results	18
3.4 Computation of biomass	18
3.4.1 Useful information	18
3.4.2 Plantation	18
3.4.2.1 Useful information	19
3.4.2.2 Input window entries	20
3.4.2.3 Calculation details	24
3.4.2.4 Results	24
3.4.2.5 Area computation	25
3.4.2.6 Error and warning messages	26
3.4.3 Fallow lands	27
3.4.3.1 Useful information	27
3.4.3.2 Input window entries	29
3.4.3.3 Computation details	31
3.4.3.4 Results	31
3.4.3.5 Error and warning messages	31

3.4.3.6	Input of new equations	33
3.4.3.7	Importing equations	35
Appendix 1.	Information about the sample sites and plantations	36
Appendix 2.	Stem characteristics of clones sampled for the development of allometric equations	37
Appendix 3.	Selected equations for willow clones and species	38
Appendix 4.	Selected equations for hybrid poplar clones and groups of clones	40
Appendix 5.	Species list and equations	43
Appendix 6.	Reference and location of each study	47

1. Introduction

The ENBIOCAL (ENergy BIOMass CALculation) application, based on the sampling theory, was developed to estimate biomass content in fast-growing species plantations and fallow lands. For plantations, the application suggests two sampling methods that can be used to determine the minimum sample size (n) required to obtain the level of precision desired. Using this sample size (n), you will then be able to estimate the total biomass content of a plantation. The major advantage of ENBIOCAL is that it integrates both the sampling method and the computation of the sample size (n) in the calculation of the biomass content of a plantation. The application can also be used to calculate biomass content in fallow lands. ENBIOCAL fills a knowledge gap in methodological procedures to estimate biomass content in fast-growing species plantations or fallow lands for bioenergy production.

With ENBIOCAL, you can:

- Estimate the sample size (n) required to estimate total biomass in a plantation;
- Compute the biomass of a plantation;
- Compute the biomass of small-diameter woody species in fallow lands;
- Compute the area of a plantation/fallow land using GPS or other coordinates.

This user's guide for the ENBIOCAL application is divided into two sections. The first section outlines the theoretical concepts used to develop the application, and the second one contains a detailed description of the input windows and functions of the application. Related complementary information can be viewed in the appendices.

2. Theory

2.1 Random sampling

It is important that sampling be carried out randomly over the entire area of the population studied, which can be a fast-growing species plantation or a fallow land. Random sampling provides the best chance for the samples to be unbiased and representative of the population of interest. Two sampling methods are suggested for data collection: simple random sampling or stratified random sampling.

2.1.1 Suggested field sampling procedures

For maximum efficiency, you should sample without replacement, meaning that you should avoid sampling an individual from a population more than once. The following procedures are suggested for random sampling in the field.

- Given the required number of samples (n), the first procedure suggested consists in assigning a number to each tree in a plantation, sort trees based on the assigned numbers, and randomly select (n) trees. For example, if you have 1000 trees in a

plantation and need to collect a representative sample (n) of 50 trees, use a spreadsheet (e.g. Microsoft Excel) to assign a number to each tree and then use a spreadsheet function (e.g. RAND in Excel) to randomly select 50 trees.

- Using the same example of a 1000-tree plantation of ten 100-tree rows, a second procedure would be to randomly select a row, and then to randomly select a tree within that row. You would first draw a number between 1 and 10 to choose the row, and then draw a number between 1 and 100 to choose the tree in that row. For example, if you draw the numbers 7 and 58, you would sample the 58th tree of the 7th row.
- A third procedure that could be considered as a random sampling method would be to apply a systematic grid on an aerial photo or map of the plantation, and then to randomly select on the grid the (n) points (coordinates) that will be used as sampling locations. In the case of a plantation, you would measure the tree closest to that point; in fallow lands, you can use the point as the centre of the sample plot.
- A fourth procedure would be to use a GPS. Using a GPS, delimit the boundaries of the sampling area and use either the GPS itself or a GIS to assign (n) random points. For fallow lands, each point will be the centre of the sampled plot. For a plantation, you should sample the tree closest to the coordinate.

2.1.2 Simple random sampling method

This sampling method is used for a population considered homogeneous. It is based on a selection procedure in which every individual of a population has an equal chance of being selected.

Table 1 contains a list of the different species already included in ENBIOCAL for sample size (n) estimation. The application provides the average dry leafless aboveground biomass (in grams) per plant and the variance derived from our own sampling. Both of these values can be replaced with other average biomass or variance values that better represent the population.

Table 1. Clones available for calculation of the sample size.

<i>Populus deltoides</i> x <i>Populus nigra</i> x <i>Populus maximowiczii</i>
<i>Populus deltoides</i> x <i>Populus nigra</i> x <i>Populus maximowiczii</i> (916401)
<i>Populus maximowiczii</i> x <i>Populus balsamifera</i>
<i>Populus maximowiczii</i> x <i>Populus balsamifera</i> (915311)
<i>Populus maximowiczii</i> x <i>Populus nigra</i>
<i>Populus maximowiczii</i> x <i>Populus nigra</i> (102377)
<i>Populus maximowiczii</i> x <i>Populus nigra</i> (102380)
<i>Populus nigra</i> x <i>Populus maximowiczii</i>
<i>Populus nigra</i> x <i>Populus maximowiczii</i> (3478)
<i>Populus nigra</i> x <i>Populus maximowiczii</i> (3729)
<i>Populus trichocarpa</i> x <i>Populus nigra</i> (2293-19)
<i>Salix dasyclados</i> (India)
<i>Salix miyabeana</i>
<i>Salix miyabeana</i> (SX64)
<i>Salix miyabeana</i> (SX67)
<i>Salix miyabeana</i> (SX64 + SX67)
<i>Salix sachalinensis</i> (SX61)
<i>Salix viminalis</i> (5027)
<i>Salix viminalis</i> x <i>Salix miyabeana</i> (Tully Champion)

2.1.3 Stratified random sampling method

This method is used for a heterogeneous population that can be divided into several relatively homogenous strata. Each stratum is treated as a separate sub-population and sampled independently from the other strata using simple random sampling. Stratification can be based on different variables, such as mortality rate, drainage capacity, slope of the terrain, position inside the plantation (border rows vs interior rows) or any other variable that affects biomass production in the plantation. Once the strata have been delimited and sampled, estimates obtained from the different strata are then put together using appropriate relative weights to obtain an overall estimate for the population. A minimum of two strata are required to use this type of sampling since only one stratum would be considered a homogenous area, in which case simple random sampling would apply.

Average dry biomass and variance must be estimated for each stratum to enable the calculation of 1) the sample size required for every stratum; and 2) the total sample size required for estimates at the population level.

2.2 Field measurements

For plantations, diameter measurements are taken at a height of 15 cm from the base of the stem itself (not 15 cm from the ground). A mark is drawn on the stem at 15 cm, and the

diameter is taken with small precision calipers (in mm; e.g. digital calipers). Stem length measurements (referred to as “height” in the equations) are either taken with a measuring tape when possible (shorter plants) or with a measuring pole from the base of the plant.

For fallow lands, depending on the species and plant size (see [Appendix 4](#)), tree diameter is either measured at breast height (DBH) or at the root collar/ground level (DRC). Plant height is measured using common forestry instruments (e.g. Suunto height metre or measuring tape/pole).

2.3 Calculations

We assume that biomass is always given as aboveground, oven-dried, without the foliage.

2.3.1 Sample size

To calculate a representative sample size (n) in a plantation, the estimated average plant biomass and variance are needed. In stratified random sampling, it is important that average plant biomass and variance be estimated for each stratum (this is somewhat of an iterative concept because this information is also needed to estimate the total biomass of the plantation). The average plant biomass suggested was developed by sampling different plantations under different site conditions (see [Appendix 1](#)). We strongly recommend that application users provide their own estimates of average plant biomass and variance (e.g. from pilot surveys or from the literature).

Based on our preliminary sampling, the application provides built-in estimates of average plant biomass and its variance for five groups of clones and 13 individual clones from which you may choose to calculate a representative sample size. See [Appendix 1](#) for information on the plantations from which the clones were sampled (age of the plants, number of rotations, geographical location, etc.).

2.3.2 Biomass

For biomass calculation in fallow lands, you must estimate the number of plots to be sampled. These plots should be a good representation of the fallow land. The application cannot suggest a sample size because it most often is a case by case situation that varies according to sample plot size, type and productivity of the fallow land, time since it was abandoned, and other factors. However, the application has a list of 19 equation forms (the most common were found in the literature; see Table 2) from which you may choose to customize equations for species present in your plots, allowing the computation of plant biomass according to your needs. You may also use built-in species equations that are predefined by the application (the list of species is presented in Table 3).

Table 2. List of the equation forms included in ENBIOCAL for the customization of biomass computation.

Equations based on diameter only
1) $\log_{10} \text{Biom.} = a + b \times \log_{10} \text{diam.}$
2) $\log_{10} \text{Biom.} = a + b \times \log_{10} \text{diam.}^c$
3) $\log_{100} \text{Biom.} = a + b \times \log_{10} \text{diam.}$
4) $\ln \text{Biom.} = a + b \times \ln \text{diam.}$
5) $\ln \text{Biom.} = \ln(a) + b \times \ln \text{diam.}$
6) $\ln \text{Biom.} = a + b \times \text{diam.} + c \times \ln \text{diam.}^c$
7) $\ln \text{Biom.} = a + b \times \ln \text{diam.} + c \times (d + e \times \ln \text{diam.})$
8) $\text{Biom.} = a \times \text{diam.}^b$
9) $\text{Biom.} = a + b \times \text{diam.} + c \times (\text{diam.}^d)$
10) $\text{Biom.} = a + b \times \text{diam.} + c \times (\text{diam.}^2) + d \times (\text{diam.}^3)$
11) $\text{Biom.} = a \times (\exp(b + c \times \ln \text{diam.} + d \times \text{diam.}))$
12) $\text{Biom.} = a + ((b \times \text{diam.}^c) / (\text{diam.}^c + d))$
Equations based on diameter and height
13) $\log_{10} \text{Biom.} = a + b \times \log_{10} \left(\frac{\pi}{2} \times (\text{diam.}/2)^2 \times \text{height} \right)$
14) $\log_{10} \text{Biom.} = a + b \times \log_{10}(\text{diam.}^2 \times \text{height})$
15) $\ln \text{Biom.} = a + b \times \ln \text{diam.} + c \times \ln \text{height}$
16) $\text{Biom.} = a \times (\text{diam.}^2 \times \text{height})$
17) $\text{Biom.} = a \times \text{diam.}^b \times \text{height}^c$
18) $\text{Biom.} = a + b \times \text{diam.} + c \times \text{height} + d \times (\text{diam.}^2 \times \text{height})$
19) $\text{Biom.} = a + b \times \text{diam.} + c \times \text{diam.}^2 + d \times (\text{diam.} \times \text{height})$

Table 3. Species names and their associated three-letter code.

Scientific name	Common name	Species code
<i>Abies balsamea</i>	Balsam fir	SAB
<i>Acer pensylvanicum</i>	Striped maple	ERP
<i>Acer rubrum</i>	Red maple	ERR
<i>Acer saccharinum</i>	Silver maple	ERA
<i>Acer saccharum</i>	Sugar maple	ERS
<i>Alnus</i> spp.	Alder	AUL
<i>Amelanchier</i> spp.	Serviceberry	AME
<i>Betula alleghaniensis</i>	Yellow birch	BOJ
<i>Betula papyrifera</i>	White birch	BOP
<i>Betula populifolia</i>	Gray birch	BOG
<i>Cornus</i> sp.	Dogwood	CO
<i>Cornus stolonifera</i>	Dogwood	COR
<i>Corylus cornuta</i>	Beaked hazel	COC
<i>Fagus grandifolia</i>	American beech	HEG
<i>Fraxinus americana</i>	White ash	FRA
<i>Picea glauca</i>	White spruce	EPB

<i>Picea mariana</i>	Black spruce	EPN
<i>Pinus banksiana</i>	Jack pine	PIG
<i>Pinus resinosa</i>	Red pine	PIR
<i>Populus balsamifera</i>	Balsam poplar	PEB
<i>Populus grandidentata</i>	Large-tooth aspen	PEG
<i>Populus tremuloides</i>	Trembling aspen	PET
<i>Prunus pensylvanica</i>	Pin cherry	PRP
<i>Prunus serotina</i>	Black cherry	CET
<i>Prunus</i> spp.	Cherry	CER
<i>Prunus virginiana</i>	Chokecherry	PRV
<i>Quercus rubra</i>	Red oak	CHR
<i>Salix</i> spp.	Willow	SAL
<i>Sambucus canadensis</i>	Elder	SAC
<i>Sorbus americana</i>	American mountain ash	SOA
<i>Thuja occidentalis</i>	Eastern white cedar	THO
<i>Tsuga canadensis</i>	Eastern hemlock	PRU
<i>Tsuga heterophylla</i>	Western hemlock	TSH

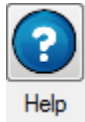
Refer to [Appendix 2](#) and [Appendix 3](#) to see the predefined equations associated with the species and their size range.

Range adjustments were made to some of the equations to standardize calculations. In some cases, the application uses **different equations**, depending on the **diameter of the tree (small or large)**, to calculate the biomass of a species. The division point of the two ranges in the application is the upper limit of the smaller diameter equation. For example, in the case of a species measured at DBH, if the range is 5-15 cm in equation 1 and 10-70 cm in equation 2, equation 2 will only be used to calculate the biomass when the diameter is greater than 15 cm (i.e. the upper limit of equation 1, which was developed on smaller trees and is therefore more appropriate for them).

For some species, **different equations** based on **different types of diameter measurements (DRC/D15/DBH)** are used for smaller or larger plants. For example, for a given species, smaller individuals can be measured using DRC or D15 (depending on the species), while larger individuals are measured using DBH. In this case, if the data entered is outside of the equation's size range (above or below), a warning window will appear to ask if you want to continue using this data. If you accept, the application will use the data even though it is outside of the range, but the result of the calculation may be inaccurate or wrong. For example, if equation 1 uses DRC with a range of 10-20 mm and equation 2 uses DBH with a range of 30-70 mm and the data entered is a DRC of 50 mm (usually within the range of larger individuals measured at DBH), the application will still use the data in equation 1 to calculate biomass if you accept.

3. Application Guide

Each window includes a **Help** button. You can click on this icon to obtain a short description of the use and functions of the window. For more detailed information, refer to the related sections in this guide.



3.1 Language of the application

When you launch ENBIOCAL, the first window asks you to select the language you wish to use (Figure 1).

Options: → [English/Anglais]
→ [Français/French]



Figure 1. ENBIOCAL initial window.

3.2 Selection of the computation type

The second window asks the user to choose among two options (Figure 2).

Options: → [Selection of sampling method and computation of sample size (n)]
→ [Computation of Biomass]

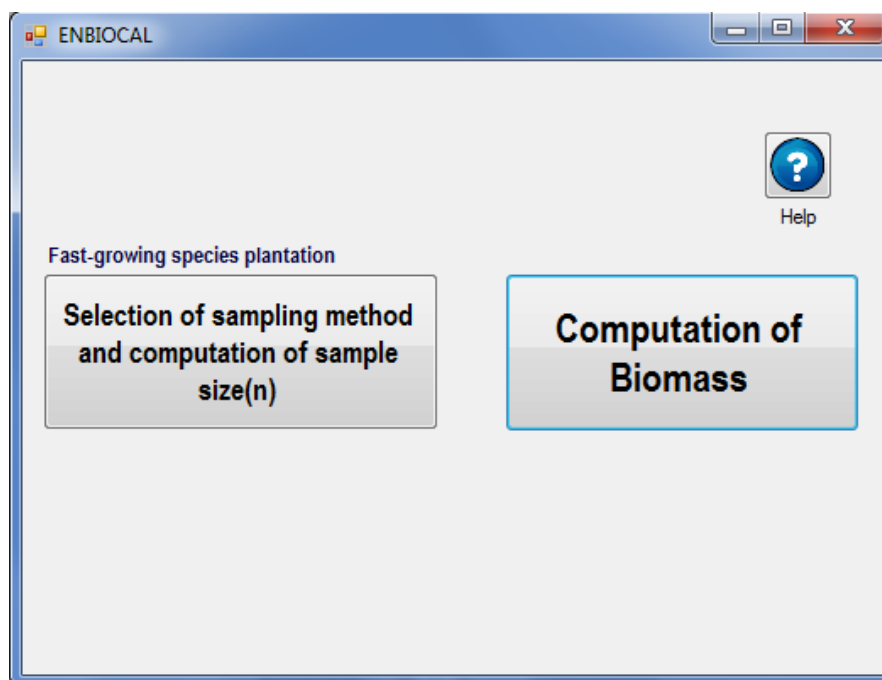


Figure 2. Calculation option window.

3.2.1 Useful information

- Select the type of computation needed.
- For a plantation, you may first use the function that allows you to estimate the minimum sample size (n) for one of the two sampling methods offered. Once you have sampled the plantation with the minimum sample size (n) suggested, you can use the “Computation of biomass” function to estimate total biomass in the plantation.
- Click on [Selection of sampling method and computation of sample size (n)] to determine the minimum sample size (n) required to obtain an accurate biomass estimation in a plantation. This step is carried out before the biomass is calculated and aims at estimating the sample size (n).
- Click on [Computation of Biomass] and enter the sampling data to calculate the biomass of a plantation or a fallow land.

3.3 Selection of sampling method and computation of sample size (n)

- [Selection of sampling method and computation of sample size (n)] (Figure 3).
- Options:
- [Simple Random Sampling]
 - [Stratified Random Sampling]
 - [Back] Return to the Calculation option window

3.3.1 Useful information

- The estimation of sample size was developed for plantations only.
- This is the first of two interrelated functions in this application.

- Choose the sampling method that is the most appropriate for the population (section 2.1). In the case of a homogeneous population, choose [Simple Random Sampling]. In the case of a heterogeneous population, choose [Stratified Random Sampling].
- You will use this function to determine the minimum sample size (n) required to obtain an estimation of the biomass content in a plantation at the desired level of precision.
- In a plantation, diameters must be measured at 15 cm from the base of the stem (D15).

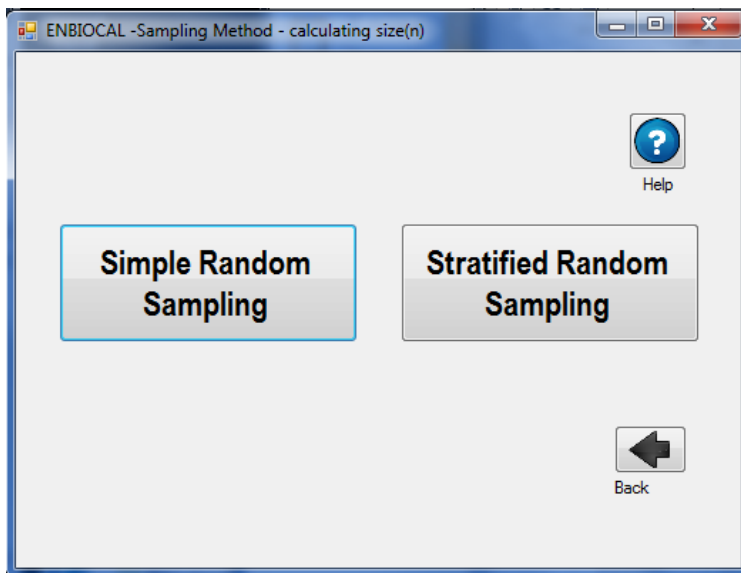


Figure 3. Sampling Method – calculating size (n) window.

3.3.2 Simple Random Sampling

- [Selection of sampling method and computation of sample size (n)]
- [Simple Random Sampling] (Figure 4).

3.3.2.1 Useful information

- This calculation is used to determine the minimum sample size (n) needed using the simple random sampling method. The application uses the average plant biomass and variance that were calculated through our own sampling for each of the clones. If you consider one or both of these parameters to be unrepresentative of the population, you may enter a different average plant biomass and/or variance if you believe you have better estimates of the parameters. Make sure that both average biomass and variance have the same units.
- Biomass is expressed in grams (g) and represents the aboveground oven-dried biomass of the plant (corresponding to multiple stems) without leaves.
- The exact size of the population is not essential to the computation of the minimum sample size (n) for this type of sampling. If the size of the population (number of trees) is unknown, the calculation assumes that the population is infinite (small sampling rate) and uses algorithms for simple random sampling with replacement. If the population size is known,

we recommend that it be entered for additional accuracy (the application uses algorithms for simple random sampling without replacement, which is generally more efficient).

- Five clone-group and 13 clone-specific estimates of average plant biomass and variance are provided, from which you may choose to calculate a representative sample size. However, if you think it is advisable, we suggest you provide your own approximate estimates since your plantation may differ in productivity, age and stand density from those sampled for the development of ENBIOCAL.
- If the mortality rate is not entered, a 0% mortality is presumed. Otherwise, sample size is adjusted for mortality.
- The desired precision is defined as the confidence limit (error margin) expressed in percentage of average plant weight and is required to calculate the sample size. The smaller the confidence interval, the larger the sample size will be because you are asking for a more precise calculation. If the precision (%) is not entered, a default confidence limit of 5% of the average is used by the application as indicated in the assigned space.
- Click on [Back] to return to the Selection of sampling method and computation of sample size (n) window.

ENBIOCAL - Calculating n - Simple Random Sampling

Precision (%) (5-50%) Mortality rate (%) (0-40%) ☐ Give Population Size (N) N

[Help](#)

Estimate of the mean biomass and variance of the clone for the calculation of sample size (n)

Clone	Mean (grams)	Variance	<input type="checkbox"/> Other Mean	<input type="checkbox"/> Other Variance
<input checked="" type="radio"/> (<i>Populus deltoides</i> x <i>P. nigra</i>) x <i>P. maximowiczii</i>	1699.9525	3179233.068	<input type="text"/>	<input type="text"/>
<input type="radio"/> (<i>P. deltoides</i> x <i>P. nigra</i>) x <i>P. maximowiczii</i> (916401)	577.8808	78811.80334	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. maximowiczii</i> x <i>P. balsamifera</i>	1823.8507	2747845.295	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. maximowiczii</i> x <i>P. balsamifera</i> (915311)	1026.2707	660098.0763	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. maximowiczii</i> x <i>P. nigra</i>	2855.994	4243746.673	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. maximowiczii</i> x <i>P. nigra</i> (102377)	4199.7353	1087956.223	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. maximowiczii</i> x <i>P. nigra</i> (102380)	2069.9193	4652136.511	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. nigra</i> x <i>P. maximowiczii</i>	1405.198	2806553.362	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. nigra</i> x <i>P. maximowiczii</i> (3478)	1486.7295	3400605.229	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. nigra</i> x <i>P. maximowiczii</i> (3729)	1327.5489	2369554.089	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>P. trichocarpa</i> x <i>P. nigra</i> (2293-19)	3107.860	4333850.437	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>S. dasyclados</i> (India)	1029.180	852594.7976	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>S. miyabeana</i> (SX64)	2120.290	3268860.746	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>S. miyabeana</i> (SX67)	2155.550	1646857.863	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>S. miyabeana</i> (SX64 + SX67)	2143.797	2093736.651	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>S. sachalinensis</i> (SX61)	2844.540	7086811.55	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>S. viminalis</i> (5027)	811.640	379987.7942	<input type="text"/>	<input type="text"/>
<input type="radio"/> <i>S. viminalis</i> x <i>S. miyabeana</i> (Tully Champion)	1103.860	566407.9642	<input type="text"/>	<input type="text"/>

Sample size (n) calculated: 0

Figure 4. Calculating (n) – Simple Random Sampling window.

3.3.2.2 Input window entries

- **Precision (%):** Specify the precision of the estimate as a percentage. You can choose a value between 5 and 50%.
- **Mortality rate (%):** Determine the mortality rate (expressed in percentage). You can choose a value between 0 and 40% of the population.
- **Population size (N):** Enter the population size if known (i.e. the number of plants in the plantation).
- **Clone:** Select the type of clone sampled.
- **Other mean:** We suggest that you manually enter an average plant biomass (g) that is more representative of the population for the calculation. Otherwise, the average and variance for the selected clone will be those observed and used for the development of the allometric equations. You can estimate average plant weight and variance based on your experience (previous harvesting of some plants) or on the literature (for similar plantations and site conditions). This is the average dry leafless biomass of a plant in the plantation.

- **Other variance:** You may choose to manually enter a variance for the calculation. It is important that the units used for average plant biomass (in grams (g) by default) be the same as those used for the standard deviation, which is related to variance (standard deviation squared).
- **[Compute]:** Click on this button to obtain the minimum required sample size (n) calculated based on the information entered.
- **[Back]:** Click on this button to return to previous window.

3.3.2.3 Results

The [Compute] function calculates the sample size (n), which appears at the bottom of the window. This is the number of samples (n) needed to provide an estimate of the population with a relatively high degree of accuracy (to the level of precision desired). You should use this minimum required sample size (i.e. the number of plants to sample) to obtain an estimate of the biomass in the population.

3.3.3 Stratified Random Sampling

→ [English] → [Selection of sampling method and computation of sample size (n)]
 → [Stratified Random Sampling] (Figure 5)

3.3.3.1 Useful information

- This calculation is used to determine the minimum required sample size (n) using the stratified random sampling method.
- The number of strata for the calculation can range from two to ten. One stratum is considered to be a homogenous area of the plantation (see section 2.1).
- You must enter the average plant biomass and variance specific to each stratum sampled, as well as the number of trees per stratum.
- You can enter a mortality rate for each stratum. If the mortality rate is not entered, a 0% mortality rate will be used by the application, as indicated in the assigned space.
- If the precision (%) is not entered, a 5% precision will be used by the application as indicated in the assigned space.
- Click on [Back] to return to the Selection of sampling method and computation of sample size (n) window.

ENBIOCAL - Calculating n - Stratified Random Sampling

Number of strata: 2

Precision (%): 5.00 (5-50%)

Help

Estimate of the mean biomass and variance for the calculation of sample size (n)

Stratum	Number of trees	Mortality (0-40%)	Mean (grams)	Variance	Stratum n Value
S1		0.00			0
S2		0.00			0

Compute

Sample size (n) calculated: 0

Back

Figure 5. Calculating (n) – Stratified Random Sampling window.

3.3.3.2 Input window entries

- **Number of strata:** Enter the number of strata in your plantation.
- **Precision (%):** Specify the precision as a percentage of the estimate. You can choose a value between 5 and 50%.
- **S1, S2, (...):** For every stratum, you must enter:
 - the number of trees in the stratum;
 - a mortality rate between 0 and 40%;
 - average plant biomass (g) in the stratum;
 - plant biomass variance in the stratum.
- **[Compute]:** Click on this button to obtain the representative sample size (n) for:
 - the total sample size (n) of the plantation (overall population);
 - the sample size (stratum (n)) of each stratum.
- **[Back]:** Click on this button to return to the previous window.

3.3.3.3 Results

The [Compute] function calculates the total sample size (n), which appears at the bottom of the window, and the sample size for each stratum, given as the stratum (n) value. The sample size (n) of each stratum is the number of plants to be sampled for that specific stratum. The total sample size (n) is the sum of all stratum (n) values. This is the number of samples (n) needed to obtain a representation of the population with a relatively high degree of accuracy (to the level of precision desired).

3.4 Computation of biomass

→[Computation of Biomass] (Figure 6)

Options: → [Plantation]
 → [Fallow lands]

3.4.1 Useful information

- This function is used to estimate biomass in a fast-growing species plantation or a fallow land.
- Information can be entered in capital or lower case letters.

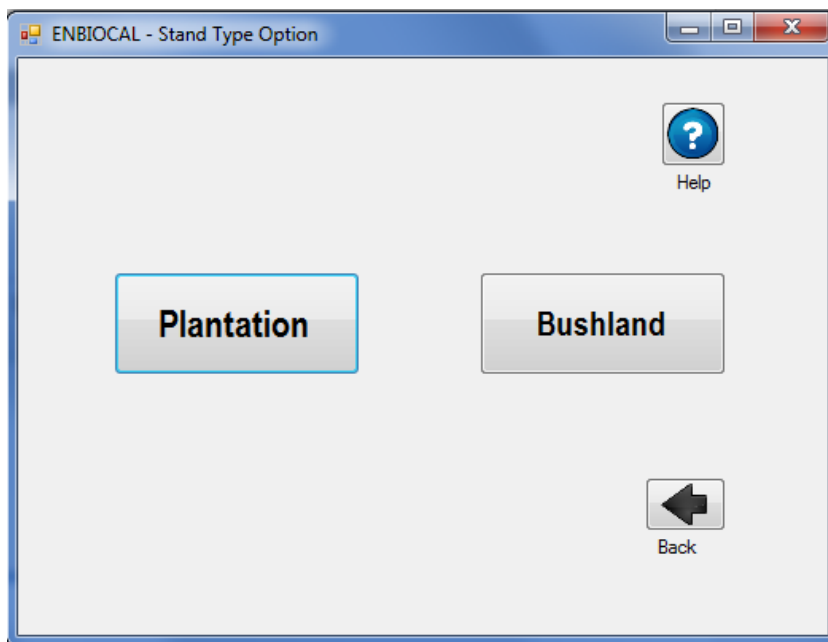


Figure 6. Stand Type Option window.

3.4.2 Plantation

→ [Computation of Biomass] → [Plantation]

3.4.2.1 Useful information

- This option makes it possible to calculate the biomass content in a plantation for a specific clone in a determined area using simple random sampling (Figure 7) or stratified random sampling (Figure 8). You can provide an area value manually or calculate the area using the [\[Calculate Area\]](#) function. Then, you must enter the sampling data for the clone; this can either be done manually, in the order indicated in the input/edit sub-window, or by uploading the data from a file. If necessary, you can modify the data imported from a file directly in the input/edit sub-window.
- All diameters are measured at D15.
- If the mortality rate is not entered, a 0% mortality is presumed, as indicated in the assigned space.
- If diameter units are not changed, the default unit is in millimetre (mm).
- If height units are not changed, the default unit is in centimetre (cm).

The screenshot shows the 'ENBIOCAL - Biomass Computation in a Plantation' window. It features several input fields and buttons. On the left, there's a 'Clone' dropdown menu. Below it, the 'Sampling method' section has two radio buttons: 'Simple random sampling' (selected) and 'Stratified random sampling'. Further down, there are input fields for 'Number of Trees in the Plantation' and 'Mortality (%)' (set to 0.00). Below these is a 'Number of strata' input field set to 2. On the right side, there's a 'Location' text field, a 'Total Plantation Area' text field with a 'Calculate Area' button, and 'Area Units' (radio buttons for 'Hectare' and 'Square metre', with 'Hectare' selected). A 'Help' button with a question mark icon is also present. The central part of the window is titled 'Tree data' and shows a header row: 'Tree number - Number of stems - Diameter - Height - Diameter - Height ...'. Below this is a large empty table area. At the bottom, there are 'Diameter units' (radio buttons for 'mm' and 'cm', with 'mm' selected) and 'Height units' (radio buttons for 'cm' and 'm', with 'cm' selected). To the right of these are a 'Select Data File' button, a 'Reset' button, a green 'Compute' button, and a 'back' button with a left arrow.

Figure 7. Input window used for the computation of biomass content in a fast-growing species plantation using simple random sampling.

Figure 8. Input window used for the computation of biomass content in a fast-growing species plantation using Stratified random sampling.

3.4.2.2 Input window entries

- You can enter the sampled data manually in the “Tree data” input/edit sub-window in the order indicated. For instance, if a clone has ten stems and the associated equation uses four stems to calculate the biomass, you may enter data for the four largest stems only. If you enter data for the ten stems, the application will automatically use the four largest ones in the calculation. However, you must still enter the **total number of stems** (i.e. ten in this case) of the plant.
- **Clone:** Select the name of the clone. Scientific names of the parent species are provided to help you identify the clone. For clone-specific equations, the code of the clone is written in parentheses after the scientific name.
- **Location:** Enter the sampling location (e.g. town, region, country).
- **Total plantation area:** Enter the surface of the plantation. Select the unit (hectare or square metre); the conversion is made automatically when you change from one unit to the other. You can also calculate the area of the plantation using the [\[Calculate Area\]](#) function.
- **Sampling method:** Select the sampling method used to obtain the sample size (n) (Simple random sampling or Stratified random sampling).
- **Population size (N):** Enter the total number of trees in the plantation (Simple random sampling only).
- **Number of strata:** Enter the total number of strata in the plantation (Stratified random sampling only).

- **Number of trees:** Enter the total number of trees per strata (Stratified random sampling only).
- **Mortality rate (%):** Determine a mortality rate (expressed in percentage). You can choose a value between 0 and 40%.
- **Select data file:** You may upload a file containing your data. It is imperative that the parameters be entered in the order indicated in the window (e.g. for Simple random sampling: tree ID number; number of stems; individual diameter; height of the k largest stems (with k depending on the clone selected, see [Appendix 2](#) and [Appendix 3](#))). An error message will appear if you do not enter the correct diameters and heights for the equation used. This file can either be in text (*.txt) or comma-separated values (*.csv) format, which can be created using Excel.

Example of a **Simple** random sampling file (you may use a space, tab, comma or semicolon to separate the values):

Tree#	Number of stems	D1	H1	D2	H2	D3	H3	D4	H4
1	4	35	523	38	256	33	458	33	458
2	6	40	256	36	369	35	569	35	569
3	7	32	369	22	458	39	563	33	523
4	7	21	458	24	569	37	532	35	256
5	8	29	569	26	563	35	540	39	369
6	8	30	563	28	532	42	538	37	458
7	8	36	532	27	540	42	596	35	569

Example of a **Stratified** random sampling file (you may use a space, tab, comma or semicolon to separate the values):

Plot	Tree	Number of stems	D1	H1	D2	H2	D3	H3	D4	H4
1	1	4	35	523	38	256	33	458	33	458
1	2	6	40	256	36	369	35	569	35	569
2	1	8	30	563	28	532	42	538	37	458
2	2	8	36	532	27	540	42	596	35	569
3	1	9	36	489	20	599	39	458	43	563
3	2	9	21	538	21	458	31	464	40	532
4	1	11	47	536	20	578	42	599	21	256
4	2	11	49	534	57	536	43	578	20	369

The data imported from the file can be modified directly in the input/edit sub-window.

- **Diameter units:** you must select the units in which the diameters were measured. All diameters must be in the same units.
 - mm (millimetre)
 - cm (centimetre)

- **Height units:** you must select the units in which the heights were measured. All heights must be in the same units.
 - cm (centimetre)
 - m (metre)
- **[Back]:** Click on this button to return to the Stand Type Option window.
- **[Reset]:** Click on this button to reset all entries.
- **[Compute]:** Click on this button to calculate total dry leafless biomass in a plantation. A results window will appear.

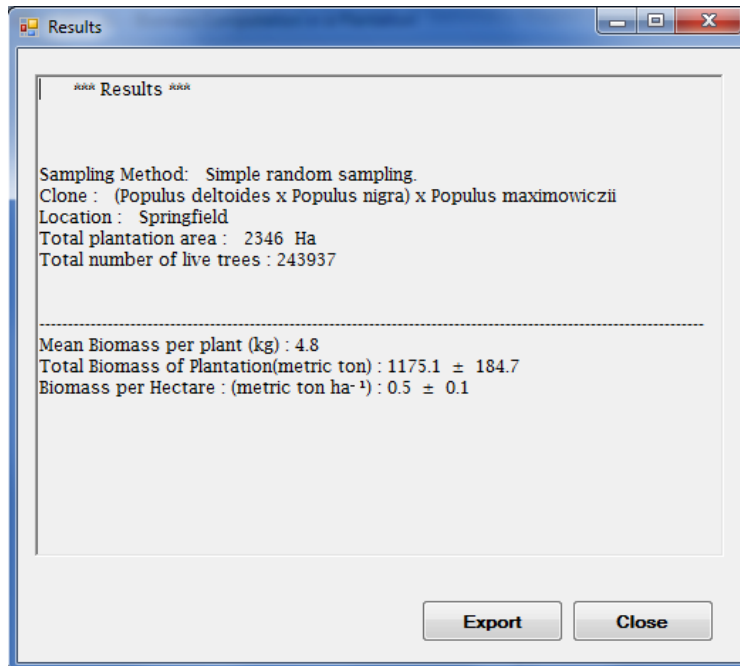


Figure 9. Example of a results window (**Simple** random sampling).

Results for **Simple** random sampling (Figure 9):

- Sampling method used.
- Clone: Clone identification and scientific name(s) of the willow or poplar species.
- Location: Location specified by the user.
- Total plantation area.
- Total number of live trees.
- Average biomass per plant (kg).
- Total biomass of the plantation (metric ton): Total biomass of the plantation with its 95% confidence interval.
- Biomass per hectare (metric ton/ha): Average plant biomass per hectare with its 95% confidence interval.

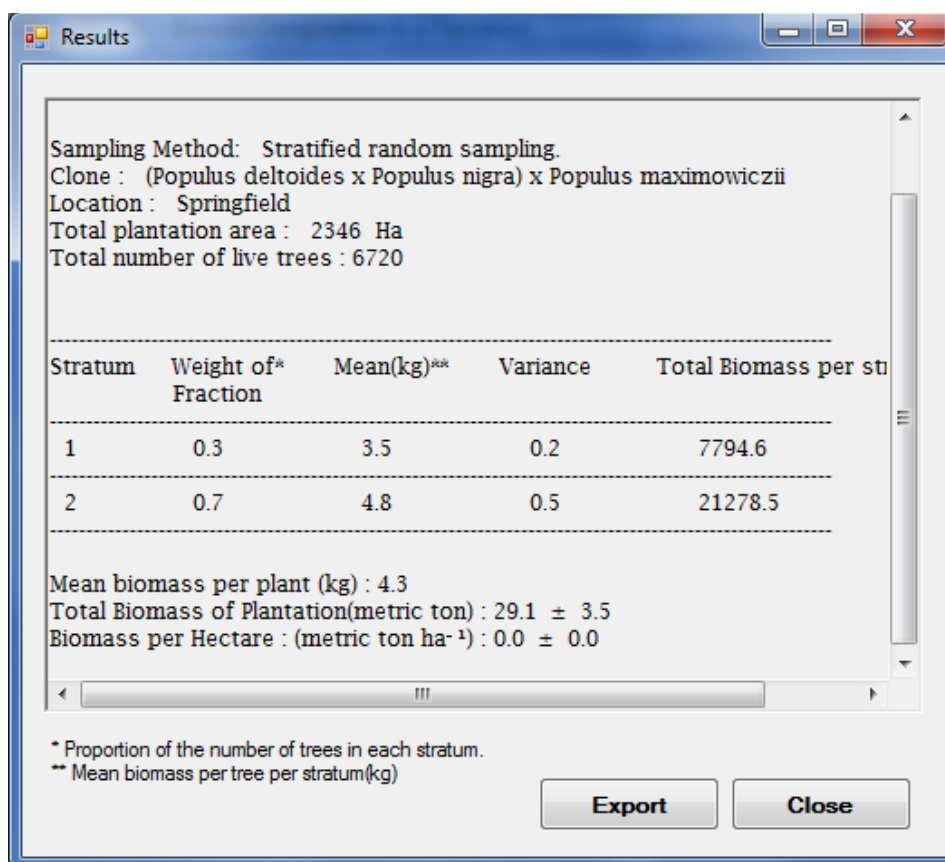


Figure 10. Example of a Results window (**Stratified** random sampling).

Results for **Stratified** random sampling (Figure 10):

- Sampling method used.
- Clone: Clone identification and scientific name(s) of the willow or poplar species.
- Location: Location specified by the user.
- Total plantation area.
- Total number of live trees.
- Weight of fraction per stratum.
- Average (kg): Average plant biomass per stratum.
- Variance: Variance per stratum.
- Total biomass per stratum (metric ton/ha): total biomass per stratum with its 95% confidence interval.
- Average biomass per plant (kg): Average overall plant biomass (for the entire plantation).
- Total biomass of the plantation (metric ton).
- Biomass per hectare (metric ton/ha) with its 95% confidence interval.

You can save the Calculation Summary Report by clicking on the button [Export Text]. Enter a name for the file and choose a location on your computer to save the report.

3.4.2.3 Calculation details

The equations used for the calculation of biomass in a plantation are based on the diameters and heights of a number of stems from each tree. The equations were developed using two, three or four stems per tree for the calculation of the biomass. This approach reduces the number of measurements needed for each plant since the data of only four stems, at the most, will be used for the equations.

For example, for an equation developed using three stems, every sampled tree should have at least three stems. We know that there will be variation in the number of stems from plant to plant. If there are more than three stems per plant, the application will choose the three largest ones. If there are less than three stems, the application will still be able to calculate the biomass using only the stem data entered for one or two stems, in this example. Consequently, a [warning](#) will be issued to allow the user to verify and correct the data entered if needed. This variation is not considered an error, but it may affect the precision of the calculation.

NOTE: You do not need to measure more than the required number of stems for the clone of interest (see [Appendix 2](#) and [Appendix 3](#)); theoretically, you only need to measure the diameter and height of the k trees with the largest D15 (not every stem of a plant), as these will be the only ones taken into account by the application for that specific clone. However, you must count and note the total number of stems of each plant sampled (a variable used in all the equations developed).

There is a size range associated with every equation. You can refer to [Appendix 4](#) for the range values of diameter, height and number of stems for each equation. A warning will be issued if the values are outside the following ranges: $5 < D15 < 100$ mm; $50 < H < 1000$ cm; Nb stems < 30 .

3.4.2.4 Results

For simple random sampling, this function calculates the average biomass per plant (kg), total biomass (metric ton) and biomass per hectare (metric ton/ha) in the plantation.

For stratified random sampling, this function calculates the average biomass per stratum (kg), total biomass per stratum, plant biomass variance per stratum, overall average biomass per plant (kg), biomass per hectare (metric ton/ha), and total biomass in the plantation (metric ton).

3.4.2.5 Area computation

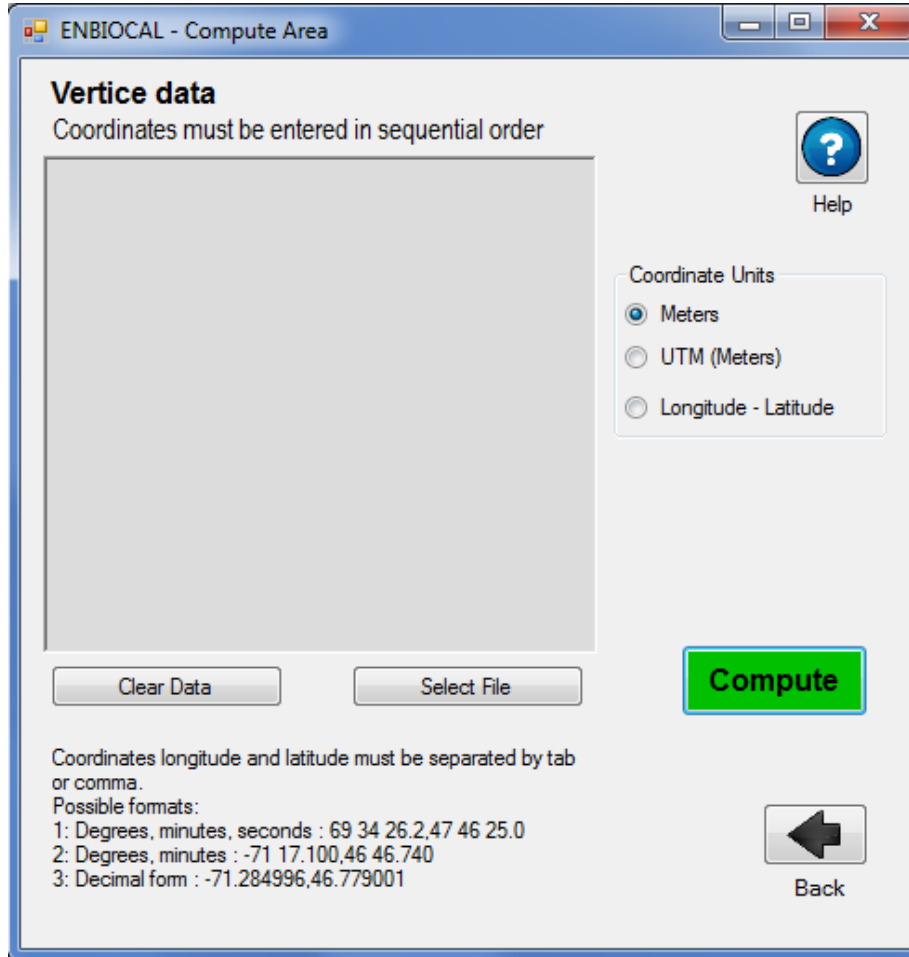


Figure 11. Compute Area window.

- Three different types of coordinate units can be used to enter data (Figure 11). All coordinates must be separated by a tab or a comma. Using a space as a separator will cause an error because a space is needed for longitude and latitude coordinates expressed in minute and seconds. See the examples below:
 - Metres: (345.45 64.78) or (345.45,64.78);
 - UTM (metres): (325616.344936436 5183177.45434031) or (325616.344936436,5183177.45434031);
 - Longitude and latitude (in the respective order):
(-71 17.284996 46 17.779001) or (-71 17.284996,46 17.779001).
- For the GPS coordinate system used, there are three possible options:
 - 1- No GPS (unknown coordinate system).
 - 2- WGS 84 (the most commonly used with GPS devices). Use this option if coordinates were taken using NAD 83 (the results are approximately equal).
 - 3- NAD 27.

- [Select File]: You may use a file containing the coordinates. This file can either be in text (*.txt) or comma-separated values (*.csv) format.
- [Clear Data]: Click on this button to clear all data in the entry area.
- [Compute]: Click on this button to calculate the area. The window will close and the area calculated will be automatically assigned to the Plantation Information window.

3.4.2.6 Error and warning messages

If you enter a number of stems that is smaller than the number of stems used by the equation (see [Appendix 2](#) and [Appendix 3](#)), a warning message will appear (Figure 12). It will ask if the number of stems entered is correct. If it is in fact a valid entry, click on [OK] to continue using it in the calculation. If it is an error, click on [Cancel] to stop the calculation. You can either change or erase the data if they are invalid.

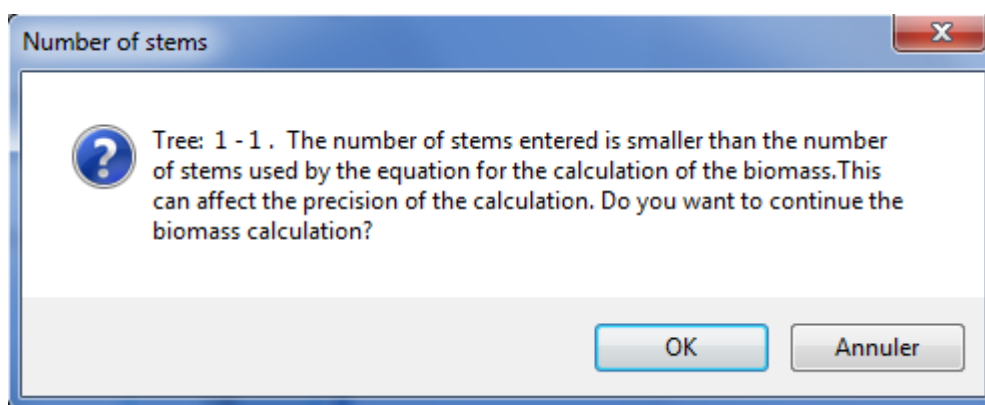


Figure 12. Example of a warning window (Number of stems).

If any diameter value, height value or number of stems entered is very high (i.e. outside of the range), the following warning window will appear to ask if the data is valid.

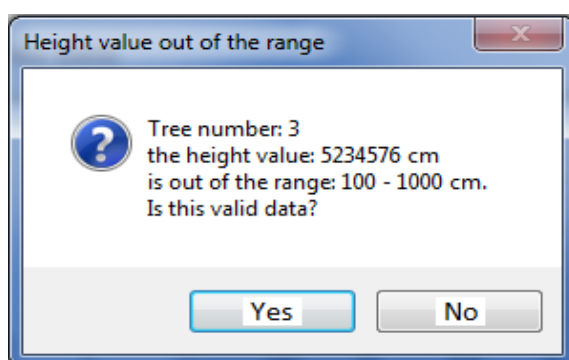


Figure 13. Example of a warning window (Height value outside of the range).

Some equations will use a maximum of four stems to calculate the biomass of a plant. Therefore, for any plant that has more than four stems, enter only the data of the four largest stems. If you indicate that a plant has a total of eight stems but enter data for only two stems while the associated equation uses three stems, a window will appear with an error message and the calculation will stop (Figure 14).

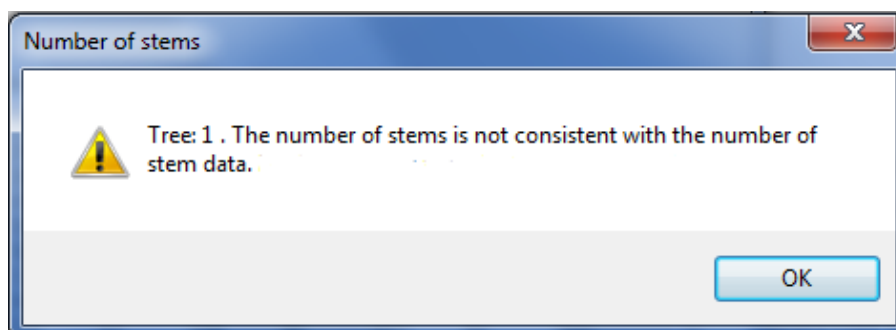


Figure 14. Example of an error window (Number of stems).

If data is missing or if there is an error in the way data was entered (e.g. if you entered a stem D15 value but did not enter its height), an error window will appear and the calculation will stop (Figure 15).

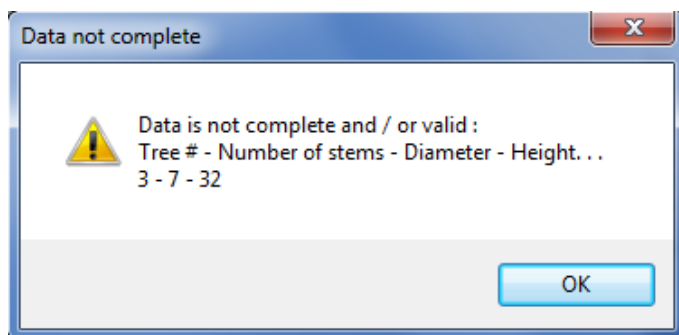


Figure 15. Example of error window (Data not complete).

3.4.3 Fallow lands

→English →Computation of Biomass →Fallow lands

3.4.3.1 Useful information

- This option will allow you to calculate the biomass of fallow lands over a determined area (Figure 16). You can either enter the area manually or calculate it using the [\[Calculate Area\]](#) function. You must also enter the sampling data for the species sampled, either manually in the order indicated in the window or by uploading the data from a file.
- If you enter species that are not already defined in ENBIOCAL, a [warning window](#) will ask you to customize them using the [\[Input of New Equations\]](#) window. You will be asked to choose from a predetermined selection of 19 equation forms and to enter the appropriate parameters specific to each equation. We recommend that you create a file containing all the customized species before using the [\[Input of New Equations\]](#) window function instead of letting ENBIOCAL identify unknown species every time.
- You may also choose to customize the equation of a species already defined in ENBIOCAL by using the [Input of New Equations window](#) and entering the species code used by the

application (see [Table 2](#)). You can then choose an equation from the 19 equation forms suggested; it will become the species' default equation for the active session. As long as the Fallow land Information window is not closed, this information is saved in the background. It is important to load this new equation every time you open a new Fallow land Information window if you wish to use the new customized equation for the species. If previously saved in a file, click on [[Import Equations](#)] to select the saved customized equation.

- For some equations, stem height is not used in the biomass calculation, but the height column cannot be left blank. Data must be entered or else an [error window](#) will appear. If stem height required for the equation (see [Appendix 5](#)), you can enter any value (negative or positive) in the height column. If height is required in the equation and the data entered is negative, an [error window](#) will appear.
- It is important to understand that the samples used to calculate the biomass of fallow lands are plots, not individual trees or shrubs.
- If diameter units are not changed, the default unit in the selection is cm.
- If height units are not changed, the default unit in the selection is m.

Figure 16. Biomass Computation on Fallow Lands window.

3.4.3.2 Input window entries

- **Location:** Enter the location of the fallow land.
- **Area:** Enter the area of the fallow land. Select the units used: hectares (ha) or square metres (m²). The conversion is made automatically when you change from unit to the other.
- **Calculate Area:** Refer to [section 3.4.2.5](#) for details on the calculation and data entry procedure.
- **Select data file:** You may upload data from a file. It is imperative that the values appear in the order indicated in the window (e.g. plot number, species code, ID tree number, type of diameter measured, diameter and height values). This file can either be in text (*.txt) or “comma-separated values” (*.csv) format, which can be created using Excel.

Example of a data entry file (you may use a space, a tab, a comma or a semicolon to separate the parameters):

Plot	Code	Tree	Type	D	H
1	SAB	1	DBH	34	454
1	SAB	2	DBH	59	603
1	SAB	3	DBH	76	687
1	SAB	4	DBH	74	678
1	BOJ	7	DBH	8	300
1	BOJ	8	DBH	10	300
2	BOJ	6	DBH	10	388
2	BOJ	1	DBH	5	150
2	BOJ	5	DBH	130	1000
2	BOJ	2	DBH	125	800
2	BOJ	3	DBH	150	900

If you wish, you may modify the data previously imported from the file directly in the window.

- **Diameter units:** You must select the measurement unit for the diameter. All diameters must be in the same unit.
 - mm (millimetre)
 - cm (centimetre)
- **Height units:** You must select the measurement unit for height. All heights must be in the same unit.
 - cm (centimetre)
 - m (metre)
- **Compute:** Click on this button to calculate the total biomass (in metric ton) of the fallow land area. A results window will appear, showing the following (Figure 17):
 - Location: The location specified by the user.
 - Biomass per hectare (metric ton/ha): Biomass per hectare and the associated 95% confidence interval.
 - Total biomass (metric ton): Total dry biomass of the plantation and the associated 95% confidence interval.
- **[Back]:** Click on this button to return to the Stand Type Option window.
- **[Reset]:** Click on this button to reset all entries.

You can save the Results by clicking on the [Export] button. Enter a name for the file and choose the computer location where you wish to save the report.

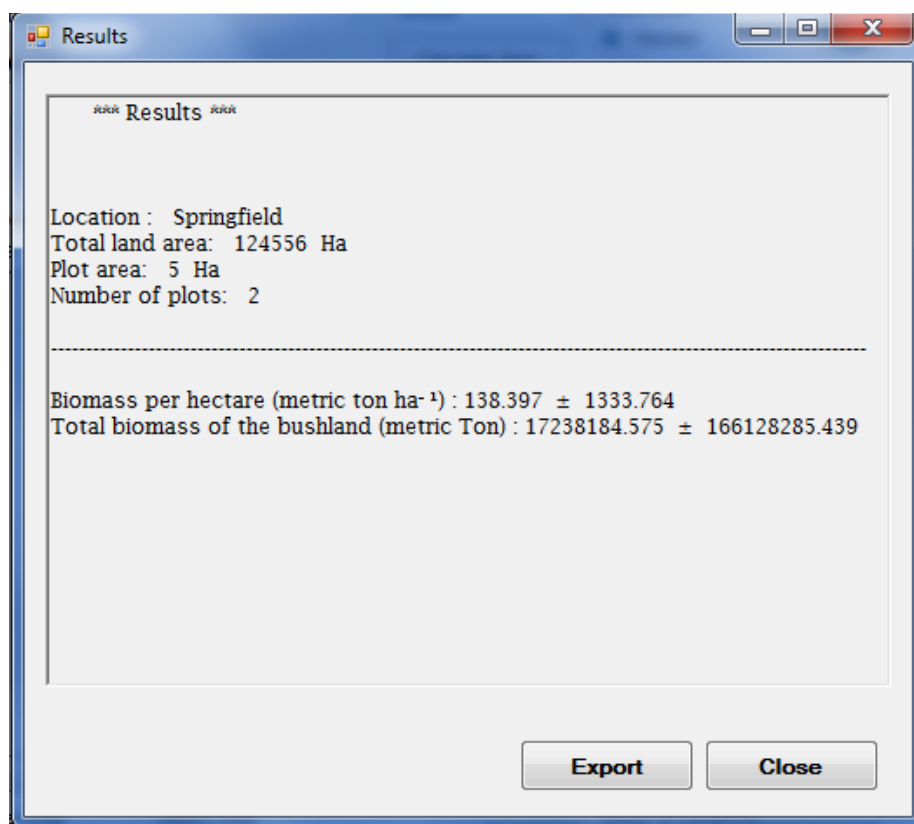


Figure 17. Example of a Results window (**Simple** Random Sampling).

3.4.3.3 Calculation details

Some of the equations used for the calculation of the biomass of fallow lands are based on the diameter and the height of the tree while others are based on the diameter only (see [Appendix 5](#) for details).

3.4.3.4 Results

This function calculates the total biomass (metric ton) of fallow lands. It also gives the biomass per hectare (metric ton/ha).

3.4.3.5 Error and warning messages

If you enter a diameter that is not within the range of the equation, a warning window will appear to ask if this is a valid entry. If this entry is in fact valid data, click on [OK] to continue using it in the calculation. If it is an error, click on [Cancel] to stop the calculation. You can either change or erase the data if it is invalid.

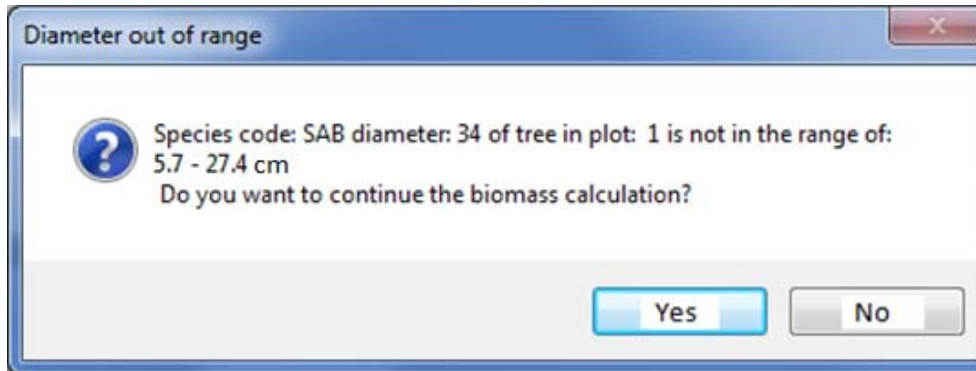


Figure 18. Example of a warning window (Diameter outside of the range).

If data is missing or if there is an error in the way data was entered, a warning window will appear (Figure 19).

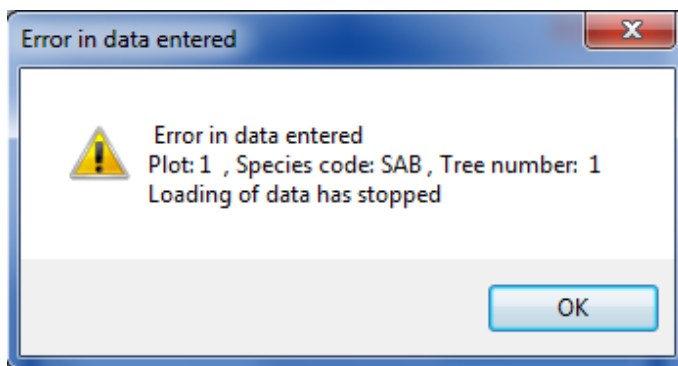


Figure 19. Example of an error window (Error in data entered).

If you enter a species code that is not in the application database and have not customized an equation for it, a warning message will appear (Figure 20). If you click on [Yes], the [Input of New Equations](#) window will appear and allow you to customize this species code. If you click on [No], an error window will appear to indicate the data is invalid and cannot be used for the calculation (Figure 21). The calculation will stop. You can change the data associated with the species code.

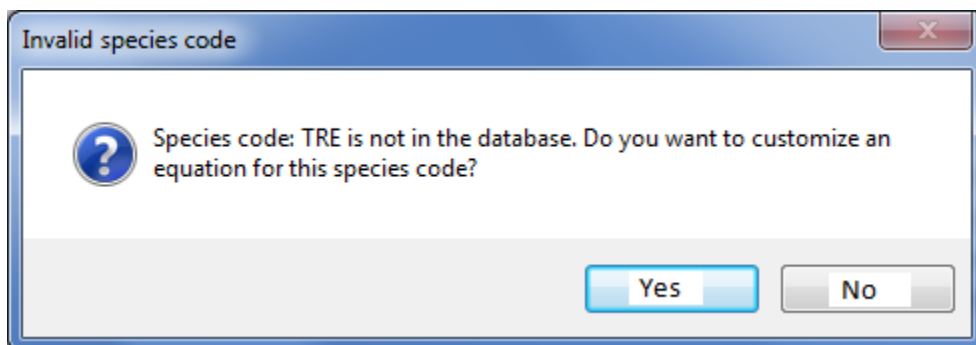


Figure 20. Example of warning window (Invalid species code).

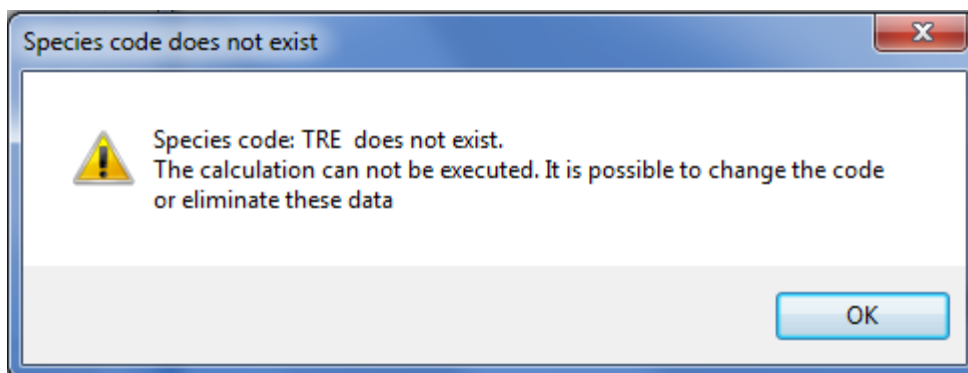


Figure 21. Example of an error window (Species code does not exist).

The following error window will appear if the wrong measurement type (DRC/D15/DBH) is entered for the equation (Figure 22). This message will also appear if the data entered for the height parameter is invalid (e.g. negative value).

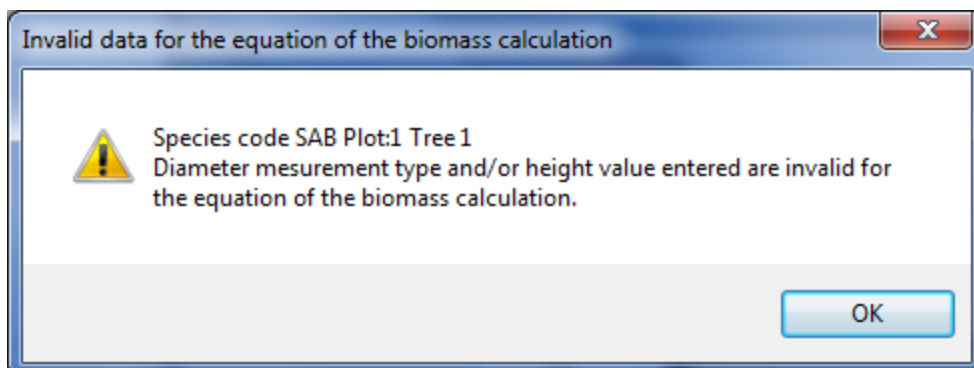


Figure 22. Example of an error window (Invalid data for the equation of the biomass calculation).

3.4.3.6 *Input of New Equations window*

This function allows you to modify the equation of a species already defined in ENBIOCAL, to enter a new species and its equation, or to define a new equation for a species in the database (Figure 23).

To assign a new biomass calculation equation to the species, choose from the list of 19 predefined equation forms (Figure 23). The first 12 equations are based on diameter only while the last seven equations are based on plant diameter and height. You must enter a value for each parameter used by the equation (at the bottom of the window, just above the [\[Delete previous customizations\]](#) button).

You can save the customized equations in a permanent file by clicking on [OK] when asked if you wish to export file.

ENBIOCAL - Input of New Equations

Species code

Help

Equations based on the diameter

- 1) $\log_{10} \text{Biom.} = a + b \times \log_{10} \text{diam.}$
- 2) $\log_{10} \text{Biom.} = a + b \times \log_{10} \text{diam.}^c$
- 3) $\log_{100} \text{Biom.} = a + b \times \log_{10} \text{diam.}$
- 4) $\ln \text{Biom.} = a + b \times \ln \text{diam.}$
- 5) $\ln \text{Biom.} = \ln(a) + b \times \ln \text{diam.}$
- 6) $\ln \text{Biom.} = a + b \times \text{diam.} + c \times \ln \text{diam.}^c$
- 7) $\ln \text{Biom.} = a + b \times \ln \text{diam.} + c \times (d + e \times \ln \text{diam.})$
- 8) $\text{Biom.} = a \times \text{diam.}^b$
- 9) $\text{Biom.} = a + b \times \text{diam.} + c \times (\text{diam.}^d)$
- 10) $\text{Biom.} = a + b \times \text{diam.} + c \times (\text{diam.}^2) + d \times (\text{diam.}^3)$
- 11) $\text{Biom.} = a \times (\exp(b + c \times \ln \text{diam.} + d \times \text{diam.}))$
- 12) $\text{Biom.} = a + ((b \times \text{diam.}^c) / (\text{diam.}^c + d))$

Eq. 1 (selected), Eq. 2, Eq. 3, Eq. 4, Eq. 5, Eq. 6, Eq. 7, Eq. 8, Eq. 9, Eq. 10, Eq. 11, Eq. 12

Eq. 13, Eq. 14, Eq. 15, Eq. 16, Eq. 17, Eq. 18, Eq. 19

Equations based on the diameter and height

- 13) $\log_{10} \text{Biom.} = a + b \times \log_{10} \left(\frac{\pi}{2} \times (\text{diam.}/2)^2 \times \text{height} \right)$
- 14) $\log_{10} \text{Biom.} = a + b \times \log_{10} (\text{diam.}^2 \times \text{height})$
- 15) $\ln \text{Biom.} = a + b \times \ln \text{diam.} + c \times \ln \text{height}$
- 16) $\text{Biom.} = a \times (\text{diam.}^2 \times \text{height})$
- 17) $\text{Biom.} = a \times \text{diam.}^b \times \text{height}^c$
- 18) $\text{Biom.} = a + b \times \text{diam.} + c \times \text{height} + d \times (\text{diam.}^2 \times \text{height})$
- 19) $\text{Biom.} = a + b \times \text{diam.} + c \times \text{diam.}^2 + d \times (\text{diam.} \times \text{height})$

Parameters a: b:

Units

Diameter units: ☐ mm ☒ cm

Height units: ☐ cm ☒ m

Biomass units: ☐ g ☒ kg

Delete Previous Customizations Save and Add Another Species Save and Finish Close

Figure 23. Input of New Equations window.

Window entries:

- **Species code:** Enter the species code associated with the full name of the species. It is suggested to use a code of three or four letters (see [Table 2](#)).
- **Parameters:** You must enter values for the number of parameters specific to each equation.
- **Diameter units:** You must select the diameter unit with which the equation was developed.
 - mm (millimetre)
 - cm (centimetre)
- **Height units:** You must select the height unit with which the equation was developed.
 - cm (centimetre)
 - m (metre)
- **Biomass units:** you must select the unit in which the equation will estimate biomass.
 - g (gram)
 - kg (kilogram)
- **[Delete Previous Customizations]:** Click on this button to delete all previously customized species saved in the background of the Fallow Lands Information window. This function resets all customized equations to the default equations established by ENBIOCAL.
- **[Save and Add Another]:** Click on this button to save the information entered for the customized species and to immediately create another equation.

- **[Save and Finish]:** Click on this button to save the current and all previously customized species. A window will appear to ask if you wish to export the customized equations. If you click on **[OK]** when asked to export the file, you must enter a name for it and choose a location on your computer where you wish to save the customized species. If you click on **[Cancel]**, the customized species will only be used for the present calculation and will not be saved. It will not be possible to use them again.
- **[Close]:** Click on this button to close the window when you are done customizing species. The same procedure as **[Save and Finish]** applies.

3.4.3.7 Importing equations

This function allows you to select a file that contains previously saved customized species equations instead of manually entering them each time (Figure 23). We recommend that you create this file using the application button **[Input of New Equations]** and that you click on **[OK]** when asked if you wish to export the file to save the customized equations on your computer. You may also create or edit this file manually, but it is important that the data be kept in the following order: species code, ID equation number, diameter unit, height unit, output biomass unit). You may use a space, a tab, a comma or a semicolon to separate the parameters.

Example of a file containing customized equations with parameters:

SpeciesCode	EqID	D unit	H unit	B unit	a	b	c	d
ALb	1	cm	m	Kg	1	0	9	
Col	18	cm	m	Kg	1	2	3	3
Can	1	cm	m	Kg	3	3	1	
hol	19	cm	m	Kg	1	2	8	7

Appendix 1. Information about the sample sites and plantations.

Municipality, province	Boisbriand, QC	Beaverlodge, AB	Guelph, ON	Saint-Augustin-de-Desmaures, QC	Saint-Paul-de-la-Croix, QC	Cacouna, QC
Latitude	45°37'48.5"N	55°11'44.62"N	43°32'28"N	46°43'37.8"N	47°57'49.4"N	47°58'32.9"N
Longitude	73°53'42.0"W	119°25'13.81"W	80°12'32"W	71°29'12.0"W	69°07'18.0"W	69°26'09.5"W
Altitude	122 m	716 m	325 m	2 m	207 m	32 m
Site code	BB	BL	GU	SA	SP	CA
Plantation year	2011	2010	2006	2010	2012	2012
Stem age at sampling (years)	3	4	2	2	2	2
Cutback? Harvest year?	Yes (end of 1 st year)	Yes (end of 1 st year)	Yes (end of 1 st year & 2009 and 2012)	No (cut in 2012)	Yes (end of 1 st year)	Yes (end of 1 st year)
Plantation density	16,000 plants ha ⁻¹	15,000 plants ha ⁻¹	16,000 plants ha ⁻¹	5164 plants ha ⁻¹	10,101 plants ha ⁻¹	10,101 plants ha ⁻¹
Spacing	Single row (0.34 m w.row × 1.8m b.row)	Double row (0.6 m w row × 0.6 m b.row × 2.2 m b.dbl.row)	Double row (0.5 m w.row × 0.75 m b.row × 1.5 m b.dbl.row)	Single row (1.0 m w.row × 1.8 m b.row, with some exceptions)	Single row (0.55 m w.row × 1.8 m b.row)	Single row (0.55 m w.row × 1.8 m b.row)
Type of plantation	Willow clones	Willow clones	1 willow clones and 1 hybrid poplars	Hybrid poplars	Hybrid poplars	Hybrid poplars
Clones sampled (nb. of plants)	SX61 (10), SX64 (10), SX67 (10), 5027 (10)	India (10), Tully Champion (10)	Willow: SX67 (10) Hybrid poplar: 2293-19 (10)	3478 (8), 3729 (6), 102377 (24), 102380 (6), 915311 (5), 915318 (6), 915508 (6)	3478 (6), 3729 (6), 915311 (6), 916401 (6)	3478 (8), 3729 (9), 102380 (9), 102890 (8), 915311 (6), 916401 (6)

* For spacing: w.row indicates distance between plants within the row; b.row, indicates distance between single rows or between rows in a bed (for double rows); b.dbl.row, indicates distance between double rows, from bed centre to bed centre.
Sampling took place in autumn 2014.

Appendix 2. Stem characteristics of clones sampled for the development of allometric equations.

	Clone	Parentage*	Site**	DBH range (mm) (stems)	H range (cm) (stems)
Willow clones	5027	<i>Salix viminalis</i>	BB	3-27	113-475
	SX61	<i>S. sachalinensis</i>	BB	10-38	324-649
	SX64	<i>S. miyabeana</i>	BB	10-38	278-625
	SX67	<i>S. miyabeana</i>	BB	3-40	181-660
			GU	1-16	130-410
	India	<i>S. dasyclados</i>	BL	10-23	49-423
	Tully	<i>S. viminalis</i> × <i>S. miyabeana</i>	BL	11-22	79-399
Hybrid poplars	3478	N×M	CA	5-17	60-310
			SP	6-21	101-349
			SA	13-60	122-631
	3729	N×M	CA	11-24	66-349
			SP	6-21	44-372
			SA	6-48	109-654
	102377	M×N	SA	9-45	112-705
	102380	M×N	CA	7-20	79-325
			SA	12-41	108-714
	102890	M×N	CA	11-20	51-309
	750301	M×T	CA	17-25	62-403
	915311	M×B	CA	9-22	72-313
			SP	8-20	75-356
			SA	8-30	131-527
	915318	M×B	SA	12-47	143-677
	915508	DN×M	SA	15-39	125-579
	916401	DN×M	CA	23-24	75-370
			SP	11-25	105-350
	2293-19	T×N	GU	13-56	154-731

*Codes for hybrid poplars: N = *Populus nigra*; M = *P. maximowiczii*; T = *P. trichocarpa*; B = *P. balsamifera*; DN = *P. deltoides* × *P. nigra*.

**Codes for sites: GU = Guelph (ON), BB = Boisbriand (QC), BL = Beaverlodge (AB), CA = Cacouna (QC), SA = Saint-Augustin-de-Desmaures (QC), SP = Saint-Paul-de-la-Croix (QC)

Appendix 3. Equations selected for willow clones and species.

Selected model – equation(s)	n.obs.	RMSE%	R ²	ME%
<i>Clones</i>				
<i>Salix viminalis</i> 5027***	10	13.78	0.9634	-3.40
1) Individual stem model: $DryW_{stem} = 1.0652 \times \exp(-5.2763 + 0.9248 \times \ln(D15^2 \times H))$				
2) Ratio model: $y' = 2.3693 - 0.3588 \times Nbstems - 0.2221 \times D15_{2Dmax} + 0.0160 \times H_{2Dmax}$				
<i>Salix sachalinensis</i> SX61***	10	6.36	0.9949	0.56
1) Individual stem model: $DryW_{stem} = 1.0094 \times \exp(-6.5944 + 0.9974 \times \ln(D15^2 \times H))$				
2) Ratio model: $y' = 2.5079 - 0.8237 \times Nbstems - 0.0221 \times D15_{3Dmax} + 0.0063 \times H_{3Dmax}$				
<i>Salix miyabeana</i> SX64	10	6.35	0.9401	-3.40
$DryW_{tree} = [94.05264 + 0.00362 \times (D15_{4Dmax}^2 \times H_{4Dmax})] \times \ln(Nbstems + 1)$				
<i>Salix miyabeana</i> SX67	20	21.98	0.8565	-20.77
$DryW_{tree} = 3365.3397 \times (D15_{2Dmax})^{2.4646} \times (H_{2Dmax})^{-1.4839} \times \ln(Nbstems + 1)$				
<i>Salix dasyclados</i>, India	10	6.70	0.9938	-0.43
$DryW_{tree} = 0.0066 \times (D15_{4Dmax})^{0.7290} \times (H_{4Dmax})^{1.6073} \times \ln(Nbstems + 1)$				
<i>Salix viminalis</i> × <i>Salix miyabeana</i>, Tully Champion	10	9.32	0.9792	-4.10
$DryW_{tree} = 2.0350 \times (D15_{3Dmax})^{2.2138} \times (H_{3Dmax})^{-0.1781} \times \ln(Nbstems + 1)$				

<i>Species</i>				
<i>Salix miyabeana</i> (SX64+SX67)	30	21.57	0.8944	-24.05
$DryW_{tree} = 1977.8989 \times (D15_{2Dmax})^{2.4233} \times (H_{2Dmax})^{-1.3784} \times \ln(Nbstems + 1)$				

***Computations steps for models combining individual stem equations and ratios:

- 1) For each selected stem, calculate stem biomass using

$$DryW_{stem} = CF \times e^{a+b \times \ln((D15)^2 \times H)}.$$

- 2) Sum individual stem biomass for the selected stems (this value will be used in the last step of the computation).

- 3) For the plant, calculate y' using the ratio model reported in the table above:

$$y' = a + b \times D15_{nDmax} + c \times H_{nDmax} + d \times Nbstems.$$

- 4) Convert y' to $Ratio_transf_{nDmax}$ using the following model:

$$Ratio_transf_{nDmax} = expit(y') = \frac{e^{y'}}{1+e^{y'}}.$$

- 5) Calculate $Ratio_{nDmax}$ using the nobs parameter reported in the table above:

$$Ratio_{nDmax} = transf^{-1}(Ratio_transf_{nDmax}) = \frac{(Ratio_transf_{nDmax} \times nobs - 0.5)}{nobs - 1}.$$

- 6) Calculate plant weight by dividing the sum of the biomass of the selected stem by $Ratio_{nDmax}$:

$$DryW_{tree} = \frac{\sum_1^{n_{Dmax}} DryW_{stem}}{Ratio_{nDmax}}.$$

Appendix 4. Equations selected for hybrid poplar clones and groups of clones.

Selected model – equation(s)	n.obs.	RMSE%	R ²	ME%
<i>Clones</i>				
<i>Populus nigra</i> x <i>Populus maximowiczii</i> (3478)	19	10.91	0.9916	-9.48
$DryW_{tree} = 0.0485 \times (D15_{2Dmax})^{1.1950} \times (H_{2Dmax})^{0.9362} \times \ln(Nbstems + 1)$				
<i>Populus nigra</i> x <i>Populus maximowiczii</i> (3729)	21	24.99	0.9512	-0.28
$DryW_{tree} = 1.0562 \times (D15_{2Dmax})^{2.5382} \times (H_{2Dmax})^{-0.3548} \times \ln(Nbstems + 1)$				
<i>Populus maximowiczii</i> x <i>Populus nigra</i> (102377)***	24	6.57	0.9269	-0.30
1) Individual stem model:				
$DryW_{stem} = 1.0143 \times \exp(-4.8874 + 0.8724 \times \ln(D15^2 \times H))$				
2) Ratio model:				
$y' = 1.5345 - 0.0955 \times Nbstems + 0.0797 \times D15_{4Dmax} - 0.0021 \times H_{4Dmax}$				
<i>Populus maximowiczii</i> x <i>Populus nigra</i> (102380)	14	6.22	0.9967	-15.24
$DryW_{tree} = 0.0888 \times (D15_{4Dmax})^{1.0111} \times (H_{4Dmax})^{0.9934} \times \ln(Nbstems + 1)$				
<i>Populus maximowiczii</i> x <i>Populus balsamifera</i> (915311)	17	11.43	0.9779	-2.69
$DryW_{tree} = [94.0522 + 0.0026 \times (D15^2_{3Dmax} \times H_{3Dmax})] \times \ln(Nbstems + 1)$				
<i>Populus deltoides</i> x <i>Populus maximowiczii</i> (916401)	12	11.05	0.9436	-0.12
$DryW_{tree} = 0.0055 \times (D15_{3Dmax})^{0.8110} \times (H_{3Dmax})^{1.6333} \times \ln(Nbstems + 1)$				
<i>Populus trichocarpa</i> x <i>Populus nigra</i> 2293-19***	10	13.75	0.9532	-0.56
1) Individual stem model:				
$DryW_{stem} = 1.0095 \times \exp(-3.8801 + 0.8233 \times \ln(D15^2 \times H))$				
2) Ratio model:				

Selected model – equation(s)	n.obs.	RMSE%	R ²	ME%
$y' = 5.0406 - 0.9274 \times Nbstems + 0.1257 \times D15_{Dmax} - 0.0140 \times H_{Dmax}$				
<i>Groups of clones</i>				
N×M [<i>Populus nigra</i> × <i>Populus maximowiczii</i>] $DryW_{tree} = 0.0648 \times (D15_{2Dmax})^{1.2975} \times (H_{2Dmax})^{0.8281} \times \ln(Nbstems + 1)$	40	22.11	0.9642	-6.90
M×N*** [<i>Populus maximowiczii</i> × <i>Populus nigra</i>] 1) Individual stem model: $DryW_{stem} = 1.0151 \times \exp(-4.9661 + 0.8755 \times \ln(D15^2 \times H))$ 2) Ratio model: $y' = 2.8218 - 0.1393 \times Nbstems + 0.0025 \times D15_{4Dmax} + 0.0001 \times H_{4Dmax}$	46	9.52	0.9828	-0.50
M×B*** [<i>Populus maximowiczii</i> × <i>Populus balsamifera</i>] 1) Individual stem model: $DryW_{stem} = 1.0203 \times \exp(-4.4792 + 0.8422 \times \ln(D15^2 \times H))$ 2) Ratio model: $y' = 3.5726 - 0.1848 \times Nbstems - 0.0237 \times D15_{4Dmax} + 0.0025 \times H_{4Dmax}$	23	8.72	0.9904	-2.06
DN×M [(<i>Populus deltoides</i> × <i>Populus nigra</i>) × <i>Populus maximowiczii</i>] $DryW_{tree} = 0.5881 \times (D15_{3Dmax})^{2.3639} \times (H_{3Dmax})^{-0.0630} \times \ln(Nbstems + 1)$	18	9.10	0.9920	-7.95

***Computation steps for models combining individual stem equations and ratios:

- 1) For each selected stem, calculate stem biomass using

$$DryW_{stem} = CF \times e^{a+b \times \ln((D15)^2 \times H)}.$$

- 2) Sum individual stem biomass for the selected stems (this value will be used in the last step of the computation).

- 3) For the plant, calculate y' using the ratio model reported in the table above:

$$y' = a + b \times D15_{nDmax} + c \times H_{nDmax} + d \times Nbstems.$$

Selected model – equation(s)	n.obs.	RMSE%	R ²	ME%
4) Convert y' to $Ratio_transf_{nDmax}$ using the following model:				
$Ratio_transf_{nDmax} = expit(y') = \frac{e^{y'}}{1+e^{y'}}.$				
5) Calculate $Ratio_{nDmax}$, using the nobs parameter reported in the table above:				
$Ratio_{nDmax} = transf^{-1}(Ratio_transf_{nDmax}) = \frac{(Ratio_transf_{nDmax} \times nobs - 0.5)}{nobs - 1}.$				
6) Calculate plant weight by dividing the sum of the biomass of the selected stem by $Ratio_{nDmax}$:				
$DryW_{tree} = \frac{\sum_1^{n_{Dmax}} DryW_{stem}}{Ratio_{nDmax}}.$				

Appendix 5. Species list and equations.

Unique ID	Instructions	Diameter size used	Species code	Diameter range	Measurement units	Equation	Tree part	Reference
1	#2 - #1	All sizes	SAB	5.7-27.4 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.002258 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
2	#2 - #1	All sizes	SAB	5.7-27.4 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.018308 \times (diam.^2 \times height)$	Whole tree (AG)**	Alemdag 1983
3	#3	All sizes	ERP	0.6-7.5 cm (DBH)	Biom. (g), diam. (cm)	$\ln Biom. = 4.68 + 2.38 \times \ln diam.$	AG leafless biomass	Hocker and Early 1983
4	#5 - #4	All sizes	ERR	5.7-45.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000499 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
5	#5 - #4	All sizes	ERR	5.7-45.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.02172 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
6	#7 - #6	All sizes	ERA	5.3-45.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000394 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
7	#7 - #6	All sizes	ERA	5.3-45.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.022011 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
8	#9 - #8	All sizes	ERS	5.1-57.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000526 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
9	#9 - #8	All sizes	ERS	5.1-57.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.026724 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
63	#63	All sizes	AUL	11-68 mm (DBH)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.11644 \times diam.^{2.17022} \times height^{0.30955}$	AG leafless biomass	THIS STUDY
62	#62	All sizes	AME	8-30 mm (DRC)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.0005904 \times diam.^{1.5485591} \times height^{1.5153692}$	AG leafless biomass	THIS STUDY
11	#12 - #11	SMALL, check DBH range	BOJ	2-12 cm (DBH)	Biom. (g), diam. (cm), height (cm)	$\log_{10} Biom. = 0.682 + 0.455 \times \log_{10} \left(\frac{\pi}{2} \times (diam./2)^2 \times height \right)$	Foliage and twigs	Fatemi et al. 2011
12	#12 - #11	SMALL, check DBH range	BOJ	2-12 cm (DBH)	Biom. (g), diam. (cm), height (cm)	$\log_{10} Biom. = 0.0366 + 0.931 \times \log_{10} \left(\frac{\pi}{2} \times (diam./2)^2 \times height \right)$	Whole tree (AG)	Fatemi et al. 2011
13	#14 - #13	LARGE, check DBH range	BOJ	6.2-70.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000343 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
14	#14 - #13	LARGE, check DBH range	BOJ	6.2-70.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.024822 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
15	#16 - #15	LARGE, check DBH range	BOP	5.4-32.7 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000859 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
16	#16 - #15	LARGE, check DBH range	BOP	5.4-32.7 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.023468 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984

64	#64	SMALL, check DBH range	BOP	15-63 mm (DBH)	Biom. (g), diam. (mm), height (cm)	$Biom. = 16.134 \times diam.^{2.4408} \times height^{-0.6207}$	AG leafless biomass	THIS STUDY
17	#17	All sizes	BOG	1-23 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$\ln Biom. = -2.3174 + 2.0483 \times \ln diam. + 0.3728 \times \ln height$	Whole tree (AG)*	Ker 1980
70	#70	All sizes	CO, COC, CON, SAC	11- 45 mm (DRC)	Biom. (g), diam. (mm), height (cm)	$Biom. = 412.93011 - 58.33215 \times diam. + 0.85505 \times (diam.^2) + 0.12816 \times (diam.^3)$	AG leafless biomass	THIS STUDY
19	#20 - #19	All sizes	HEG	6.1-46.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000356 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
20	#20 - #19	All sizes	HEG	6.1-46.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.024903 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
21	#21	SMALL, if DRC use this	FRA	0.5-6.14 cm (DRC)	Biom. (g), diam. (cm), height (m)	$\log_{10} Biom. = 1.3518 + 0.9923 \times \log_{10}(diam.^2 \times height)$	Whole tree (AG)	Williams and McClenahan 1984
22	#23 - #22	LARGE, if DBH use this	FRA	5.9-53.7 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000328 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
23	#23 - #22	LARGE, if DBH use this	FRA	5.9-53.7 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.023684 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
24	# 25 - #24	All sizes	EPB	6.3-35.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.001657 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
25	# 25 - #24	All sizes	EPB	6.3-35.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.018219 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983
26	#26 + #27	SMALL, if DRC use this	EPN	5-21 mm (DRC)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.1533 \times diam.^b \times height^c$	Branches	Wagner and Ter-Mikaelian 1999
27	#26 + #27	SMALL, if DRC use this	EPN	5-21 mm (DRC)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.0194 \times diam.^b \times height^c$	Stem	Wagner and Ter-Mikaelian 1999
28	#29 - #28	LARGE, if DBH use this	EPN	5.2-22.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.003031 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
29	#29 - #28	LARGE, if DBH use this	EPN	5.2-22.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.02267 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983
30	#30 + #31	SMALL, if DRC use this	PIG	8-39 mm (DRC)	Biom. (g), diam. (mm)	$Biom. = 0.0072 \times diam.^b$	Branches	Wagner and Ter-Mikaelian 1999
31	#30 + #31	SMALL, if DRC use this	PIG	8-39 mm (DRC)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.0098 \times diam.^b \times height^c$	Stem	Wagner and Ter-Mikaelian 1999
32	#33 - #32	LARGE, if DBH use this	PIG	8.8-26.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.001042 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
33	#33 - #32	LARGE, if DBH use this	PIG	8.8-26.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.018994 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983

34	#34 + #35	SMALL, if DRC use this	PIR	5-21 mm (DRC)	Biom. (g), diam. (mm)	$Biom. = 0.0037 \times diam.^{2.9005}$	Branches	Wagner and Ter-Mikaelian 1999
35	#34 + #35	SMALL, if DRC use this	PIR	5-21 mm (DRC)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.0215 \times diam.^{1.6522} \times height^{0.6531}$	Stem	Wagner and Ter-Mikaelian 1999
36	#37 - #36	LARGE, if DBH use this	PIR	5.4-55.1 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.001048 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
37	#37 - #36	LARGE, if DBH use this	PIR	5.4-55.1 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.017147 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983
38	#39 - #38	LARGE, check DBH range	PEB	6.6-53.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.018505 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
39	#39 - #38	LARGE, check DBH range	PEB	6.6-53.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000677 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
65	#65	SMALL, check DBH range	PEB	12-76 mm (DBH)	Biom. (g), diam. (mm), height (cm)	$Biom. = 3.273 \cdot 10^{-7} \times diam.^{8.681} \times height^{3.097}$	AG leafless biomass	THIS STUDY
40	#40	SMALL, if DRC use this	PEG	0.68-7.49 cm (DRC)	Biom. (g), diam. (cm), height (m)	$\log_{10} Biom. = 1.2575 + 0.9326 \times \log_{10}(diam.^2 \times height)$	AG leafless biomass	Williams and McClenahan 1984
41	#42 - #41	LARGE, if DBH use this	PEG	5.4-39.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000379 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
42	#42 - #41	LARGE, if DBH use this	PEG	5.4-39.2 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.018577 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
43	#44 - #43	LARGE, check DBH range	PET	5.2-43.5 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.00051 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
44	#44 - #43	LARGE, check DBH range	PET	5.2-43.5 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.020785 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
66	#66	SMALL, check DBH range	PET	13-57 mm (DBH)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.34905 \times diam.^{2.22387} \times height^{0.06639}$	AG leafless biomass	THIS STUDY
45	#46 - #45	LARGE, check DBH range	PRP	2-12 cm (DBH)	Biom. (g), diam. (cm), height (cm)	$\log_{10} Biom. = 0.753 + 0.739 \times \log_{10} \left(\frac{\pi}{2} \times (diam./2)^2 \times height \right)$	Foliage and twigs	Fatemi et al. 2011
46	#46 - #45	LARGE, check DBH range	PRP	2-12 cm (DBH)	Biom. (g), diam. (cm), height (cm)	$\log_{10} Biom. = 0.187 + 0.899 \times \log_{10} \left(\frac{\pi}{2} \times (diam./2)^2 \times height \right)$	Whole tree (AG)	Fatemi et al. 2011
47	#47	SMALL, if DRC use this	CET	0.37-6.83 cm (DRC)	Biom. (g), diam. (cm), height (m)	$\log_{10} Biom. = 1.2138 + 1.0748 \times \log_{10}(diam.^2 \times height)$	AG leafless biomass	Williams and McClenahan 1984
48	#49 - #48	LARGE, if DBH use this	CET	6.4-49.6 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000275 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
49	#49 - #48	LARGE, if DBH use this	CET	6.4-49.6 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.022124 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984

67	#67	SMALL, check DBH range (use for PRP and PRV when DBH <4.4 cm)	CER	15-44 mm (DBH)	Biom. (g), diam. (mm), height (cm)	$Biom. = -1.56 \cdot 10^3 + 92.69 \times diam. - 2.473 \times diam.^2 + 0.2362 \times (diam. \times height)$	AG leafless biomass	THIS STUDY
50	#50 + #51	BIG, check DBH range	PRV	2.5-7.62 cm (DBH)	Biom. (g), diam. (cm)	$\log_{10} Biom. = 2.554 + 1.2191 \times \log_{10} diam.$	Branches	Ribe 1973
51	#50 + #51	BIG, check DBH range	PRV	2.5-7.62 cm (DBH)	Biom. (g), diam. (cm)	$\log_{10} Biom. = 2.876 + 2.0038 \times \log_{10} diam.$	Stem	Ribe 1973
52	#53 - #52	SMALL, if DRC use this	CHR	0.22-3.99 cm (DRC)	Biom. (g), diam. (cm)	$Biom. = 11.694 \times diam.^{2.198}$	Foliage and twigs	Telfer 1969
53	#53 - #52	SMALL, if DRC use this	CHR	0.22-3.99 cm (DRC)	Biom. (g), diam. (cm)	$Biom. = 44.726 \times diam.^{2.649}$	Whole tree (AG)	Telfer 1969
54	#55 - #54	BIG, if DBH use this	CHR	5.5-55.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.000669 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
55	#55 - #54	BIG, if DBH use this	CHR	5.5-55.3 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.02971 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
68	#68	All sizes (range limited)	SAL	8-46 mm (DBH)	Biom. (g), diam. (mm), height (cm)	$Biom. = 0.005941 \times diam.^{1.233489} \times height^{1.346887}$	AG leafless biomass	THIS STUDY
69	#69	All sizes (range limited)	SOA	8-35 mm (DBH)	Biom. (g), diam. (mm), height (cm)	$Biom. = 13.4382 \times diam.^{2.0951} \times height^{-0.4311}$	AG leafless biomass	THIS STUDY
56	#56	SMALL, if D15(!) use this	THO	0.3-5.1 cm (D15)	Biom. (g), diam. (cm)	$Biom. = 30.8 \times diam.^{2.244}$	AG leafless biomass	Rousopoulos and Loomis 1979
57	#58 - #57	LARGE, if DBH use this	THO	5.1-38.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.001766 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
58	#58 - #57	LARGE, if DBH use this	THO	5.1-38.8 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.014242 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983
59	#60 - #59	LARGE, if DBH use this	PRU	5.3-51.4 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.00132 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
60	#60 - #59	LARGE, if DBH use this	PRU	5.3-51.4 cm (DBH)	Biom. (kg), diam. (cm), height (m)	$Biom. = 0.019949 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983
61	#61	SMALL, if DRC use this	TSH	1-29 mm (DRC)	Biom. (g), diam. (mm)	$\ln Biom. = -3.0539 + 2.789 \times \ln diam.$	AG leafless biomass	Alaback 1986

* Equations for this species were only available for aboveground biomass including leaves.

**AG = Aboveground.

Appendix 6. Reference and location of each study.

Reference	Full reference	Location
Alaback 1986	Alaback, P. B. 1986. Biomass regression equations for understory plants in coastal Alaska: effects of species and sampling design on estimates. <i>Northwest Science</i> 60:90-103.	Alaska, USA
Alemdag 1983	Alemdag, S. 1983. Mass equation and merchantability factors for Ontario softwoods. Information Report PI-X-23, Petawawa National Forestry Institute, Canadian Forestry Service, Environment Canada.	Ontario, CANADA
Alemdag 1984	Alemdag, I. 1984. Total tree and merchantable stem biomass equations for Ontario hardwoods. Information Report PI-X-46, Petawawa National Forestry Institute, Canadian Forestry Service, Agriculture Canada.	Ontario, CANADA
Fatemi et al. 2011	Fatemi, F. R., R. D. Yanai, S. P. Hamburg, M. A. Vadeboncoeur, M. A. Arthur, R. D. Briggs and C. R. Levine. 2011. Allometric equations for young northern hardwoods: the importance of age-specific equations for estimating aboveground biomass. <i>Canadian Journal of Forest Research</i> 41:881-891.	New Hampshire, USA
Hocker and Early 1983*	Hocker, H. W. and Early, D. J. 1983. Biomass and leaf area equations for northern forest species. Research Paper 102, Agricultural Experiment Station, University of New Hampshire.	New Hampshire, USA
Ker 1980*	Ker, M. 1980 Tree biomass equations for ten major species in Cumberland County, Nova Scotia. Information Report M-X-108, Maritimes Forest Research Centre, Canadian Forestry Service, Environment Canada.	Nova Scotia, CANADA
Ribe 1973*	Ribe, J. 1973. Puckerbrush weight tables. Miscellaneous Report 152. Life Sciences and Agriculture Experiment Station, University of Maine.	Maine, USA
Roussopoulos and Loomis 1979	Roussopoulos, P. J. and R. M. Loomis. 1979. Weights and dimensional properties of shrubs and small trees of the Great Lakes conifer forest. North Central Forest Experiment Station, USDA Forest Service.	Minnesota, USA
Telfer 1969	Telfer, E. S. 1969. Weight–diameter relationships for 22 woody plant species. <i>Canadian Journal of Botany</i> 47:1851-1855.	Maritime Provinces, CANADA
THIS STUDY		Quebec, CANADA
Wagner and Ter-Mikaelian 1999	Wagner, R. G. and M. T. Ter-Mikaelian. 1999. Comparison of biomass component equations for four species of northern coniferous tree seedlings. <i>Annals of Forest Science</i> 56:193-199.	Ontario, CANADA
Williams and McClenahan 1984	Williams, R. and J. McClenahan. 1984. Notes: Biomass prediction equations for seedlings, sprouts, and saplings of ten central hardwood species. <i>Forest Science</i> 30:523-527.	Ohio, USA

*Original study not found; equation cited in Jenkins, C. J., Chojnacky, D. C., Heath, L. S., Birdsey, R. A. 2004. Comprehensive database of diameter-based biomass regressions for North American tree species. General Technical Report NE-319, Northeastern Research Station, USDA Forest Service.