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

Version 1.0

User's guide

Carlo Lupi, Mildred Deldago, Laurent Lemay

and Guy R. Larocque[1]

Natural Resources Canada

Laurentian Forestry Centre

1055 du P.E.P.S., POB 10380, Stn. Ste-Foy

Quebec (QC) Canada G1V 4C7

[1] Corresponding author: Guy.Larocque@NRCan.gc.ca

Table of contents

1. Context

The application ENBIOCAL was developed as a tool to assist in the computation of the estimates in biomass contents in short rotation plantations or forested area (bushlands). In the case of a plantation, the application provides two sampling methods from which to choose. These sampling methods will be used to determine the minimum sample size (n) of a plantation. From this sample size, you will then be able to estimate the biomass content in the plantation with a desired precision. The strong point of this application is that it integrates both the sampling method and the computation of the sample size (n) for the calculation of the biomass content of a plantation. The application can also be used to calculate the biomass of forest lands (uncultivated).

With ENBIOCAL you can:

- Estimate required sample size (n) for accurate estimation of biomass in a plantation
- Compute the biomass in a plantation
- Compute the biomass of small-diameter woody species in bushlands
- Compute the area of a plantation/forested area, via GPS or other coordinates

1.1 Introduction

This user guide for the application ENBIOCAL has been divided into two sections; the first is a theory section in which the concepts used to develop the application are defined and the second is a detailed description of the windows and functions of the application. Related complementary information can be viewed in the appendixes.

2. Theory

2.1 Random Sampling

It is important that sampling be carried out randomly on the entire area of the studied population. This is why a random sampling method must be applied as a way of collecting representative data. We suggest two sampling methods that can be used to collect data which are simple random sampling or stratified random sampling.

2.1.1 Sampling methodology suggested

Random sampling is very important to ensure an unbiased and precise estimate. For maximum efficiency, you should sample without replacement, meaning that you avoid choosing an individual from a population more than once. The following methodologies are suggestions on how to proceed when sampling randomly.

- Given the required number of samples (n), the first methodology would be to assign a random number to each tree in a plantation, sort trees based on the assigned random number, and select the first (n) trees. For example, if you have 1000 trees in a plantation and you need to collect a representative sample (n) of 50 trees, using a spreadsheet (e.g. Microsoft Excel) you can assign a random number to each tree; then copy and paste random numbers as values and sort them in ascending order selecting the first 50

trees. If the plantation has 10 rows of 100 trees and that the first number drawn is 123, then the 23rd tree of the second row will be measured. The other 49 trees will be sampled in the same way using a different unique number.

- A second methodology using the same example of a 1000 tree plantation of ten 100-tree rows would be to first randomly choose a row and secondly choose a tree in 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 7 and 58, you would sample the 58th tree in the 7th row.
- A third methodology that could be considered as a random sampling method could be to apply a systematic grid on an aerial photo or map of the sampling area; then select random relative coordinates of the points in the grid and select the (n) points you need to sample. In a plantation you would measure the closest tree to that point and in an uncultivated land you could use the point as the center of the sample plot.
- A fourth methodology could be to use a GPS. With your GPS, delimit the boundaries of the sampling area and use either the GPS itself or a GIS to assign (n) random points. For an uncultivated land, each point will be the center of the sampled plot. For a plantation, you should sample the tree closest to the coordinate.

2.1.2 Simple Random Sampling method - PLANTATION:

This is a very basic sampling method and it is used for a population considered homogeneous. It is based on a selection procedure whereby every element in a population has an equal chance of being selected.

The following table illustrates the different species already considered in ENBIOCAL for sample size estimation. The application provides a mean dry leafless aboveground biomass (in grams) per plant and variance derived from our own sampling. Both of these values can be replaced with other mean biomass or variance values that could better represent your population.

Table 1. Clones available for the calculation of sample size

Populus deltoides x Populus nigra) x Populus maximowiczii
P.deltoides x P. nigra) x P. maximowiczii (916401)
Populus maximowiczii x Populus balsamifera
Populus maximowiczii x Populus balsamifera (915311)
Populus maximowiczii x Populus nigra
Populus maximowiczii x Populus nigra (102377)
Populus maximowiczii x Populus nigra (102380)
Populus nigra x Populus maximowiczii
Populus nigra x Populus maximowiczii(3478)
Populus nigra x Populus maximowiczii(3729)
Populus trichocarpa x Populus nigra (2293-19)
Salix dasyclados (India)
Salix miyabeana (SX64)
Salix miyabeana (SX67)

Salix miyabeana (SX64 + SX67)
Salix sachalinensis (SX61)
Salix viminalis (5027)
Salix viminalis x Salix miyabeana (Tully Champion)

2.1.3 Stratified Random Sampling - PLANTATION:

This method is used for a heterogeneous population which can be divided in different more or less homogenous strata. Each stratum is treated as a separate sub-population and sampled independently from the other strata, via Simple Random Sampling. Stratification can be based upon different variables, for example mortality rate, drainage capacity, slope of the terrain, position inside the plantation (border rows vs interior rows) or any other variable which you consider affects biomass production in your plantation. Once you have delimited and sampled your strata, the estimates 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, one stratum would be considered a homogenous area and thus the Simple Random Sampling method would apply.

A mean dry biomass and variance must be estimated for each stratum to enable the calculation of first, a sample size required for every stratum and second, the total sample size required for the estimate at the level of the population.

2.2 Measurements

For plantations, diameter measurements were taken at a height of 15 cm from the base of the stem itself and not 15 cm from the ground. A mark was drawn on the stem at 15 cm and the diameter was taken with small precision calipers (mm; e.g. digital calipers). Stem length (referred to as height in the equations) measurements were either taken with a measuring tape if it was possible (shorter plants) or with a measuring pole from the base of the plant.

For uncultivated land, depending on the species and plant size (See Appendix 4), tree diameters were either measured at breast height (DBH) or at root-collar/ground-level (DRC). Plant height was measured using common forestry instruments (e.g. Suunto height meter or measuring tape/pole).

2.3 Calculations:

We assume that all biomasses are given as aboveground, oven-dried, without the foliage.

2.3.1 Sample size

For the calculation of a representative sample size (n) in a plantation, an estimated mean plant biomass and variance is needed. In stratified random sampling, it is important that a mean plant biomass and variance be estimated for each stratum. We know this is somewhat an iterative concept because this information is needed to estimate the total biomass of the plantation. The suggested mean plant biomasses were developed by sampling different plantations at different site conditions (see Appendix 1). We strongly advice the user of the applications to provide their own estimates of mean plant biomass and variance (e.g. from pilot surveys or the literature).

Based on our preliminary sampling, the application provides built-in estimates of mean plant biomass and its variance for 5 groups of clones and 13 individual clones from which you may choose to calculate a representative sample size. See Appendix 1 for information on plantations from which the clones were sampled (age of plants, number of rotations, geographical location, etc.).

2.3.2 Biomass

For the calculation of the biomass of an uncultivated land, you must estimate a number of plots which will be sampled and represent the forested land. The application cannot suggest a sample size because this is most often a case by case situation (varying according to sample plot size, type and productivity of forested area, time since abandonment and other factors). However, the application has a list of 19 equation forms (the most common we found in the literature Table 2) that you may choose from to customize specific species that are present in your area, 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 provided for the customization of biomass computation

Equation forms based on diameter only:

1) $\log_{10} Biom. = a + b \times \log_{10} diam.$

2) $\log_{10} Biom. = a + b \times \log_{10} diam.^c$

3) $\log_{100} Biom. = a + b \times \log_{10} diam.$

4) $\ln Biom. = a + b \times \ln diam.$

5) $\ln Biom. = \ln(a) + b \times \ln diam.$

6) $\ln Biom. = a + b \times diam. + c \times \ln diam.^c$

7) $\ln Biom. = a + b \times \ln diam. + c \times (d + e \times \ln diam.)$

8) $Biom. = a \times diam.^b$

9) $Biom. = a + b \times diam. + c \times (diam.^d)$

10) $Biom. = a + b \times diam. + c \times (diam.^2) + d \times (diam.^3)$

11) $Biom. = a \times (\exp(b + c \times \ln diam. + d \times diam.))$

12) $Biom. = a + ((b \times diam.^c)/(diam.^c + d))$

Equation forms based on diameter and height:

13) $\log_{10} Biom. = a + b \times \log_{10} \left(\frac{\pi}{2} \times (diam./2)^2 \times height\right)$

14) $\log_{10} Biom. = a + b \times \log_{10}(diam.^2 \times height)$

15) $\ln Biom. = a + b \times \ln diam. + c \times \ln height$

16) $Biom. = a \times (diam.^2 \times height)$

17) $Biom. = a \times diam.^b \times height^c$

18) $Biom. = a + b \times diam. + c \times height + d \times (diam.^2 \times height)$

19) $Biom. = a + b \times diam. + c \times diam.^2 + d \times (diam. \times height)$

Table 3. Species names and associated three letter code

Scientific name	Name	Specie code
Abies balsamea	Balsam fir	SAB
Acer pensylvanicum	Striped maple	ERP
Acer rubrum	Red maple	ERR
Acer saccharinum	Silver maple	ERA
Acer saccharum	Sugar maple	ERS
Alnus spp.	Alder	AUL
Amelanchier spp.	Serviceberry	AME
Betula alleghaniensis	Yellow birch	BOJ
Betula papyrifera	White birch	BOP
Betula populifolia	Gray birch	BOG
Cornus sp.	Dogwood	CO
Cornus stolonifera	Dogwood	COR
Corylus cornuta	Beaked hazel	COC
Fagus grandifolia	American beech	HEG
Fraxinus americana	White ash	FRA
Picea glauca	White spruce	EPB
Picea mariana	Black Spruce	EPN
Pinus banksiana	Jack pine	PIG
Pinus resinosa	Red Pine	PIR
Populus balsamifera	Balsam Poplar	PEB
Populus grandidentata	Largetooth Aspen	PEG
Populus tremuloides	Trembling Aspen	PET
Prunus pensylvanica	Pin Cherry	PRP
Prunus serotina	Black Cherry	CET
Prunus spp.	Cherry	CER
Prunus virginiana	Chokecherry	PRV
Quercus rubra	Red oak	CHR
Salix spp.	Willow	SAL
Sambucus canadensis	Elder	SAC
Sorbus americana	American mountain ash	SOA
Thuja occidentalis	Eastern white cedar	THO
Tsuga canadensis	Eastern hemlock	PRU
Tsuga heterophylla	Western hemlock	TSH

Refer to Appendix 2 and Appendix 3 to see the predefined equations associated to the species and their size range.

Range adjustments were brought 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 one species. The division point of the two ranges established in the application is the upper limit of the smaller diameter equation. For example, in the case of a species measured at DBH, if in equation 1 the range is 5-15cm and in equation 2 the range is 10-70cm, equation 2 will only be used to calculate the biomass when the diameter is above 15cm (the upper limit of equation 1 which was developed on smaller trees and which is more adequate for them).

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

3. **Application Guide**

Each window includes a [Help] button: You can click on this icon for a short description of the use and functions of the window. For more detailed information refer to related sections in this guide (user's guide).
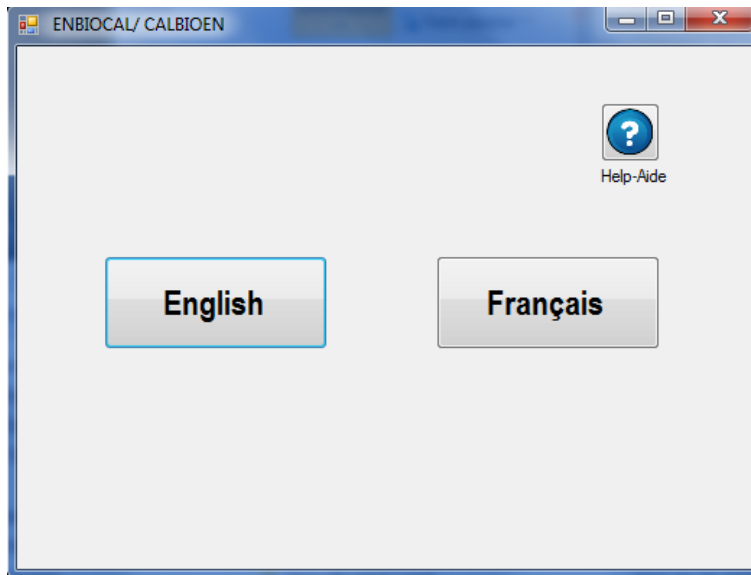

3.1 Input language of the application

Options: → [English/Anglais]

→ [Français/French]

Select the language in which the application will function.

Figure 1. ENBIOCAL window

3.2 Selection of computation type

→[English]

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

→ [Computation of Biomass]

3.2.1 Useful information
- Select the calculation needed.
- For a plantation you must first use the function which estimates minimum sample size (n) using one of the two sampling methods offered. Once you have sampled your plantation with the minimum sample size (n) suggested, you can use the computation of biomass function to estimate the total biomass of your plantation.
- Click on [Selection of sampling method and computation of sample size (n)] to determine the minimum sample size (n) required to estimate biomass in a plantation with a desired precision. This step is carried out before the computation of biomass and aims at estimating the sample size (n).
- Click on [Computation of Biomass] to enter your sampling data and calculate an estimate of biomass either for a plantation or forested area (bushland).

Figure 2. Calculation Option window
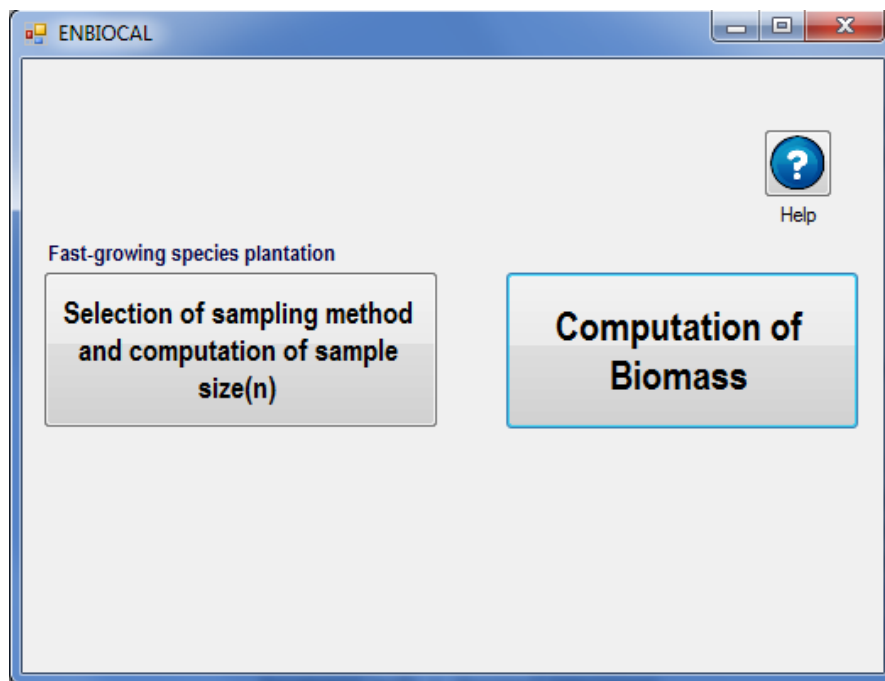
3.3 Selection of sampling method and computation of sample size (n):
→ [English]→ [Selection of sampling method and computation of sample size (n)]

Options: → [Simple Random Sampling]

→ [Stratified Random Sampling]

→ [Back] return to calculation Option Window

3.3.1 Useful information
- The estimation of sample size is only developed for a plantation.
- This is the first of two interrelated functions of this application.

- Choose the appropriate sampling method that applies to your population. You either have a rather homogenous population or a more heterogeneous population. In the case of a homogeneous population choose the [Simple Random Sampling method]. In the case of a heterogeneous population choose the [Stratified Random Sampling method].
- You will use this function to determine the minimum sample size (n) required to estimate biomass with a desired precision.
- In a plantation, diameters must be measured at 15 cm from the base of the stem (D15).
- In a forested area (bushland), make sure you know what equations use diameter measurements at breast height (DBH), at root-collar/ground-level (DRC) or at 15 cm form the base of the stem (D15). These equations requiring different variables will be used for the types of plants you are sampling.

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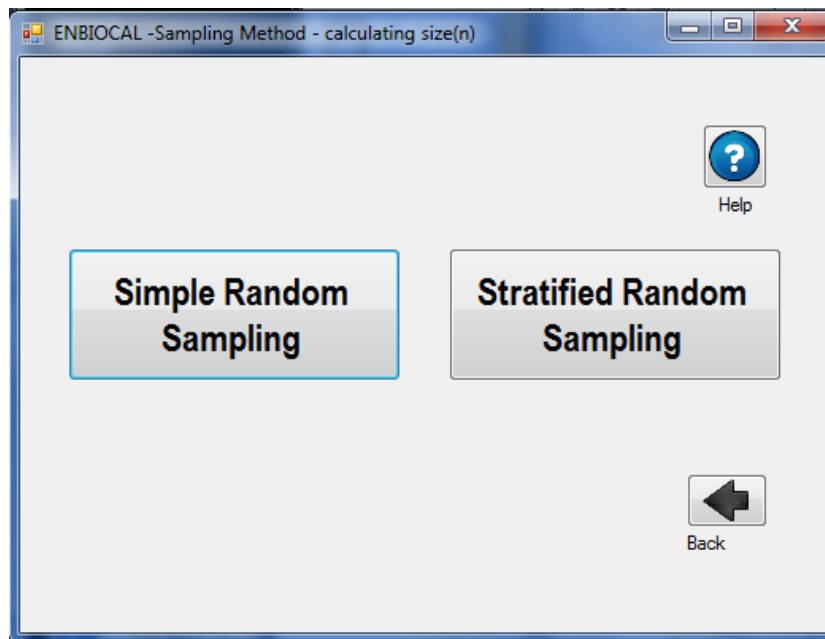

3.3.2 Simple Random Sampling
→ [English]→ [Selection of sampling method and computation of sample size (n)]→ [Simple Random Sampling]

3.3.2.1 Useful information
- This calculation is used to determine the minimum sample size (n) by using the Simple Random Sampling method. The application uses a determined mean plant weight and variance for the clone which has been established by our own sampling. If you consider one or both of these parameters to be unrepresentative of your population, you may enter a different mean plant weight and/or variance to better evaluate your plantation. Make sure the both mean weight and variance are in the same units.
- Weight is expressed in grams (g) and is the aboveground oven-dried weight of the plant (corresponding to multiple stems) without leaves.
- The exact size of the population is not essential in this sampling. If the size of the population (number of trees) is unknown, the calculation assumes 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 added precision (the application uses algorithms for simple random sampling without replacement, which is generally more efficient).

- 5 clone-group and 13 clone-specific estimates of mean plant biomass and its variance are provided from which you may choose to calculate a representative sample size. However, 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 this application.
- 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 the mean 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 mean is used by the application as indicated in the assigned space.
- Click [Back] to return to the Selection of sampling method and computation of sample size (n) window.

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

ENBIOCAL - Calculating n - Simple Random Sampling					

Precision (%) 5.00 (5-50%)   Mortality rate (%) 0.00 (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	☐ Other Mean	☐ Other Variance
⦿ (Populus deltoides x P. nigra) x P. maximowiczii	1699.9525	3179233.068		
○ (P. deltoides x P. nigra) x P. maximowiczii (916401)	577.8808	78811.80334		
○ P. maximowiczii x P. balsamifera	1823.8507	2747845.295		
○ P. maximowiczii x P. balsamifera (915311)	1026.2707	660098.0763		
○ P. maximowiczii x P. nigra	2855.994	4243746.673		
○ P. maximowiczii x P. nigra (102377)	4199.7353	1087956.223		
○ P. maximowiczii x P. nigra (102380)	2069.9193	4652136.511		
○ P. nigra x P. maximowiczii	1405.198	2806553.362		
○ P. nigra x P. maximowiczii(3478)	1486.7295	3400605.229		
○ P. nigra x P. maximowiczii(3729)	1327.5489	2369554.089		
○ P. trichocarpa x P. nigra (2293-19)	3107.860	4333850.437		
○ S dasyclados (India)	1029.180	852594.7976		
○ S miyabeana (SX64)	2120.290	3268860.746		
○ S miyabeana (SX67)	2155.550	1646857.863		
○ S miyabeana (SX64 + SX67)	2143.797	2093736.651		
○ S sachalinensis (SX61)	2844.540	7086811.55		
○ S viminalis (5027)	811.640	379987.7942		
○ S viminalis x S miyabeana (Tully Champion)	1103.860	566407.9642		

Compute   Sample size (n) calculated: 0   ⬅ Back

3.3.2.2 Window entries

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

same as those used for standard deviation which is related to the variance (standard deviation squared)).

- **[Compute]**: click to obtain the minimum required sample size (n) calculated from the entered information
- **[Back]**: click to return to previous window

3.3.2.3 Results:

- This function calculates a sample size (n) which appears at the bottom of the window. This (n) is the number of samples needed to give an accurate representation of the population (to the level of precision desired). You should use this minimum required sample size as a guidance (i.e. number of plants to sample) to estimate the biomass of your population with a desired precision.

3.3.3 Stratified Random Sampling

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

3.3.3.1 Useful information

- This calculation is used to determine minimum required sample size (n) by using the Stratified Random Sampling method.
- The number of strata is assumed at a minimum of two and a maximum of ten for the calculation. One stratum would be considered a homogenous area and thus the Simple Random Sampling method would apply.
- You must enter a mean plant weight and variance specific to every stratum sampled as well as the number of trees per stratum
- You must enter a mortality rate for each stratum. If the mortality rate is not entered, a 0% mortality is presumed as indicated in the assigned space.
- If the precision (%) is not entered, a 5% precision is presumed as indicated in the assigned space.
- Click [Back] to return to the Selection of sampling method and computation of sample size (n) window.

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

3.3.3.2 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 0-40%
  - the mean plant biomass (Kg) in that stratum
  - the variance of plant biomass in the stratum
- **[Compute]**: click 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 to return to previous window

3.3.3.3 Results

- This function calculates the total sample size (n) which appears at the bottom of the window and the sample size for each stratum which appears under Stratum (n) value. The

(n) of each stratum is the number of plants needed to be sampled for that specific stratum. The global sample size (n) is the sum of Stratum (n) values. This (n) is the number of samples needed to give an accurate representation of the population (to the level of precision desired).

3.4 Computation of Biomass

→ [English] →[Computation of Biomass]

Options: → [Plantation]

             → [Uncultivated land]

3.4.1 Useful information
- This calculation is used to estimate the biomass of either a plantation or a forested area (bushland).
- Information can be entered in capital or lower case letters.

Figure 6. Stand Type Option window
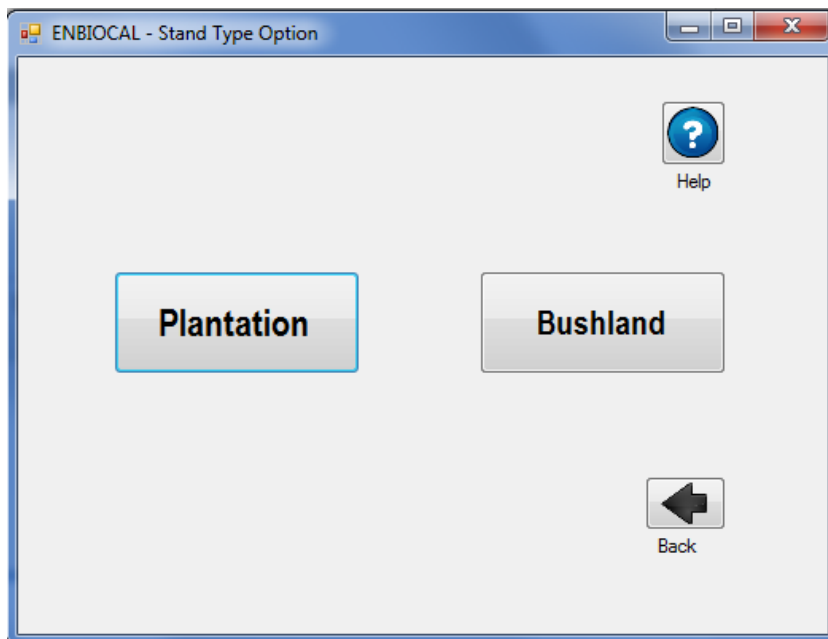
3.4.2 Plantation

→ [English] → [Computation of Biomass] → [Plantation]

3.4.2.1 Useful information
- This option will allow you to calculate the biomass of a plantation of specific clone in a determined area. You must enter the value of an area either manually or calculate the

area using the [Calculate Area] command. You must also enter your sampling data for the specific clone. You may enter data manually in the respective order established in the window or you can load the data from a file. You can modify the data imported from a file directly in the window if need be.

- All diameters were 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, millimetre (mm) is the default unit in the selection.
- If height units are not changed, centimetre (cm) is the default unit in the selection.

Figure 7. Plantation Information window (Simple random sampling)
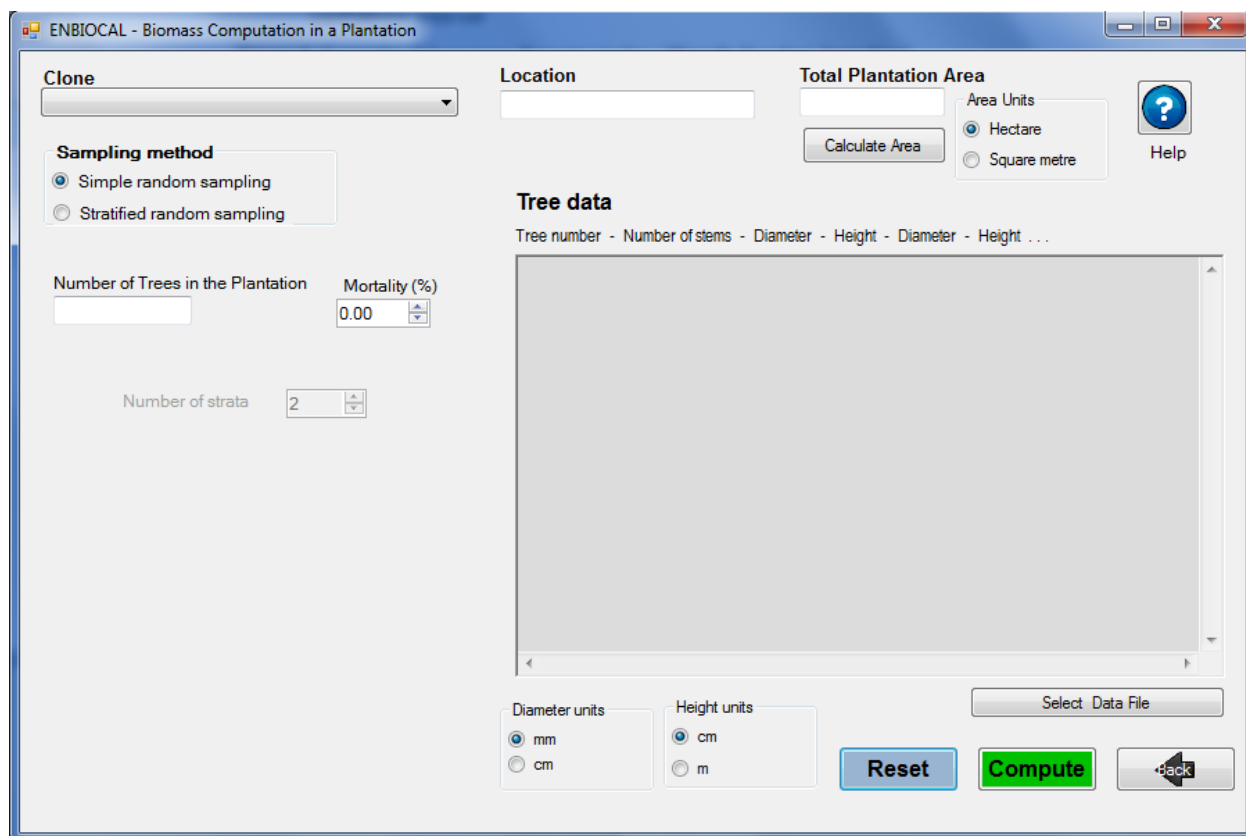
Figure 8. Plantation Information window (Stratified random sampling)

3.4.2.2 Window entries

- You can manually enter your sampled data in the Tree data available space. It is very important that you respect the established entry sequence for the data. If a clone has 10 stems and the associated equations uses 4 stems to calculate the biomass you can decide to enter the stem data of only the 4 largest stems. If you enter the data for 10 stems the application will automatically use the 4 largest ones in the calculation. Having said this, you must still enter the **total number of stems(10)** of the plant.
- **Clone**: select the name of the clone (Latin names of the parent species are provided to help you identify your clone in the list. For clone-specific equations, the code of the clone is written in parentheses after the Latin names).
- **Location**: enter location of sampling (e.g. Town, Region, Country)
- **Area**: enter the surface of the plantation
    - Select unit: hectare or square metre
    - The conversion is made automatically when you change from one unit to the other

    You can calculate the area of your plantation using the [Calculate Area] command.

- Sampling method: select proper sampling method used to obtain the sample size (n) (Simple random or Stratified random)
- **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 population (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% of the population
- **Select data file**: you may load a file containing your data. It is imperative that the parameters be entered in the respective order established in the window: e.g. for Simple Random Sampling; ID tree number, number of stems, the individual diameter and 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 assign the right amount of diameters and heights for the equation. This file can either be in the form of a:
    - text files (*.txt)
    - Comma Separated Values files (*.csv).
    - Example of **Simple** Random Sampling file (you may use a space, a tab, a comma or a semicolon to separate the parameters)

Tree	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 **Stratified** Random Sampling file (you may use a space, a tab, a comma or a semicolon to separate the parameters)

Plot	Tree	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

If you wish, you can modify the data previously selected from the file directly in the window.

- **Diameter units**: you must select in which units the diameters were recorded. All diameters must be in the same units.
    - mm (millimeters)
    - cm (centimeters)
- **Height units**: you must select in which units the heights were recorded. All heights must be in the same units.
    - cm (centimeters)
    - m (meters)
- **[Back]**: click to return to Stand type option window
- **[Reset]**: resets all entries
- **[Compute]**: click to calculate the total dry leafless biomass. A Results window will appear for **Simple** Random Sampling;

Figure 9. Example of Results window (**Simple** Random Sampling)
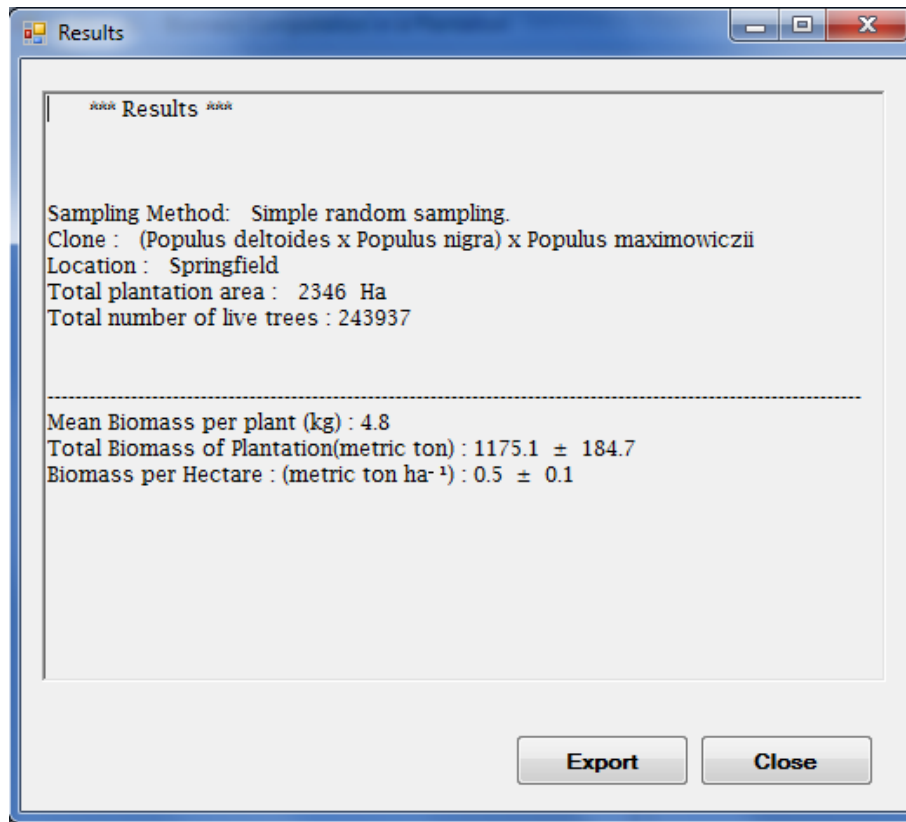
```
Results                                              ▢ ▢ ✕

     *** Results ***



Sampling Method:   Simple random sampling.
Clone :   (Populus deltoides x Populus nigra) x Populus maximowiczii
Location :   Springfield
Total plantation area :   2346  Ha
Total number of live trees : 243937


----------------------------------------------------------------------------------------
Mean Biomass per plant (kg) : 4.8
Total Biomass of Plantation(metric ton) : 1175.1  ±  184.7
Biomass per Hectare : (metric ton ha⁻¹) : 0.5  ±  0.1




                                        [  Export  ]   [  Close  ]
```

Results for **Simple** Random Sampling

- Sampling method: sampling method used
- Clone: clone identification and Latin name(s) of the willow and poplars species
- Location: the location specified by the user
- Total plantation area:
- Total number of live trees:
- Mean biomass per plant (Kg):
- Total biomass of plantation(metric ton): total biomass of the plantation with its 95% confidence interval
- Biomass per hectare (metric ton ha^{-1}): mean plant biomass per hectare with its 95% confidence interval

Figure 10. Example of Results window (**Stratified** Random Sampling)
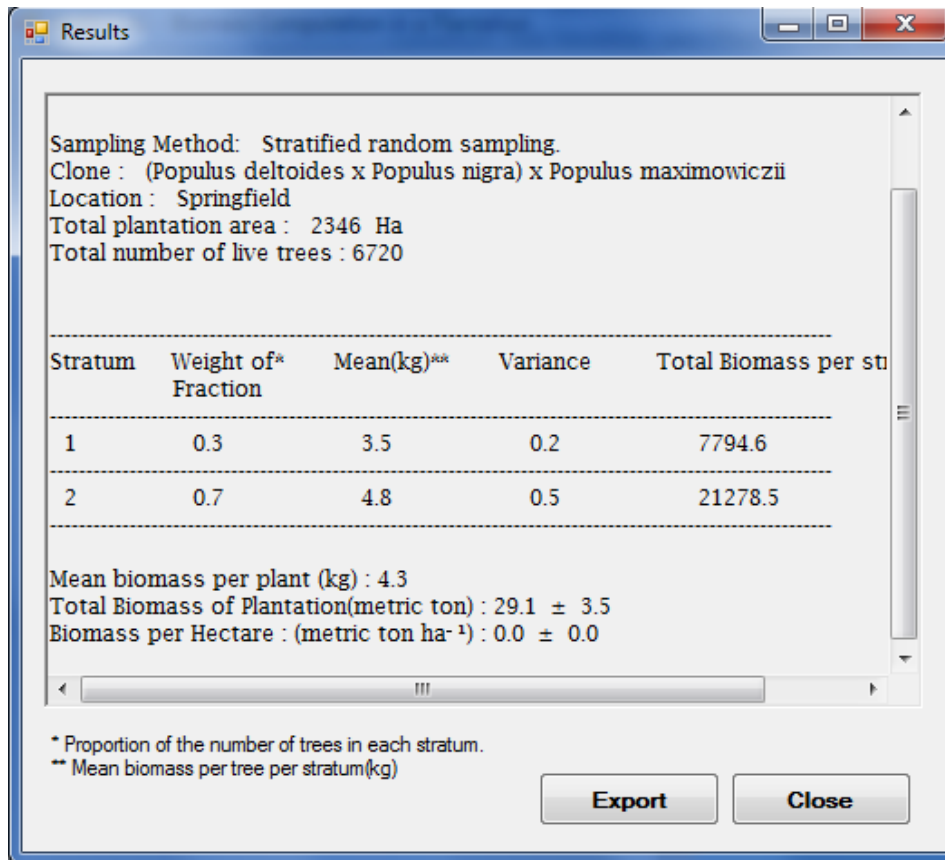
Results for **Stratified** Random Sampling;
-   Sampling method: sampling method used
-   Clone: clone identification and Latin name(s) of the willow and poplars species
-   Location: the location specified by the user
-   Total plantation area:
-   Total number of live trees:
-   Weight of fraction per stratum:
-   Mean (Kg): mean plant biomass per stratum
-   Variance: per stratum
-   Total Biomass per stratum(Kg): total biomass per stratum with its 95% confidence interval
-   Mean biomass per plant (Kg): mean overall plant biomass (for the entire plantation)
-   Total Biomass of plantation (metric ton):

Biomass per hectare (metric ton/ha): biomass per hectare 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 Details on calculations:

The equations used for the calculation of the biomass of a plantation are based on the diameters and heights of a number of stems. The equations vary in the number of stems

used for the calculation of the biomass. This approach reduces the number of measurements needed for each plant because at most 4 stem data will be used by the equations. Some were developed for two, three or four stems per tree. For example, for an equation developed using three stems, every sampled tree would have to have at least three stems. We know that there will be variations 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 1 or 2 stems, in this example. Consequently, a warning will be issued to allow the user to verify and eventually correct the data entered if need be. This variation is not considered an error but 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 have to measure the k trees of largest D15 for their diameter and height (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 to every equation. You can refer to Appendix 4 for the range of diameter, height and number of stems values for each equation. A warning is 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 mean biomass per plant in (Kg), the total biomass in (metric ton) and the biomass per hectare (metric ton/ha) of the plantation.

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

3.4.2.5 Compute area: a window allowing you to enter geographical (or relative) coordinates will appear

Figure 11. Compute area Window
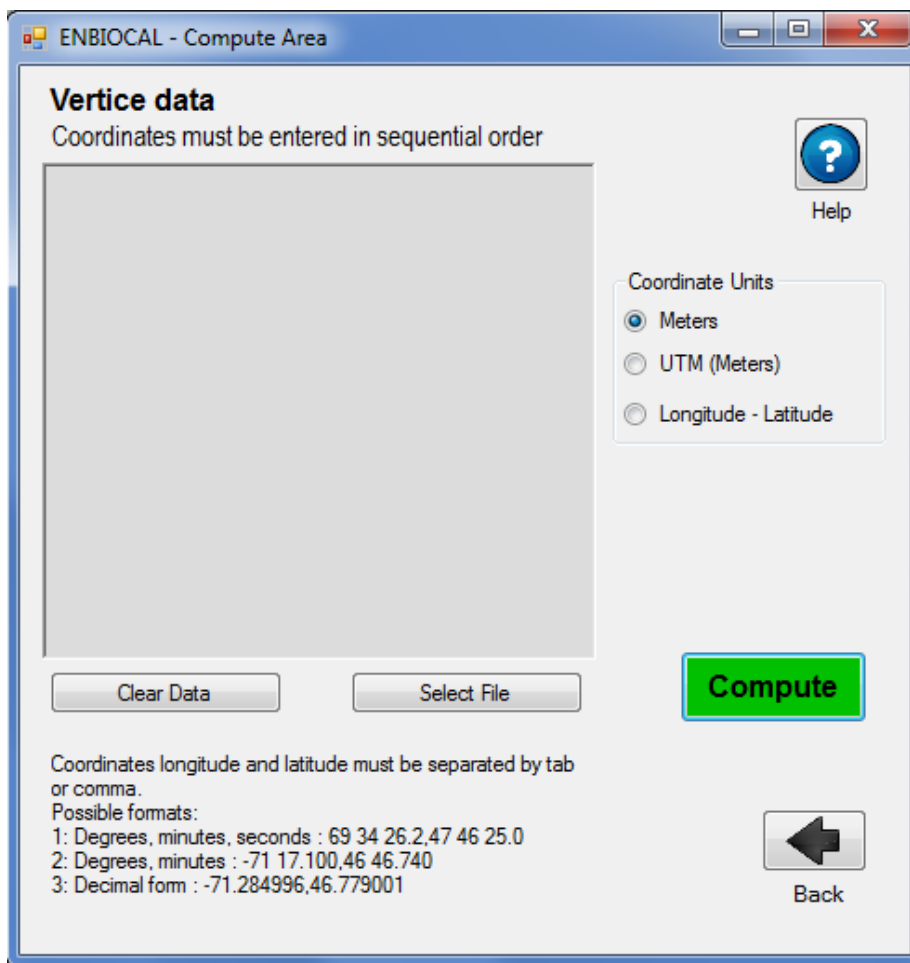
- Three different coordinate units can be used to enter data. All coordinates must be separated by tab or a comma. A space using the space bar will cause an error because a space is needed for longitude and latitude coordinates, for example in minute seconds.
    - Meters (e.g. 345.45   64.78) or (e.g. 345.45,64.78)
    - UTM (meters) (e.g. 325616.344936436 5183177.45434031)
    - Longitude and Latitude (in respective order)
      (e.g. -71 17.284996   46 17.779001) or (e.g. -71 17.284996,46 17.779001)

        - No GPS (unknown coordinate system)
        - WGS 84 (the most commonly used in GPS devices). If coordinates are taken in NAD 83 use this option (the result is approximately equal).
        - NAD 27

- Select file: you may enter a file containing your data coordinates. This file can either be in the form of

- text files(*.txt)
- Comma Separated Values files(*.csv).
- Clear data: click to clear data in entry area
- Compute: click to calculate 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 less than the number of stems used by the equation (see Appendix 2 and Appendix 3), a window will appear to warn you. It will ask you if the entered number of stems is right. If it is in fact a valid entry, click [OK] to continue and use it in the calculation. If it is an error click [Cancel] to stop calculation. You can either change or erase the data if it is invalid.

Figure 12. Example of warning window
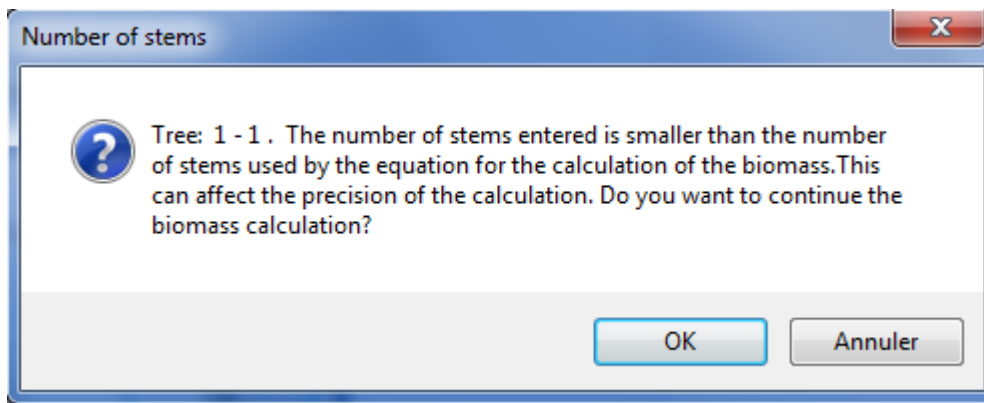
Some equation forms will use at most 4 stems to calculate the biomass of the plant. Therefore, if any plant has more than 4 stems, only enter the data of the 4 largest ones. If you write that a plant had a total of 8 stems and the associated equation uses 3 stems, but you enter the data for only 2 stems a window will appear with an error message and the calculation will stop.

Figure 13. Example of error window
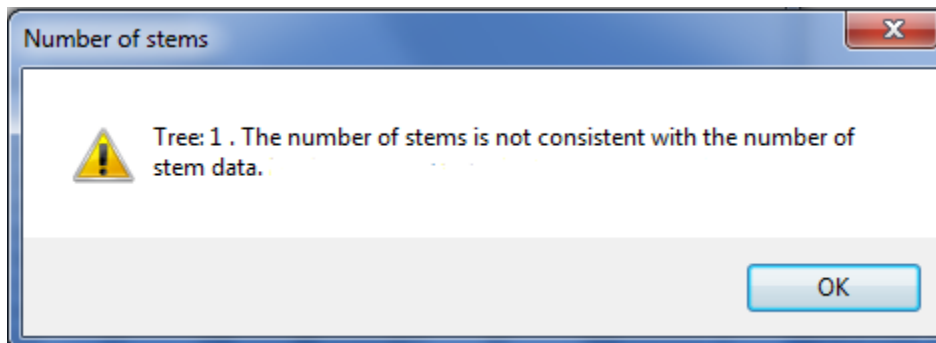
If data is missing or if there is an error in the way data is entered (for example you give a D15 value for a stem but not its height), an error window will appear and the calculation will stop.

Figure 14. Example of error window
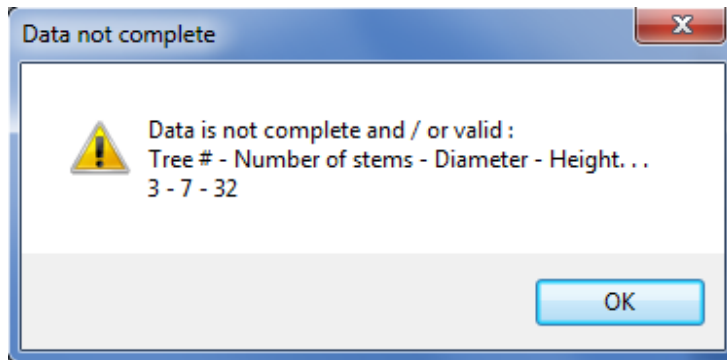
If any diameter value, height value or number of stems entered is very high (out of range) a warning window will appear asking you if this is valid data.

Figure 15. Example of warning window
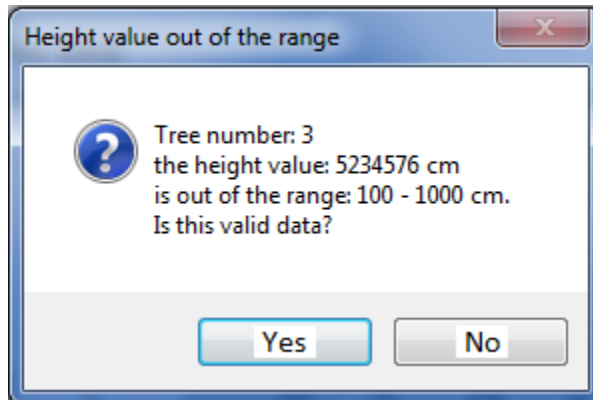
3.4.3 Forested Area (bushland)
→English→Computation of Biomass→Uncultivated land

3.4.3.1 Useful information
- This option will allow you to calculate the biomass of a bushland in a determined area. You must enter an area either manually or calculate the area using the [Calculate Area] command. You must also enter your sampling data for the species sampled. You may enter data manually in the respective order established in the window or you can load the data from a file.
- If you enter species that are not already defined by the application, they will be recognized by the application and a warning window will ask you to customize them using the Input of New Equations window. You must assign an equation to the species to calculate their biomass. You will choose from a predetermined selection of 19 equation forms and enter the appropriate parameters specific to each equation. We recommend that you create a file containing all the customized species beforehand using the Input of New Equations window function instead of letting the application recognize new species every time. By creating a file in advance, you will be able to customize many species in a row instead of one species at a time when recognised by the app.

- You may also choose to customize the equation of a species already defined by the application. To do this, you must go through the Input of New Equations window and enter the Species code used by the application (see Table 2). You can then choose an equation from the 19 suggested which will become its default equation for the active session. As long as the Bushland Information window is not closed this information is saved in the background. It is important to remember to load this new equation every time you open a new Bushland Information window and want to use the new customized equation for this species. If previously saved in a file, click on [Customized Equation File] to select the saved customized equation.
- For some equations, height is not used in the calculation of the biomass but the column height cannot be left blank. Data must be entered or else an error window will appear. If height is not a required parameter for the equation (see Appendix 5) you can enter any value (negative or positive) in the height column. If height is a required parameter in the equation and the data entered is negative an error window will appear.
- It is important to understand that the samples for the calculation of the biomass of an uncultivated land are plots and not individual trees or shrubs.
- If diameter units are not changed, (cm) is the default unit in the selection.
- If height units are not changed, (m) is the default unit in the selection.

Figure 16. Biomass computation on Bushland window

3.4.3.2 Window entries

- **Location**: enter location of sampling
- **Area**: enter the size of the area
    - Select unit: hectare (ha) or square metres (m^2)
    - The conversion is calculated automatically when you change from one 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 load a file containing your data. It is imperative that the parameters be entered in the respective order established in the window: plot number, species code, ID tree number, type of diameter measured, diameter and height values. This file can either be in the form of
    - text files(*.txt)
    - Comma Separated Values files(*.csv)
    - Example of 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 in which units the diameters were measured. All diameters must be in the same units.
    - mm (millimeters)
    - cm (centimeters)
- **Height units**: you must select in which units the heights were measured. All heights must be in the same units.
    - cm (centimeters)
    - m (meters)
- **Compute**: click to calculate the total biomass (metric ton) of the forested area. A Results window will appear showing the following;
    - Sampling method: sampling method used
    - Location: entered location
    - 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 to return to Stand type option window
- **[Reset]**: reset all entries

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

Figure 17. Example of Results
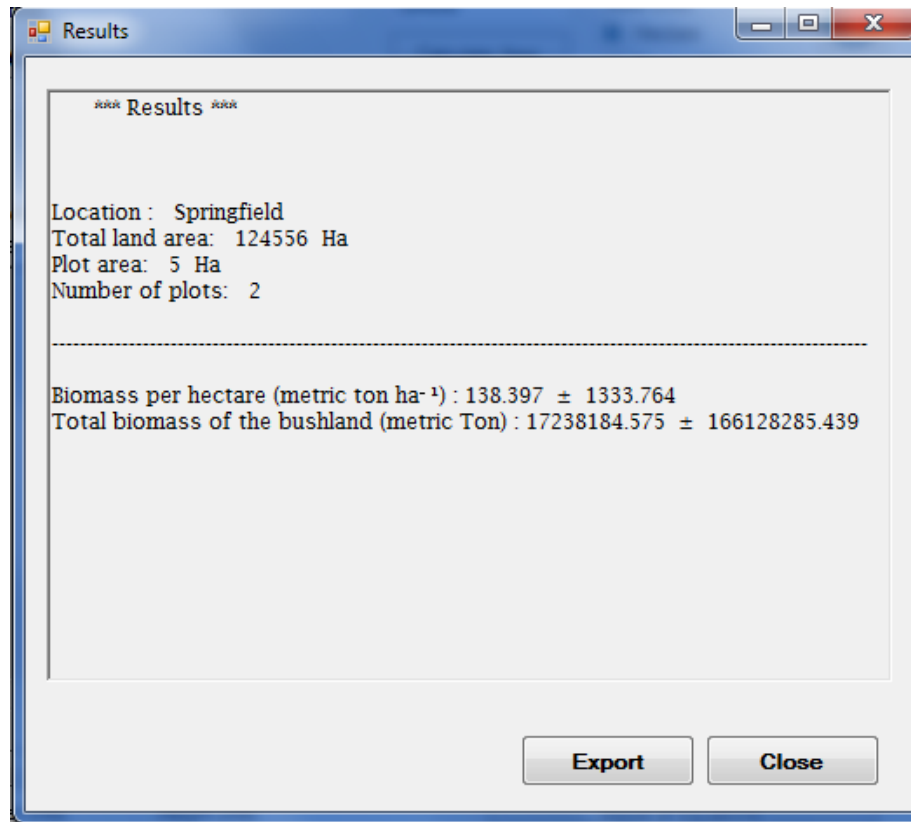
Results for **Simple** Random Sampling;

- Sampling method: sampling method used
- Location: the location specified by the user
- Biomass per hectare (metric ton ha^{-1}): mean biomass per hectare with its 95% confidence interval
- Total biomass (metric ton): total biomass of the plantation with its 95% confidence interval

3.4.3.3 Details on calculations

Some equations used for the calculation of the biomass of forested area (bushland) are based on the diameter and the height of the tree and others based only on the diameter (see Appendix 5 for details).

3.4.3.4 Results

- This function calculates the total biomass (metric ton) of a bushland. It also gives the biomass per hectare (metric ton ha^{-1}).

3.4.3.5 Error and warning messages

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

Figure 18. Example of warning window
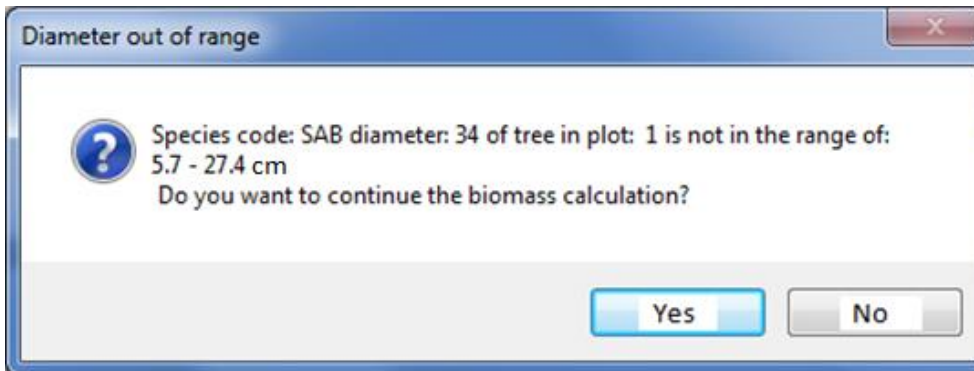
If data is missing or if there is an error in the way data is entered a warning will appear.

Figure 19. Example of error window cm
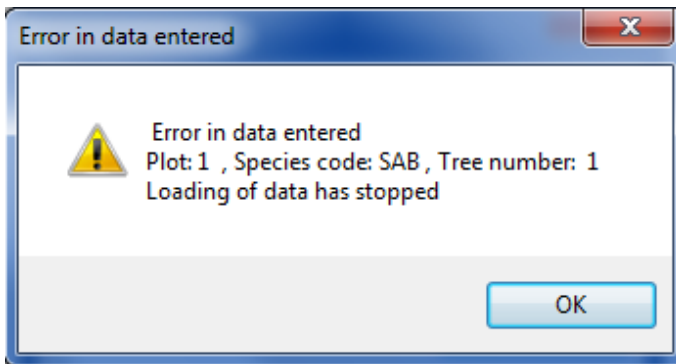
If you enter a species code that is not in the application database and you haven't customized an equation for it a warning message will appear. If you click [Yes] the Input of New Equations window will appear for you to customize this species code. If you click [No] an error window will appear and say that this is invalid data and that it cannot be used for the calculation. Calculation is stopped and you can change data associated with that species code.

Figure 20. Example of window warning
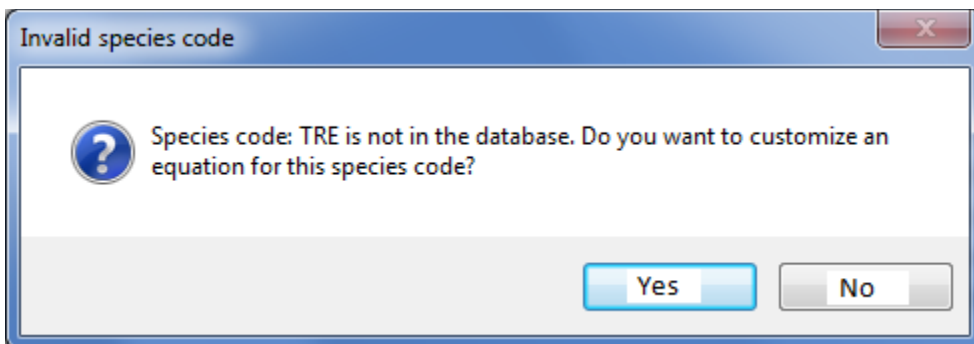
Figure 21. Example of error window
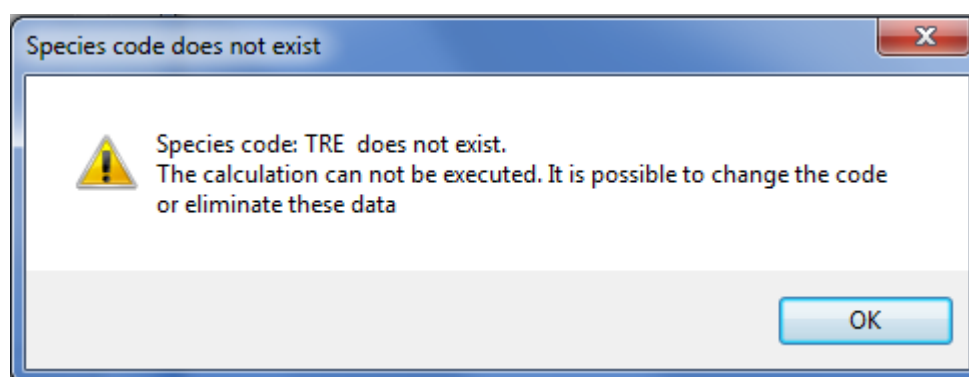
The following error window can appear if the wrong measurement type (DRC/D15/DBH) associated to the equation is entered. This message will also appear if data entered is invalid for the height parameter (e.g. negative value).

Figure 22. Example error window
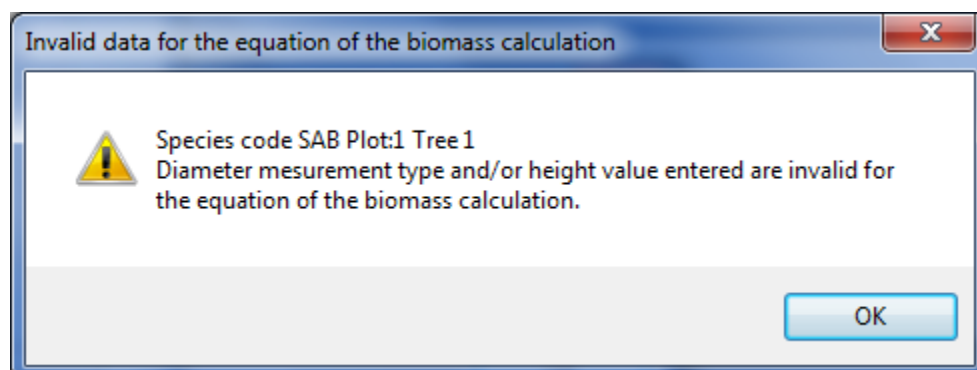
3.4.3.6 Input of New Equations Window
- This function allows you to modify the equation for a species already defined by the application or, allows you to enter a new species and its equation or to define a new equation for species in DB.
- You will assign a new biomass calculation equation to the species. Choose from a predefined selection of 19 equation forms. The first twelve equations are based on the diameter only and the last seven equations are based on the diameter and height of the plant. 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 [OK] when asked to export file.

Figure 23. Input of New Equations window
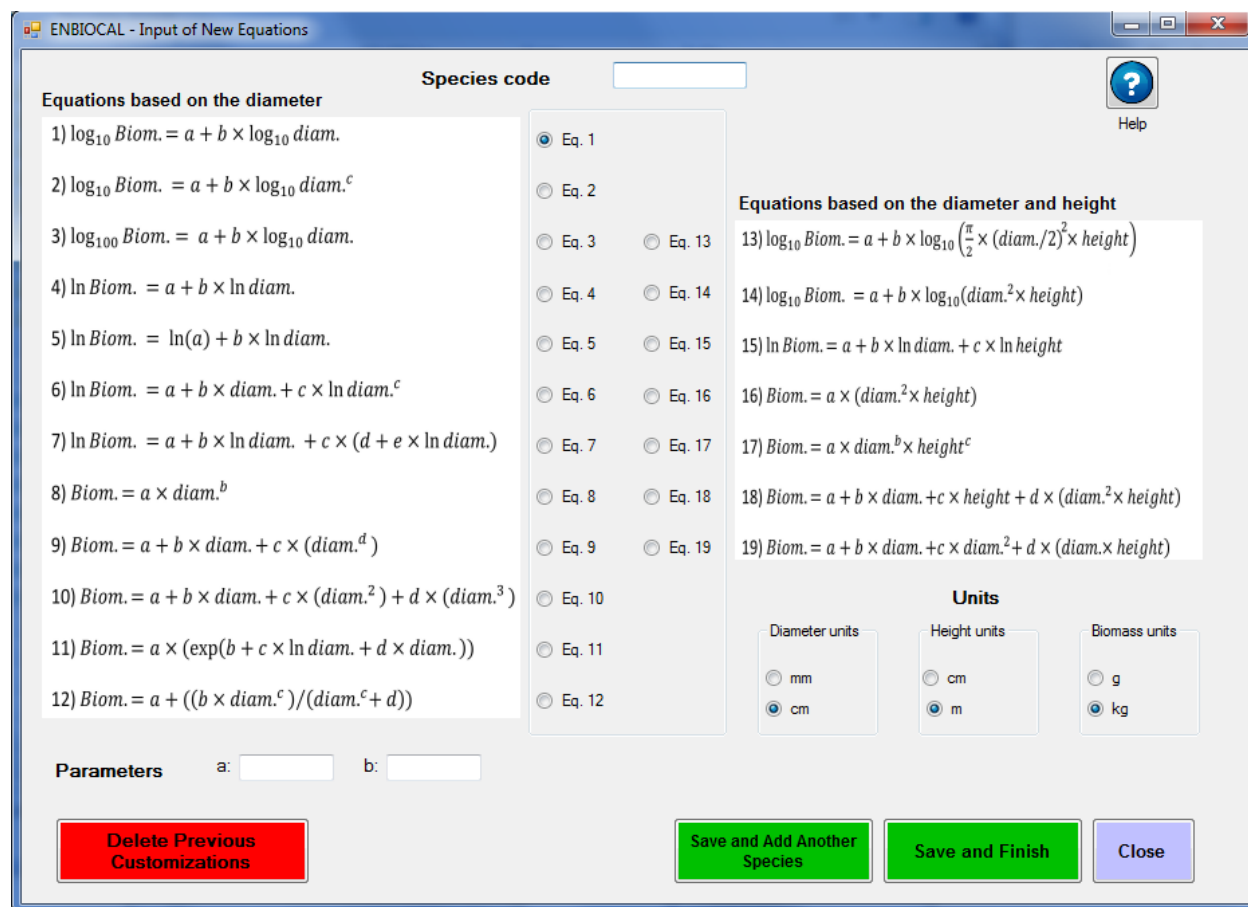
Window entries:

- **Species code**: enter the species code associated to full name of the species. It is suggested to use a code of 3 or 4 letters (see Table 2)
- **Parameters**: you must enter values for the number of parameters specific to each equation
- **Diameter units**: you must select in which diameter units the equation was developed.
  - mm (millimeters)
  - cm (centimeters)
- **Height units**: you must select in which height units the equation was developed.
  - cm (centimeters)
  - m (meters)
- **Biomass units**: you must select in which units your equation predicts biomass.
  - g (grams)
  - Kg(kilograms)
- **[Delete Previous Customizations]**: click to delete all previous customized species saved in the background of the Uncultivated Information window. This function resets all customized equations to the default equations established by the application.
- **[Save and Add Another]**: click to save the entered information on the customized species and to immediately create another.

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

3.4.3.7 Import Equations (file)

This function allows you to select a file with formerly saved customized species instead of manually entering them every time. We recommend that you create this file using the application button [Input of New Equations] and that you click [OK] when asked to "export file" to save the customized equations on your computer. You may also create or edit this file manually. In this case, it is imperative that you respect the established parameter entry order and that you enter the appropriate number of parameters associated with the specific equation. For example; species code, ID equation number, diameter unit, height unit, output biomass unit and the right number of parameters associated with the equation. You may use a space, a tab, a comma or a semicolon to separate the parameters.

Example of file containing customized equations with parameters

SpeciesCode	EqID	D unit	H unit	B unit	a	b	c	d
ALb	1	cm	m	Kg	10	9		
Col	18	cm	m	Kg	1	2	3	3
Can	1	cm	m	Kg	33	1		
hol	19	cm	m	Kg	1	2	8	7

Appendix 1: Information about sample sites and plantations

Site (Canadian Province)	Boisbriand, QC	Bearverlodge, 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 1st year)	Yes (end 1st year)	Yes (end 1st year, + 2009 and 2012)	No (cut in 2012)	Yes (end 1st year)	Yes (end 1st year)
Plantation density	16000 plants ha^{-1}	15000 plants ha^{-1}	16000 plants ha^{-1}	5164 plants ha^{-1}	10101 plants ha^{-1}	10101 plants ha^{-1}
Spacing	Single row (0.34m w.row × 1.8m b.row)	Double row (0.6m w.row × 0.6m b.row × 2.2m b.dbl.row)	Double row (0.5m w.row × 0.75m b.row × 1.5m b.dbl.row)	Single row (1.0m w.row × 1.8m b.row, with some exceptions)	Single row (0.55m w.row × 1.8m b.row)	Single row (0.55m w.row × 1.8m b.row)
Type of plantations	Willow clones	Willow clones	1 willow clone and 1 hybrid poplar	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 distances between plants within the row; b.row, indicates distances between single rows or between rows in a bed (for double rows); b.dbl.row, indicates distances between double rows, from bed centre to bed centre.

Sampling took place in autumn 2014.

	clone	Parentage*	Site **	DBH range (mm)(stems)	H range (cm)(stems)
Willow clones	5027	*Salix viminalis*	BB	3-27	113-475
	SX61	*S. sachalinensis*	BB	10-38	324-649
	SX64	*S. miyabeana*	BB	10-38	278-625
	SX67	*S. miyabeana*	BB	3-40	181-660
			GU	1-16	130-410
	India	*S. dasyclados*	BL	10-23	49-423
	Tully Champion	*S. viminalis* × *S. miyabeana*	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=Populus deltoides × P.nigra

**codes for site: 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: Selected models for clone-specific and species-group equations for willow clones and species (i.e. S*alix miyabeana*)

Selected model – equation(s)	n.obs	RMSE%	R^2	ME%
Clones				
Salix viminalis 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				
$y' = 2.3693 - 0.3588 \times Nbstems - 0.2221 \times D15_{2Dmax} + 0.0160 \times H_{2Dmax}$				
Salix sachalinensis 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				
$y' = 2.5079 - 0.8237 \times Nbstems - 0.0221 \times D15_{3Dmax} + 0.0063 \times H_{3Dmax}$				
Salix miyabeana SX64	10	6.35	0.9401	-3.40
$DryW_{tree} = [94.05264 + 0.00362 \times (D15^2{}_{4Dmax} \times H_{4Dmax})] \times \ln(Nbstems + 1)$				
Salix miyabeana SX67	20	21.98	0.8565	-20.77
$DryW_{tree} = 3365.3397 \times (D15_{2Dmax})^{2.4646} \times (H_{2Dmax})^{-1.4839} \times \ln(Nbstems + 1)$				
Salix dasyclados, India	10	6.70	0.9938	-0.43
$DryW_{tree} = 0.0066 \times (D15_{4Dmax})^{0.7290} \times (H_{4Dmax})^{1.6073} \times \ln(Nbstems + 1)$				
Salix viminalis × Salix miyabeana, Tully Champion	10	9.32	0.9792	-4.10
$DryW_{tree} = 2.0350 \times (D15_{3Dmax})^{2.2138} \times (H_{3Dmax})^{-0.1781} \times \ln(Nbstems + 1)$				
Species				
Salix miyabeana (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 at 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 RationDmax, using the nobs parameter reported 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 selected stem biomass for Ratio$_{nDmax}$

$$DryW_{tree} = \frac{\sum_{1}^{n\_Dmax} DryW_{stem}}{Ratio_{nDmax}}$$

Appendix 4: Selected models for clone-specific and clone-group specific equations for hybrid poplar clones and groups of clones

Selected model – equation(s)	n.obs	RMSE%	R^2	ME%
Clones				
Populus nigra x P.maximowiczii **(3478)** $$DryW_{tree} = 0.0485 \times (D15_{2Dmax})^{1.1950} \times (H_{2Dmax})^{0.9362} \times \ln(Nbstems + 1)$$	19	10.91	0.9916	-9.48
Populus nigra x P.maximowiczii **(3729)** $$DryW_{tree} = 1.0562 \times (D15_{2Dmax})^{2.5382} \times (H_{2Dmax})^{-0.3548} \times \ln(Nbstems + 1)$$	21	24.99	0.9512	-0.28
P.maximowiczii x Populus nigra **(102377)** *** 1) Individual stem model $$DryW_{stem} = 1.0143 \times \exp((-4.8874 + 0.8724 \times \ln(D15^2 \times H))$$ 2) Ratio model $$y' = 1.5345 - 0.0955 \times Nbstems + 0.0797 \times D15_{4Dmax} - 0.0021 \times H_{4Dmax}$$	24	6.57	0.9269	-0.30
P.maximowiczii x Populus nigra **(102380)** $$DryW_{tree} = 0.0888 \times (D15_{4Dmax})^{1.0111} \times (H_{4Dmax})^{0.9934} \times \ln(Nbstems + 1)$$	14	6.22	0.9967	-15.24
P.maximowiczii x P.balsamifera **(915311)** $$DryW_{tree} = [94.0522 + 0.0026 \times (D15^2_{3Dmax} \times H_{3Dmax})] \times \ln(Nbstems + 1)$$	17	11.43	0.9779	-2.69
Populus deltoids x P.maximowiczii **(916401)** $$DryW_{tree} = 0.0055 \times (D15_{3Dmax})^{0.8110} \times (H_{3Dmax})^{1.6333} \times \ln(Nbstems + 1)$$	12	11.05	0.9436	-0.12
P.trichocarpa x Populus nigra **2293-19***** 1) Individual stem model $$DryW_{stem} = 1.0095 \times \exp((-3.8801 + 0.8233 \times \ln(D15^2 \times H))$$ 2) Ratio model $$y' = 5.0406 - 0.9274 \times Nbstems + 0.1257 \times D15_{Dmax} - 0.0140 \times H_{Dmax}$$	10	13.75	0.9532	-0.56
Group of clones				
N×M [*P. nigra × P. maximowiczii*] $$DryW_{tree} = 0.0648 \times (D15_{2Dmax})^{1.2975} \times (H_{2Dmax})^{0.8281} \times \ln(Nbstems + 1)$$	40	22.11	0.9642	-6.90
M×N*** [*P. maximowiczii × P. nigra*] 1) Individual stem model $$DryW_{stem} = 1.0151 \times \exp(-4.9661 + 0.8755 \times \ln(D15^2 \times H))$$ 2) Ratio model	46	9.52	0.9828	-0.50

Selected model – equation(s)	n.obs	RMSE%	R^2	ME%
$y' = 2.8218 - 0.1393 \times Nbstems + 0.0025 \times D15_{4Dmax} + 0.0001 \times H_{4Dmax}$				
M×B* [*P. maximowiczii × P. balsamifera*]	23	8.72	0.9904	-2.06
1) Individual stem model $DryW_{stem} = 1.0203 \times \exp(-4.4792 + 0.8422 \times \ln(D15^2 \times H))$				
2) Ratio model $y' = 3.5726 - 0.1848 \times Nbstems - 0.0237 \times D15_{4Dmax} + 0.0025 \times H_{4Dmax}$				
DN×M [*(P. deltoids × P. nigra) × P. maximowiczii*] $DryW_{tree} = 0.5881 \times (D15_{3Dmax})^{2.3639} \times (H_{3Dmax})^{-0.0630} \times \ln(Nbstems + 1)$	18	9.10	0.9920	-7.95

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

7) For each selected stem, calculate stem biomass using

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

8) Sum individual stem biomass for the selected stems (this value will be used at the last step of the computation)

9) For the plant, calculate y' using the ratio model reported in the table above

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

10) Convert y' to Ratio_transf$_{nDmax}$ using the following model:

$Ratio\_transf_{nDmax} = expit(y') = \dfrac{e^{y'}}{1 + e^{y'}}$

11) Calculate RationDmax, using the nobs parameter reported the table above:

$Ratio_{nDmax} = transf^{-1}(Ratio\_transf_{nDmax}) = \dfrac{(Ratio\_transf_{nDmax} \times nobs - 0.5)}{nobs - 1}$

12) Calculate plant weight by dividing the sum of selected stem biomass for Ratio$_{nDmax}$

$DryW_{tree} = \dfrac{\sum_{1}^{n\_Dmax} DryW_{stem}}{Ratio_{nDmax}}$

Appendix 5: Species List and Equations

Unique ID	Instructions	Diameter size used	Specie code	Diam. Range	Measure. units	Equation	Part	Reference
1	#2 - #1	All sizes	SAB	5.7-27.4cm(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	5.7-27.4cm(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	5.7-45.2cm(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	5.7-45.2cm(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	5.3-45.3cm(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	5.3-45.3cm(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	5.1-57.8cm(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	5.1-57.8cm(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 to 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)	$\log_{10} Biom. = .0366 + 0.931 \times \log_{10}\left(\frac{\pi}{2} \times (diam./2)^2 \times height\right)$	Whole tree (AG)	Fatemi et al. 2011
13	#14 -#13	BIG, check DBH range	BOJ	6.2-70.3cm(DBH)	Biom (kg),	$Biom. = 0.000343 \times (diam.^2 \times height)$	Foliage	Alemdag 1984

					diam (cm), height (m)		and twigs	
14	#14 -#13	BIG, check DBH range	BOJ	6.2-70.3cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.024822 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
15	#16 - #15	BIG, check DBH range	BOP	5.4-32.7cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.000859 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
16	#16 - #15	BIG, check DBH range	BOP	5.4-32.7cm(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 to 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	6.1-46.3cm(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	6.1-46.3cm(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	BIG, if DBH use this	FRA	5.9-53.7cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.000328 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
23	#23 - #22	BIG, if DBH use this	FRA	5.9-53.7cm(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	6.3-35.8cm(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	6.3-35.8cm(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),	$Biom. = 0.0194 \times diam.^b \times height^c$	Stem	Wagner and Ter-Mikaelian

					height (cm)			1999
28	#29 - #28	BIG, if DBH use this	EPN	5.2-22.2cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.003031 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
29	#29 - #28	BIG, if DBH use this	EPN	5.2-22.2cm(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	BIG, if DBH use this	PIG	8.8-26.8cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.001042 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
33	#33 - #32	BIG, if DBH use this	PIG	8.8-26.8cm(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	BIG, if DBH use this	PIR	5.4-55.1cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.001048 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
37	#37 - #36	BIG, if DBH use this	PIR	5.4-55.1cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.017147 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983
38	#39 - #38	BIG, check DBH range	PEB	6.6-53.2cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.018505 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
39	#39 - #38	BIG, check DBH range	PEB	6.6-53.2cm(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	BIG, if DBH use this	PEG	5.4-39.2cm(DBH)	Biom (kg), diam (cm),	$Biom. = 0.000379 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984

								height (m)		

42	#42 - #41	BIG, if DBH use this	PEG	5.4-39.2cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.018577 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984
43	#44 - #43	BIG, check DBH range	PET	5.2-43.5cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.00051 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
44	#44 - #43	BIG, check DBH range	PET	5.2-43.5cm(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	BIG, 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	BIG, 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	BIG, if DBH use this	CET	6.4-49.6cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.000275 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1984
49	#49 - #48	BIG, if DBH use this	CET	6.4-49.6cm(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 <4.4 cm at DBH)	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	5.5-55.3cm(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	5.5-55.3cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.02971 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1984

68	#68	All sizes (attention 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 (attention 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	Roussopoulos and Loomis 1979
57	#58 - #57	BIG, if DBH use this	THO	5.1-38.8cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.001766 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
58	#58 - #57	BIG, if DBH use this	THO	5.1-38.8cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.014242 \times (diam.^2 \times height)$	Whole tree (AG)	Alemdag 1983
59	#60 - #59	BIG, if DBH use this	PRU	5.3-51.4cm(DBH)	Biom (kg), diam (cm), height (m)	$Biom. = 0.00132 \times (diam.^2 \times height)$	Foliage and twigs	Alemdag 1983
60	#60 - #59	BIG, if DBH use this	PRU	5.3-51.4cm(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

*attention, this species equations were available only for aboveground biomass including leaves

AG = aboveground

Appendix 6: Reference and geographical area of each study

Reference	Full Reference	Geographical area
Alaback 1986	Alaback, P. B. 1986. Biomass regression equations for understory plants in coastal Alaska: effects of species and sampling design on estimates. Northwest Science 60:90-103.	Alaska, USA
Alemdag 1983	Alemdag, S. 1983. Mass Equation And Mercltantability 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. Canadian Journal of Forest Research 41:881-891.	New Hampshire, USA
Hocker and Early 1983*	Hocker, H. W., Early, D. J. 1983. Biomass and leaf area equations for northern forest species. Res. Pap. 102. Durnham, NH: University of New Hampshire Agricultural Experiment Station	New Hampshire, USA
Ker 1980*	Ker, M. 1980 Tree biomass equations for ten major species in Cumberland County, Nova Scotia. Inf. Rep. M-X-108. Fredericton, NS: Canadian Forestry Service, Maritime Forest Research Center	Nova Scotia, CANADA
Ribe 1973*	Ribe, J. 1973. Puckerbrush weight tables. Misc. Rep. 152. Orono, ME: University of Maine, Life Sciences and Agriculture Experiment Station.	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, Forest Service, US Department of Agriculture.	Minnesota, USA
Telfer 1969	Telfer, E. S. 1969. Weight–diameter relationships for 22 woody plant species. Canadian Journal of Botany 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. Annals of forest science 56:193-199.	Ontario, CANADA
Williams and McClenahen 1984	Williams, R. and J. McClenahen. 1984. Notes: Biomass prediction equations for seedlings, sprouts, and saplings of ten central hardwood species. Forest Science 30:523-527.	Ohio, USA

*original study not found; equation cited by 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. USDA, For. Serv., Northeastern Res. Station, General Tech. Rep. NE-319