# **Canada's National Forest Inventory**

# National Standards for Ground Plots Compilation Procedures

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# **Table of Contents**

1.	Introduction	1
2.	Compiled Attributes	1
3.	Notation and constants	12
4.	Large Tree List	12
	HEIGHT_PRJ	12
	CROWN LENGTH	13
	VOL TOTAL, VOL PRJ	13
	BIOMASS_TOTAL, BIOMASS_STEMWOOD, BIOMASS_STEMBARK, BIOMASS_BRANCHES,	
	BIOMASS_FOLIAGE, BMEQ_WOOD, BMEQ_BARK, BMEQ_BRANCHES, BMEQ_FOLIAGE	14
5.	Large Tree Plot Summary	
	SITE INDEX	
	SITE INDEX GENUS	18
	SITE INDEX SPECIES	
	SITE HEIGHT	
	LOREY HEIGHT	
	BASAL AREA STANDLIVE	
	BASAL AREA STANDDEAD	
	BASAL AREA FALLLIVE	
	STEM DENSITY STANDLIVE	
	STEM DENSITY STANDDEAD	
	STEM_DENSITY_FALLLIVE	
	PLOTBIO STEMWOOD LIVE	
	PLOTBIO STEMBARK LIVE	
	PLOTBIO BRANCHES LIVE	
	PLOTBIO FOLIAGE LIVE	
	PLOTBIO STEMWOOD DEAD	
	PLOTBIO STEMBARK DEAD	
	PLOTBIO BRANCHES DEAD	
	PLOTVOL STANDLIVE	
	PLOTVOL STANDDEAD	
	PLOTVOL FALLLIVE	
	PLOTBIO LGTR LIVE	
	PLOTBIO LGTR DEAD	
	SITE AGE, NUM LAB, NUM FIELD, AGE CORR YEARS, AGE TOTAL	
	GROSSVOL INCR	
	GROSSVOL MAI	
	PERCENT, SPECIES NUM	
6.		
	SMTREE_VOL_TOTAL, SMTREE_HT_PRJ, SMTREE_VOL_PRJ	
	SMTREE_BIOMASS, BIOMASS_STEMWOOD, BIOMASS_STEMBARK, BIOMASS_BRANCHES,	
	BIOMASS_FOLIAGE, BMEQ_WOOD, BMEQ_BARK, BMEQ_BRANCHES, BMEQ_FOLIAGE	31
7.		
	PLOTVOL SMTR LIVE	
	PLOTVOL SMTR DEAD	
	PLOTBIO SMTR LIVE	
	PLOTBIO_SMTR_DEAD	
	PLOTBIO SMT STEMWOOD LIVE	
	PLOTBIO SMT STEMBARK LIVE	
	PLOTBIO SMT BRANCHES LIVE	

	OTBIO_SMT_FOLIAGE_LIVE	
	OTBIO_SMT_STEMWOOD_DEAD	
	OTBIO_SMT_STEMBARK_DEAD	
	OTBIO_SMT_BRANCHES_DEAD	
S۱	/ITREE_PERCENT, SMTREE_SPECIES_NUM	
8.	Shrub List and Summary	
	OMASS_TOTAL, BIOMASS_WOOD, BIOMASS_FOLIAGE	
PL	OTBIO_LGSHRUB_LIVE, PLOTBIO_LGSHRUB_DEAD	
9.	Stump List and Summary	
	UMP_VOLUME, STUMP_BIOMASS	
PL	OTVOL_STUMP, PLOTBIO_STUMP	. 41
10.	Species list	. 41
11.	Biodiversity Indices – Number of Unique Species and Shannon, Pielou Evenness and Margalef	
Indic	res 42	
12.	Fine Woody Debris, Small Shrubs, Small Stumps and Herbs	
PL	OTBIO_SMSHRUB	. 46
PL	OTBIO_HERB	. 47
PL	OTBIO_FWD	. 47
PL	OTBIO_BRYO	. 47
PL	OTBIO_SMSTUMP	. 48
13.	Coarse and Small Woody Debris – Plot-level Summary	. 48
DE	ENSITY	. 49
PL	OTVOL_ROUNDWD, PLOTBIO_ROUNDWD	. 49
CV	ND_LEAD_SPECIES	. 52
PL	OTVOL_SWD, PLOTBIO_SWD	. 54
PL	OTVOL_ODDWD, PLOTBIO_ODDWD	. 55
PL	OTVOL_CWD, PLOTBIO_CWD	. 57
14.	Coarse and Small Woody Debris – Plot-Level Summary by Decay Class	. 57
PL	OTVOL_ROUNDWD, PLOTBIO_ROUNDWD, PLOTVOL_ODDWD, PLOTBIO_ODDWD, PLOTVOL_WD,	
PL	OTBIO WD, PLOTVOL SWD, PLOTBIO SWD	. 57
15.	Soil Carbon	. 58
TΑ	ALLY_SS_BED, TALLY_SS_ROCK, TALLY_SS_MIN, TALLY_SS_WATER, TALLY_SS_ORG, TALLY_SS_BURI	ED,
	ALLY_SS_DECAY, TOTAL_MEAS	
	JLK DENSITY 2MM, BULK DENSITY TOTAL, CF GRAV, CF COBB, CF STONE (mineral soil samples)	
	YER_CC (mineral soil samples)	
	C_MIN0_15, CC_MIN15_35, CC_MIN35_55	
	YER_CC_8MM, LAYER_CC_TOTAL (forest floor & organic soil samples)	
	C_FOR_FLOOR_8MM, CC_FOR_FLOOR_TOTAL, CC_ORGANIC0_15_8MM, CC_ORGANIC15_35_8MM	
	C_ORGANIC35_55_8MM, CC_ORGANIC0_15_TOTAL, CC_ORGANIC15_35_TOTAL,	.,
		. 67
	PTH ORG, DEPTH MIN	
16.	Computational References for Tree Volume	
17.	Computational References for Biomass	
18.	Wood Density	

March 2021 iii

#### 1. Introduction

This document outlines the equations and rules that have been developed to compile the National Forest Inventory (NFI) ground plot raw data. Raw data from ground plots include field measurements and descriptions made at a point inside or adjacent to a photo plot. These raw ground plot data include individual large-tree and small-tree measurements, shrub tallies, understory vegetation sampling, vegetation cover, stump assessments, woody debris data, surface substrates, site descriptions and soil measurements.

Compilation of the ground plot raw data involves aggregating the individual-tree, understory-vegetation, woody-debris, and soil-pit measurements into plot averages and per-hectare values. For example, the plot basal area of large trees is obtained as a sum of the individual large tree basal areas converted to a per hectare value.

<u>Section 2</u> provides a list of calculated attributes; <u>Section 3</u> gives some notation and the remaining sections outline the compilation algorithms (routines) for each attribute. Reference to the NFI's *National Standards for Ground Plots Data Dictionary* and *Ground Sampling Guidelines* can improve understanding of terminology and processes described below.

# 2. Compiled Attributes

Compilation routines were developed to derive the attributes listed in the tables below based on field measurements and other data sources. The definitions of these attributes are based on the descriptions in the NFI document *National Standards for Ground Plots Data Dictionary*. Definitions of input variables stated in this manual (upper case) such as DBH and HEIGHT can be found in the same document, unless otherwise stated.

**Table 1.** Site information (table site info).

Variable Name	Attribute (Units)
EC_REGION	A subdivision of an ecoprovince characterized by distinctive
(Not yet implemented)	regional ecological factors, including climate, physiography, vegetation, soil, water, and fauna.
EC_DISTRICT	A subdivision of an ecoregion (different from ecoclimatic region)
(Not yet implemented)	characterized by a distinctive assemblages of relief, landforms, geology, soil, vegetation, water bodies and fauna.
PLOTVOL_STANDLIVE	Total volume ( $m^3$ $ha^{-1}$ ) of all trees that are longer than 1.3 m, having roots attached to the bole or an identifiable root collar; with DBH $\geq 9.0$ cm. Includes volume inside bark of the main stem, including stump and top of all <b>standing live trees</b> .
PLOTVOL_STANDDEAD	Total volume ( $m^3$ $ha^{-1}$ ) of all trees that are longer than 1.3 m, having roots attached to the bole or an identifiable root collar; and DBH $\geq$ 9.0 cm. Includes volume inside bark of the main stem, including stump and top of all <b>standing dead trees.</b>
PLOTVOL_FALLLIVE	Total volume ( $m^3$ $ha^{-1}$ ) of all trees that are longer than 1.3 m, having roots attached to the bole or an identifiable root collar; and DBH $\geq$ 9.0 cm. Includes volume inside bark of the main stem, including stump and top of all <b>fallen live trees</b> .
PLOTVOL_SMTR_LIVE	Total volume (m³ ha⁻¹) of all live small trees with a measurable DBH < 9.0 cm. For the purposes of this inventory attribute, a tree is defined as a woody plant, usually with a single stem and a

March 2021

Variable Name	Attribute (Units)
PLOTVOL_SMTR_DEAD	definite crown that is capable of reaching a mature height of 5.0 m somewhere within its natural range.  Total volume (m³ ha¹¹) of all dead small trees with a measurable
FEOTVOL_SWITK_DEAD	DBH < 9.0 cm. For the purposes of this inventory attribute, a tree is defined as a woody plant, usually with a single stem and a definite crown that is capable of reaching a mature height of 5.0
GROSSVOL_INCR	m somewhere within its natural range.  Current annual gross volume increment (m³ ha⁻¹ yr⁻¹) of the
(Not yet implemented)	entire plot. Calculated from growth and yield models or tree measurement information. Calculation includes accretion, ingrowth and mortality.
GROSSVOL_MAI	Mean annual gross volume increment (m³ ha-1 yr-1) of the entire
	plot. Calculated from volume and age data summaries.
	Calculation includes standing live, standing fallen and standing dead trees.
PLOTVOL_STUMP	Total volume ( $m^3 ha^{-1}$ ) of stumps $\leq 1.3 m$ in length and $\geq 4.0 cm$
	top diameter inside bark.
PLOTBIO_STUMP	Total above ground biomass of stumps ≤ 1.3 m in length and ≥ 4.0 cm top diameter inside bark ( <b>Mg ha</b> <sup>-1</sup> oven-dry material).
PLOTBIO_LGTR_LIVE	Total above ground biomass (Mg ha-1 oven-dry material) of all
	standing live and fallen live trees that are longer than 1.3 m,
	having roots attached to the bole or an identifiable root collar; and DBH $\geq$ 9.0 cm.
PLOTBIO_LGTR_DEAD	Total above ground biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) of all
1201510_2011527.5	standing dead trees that are longer than 1.3 m, having roots
	attached to the bole or an identifiable root collar; and DBH $\geq$ 9.0
	cm.
PLOTBIO_SMTR_LIVE	Total above ground biomass ( <b>Mg ha</b> -¹ oven-dry material) of live
	small trees. For the purposes of this inventory attribute, a small tree is defined as a woody plant, usually with a single trunk and
	definite crown that is greater than 1.3 m in height and < 9.0 cm
	DBH.
PLOTBIO_SMTR_DEAD	Total above ground biomass (Mg ha-1 oven-dry material) of dead
	small trees. For the purposes of this inventory attribute, a small
	tree is defined as a woody plant, usually with a single trunk and
	definite crown that is greater than 1.3 m in height and $<$ 9.0 cm DBH.
PLOTBIO_LGSHRUB_LIVE	Total above ground biomass of live shrubs $\geq 1.3$ m in height. (Mg $ha^{-1}$ oven-dry material).
PLOTBIO LGSHRUB DEAD	Total above ground biomass of dead shrubs ≥ 1.3 m in height.
	( <b>Mg ha</b> <sup>-1</sup> oven-dry material).
PLOTBIO_SMSHRUB	Total above ground biomass of small shrubs (live and/or dead) <
	1.3 m in height ( <b>Mg ha</b> <sup>-1</sup> oven-dry material).
PLOTBIO_HERB	Total above ground biomass of the herb layer ( <b>Mg ha</b> <sup>-1</sup> oven-dry material).
PLOTBIO_BRYO	Total above ground biomass of the bryophyte layer (Mg ha <sup>-1</sup>
DIOTRIO CNACTURAS	oven-dry material).
PLOTBIO_SMSTUMP	Total above ground biomass of small stumps with a top diameter inside bark of < 4 cm ( <b>Mg ha</b> <sup>-1</sup> oven-dry material).
PLOTBIO_FWD	Total above ground biomass of fine woody debris ( <b>Mg ha</b> <sup>-1</sup> oven-
	dry material). Fine woody debris measurements obtained from

Variable Name	Attribute (Units)
PLOTVOL_CWD	destructive sampling of microplots. Defined as material 0.5 cm to < 1.0 cm in diameter. Includes bark where present.  Total volume (m³ ha⁻¹) for all coarse woody debris > 7.5 cm in diameter. Includes all round and odd-shaped pieces. Includes
PLOTBIO_CWD	bark where present.  Total above ground biomass ( <b>Mg ha</b> -1 oven-dry material) for all coarse woody debris > 7.5 cm in diameter. Includes all round
PLOTVOL_SWD	and odd-shaped pieces. Includes bark where present. Total volume ( $m^3 ha^{-1}$ ) for all small woody debris $\geq 1$ cm and $\leq$ 7.5 cm in diameter. Includes bark where present.
PLOTBIO_SWD	Total above ground biomass (Mg ha <sup>-1</sup> oven-dry material) for all small woody debris $\geq 1$ cm and $\leq 7.5$ cm in diameter. Includes
PLOTVOL_ROUNDWD	bark where present.  Total volume (m³ ha⁻¹) for all coarse woody debris round pieces  > 7.5 cm in diameter. Includes bark where present.
PLOTBIO_ROUNDWD	Total above ground biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) for all coarse woody debris round pieces > 7.5 cm in diameter. Includes bark where present.
PLOTVOL_ODDWD	Total volume ( <b>m³ ha⁻¹</b> ) for all coarse woody debris odd-shaped pieces > 7.5 cm in diameter. Includes bark where present.
PLOTBIO_ODDWD	Total above ground biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) for all coarse woody debris odd-shaped pieces > 7.5 cm in diameter.
SAMPLE_DEPTH_MIN	Includes bark where present.  Maximum depth to which carbon content was calculated for mineral soil samples (cm).
SAMPLE_DEPTH_ORG	Maximum depth to which carbon content was calculated for organic soil samples (cm).
CC_FOR_FLOOR_8MM	Carbon content of the ≤ 8 mm fraction of the forest floor, plot level (Mg C ha <sup>-1</sup> )
CC_FOR_FLOOR_TOTAL CC_MINO_15	Carbon content of the total forest floor, plot level (Mg C ha <sup>-1</sup> ) Carbon content of the 0-15 cm mineral soil layer, plot level (Mg C ha <sup>-1</sup> )
CC_MIN15_35	Carbon content of the 15-35 cm mineral soil layer, plot level (Mg C ha <sup>-1</sup> )
CC_MIN35_55	Carbon content of the 35-55 cm mineral soil layer, plot level ( <b>Mg C ha</b> <sup>-1</sup> )
CC_ORGANICO_15_8MM	Carbon content of the ≤ 8 mm fraction of the organic soil occurring 0 - 15 cm below surface, plot level (Mg C ha <sup>-1</sup> )
CC_ORGANICO_15_TOTAL	Carbon content of the organic soil occurring 0 - 15 cm below surface, plot level ( <b>Mg C ha</b> <sup>-1</sup> )
CC_ORGANIC15_35_8MM	Carbon content of the ≤ 8 mm fraction of the organic soil occurring 15 - 35 cm below surface, plot level (Mg C ha <sup>-1</sup> )
CC_ORGANIC15_35_TOTAL	Carbon content of the organic soil occurring 15 - 35 cm below surface, plot level ( <b>Mg C ha</b> -1)
CC_ORGANIC35_55_8MM	Carbon content of the ≤ 8 mm fraction of the organic soil occurring 35 - 55 cm below surface, plot level (Mg C ha <sup>-1</sup> )
CC_ORGANIC35_55_TOTAL	Carbon content of the organic soil occurring 35 - 55 cm below surface, plot level ( <b>Mg C ha</b> -1)
AVG_ORG_CARB	The average carbon concentration of $\leq 8$ mm fraction organic soil and forest floor samples ( $\mathbf{g} \ \mathbf{kg}^{-1}$ )

Variable Name	Attribute (Units)
AVG_BULK_DENSITY_ORG	The average bulk density of $\leq$ 8 mm fraction of organic soil and forest floor samples ( <b>g cm</b> <sup>-3</sup> )

Table 2. Large tree plot header (table ltp header).

Variable Name	Attribute (Units)
SITE_INDEX	An expression of forest site quality based on the height (m), at a breast-height age of 50 years, of the dominant and co-dominant trees (site trees) in the large tree plot.
SITE_INDEX_GENUS	Site index genus code. Uses the first four letters of the scientific genus name. If unknown conifer, use code <b>GENC</b> , if unknown hardwood, use code <b>GENH</b> . For a list of acceptable genus codes, refer to the <i>NFI Tree Species List</i> .
SITE_INDEX_SPECIES	Site index species code. Uses the first three letters of the scientific species name. If unknown species, use code <b>SPP</b> . For a list of acceptable species codes, refer to the <i>NFI Tree Species List</i> .
SITE_HEIGHT	The average height (m) of intact live standing dominant and codominant trees forming the stand (site trees).
LOREY_HEIGHT	The average height (m) of all intact live trees (LF, LS) in the plot, weighted by their basal area.
SITE_AGE	The average total age ( <b>years</b> ) of the dominant and co-dominant trees forming the stand (site trees).
NUM_LAB	A field to indicate the number of lab-counted tree cores used in the determination of site age.
NUM_FIELD	A field to indicate the number of field-counted tree cores used in the determination of site age.
BASAL_AREA_STANDLIVE	Summed cross-sectional area ( $m^2 ha^{-1}$ ), measured at breast height, of tree boles for all standing live trees within the LTP. Minimum DBH measured = 9.0 cm.
BASAL_AREA_STANDDEAD	Summed cross-sectional area ( $m^2 ha^{-1}$ ), measured at breast height, of tree boles for all standing dead trees within the LTP. Minimum DBH measured = 9.0 cm.
BASAL_AREA_FALLLIVE	Summed cross-sectional area (m² ha-1), measured at breast height, of tree boles for all fallen live trees within the LTP.  Minimum DBH measured = 9.0 cm.
STEM_DENSITY_STANDLIVE	The number of standing live <b>stems ha</b> <sup>-1</sup> including stems with minimum DBH = 9.0 cm
STEM_DENSITY_STANDDEAD	The number of standing dead <b>stems ha</b> <sup>-1</sup> including stems with minimum DBH = 9.0 cm
STEM_DENSITY_FALLLIVE	The number of fallen live <b>stems ha</b> <sup>-1</sup> including stems with minimum DBH = 9.0 cm
SPECIES_LTNUM	This is the total number of unique species of live standing large tree in an area (species richness).
BINDEX_LTSHANNON	The Shannon diversity index, which is a measure of the species richness and evenness for live standing large trees.
BINDEX_LTEVEN	The Pielou evenness index, which measures how close the numbers of individual live large trees of each species are to each other.
BINDEX_LTMARGALEF	The Margalef richness index, which measures the total number o large tree species in an area.

Variable Name	Attribute (Units)
PLOTBIO_STEMWOOD_LIVE	Total biomass (Mg ha <sup>-1</sup> oven-dry material) of stem wood of all live standing and live fallen trees $\geq 1.3$ m in height and DBH $\geq 9.0$ cm.
PLOTBIO_STEMBARK_LIVE	Total biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) of stem bark of all live standing and live fallen trees $\geq 1.3$ m in height DBH $\geq 9.0$ cm.
PLOTBIO_BRANCHES_LIVE	Total biomass (Mg ha <sup>-1</sup> oven-dry material) of branches of all live standing and live fallen trees $\geq 1.3$ m in height and DBH $\geq 9.0$ cm.
PLOTBIO_FOLIAGE_LIVE	Total biomass (Mg ha <sup>-1</sup> oven-dry material) of foliage of all live standing and live fallen trees $\geq 1.3$ m in height and DBH $\geq 9.0$ cm.
PLOTBIO_STEMWOOD_DEAD	Total biomass (Mg ha <sup>-1</sup> oven-dry material) of stem wood of all dead standing trees $\geq 1.3$ m in height and DBH $\geq 9.0$ cm.
PLOTBIO_STEMBARK_DEAD	Total biomass (Mg ha <sup>-1</sup> oven-dry material) of stem bark of all dead standing trees $\geq 1.3$ m in height and DBH $\geq 9.0$ cm. The biomass of stem bark is 0 for unidentifiable conifer or hardwood dead standing trees.
PLOTBIO_BRANCHES_DEAD	Total biomass (Mg ha <sup>-1</sup> oven-dry material) of branches of all dead standing trees $\geq$ 1.3 m in height and DBH $\geq$ 9.0 cm. The biomass of branches is 0 for unidentifiable conifer or hardwood dead standing trees.

 Table 3. Large tree species composition (table ltp\_tree\_species\_comp).

Variable Name	Attribute (Units)
SPECIES_NUM	Identifies the species ranked abundance in the plot by percentage of basal area per hectare.
PERCENT	Percentage (%) of the species in the plot determined by live basal area per hectare in the large tree plot.

**Table 4.** Large tree list (table ltp\_tree).

Variable Name	Attribute (Units)
HEIGHT_PRJ	The projected height ( <b>m</b> ) to the top of the tree before the break occurred. Calculated for broken trees and trees with missing height values. Projected tree height is reported to the nearest 0.1 m. Reported if HEIGHT_PRJ ≥ HEIGHT.
CROWN_LENGTH	The crown length ( <b>m</b> ) for all trees in the large tree plot with a HEIGHT_LIVE > 0.
VOL_TOTAL	The total volume ( $m^3$ ) by tree for all trees in the large tree plot $\geq$ 1.3 m in height and DBH $\geq$ 9.0 cm. Includes volume inside bark of the main stem including stump and top.
VOL_PRJ	The total volume ( $m^3$ ) calculated to the projected height (HEIGHT_PRJ) by tree for all trees in the large tree plot $\geq 1.3$ m in height and DBH $\geq 9.0$ cm. Includes volume inside bark of the main stem including stump and reconstructed top.
BIOMASS_TOTAL	The total aboveground biomass ( $kg$ oven-dry material) by tree for all trees in the large tree plot $\geq 1.3$ m in height having roots attached to the bole or an identifiable root collar and DBH $\geq 9.0$ cm.
BIOMASS_STEMWOOD	The stem wood biomass (kg oven-dry material) by tree for all trees in the large tree plot $\geq$ 1.3 m in height having roots attached to the bole or an identifiable root collar and DBH $\geq$ 9.0 cm.

Variable Name	Attribute (Units)
BIOMASS_STEMBARK	The stem bark biomass (kg oven-dry material) by tree for all
	trees in the large tree plot ≥ 1.3 m in height having roots
	attached to the bole or an identifiable root collar and DBH $\geq$ 9.0
	cm.
BIOMASS_BRANCHES	The branch biomass (kg oven-dry material) by tree for all trees in
	the large tree plot $\geq$ 1.3 m in height having roots attached to the
	bole or an identifiable root collar and DBH ≥ 9.0 cm.
BIOMASS_FOLIAGE	The foliage biomass (kg oven-dry material) by tree for all trees in
	the large tree plot $\geq$ 1.3 m in height having roots attached to the
BIOMASS_STEMBARK BIOMASS_BRANCHES	bole or an identifiable root collar and DBH ≥ 9.0 cm. Dead trees
	are assumed to have zero foliage biomass.
BMEQ_WOOD	The biomass equation ID for computing stem wood biomass
	(eqid from support table gpcsd_tree_biom_eqs)
BMEQ_BARK	The biomass equation ID for computing stem bark biomass (eqid
	from support table <pre>gpcsd_tree_biom_eqs</pre>
BMEQ_BRANCHES	The biomass equation ID for computing branch biomass (eqid
	from support table <pre>gpcsd_tree_biom_eqs</pre>
BMEQ_FOLIAGE	The biomass equation ID for computing foliage biomass (eqid
	from support table <pre>gpcsd_tree_biom_eqs</pre>

**Table 5.** Large tree plot, site tree and age information (table ltp\_tree\_age).

Variable Name	Attribute (Units)
AGE CORR YEARS	Estimated number of full years of the tree growth below the
<b>- -</b>	boring height.
AGE_TOTAL	An estimate of the total age of the tree.

<b>Table 6.</b> Small tree plot header (table st	:p header).
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Variable Name	Attribute (Units)
SPECIES_SMTNUM	This is the total number of all unique live standing small tree species in an area (species richness).
BINDEX_STSHANNON	The Shannon diversity index, which is a measure of the species richness and evenness for small trees.
BINDEX_STEVEN	The Pielou evenness index, which measures how close the numbers of individual live small trees of each species are to each other.
BINDEX_STMARGALEF	The Margalef richness index, which measures the total number of small tree species in an area.
PLOTBIO_SMT_STEMWOOD_LIVE	Total biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material), of stem wood of all small live standing trees ≥ 1.3 m in height and DBH < 9.0 cm.
PLOTBIO_SMT_STEMBARK_LIVE	Total biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material), of stem bark of all small live standing trees ≥ 1.3 m in height and DBH < 9.0 cm.
PLOTBIO_SMT_BRANCHES_LIVE	Total biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material), of branches of all small live standing trees ≥ 1.3 m in height and DBH < 9.0 cm.
PLOTBIO_SMT_FOLIAGE_LIVE	Total biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material), of foliage of all small live standing trees ≥ 1.3 m in height and DBH < 9.0 cm.
PLOTBIO_SMT_STEMWOOD_DEAD	Total biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material), of stem wood of all small dead standing trees ≥ 1.3 m in height and DBH < 9.0 cm.
PLOTBIO_SMT_STEMBARK_DEAD	Total biomass ( <b>Mg ha</b> -¹ oven-dry material), of bark of all small dead standing trees ≥ 1.3 m in height and DBH < 9.0 cm. The

Variable Name	Attribute (Units)
PLOTBIO_SMT_BRANCHES_DEAD	biomass of stem bark is 0 for unidentifiable conifer or hardwood dead standing trees.  Total biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material), of branches of all small dead standing trees ≥ 1.3 m in height and DBH < 9.0 cm.  The biomass of branches is 0 for unidentifiable conifer or hardwood dead standing trees.

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Variable Name	Attribute (Units)
SMTREE_VOL_TOTAL	The total volume (m³) by tree for all trees in the small tree plot ≥
	1.3 m in height and DBH < 9.0 cm. Includes volume inside bark
	of the main stem including stump and top.
SMTREE_HT_PRJ	The projected height (m) to the top of the small tree before the
	break occurred. Calculated for broken trees and for trees with
	missing height values. Projected height is reported to the
	nearest 0.1 m. SMTREE_HT_PRJ ≥ SMTREE_HT.
SMTREE_BIOMASS	The total aboveground biomass (kg oven-dry material) by tree
	for all trees in the small tree plot ≥ 1.3 m in height and DBH < 9.0
	cm having roots attached to the bole or an identifiable root
	collar.
BIOMASS_STEMWOOD	The stem wood biomass (kg oven-dry material) by tree for all
	trees in the small tree plot $\geq$ 1.3 m in height and DBH < 9.0 cm
	having roots attached to the bole or an identifiable root collar.
BIOMASS_STEMBARK	The stem bark biomass (kg oven-dry material) by tree for all
	trees in the small tree plot $\geq$ 1.3 m in height and DBH < 9.0 cm
	having roots attached to the bole or an identifiable root collar.
BIOMASS_BRANCHES	The branch biomass (kg oven-dry material) by tree for all trees in
	the small tree plot $\geq$ 1.3 m in height and DBH < 9.0 cm having
	roots attached to the bole or an identifiable root collar.
BIOMASS_FOLIAGE	The foliage biomass (kg oven-dry material) by tree for all trees in
	the small tree plot $\geq$ 1.3 m in height and DBH < 9.0 cm having
	roots attached to the bole or an identifiable root collar.
BMEQ_WOOD	The biomass equation ID for computing stem wood biomass
	(eqid from support table gpcsd_tree_biom_eqs)
BMEQ_BARK	The biomass equation ID for computing stem bark biomass (eqid
	from support table <i>gpcsd_tree_biom_eqs</i> )
BMEQ_BRANCHES	The biomass equation ID for computing branch biomass (eqid
	from support table <i>gpcsd_tree_biom_eqs</i> )
BMEQ_FOLIAGE	The biomass equation ID for computing foliage biomass (eqid
	from support table <i>gpcsd_tree_biom_eqs</i> )
SMTREE_VOL_PRJ	Total tree volume (m³) to the projected height of a broken top
	tree

 Table 8. Small tree species composition (table stp\_tree\_species\_comp).

Variable Name	Attribute (Units)
SMTREE_SPECIES_NUM	Identifies the species ranked abundance in the plot by
	percentage of basal area per hectare
SMTREE_PERCENT	Percent (%) composition of the small tree species based on
	proportion of live basal area in the small tree plot.

March 2021

<b>Table 9.</b> Shrub plot, species	list (table shrub_list).
Variable Name	Attribute (Units)
BIOMASS_TOTAL	Total above ground biomass (kg of oven dry material)
BIOMASS_WOOD	Total above ground woody biomass (kg of oven dry material)
BIOMASS_FOLIAGE	Total foliage biomass (kg of oven dry material)
BMEQ_TOTAL	Biomass equation ID for computing total above ground biomass
BMEQ_WOOD	Biomass equation ID for computing above ground woody
	biomass

Biomass equation ID for computing foliage biomass

<b>Table 10.</b> Stump list (table stump
--

BMEQ\_FOLIAGE

Variable Name	Attribute (Units)
STUMP_VOLUME	The total volume (m³) of each stump in the stump plot with
	diameter inside bark ≥ 4 cm.
STUMP_BIOMASS	The total aboveground biomass (kg oven-dry material) of each
	stump in the stump plot.

**Table 11.** Ecological biodiversity (table biodiversity\_ec).

	7 \ 7 = 7
Variable Name	Attribute (Units)
SPECIES_ECNUM	Total number of all unique ecological species (species richness).
	Reported by ecological layer (trees, tall shrubs, low shrubs,
	herbs and bryoids).
BINDEX_ECSHANNON	Shannon diversity index for ecological species
BINDEX_ECEVEN	Pielou evenness index for ecological species, which measures
	how close, in percent cover, each species are within an
	ecological layer.

**Table 12.** Round coarse woody debris (table woody\_debris\_round).

Variable Name	Attribute (Units)
DENSITY	The wood density ( <b>g cm</b> <sup>-3</sup> ) associated with each piece of round woody debris, based on a combination of the species codes and wood condition (DECAY_CLASS).

**Table 13.** Odd coarse woody debris (table woody\_debris\_odd).

Variable Name	Attribute (Units)
DENSITY	The wood density ( <b>g cm</b> <sup>-3</sup> ) associated with each piece of odd woody debris, based on a combination of the species codes and wood condition (DECAY_CLASS).

**Table 14.** Woody debris summary (table wd\_summary).

Variable Name	Attribute (Units)
PLOTVOL_SWD	Total volume ( $m^3 ha^{-1}$ ) for all small woody debris $\geq 1$ cm and $\leq$ 7.5 cm in diameter by decay class. Includes bark where present.
PLOTBIO_SWD	Total above ground biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) for all small woody debris $\geq 1$ cm and $\leq 7.5$ cm in diameter by decay class. Includes bark where present.
PLOTVOL_WD	Total volume ( <b>m³ ha⁻¹</b> ) for all coarse woody debris > 7.5 cm in diameter by decay class. Includes all round and odd-shaped pieces. Includes bark where present.

Variable Name	Attribute (Units)
PLOTBIO_WD	Total above ground biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) for all coarse woody debris > 7.5 cm in diameter by decay class. Includes all round and odd-shaped pieces. Includes bark where present.
PLOTVOL_ROUNDWD	Total volume (m³ ha⁻¹) for all coarse woody debris round pieces > 7.5 cm in diameter by decay class. Includes bark where present.
PLOTBIO_ROUNDWD	Total above ground biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) for all coarse woody debris round pieces > 7.5 cm in diameter by decay class. Includes bark where present.
PLOTVOL_ODDWD	Total volume (m³ ha-¹) for all coarse woody debris odd-shaped pieces > 7.5 cm in diameter by decay class. Includes bark where present.
PLOTBIO_ODDWD	Total above ground biomass ( <b>Mg ha</b> <sup>-1</sup> oven-dry material) for all coarse woody debris odd-shaped pieces > 7.5 cm in diameter by decay class. Includes bark where present.

**Table 15.** Surface substrate header (table surface\_substrate\_header).

Variable Name	Attribute (Units)
TOTAL_MEAS	Total number of surface substrate measurements made along the transect.
TALLY_SS_ORG	Number of surface substrate measurements along the transect line with organic matter cover (includes: organic layers ≥ 1 cm thick overlying mineral soil, cobbles, stones or bedrock; layers of decaying wood < 10 cm thick; large animal droppings; and areas covered by mats of bunchgrass [mats include L horizons]).
AVG_ORG_THICK	The average depth (cm) of the organic matter surface substrate (if present).
TALLY_SS_BURIED	Number of surface substrate measurements along the transect line with buried wood cover (includes: class 5 woody debris with > 50 % thickness below surrounding surface; may be covered with mosses, lichens, liverworts, or other plants; if an organic layer has developed over the wood, buried wood must be > 10 cm thick otherwise it is classed as 'organic matter').
AVG_BURIED_THICK	The average depth (cm) of the buried wood surface substrate (if present).
TALLY_SS_DECAY	Number of surface substrate measurements along the transect line with decaying wood cover (includes: fallen trees, large branches on the ground surface, and partially buried stumps with an exposed edge; may be covered with mosses, lichens, liverworts, or other plants; if an organic layer developed over the wood, decaying wood must have > 50 % of its thickness above the surrounding surface, otherwise it is classed as 'buried wood').
TALLY_SS_BED	Number of surface substrate measurements along the transect line with bedrock cover (includes: exposed consolidated mineral material; may have a partial covering of mosses, lichens, liverworts, or other epilithic plants; does not qualify as bedrock if covered by unconsolidated mineral material or organic matter ≥ 1 cm in thickness).

Variable Name	Attribute (Units)
TALLY_SS_ROCK	Number of surface substrate measurements along the transect line with rock or cobble and stones cover (includes: exposed unconsolidated rock fragments > 7.5 cm in diameter; may be covered by mosses, lichens, liverworts, epilithic plants, or an organic layer < 1 cm in thickness; does not include gravels < 7.5 cm in diameter).
TALLY_SS_MIN	Number of surface substrate measurements along the transect line with mineral soil cover (includes: unconsolidated mineral material of variable texture not covered by organic matter; may have a partial cover of mosses, lichens, and liverworts; includes small cobbles and gravel < 7.5 cm in diameter; areas of living grass or forb cover where mineral soil is visible between stems are classed as mineral soil, as are exposed Ah or Ae horizons.
TALLY_SS_WATER	Number of surface substrate measurements along the transect line covered with streams, puddles, or areas of open water in bogs or fens (does not include 'casual' or non-permanent water)

**Table 16.** Soil pit depth (table soil\_pit\_depth).

Variable Name	Attribute (Units)
DEPTH_MIN	Total depth to which mineral soil samples were collected in a pit (cm).
DEPTH_ORG	Total depth to which forest floor and/or organic soil samples were collected in a pit (cm).

**Table 17.** Forest floor organic sample (table for\_flr\_org\_sample).

Variable Name	Attribute (Units)
BULK_DENSITY_8MM	The bulk density of the $\leq$ 8 mm portion of the forest floor (g cm <sup>-3</sup> oven-dry material)
BULK_DENSITY_TOTAL	The bulk density of the total forest floor (g cm <sup>-3</sup> oven-dry material)
LAYER_CC_8MM	Carbon content per unit area of the $\leq 8$ mm component of the forest floor sample (kg m <sup>-2</sup> )
LAYER_CC_TOTAL	Carbon content per unit area of the total forest floor sample (kg m <sup>-2</sup> )

 Table 18. Mineral soil sample (table soil\_mineral\_sample).

Variable Name	Attribute (Units)
CF_GRAV	The % content of gravel (diameter < 7.5 cm or length < 15 cm) in the mineral horizon represented by the sample.
CF_COBB	The % content of cobble (diameter = 7.5 to 25 cm or length = 15 to 38 cm) in the mineral horizon represented by the sample.
CF_STONE	The % content of stone (diameter > 25 cm or length > 38 cm) in the mineral horizon represented by the sample.
BULK_DENSITY_2MM	The bulk density of the $\leq$ 2 mm portion of the mineral soil ( <b>g cm</b> <sup>-3</sup> oven-dry material)
BULK_DENSITY_TOTAL	The bulk density of the total mineral soil sample ( <b>g cm</b> <sup>-3</sup> oven-dry material)
LAYER_CC	Carbon content per unit area of the mineral soil sample (kg m <sup>-2</sup> )

Table 19.	Organic soil sam	ple (table so	oil org sample).

Variable Name	Attribute (Units)
BULK_DENSITY_8MM	The bulk density of the $\leq$ 8 mm portion of the organic soil (g cm <sup>-3</sup> oven-dry material)
BULK_DENSITY_TOTAL	The bulk density of the total organic soil sample ( <b>g cm</b> <sup>-3</sup> oven-dry material)
LAYER_CC_8MM	Carbon content per unit area of the $\leq 8$ mm component of the organic soil sample (kg m <sup>-2</sup> )
LAYER_CC_TOTAL	Carbon content per unit area of the total organic soil sample (kg m <sup>-2</sup> )

**Table 20.** Relative abundance of large tree species (table rel\_abundance\_lgtree).

Variable Name	Attribute (Units)
SPECIES_NUM	Ranked abundance number
SPECIES_LTREL	The relative abundance of each large tree taxon in an area,
	expressed as a proportion.

**Table 21.** Relative abundance of small tree species (table rel\_abundance\_smtree).

Variable Name	Attribute (Units)
SPECIES_NUM	Ranked abundance number
SPECIES_STREL	The relative abundance of each small tree taxon in an area,
	expressed as a proportion.

 Table 22. Relative abundance of ecological species (table rel\_abundance\_ec).

Variable Name	Attribute (Units)
SPECIES_NUM	Ranked abundance number
SPECIES_ECREL	The relative abundance, by taxon, in an ecological layer, based
	on forest cover

**Table 23.** Unique species list (table species\_list).

Variable Name	Attribute (Units)
SPECIES_INDEX	A unique number assigned to each taxon in the NFI plot.
GENUS	The genus of each plant taxon detected in the NFI plot.
SPECIES	The species of each plant taxon detected in the NFI plot.
VARIETY	The variety of each plant taxon detected in the NFI plot.

#### 3. Notation and constants

Throughout this document, the following conventions are observed:

The value of  $\pi$  (pi) has been set to the constant 3.14159265.

Tree, shrub and stump biomass estimates are all above ground and expressed on an oven-dry basis. Tree volume refers only to the above-ground volume inside bark of the main stem, from the base of the stump to the top of the main leader, excluding branches and other bifurcations.

The scaling of units to per-hectare values make use of measured plot sizes (MEAS\_PLOT\_SIZE) when these are available, else nominal plot sizes (NOM\_PLOT\_SIZE) are used and, if information was collected before August 1, 2007, adjusted accordingly when plot measurement was split by half or a quarter (PLOT\_SPLIT).

```
IF MEAS_PLOT_SIZE > 0 then PLOT_SIZE = MEAS_PLOT_SIZE

ELSE IF PLOT_SPLIT = 'F' then PLOT_SIZE = NOM_PLOT_SIZE

ELSE IF PLOT_SPLIT = 'H' then PLOT_SIZE = NOM_PLOT_SIZE * 0.5

ELSE IF PLOT_SPLIT = 'Q' then PLOT_SIZE = NOM_PLOT_SIZE * 0.25
```

Wood density (DENSITY; g cm<sup>-3</sup>) coefficients are used to convert woody debris volume to biomass. These coefficients vary by genus, species and variety (WD\_GENUS, WD\_SPECIES, WD\_VARIETY) and decay class (DECAY\_CLASS) and are contained in the wood\_density dataset. More information regarding the source and derivation of these coefficients is contained in section 18.

Carbon content in soil samples and soil layers were reported on an oven-dry basis, where soil samples were dried in a forced-air oven (at  $105^{\circ}C \pm 3^{\circ}C$  for mineral soil and  $70^{\circ}C \pm 3^{\circ}C$  for forest floor, organic soil and other organic matter) for 24 to 48 hours or until no change in sample mass was detected (Alemdag, I.S. 1980. Manual of data collection and processing for the development of forest biomass relationships. Canadian Forestry Service Information Report PI-X-4. 38p). The mass of mineral soil fractions used in compilations were reported on an air-dried basis (25°C) and adjusted for moisture content in the fraction less than 2 mm after oven drying at  $105^{\circ}C \pm 3^{\circ}C$ .

Given the quasi-ubiquitous requirement for plot number (NFI\_PLOT) and measurement period (MEAS\_NUM) in computing the values listed below, these two attributes were omitted from 'inputs' subsections.

# 4. Large Tree List

#### **Compiler routines**

lgtree\_volume\_all.sas lgtree\_biomass.sas

#### Output written to:

ltp\_tree

#### **HEIGHT\_PRJ**

**Compiler routines** 

gp\_ht\_dbh\_prj.sas (called from the large tree volume routines gp\_tree\_volume\_ab.sas, gp\_tree\_volume\_bc.sas, etc. which are called from lgtree\_volume\_all.sas; also called from the large tree biomass routines)

#### Inputs

TREE\_NUM; LGTREE\_GENUS; LGTREE\_SPECIES; LGTREE\_VARIETY; LGTREE\_STATUS; STEM\_COND; DBH; HEIGHT

#### **Computations**

If the tree has a broken top (STEM\_COND = 'B') or is missing height value (HEIGHT = -1), estimate the projected total height of the tree in meters (HEIGHT\_PRJ). The computations are described in more detail in section 16.

#### Output

HEIGHT PRJ

#### **CROWN\_LENGTH**

#### **Compiler routines**

Lgtree\_volume\_all.sas

#### Inputs

TREE NUM; CROWN BASE; CROWN TOP; HEIGHT

#### **Computations**

Set crown length (CROWN\_LENGTH) to missing when the height to the base of the live crown (CROWN\_BASE) is missing (i.e. -1) or not applicable (i.e. -9) (e.g. when tree status is dead standing). If the height to the top of the live crown (CROWN\_TOP) is missing or not applicable yet the height to the base of the live crown is measured then assume the height of the top of the live crown is equal to the height of the tree. Calculate crown length (m) as the difference between the top and base of the live crown.

```
If \ CROWN\_BASE_{mpt} = -9 \ then \ CROWN\_LENGTH_{mpt} = -9 If \ CROWN\_TOP_{mpt} \leq 0 \ and \ CROWN\_BASE_{mpt} \geq 0 \ then \ CROWN\_TOP_{mpt} = HEIGHT_{mpt} If \ (CROWN\_BASE_{mpt} = -1 \ or \ CROWN\_TOP_{mpt} = -1) \ then \ CROWN\_LENGTH_{mpt} = -1 If \ CROWN\_BASE_{mpt} \geq 0 \ and \ CROWN\_TOP_{mpt} > 0 \ then \ CROWN\_LENGTH_{mpt} = CROWN\_TOP_{mpt} - CROWN\_BASE_{mpt}
```

where t is a unique tree (TREE\_NUM) within a plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

CROWN\_LENGTH

#### VOL TOTAL, VOL PRJ

#### **Compiler routines**

Tree volumes use provincial volume estimation routines, gp\_tree\_volume\_ab.sas, gp\_tree\_volume\_bc.sas etc., which are called from lgtree\_volume\_all.sas)

#### Inputs

TREE\_NUM; LGTREE\_GENUS; LGTREE\_SPECIES; LGTREE\_VARIETY; LGTREE\_STATUS; STEM\_COND; DBH; HEIGHT; HEIGHT PRJ

#### **Computations**

The computations are described in more detail in section 16.

1) Calculate the total tree volume (m³) of each tree ≥ 1.3 m in height. If the tree has a broken top (STEM\_COND = 'B'), the volume to the estimated projected height of the tree before the break occurred is labelled VOL PRJ and the volume to the break is VOL TOTAL.

#### Output

VOL\_TOTAL, VOL\_PRJ

# BIOMASS\_TOTAL, BIOMASS\_STEMWOOD, BIOMASS\_STEMBARK, BIOMASS\_BRANCHES, BIOMASS\_FOLIAGE, BMEQ\_WOOD, BMEQ\_BARK, BMEQ\_BRANCHES, BMEQ\_FOLIAGE

#### **Compiler routines**

Lgtree biomass.sas

#### Inputs

TREE\_NUM; LGTREE\_GENUS; LGTREE\_SPECIES; LGTREE\_VARIETY; LGTREE\_STATUS; DBH; HEIGHT; HEIGHT\_PRJ; PROVINCE; ECOZONE; STEM\_COND; VOL\_TOTAL; VOL\_PRJ

#### **Computations**

The computations are described in more detail in <u>section 17</u>. In some cases biomass equations jointly treat stem wood with stem bark or branches with foliage. In such cases, biomass for stem bark (BIOMASS\_STEMBARK) or foliage (BIOMASS\_FOLIAGE) is set to zero, however these components are included in stem wood (BIOMASS\_STEMWOOD) or branches (BIOMASS\_BRANCHES) components, respectively.

1) Estimate the total biomass (kg) of each tree using existing tree biomass equations and coefficients. For broken top trees, use the projected height. Keep track of which equation number (eqid) is used (reported as BMEQ WOOD, BMEQ BARK, BMEQ BRANCHES and BMEQ FOLIAGE).

```
BIOMASS\_STEMWOOD_{mpt} = f(DBH_{pmt}, HEIGHT_{mpt})

BIOMASS\_STEMBARK_{mpt} = f(DBH_{pmt}, HEIGHT_{mpt})

BIOMASS\_BRANCHES_{mpt} = f(DBH_{pmt}, HEIGHT_{mpt})

BIOMASS\_FOLIAGE_{mpt} = f(DBH_{pmt}, HEIGHT_{mpt})
```

where t is a unique tree (TREE\_NUM) within a plot p (NFI\_PLOT) at measurement m (MEAS\_NUM) and equation forms and coefficients are based on genus, species, variety, province and ecozone. Note that some species use only diameter as the predictor for biomass

- 2) For broken top trees (STEM\_COND = 'B'), multiply each biomass component by a correction factor to correct biomass estimates to the height of the break. The correction for broken top trees is the ratio between the volume to the broken top and the volume to the projected height ( $VOL\_TOTAL_{mot}/VOL\_PRI_{mot}$ ).
- 3) Add some logic checks:

Set foliage biomass to zero for dead standing (DS) trees when information on crown condition is missing (CROWN COND = -1).

```
If LGTREE\_STATUS_{mnt} = 'DS' and CROWN\_COND_{mnt} = -1 then BIOMASS\_FOLIAGE_{mnt} = 0
```

When missing information on bark retention or crown condition, set bark or branch biomass, respectively, to zero for dead standing (DS) trees if the genus is unknown (it is assumed that if the genus is unknown, there was no bark or branches to identify the species).

```
If LGTREE\_STATUS_{mpt}

= 'DS' and LGTREE\_GENUS_{mpt} in ('GENC', 'GENH', 'UNKN') and CROWN\_COND_{mpt}

= -1 then BIOMASS\_FOLIAGE_{mpt} = 0

If LGTREE\_STATUS_{mpt}

= 'DS' and LGTREE\_GENUS_{mpt} in ('GENC', 'GENH', 'UNKN') and BARK\_RET_{mpt}

= -1 then BIOMASS\_STEMBARK_{mpt} = 0
```

Set biomass values less than zero to missing ('.')

```
\begin{array}{l} \textit{If BIOMASS\_STEMWOOD}_{mpt} < 0 \; \textit{then BIOMASS\_STEMWOOD}_{mpt} = . \\ \textit{If BIOMASS\_STEMBARK}_{mpt} < 0 \; \textit{then BIOMASS\_STEMBARK}_{mpt} = . \\ \textit{If BIOMASS\_BRANCHES}_{mpt} < 0 \; \textit{then BIOMASS\_BRANCHES}_{mpt} = . \\ \textit{If BIOMASS\_FOLIAGE}_{mpt} < 0 \; \textit{then BIOMASS\_FOLIAGE}_{mpt} = . \\ \end{array}
```

Set foliage biomass (BIOMASS\_FOLIAGE) to zero when crown condition (CROWN\_COND) is greater or equal to 3. Reduce foliage biomass by 50% when crown condition is equal to 2.

```
If \ CROWN\_COND_{mpt} = 2 \ then \ BIOMASS\_FOLIAGE_{mpt} = BIOMASS\_FOLIAGE_{mpt} * 0.5 \\ If \ CROWN\_COND_{mpt} \ge 3 \ then \ BIOMASS\_FOLIAGE_{mpt} = 0
```

Set branch biomass (BIOMASS\_BRANCHES) to zero when crown condition is 6. Adjust branch biomass to 75% or 25% when crown condition is 4 or 5 respectively.

```
\begin{split} If \ CROWN\_COND_{mpt} = 4 \ then \ BIOMASS\_BRANCHES_{mpt} = BIOMASS\_BRANCHES_{mpt} * 0.75 \\ If \ CROWN\_COND_{mpt} = 5 \ then \ BIOMASS\_BRANCHES_{mpt} = BIOMASS\_BRANCHES_{mpt} * 0.25 \\ If \ CROWN\_COND_{mpt} = 6 \ then \ BIOMASS\_BRANCHES_{mpt} = 0 \end{split}
```

Set stem bark biomass (BIOMASS\_STEMBARK) to zero when bark retention (BARK\_RET) is equal to 7. When the bark retention is 2-6, adjust the stem bark biomass by the midpoint of the range of % stem bark remaining defined by a given bark retention class.

```
If \ BARK\_RET_{mpt} = 2 \ then \ BIOMASS\_STEMBARK_{mpt} = BIOMASS\_STEMBARK_{mpt} * (1-0.025) If \ BARK\_RET_{mpt} = 3 \ then \ BIOMASS\_STEMBARK_{mpt} = BIOMASS\_STEMBARK_{mpt} * (1-0.15) If \ BARK\_RET_{mpt} = 4 \ then \ BIOMASS\_STEMBARK_{mpt} = BIOMASS\_STEMBARK_{mpt} * (1-0.38) If \ BARK\_RET_{mpt} = 5 \ then \ BIOMASS\_STEMBARK_{mpt} = BIOMASS\_STEMBARK_{mpt} * (1-0.63) If \ BARK\_RET_{mpt} = 6 \ then \ BIOMASS\_STEMBARK_{mpt} = BIOMASS\_STEMBARK_{mpt} * (1-0.875) If \ BARK\_RET_{mpt} = 7 \ then \ BIOMASS\_STEMBARK_{mpt} = 0
```

where t is a unique tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

4) Sum the biomass components for each tree:

```
BIOMASS\_TOTAL_{mpt} \\ = BIOMASS\_STEMWOOD_{mpt} + BIOMASS\_STEMBARK_{mpt} \\ + BIOMASS\_BRANCHES_{mpt} + BIOMASS\_FOLIAGE_{mpt}
```

where t is a unique tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

BIOMASS\_STEMWOOD, BIOMASS\_STEMBARK, BIOMASS\_BRANCHES, BIOMASS\_FOLIAGE, BIOMASS\_TOTAL, BMEQ\_WOOD, BMEQ\_BARK, BMEQ\_BRANCHES, BMEQ\_FOLIAGE

## 5. Large Tree Plot Summary

#### **Compiler routines**

```
gp_compile_lgtree.sas
gp_ltp_tree_age_corr_years.sas
gp_ltp_tree_age_total.sas
gp_siteindex_macro.sas (which calls upon gp_siteindex_bc.sas and a temporary output table from
gp_ltp_tree_age_corr_years.sas)
```

#### **Output written to:**

ltp\_header
site\_info
ltp\_tree\_species\_comp
ltp\_tree\_age

#### SITE INDEX

#### Inputs

TREE\_NUM; AGE\_TOTAL; HEIGHT

#### **Computations**

1) For each tree deemed suitable for compiling site height (SUIT\_HT = 'Y' or 'M') and site age (SUIT\_AGE = 'Y' or 'M'), of dominant or co-dominant crown class (CROWN\_CLASS = 'D' or 'C') and not selected as a residual or non-standard tree (SITE\_TYPE = 'T', 'TL', 'TS', 'TO', 'TR', 'L', 'S', 'O', or 'U'), calculate site index at breast-height age of 50 years using the appropriate tree age specified by each site index equation (i.e. breast-height age, stump-height age or total age) or geospatial coordinates of plot centers in the case of trees in British Columbia. Tree age for calculating site-index (SI\_AGE) is based on total tree age (AGE\_TOTAL) minus the proportion of appropriate species- and jurisdiction-specific age correction factors (AGE\_CORR\_YEARS unadjusted for boring height) between total age and breast-height age (i.e. 1.3m). Tree height (HEIGHT) was used for calculating site index per tree:

```
SITE\_INDEX_{mpt} = f(SI\_AGE_{mpt}; HEIGHT_{mpt}; LGTREE\_GENUS_{mpt}; LGTREE\_SPECIES_{mpt})

Or in the case of trees in British Columbia:

SITE\_INDEX_{mpt} = f(UTM\_E_{mpt}; UTM\_N_{mpt}; UTM\_ZONE_{mpt}; LGTREE\_GENUS_{mpt}; LGTREE\_SPECIES_{mpt})
```

where t is a unique site tree (SUIT\_HT = 'Y' or 'M' and SUIT\_AGE = 'Y' or 'M' and CROWN\_CLASS = 'D' or 'C' and SITE\_TYPE = 'T', 'TL', 'TS', 'TO', 'TR', 'L', 'S', 'O', or 'U') within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate the average site index for the plot regardless of species by summing the site indices of all trees within a plot and dividing by the number of site trees:

$$SITE\_INDEX_{mp} = \left[\sum_{t=1}^{n} SITE\_INDEX_{mpt}\right] / n_{mp}$$

where t is a unique site tree (SUIT\_HT = 'Y' or 'M' and SUIT\_AGE = 'Y' or 'M' and CROWN\_CLASS = 'D' or 'C' and SITE\_TYPE = 'T', 'TL', 'TS', 'TO', 'TR', 'L', 'S', 'O', or 'U') among n number of site trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

Site index calculations use jurisdiction-based and taxon-specific equations or maps provided by jurisdictions (Cieszewski et al. 1993; Huang et al. 1994; Ker 1991; NS Forest Research Section 1987; Pothier and Savard 1998). When a species-specific equation or map does not exist for a particular species, then substitutions are done based on genus or vegetation type (hardwood versus softwood). Site index calculations for species in BC make use of the 'SIInBC' function of the 'FAIBBase' package for R (Y. Luo 2020). Site indexes were only calculated for trees with breast-height age greater or equal to 3, except for plots within British Columbia, and height greater or equal to 1.3 m. Site index was capped at 45 m except for plots within British Columbia. Short trees and really old trees can lead to misleading site index values (Comeau 2020), however these were included in our calculations due to the limited number of site trees in some plots and the plot selection design that includes non-productive stands (i.e. plots where site index could realistically be small). Tests of our site index calculations indicate values are within expected ranges for jurisdictions (e.g. 2 – 35 m for New Brunswick, Hennigar et al. 2017) or reasonable given site tree attributes (e.g. 1.5 m tall 50 year old tree).

#### References:

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#### Output

SITE INDEX

#### SITE\_INDEX\_GENUS

#### Inputs

LGTREE\_GENUS of site trees; DBH

#### **Computations**

Site index genus (SITE\_INDEX\_GENUS) was assigned as the genus of the most abundant taxon, by basal area, of site index trees used in calculations of site index (SITE\_INDEX).

#### Output

SITE\_INDEX\_GENUS

#### SITE INDEX SPECIES

#### Inputs

LGTREE SPECIES of site trees

#### **Computations**

Site index species (SITE\_INDEX\_SPECIES) was assigned as the species of the most abundant taxon, by basal area, of site index trees used in calculations of site index (SITE\_INDEX).

#### Output

SITE\_INDEX\_SPECIES

#### SITE\_HEIGHT

#### Inputs

TREE\_NUM; HEIGHT; LGTREE\_STATUS; CROWN\_CLASS; MEAS\_EST\_HEIGHT; STEM\_COND

#### **Computations**

NOTE: This should only use the trees suitable for calculating height and site indices from the LTP\_TREE\_AGE table (i.e. SUIT\_HT = 'Y'), however there were not always enough suitable site trees in the LTP\_TREE\_AGE table for this calculation so trees meeting conditions to be a site-representative tree (see below) and with missing indicators of site height suitability (i.e. SUIT\_HT = 'M') were also used following the constraint.

1) Calculate the arithmetic average height (m) of all large site trees with live standing status (LGTREE\_STATUS = 'LS'), dominant or co-dominant crown class (CROWN\_CLASS = 'C' or 'D'), intact stems (STEM\_COND not = 'B'), measured (or not specified) height values (MEAS\_EST\_HEIGHT = 'M' or 'S') and not selected as a residual or non-standard tree (SITE\_TYPE not = 'N' or 'R'). Site height considered trees within the plot with height suitable for calculating site height (SUIT\_HT = 'Y') or with missing suitable height indicator (SUIT\_HT = 'M') and no recorded damage (damage\_agent = 'O' or 'S'). Site height also considered site trees outside the plot when trees were suitable for calculating site height (SUIT\_HT = 'Y' or 'M') and dominant, co-dominant or missing crown class (CROWN\_CLASS = 'C', 'D' or 'M'):

$$SITE\_HEIGHT_{mp} = \left[\sum_{t=1}^{n} HEIGHT_{mpt}\right] / n_{mp}$$

where t is a unique tree among n number of site-representative trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

SITE\_HEIGHT

#### LOREY\_HEIGHT

#### Inputs

TREE\_NUM; LGTREE\_STATUS; DBH; HEIGHT; STEM\_COND

#### **Computations**

1) Estimate the basal area of each intact (STEM\_COND not ='B') live fallen and live standing (LGTREE STATUS = 'LF' or 'LS') tree, using DBH (cm) and converting basal area to m<sup>2</sup>:

$$BASAL\_AREA_{mpt} = \frac{\pi * DBH_{mpt}^2}{40.000}$$

where t is a unique intact live fallen and live standing tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate Lorey height (m) as a basal area-weighted average of HEIGHT for intact live fallen and live standing trees. If tree height is missing (HEIGHT = -1), then it is set equal to the projected height of that tree (HEIGHT = HEIGHT\_PRJ):

$$LOREY\_HEIGHT_{mp} = \left[\sum_{t=1}^{n} BASAL\_AREA_{mpt} * HEIGHT_{mpt}\right] \bigg/ \sum_{t=1}^{n} BASAL\_AREA_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of intact live fallen and live standing trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

LOREY\_HEIGHT

#### **BASAL AREA STANDLIVE**

#### Inputs

TREE NUM; LGTREE STATUS; DBH; MEAS PLOT SIZE

#### **Computations**

1) Estimate the basal area of each live standing (LGTREE\_STATUS = 'LS') large tree in large tree plot, using DBH (cm) and converting basal area to m<sup>2</sup>:

$$BASAL\_AREA_{mpt} = \frac{\pi * DBH_{mpt}^2}{40.000}$$

where t is a unique live standing tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Sum the basal area estimates of all live standing (LGTREE\_STATUS = 'LS') large trees in the large tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare basal area (m² ha<sup>-1</sup>):

$$BASAL\_AREA\_STANDLIVE_{mp} \ = \ \left[ \sum_{t=1}^{n} BASAL\_AREA_{mpt} \right] \Big/ MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique tree (TREE\_NUM) among n number of live standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

BASAL AREA STANDLIVE

#### BASAL\_AREA\_STANDDEAD

#### Inputs

TREE\_NUM; LGTREE\_STATUS; DBH; MEAS\_PLOT\_SIZE

#### **Computations**

1) Estimate the basal area of each dead standing (LGTREE\_STATUS = 'DS') large tree in the large tree plot, using DBH (cm) and converting basal area to m<sup>2</sup>:

$$BASAL\_AREA_{mpt} = \frac{\pi * DBH_{mpt}^{2}}{40.000}$$

where t is a unique dead standing tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Sum the basal area estimates of all dead standing (LGTREE\_STATUS = 'DS') large trees in the large tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare basal area ( $m^2$  ha<sup>-1</sup>):

$$BASAL\_AREA\_STANDDEAD_{mp} = \left[\sum_{t=1}^{n} BASAL\_AREA_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique tree (TREE\_NUM) among n number of dead standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

BASAL\_AREA\_STANDDEAD

#### **BASAL\_AREA\_FALLLIVE**

#### Inputs

TREE NUM; LGTREE STATUS; DBH; MEAS PLOT SIZE

#### Computations

1) Estimate the basal area of each live fallen (LGTREE\_STATUS = 'LF') large tree in the large tree plot, using DBH (cm) and converting basal area to m<sup>2</sup>:

$$BASAL\_AREA_{mpt} = \frac{\pi * DBH_{mpt}^2}{40,000}$$

where t is a unique live fallen tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Sum the basal area estimates of all live fallen (LGTREE\_STATUS = 'LF') large trees in the large tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare basal area (m² ha⁻¹):

$$BASAL\_AREA\_FALLLIVE_{mp} = \left[\sum_{t=1}^{n} BASAL\_AREA_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique tree (TREE\_NUM) among n number of live fallen large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

BASAL AREA FALLLIVE

#### STEM DENSITY STANDLIVE

#### Inputs

TREE\_NUM; LGTREE\_STATUS; MEAS\_PLOT\_SIZE

#### **Computations**

Count the number of live standing (LGTREE\_STATUS = 'LS') large trees in the large tree plot, and then divide by measured plot size (MEAS PLOT SIZE) to calculate per-hectare stem density (trees ha<sup>-1</sup>):

$$STEM\_DENSITY\_STANDLIVE_{mp} = \frac{n_{mp}}{MEAS\_PLOT\_SIZE_{mp}}$$

where n is the number of live standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

STEM\_DENSITY\_STANDLIVE

#### STEM\_DENSITY\_STANDDEAD

#### Inputs

TREE\_NUM; LGTREE\_STATUS; MEAS\_PLOT\_SIZE

#### **Computations**

Count the number of dead standing (LGTREE\_STATUS = 'DS') large trees in the large tree plot, and then divide by measured plot size (MEAS PLOT SIZE) to calculate per-hectare stem density (trees ha<sup>-1</sup>):

$$STEM\_DENSITY\_STANDDEAD_{mp} = \frac{n_{mp}}{MEAS\_PLOT\_SIZE_{mp}}$$

where n is the number of dead standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

STEM DENSITY STANDDEAD

#### STEM\_DENSITY\_FALLLIVE

#### Inputs

TREE NUM; LGTREE STATUS; MEAS PLOT SIZE

#### Computations

Count the number of live fallen (LGTREE\_STATUS = 'LF') large trees in the large tree plot, and then divide by measured plot size (MEAS PLOT SIZE) to calculate per-hectare stem density (trees ha<sup>-1</sup>):

$$STEM\_DENSITY\_FALLLIVE_{mp} = \frac{n_{mp}}{MEAS\_PLOT\_SIZE_{mp}}$$

where n is the number of live fallen large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

STEM\_DENSITY\_FALLLIVE

#### PLOTBIO\_STEMWOOD\_LIVE

#### Inputs

TREE\_NUM; LGTREE\_STATUS; MEAS\_PLOT\_SIZE; BIOMASS\_STEMWOOD

#### Computations

Sum the stem wood biomass estimates (BIOMASS\_STEMWOOD) of all live large trees (LGTREE\_STATUS = 'LS' or 'LF') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the per-hectare biomass of live large tree stem wood (Mg ha<sup>-1</sup>):

$$PLOTBIO\_STEMWOOD\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_STEMWOOD_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of live large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_STEMWOOD\_LIVE

#### PLOTBIO STEMBARK LIVE

#### Inputs

TREE NUM; LGTREE STATUS; MEAS PLOT SIZE; BIOMASS STEMBARK

#### **Computations**

Sum the stem bark biomass estimates (BIOMASS\_STEMBARK) of all live large trees (LGTREE\_STATUS = 'LS' or 'LF') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the per-hectare biomass of live large tree stem bark (Mg ha<sup>-1</sup>):

$$PLOTBIO\_STEMBARK\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_STEMBARK_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of live large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_STEMBARK\_LIVE

#### PLOTBIO\_BRANCHES\_LIVE

#### Inputs

TREE\_NUM; LGTREE\_STATUS; MEAS\_PLOT\_SIZE; BIOMASS\_BRANCHES

#### **Computations**

Sum the branches biomass estimates (BIOMASS\_BRANCHES) of all live large trees (LGTREE\_STATUS = 'LS' or 'LF') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the per-hectare biomass of live large tree branches (Mg ha<sup>-1</sup>):

$$PLOTBIO\_BRANCHES\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_BRANCHES_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of live large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_BRANCHES\_LIVE

#### PLOTBIO\_FOLIAGE\_LIVE

#### Inputs

TREE NUM; LGTREE STATUS; MEAS PLOT SIZE; BIOMASS FOLIAGE

#### Computations

Sum the foliage biomass estimates (BIOMASS\_FOLIAGE) of all live large trees (LGTREE\_STATUS = 'LS' or 'LF') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the per-hectare biomass of live large tree foliage (Mg ha<sup>-1</sup>):

$$PLOTBIO\_FOLIAGE\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_FOLIAGE_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of live large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO FOLIAGE LIVE

#### PLOTBIO\_STEMWOOD\_DEAD

#### Inputs

TREE\_NUM; LGTREE\_STATUS; MEAS\_PLOT\_SIZE; BIOMASS\_STEMWOOD

#### **Computations**

Sum the stem wood biomass estimates (BIOMASS\_STEMWOOD) of all dead standing large trees (LGTREE\_STATUS = 'DS') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the per-hectare biomass of dead standing large tree stem wood (Mg ha<sup>-1</sup>):

$$PLOTBIO\_STEMWOOD\_DEAD_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_STEMWOOD_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of dead standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO STEMWOOD DEAD

#### PLOTBIO STEMBARK DEAD

#### Inputs

TREE\_NUM; LGTREE\_STATUS; MEAS\_PLOT\_SIZE; BIOMASS\_STEMBARK; LGTREE\_GENUS

#### **Computations**

Sum the stem bark biomass estimates (BIOMASS\_STEMBARK) of all dead standing large trees (LGTREE\_STATUS = 'DS') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS PLOT SIZE) to get the per-hectare biomass of dead standing large tree stem bark (Mg ha<sup>-1</sup>):

$$PLOTBIO\_STEMBARK\_DEAD_{mp} \ = \ \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_STEMBARK_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of dead standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

Note that the biomass of stem bark is 0 for unidentifiable conifer or hardwood dead standing trees (LGTREE STATUS = 'DS' and LGTREE GENUS = 'GENC', 'GENH' or 'UNKN').

#### Output

PLOTBIO STEMBARK DEAD

#### PLOTBIO\_BRANCHES\_DEAD

#### Inputs

TREE\_NUM; LGTREE\_STATUS; MEAS\_PLOT\_SIZE; BIOMASS\_BRANCHES

#### Computations

Sum the branches biomass estimates (BIOMASS\_BRANCHES) of all dead standing large trees (LGTREE\_STATUS = 'DS') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the per-hectare biomass of dead standing large tree branches (Mg ha<sup>-1</sup>):

$$PLOTBIO\_BRANCHES\_DEAD_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_BRANCHES_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of dead standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

Note that the biomass of branches is 0 for unidentifiable conifer or hardwood dead standing trees (LGTREE STATUS = 'DS' and LGTREE GENUS = 'GENC', 'GENH' or 'UNKN').

#### Output

PLOTBIO\_BRANCHES\_DEAD

#### PLOTVOL STANDLIVE

#### Inputs

TREE\_NUM; LGTREE\_STATUS; VOL\_TOTAL; MEAS\_PLOT\_SIZE

#### **Computations**

Sum the volume estimates (VOL\_TOTAL) of all live standing trees (LGTREE\_STATUS = 'LS') in the large tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare volume (m³ ha⁻¹):

$$PLOTVOL\_STANDLIVE_{mp} = \left[\sum_{t=1}^{n} VOL\_TOTAL_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique tree (TREE\_NUM) among n number of live standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_STANDLIVE

#### PLOTVOL STANDDEAD

#### Inputs

TREE\_NUM; LGTREE\_STATUS; VOL\_TOTAL; MEAS\_PLOT\_SIZE

#### Computations

Sum the volume estimates (VOL\_TOTAL) of all dead standing trees (LGTREE\_STATUS = 'DS') in the large tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare volume (m³ ha<sup>-1</sup>):

$$PLOTVOL\_STANDDEAD_{mp} = \left[\sum_{t=1}^{n} VOL\_TOTAL_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique tree (TREE\_NUM) among n number of dead standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_STANDDEAD

#### PLOTVOL\_FALLLIVE

#### Inputs

TREE\_NUM; LGTREE\_STATUS; VOL\_TOTAL; MEAS\_PLOT\_SIZE

#### **Computations**

Sum the volume estimates (VOL\_TOTAL) of all live fallen trees (LGTREE\_STATUS = 'LF') in the large tree plot and divide by measured plot size (MEAS PLOT SIZE) to get per-hectare volume (m³ ha-1):

$$PLOTVOL\_FALLLIVE_{mp} = \left[\sum_{t=1}^{n} VOL\_TOTAL_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique tree (TREE\_NUM) among n number of live fallen large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_FALLLIVE

#### PLOTBIO\_LGTR\_LIVE

#### Inputs

TREE\_NUM; BIOMASS\_TOTAL; LGTREE\_STATUS; MEAS\_PLOT\_SIZE.

#### **Computations**

Sum the biomass estimates (BIOMASS\_TOTAL) of all live large trees (LGTREE\_STATUS = 'LS' or 'LF') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_LGTR\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_TOTAL_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of live large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_LGTR\_LIVE

#### PLOTBIO\_LGTR\_DEAD

#### Inputs

TREE NUM; BIOMASS TOTAL; LGTREE STATUS; MEAS PLOT SIZE.

#### Computations

Sum the biomass estimates (BIOMASS\_TOTAL) of all dead standing large trees (LGTREE\_STATUS = 'DS') in the large tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_LGTR\_DEAD_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_TOTAL_{mpt}$$

where t is a unique tree (TREE\_NUM) among n number of dead standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_LGTR\_DEAD

## SITE\_AGE, NUM\_LAB, NUM\_FIELD, AGE\_CORR\_YEARS, AGE\_TOTAL

#### Inputs

TREE\_NUM; LAB\_AGE; FIELD\_AGE; SUIT\_AGE; BORE\_HT; BORE\_DOB; DBH; LGTREE\_GENUS; LGTREE SPECIES; LGTREE VARIETY; PROVINCE; ECOZONE

#### **Computations**

1) Calculate age correction factor (AGE\_CORR\_YEARS) according to bore height (BORE\_HT), tree taxon (LGTREE\_GENUS; LGTREE\_SPECIES; LGTREE\_VARIETY), province (PROVINCE) and ecozone (ECOZONE):

A lookup table of age correction factors, derived from jurisdictional years-to-breast-height values, were used to compute age correction years for most jurisdictions, except for BC, NL, and NS where age correction factors were not provided or readily available. While species-specific 'years-to-breast-height' equations are provided for BC, the equations require site index as an input parameter, which can only be compiled with site age (i.e. total age of trees in the plot). Similarly, age correction factors provided by NL require site index as an input parameter. Therefore, age correction years provided during baseline sampling (provided by jurisdictions for all established NFI plots [NFI\_PLOT]) are used to calculate age correction years for trees in BC, NL and NS, as well as for cases where years-to-breast-height values for particular species-location combinations were unavailable. To this end, mean age correction years by plot (NFI\_PLOT) or ecozone and species or vegetation type (hardwood versus softwood) provided by jurisdictions during baseline sampling were considered to estimate age correction years (AGE\_CORR\_YEARS) for BC, NL, and NS. When estimating age correction years from baseline data, only age corrections years less than 100 years were used for particular combinations of plot or ecozone and species or vegetation type. Age correction years assigned to each tree is then adjusted (BORE\_HT\_ADJ) using the ratio of bore height (BORE\_HT) to breast height (1.3 m). When a tree core was collected during a

previous sampling period and can be used for calculating the tree's age during a subsequent sampling period (i.e. FIELD\_AGE = -8), then the bore height (BORE\_HT) of the site tree during the previous sampling period is used in lieu of current missing bore height:

$$BORE\_HT\_ADJ_{mpt} = \frac{BORE\_HT_{mpt}}{1.3}$$

 $AGE\_CORR\_YEARS_{mpt}$ 

 $= f(BORE\_HT_{mpt}; LGTREE\_GENUS SPECIES VARIETY_{mpt}; PROVINCE_{mp}; ECOZONE_{mp}) *BORE\_HT\_ADJ_{mpt}$ 

where t is a unique aged site tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate estimated total age (AGE\_TOTAL) using age correction factors (AGE\_CORR\_YEARS) and age calculated in the lab (LAB\_AGE) or, if not available, age determined in the field (FIELD\_AGE). If age determined in both the lab and field are missing then total age is recorded as missing. When a tree core was collected during a previous sampling period and can be used for calculating the tree's age during a subsequent sampling period (i.e. FIELD\_AGE = -8), then the lab age (LAB\_AGE) and field age (FIELD\_AGE) of the site tree during the previous sampling period plus the time elapsed between sampling periods are used in lieu of current missing lab and field ages:

$$\begin{split} if \ \mathit{FIELD\_AGE}_{mpt} - 8, then \ \mathit{LAB\_AGE}_{mpt} \\ &= \mathit{LAB\_AGE}_{(m-1)pt} + \left( \mathit{MEAS\_DATE}_{mpt} - \mathit{MEAS\_DATE}_{(m-1)pt} \right) \ and \ \mathit{FIELD\_AGE}_{mpt} \\ &= \mathit{FIELD\_AGE}_{(m-1)pt} + \left( \mathit{MEAS\_DATE}_{mpt} - \mathit{MEAS\_DATE}_{(m-1)pt} \right) \end{split}$$

$$\begin{array}{ll} \textit{if LAB\_AGE}_{mpt} > \textit{0, then AGE\_TOTAL}_{mpt} = \textit{LAB\_AGE}_{mpt} + \textit{AGE\_CORR\_YEARS}_{mpt} \\ \textit{if LAB\_AGE}_{mpt} = -1 \textit{ and FIELD\_AGE}_{mpt} \neq -1, \textit{then AGE\_TOTAL}_{mpt} \\ = \textit{FIELD\_AGE}_{mpt} + \textit{AGE\_CORR\_YEARS}_{mpt} \\ \textit{if LAB\_AGE}_{mpt} = -1 \textit{ and FIELD\_AGE}_{mpt} = -1, \textit{then AGE\_TOTAL}_{mpt} = -1 \end{array}$$

where t is a unique tree (TREE\_NUM) among n number of suitable aged site trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate the arithmetic average age of trees deemed suitable for compiling site age (SUIT\_AGE ='Y' or 'M' and CROWN\_CLASS ='D', 'C', or 'M' and SITE\_TYPE = 'T', 'TL', 'TS', 'TO', 'TR', 'L', 'S', 'O', or 'U'):

$$SITE\_AGE_{mp} = \left[\sum_{t=1}^{n} AGE\_TOTAL_{mpt}\right] / n_{mp}$$

where t is a unique tree (TREE\_NUM) among n number of suitable aged site trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Count the number of suitable aged site trees with available lab calculated ages (LAB\_AGE  $\neq$  -1) to determine the number of lab-counted tree cores used in the determination of site age (NUM\_LAB):

$$NUM_{\perp}LAB_{mn} = n_{mn}$$

where n is the number of suitable aged site trees with available lab calculated ages (LAB\_AGE  $\neq$  -1) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

4) Count the number of suitable aged site trees with available field calculated ages and no concurrent lab calculated ages (LAB\_AGE = -1 and FIELD\_AGE  $\neq -1$ ) to determine the number of lab-counted tree cores used in the determination of site age (NUM\_FIELD):

$$NUM_FIELD_{mp} = n_{mp}$$

where n is the number of suitable aged site trees with available field calculated ages and no concurrent lab calculated ages (LAB\_AGE = -1 and FIELD\_AGE  $\neq$  -1)within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

SITE\_AGE, NUM\_LAB, NUM\_FIELD, AGE\_CORR\_YEARS, AGE\_TOTAL

#### **GROSSVOL INCR**

Not yet implemented (requires multiple measurement cycles) Inputs

SITE\_AGE; PLOTVOL\_STANDLIVE; PLOTVOL\_STANDDEAD; PLOTVOL\_FALLLIVE; PLOTVOL\_SMTR\_LIVE; PLOTVOL\_SMTR\_DEAD

Growth & vield models

#### **Computations**

1) Sum large (PLOTVOL\_STANDLIVE, PLOTVOL\_STANDDEAD and PLOTVOL\_FALLLIVE) and small (PLOTVOL\_SMTR\_LIVE and PLOTVOL\_SMTR\_DEAD) tree volumes to calculate total stand-level tree volume:

$$TREE\_VOL_{mp} = PLOTVOL\_STANDLIVE_{mp} + PLOTVOL\_STANDDEAD_{mp} + PLOTVOL\_FALLLIVE_{mp} \\ + PLOTVOL\_SMTR\_LIVE_{mp} + PLOTVOLSMTR\_DEAD_{mp}$$

where m is a specific measurement (MEAS NUM) of plot p (NFI PLOT)

2) Develop appropriate cumulative volume-age relationship or growth-yield model (GROSSVOL) for a given plot using data from multiple measurement cycles (i.e. MEAS\_NUM):

$$\begin{aligned} \textit{GROSSVOL}_p \ = \ & f(\textit{SITE\_AGE}, \textit{TREE\_VOL}, \textit{MEAS\_NUM} \ldots) \\ & \textit{GROSSVOL}_p \ = \ & \alpha \ e^{-\beta t^{-1}} \end{aligned}$$

Where p is a unique plot (NFI PLOT)

3) Calculate current annual increment for the plot (GROSSVOL\_INCR) as the value of the first derivative of the volume-age relationship evaluated at time of sampling (SITE\_AGE) for each major taxon in the large plot:

$$GROSSVOL\_INCR_{mp} = \frac{dGROSSVOL_p}{dSITE\_AGE_{mp}} = f(SITE\_AGE_{mp}, \dots)$$

Where m is a specific measurement (MEAS\_NUM) of plot p (NFI\_PLOT)

#### Output

**GROSSVOL INCR** 

#### GROSSVOL\_MAI

#### Inputs

PLOTVOL\_STANDLIVE; PLOTVOL\_STANDDEAD; PLOTVOL\_FALLLIVE; SITE\_AGE

#### **Computations**

1) Sum plot-level volumes of live (PLOTVOL\_STANDLIVE and PLOTVOL\_FALLLIVE) and dead (PLOTVOL\_STANDDEAD) large trees and divide by site age (SITE\_AGE) to estimate mean gross volume annual increment (GROSSVOL MAI) in m<sup>3</sup> ha<sup>-1</sup> yr<sup>-1</sup>:

$$\frac{\textit{GROSSVOL\_MAI}_{mp}}{\textit{SITE\_AGE}_{mp}} = \frac{\textit{PLOTVOL\_STANDLIVE}_{mp} + \textit{PLOTVOL\_FALLLIVE}_{mp}}{\textit{SITE\_AGE}_{mp}}$$

#### **Output**

GROSSVOL\_MAI

#### PERCENT, SPECIES\_NUM

#### Inputs

TREE NUM; LGTREE GENUS; LGTREE SPECIES; LGTREE VARIETY; LGTREE STATUS; DBH

#### **Computations**

1) Estimate the basal area (BASAL\_AREA) of each live large tree (LGTREE\_STATUS = 'LS' or 'LF') without missing DBH (DBH not equal to -1), using DBH (cm) and converting basal area to m<sup>2</sup>:

$$BASAL\_AREA_{mpt} = \frac{\pi * DBH_{mpt}^{2}}{40,000}$$

where t is a unique tree (TREE NUM) within plot p (NFI PLOT) at measurement m (MEAS NUM)

2) Sum the basal area estimates of live large trees by taxon (i.e. unique genus-species-variety combinations):

$$BASAL\_AREA_{mps} = \sum_{t=1}^{n} BASAL\_AREA_{mpst}$$

where t is a unique tree (TREE\_NUM) among n number of trees belonging to taxon s (LGTREE\_GENUS, LGTREE\_SPECIES and LGTREE\_VARIETY) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Divide the basal area of each taxon by the summed basal area of all live large trees (LGTREE\_STATUS = 'LS' or 'LF') within the large tree plot and multiply by 100% to calculate percent basal area cover of each species in the large tree plot (PERCENT):

$$PERCENT_{mps} = BASAL\_AREA_{mps} / \sum_{s=1}^{n} BASAL\_AREA_{mps} * 100\%$$

where s is a unique taxon (LGTREE\_GENUS, LGTREE\_SPECIES and LGTREE\_VARIETY) among n number of taxa within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

4) Assign a ranked abundance number (SPECIES\_NUM) to each large tree taxon (i.e. combination of genus, species and variety) in the large tree plot, from greatest to smallest percent basal area

#### Output

PERCENT, SPECIES NUM

#### 6. Small Tree List

#### **Compiler routines**

smtree\_volume\_all.sas smtree\_biomass.sas

#### **Output written to:**

stp\_tree

#### SMTREE\_VOL\_TOTAL, SMTREE\_HT\_PRJ, SMTREE\_VOL\_PRJ

#### **Compiler routines**

Provincial volume estimation routines, gp\_tree\_volume\_ab.sas, gp\_tree\_volume\_bc.sas etc., which are called from smtree\_volume\_all.sas

#### Inputs

SMTREE\_NUM; SMTREE\_GENUS; SMTREE\_SPECIES; SMTREE\_VARIETY; SMTREE\_STATUS; SMTREE\_DBH; SMTREE\_HT

#### Computations

For measurements prior to August 1, 2007: In the small tree plots, some jurisdictions tallied smaller trees into height and DBH classes rather than recording actual height and DBH values. These classes were converted to specific DBH and height values (midpoint of the class used) before submitting the data to the CFS.

Trees are processed by the volume compiler and individual tree volumes calculated in the same manner as the large trees with the following exceptions:

- 1. There are no allowances for trees with broken tops in baseline measurement cycle prior to August 1, 2007.
- 2. There is no merchantable volume.

#### Output

SMTREE\_VOL\_TOTAL, SMTREE\_HT\_PRJ, SMTREE\_VOL\_PRJ

SMTREE\_BIOMASS, BIOMASS\_STEMWOOD, BIOMASS\_STEMBARK, BIOMASS\_BRANCHES, BIOMASS\_FOLIAGE, BMEQ\_WOOD, BMEQ\_BARK, BMEQ\_BRANCHES, BMEQ\_FOLIAGE

#### **Compiler routines**

smtree\_biomass.sas
gp\_smtree\_biomass.sas

#### Inputs

```
SMTREE_NUM; SMTREE_GENUS; SMTREE_SPECIES; SMTREE_VARIETY; SMTREE_STATUS; SMTREE_DBH; SMTREE_HT; SMTREE_HT_PRJ; SMTREE_VOL_TOTAL; SMTREE_VOL_PRJ; PROVINCE; ECOZONE
```

#### **Computations**

1) The computations for small tree biomass are the same as those for large tree biomass with one exception:

-There are no allowances for trees with broken tops in baseline measurement cycle prior to August 1, 2007.

```
BIOMASS\_STEMWOOD_{mpt} = f(SMTREE\_DBH_{mpt}, SMTREE\_HEIGHT_{mpt})

BIOMASS\_STEMBARK_{mpt} = f(SMTREE\_DBH_{mpt}, SMTREE\_HEIGHT_{mpt})

BIOMASS\_BRANCHES_{mpt} = f(SMTREE\_DBH_{mpt}, SMTREE\_HEIGHT_{mpt})

BIOMASS\_FOLIAGE_{mpt} = f(SMTREE\_DBH_{mpt}, SMTREE\_HEIGHT_{mpt})
```

where t is a unique tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Sum the biomass components for each tree:

```
\begin{split} SMTREE\_BIOMASS_{mpt} \\ &= BIOMASS\_STEMWOOD_{mpt} + BIOMASS\_STEMBARK_{mpt} \\ &+ BIOMASS\_BRANCHES_{mpt} + BIOMASS\_FOLIAGE_{mpt} \end{split}
```

where t is a unique tree (TREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

BIOMASS\_STEMWOOD, BIOMASS\_STEMBARK, BIOMASS\_BRANCHES, BIOMASS\_FOLIAGE, SMTREE\_BIOMASS, BMEQ\_WOOD, BMEQ\_BARK, BMEQ\_BRANCHES, BMEQ\_FOLIAGE

# 7. Small Tree Plot Summary

#### **Compiler routines**

gp\_compile\_smtree.sas

#### **Output written to**

```
stp_header
site_info
stp_tree_species_comp
```

### PLOTVOL\_SMTR\_LIVE

#### Inputs

SMTREE\_NUM; SMTREE\_VOL\_TOTAL; SMTREE\_STATUS; MEAS\_PLOT\_SIZE

Volume equations: See Section 16.

#### **Computations**

1) For measurements prior to August 1, 2007: In the small tree plots, some jurisdictions tallied smaller trees into height and DBH classes rather than recording actual height and DBH values. These classes were converted to specific DBH and height values (midpoint of the class used) before submitting the data to the CFS. These trees are then processed by the volume compiler and individual tree volumes calculated in the same manner as the large trees.

2) Sum the volume estimates (SMTREE\_VOL\_TOTAL) of all live small trees (SMTREE\_STATUS = 'LS' or 'LF') in the small tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare volume (m<sup>3</sup> ha<sup>-1</sup>):

$$PLOTVOL\_SMTR\_LIVE_{mp} = \left[\sum_{t=1}^{n} SMTREE\_VOL\_TOTAL_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique small tree (SMTREE\_NUM) among n number of live small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_SMTR\_LIVE

## PLOTVOL SMTR DEAD

#### Inputs

SMTREE\_NUM; SMTREE\_VOL\_TOTAL; SMTREE\_STATUS; MEAS\_PLOT\_SIZE

Volume equations: See Section 16.

## Computations

- 1) For measurements prior to August 1, 2007: In the small tree plots, some jurisdictions tallied smaller trees into height and DBH classes rather than recording actual height and DBH values. These classes were converted to specific DBH and height values (midpoint of the class used) before submitting the data to the CFS. These trees are then processed by the volume compiler and individual tree volumes calculated in the same manner as the large trees.
- 2) Sum the volume estimates (SMTREE\_VOL\_TOTAL) of all dead standing small trees (SMTREE\_STATUS = 'DS') in the small tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare volume (m³ ha-¹):

$$PLOTVOL\_SMTR\_DEAD_{mp} = \left[\sum_{t=1}^{n} SMTREE\_VOL\_TOTAL_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique small tree (SMTREE\_NUM) among n number of dead standing small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_SMTR\_DEAD

# PLOTBIO SMTR LIVE

#### Inputs

SMTREE\_NUM; SMTREE\_STATUS; SMTREE\_BIOMASS; MEAS\_PLOT\_SIZE

#### **Computations**

Sum the biomass estimates (SMTREE\_BIOMASS) of all live small trees (SMTREE\_STATUS = 'LS' or 'LF') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMTR\_LIVE_{mp} \ = \ \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} \ * \ \sum_{t=1}^{n} SMTREE\_BIOMASS_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of live small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_SMTR\_LIVE

#### PLOTBIO SMTR DEAD

#### Inputs

SMTREE NUM; SMTREE STATUS; SMTREE BIOMASS; MEAS PLOT SIZE

#### **Computations**

Sum the biomass estimates (SMTREE\_BIOMASS) of all dead standing small trees (SMTREE\_STATUS = 'DS') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMTR\_DEAD_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} SMTREE\_BIOMASS_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of live small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO SMTR DEAD

# PLOTBIO\_SMT\_STEMWOOD\_LIVE

#### Inputs

SMTREE\_NUM; SMTREE\_STATUS; BIOMASS\_STEMWOOD; MEAS\_PLOT\_SIZE

#### **Computations**

Sum the stem wood biomass estimates (BIOMASS\_STEMWOOD) of all live small trees (SMTREE\_STATUS = 'LS' or 'LF') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMT\_STEMWOOD\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_STEMWOOD_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of live small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_SMT\_STEMWOOD\_LIVE

# PLOTBIO\_SMT\_STEMBARK\_LIVE

#### Inputs

SMTREE\_NUM; SMTREE\_STATUS; BIOMASS\_STEMBARK; MEAS\_PLOT\_SIZE

#### **Computations**

Sum the stem bark biomass estimates (BIOMASS\_STEMBARK) of all live small trees (SMTREE\_STATUS = 'LS' or 'LF') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMT\_STEMBARK\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_STEMBARK_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of live small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO SMT STEMBARK LIVE

# PLOTBIO SMT BRANCHES LIVE

#### Inputs

SMTREE\_NUM; SMTREE\_STATUS; BIOMASS\_BRANCHES; MEAS\_PLOT\_SIZE

# **Computations**

Sum the branches biomass estimates (BIOMASS\_BRANCHES) of all live small trees (SMTREE\_STATUS = 'LS' or 'LF') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMT\_BRANCHES\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_BRANCHES_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of live small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_SMT\_BRANCHES\_LIVE

# PLOTBIO\_SMT\_FOLIAGE\_LIVE

#### Inputs

SMTREE\_NUM; SMTREE\_STATUS; BIOMASS\_FOLIAGE; MEAS\_PLOT\_SIZE

#### **Computations**

Sum the foliage biomass estimates (BIOMASS\_FOLIAGE) of all live small trees (SMTREE\_STATUS = 'LS' or 'LF') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMT\_FOLIAGE\_LIVE_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_FOLIAGE_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of live small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO SMT FOLIAGE LIVE

# PLOTBIO SMT STEMWOOD DEAD

#### Inputs

SMTREE NUM; SMTREE STATUS; BIOMASS STEMWOOD; MEAS PLOT SIZE

# **Computations**

Sum the stem wood biomass estimates (BIOMASS\_STEMWOOD) of all dead standing small trees (SMTREE\_STATUS = 'DS') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha-1):

$$PLOTBIO\_SMT\_STEMWOOD\_DEAD_{mp} \ = \ \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} \ * \ \sum_{t=1}^{n} BIOMASS\_STEMWOOD_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of dead standing small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_SMT\_STEMWOOD\_DEAD

# PLOTBIO\_SMT\_STEMBARK\_DEAD

#### Inputs

SMTREE NUM; SMTREE STATUS; BIOMASS STEMBARK; MEAS PLOT SIZE.

## Computations

Sum the stem bark biomass estimates (BIOMASS\_STEMBARK) of all dead standing small trees (SMTREE\_STATUS = 'DS') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS PLOT SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMT\_STEMBARK\_DEAD_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_STEMBARK_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of dead standing small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_SMT\_STEMBARK\_DEAD

# PLOTBIO SMT BRANCHES DEAD

#### Inputs

SMTREE\_NUM; SMTREE\_STATUS; BIOMASS\_BRANCHES; MEAS\_PLOT\_SIZE

## Computations

Sum the branches biomass estimates (BIOMASS\_BRANCHES) of all dead standing small trees (SMTREE\_STATUS = 'DS') in the small tree plot, convert units from kg to Mg and divide by measured plot size (MEAS\_PLOT\_SIZE) to get the total per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMT\_BRANCHES\_DEAD_{mp} = \frac{0.001}{MEAS\_PLOT\_SIZE_{mp}} * \sum_{t=1}^{n} BIOMASS\_BRANCHES_{mpt}$$

where t is a unique tree (SMTREE\_NUM) among n number of dead standing small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_SMT\_BRANCHES\_DEAD

## SMTREE PERCENT, SMTREE SPECIES NUM

#### Inputs

SMTREE NUM; SMTREE GENUS; SMTREE SPECIES; SMTREE VARIETY; SMTREE STATUS; DBH

#### **Computations**

1) Estimate the basal area (BASAL\_AREA) of each live small tree (SMTREE\_STATUS = 'LS' or 'LF') without missing DBH (SMTREE\_DBH not equal to -1), using DBH (cm) and converting basal area to m<sup>2</sup>:

$$BASAL\_AREA_{mpt} = \frac{\pi * DBH_{mpt}^{2}}{40.000}$$

where t is a unique tree (SMTREE\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Sum the basal area estimates of live small trees by taxon (i.e. unique genus-species-variety combinations):

$$BASAL\_AREA_{mps} = \sum_{t=1}^{n} BASAL\_AREA_{mpst}$$

where t is a unique tree (TREE\_NUM) among n number of trees belonging to taxon s (SMTREE\_GENUS, SMTREE\_SPECIES and SMTREE\_VARIETY) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Divide the basal area of each taxon by the summed basal area of all live small trees (LGTREE\_STATUS = 'LS' or 'LF') within the small tree plot and multiply by 100% to calculate percent basal area cover of each species in the small tree plot (PERCENT):

$$PERCENT_{mps} = BASAL\_AREA_{mps} / \sum_{s=1}^{n} BASAL\_AREA_{mps} * 100\%$$

where s is a unique taxon (SMTREE\_GENUS, SMTREE\_SPECIES and SMTREE\_VARIETY) among n number of taxa within plot p (NFI PLOT) at measurement m (MEAS NUM)

4) Assign a ranked abundance number (SMTREE\_SPECIES\_NUM) to each small tree taxon (i.e. combination of genus, species and variety) in the small tree plot, from greatest to smallest percent basal area

#### Output

SMTREE\_PERCENT, SMTREE\_SPECIES\_NUM

# 8. Shrub List and Summary

## **Compiler routines**

gp\_shrub\_biomass.sas

#### **Output written to**

shrub\_list site info

# BIOMASS\_TOTAL, BIOMASS\_WOOD, BIOMASS\_FOLIAGE

#### Inputs

SHRUB\_GENUS; SHRUB\_SPECIES; SHRUB\_VARIETY; SHRUB\_STATUS; BD\_CLASS; FREQUENCY

# Computations

1) Estimate the total (BIOMASS\_TOTAL), wood (BIOMASS\_WOOD) and foliage (BIOMASS\_FOLIAGE) biomasses in kg for each shrub record (RECORD\_NUM). The midpoint of a basal diameter class (BD\_CLASS) is used in each component- and taxon-specific biomass equations for each measured shrub record. Biomass equations are sourced from peer-reviewed publications and reports generated by jurisdictions or the US department of agriculture. When a taxon-specific biomass equation does not exist for a measured shrub, the equation for a similar taxon with equivalent genus, species, vegetation type,

and / or growth form is used. Biomass estimates for each basal diameter class of measured shrubs is then multiplied by the frequency of the shrub record to obtain plot-level biomasses.

 $BIOMASS\_TOTAL_{mpt} \\ = f(SHRUB\_GENUS_{mpt}, SHRUB\_SPECIES_{mpt}, SHRUB\_VARIETY_{mpt}, BD\_CLASS_{mpt}) \\ * FREQUENCY_{mpt} \\ BIOMASS\_WOOD_{mpt} \\ = f(SHRUB\_GENUS_{mpt}, SHRUB\_SPECIES_{mpt}, SHRUB\_VARIETY_{mpt}, BD\_CLASS_{mpt}) \\ * FREQUENCY_{mpt} \\ BIOMASS\_FOLIAGE_{mpt} \\ = f(SHRUB\_GENUS_{mpt}, SHRUB\_SPECIES_{mpt}, SHRUB\_VARIETY_{mpt}, BD\_CLASS_{mpt}) \\ * FREQUENCY_{mpt} \\$ 

where t is a unique shrub record (RECORD\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Foliage biomass (BIOMASS\_FOLIAGE) was set equal to zero and total biomass (BIOMASS\_TOTAL) was set equal to only woody biomass (BIOMASS\_WOOD) when shrubs are deemed dead standing (SHRUB\_STATUS = 'DS').

$$if SHRUB\_STATUS_{mpt} = 'DS' then BIOMASS\_FOLIAGE_{mpt} = 0$$
  
 $and BIOMASS\_TOTAL_{mpt} = BIOMASS\_WOOD_{mpt}$ 

where t is a unique shrub record (RECORD\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) When an equation for total biomass, woody biomass or foliage biomass is not available but the other two are, the biomass of the missing component is calculated from the two others. Total biomass is constrained to be equal or greater than the sum of woody biomass and foliage biomass. Total biomass is set to 0.01 when small values (i.e. less or equal to 0.005) round to zero, hence in these cases total biomass may not be equal to wood biomass for dead standing shrubs.

#### Output

BIOMASS TOTAL, BIOMASS WOOD, BIOMASS FOLIAGE, BMEQ TOTAL, BMEQ WOOD, BMEQ FOLIAGE

# PLOTBIO\_LGSHRUB\_LIVE, PLOTBIO\_LGSHRUB\_DEAD

# Inputs

BIOMASS\_TOTAL; SHRUB\_STATUS; MEAS\_PLOT\_SIZE

#### Computations

1) Total biomass records (BIOMASS\_TOTAL) of dead and live shrubs ≥ 1.3 m in height (SHRUB\_STATUS = 'DS' or 'LV') are summed separately to the plot level, divided by 1000 to convert kg to Mg and divided by measured plot size (MEAS\_PLOT\_SIZE) to compute per-hectare large shrub live biomass (PLOTBIO LGSHRUB LIVE) and large shrub dead biomass (PLOTBIO LGSHRUB DEAD):

$$PLOTBIO\_LGSHRUB\_LIVE_{mp} = \left[\sum_{t=1}^{n} BIOMASS\_TOTAL_{mpt}/1000\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique shrub record (RECORD\_NUM) among n number of live shrub records (SHRUB\_STATUS = 'LV') within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

$$PLOTBIO\_LGSHRUB\_DEAD_{mp} = \left[\sum_{t=1}^{n} BIOMASS\_TOTAL_{mpt}/1000\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique shrub record (RECORD\_NUM) among n number of dead shrub records (SHRUB\_STATUS = 'DS') within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_LGSHRUB\_LIVE, PLOTBIO\_LGSHRUB\_DEAD

# 9. Stump List and Summary

#### **Compiler routines**

gp\_compile\_stump.sas

# **Output written to**

stump\_list site\_info

# STUMP\_VOLUME, STUMP\_BIOMASS

#### Inputs

STUMP\_NUM; STUMP\_DIB; STUMP\_DIAMETER; STUMP\_LENGTH; STUMP\_DECAY; STUMP\_GENUS; STUMP\_SPECIES; STUMP\_VARIETY; PROVINCE

#### Computations

1) Estimate the inside-bark volume of each stump with diameter inside bark ≥ 4 cm in m<sup>3</sup> (STUMP\_VOLUME) assuming a cylindrical shape, using top diameter inside bark (STUMP\_DIB) to calculate basal area, converting basal area units to m<sup>2</sup> and multiplying by stump height (STUMP\_LENGTH). The top diameter outside bark (STUMP\_DIAMETER) is used if the value for diameter inside bark is missing:

$$STUMP\_VOLUME_{mpt} = \frac{\pi * STUMP\_DIB_{mpt}^{2} * STUMP\_LENGTH_{mpt}}{40,000}$$

where t is a unique stump (STUMP\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

- 2) The minimum stump volume (STUMP\_VOLUME) is set to 0.0001 m<sup>3</sup>, so smaller non-missing stump volumes are set equal to 0.0001 m<sup>3</sup>.
- 3) Estimate the biomass of each stump with diameter inside bark ≥ 4 cm in kg (STUMP\_BIOMASS) from the stump volume and the wood density (DENSITY) associated with the stump's decay class, taxon (i.e. unique genus-species-variety combinations) and province, converting units to kg:

$$STUMP\_BIOMASS_{mvt} = STUMP\_VOLUME_{mvt} * DENSITY_{isd} * 1000$$

where t is a unique stump (STUMP\_NUM) of taxon s (STUMP\_GENUS, STUMP\_SPECIES and STUMP\_VARIETY) and decay class d (STUMP\_DECAY) within province j (PROVINCE) and plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

# Output

STUMP\_VOLUME, STUMP\_BIOMASS

# PLOTVOL\_STUMP, PLOTBIO\_STUMP

#### Inputs

STUMP NUM; STUMP VOLUME; STUMP BIOMASS; MEAS PLOT SIZE

#### Computations

1) Sum the volume estimates (STUMP\_VOLUME) of all stumps with diameter inside bark  $\geq 4$  cm in the small tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare volume (m<sup>3</sup> ha<sup>-1</sup>):

$$PLOTVOL\_STUMP_{mp} = \left[\sum_{t=1}^{n} STUMP\_VOLUME_{mpt}\right] / MEAS\_PLOT\_SIZE_{mp}$$

where t is a unique stump (STUMP\_NUM) among n number of stumps within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Sum the biomass estimates (STUMP\_BIOMASS) of all stumps with diameter inside bark  $\geq$  4 cm in the small tree plot and divide by measured plot size (MEAS\_PLOT\_SIZE) to get per-hectare biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_STUMP_{mp} = \left[\sum_{t=1}^{n} STUMP\_BIOMASS_{mpt}\right] / (MEAS\_PLOT\_SIZE_{mp} * 1000)$$

where t is a unique stump (STUMP\_NUM) among n number of stumps within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

## Output

PLOTVOL STUMP, PLOTBIO STUMP

# 10. Species list

#### **Compiler routines**

gp\_unique\_species\_list.sas

# **Output written to**

species\_list

#### Inputs

LGTREE\_GENUS; LGTREE\_SPECIES; LGTREE\_VARIETY; SMTREE\_GENUS; SMTREE\_SPECIES; SMTREE\_VARIETY; EC\_GENUS; EC\_SPECIES; EC\_VARIETY; EC\_LAYERID; PROVINCE

#### **Computations**

- 1) Extract list of live taxa (LGTREE\_STATUS not = 'DS') from the large tree plot (LGTREE\_GENUS, LGTREE\_SPECIES and LGTREE\_VARIETY; TREE\_NUM < 8000). Extract list of live taxa (SMTREE\_STATUS not = 'DS') from the small tree plot (SMTREE\_GENUS, SMTREE\_SPECIES and SMTREE\_VARIETY). Extract list of live taxa (SHRUB\_STATUS not = 'DS') from the shrub plot (SHRUB\_GENUS, SHRUB\_SPECIES and SHRUB\_VARIETY). Extract list of taxa from the ecological plot (EC\_GENUS, EC\_SPECIES and EC\_VARIETY), however for records collected before August 1, 2007 exclude taxa associated with woody debris (EC\_LAYERID = 4) that were recorded in Alberta reports (PROVINCE = 'AB') and exclude taxa associated with aquatic plants (EC\_LAYERID = 8-15) that were recorded in Saskatchewan reports (PROVINCE = 'SK').
- 2) Translate all NFI codes to full latin names.
- 3) Bind the three lists of taxa, sort by GENUS, SPECIES and VARIETY and remove any duplicates.
- 4) Assign sequential numbers to each unique taxon detected in a plot, listed alphabetically by genus, species then variety (SPECIES INDEX)

## Output

GENUS, SPECIES, VARIETY, SPECIES INDEX

# 11. Biodiversity Indices – Number of Unique Species and Shannon, Pielou Evenness and Margalef Indices

#### **Compiler routines**

Gp biodiversity.sas

#### **Output written to**

ltp\_header
stp\_header
rel\_abundance\_lgtree
rel\_abundance\_smtree

# SPECIES\_LTNUM, SPECIES\_LTREL, SPECIES\_NUM, BINDEX LTSHANNON, BINDEX LTEVEN, BINDEX LTMARGALEF

#### Inputs

LGTREE GENUS; LGTREE SPECIES; LGTREE VARIETY; LGTREE STATUS

#### **Computations**

- 1) Count the number of live standing (LGTREE\_STATUS = 'LS') large tree taxa (i.e. combination LGTREE\_GENUS, LGTREE\_SPECIES and LGTREE\_VARIETY) in the large tree plot (SPECIES\_LTNUM)
- 2) Calculate the relative stem abundance (SPECIES\_LTREL) of each live standing (LGTREE\_STATUS = 'LS') large tree taxa in the large tree plot:

$$SPECIES\_LTREL_{mps} = \frac{n_{mps}}{N_{mp}}$$

Where n is the number of live standing large trees of taxon s (LGTREE\_GENUS, LGTREE\_SPECIES and LGTREE\_VARIETY) and N is the total number of live standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

- 3) Assign a ranked abundance number (SPECIES\_NUM) to each large tree taxon (i.e. combination of genus, species and variety) in the large tree plot, from most abundant to least abundant number of stems
- 4) Calculate the Shannon diversity index (BINDEX\_LTSHANNON) for live standing (LGTREE\_STATUS = 'LS') large tree taxa in the large tree plot by summing the negative product of the relative abundance and natural log of the relative abundance of each taxon:

$$BINDEX\_LTSHANNON_{mp} = -\sum_{s=1}^{n} SPECIES\_LTREL_{mps} * ln(SPECIES\_LTREL_{mps})$$

where s is a unique large tree taxon (LGTREE\_GENUS, LGTREE\_SPECIES and LGTREE\_VARIETY) among n number of taxa within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

5) Calculate the Pielou evenness index (BINDEX\_LTEVEN) for live standing (LGTREE\_STATUS = 'LS') large tree taxa in the large tree plot by dividing Shannon index (BINDEX\_LTSHANNON) by the natural log of large tree richness (SPECIES\_LTNUM); the index is recorded as missing when the number of taxa is equal to 1:

$$BINDEX\_LTEVEN_{mp} = \frac{BINDEX\_LTSHANNON_{mp}}{ln(SPECIES\_LTNUM_{mp})}$$

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

6) Calculate the Margalef richness index (BINDEX\_LTMARGALEF) for live standing (LGTREE\_STATUS = 'LS') large tree taxa in the large tree plot by dividing the total number of taxa (SPECIES\_LTNUM) less 1 by the natural log of the total number of live standing large trees; the index is recorded as 0 when the number of live standing large trees is equal to 1:

$$BINDEX\_LTMARGALEF_{mp} = \frac{SPECIES\_LTNUM_{mp} - 1}{ln(N_{mp})}$$

Where N is the total number of live standing large trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

SPECIES\_LTNUM, SPECIES\_LTREL, SPECIES\_NUM, BINDEX\_LTSHANNON, BINDEX\_LTEVEN, BINDEX\_LTMARGALEF

#### References

The formulae for estimating the biodiversity indices are as follows:

Shannon diversity index (Shannon, C.E. 1948. A mathematical theory of communication. Bell System Technical Journal, 27, 379-423), *H*:

$$H = -\sum_{i=1}^{S} p_i ln(p_i)$$

Pielou evenness index (Pielou, E.C. 1969. An introduction to mathematical ecology. Wiley-Interscience, NEW York. 286 p.), *J*:

$$J = \frac{H}{ln(S)}$$

Margalef richness index (Margalef, R. 1958. Information theory in ecology. Gen. Syst. 3:36-71), M:

$$M = \frac{S-1}{\ln(N)}$$

where

S = Number of species in the plot.

*N* = Total number of individuals in the plot.

 $n_i$  = Number of individuals of *i*th species.

 $p_i$  = Relative frequency of the *i*th species =  $n_i/N$ .

# SPECIES\_SMTNUM, SPECIES\_STREL, SPECIES\_NUM, BINDEX\_STSHANNON, BINDEX\_STEVEN, BINDEX\_STMARGALEF

#### Inputs

SMTREE\_GENUS; SMTREE\_SPECIES; SMTREE\_VARIETY; SMTREE\_STATUS

#### **Computations**

- 1) Count the number of live standing (SMTREE\_STATUS = 'LS') small tree taxa (i.e. combination SMTREE\_GENUS, SMTREE\_SPECIES and SMTREE\_VARIETY) in the small tree plot (SPECIES\_SMTNUM)
- 2) Calculate the relative stem abundance (SPECIES\_STREL) of each live standing (SMTREE\_STATUS = 'LS') small tree taxon in the small tree plot:

$$SPECIES\_STREL_{mps} = \frac{n_{mps}}{N_{mp}}$$

Where n is the number of live standing small trees of taxon s (SMTREE\_GENUS, SMTREE\_SPECIES and SMTREE\_VARIETY) and N is the total number of live standing small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

- 3) Assign a ranked abundance number (SPECIES\_NUM) to each small tree taxon (i.e. combination of genus, species and variety) in the small tree plot, from most abundant to least abundant number of stems
- 4) Calculate the Shannon diversity index (BINDEX\_STSHANNON) for live standing (SMTREE\_STATUS = 'LS') small tree taxa in the small tree plot by summing the negative product of the relative abundance and natural log of the relative abundance of each taxon:

$$BINDEX\_STSHANNON_{mp} = -\sum_{s=1}^{n} SPECIES\_STREL_{mps} * ln(SPECIES\_STREL_{mps})$$

where s is a unique small tree taxon (SMTREE\_GENUS, SMTREE\_SPECIES and SMTREE\_VARIETY) among n number of taxa within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

5) Calculate the Pielou evenness index (BINDEX\_STEVEN) for live standing (SMTREE\_STATUS = 'LS') small tree taxa in the small tree plot by dividing Shannon index (BINDEX\_STSHANNON) by the natural log of

small tree richness (SPECIES\_STNUM); the index is recorded as missing when the number of taxa is equal to 1:

$$BINDEX\_STEVEN_{mp} = \frac{BINDEX\_STSHANNON_{mp}}{ln(SPECIES\_STNUM_{mp})}$$

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

6) Calculate the Margalef richness index (BINDEX\_STMARGALEF) for live standing (SMTREE\_STATUS = 'LS') small tree taxa in the small tree plot by dividing the total number of taxa (SPECIES\_STNUM) less 1 by the natural log of the total number of live standing small trees; the index is recorded as 0 when the number of live standing large trees is equal to 1:

$$BINDEX\_STMARGALEF_{mp} = \frac{SPECIES\_STNUM_{mp} - 1}{ln(N_{mp})}$$

Where N is the total number of live standing small trees within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

SPECIES\_SMTNUM, SPECIES\_STREL, SPECIES\_NUM, BINDEX\_STSHANNON, BINDEX\_STEVEN, BINDEX\_STMARGALEF

# SPECIES\_ECNUM, SPECIES\_ECREL, SPECIES\_NUM, BINDEX\_ECSHANNON, BINDEX\_ECEVEN

#### Inputs

EC\_GENUS; EC\_SPECIES; EC\_VARIETY; EC\_LAYER

#### **Computations**

- 1) Count the number of unique taxa (i.e. combination EC\_GENUS, EC\_SPECIES and EC\_VARIETY) in each ecological layer (EC\_LAYERID) to calculate taxa richness in an area (SPECIES\_ECNUM)
- 2) Calculate the relative percent cover (SPECIES\_ECREL) of each taxon in an ecological layer:

$$SPECIES\_ECREL_{mpls} = \frac{n_{mpls}}{N_{mpl}}$$

Where n is the percent cover of taxon s (EC\_GENUS, EC\_SPECIES and EC\_VARIETY) and N is the plant cover within ecological layer I (EC\_LAYER) of plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

- 3) Assign a ranked abundance number (SPECIES\_NUM) to each taxon (i.e. combination of genus, species and variety) in an ecological layer, from most abundant to least abundant percent cover
- 4) Calculate the Shannon diversity index (BINDEX\_ECSHANNON) for taxa in each ecological layer by summing the negative product of the relative abundance and natural log of the relative abundance of each taxon:

$$BINDEX\_ECSHANNON_{mpl} = -\sum_{s=1}^{n} SPECIES\_ECREL_{mpls} * ln(SPECIES\_ECREL_{mpls})$$

where s is a unique ecological taxon (EC\_GENUS, EC\_SPECIES and EC\_VARIETY) among n number of taxa within ecological layer I (EC\_LAYER) of plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

5) Calculate the Pielou evenness index (BINDEX\_ECEVEN) for taxa in each ecological layer by dividing Shannon index (BINDEX\_ECSHANNON) by the natural log of ecological taxa richness (SPECIES\_ECNUM); the index is recorded as missing when the number of taxa is equal to 1 while species with missing percent ground cover were included in calculations of taxa richness:

$$BINDEX\_ECEVEN_{mpl} = \frac{BINDEX\_ECSHANNON_{mpl}}{ln(SPECIES\_ECNUM_{mpl})}$$

Where I is an ecological layer (EC\_LAYER) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

SPECIES\_ECNUM, SPECIES\_ECREL, SPECIES\_NUM, BINDEX\_ECSHANNON, BINDEX\_ECEVEN

# 12. Fine Woody Debris, Small Shrubs, Small Stumps and Herbs

#### **Compiler routines**

gp fwd shrubherb.sas

#### **Output written to**

site\_info

## PLOTBIO SMSHRUB

#### Inputs

MICRO LAYER BIOMASS; MICRO LAYER ID; MEAS PLOT SIZE; MICRO PLOT NUM

#### **Computations**

For each microplot, divide the biomass of small shrubs (MICRO\_LAYER\_ID = 1) by the measured microplot size (MEAS\_PLOT\_SIZE) and convert units from g to Mg. Sum these ratios across all microplots (usually 4) and divide by the number of measured microplots to get per-hectare small shrub biomass (Mg ha<sup>-1</sup>):

$$\begin{split} &PLOTBIO\_SMSHRUB_{mp} \\ &= \left[\sum_{u=1}^{n} \left(MICRO\_LAYER\_BIOMASS_{mpu} / \left[1,000,000*MEAS\_PLOT\_SIZE_{mpu}\right]\right)\right] \middle/ n_{mp} \end{split}$$

Where u is a unique microplot (MICRO\_PLOT\_NUM) among n number of microplots where the biomass of small shrubs was measured, within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

# Output

PLOTBIO SMSHRUB

#### PLOTBIO\_HERB

#### Inputs

MICRO LAYER BIOMASS; MICRO LAYER ID; MEAS PLOT SIZE; MICRO PLOT NUM

#### **Computations**

For each microplot, divide the biomass of herbs (MICRO\_LAYER\_ID = 2) by the measured microplot size (MEAS\_PLOT\_SIZE) and convert units from g to Mg. Sum these ratios across all microplots (usually 4) and divide by the number of measured microplots to get per-hectare herb biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_HERB_{mp} = \left[ \sum_{u=1}^{n} (MICRO\_LAYER\_BIOMASS_{mpu} / [1,000,000 * MEAS\_PLOT\_SIZE_{mpu}]) \right] / n_{mp}$$

Where u is a unique microplot (MICRO\_PLOT\_NUM) among n number of microplots where the biomass of herbs was measured, within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO HERB

## PLOTBIO FWD

#### Inputs

MICRO\_LAYER\_BIOMASS; MICRO\_LAYER\_ID; MEAS\_PLOT\_SIZE; MICRO\_PLOT\_NUM

#### **Computations**

For each microplot, divide the biomass of fine woody debris (MICRO\_LAYER\_ID = 4) by the measured microplot size (MEAS\_PLOT\_SIZE) and convert units from g to Mg. Sum these ratios across all microplots (usually 4) and divide by the number of measured microplots to get per-hectare fine woody debris biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_FWD_{mp} = \left[ \sum_{u=1}^{n} \left( MICRO\_LAYER\_BIOMASS_{mpu} / [1,000,000 * MEAS\_PLOT\_SIZE_{mpu}] \right) \right] / n_{mp}$$

Where u is a unique microplot (MICRO\_PLOT\_NUM) among n number of microplots where the biomass of fine woody debris was measured, within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO FWD

#### PLOTBIO BRYO

#### Inputs

MICRO\_LAYER\_BIOMASS; MICRO\_LAYER\_ID; MEAS\_PLOT\_SIZE; MICRO\_PLOT\_NUM

#### Computations

For each microplot, divide the biomass of bryoids (MICRO\_LAYER\_ID = 3) by the measured microplot size (MEAS\_PLOT\_SIZE) and convert units from g to Mg. Sum these ratios across all microplots (usually 4) and divide by the number of measured microplots to get per-hectare bryoid biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_BRYO_{mp} = \left[ \sum_{u=1}^{n} \left( MICRO\_LAYER\_BIOMASS_{mpu} / \left[ 1,000,000 * MEAS\_PLOT\_SIZE_{mpu} \right] \right) \right] / n_{mp}$$

Where u is a unique microplot (MICRO\_PLOT\_NUM) among n number of microplots where the biomass of bryoids was measured, within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO BRYO

# PLOTBIO\_SMSTUMP

#### Inputs

MICRO LAYER BIOMASS; MICRO LAYER ID; MEAS PLOT SIZE; MICRO PLOT NUM

#### **Computations**

For each microplot, divide the biomass of small stumps (MICRO\_LAYER\_ID = 5) by the measured microplot size (MEAS\_PLOT\_SIZE) and convert units from g to Mg. Sum these ratios across all microplots (usually 4) and divide by the number of measured microplots to get per-hectare small stump biomass (Mg ha<sup>-1</sup>):

$$PLOTBIO\_SMSTUMP_{mp} = \left[ \sum_{u=1}^{n} \left( MICRO\_LAYER\_BIOMASS_{mpu} / [1,000,000 * MEAS\_PLOT\_SIZE_{mpu}] \right) \right] / n_{mp}$$

Where u is a unique microplot (MICRO\_PLOT\_NUM) among n number of microplots where the biomass of small stumps was measured, within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO SMSTUMP

# 13. Coarse and Small Woody Debris – Plot-level Summary

#### **Compiler routines**

gp\_woody\_debris.sas
gp\_cwd\_lead\_species.sas

#### **Output written to**

woody\_debris\_round woody\_debris\_odd site\_info

#### DENSITY

#### Inputs

TRANSECT\_NUM; WD\_PIECE\_NUM; WD\_GENUS; WD\_SPECIES; DECAY\_CLASS; PROVINCE (from each woody\_debris\_round and woody\_debris\_odd tables)
GENUS; SPECIES; VARIETY; PERCENT (from gp\_ltp\_tree\_species\_comp table)
SMTREE\_GENUS; SMTREE\_SPECIES; SMTREE\_VARIETY; SMTREE\_PERCENT (from gp\_stp\_tree\_species\_comp table)

#### **Computations**

Assign variety classifications (WD\_VARIETY) to woody-debris species (WD\_GENUS and WD\_SPECIES) when the most abundant associated taxon (LGTREE\_GENUS, LGTREE\_SPECIES and LGTREE\_VARIETY or SMTREE\_GENUS, SMTREE\_SPECIES and SMTREE\_VARIETY) by basal area (PERCENT or SMTREE\_PERCENT) in the large or small tree species composition tables (LTP\_TREE\_SPECIES\_COMP; STP\_TREE\_SPECIES\_COMP) define this level of classification.

For each piece of round woody debris, attribute a wood density value (g cm<sup>-3</sup>) according to the 'wood\_density' support-data table (gpcsd\_wood\_density) based on the province (PROVINCE), genus (WD GENUS), species (WD SPECIES), variety (WD VARIETY) and decay class (DECAY CLASS) of the piece.

For each piece of odd woody debris, attribute a wood density value (g cm<sup>-3</sup>) according to the 'wood\_density' support-data table (gpcsd\_wood\_density) based on the province (PROVINCE), genus (WD\_GENUS), species (WD\_SPECIES), variety (WD\_VARIETY) and decay class (DECAY\_CLASS) of the piece.

The methods used to derive wood density by decay class (i.e. 'wood\_density' support-data table) are described in <u>section 18</u>. The average wood density for decay classes 1 to 5 is used when the decay class is not specified for a piece of woody debris.

#### Output

DENSITY

## PLOTVOL ROUNDWD, PLOTBIO ROUNDWD

#### Inputs

TRANSECT\_NUM; WD\_PIECE\_NUM; WD\_DIAMETER; DENSITY; TILT\_ANGLE; MCWD\_MEASLEN; LCWD\_MEASLEN

#### **Computations**

1) Calculate a volume proxy (V\_ROUND) for each round coarse woody debris, using woody debris diameter (WD\_DIAMETER) and tilt angle (in degrees) of woody debris with the soil plane (TILT\_ANGLE). The tilt angle is constrained to be  $\leq 80^{\circ}$ , namely tilts greater than  $80^{\circ}$  are set equal to  $80^{\circ}$ :

$$V\_ROUND_{mpzw} = \frac{WD\_DIAMETER_{mpzw}^{2}}{cos(\pi * TILT\_ANGLE_{mpzw}/180)}$$

where w is a unique round coarse woody debris (WD\_PIECE\_NUM) along transect z (TRANSECT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate a biomass proxy (BIOM\_ROUND) for each round coarse woody debris, using the product of volume proxy estimates (V\_ROUND) and wood density (DENSITY):

$$BIOM\_ROUND_{mpzw} = V\_ROUND_{mpzw} * DENSITY_{isd}$$

where w is a unique round coarse woody debris (WD\_PIECE\_NUM) of taxon s (WD\_GENUS, WD\_SPECIES and WD\_VARIETY) and decay class d (DECAY\_CLASS) along transect z (TRANSECT\_NUM) within province j (PROVINCE) and plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) The per-hectare volume and biomass estimates for each size class of round coarse woody debris is then calculated using values to complete volume calculations ( $\pi$ \*length of debris/4), convert units to meters (1/10,000) and account for the probability of intersecting a transect given an area of interest [10,000 \*  $\pi$  / (2 \* transect length \* length of debris)]. The round coarse woody debris are stratified into two size classes: medium (7.5 < WD\_DIAMETER  $\leq$  30 cm) and large (WD\_DIAMETER > 30 cm) according to diameter size (WD\_DIAMETER); and appropriate transect lengths for medium (MCWD\_MEASLEN) and large (LCWD\_MEASLEN) size classes are used to calculate per-hectare estimates.

For large round pieces (weighted by transect length)

$$WD\_ROUND\_LARGE\_VOLUME_{mp} = \left[\sum_{z=1}^{k} \sum_{w=1}^{n} \frac{V\_ROUND_{mpzw} * \pi^{2}}{8}\right] / \sum_{z=1}^{k} LCWD\_MEASLEN_{mpz}$$

$$WD\_ROUND\_LARGE\_BIOMASS_{mp} = \left[\sum_{z=1}^{k} \sum_{w=1}^{n} \frac{BIOM\_ROUND_{mpzw} * \pi^{2}}{8}\right] / \sum_{z=1}^{k} LCWD\_MEASLEN_{mpz}$$

where w is a unique round coarse woody debris (WD\_PIECE\_NUM) among n number of round coarse woody debris along transect z (TRANSECT\_NUM) among k number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

For medium round pieces (weighted by transect length)

$$WD\_ROUND\_MED\_VOLUME_{mp} = \left[\sum_{z=1}^{k} \sum_{w=1}^{n} \frac{V\_ROUND_{mpzw} * \pi^{2}}{8}\right] / \sum_{z=1}^{k} MCWD\_MEASLEN_{mpz}$$

$$WD\_ROUND\_MED\_BIOMASS_{mp} = \left[\sum_{z=1}^{k} \sum_{w=1}^{n} \frac{BIOM\_ROUND_{mpzw} * \pi^{2}}{8}\right] / \sum_{z=1}^{k} MCWD\_MEASLEN_{mpz}$$

where w is a unique round coarse woody debris (WD\_PIECE\_NUM) among n number of round coarse woody debris along transect z (TRANSECT\_NUM) among k number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Sum the volumes and biomass estimates across medium and large size classes to calculate total round coarse woody debris volume (PLOTVOL\_ROUNDWD) and biomass (PLOTBIO\_ROUNDWD) per hectare:

$$PLOTVOL\_ROUNDWD_{mp} = WD\_ROUND\_LARGE\_VOLUME_{mp} + WD\_ROUND\_MED\_VOLUME_{mp}$$
 
$$PLOTBIO\_ROUNDWD_{mp} = WD\_ROUND\_LARGE\_BIOMASS_{mp} + WD\_ROUND\_MED\_BIOMASS_{mp}$$

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTBIO\_ROUNDWD, PLOTVOL\_ROUNDWD

#### References

The per-hectare biomass and volume calculations for round woody debris described above are based on the following line-intersect sampling formulae:

volume 
$$(m^3 ha^{-1}) = 10,000 * \frac{\pi}{2} * \frac{\pi}{4} * \frac{1}{L_i} * \sum_{j=1}^{m_i} \frac{1}{\cos(\pi * h_{ij}/180)} * \left[\frac{d_{ij}}{100}\right]^2$$

$$biomass (Mg \ ha^{-1}) = \sum_{j=1}^{m_i} volume_{ij} * \rho_{ij}$$

where,

 $\rho_{ij}$  = wood density (**g cm**<sup>-3</sup>) of the jth piece in the *i*th plot  $m_i$  = number of pieces intersected by transect in the *i*th plot  $h_{ij}$  = tilt angle (**degrees**) of the jth piece in the *i*th plot  $d_{ij}$  = diameter (**cm**) of the jth piece in the *i*th plot  $L_i$  = total measured transect length (**m**)

The corresponding equations for odd pieces and accumulations (attributes calculated below) are:

$$volume\ (m^3\ ha^{-1}) = 10,000 * \frac{1}{L} * \sum_{j=1}^{m_i} \frac{Length}{100} * \frac{Depth}{100}$$

$$biomass (Mg \ ha^{-1}) = \sum_{j=1}^{m_i} volume_{ij} * \rho_{ij}$$

#### Notes:

- 1. The value  $\pi/2$  in is a constant for horizontal tilt correction. This correction accounts for the fact that we do not always cross the woody debris at right angles to the line intersect. That is why we do not measure the horizontal tilt angle.
- 2. The vertical tilt correction is  $[1/\cos(\pi * h_{ij}/180)]$ . This correction accounts for the fact that the woody debris does not always lie horizontally on the forest floor or ground, and converts degrees into radians.
- 3. The value  $\pi/4$  converts the cross-sectional diameters  $d_{ij}$  into circular cross-sectional areas.
- 4. The numerator 10,000 in all the equations converts the biomass and volumes onto a one-hectare basis (1 hectare =  $10,000 \text{ m}^2$ ).
- 5. Be careful about the units of L, d, and  $\rho_{ij}$ ; they are **m**, **cm** and **g** cm<sup>-3</sup>, respectively. The equations must be modified if the units are changed.
- 6. For odd pieces and accumulations, *Length* and *Depth* of are in **cm**.

#### Source literature:

Marshall, P.L., Davis, G. and LeMay, V.M., 2000. Using line intersect sampling for coarse woody debris. Research Section, Vancouver Forest Region, BC Ministry of Forests, Nanaimo, BC, Canada.

Technical Report TR-003. 34 pp. See equations 8 and 16. (www.for.gov.bc.ca/rco/research/cwd/tr003.pdf)

Van Wagner, C.E., 1982. Practical aspects of the line intersect sampling method. Canadian Forest Service. Information Report PI-X-12. See equations 1 and 2 (page 2).

# CWD\_LEAD\_SPECIES

#### **Compiler routines**

gp\_cwd\_lead\_species.sas

#### Inputs

TRANSECT\_NUM, LCWD\_MEASLEN, MCWD\_MEASLEN (from woody\_debris\_header table) TRANSECT\_NUM, WD\_PIECE\_NUM; WD\_GENUS; WD\_SPECIES; WD\_DIAMETER; TILT\_ANGLE (from woody\_debris\_round table)

TRANSECT\_NUM, WD\_PIECE\_NUM; WD\_GENUS; WD\_SPECIES; HOR\_LENGTH; VER\_DEPTH (from woody debris odd table)

#### **Computations**

1) Calculate the volume of round coarse woody debris by species for medium (V\_ROUND\_MED) and large (V\_ROUND\_LARGE) pieces by stratifying debris into medium (7.5 < WD\_DIAMETER ≤ 30 cm) and large (WD\_DIAMETER > 30 cm) size classes according to diameter size (WD\_DIAMETER) and using appropriate transect lengths for medium (MCWD\_MEASLEN) and large (LCWD\_MEASLEN) size classes to calculate perhectare estimates:

For large round coarse woody debris:

$$V\_ROUND\_LARGE_{mps} = \left[\sum_{z=1}^{k} \sum_{w=1}^{n} \frac{WD\_DIAMETER_{mpsw}^{2}}{cos(\pi * TILT\_ANGLE_{mpsw}/180)} * \frac{\pi^{2}}{8}\right] * \sum_{z=1}^{k} \frac{1}{LCWD\_MEASLEN_{mpz}}$$

For medium round coarse woody debris:

$$V\_ROUND\_MED_{mps} = \left[\sum_{z=1}^{k} \sum_{w=1}^{n} \frac{WD\_DIAMETER_{mpsw}^{2}}{cos(\pi * TILT\_ANGLE_{mpsw}/180)} * \frac{\pi^{2}}{8}\right] * \sum_{z=1}^{k} \frac{1}{MCWD\_MEASLEN_{mpz}}$$

where w is a unique round coarse woody debris (WD\_PIECE\_NUM) among n number of round coarse woody debris of species s (WD\_GENUS, WD\_SPECIES) along transect z (TRANSECT\_NUM) among k number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM).

Then sum these volumes for medium and large pieces to calculate total volume of round coarse woody debris by species per hectare (V\_ROUND):

$$V_ROUND_{mps} = V_ROUND_LARGE_{mps} + V_ROUND_MED_{mps}$$

where s is a unique species (WD\_GENUS, WD\_SPECIES) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM).

2) Assign a variety label (WD\_VARIETY) to the woody debris species if the most abundant associated taxon in the large or small tree species composition table (LTP\_TREE\_SPECIES\_COMP; STP\_TREE\_SPECIES\_COMP) defines this level of classification.

3) The cross sectional area of each odd-shaped coarse woody debris and woody debris accumulation is calculated using the product of length (HOR\_LENGTH) and depth (VER\_DEPTH). Odd-shaped debris and accumulations are then stratified into two size classes according to the round-diameter equivalents (EQ\_DIAMETER) to cross sectional areas as defined below: medium (7.5 < EQ\_DIAMETER ≤ 30 cm) and large (EQ\_DIAMETER > 30 cm):

$$EQ\_DIAMETER_{mpzw} = \sqrt{\frac{HOR\_LENGTH_{mpzw} * VER\_DEPTH_{mpzw} * 4}{\pi}}$$

where w is a unique odd shaped coarse woody debris (WD\_PIECE\_NUM) along transect z (TRANSECT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

4) Calculate the volume of odd-shaped coarse woody debris by species for medium (V\_ODD\_MED) and large (V\_ODD\_LARGE) pieces using appropriate transect lengths for medium (MCWD\_MEASLEN) and large (LCWD\_MEASLEN) size classes to calculate per-hectare estimates:

For large odd-shaped coarse woody debris:

$$V\_ODD\_LARGE_{mps} = \left[\sum_{z=1}^{k}\sum_{w=1}^{n}HOR\_LENGTH_{mpsw} * VER\_DEPTH_{mpsw}\right] * \sum_{z=1}^{k}\frac{1}{LCWD\_MEASLEN_{mpz}}$$

For medium odd-shaped coarse woody debris:

$$V\_ODD\_MED_{mps} = \left[\sum_{z=1}^{k} \sum_{w=1}^{n} HOR\_LENGTH_{mpsw} * VER\_DEPTH_{mpsw}\right] * \sum_{z=1}^{k} \frac{1}{MCWD\_MEASLEN_{mpz}}$$

where w is a unique odd-shaped coarse woody debris (WD\_PIECE\_NUM) among n number of odd-shaped coarse woody debris of species s (WD\_GENUS, WD\_SPECIES) along transect z (TRANSECT\_NUM) among k number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM).

Then sum these volumes for medium and large pieces to calculate total volume of odd-shaped coarse woody debris by species per hectare (V ODD):

$$V_{-}ODD_{mns} = V_{-}ODD_{-}LARGE_{mns} + V_{-}ODD_{-}MED_{mns}$$

where s is a unique species (WD\_GENUS, WD\_SPECIES) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM).

- 5) Assign a variety label (WD\_VARIETY) to the woody debris species if the most abundant associated taxon in the large or small tree species composition table (LTP\_TREE\_SPECIES\_COMP; STP\_TREE\_SPECIES\_COMP) defines this level of classification.
- 6) Sum the volume of odd-shaped woody debris (V\_ODD) with the volume of round woody debris (V\_ROUND) by taxon. Select the taxon with the largest combined coarse woody-debris volume (V\_CWD) and designate as the leading woody debris species (i.e. WD\_GENUS, WD\_SPECIES and WD\_VARIETY).

$$V_{-}CWD_{mps} = V_{-}ODD_{mps} + V_{-}ROUND_{mps}$$

where s is a unique taxon (WD\_GENUS, WD\_SPECIES, WD\_VARIETY) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM).

- 7) If a plot has small woody debris but no coarse woody debris, select the most common taxon from the large tree plot as the leading woody debris species. This is the species in the large tree species composition table (LTP\_TREE\_SPECIES\_COMP) with the first ranked abundance (species\_num = 1).
- 8) If a plot has small woody debris but no large woody debris or large trees, then select the most common taxon from the small tree plot as the leading woody debris species. This is the species in the small tree species composition table (STP\_TREE\_SPECIES\_COMP) with the first ranked abundance (species\_num = 1).
- 9) If a plot has small woody debris but no large woody debris, no large trees and no small trees, then assign the leading woody debris species as unknown (i.e. WD GENUS = 'UNKN' and WD SPECIES = 'SPP').
- 10) If no coarse or small woody debris were measured, then select the most common taxon from the large tree plot, else the small tree plot, as the leading woody debris species. This is the species in the large or small tree species composition table (LTP\_TREE\_SPECIES\_COMP; STP\_TREE\_SPECIES\_COMP) with the first ranked abundance (species num = 1).

#### Output

WD\_GENUS, WD\_SPECIES, WD\_VARIETY

# PLOTVOL\_SWD, PLOTBIO\_SWD

#### Inputs

TRANSECT\_NUM; SWD\_DIAM\_CLASS; SWD\_TALLY; SWD\_DECAY\_CLASS; SWD\_MEASLEN; PROVINCE

#### **Computations**

1) Calculate the per-hectare volume of small woody debris (SWD\_VOLUME; m³ ha⁻¹) for each diameter class (SWD\_DIAM\_CLASS), weighted by transect length (SWD\_MEASLEN). Small woody debris is assumed parallel with the ground, there is therefore no need to account for the tilt angle where debris intercept with sampling transects.

Woody debris diameter is set to 2 cm if the diameter small woody debris is 1 to 3 cm (SWD\_DIAM\_CLASS = 1):

$$SWD\_VOLUME_{mpc} = \left[ \sum_{z=1}^{k} \frac{\pi^2 * SWD\_TALLY_{mpcz} * 2^2}{8} \right] / \sum_{z=1}^{k} SWD\_MEASLEN_{mpz}$$

Woody debris diameter is set to 4 cm if the diameter small woody debris is 3 to 5 cm (SWD\_DIAM\_CLASS = 2):

$$SWD\_VOLUME_{mpc} = \left[ \sum_{z=1}^{k} \frac{\pi^2 * SWD\_TALLY_{mpcz} * 4^2}{8} \right] / \sum_{z=1}^{k} SWD\_MEASLEN_{mpz}$$

Woody debris diameter is set to 6.25 cm if the diameter small woody debris is 4 to 7.5 cm (SWD\_DIAM\_CLASS = 3):

$$SWD\_VOLUME_{mpc} = \left[ \sum_{z=1}^{k} \frac{\pi^2 * SWD\_TALLY_{mpcz} * 6.25^2}{8} \right] / \sum_{z=1}^{k} SWD\_MEASLEN_{mpz}$$

where c is one of three diameter classes for small woody debris (SWD\_DIAM\_CLASS) along transect z (TRANSECT\_NUM) among k number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Volumes are converted to biomass (SWD\_BIOMASS; Mg ha<sup>-1</sup>) by multiplying volume estimates (SWD\_VOLUME) by wood density (DENSITY), which is based on small woody debris decay class (SWD\_DECAY\_CLASS) and the leading woody debris taxon (WD\_GENUS, WD\_SPECIES, WD\_VARIETY) in the plot, determined by the CWD\_LEAD\_SPECIES routine documented above.

$$SWD\_BIOMASS_{mpc} = SWD\_VOLUME_{mpc} * DENSITY_{jsd}$$

where c is one of three diameter classes for small woody debris (SWD\_DIAM\_CLASS) of taxon s (WD\_GENUS, WD\_SPECIES, WD\_VARIETY) and decay class d (SWD\_DECAY\_CLASS) within province j (PROVINCE) and plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Sum the volume (SWD\_VOLUME) and biomass (SWD\_BIOMASS) estimates across diameter classes (SWD\_DIAM\_CLASS) to get total small woody debris volume (PLOTVOL\_SWD) and biomass (PLOTBIO\_SWD) per hectare:

$$PLOTVOL\_SWD_{mp} = \sum_{c=1}^{n} SWD\_VOLUME_{mpc}$$

$$PLOTBIO\_SWD_{mp} = \sum_{c=1}^{n} SWD\_BIOMASS_{mpc}$$

where c is a unique diameter class of small woody debris (SWD\_DIAM\_CLASS) among n number of diameter classes within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_SWD, PLOTBIO\_SWD

# PLOTVOL\_ODDWD, PLOTBIO\_ODDWD

#### Inputs

TRANSECT\_NUM; WD\_PIECE\_NUM; DENSITY; HOR\_LENGTH; VER\_DEPTH; MCWD\_MEASLEN; LCWD\_MEASLEN

#### Computations

1) The cross sectional area of each odd shaped coarse woody debris and woody debris accumulation is calculated using the product of length (HOR\_LENGTH) and depth (VER\_DEPTH). Odd shaped debris and accumulations are then stratified into two size classes according to the round-diameter equivalents (EQ\_DIAMETER) to cross sectional areas as defined below: medium (7.5 < EQ\_DIAMETER ≤ 30 cm) and large (EQ\_DIAMETER > 30 cm):

$$EQ\_DIAMETER_{mpzw} = \sqrt{\frac{HOR\_LENGTH_{mpzw}*VER\_DEPTH_{mpzw}*4}{\pi}}$$

where w is a unique odd shaped coarse woody debris (WD\_PIECE\_NUM) along transect z (TRANSECT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate the volume per hectare for each size class of odd shaped coarse woody debris and woody debris accumulations (WD\_ODD\_MED\_VOLUME; WD\_ODD\_LARGE\_VOLUME), using the product of debris length (HOR\_LENGTH) and depth (VER\_DEPTH) and weighing the sum of cross sectional areas by the total measured transect length for medium (MCWD\_MEASLEN) and large (LCWD\_MEASLEN) size classes:

 $WD\_ODD\_MED\_VOLUME_{mp}$ 

$$= \left[ \sum_{z=1}^{k} \sum_{w=1}^{n} HOR\_LENGTH_{mpzw} * VER\_DEPTH_{mpzw} \right] / \sum_{z=1}^{k} MCWD\_MEASLEN_{mpz}$$

 $WD\_ODD\_LARGE\_VOLUME_{mp}$ 

$$= \left[ \sum_{z=1}^{k} \sum_{w=1}^{n} HOR\_LENGTH_{mpzw} * VER\_DEPTH_{mpzw} \right] / \sum_{z=1}^{k} LCWD\_MEASLEN_{mpz}$$

where w is a unique odd shaped coarse woody debris (WD\_PIECE\_NUM) among n number of odd woody debris along transect z (TRANSECT\_NUM) among k number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Biomass estimates for each size class of odd shaped coarse woody debris and woody debris accumulations (WD\_ODD\_MED\_BIOMASS; WD\_ODD\_LARGE\_BIOMASS) are calculated similarly to volume estimates however account for debris density (DENSITY):

 $WD\_ODD\_MED\_BIOMASS_{mp}$ 

$$= \left[ \sum_{z=1}^{k} \sum_{w=1}^{n} HOR\_LENGTH_{mpzw} * VER\_DEPTH_{mpzw} * DENSITY_{jsd} \right] \bigg/ \sum_{z=1}^{k} MCWD\_MEASLEN_{mpz}$$

 $WD\_ODD\_LARGE\_BIOMASS_{mp}$ 

$$= \left[ \sum_{z=1}^{k} \sum_{w=1}^{n} HOR\_LENGTH_{mpzw} * VER\_DEPTH_{mpzw} * DENSITY_{jsd} \right] / \sum_{z=1}^{k} LCWD\_MEASLEN_{mpz}$$

where w is a unique odd shaped coarse woody debris (WD\_PIECE\_NUM) of taxon s (WD\_GENUS, WD\_SPECIES, WD\_VARIETY) and decay class d (SWD\_DECAY\_CLASS) among n number of odd woody debris along transect z (TRANSECT\_NUM) among k number of transects within province j (PROVINCE) and plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

4) Sum the volumes and biomass estimates across medium and large size classes to calculate total odd shaped coarse woody debris volume (PLOTVOL\_ODDWD) and biomass (PLOTBIO\_ODDWD) per hectare:

$$PLOTVOL\_ODDWD_{mp} = WD\_ODD\_LARGE\_VOLUME_{mp} + WD\_ODD\_MED\_VOLUME_{mp}$$

$$PLOTBIO\_ODDWD_{mp} = WD\_ODD\_LARGE\_BIOMASS_{mp} + WD\_ODD\_MED\_BIOMASS_{mp}$$

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_ODDWD, PLOTBIO\_ODDWD

# PLOTVOL\_CWD, PLOTBIO\_CWD

#### Inputs

PLOTVOL ROUNDWD; PLOTVOL ODDWD; PLOTBIO ROUNDWD; PLOTBIO ODDWD

#### **Computations**

Pool the biomass and volume estimates for round (PLOTVOL\_ROUNDWD; PLOTBIO\_ROUNDWD) and odd shaped (PLOTVOL\_ODDWD; PLOTBIO\_ODDWD) coarse woody debris to get the total coarse woody debris volume (PLOTVOL\_CWD) and biomass (PLOTBIO\_CWD) per hectare:

$$PLOTVOL\_CWD_{mp} = PLOTVOL\_ROUNDWD_{mp} + PLOTVOL\_ODDWD_{mp}$$
 
$$PLOTBIO\_CWD_{mp} = PLOTBIO\_ROUNDWD_{mp} + PLOTBIO\_ODDWD_{mp}$$

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

PLOTVOL\_CWD, PLOTBIO\_CWD

# 14. Coarse and Small Woody Debris – Plot-Level Summary by Decay Class

#### **Compiler routines**

gp\_woody\_debris.sas

#### **Output written to**

wd summary

# PLOTVOL\_ROUNDWD, PLOTBIO\_ROUNDWD, PLOTVOL\_ODDWD, PLOTBIO\_ODDWD, PLOTVOL\_WD, PLOTBIO\_WD, PLOTVOL\_SWD, PLOTBIO\_SWD

#### Inputs

ROUND COARSE WOODY DEBRIS (from woody\_debris\_round table): TRANSECT\_NUM; WD\_PIECE\_NUM; WD\_GENUS; WD\_SPECIES; WD\_DIAMETER; DECAY\_CLASS; TILT\_ANGLE; MCWD\_MEASLEN; LCWD\_MEASLEN

SMALL WOODY DEBRIS (from woody\_debris\_small table): TRANSECT\_NUM; SWD\_DIAM\_CLASS; SWD\_TALLY; SWD\_DECAY\_CLASS; SWD\_MEASLEN

ODD COARSE WOODY DEBRIS (from woody\_debris\_odd table): TRANSECT\_NUM; WD\_PIECE\_NUM; WD\_GENUS; WD\_SPECIES; DECAY\_CLASS; HOR\_LENGTH; VER\_DEPTH; MCWD\_MEASLEN; LCWD\_MEASLEN

TOTAL WOODY DEBRIS (from wd\_summary table, calculated using attributes above): PLOTVOL\_ROUNDWD; PLOTVOL\_ODDWD; PLOTBIO\_ROUNDWD; PLOTBIO\_ODDWD; PLOTVOL SWD; PLOTBIO\_SWD

#### **Computations**

Essentially, these are a repeat of the previous woody debris calculations but the summaries are calculated by measurement number (MEAS\_NUM), plot (NFI\_PLOT) and decay class (DECAY\_CLASS) rather than only by measurement number and plot. Note that, unlike total coarse woody debris estimates in the site\_info table (PLOTVOL\_CWD and PLOTBIO\_CWD), total woody debris estimates in the wd\_summary table (PLOTVOL\_WD and PLOTBIO\_WD) include the volume and biomass of small woody debris.

#### Output

PLOTVOL\_WD, PLOTBIO\_WD, PLOTVOL\_SWD, PLOTBIO\_SWD, PLOTVOL\_ROUNDWD, PLOTBIO\_ROUNDWD, PLOTVOL\_ODDWD, PLOTBIO\_ODDWD

# 15. Soil Carbon

## **Compiler routines**

gp\_carbon\_content.sas gp\_substrate\_tally.sas gp\_soil\_layer\_cc.sas gp\_soil\_layer\_cc\_org\_rev.sas gp\_soil\_layer\_cf\_horizons.sas gp\_cwd\_lead\_species.sas

#### **Output written to**

surface\_substrate\_header site\_info soil\_pit\_depth soil\_mineral\_sample soil\_org\_sample for\_flr\_org\_sample

# TALLY\_SS\_BED, TALLY\_SS\_ROCK, TALLY\_SS\_MIN, TALLY\_SS\_WATER, TALLY\_SS\_ORG, TALLY\_SS\_BURIED, TALLY\_SS\_DECAY, TOTAL\_MEAS

#### Inputs

TRANSECT NUM; STATION NUM; SUBSTRATE TYPE

# Computations

Surface substrate information is collected for computing per-hectare estimates of carbon content in the forest floor, mineral soil layer and organic soil layer.

1) Count the total number of sampling stations (STATION\_NUM) along each transect (TOTAL\_MEAS):

$$TOTAL\_MEAS_{mpz} = n_{mpz}$$

where z is a unique transect (TRANSECT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Count the number of sampling stations (STATION\_NUM) with bedrock surface coverage (SUBSTRATE TYPE = 'BR') along each transect (TALLY SS BED):

$$TALLY\_SS\_BED_{mpz} = n_{mpz}$$

where z is a unique transect (TRANSECT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

Tallies of surface coverage for water (TALLY\_SS\_WATER; SUBSTRATE\_TYPE = 'WA'), mineral soil (TALLY\_SS\_MIN; SUBSTRATE\_TYPE = 'MS'), rock (TALLY\_SS\_ROCK; SUBSTRATE\_TYPE = 'RC'), decaying wood (TALLY\_SS\_DECAY; SUBSTRATE\_TYPE = 'DW'), organic matter (TALLY\_SS\_ORG; SUBSTRATE\_TYPE = 'OM') and buried wood (TALLY\_SS\_BURIED; SUBSTRATE\_TYPE = 'BW') substrate types are calculated in the same manner.

3) Calculate the average depth (DEPTH) of organic matter (SUBSTRATE\_TYPE = 'OM') at sampling stations for each transect (AVG\_ORG\_THICK):

$$AVG\_ORG\_THICK_{mpz} = \sum_{a=1}^{n} DEPTH_{mpza} / n_{mpz}$$

where z is a unique transect (TRANSECT\_NUM) with n number of sampling stations (STATION\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

4) The average depth (DEPTH) of buried wood (SUBSTRATE\_TYPE = 'BW') along each transect is calculated in the same manner (AVG\_BURIED\_THICK):

$$AVG\_BURIED\_THICK_{mpz} = \sum_{a=1}^{n} DEPTH_{mpza} / n_{mpz}$$

where z is a unique transect (TRANSECT\_NUM) with n number of sampling stations (STATION NUM) within plot p (NFI PLOT) at measurement m (MEAS NUM)

5) For each plot, calculate the percent surface coverage of bedrock (PCT\_SS\_BED) by dividing the total number of surface substrate sampling stations with bedrock cover (TALLY\_SS\_BED) with the total number of surface substrate sampling stations (TOTAL MEAS) across transects:

$$PCT\_SS\_BED_{mp} = 100 * \sum_{z=1}^{n} TALLY\_SS\_BED_{mpz} / \sum_{z=1}^{n} TOTAL\_MEAS_{mpz}$$

where z is a unique transect (TRANSECT\_NUM) among n number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

Percent surface substrate cover for water (PCT\_SS\_WATER), organic matter (PCT\_SS\_ORG), decayed wood (PCT\_SS\_DECAY), buried wood (PCT\_SS\_BURIED), rock (PCT\_SS\_ROCK) and mineral soil (PCT\_SS\_MIN) are all calculated in the same manner. Note that percent surface coverage values are intermediate variables that are not written to the database.

7) For each plot, calculate the average thickness of organic matter (PLOT\_AVG\_ORG\_THICK) and buried wood (PLOT\_AVG\_BURIED\_THICK) by summing average substrate thickness (AVG\_ORG\_THICK and AVG\_BURIED\_THICK, respectively) across transects and dividing by the number of transects. Note that

plot-level averages of surface substrates thickness are intermediate variables that are not written to the database:

$$PLOT\_AVG\_ORG\_THICK_{mp} = \sum_{z=1}^{n} AVG\_ORG\_THICK_{mpz} \Big/ n_{mp}$$
 
$$PLOT\_AVG\_BURIED\_THICK_{mp} = \sum_{z=1}^{n} AVG\_BURIED\_THICK_{mpz} \Big/ n_{mp}$$

where z is a unique transect (TRANSECT\_NUM) among n number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

TALLY\_SS\_ORG, AVG\_ORG\_THICK, TALLY\_SS\_BURIED, AVG\_BURIED\_THICK, TALLY\_SS\_DECAY, TALLY\_SS\_BED, TALLY\_SS\_MIN, TALLY\_SS\_WATER, TALLY\_SS\_ROCK (surface\_substrate\_header table)

# BULK\_DENSITY\_2MM, BULK\_DENSITY\_TOTAL, CF\_GRAV, CF\_COBB, CF\_STONE (mineral soil samples)

#### Inputs

MASS\_DISC\_ROCKS; MASS\_TOTAL; MASS\_ROOT; MASS\_COBBLE; MASS\_GRAVEL; MASS\_2MM; VOLUME; PIT\_NUM; SAMPLE\_NUM

#### **Computations**

Warning: These compiled attributes (or their precursors) were not compiled by the NFI office prior to August 1, 2007 and therefore may not follow the procedures outlined below.

Note: Cobble may be included in rocks discarded from mineral soil samples (MASS\_DISC\_ROCKS) therefore potentially overestimating actual percent content of stones (CF\_STONE) and underestimating percent content of cobble (CF\_COBB) in small soil pit samples. Volume occupied by roots (MASS\_ROOT) is not accounted for when calculating bulk density of mineral soil fraction less than 2mm (BULK\_DENSITY\_2MM). The air-dried mass of gravel, cobbles and stones is assumed equal to their ovendried mass (at 105 °C).

1) For small soil pits in microplots or other locations (PIT\_NUM = MP1 –MP8 or PT1 – PT4; note: for measurements prior to August 1, 2007 small soil pits may also have been collected where large pits were dug), calculate coarse fragment content of gravel (CF\_GRAV), cobble (CF\_COBB) and stones (CF\_STONE) by dividing the mass of gravel (MASS\_GRAVEL), cobble (MASS\_COBBLE), or stones (MASS\_DISC\_ROCKS) in the sample by the total sample mass (MASS\_TOTAL):

$$CF\_GRAV_{mpuh} = \frac{MASS\_GRAVEL_{mpuh}}{MASS\_TOTAL_{mpuh} + MASS\_DISC\_ROCKS_{mpuh}} * 100$$
 
$$CF\_COBB_{mpuh} = \frac{MASS\_COBB_{mpuh}}{MASS\_TOTAL_{mpuh} + MASS\_DISC\_ROCKS_{mpuh}} * 100$$
 
$$CF\_STONE_{mpuh} = \frac{MASS\_DISK\_ROCKS_{mpuh}}{MASS\_TOTAL_{mpuh} + MASS\_DISC\_ROCKS_{mpuh}} * 100$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate total bulk density (BULK\_DENSITY\_TOTAL) by dividing total sampled mass (MASS\_TOTAL + MASS\_DISC\_ROCKS) adjusted for moisture content in mineral soil fraction less than 2 mm (MASS\_2MM \*(1 – SOIL\_MOISTURE)) by total sampled volume (VOLUME):

```
BULK\_DENSITY\_TOTAL_{mpuh} \\ = \frac{MASS\_TOTAL_{mpuh} - MASS\_2MM_{mpuh} + (MASS\_2MM_{mpuh} * (1 - SOIL\_MOISTURE_{mpuh})) + MASS\_DISC\_ROCKS_{mpuh}}{VOLUME_{mpuh}}
```

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Calculate the bulk density of the mineral soil fraction ≤ 2 mm (BULK\_DENSITY\_2MM) by dividing the mass of the mineral soil fraction ≤ 2 mm (MASS\_2MM) adjusted for moisture content (SOIL\_MOISTURE) by the sample volume (VOLUME) adjusted for volume occupied by gravel, cobble and stones (i.e. the mass of coarse mineral fragments [MASS\_GRAVEL + MASS\_COBBLE + MASS\_DISC\_ROCKS] divided by the bulk density of quartz [2.65 g cm<sup>-3</sup>]):

```
BULK\_DENSITY\_2MM_{mpuh} \\ = \frac{MASS\_2MM_{mpuh}*(1-SOIL\_MOISTURE_{mpuh})}{VOLUME_{mpuh}-((MASS\_GRAVEL_{mpuh}+MASS\_COBBLE_{mpuh}+MASS\_DISC\_ROCKS_{mpuh})/2.65)}
```

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

BULK\_DENSITY\_2MM, BULK\_DENSITY\_TOTAL, CF\_GRAV, CF\_COBB, CF\_STONE (soil\_mineral\_sample table)

# LAYER\_CC (mineral soil samples)

#### Inputs

MASS\_2MM; VOLUME; CF\_GRAV; CF\_COBB; CF\_STONE; TOC; TC; SAMPLE\_UPPER; SAMPLE\_BOTTOM

#### Computations

Warning: These compiled attributes (or their precursors) were not compiled by the NFI office prior to August 1, 2007 and therefore may not follow the procedures outlined below.

1) Calculate the thickness (THICKNESS) of each mineral soil samples as the difference between upper and bottom depths of each sample (SAMPLE UPPER, SAMPLE BOTTOM)

$$THICKNESS_{mpuh} = SAMPLE\_BOTTOM_{mpuh} - SAMPLE\_UPPER_{mpuh}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate effective bulk density of mineral soil ≤ 2 mm (BULK\_DENSITY\_EFFECTIVE\_2MM) and roots (BULK\_DENSITY\_EFFECTIVE\_ROOT) by dividing respective masses (MASS\_2MM, MASS\_ROOT), when applicable adjusted for moisture content (SOIL MOISTURE), by sample volume (VOLUME):

$$BULK\_DENSITY\_EFFECTIVE\_2MM_{mpuh} = \frac{MASS\_2MM_{mpuh}*(1-SOIL\_MOISTURE_{mpuh})}{VOLUME_{mpuh}}$$

$$BULK\_DENSITY\_EFFECTIVE\_ROOT_{mpuh} = \frac{MASS\_ROOT_{mpuh}}{VOLUME_{mpuh}}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Calculate the carbon content of each sampled layer within each soil pit (LAYER\_CC) by multiplying effective bulk density of mineral soil  $\leq$  2 mm (BULK\_DENSITY\_EFFECTIVE\_2MM) or roots (BULK\_DENSITY\_EFFECTIVE\_ROOT) with soil sample thickness (THICKNESS) and organic carbon content of the  $\leq$  2 mm (TOC) or root (46 g kg<sup>-1</sup>; Ma et al. 2018) fraction of mineral soil and convert units to kg m<sup>-2</sup> (use total carbon content [TC] if total organic carbon [TOC] is missing):

$$\begin{split} LAYER\_CC_{mpuh} &= \frac{TOC_{mpuh}}{1000} *BULK\_DENSITY\_EFFECTIVE\_2MM_{mpuh} *THICKNESS_{mpuh} *10\\ &+ \frac{46}{1000} *BULK\_DENSITY\_EFFECTIVE\_ROOT_{mpuh} *THICKNESS_{mpuh} *10 \end{split}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

LAYER CC (soil mineral sample table)

# CC\_MIN0\_15, CC\_MIN15\_35, CC\_MIN35\_55

#### Inputs

SAMPLE\_UPPER; SAMPLE\_BOTTOM; LAYER\_CC; PCT\_SS\_BED; PCT\_SS\_WATER

#### Computations

Warning: These compiled attributes (or their precursors) were not compiled by the NFI office prior to August 1, 2007 and therefore may not follow the procedures outlined below.

Note: Carbon content in mineral soil layers was adjusted for coarse fragment occupancy in both small and large (representative) soil pits. Since small soil pits are unlikely to effectively capture cobbles (75 – 250 mm) and stones ( > 250 mm), the carbon content of each sampled layer within small soil pits (LAYER\_CC) is adjusted to only reflect gravel content (LAYER\_CC\_GRAVADJ). Therefore, adjustments for coarser soil fragments (i.e. cobbles and stones) rely on percent cobble and percent stone determined by a large representative soil pit. The carbon content of the mineral soil at each depth layer should therefore be considered overestimated if data from a large representative soil pit is not available for a site.

1) Multiply the carbon content of each sampled layer within each soil pit (LAYER\_CC) by the ratio of total sample volume (VOLUME) to volume not occupied by cobble (MASS\_COBBLE/2.65) and stone (MASS\_COBBLE/2.65) coarse fragments assuming these have the bulk density of quartz (2.65 g cm<sup>-3</sup>), to

adjust carbon content of each sampled layer within each soil pit to only reflect gravel content (LAYER\_CC\_GRAVADJ):

$$\begin{aligned} LAYER\_CC\_GRAVADJ_{mpuh} \\ &= LAYER\_CC_{mpuh} \\ &* \frac{VOLUME_{mpuh}}{VOLUME_{mpuh} - ((MASS\_COBBLE_{mpuh} + MASS\_DISC\_ROCKS_{mpuh})/2.65)} \end{aligned}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

For reporting, the original mineral soil layers are reapportioned to three standardized layers of 0-15 cm, 15-35 cm and 35-55 cm. The carbon content of the mineral soil is reported to the maximum depth for which all required data are available.

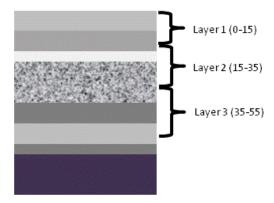


Figure 1. The original soil horizons are reapportioned to three layers of standardized depth.

2) For each standardized layer within a pit, determine the portion ( $\epsilon$  0 – 15) of each sample's thickness (SAMPLE\_BOTTOM – SAMPLE\_UPPER) and carbon content adjusted only for gravel content (LAYER\_CC\_GRAVADJ) contained within the depth range of a layer, and sum to calculate the total measured thickness (i.e. sampled interval; THICKNESS\_0\_15) and carbon content (CC0\_15) corresponding to each layer. The calculations for the 0-15 cm layer are as follows:

$$THICKNESS\_0\_15_{mpu} = \sum_{h=1}^{n} (SAMPLE\_BOTTOM_{mpuh} - SAMPLE\_UPPER_{mpuh}) * (\epsilon \ 0 \ -15)$$

$$CC0\_15_{mpu} = \sum_{h=1}^{n} LAYER\_CC\_GRAVADJ_{mpuh} * (\epsilon \ 0 \ -15)$$

where h is a unique sample (SAMPLE\_NUM) among n number of samples where the midpoint of the sampled interval lies in the layer range (e.g. 0-15 cm) within pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM). The term ( $\epsilon$  0-15) stands for the proportion of each sample that lies in the designated range of a layer. For example, if the interval sampled runs from 11-21 cm, the midpoint of that interval is 16. Therefore, only the portion of the sample that is in the 15-35 cm layer (15-21 cm) will be used in calculating carbon content in the 15-35 cm layer (CC15\_35). The portion that is in the 0-15 cm layer (11-14 cm) will not be used since the midpoint lies outside of the 0-15 cm layer. Exceptions were made for thick soil samples with

midpoints lying outside the range of a soil layer being completely enclosed in the sample. In these cases, the portion of the sample associated with the enclosed soil layer is used to calculate that layer's thickness and carbon content.

3) Calculate the adjusted carbon content (kg m<sup>-2</sup>) for each standard layer across all soil pits (CCO\_15\_ADJ) and for all layers combined (PLOT TOT CC) by dividing the carbon content (CCO 15) by measured thickness (THICKNESS 0 15) in each standardized layer in a pit, then dividing the summed fractions across all pits by the number of pits in a plot and multiplying by the nominal thickness of each layer (NOM\_THICKNESS):

$$CC0\_15\_ADJ_{mp} = \left[ \left[ \sum_{u=1}^{n} (CC0\_15_{mpu}/THICKNESS\_0\_15_{mpu}) \right] / n \right] * NOM\_THICKNESS_{mp}$$

$$PLOT\_TOT\_CC_{mp} = CC0\_15\_ADJ_{mp} + CC15\_35\_ADJ_{mp} + CC35\_55\_ADJ_{mp}$$

where u is a unique pit (PIT NUM) among n number of pits within plot p (NFI PLOT) at measurement m (MEAS NUM) and where the nominal thickness (NOM THICKNESS) of the standardized layer / is 15 cm for the 0-15 cm layer, 20 cm for the 15-35 cm layer and 20 cm for the 35-55 cm layer or, alternatively, the portion of the nominal thickness which corresponds to the maximum depth for which all required data are available for computing carbon content.

4) Calculate total depth of sampled mineral soil (SAMPLE DEPTH MIN) as the sum of nominal thickness values (NOM THICKNESS) used to calculate adjusted carbon content for each standard layer across all soil pits:

$$SAMPLE\_DEPTH\_MIN_{mp} = \sum_{l=1}^{n} NOM\_THICKNESS_{mpl}$$

where I is one of three standardized soil layers (0-15 cm, 15-35 cm, 35-55 cm) within plot p(NFI\_PLOT) at measurement m (MEAS\_NUM)

5) For the latest sampled, large representative soil pit within each plot, calculate percent cobble and percent stone for each standardized layer adjusting percent values contributed by each sample according to the proportion of total measured thickness within a layer:

$$CCOBB0\_15_{pu} = \left[\sum_{h=1}^{n} CF\_COBB_{puh} * THICKNESS_{puh} * (\epsilon \ 0 \ -15)\right] / \left[\sum_{h=1}^{n} THICKNESS_{puh} * (\epsilon \ 0 \ -15)\right]$$

$$CSTONE0\_15_{pu}$$

$$= \left[ \sum_{h=1}^{n} CF\_STONE_{puh} * THICKNESS_{puh} * (\epsilon \ 0 \ -15) \right] / \left[ \sum_{h=1}^{n} THICKNESS_{puh} * (\epsilon \ 0 \ -15) \right]$$

where h is a unique sample (SAMPLE NUM) among n number of samples with sampled interval lying in the layer range (e.g. 0-15 cm) within large representative pit number u (PIT NUM = LPO, PT1, PT2, PT3 or PT4) within plot p (NFI PLOT). The term ( $\epsilon$  0 – 15) stands for the proportion of each sample that lies in the designated range of a layer. For example, if the interval sampled runs from 11-21 cm, only the portion of the sample that is in the 0-15 cm layer (11-14 cm) will be used in calculating percent coarse fragments in the 0-15 cm layer (CCOBBO 15, CSTONEO 15). The

64 March 2021

portion that is in the 15-35 cm layer (15-21 cm) will be used in calculating percent coarse fragments in the 15-35 cm layer (CCOBB15 35, CSTONE15 35).

6) If the latest measurement of a plot included more than one large representative pit, then take the mean percent cobble (CCOBBO\_15) and percent stone (CSTONEO\_15) across large representative pits:

$$CCOBB0\_15_p = \left[\sum_{u=1}^{n} CCOBB0\_15_{pu}\right]/n$$

$$CSTONE0\_15_p = \left[\sum_{u=1}^{n} CSTONE0\_15_{pu}\right]/n$$

where u is a unique large representative soil pit (PIT\_NUM = LPO, PT1, PT2, PT3 or PT4) among n number of large representative soil pits within plot p (NFI PLOT).

7) Adjust carbon content in mineral soil layers (CCO\_15\_ADJ) to account for percent volume occupied by cobble (CCOBBO\_15) and stone (CSTONEO\_15):

$$CC0_{15}HADJ_{mp} = CC0_{15}ADJ_{mp} * (100 - (CCOBB0_{15}_p + CSTONE0_{15}_p))/100$$

8) Calculate the per hectare carbon content in a mineral soil layer (CC\_MIN0\_15, CC\_MIN15\_35, CC\_MIN35\_55) by multiplying the adjusted carbon content in a layer (CC0\_15\_HADJ, CC15\_35\_HADJ, CC35\_55\_HADJ) with the percent surface substrate not occupied by bedrock (PCT\_SS\_BED), rock (PCT\_SS\_ROCK), and water (PCT\_SS\_WATER) and convert units to Mg C ha<sup>-1</sup>:

$$= \frac{CCO\_15\_HADJ_{mp} * \left[ (100 - (PCT\_SS\_BED_{mp} + PCT\_SS\_ROCK_{mp} + PCT\_SS\_WATER_{mp}))/100 \right] * 10000}{1000}$$

Where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

CC\_MINO\_15, CC\_MIN15\_35, CC\_MIN35\_55, SAMPLE\_DEPTH\_MIN (site\_info table)

# BULK\_DENSITY\_8MM, BULK\_DENSITY\_TOTAL (forest floor & organic soil samples)

#### Inputs

MASS\_TOTAL; MASS\_LIVE\_ROOT; MASS\_GRAVEL; MASS\_GT8MM; MASS\_8MM; VOLUME; PIT\_NUM; SAMPLE\_NUM

#### **Computations**

Warning: These compiled attributes (or their precursors) were not compiled by the NFI office prior to August 1, 2007 and therefore may not follow the procedures outlined below.

Note: The density of roots and organic fractions > 8 mm is assumed to be the same as organic fractions  $\le 8$  mm when calculating the bulk density of organic fractions  $\le 8$  mm.

1) Calculate total bulk density (BULK\_DENSITY\_TOTAL) by dividing total sampled mass (MASS\_TOTAL) by total sampled volume (VOLUME):

$$BULK\_DENSITY\_TOTAL_{mpuh} = \frac{MASS\_TOTAL_{mpuh}}{VOLUME_{mpuh}}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate the bulk density of the forest floor or organic soil fraction  $\leq$  8 mm (BULK\_DENSITY\_8MM) by dividing the mass of the forest floor or organic soil fraction  $\leq$  8 mm (MASS\_8MM) by the sample volume (VOLUME) adjusted for volume occupied by gravel (i.e. MASS\_GRAVEL divided by the bulk density of quartz [2.65 g cm<sup>-3</sup>]) and by live roots and fraction > 8 mm:

 $BULK_DENSITY_8MM_{mnuh}$ 

$$MASS\_8MM_{mpuh}$$

$$=\frac{-\frac{1}{(VOLUME_{mpuh}-(MASS\_GRAVEL_{mpuh}/2.65))*(MASS\_8MM_{mpuh}/(MASS\_TOTAL_{mpuh}-MASS\_GRAVEL_{mpuh}))}}{(VOLUME_{mpuh}-(MASS\_GRAVEL_{mpuh}/2.65))*(MASS\_8MM_{mpuh}/(MASS\_TOTAL_{mpuh}-MASS\_GRAVEL_{mpuh}))}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

BULK\_DENSITY\_8MM, BULK\_DENSITY\_TOTAL (for\_flr\_org\_sample and soil\_org\_sample tables)

# LAYER\_CC\_8MM, LAYER\_CC\_TOTAL (forest floor & organic soil samples)

#### Inputs

MASS\_8MM; MASS\_GT8MM; MASS\_LIVE\_ROOT; VOLUME; SAMPLE\_UPPER; SAMPLE\_BOTTOM; TOC 8MM; TOC GT8MM

#### Computations

Warning: These compiled attributes (or their precursors) were not compiled by the NFI office prior to August 1, 2007 and therefore may not follow the procedures outlined below.

Note: 'Effective density' values for small pit samples include volumes occupied by gravel and roots, therefore can be integrated with organic depth measurements along transects to calculate carbon content at plot level.

1) Calculate the thickness (THICKNESS) of forest floor or organic soil samples as the difference between upper and bottom depths of each sample (SAMPLE\_UPPER, SAMPLE\_BOTTOM):

$$THICKNESS_{mpuh} = SAMPLE\_BOTTOM_{mpuh} - SAMPLE\_UPPER_{mpuh}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) Calculate effective bulk density of the forest floor or organic soil fractions > 8 mm (BULK\_DENSITY\_EFFECTIVE\_GT8MM), ≤ 8 mm (BULK\_DENSITY\_EFFECTIVE\_8MM) and/or of live roots (BULK\_DENSITY\_EFFECTIVE\_ROOT) by dividing the mass of the soil fractions > 8 mm, ≤ 8 mm and/or of live roots (i.e. those used to quantify carbon; MASS\_8MM, MASS\_GT\_8MM, MASS\_LIVE\_ROOT) by total sampled volume:

$$BULK\_DENSITY\_EFFECTIVE\_8MM_{mpuh} = \frac{MASS\_8MM_{mpuh}}{VOLUME_{mpuh}}$$
 
$$BULK\_DENSITY\_EFFECTIVE\_GT8MM_{mpuh} = \frac{MASS\_GT8MM_{mpuh}}{VOLUME_{mpuh}}$$
 
$$BULK\_DENSITY\_EFFECTIVE\_ROOT_{mpuh} = \frac{MASS\_LIVE\_ROOT_{mpuh}}{VOLUME_{mpuh}}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) Calculate the total carbon content (LAYER\_CC\_TOTAL) and carbon content from the fraction  $\leq 8$  mm (LAYER\_CC\_8MM) in each of the forest floor or organic soil samples by multiplying the effective bulk density of the  $\leq 8$  mm (BULK\_DENSITY\_EFFECTIVE\_8MM), > 8 mm (BULK\_DENSITY\_EFFECTIVE\_GT8MM) or live roots (BULK\_DENSITY\_EFFECTIVE\_ROOT) fractions with soil sample thickness (THICKNESS) and organic carbon content of the  $\leq 8$  mm (TOC\_8MM), > 8 mm (TOC\_GT8MM) or root (46 g kg<sup>-1</sup>; Ma et al. 2018) fractions of forest floor or organic soil and convert units to kg m<sup>-2</sup>. Use total carbon content [TC\_8MM, TC\_GT8MM] if total organic carbon [TOC\_8MM, TOC\_GT8MM] is missing. If no values of carbon content are available for the fraction > 8mm [TC\_GT8MM, TOC\_GT8MM], then carbon content in the fraction  $\leq 8$  mm [TC\_8MM, TOC\_8MM] is used as a substitute. Total carbon content is the sum of carbon content in  $\leq 8$  mm, > 8 mm and live root fractions:

$$LAYER\_CC\_8MM_{mpuh} \\ = \frac{TOC\_8MM_{mpuh}}{1000} *BULK\_DENSITY\_EFFECTIVE\_8MM_{mpuh} *THICKNESS_{mpuh} \\ *10$$

$$\begin{split} LAYER\_CC\_TOTAL_{mpuh} \\ &= \left[\frac{TOC\_8MM_{mpuh}}{1000} *BULK\_DENSITY\_EFFECTIVE\_8MM_{mpuh} *THICKNESS_{mpuh} \right. \\ &* 10 \right] \\ &+ \left[\frac{TOC\_GT8MM_{mpuh}}{1000} *BULK\_DENSITY\_EFFECTIVE\_GT8MM_{mpuh} \right. \\ &* THICKNESS_{mpuh} *10 \right] \\ &+ \left[\frac{46}{1000} *BULK\_DENSITY\_EFFECTIVE\_ROOT_{mpuh} *THICKNESS_{mpuh} *10 \right] \end{split}$$

where h is a unique sample (SAMPLE\_NUM) of pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

#### Output

LAYER CC 8MM, LAYER CC TOTAL (for flr org sample and soil org sample tables)

CC\_FOR\_FLOOR\_8MM, CC\_FOR\_FLOOR\_TOTAL, CC\_ORGANIC0\_15\_8MM, CC\_ORGANIC15\_35\_8MM,

# CC\_ORGANIC35\_55\_8MM, CC\_ORGANIC0\_15\_TOTAL, CC\_ORGANIC15\_35\_TOTAL, CC\_ORGANIC35\_55\_TOTAL

#### Inputs

BULK\_DENSITY\_8MM; BULK\_DENSITY\_TOTAL; TOC\_8MM; TOC\_GT8MM; THICKNESS; LAYER\_CC\_8MM; LAYER\_CC\_TOTAL; AVG\_ORG\_THICK; AVG\_BURIED\_THICK; PCT\_SS\_ORG; PCT\_SS\_DECAY; PCT\_SS\_BURIED; DENSITY; ORG\_CARB\_WD

#### **Computations**

Warning: These compiled attributes (or their precursors) were not compiled by the NFI office prior to August 1, 2007 and therefore may not follow the procedures outlined below.

#### **For Forest Floor**

1) Compute the weighted average organic carbon (AVG\_ORG\_CARB\_PIT) and bulk density (AVG\_BULK\_DENSITY\_PIT) for the < 8 mm fraction in each soil pit (in case there are multiple samples in the pit) by multiplying total organic carbon of the < 8 mm fractions (TOC\_8MM) with sample thickness (THICKNESS), summing these products across all samples in a pit and dividing the result by the summed thickness of all samples in a pit:

$$AVG\_ORG\_CARB\_PIT_{mpu} = \sum_{h=1}^{n} TOC\_8MM_{mpuh} * THICKNESS_{mpuh} \bigg/ \sum_{h=1}^{n} THICKNESS_{mpuh}$$

 $AVG\_BULK\_DENSITY\_PIT_{mpu}$ 

$$= \sum_{h=1}^{n} BULK\_DENSITY\_8MM_{mpuh} * THICKNESS_{mpuh} / \sum_{h=1}^{n} THICKNESS_{mpuh}$$

where h is a unique sample (SAMPLE\_NUM) among n number of samples in pit u (PIT\_NUM) within plot p (NFI PLOT) at measurement m (MEAS NUM)

2) Then calculate the average organic carbon (AVG\_ORG\_CARB\_FF) and bulk density (AVG\_BULK\_DENSITY\_FF) of the < 8mm fraction of forest floor for the plot as a whole, by summing the weighted average organic carbon (AVG\_ORG\_CARB\_PIT) or bulk density (AVG\_BULK\_DENSITY\_PIT) across soil pits and dividing by the number of soil pits in a plot:

$$AVG\_ORG\_CARB\_FF_{mp} = \sum_{u=1}^{n} AVG\_ORG\_CARB\_PIT_{mpu} / n_{mp}$$

$$AVG\_BULK\_DENSITY\_FF_{mp} = \sum_{u=1}^{n} AVG\_BULK\_DENSITY\_PIT_{mpu} / n_{mp}$$

where u is a unique pit number (PIT\_NUM) among n number of pits within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) For each pit, determine the carbon content per cm depth in the < 8 mm fraction (LAYER\_CC\_CM\_PIT) and total forest floor layer (LAYER\_CCTOTAL\_CM\_PIT) within each pit by dividing the sum of carbon content values in each sample (LAYER\_CC\_8MM, LAYER\_CC\_TOTAL) by the sum of forest floor thickness sampled (THICKNESS).

$$LAYER\_CC\_CM\_PIT_{mpu} = \left[\sum_{h=1}^{n} LAYER\_CC\_8MM_{mpuh}\right] / \sum_{h=1}^{n} THICKNESS_{mpuh}$$

$$LAYER\_CCTOTAL\_CM\_PIT_{mpu} = \left[\sum_{h=1}^{n} LAYER\_CC\_TOTAL_{mpuh}\right] / \sum_{h=1}^{n} THICKNESS_{mpuh}$$

where h is a unique sample (SAMPLE\_NUM) among n number of samples in pit u (PIT\_NUM) within plot p (NFI PLOT) at measurement m (MEAS NUM)

4) For each NFI plot, Calculate the average carbon content per cm depth in the < 8 mm fraction (LAYER CC CM) and total forest floor layer (LAYER CCTOTAL CM) across all small soil pits in the plot:

$$LAYER\_CC\_CM_{mp} = \left[\sum_{u=1}^{n} LAYER\_CC\_CM_{mpu}\right] / n_{mp}$$
 
$$LAYER\_CCTOTAL\_CM_{mp} = \left[\sum_{u=1}^{n} LAYER\_CCTOTAL\_CM_{mpu}\right] / n_{mp}$$

where u is a unique pit (PIT\_NUM) among n number of pits in plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

5) Calculate the plot-level average organic (PLOT\_AVG\_ORG\_THICK) and buried wood (PLOT\_AVG\_BURIED\_THICK) thicknesses (cm) determined from surface substrate sampling, by averaging organic (AVG\_ORG\_THICK) and buried wood (AVG\_BURIED\_THICK) thicknesses across transects. Then calculate an average layer carbon content (kg m<sup>-2</sup>) in the < 8 mm fraction (AVG\_LAYER\_CC) and total forest floor layer (AVG\_LAYER\_CC\_TOTAL) using the plot-level average organic thickness determined from surface substrate sampling along transects (PLOT\_AVG\_ORG\_THICK):

$$PLOT\_AVG\_ORG\_THICK_{mp} = \left[\sum_{z=1}^{n} AVG\_ORG\_THICK_{mpz}\right] / n_{mp}$$
 
$$PLOT\_AVG\_BURIED\_THICK_{mp} = \left[\sum_{z=1}^{n} AVG\_BURIED\_THICK_{mpz}\right] / n_{mp}$$
 
$$AVG\_LAYER\_CC_{mp} = LAYER\_CC\_CM_{mp} * PLOT\_AVG\_ORG\_THICK_{mp}$$
 
$$AVG\_LAYER\_CC\_TOTAL_{mp} = LAYER\_CCTOTAL\_CM_{mp} * PLOT\_AVG\_ORG\_THICK_{mp}$$

where z is a unique transect (TRANSECT\_NUM) among n number of transects within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

6) Determine the leading taxon of coarse woody debris in the plot using the same algorithms as in <a href="section13">section13</a> and use that to determine the wood density (DENSITY; refer to support-data table <a href="gpcsd\_wood\_density">gpcsd\_wood\_density</a>) and organic carbon content of the buried wood (ORG\_CARB\_WD; refer to support-data table <a href="gpcsd\_cwd\_org\_carb">gpcsd\_cwd\_org\_carb</a>) tallied during surface substrate sampling (PCT\_SS\_BURIED), assuming a decay class of 5.

7) Determine the total carbon content per hectare in the forest floor (CCTOTAL\_FOR\_FLOOR), by multiplying the average layer carbon content (AVG\_LAYER\_CC) with the fractions of the plot that is covered by organics (PCT\_SS\_ORG) and decaying wood (PCT\_SS\_DECAY) and adding the carbon content contained in buried wood (i.e. the fraction of the plot that is covered by buried wood [PCT\_SS\_BURIED] multiplied by buried wood carbon content [ORG\_CARB\_WD], density [DENSITY] and thickness [PLOT\_AVG\_BURIED\_THICK]) then converting units to Mg ha<sup>-1</sup>:

```
\begin{split} CCTOTAL\_FOR\_FLOOR_{mp} \\ &= (AVG\_LAYER\_CC\_TOTAL_{mp} * (PCT\_SS\_ORG_{mp}/100) * 10000 \\ &+ AVG\_LAYER\_CC\_TOTAL_{mp} * (PCT\_SS\_DECAY_{mp}/100) * 10000 \\ &+ PLOT\_AVG\_BURIED\_THICK_{mp} * DENSITY_{mp} * (ORG\_CARB\_WD_{mp}/1000) * 10 \\ &* (PCT\_SS\_BURIED_{mp}/100) * 10000)/1000 \end{split}
```

If the average thickness of organic matter along transects (PLOT\_AVG\_ORG\_THICK) is greater than the average thickness of buried wood along transects (PLOT\_AVG\_BURIED\_THICK), then calculation of total carbon content per hectare in the forest floor (CCTOTAL\_FOR\_FLOOR) needs to include a term to account for organic content surrounding buried wood using:

```
\begin{split} &CCTOTAL\_FOR\_FLOOR_{mp} \\ &= (AVG\_LAYER\_CC\_TOTAL_{mp}*(PCT\_SS\_ORG_{mp}/100)*10000 \\ &+ AVG\_LAYER\_CC\_TOTAL_{mp}*(PCT\_SS\_DECAY_{mp}/100)*10000 \\ &+ PLOT\_AVG\_BURIED\_THICK_{mp}*DENSITY_{mp}*(ORG\_CARB\_WD_{mp}/1000)*10 \\ &* (PCT\_SS\_BURIED_{mp}/100)*10000 + (PLOT\_AVG\_ORG\_THICK_{mp} \\ &- PLOT\_AVG\_BURIED\_THICK_{mp})/PLOT\_AVG\_ORG\_THICK_{mp} \\ &* AVG\_LAYER\_CC\_TOTAL_{mp}*(PCT\_SS\_BURIED_{mp}/100)*10000)/1000 \end{split}
```

where p is a unique plot (NFI PLOT) at measurement m (MEAS NUM)

8) Determine the carbon content per hectare in the < 8 mm fraction of the forest floor (CC\_FOR\_FLOOR), by multiplying the average layer carbon content (AVG\_LAYER\_CC) with the fractions of the plot that is covered by organics (PCT\_SS\_ORG) then converting units to Mg ha<sup>-1</sup>:

```
CC\_FOR\_FLOOR_{mp} = (AVG\_LAYER\_CC_{mp} * (PCT\_SS\_ORG_{mp}/100) * 10000)/1000
```

If the average thickness of organic matter along transects (PLOT\_AVG\_ORG\_THICK) is greater than the average thickness of buried wood along transects (PLOT\_AVG\_BURIED\_THICK), then calculation of total carbon content per hectare in the < 8 mm fraction of the forest floor (CC\_FOR\_FLOOR) needs to include a term to account for organic content surrounding buried wood using:

```
 \begin{split} \textit{CC\_FOR\_FLOOR}_{mp} &= (\textit{AVG\_LAYER\_CC}_{mp} * (\textit{PCT\_SS\_ORG}_{mp}/100) * 10000 \\ &+ (\textit{PLOT\_AVG\_ORG\_THICK}_{mp} \\ &- \textit{PLOT\_AVG\_BURIED\_THICK}_{mp})/\textit{PLOT\_AVG\_ORG\_THICK}_{mp} * \textit{AVG\_LAYER\_CC}_{mp} \\ &* (\textit{PCT\_SS\_BURIED}_{mp}/100) * 10000)/1000 \end{split}
```

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

9) If forest floor and organic soil samples are taken from the same NFI plot, then the forest floor is only considered as a surface litter layer. Therefore, the carbon content in the total forest floor or fraction < 8 mm is determined by multiplying the carbon content per cm of depth (LAYER\_CCTOTAL\_CM or LAYER\_CC\_CM, respectively), the average depth of the forest floor sample pits (TOT\_THICKNESS) and the fraction of the plot that is covered by organic matter (PCT\_SS\_ORG), then converting units to Mg ha<sup>-1</sup>:

First calculate the total thickness of each plot (TOT\_THICKNESS) by summing the thickness (THICKNESS) of all samples in a pit:

$$TOT\_THICKNESS_{mpu} = \left[\sum_{h=1}^{n} THICKNESS_{mpuh}\right]$$

where h is a unique sample (SAMPLE\_NUM) among n number of samples in pit u (PIT\_NUM) within plot p (NFI PLOT) at measurement m (MEAS NUM)

Then calculate the carbon content in the forest floor layer using the average depth of forest sample pits:

$$\begin{split} \textit{CCTOTAL\_FOR\_FLOOR\_LITTER}_{mp} \\ &= \left(\textit{LAYER\_CCTOTAL\_CM}_{mp} * \left[\sum_{u=1}^{n} \textit{TOT\_THICKNESS}_{mpu}\right] / n_{mp} \\ &* \left(\textit{PCT\_SS\_ORG}_{mp} / 100\right) * 10000\right) / 1000 \end{split}$$

 $CC\_FOR\_FLOOR\_LITTER_{mp}$ 

$$= (LAYER\_CC\_CM_{mp} * \left[\sum_{u=1}^{n} TOT\_THICKNESS_{mpu}\right] / n_{mp} * (PCT\_SS\_ORG_{mp}/100)$$

$$* 10000)/1000$$

where u is a unique pit (PIT\_NUM) among n number of pits within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

## **For Organic Soil**

1) Compute the weighted average organic carbon (AVG\_ORG\_CARB\_PIT) and bulk density (AVG\_BULK\_DENSITY\_PIT) for the < 8 mm fraction in each soil pit (in case there are multiple samples in the pit) by multiplying total organic carbon of the < 8 mm fractions (TOC\_8MM) with sample thickness (THICKNESS), summing these products across all samples in a pit and dividing the result by the summed thickness of all samples in a pit:

$$AVG\_ORG\_CARB\_PIT_{mpu} = \sum_{h=1}^{n} TOC\_8MM_{mpuh} * THICKNESS_{mpuh} / \sum_{h=1}^{n} THICKNESS_{mpuh}$$

 $AVG\_BULK\_DENSITY\_PIT_{mvu}$ 

$$= \sum_{h=1}^{n} BULK\_DENSITY\_8MM_{mpuh} * THICKNESS_{mpuh} / \sum_{h=1}^{n} THICKNESS_{mpuh}$$

where h is a unique sample (SAMPLE\_NUM) among n number of samples in pit u (PIT\_NUM) within plot p (NFI PLOT) at measurement m (MEAS NUM)

2) Then calculate the average organic carbon (AVG\_ORG\_CARB\_OS) and bulk density (AVG\_BULK\_DENSITY\_OS) of the < 8 mm fraction of organic soils for the plot as a whole, by summing the weighted average organic carbon (AVG\_ORG\_CARB\_PIT) or bulk density (AVG\_BULK\_DENSITY\_PIT) across soil pits and dividing by the number of soil pits in a plot:

$$AVG\_ORG\_CARB\_OS_{mp} = \sum_{u=1}^{n} AVG\_ORG\_CARB\_PIT_{mpu} / n_{mp}$$

$$AVG\_BULK\_DENSITY\_OS_{mp} = \sum_{u=1}^{n} AVG\_BULK\_DENSITY\_PIT_{mpu} / n_{mp}$$

where u is a unique pit number (PIT\_NUM) among n number of pits within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) For reporting, the original organic soil layers are reapportioned to three standardized layers of 0-15 cm, 15-35 cm and 35-55 cm. The carbon content of the organic soil is reported to the maximum depth for which all required data are available, up to a depth of 55 cm. For each standardized layer within a pit, determine the portion ( $\epsilon$  0 – 15) of each sample's thickness (SAMPLE\_BOTTOM – SAMPLE\_UPPER) and carbon content (LAYER\_CCTOTAL for the entire organic soil, LAYER\_CC for the < 8mm fraction) contained within the depth range of a layer, and sum to calculate the total measured thickness (i.e. sampled interval; THICKNESS\_0\_15) and carbon content in the entire organic soil (CCTOTAL0\_15) and the < 8 mm fraction (CC0\_15) corresponding to each layer. The calculations for the 0-15 cm layer are as follows:

$$THICKNESS\_0\_15_{mpu} = \sum_{h=1}^{n} (SAMPLE\_BOTTOM_{mpuh} - SAMPLE\_UPPER_{mpuh}) * (\epsilon \ 0 \ -15)$$

$$CCTOTAL0\_15_{mpu} = \sum_{h=1}^{n} LAYER\_CCTOTAL_{mpuh} * (\epsilon \ 0 \ -15)$$

$$CC0\_15_{mpu} = \sum_{h=1}^{n} LAYER\_CC_{mpuh} * (\epsilon \ 0 \ -15)$$

where h is a unique sample (SAMPLE\_NUM) among n number of samples where the midpoint of the sampled interval lies in the layer range (e.g. 0-15 cm) within pit number u (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM). The term ( $\epsilon$  0-15) stands for the proportion of each sample that lies in the designated range of a layer. For example, if the interval sampled runs from 11-21 cm, the midpoint of that interval is 16. Therefore, only the portion of the sample that is in the 15-35 cm layer (15-21 cm) will be used in calculating carbon content in the 15-35 cm layer (CC15\_35). The portion that is in the 0-15 cm layer (11-14 cm) will not be used since the midpoint lies outside of the 0-15 cm layer. The midpoint constraint is ignored in cases where all samples spanning a higher layer's standardized depth have midpoints in lower layers. For example, in the case where the first sampled horizon ranged from 0-40 cm, the portion that is in the 0-15 cm layer will be used to calculate that layer's carbon content, while the 15-35 cm portion will be used to calculate the second standardized layer's carbon content (where the midpoint lies) and the 35-40 cm portion will not be used.

4) Calculate the adjusted carbon content (kg m<sup>-2</sup>) for each standard layer across all soil pits (CCTOTALO\_15\_ADJ and CCO\_15\_ADJ for the entire and < 8 mm fraction of organic soil, respectively) and for all layers combined (PLOT\_TOT\_CC\_TOTAL and PLOT\_TOT\_CC for the entire and < 8 mm fraction of organic soil, respectively) by dividing the carbon content (CCTOTALO\_15 and CCO\_15 for the entire and < 8 mm fraction of organic soil, respectively) by the measured thickness (THICKNESS\_0\_15) in standardized layers for each pit, then dividing the summed fractions across pits by the number of pits in a plot and multiplying by the nominal thickness of each layer (NOM\_THICKNESS):

$$\begin{split} &CCTOTAL0\_15\_ADJ_{mp} \\ &= \left[ \left[ \sum_{u=1}^{n} \left( CCTOTAL0\_15_{mpu} / THICKNESS\_0\_15_{mpu} \right) \right] / n \right] * NOM\_THICKNESS_{mp} \\ &CC0\_15\_ADJ_{mp} = \left[ \left[ \sum_{u=1}^{n} \left( CC0\_15_{mpu} / THICKNESS\_0\_15_{mpu} \right) \right] / n \right] * NOM\_THICKNESS_{mp} \\ &PLOT\_TOT\_CC\_TOTAL_{mp} \\ &= CCTOTAL0\_15\_ADJ_{mp} + CCTOTAL15\_35\_ADJ_{mp} + CCTOTAL35\_55\_ADJ_{mp} \end{split}$$

$$PLOT\_TOT\_CC_{mp} = CC0\_15\_ADJ_{mp} + CC15\_35\_ADJ_{mp} + CC35\_55\_ADJ_{mp}$$

where u is a unique pit (PIT\_NUM) among n number of pits within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM) and where the nominal thickness (NOM\_THICKNESS) of the standardized layer I is 15 cm for the 0-15 cm layer, 20 cm for the 15-35 cm layer and 20 cm for the 35-55 cm layer or, alternatively, the portion of the nominal thickness which corresponds to the maximum depth for which all required data are available for computing carbon content.

Note: The average thickness of organic matter along transects (PLOT\_AVG\_ORG\_THICK) and the maximum depth sampled (the maximum value of SAMPLE\_BOTTOM among samples used to calculate carbon content in a standardized layer [LAYER\_CC]) in a plot govern the nominal thickness applied to the calculation of the adjusted carbon content of standardized layers.

If the average thickness of organic matter along transects is 40 cm or more, then the nominal thickness of the third layer is 20 – (55 – maximum depth) when the maximum depth sampled is 35-55cm, otherwise the nominal thickness of the third layer is 20 cm when the maximum depth sampled is 55 cm or more.

Where the average thickness of organic matter along transects is less than 40 cm, the midpoint of the layer is either the middle of the standardized layer thickness (e.g. [15 + 35] / 2 = 25 for the second layer) or the middle of the interval in which the average thickness of organic matter along transects lies within the standardized layer, whichever is less. For example, if the average thickness of organic matter along transects is 32, then the middle of the interval running from 15 to 32 in the second standardized layer is 23.5 ([15 + 32] / 2)) whereas the middle of the layer itself is 25. The midpoint chosen is therefore 23.5. The maximum depth is then used to determine the nominal thickness of the second layer. If the maximum depth is *less* than 35 cm but higher than the midpoint and the average thickness of organic matter along transects is more than 35 cm, then the nominal thickness of the second layer is 20, otherwise it is only as thick as the depth allowed by the average thickness of organic matter along transects (i.e., 20 - [35-plot average organic thickness]). If the maximum depth is less than the midpoint, then the maximum depth dictates the nominal thickness of the second layer (i.e., 20 - [35-maximum depth]). If the maximum depth is 35 cm or more, then the average thickness of organic matter along transects determines the nominal thickness of the second layer. If it is 35 cm or more, then the nominal thickness of the second layer is 20, otherwise it is constrained by the average thickness of organic matter along transects.

5) Calculate total depth of sampled organic soil (SAMPLE\_DEPTH\_ORG) as the sum of nominal thickness values (NOM\_THICKNESS) used to calculate adjusted carbon content for each standard layer across all soil pits:

$$SAMPLE\_DEPTH\_ORG_{mp} = \sum_{l=1}^{n} NOM\_THICKNESS_{mpl}$$

where l is one of three standardized soil layers (0-15 cm, 15-35 cm, 35-55 cm) within plot p (NFI PLOT) at measurement m (MEAS NUM)

- 6) Determine the leading taxon of coarse woody debris in the plot using the same algorithms as in <a href="section13">section 13</a> and use that to determine the wood density (DENSITY; refer to support-data table gpcsd\_wood\_density) and organic carbon content of the buried wood (ORG\_CARB\_WD; refer to support-data table gpcsd\_cwd\_org\_carb) tallied during surface substrate sampling (PCT\_SS\_BURIED), assuming a decay class of 5.
- 7) The sum of the nominal thicknesses of the first, second and third standardized layers (SAMPLE\_DEPTH\_ORG) is reapportioned to each of three standardized layers: ORG\_SOIL\_THICK0-15, ORG\_SOIL\_THICK15-35 and ORG\_SOIL\_THICK35-55. The plot average buried thickness (PLOT\_AVG\_BURIED\_THICK) is similarly reapportioned to three standardized layers: PLOT\_AVG\_BURIED\_THICK0\_15, PLOT\_AVG\_BURIED\_THICK15\_35 and PLOT\_AVG\_BURIED\_THICK35\_55.
- 8) For each of the standardized layer, determine the total carbon content per hectare in the organic soil (CCTOTAL\_ORGANICO\_15) by multiplying the adjusted carbon content in a layer (CCTOTALO\_15\_ADJ) with the fractions of the plot that is covered by organics (PCT\_SS\_ORG) and decaying wood (PCT\_SS\_DECAY), adding the carbon content contained in buried wood in the layer (i.e. the fraction of the plot that is covered by buried wood [PCT\_SS\_BURIED) multiplied by buried wood carbon content [ORG\_CARB\_WD], density [DENSITY] and thickness [PLOT\_AVG\_BURIED\_THICKO\_15]) and including a term to account for organic content surrounding buried wood if the average thickness of organic matter along transects (ORG\_SOIL\_THICKO\_15) is greater than the average thickness of buried wood along transects (PLOT\_AVG\_BURIED\_THICKO\_15) within a layer. Units are then converted to Mg ha<sup>-1</sup>:

```
\begin{split} \textit{CCTOTAL\_ORGANICO}\_15_{mp} \\ &= (\textit{CCTOTALO}\_15\_\textit{ADJ}_{mp} * (\textit{PCT\_SS\_ORG}_{mp}/100) * 10000 + \textit{CCTOTALO}\_15\_\textit{ADJ}_{mp} \\ &* (\textit{PCT\_SS\_DECAY}_{mp}/100) * 10000 + \textit{PLOT\_AVG\_BURIED\_THICKO}\_15_{mp} \\ &* \textit{DENSITY}_{mp} * (\textit{ORG\_CARB\_WD}_{mp}/1000) * 10 * (\textit{PCT\_SS\_BURIED}_{mp}/100) \\ &* 10000 + ((\textit{ORG\_SOIL\_THICKO}\_15_{mp} \\ &- \textit{PLOT\_AVG\_BURIED\_THICKO}\_15_{mp})/\textit{ORG\_SOIL\_THICKO}\_15_{mp}) \\ &* \textit{CCTOTALO}\_15\_\textit{ADJ}_{mp} * (\textit{PCT\_SS\_BURIED}_{mp}/100) * 10000)/1000 \end{split}
```

where p is a unique plot (NFI PLOT) at measurement m (MEAS NUM)

9) For each of the standardized layer, determine the carbon content per hectare in the < 8 mm fraction of organic soil (CC\_ORGANICO\_15) by multiplying the adjusted carbon content in a layer (CCO\_15\_ADJ) with the fractions of the plot that is covered by organics (PCT\_SS\_ORG) and including a term to account for organic content surrounding buried wood if the average thickness of organic matter along transects (ORG\_SOIL\_THICKO\_15) is greater than the average thickness of buried wood along transects (PLOT\_AVG\_BURIED\_THICKO\_15) within a layer. Units are then converted to Mg ha<sup>-1</sup>:

```
 \begin{split} CC\_ORGANICO\_15_{mp} &= (CCO\_15\_ADJ_{mp} * (PCT\_SS\_ORG_{mp}/100) * 10000 + ((ORG\_SOIL\_THICKO\_15_{mp} \\ &- PLOT\_AVG\_BURIED\_THICKO\_15_{mp})/ORG\_SOIL\_THICKO\_15_{mp}) * CO\_15\_ADJ_{mp} \\ &* (PCT\_SS\_BURIED_{mp}/100) * 10000)/1000 \end{split}
```

where p is a unique plot (NFI PLOT) at measurement m (MEAS NUM)

10) For organic soil, calculate the products of the total depth of sampled organic soil standardized to 55 cm (SAMPLE DEPTH ORG; i.e. sum of nominal thickness of standardized layers) with the average organic

carbon (AVG\_ORG\_CARB\_OS) and the average bulk density (AVG\_BULK\_DENSITY\_OS) in the < 8 mm fraction:

$$WT\_AVG\_ORG\_CARB\_OS_{mp} = AVG\_ORG\_CARB\_OS_{mp} * SAMPLE\_DEPTH\_ORG_{mp}$$
 
$$WT\_AVG\_BULK\_DENSITY\_OS_{mp} = AVG\_BULK\_DENSITY\_OS_{mp} * SAMPLE\_DEPTH\_ORG_{mp}$$

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

For forest floor, calculate the products of the average thickness of organic matter along transects (PLOT\_AVG\_ORG\_THICK) with the average organic carbon (AVG\_ORG\_CARB\_FF) and the average bulk density (AVG\_BULK\_DENSITY\_FF) in the < 8 mm fraction:

$$WT\_AVG\_ORG\_CARB\_FF_{mp} = AVG\_ORG\_CARB\_FF_{mp} * PLOT\_AVG\_ORG\_THICK_{mp}$$
 
$$WT\_AVG\_BULK\_DENSITY\_FF_{mp} = AVG\_BULK\_DENSITY\_FF_{mp} * PLOT\_AVG\_ORG\_THICK_{mp}$$

where p is a unique plot (NFI\_PLOT) at measurement m (MEAS\_NUM)

11) Calculate the weighted average organic carbon (AVG\_ORG\_CARB; g kg<sup>-1</sup>) and weighted average bulk density (AVG\_BULK\_DENSITY; g cm<sup>-3</sup>) for the joint forest floor and organic soil components using the average thickness of organic matter along transects (for forest floor overlying mineral soil; PLOT\_AVG\_ORG\_THICK) and organic soil thickness standardized to 55 cm (for organic soils; SAMPLE\_DEPTH\_ORG).

$$AVG\_ORG\_CARB_{mp} = \frac{(WT\_AVG\_ORG\_CARB\_FF_{mp} + WT\_AVG\_ORG\_CARB\_OS_{mp})}{(PLOT\_AVG\_ORG\_THICK_{mp} + ORG\_SOIL\_THICK_{mp})}$$

$$AVG\_BULK\_DENSITY\_ORG_{mp} = \frac{(WT\_AVG\_BULK\_DENSITY\_FF_{mp} + WT\_AVG\_BULK\_DENSITY\_OS_{mp})}{(PLOT\_AVG\_ORG\_THICK_{mp} + ORG\_SOIL\_THICK_{mp})}$$

where p is a unique plot (NFI PLOT) at measurement m (MEAS NUM)

Note: Values for the weighted average organic carbon (AVG\_ORG\_CARB) and weighted average bulk density (AVG\_BULK\_DENSITY) are equivalent to plot-level average organic carbon and average bulk density in only forest floors or only organic soils when the other soil type is absent.

## Output

CC\_FOR\_FLOOR\_8MM, CC\_FOR\_FLOOR\_TOTAL, CC\_ORGANICO\_15\_8MM, CC\_ORGANIC15\_35\_8MM, CC\_ORGANIC35\_55\_8MM, CC\_ORGANIC0\_15\_TOTAL, CC\_ORGANIC15\_35\_TOTAL, CC\_ORGANIC35\_55\_TOTAL, AVG\_ORG\_CARB, AVG\_BULK\_DENSITY\_ORG, SAMPLE\_DEPTH\_ORG (site\_info table)

# DEPTH\_ORG, DEPTH\_MIN

Inputs

SAMPLE BOTTOM

**Computations** 

1) For forest floor, the depth of the organic layer (DEPTH\_ORG\_FLOOR) is the maximum bottom-depth value (SAMPLE\_BOTTOM) among forest floor samples collected in the pit:

$$DEPTH\_ORG\_FLOOR_{mpu} = MAX(SAMPLE\_BOTTOM_{mpu})$$

where u is a unique pit number (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

2) For organic soil, the depth of the organic layer (DEPTH\_ORG\_FLOOR) is the maximum bottom-depth value (SAMPLE BOTTOM) among organic soil samples collected in the pit:

$$DEPTH\_ORG\_ORGANIC_{mpu} = MAX(SAMPLE\_BOTTOM_{mpu})$$

where u is a unique pit number (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

3) For mineral soil, the depth of the mineral layer (DEPTH\_MIN) is the maximum bottom-depth value (SAMPLE BOTTOM) among mineral soil samples collected in the pit:

$$DEPTH\_MIN_{mpu} = MAX(SAMPLE\_BOTTOM_{mpu})$$

where u is a unique pit number (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

4) The organic soil depth (DEPTH\_ORG) is the sum of the depths of the forest floor (DEPTH\_ORG\_FLOOR) and organic soil (DEPTH\_ORG\_ORGANIC) in the pit:

$$DEPTH\_ORG_{mpu} = DEPTH\_ORG\_FLOOR_{mpu} + DEPTH\_ORG\_ORGANIC_{mpu}$$

where u is a unique pit number (PIT\_NUM) within plot p (NFI\_PLOT) at measurement m (MEAS\_NUM)

# Output

DEPTH\_ORG, DEPTH\_MIN (soil\_pit\_depth table)

# 16. Computational References for Tree Volume

Tree volume equations and systems were requested from the provinces and territories to be used for compilation of tree volumes within their respective jurisdictions. In some cases these compilation procedures were modified by the NFI office to accommodate the unique format and structure of the NFI ground plot program. The following includes a listing by province/territory of the tree volume equations and systems that are used by the NFI, along with jurisdictional contacts. Volume and taper coefficients used by the NFI compiler are available upon request.

# Height estimation for broken top trees

Some trees have broken tops or have missing height values, in which cases total tree heights are projected (HT\_PRJ). The projected height (HT\_PRJ) of broken top trees is used to adjust quantification of volume and biomass. Total projected heights are calculated using Chapman-Richard's model for tree height prediction (Huang et al. 2009; gp\_ht\_dbh\_prj.sas).

Coefficients for height projection equations are parameterized by plot, measurement and species using only measured (or unspecified) tree heights (MEAS\_EST\_HEIGHT = 'M' or 'S'). The minimum sample size for calibrating the equation is three trees. If the sample size requirement is not met, curves are generated by plot, measurement and vegetation type (hardwood vs. softwood). If the sample size requirement is still not met, equations are fit (within jurisdiction) by ecozone and species. If the sample size requirement is still not met, equations are fit (within jurisdiction) by ecozone and vegetation type (hardwood vs. softwood).

$$HT_PRJ = 1.3 + a * (1 - e^{-b*DBH})^c$$

where a > 0

If a projected tree height (HT\_PRJ) is less or equal to 1.3 m, then that projected tree height is set to missing. If a projected tree height is less than the measured tree height, then that projected height is set equal to the measured height. Projected height for small trees (i.e. trees with diameter at breast height less than 9 cm) is set to missing when greater than 20 m.

## Merchantability limits

The merchantable volume is the inside bark stem wood volume excluding the stump and top, unless otherwise stated.

Province/territory	Stump height (m)	Top diameter (cm)	Additional requirement
Alberta	0.3	10.0	stump diameter ≥ 15 cm
British Columbia	0.3	10.0	DBH ≥ 17.5 cm for CWH and CDF
			BEC zones
			DBH ≥ 12.5 cm otherwise
Manitoba	0.3	7.62	DBH > 9.0 cm
Newfoundland & Labrador	0.15	7.6	DBH > 9.0 cm
New Brunswick	0.15	6.6 hardwoods	DBH ≥ 9.1 cm
		6.7 softwoods	
Northwest Territory	0.3	7.0	DBH > 10.1 cm
Nova Scotia	0.15	7.0	DBH ≥ 9.0 cm
Ontario	0.3	7.0	DBH ≥ 9.0 cm
Prince Edward Island	0.2	8.0	DBH ≥ 9.0 cm
Quebec	0.15	9.0	DBH ≥ 9.0 cm
Saskatchewan	0.3	8.01	DBH ≥ 7.0 cm
Yukon Territory	0.3	7.5	

**Table 24.** The merchantability limits used, when necessary, in calculations of total volume.

#### **Alberta**

Kozak's variable-exponent taper equation (Kozak 1988) was tested and proven to be appropriate for major tree species in Alberta (Huang 1994, Huang et al. 2000). Tree volumes in Alberta are calculated using Kozak's taper function (equation 1) and the following calculations.

- 1. Calculate the diameter inside bark (DIB) at stump height (0.3 m).
- 2. Calculate the merchantable height (height at which the top diameter is 10.0 cm).
- 3. Calculate the volume for stump (assumed to be a cylinder with diameter equal to the stump diameter) and top (assumed to be a cone).
- 4. Split the merchantable length (between stump and merchantable height) into 20 segments and calculate the top diameters for each segment.
- 5. Calculate the volume for each log using Newton's formula.

(1) 
$$d_i = a_0 D^{a_1} a_2^D X_i^{b_1 z_i^2 + b_2 \ln(z_i + 0.001) + b_3 \sqrt{z_i} + b_4 e^{z_i} + b_5 (D/H)} + \varepsilon_i$$

where  $d_i$  is the diameter inside bark (cm) at  $h_i$ ,  $h_i$  is the height (m) above ground (0< hi < H), H is the total tree height (m), D is the breast height diameter outside bark (cm), p is the relative height constraint (input as a parameter), e = 2.718282,  $a_0 - a_2$  and  $b_1 - b_5$  are taxon-specific input

parameters, 
$$\varepsilon_i$$
 is the error term,  $X_i = \frac{1 - \sqrt{h_i/H}}{1 - \sqrt{p}}$ , and  $z_i = h_i/H$ .

## References

Huang, S. 1994. Ecologically based Individual Tree Volume Estimation for Major Alberta Tree Species: Report #1 Methods of Formulation and Statistical Functions. Alberta Environmental Protection, Land and Forest Service, Forest Mngmt. Division. Tech. Rep. Pub. No. T/288. 80 p.

Huang, S., D. Price, D. Morgan, and K. Peck. 2000. Kozak's variable-exponent taper equation regionalized for white spruce in Alberta. W. J. App. For. 15: 75-85.

Kozak, A. 1988. A variable-exponent taper equation. Can. J. For. Res. 18: 1363-1368.

## **Alberta Contact:**

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#### **British Columbia**

Kozak's variable-exponent taper equation (Kozak 1997; equation 2) is used in BC. The procedure is as follows.

- 1. Calculate the diameter inside bark (DIB) at stump height (0.3 m).
- 2. Calculate the merchantable height (height at which the top diameter is 10.0 cm).
- 3. Calculate the volume for stump (assumed to be a cylinder with diameter equal to the stump diameter).
- 4. Split the merchantable length (between stump and merchantable height) into 10 cm slices and calculate the top diameters for each slice.
- 5. Calculate the volume for each slice using Smalian's formula.
- 6. The top volume is calculated using 10 cm slices and Smalian's formula.

Merchantable volume is the stem wood volume between the stump and the top diameter for trees with DBH ≥ 17.5 cm for CWH and CDF BEC zones, else the minimum DBH is 12.5 cm.

(2) 
$$d_{i} = e^{\frac{err}{2}} \cdot b_{1} Dbh^{b_{2}} b_{3}^{Dbh} X^{b_{4} + b_{5}z_{i}^{0.25} + b_{6} \cdot z_{i}^{1/3} + b_{7} \sqrt{z_{i}} + b_{8} \cdot \arcsin(1 - \sqrt{z_{i}}) + b_{9} \cdot (z_{i} + Dbh/height)^{-1} + b_{10} \cdot height} + \varepsilon_{i}$$

where 
$$X_i = \frac{1 - \sqrt{h_i / H}}{1 - \sqrt{p}}$$
,  $p = 0.01$  and  $z_i = h_i / H$ 

#### References

Kozak, A. 1997. Effects of multicollinearity and autocorrelation on the variable-exponent taper functions. Can. J. For. Res. 27:619-629.

#### Manitoba

Kozak's variable-exponent tape equation (Kozak 1988) was tested for Manitoba (Klos et al. 2007). Taxon-specific coefficients parameterized for Manitoba are used when available, with the exception of Balsam poplar (Klos et al. 2007), else those for Saskatchewan (Gal and Bella 1994) and Alberta (Huang 1994; Huang et al. 2000) are used. The procedure is as follows.

- 1. Calculate the diameter inside bark (DIB) at stump height (0.3 m).
- 2. Calculate the merchantable height (height at which the top diameter is 7.62 cm).
- 3. Calculate the volume for stump (assumed to be a cylinder with diameter equal to the stump diameter) and top (assumed to be a cone).
- 4. Split the merchantable length (between stump and merchantable height) into 20 segments and calculate the top diameters for each segment (equation 1).
- 5. Calculate the volume for each log using Newton's formula.

Merchantable volume is the stem wood volume between the stump and the top diameter for trees with DBH > 9.0 cm.

#### References

Huang, S. 1994. Ecologically based individual tree volume estimation for major Alberta tree species.

Report #1, Individual tree volume estimation procedures for Alberta: methods of formulation and statistical foundations. Alberta Environmental Protection, Land and Forest Services, Forest Management Division. Edmonton Alberta.

Huang, S., D. Price, D. Morgan, and K. Peck. 2000. Kozak's variable-exponent taper equation regionalized for white spruce in Alberta. W. J. App. For. 15: 75-85.

Kozak, A. 1988. A variable-exponent taper equation. Can. J. For. Res. 18: 1363-1368.

Klos, R.J., G.G. Wang, Q.-L. Dang, and E.W. East. 2007. Taper equations for five major commercial tree species in Manitoba, Canada. West. J. Appl. For. 22(3): 163-170.

Gal, J. and I.E. Bella. 1994. New stem taper function for 12 Saskatchewan timber species. CFS Northwest Region, Information Report NOR-X-338.

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## **Newfoundland & Labrador**

Total and merchantable tree volume calculations use species- and district-specific coefficients when these are available for Balsam fir and black spruce (Warren and Meades 1986; equations 3 and 5), else species-specific coefficients from Ker (1974; equations 4 and 5). Customized equations and coefficients were used for merchantable volume of Balsam fir and black spruce in Labrador (i.e. district  $\geq$  19; equation 6). Merchantable volume calculations use a stump height of 0.15 m (Height<sub>stump</sub>) and a top diameter of 7.6 cm (Diameter<sub>merch</sub>) for trees with DBH > 9.0 cm.

- 1. Plots within district 50 (federal lands) were assign equations from district 2 when these lie in Terra Nova National Park and district 16 when in Gros Morne National Park
- 2. Assign coefficients based on tree genus and species as well as the district where the plot lies
- 3. Calculate total and merchantable volumes using respective equations according to tree taxon and the district where the plot lies (i.e. Balsam fir and black spruce are treated differently).

(3) 
$$volume_{total} = 0.00439 * (DBH)^2 * \left(\frac{(1-0.04365*f)^2}{a+0.3048*b/HEIGHT}\right)$$

(4) 
$$volume_{total} = \frac{(DBH)^2}{(a+b/_{HEIGHT})}$$

if Balsam fir or black spruce in district other than 1 or 3  $\,$ 

- (5)  $volume_{merch} = volume_{total} * (c + x * (d + e * x))$
- (6)  $volume_{merch} = volume_{total} * (d + x * (c + e * x))$ if Balsam fir or black spruce in district greater or equal to 19

where

$$x = \left(\frac{Diameter_{merch}}{DBH}\right)^{2} * \left(1 + \frac{Height_{stump}}{HEIGHT}\right) * (1 - 0.04365 * f)^{-2}$$

$$x = \left(\frac{Diameter_{merch}}{DBH}\right)^{2} * \left(1 + \frac{Height_{stump}}{HEIGHT}\right)$$
if Balsam fir or black spruce in district other than 1 or 3

#### References

Ker, M.F. 1974. Metric tree volume tables for Newfoundland. CFS Report N-X-122, Warren, G.R. and J. P. Meades. 1986. Wood defect and density studies II. Total and net volume equations for Newfoundland forest management units. CFS Report N-X-242.

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## **New Brunswick**

Kozak's variable-exponent taper equation (equation 7; Kozak 2004, model 02) is used when taxon-specific coefficients are available for NB, else Honer *et al.* (1983) model and coefficients are used. Coefficients for inside-bark taper models are used for most softwood species (Li et al. 2012, Hennigar 2019), while coefficients for outside bark taper models (Li et al. 2012, Hennigar 2019) combined with bark thickness models (equation 8; Li and Weiskittel 2011, Hennigar 2019) are used for eastern hemlock and tamarack. Most hardwood species use coefficients for outside-bark taper models combined with bark thickness models (equation 8; Weiskittel and Li 2011, Hennigar 2019). When taxon-specific or applicable taper coefficients are not available (e.g. rarer/non-commercial softwoods and hardwoods), Honer et al. (1983) equations for lodgepole pine (equation 9; total volume) and softwoods (equation 10; merchantable volume) or for maple (equation 11; total volume) and hardwoods (equation 12; merchantable volumes) are used.

Taper equations (equation 7) were implemented as follows.

- Calculate the volume of stump (from ground to 0.15 m) by dividing stump into 10 cm slices, calculate the top and bottom diameters inside bark for each slice, and calculate the volume of each slice using Smalian's formula
- 2. Calculate the merchantable height (height at which the top diameter is 6.7 cm for softwoods and 6.6 for hardwoods).
- 3. Split the merchantable length (between stump and merchantable height) into 10 cm slices, calculate the top and bottom diameters for each slice, and calculate the volume for each slice using Smalian's formula.

4. The volume above merchantable height is calculated using 10 cm slices, calculate the top and bottom diameters for each slice, and calculate the volume for each slice using Smalian's formula. Merchantable volume is the stem wood volume between the stump and the top diameter for trees with DBH ≥ 9.1 cm.

(7) 
$$dib \ or \ dob = a_0 * DBH^{a_1} * HEIGHT^{a_2} *$$

$$\chi((b_1*z^4) + (b_2*(1/e^{DBH/HEIGHT})) + (b_3*x^{0.1}) + (b_4*(1/DBH)) + (b_5*HEIGHT^Q) + (b_6*x))$$

where dib = diameter inside bark at  $h_i$  height from the ground (cm), dob = diameter outside bark at  $h_i$  height from the ground (cm),  $h_i$  = height of the slice from the ground (cm)

$$p = \frac{1.3}{HEIGHT}$$

$$z = \frac{h_i}{HEIGHT}$$

$$x = \frac{1 - z^{1/3}}{1 - p^{1/3}}$$

$$Q = 1 - z^{1/3}$$

$$(8) \quad dib = c_0 * dob^{c_1}$$

When taper coefficients are not available for a given taxon, equations from Honer *et al.* (1983) were implemented as follows. For softwood total volume, the equation for lodgepole pine (Honer *et al.* 1983, Table 3) is used (equation 9).

(9) 
$$Volume_{total} = 0.0043891 * DBH^2 * \frac{(1-0.04365*0.118)^2}{0.694+0.3048*^{343.896}/_{HEIGHT}}$$

For softwood merchantable volume, the equation parameterized for softwoods is used (Honer *et al.* 1983, Table 6), where top diameter (Diameter<sub>merch</sub>) is set to 6.7 cm and stump height (Height<sub>stump</sub>) is set to 0.15 cm (equation 10).

(10) 
$$Volume_{merch} = Volume_{total} * (0.9645 - 0.1616 * x - 0.7945 * x^2)$$

where

$$x = \left(\frac{Diameter_{merch}}{DBH}\right)^{2} * \left(1 + \frac{Height_{stump}}{HEIGHT}\right) * (1 - 0.04365 * 0.155)^{-2}$$

For hardwood total volume, the equation parameterized for maple (Honer *et al.* 1983, Table 3) is used (equation 11).

(11) 
$$Volume_{total} = 0.0043891 * DBH^2 * \frac{(1-0.04365*0.145)^2}{1.046+0.3048*^{383.972}/HEIGHT}$$

For hardwood merchantable volume, the equation parameterized for hardwoods is used (Honer *et al.* 1983, Table 6), where top diameter (Diameter<sub>merch</sub>) is set to 6.6 cm and stump height (Height<sub>stump</sub>) is set to 0.15 cm (equation 12).

(12) 
$$Volume_{merch} = Volume_{total} * (0.9057 - 0.0708 * x - 0.8375 * x^2)$$

where

$$x = \left(\frac{Diameter_{merch}}{DBH}\right)^{2} * \left(1 + \frac{Height_{stump}}{HEIGHT}\right) * (1 - 0.04365 * 0.145)^{-2}$$

#### References:

- Honer, T.G., M.F. Ker, and I.S. Alemdag. 1983. Metric Timber Tables for the Commercial Tree Species of Central and Eastern Canada. Canadian Forestry Service, Inf. Rep. M-X-140. 139p.
- Li, R., A.R. Weiskittel, J.A. Kershaw Jr, A. Dick, and R.S. Seymour. 2012. Regional stem taper equations for eleven conifer species in the Acadian Region of North America: Development and assessment. North. J. Appl. For. 29, 5-14.
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### **Northwest Territories**

The Alberta volume coefficients are used for the Northwest Territories. The Alberta Northern Mixedwood sub-region is used for the Northwest Territories.

# Ontario, Quebec and Nova Scotia

For Ontario, Quebec and Nova Scotia, Honer et al.'s (1983) volume equations are used (equation 13).

(13) 
$$Volume_{total} = \frac{0.0043891*DBH^2*(1-0.04365*b_2)^2}{c_1+0.3048*^{c_2}/_{HEIGHT}}$$

Merchantable volume is estimated for trees larger than the merchantable DBH limit using merchantable model form from Honer *et al.* (1983; equation 14).

For Ontario, the stump height is 0.30m, the top diameter (diameter<sub>merch</sub>) is 7.0 cm. For Quebec, the stump height is 0.15m, the top diameter (diameter<sub>merch</sub>) is 9.0 cm.

For Nova Scotia, the stump height is 0.15m, the top diameter (diameter<sub>merch</sub>) is 7.0 cm.

The merchantable DBH for Ontario, Quebec and Nova Scotia is 9 cm.

(14) 
$$Volume_{merch} = Volume_{total} * (a + b * x + c * x^2)$$

Where

$$x = \left(1 + \frac{Height_{stump}}{HEIGHT}\right) * \left(\frac{Diameter_{merch}^2}{DBH^2}\right) * (1 - 0.04365 * b_2)^{-2}$$

## **References:**

Honer, T.G., M.F. Ker, and I.S. Alemdag. 1983. Metric Timber Tables for the Commercial Tree Species of Central and Eastern Canada. Canadian Forestry Service, Inf. Rep. M-X-140. 139p.

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#### **Prince Edward Island**

The Schumacher total volume equations for PEI (equation 15) are taken from Hutchinson (1986) for all species except white pine, which is from Hutchinson (1992). Honer et al's (1983) volume equations for Central and Eastern Canada (equation 13) are used when taxon-specific coefficients for Schumacher total volume equations for PEI are not available.

(15) 
$$Volume_{total} = e^a * DBH^b * HEIGHT^c$$

Merchantable volume is estimated for trees larger than the merchantable DBH limit using merchantable model form from Honer *et al.* (1983; Hutchinson 1986; equation 16). The stump height is 0.2m; the top diameter (diameter<sub>merch</sub>) is 8.0 cm. The merchantable DBH is 9 cm.

(16) 
$$Volume_{merch} = Volume_{total} * (a + b * x + c * x^2)$$

Where

$$x = \left(1 + \frac{Height_{stump}}{HEIGHT}\right) * \left(\frac{Diameter_{merch}^{2}}{DBH^{2}}\right)$$

# References

Honer, T.G., M.F. Ker, and I.S. Alemdag. 1983. Metric Timber Tables for the Commercial Tree Species of Central and Eastern Canada. Canadian Forestry Service, Inf. Rep. M-X-140. 139p.

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#### Saskatchewan:

Volumes are estimated using Kozak's taper function (equation 1) calibrated for Saskatchewan by Gal and Bella (1994).

- 1. Calculate the diameter inside bark (DIB) at stump height (0.3 m).
- 2. Calculate the merchantable height (height at which the top diameter is 8.01 cm).
- 3. Calculate the volume for stump (assumed to be a cylinder with diameter equal to the stump diameter) and top.
- 4. Calculate the top diameters for each log (log length = 2.6 m).
- 5. Calculate the volume for each log using Newton's formula.

#### References:

Gal, J. and I.E. Bella. 1994. New stem taper function for 12 Saskatchewan timber species. CFS Northwest Region, Information Report NOR-X-338.

Kozak, A. 1988. A variable-exponent taper equation. Can. J. For. Res. 18: 1363-1368.

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## **Yukon Territory**

Bonnor and Boudewyn's (1990) calibration of Kozak's (1988) taper model is used to estimate tree volumes in the Yukon.

- 1. Calculate the diameter inside bark (DIB) at stump height (0.3 m).
- 2. Calculate the merchantable height (height at which the top diameter is 7.5 cm).
- 3. Calculate the volume for stump (assumed to be a cylinder with diameter *equal* to the stump diameter) and top (assumed to be a cone).
- 4. Split the merchantable length (between stump and merchantable height) into 20 segments and calculate the top diameters for each segment.
- 5. Calculate the volume for each log using Newton's formula.
- 6. Merchantable volume is the stem wood volume between the stump and the top diameter.

There is no provision yet in the volume estimation routine for estimating the virtual height of broken top trees. The taper model assumes total height is being input. If the height to the break is supplied, this will lead to an underestimate of total and merchantable volume.

#### References:

Bonnor, G.M. and Boudewyn, P. 1990. Taper-volume equations for major tree species of the Yukon Territory. Forestry Canada, Pacific and Yukon Region, Pacific Forestry Centre.

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# 17. Computational References for Biomass

There are three sets of equations for estimating biomass. All deal with aboveground biomass only.

- 1. National equations were calibrated from the ENFOR data for all provinces and ecozones combined (Lambert et al. 2005 and Ung et al. 2008).
- 2. Regional equations were calibrated using the same data but by species and ecozone. These are not published.
- 3. Preferred equations were taken from literature and generally calibrated at the provincial or territorial scale.

The biomass components (stem wood, stem bark, branches, foliage) for the national and regional equations were fit simultaneously ensuring the components sum to the total biomass. As well, the national and regional equations have a standard equation form and predict biomass in kg using inputs of DBH in cm and height (if used) in m. The preferred equations are a mix of model forms, units (metric and imperial), and were not necessarily fit considering the correlation between components or even including all the components.

In general, the regional equations are recommended followed by the national equations and then the preferred equations.

# **References:**

Lambert, M.-C., C.-H. Ung and F. Raulier. 2005. Canadian national tree aboveground biomass equations. Can. J. For. Res. 35:1996-2018.

Ung, C.-H., P. Bernier and X.-J. Guo. 2009. Canadian national biomass equations: new parameter estimates that include British Columbia data. Can. J. For. Res. 38:1123-1132.

# 18. Wood Density

This section describes the procedures followed for the development of a wood density support table for use in the compilation of NFI ground plot attributes (support-data table name: gpcsd\_wood\_density).

Wood density data used to generate our support table included: 1- density of undecayed 'green' wood (i.e. harvested live wood; e.g. Alden 1997, Alden 1995, Alemdag 1984, Gonzalez 1990, Mullins and McKnight 1981) and density of woody debris based on decay classes (all of which following the standard by Sollins [1981; e.g. Adams and Owens 2001, Dauthieu 2003, Harmon and Secton 1996, Harmon et al. 1995, Harmon et al. 2000, Harmon et al 2011, Liu et al. 2006, Renninger et al. 2014, Preston et al. 2006, Seedre et al. 2013], or harmonized to this standard [Harmon et al 2008]). References such as Harmon et al. (2008) have separated undecayed 'green' wood density from densities by decay class in their reports. Advantages of separating 'decay class 1' from undecayed 'green' wood include ensuring that starting (time 0) density values for modelling (i.e. undecayed 'green' wood) do not risk being swayed by the subjective bias of field workers and processes taking place while the wood still appears intact and hard. Therefore, decay class 1 may include undecayed 'green' wood but the reverse is not true.

The mean wood densities per decay class (including undecayed 'green' wood) per taxon per publication were compiled and separated into wood from Canadian and foreign (e.g. USA, boreal Russia) sources. We only selected densities based on oven-dried weight and volume not corrected for moisture content (i.e. green volume basis). Care was taken to remove values previously computed or estimated by publications' authors from our compiled list.

Undecayed 'green' wood density was assigned to each taxon in the NFI tree species list for each jurisdiction. Values were first assigned on a taxon-specific basis using province/territory-specific values when these were available, else the mean of Canadian-sourced values when these are available, else the mean of foreign-sourced values when these are available. If taxon-specific values of undecayed 'green' wood are not available, then these were assigned respective genus-level means from Canadian sources when available, else from foreign sources. If genus-specific values of undecayed 'green' wood are not available, then these were assigned respective vegetation-type-level (hardwood versus softwood) means from Canadian sources. Undecayed 'green' wood density for unknown taxa were assigned the mean of the hardwood and softwood means from Canadian sources, in order not to weight the overall mean by the number of available values for hardwood and softwood species.

Exponential, sigmoidal and polynomial model structures were tested using non-linear mixed effect modeling with species as a random effect (R package nlme v3.1-140) and the best fit model structure was selected based on log-likelihood, AIC and BIC. Thus, missing wood density values for each taxon in each province/territory were modeled using a sigmoidal model structure that can account for possible lag in decay at the onset of decay and later reduction in decay rates (Preston et al. 2012):

$$WOOD\_DENSITY = a * e^{-(b*DECAY\_CLASS)^2}$$

where a and b are constants; and a DECAY\_CLASS of zero is equivalent to wood density for undecayed 'green' wood, such that the constant a will be equal to undecayed 'green' wood density.

Taxon-specific model parameterization and computation of missing wood densities for particular decay classes were done for each province/territorial-specific, Canadian or foreign data sources when wood densities were available for at least 3 decay classes (including undecayed 'green' wood) in a taxon's decay trajectory. Otherwise, models were parameterized by genus or vegetation type (hardwood versus softwood) from province/territorial-specific data or from all data sources combined when wood densities were available for at least 3 decay classes in a decay trajectory. These parameters were then used to compute missing wood densities for a particular taxon using its associated undecayed 'green' wood density.

In summary, assigning the best wood density values per decay class for each taxon prioritized 1- published values and associated 'gap-filled' wood densities calculated using taxon-specific parameterized decay trajectories (from province/territorial-specific data sources when available, else from Canadian sources when these are available, else from foreign sources), 2- wood density values predicted from the best available undecayed 'green' wood density and decay trajectories parameterized from province/territorial-specific data sources (using data sharing the taxon's genus if available, else its vegetation type), 3- wood density values predicted from the best available undecayed 'green' wood density and decay trajectories parameterized from all data sources combined (using data sharing the taxon's genus when available, else its vegetation type).

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