**Region 6 Biomass Sampling Protocol**

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**Objectives**

The goal of this project is to determine canopy biomass equations for species of interest in the northwest. Field data will be collected to develop new equations to determine crown (branch and non-merch) biomass weight based on common tree metrics (species, dbh, height). Initial estimates based in part on published error rates indicate that sample sizes of 40 to 50 trees per species are needed to achieve crown biomass equation errors approaching 10% (with 90% confidence) if individual crowns are subsampled for biomass. Subsampling of crowns greatly reduces the measurement costs for individual trees and allows more trees to be selected, thereby providing a richer data set for equation development.

**Stand and Tree Selection**

This project will develop new biomass equations for use in timber sales. As such, biomass data must be drawn from the full range of sites, stand types, and trees that are of management interest or are part of the current or upcoming timber sale. Within an individual stand, trees must be selected in an objective manner while still capturing a range of species and diameter classes.

Candidate trees must meet all of the following conditions when observed from the ground:

 i. live, intact top with no noticeable forks;

 ii. minimum diameter at breast-height of 4 cm (1.6 inches);

 iii. no noticeable mistletoe brooms, visible conks, or marked defoliation;

 iv. no sign of successful beetle attack or root rot disease;

 v. if possible, avoid sampling on days where branches have excessive moisture (rain/snow).

**Tree Measurements**

Measuring selected trees will proceed in 3 steps:

1. Standing tree measurements

Measure and mark breast-height on the stem, then record the tree’s species and its DBH (nearest lower 0.1 inch) using a diameter-tape.

Using a laser rangefinder measure total height.

*Remarks*

» Breast-height is at 4.5 feet above the ground line on the uphill side of the tree, or as close to this height as possible but above or below irregularities such as branches, swellings, or depressions.

2. Downed tree initial measurements

Observe the sample tree as it falls and recover/reassemble the major components of the top and crown once the tree is down.

Keeping crown breakage to a minimum, extend a tape from the base\* to the top of the tree and record total length\*\* (±0.1 foot) and mark each of the following points on the stem:

 i. height of the lowest live branch (exclusive of epicormic shoots)\*

 ii. base of the 1” top

 iii. 3’ segment ends starting at first live branch

\*Include/add stump height to total length measurement.

\*\*Height (nearest 0.1 foot) to the first live branch and to the top must be recorded/confirmed using a tape.

 3. Branch sampling

For this study, five branches is the recommended sample size per tree, however, conditions (i.e., smaller trees, homogeneous branch form, etc.) may warrant fewer branch selections. Branches will be selected from each tree using randomized branch sampling (RBS) with branch selection probabilities made proportional to diameter squared (i.e., proportional to branch cross-sectional area). This design concentrates branch sampling in the lower portion of the crown where most of the biomass is located, but controls branch selection in such a way that whole-crown biomass components can be estimated without bias.

Beginning at the lowest live branch, one crew member will caliper the basal diameters (± 0.1 inch) of all live first-order branches in the next 3-foot stem section, as well as the stem diameter at the top of that 3-foot section. A second crew member will record these measurements (see detailed data recorder instructions in user’s manual) and indicate which branches, if any, from that stem section should be selected and marked.

If fewer than 5 branches are selected on that segment, then sampling proceeds to the next 3-foot stem section, where all live branch diameters and the segment end diameter are measured and recorded. Branches are again checked for selection and marked, and or cut and weighted. Sampling may or may not proceed to the next 3-foot section. After a total of 5 branches have been selected, branch sampling stops and the portion of the crown further up the bole need not be assessed. In the course of this branch selection procedure, do not measure (or select) dead branches or small epicormic shoots.

Following branch selection cut the individual sample branches from the stem and weigh them using an appropriate scale and enters the weights in the data recorder. Record the weights to the nearest 0.1 lbs.

*Remarks*

» RBS is a with-replacement sampling design; though it is unlikely, the same branch can be selected more than once.

» All basal branch diameter measurements for RBS should be made within 2” of the bole beyond the butt swell. Callipered diameters should measure to 1/10 (0.1) inch.

» Carrying out RBS on 3-foot stem sections effectively collapses the crown into an equally spaced sequence of whorls.

» Five branches are selected from each sample tree to allow precise estimation of whole-crown biomass as well as estimates of precision.

» Should RBS proceed to the uppermost portion of the stem, the top (1” diameter) is treated the same as a branch. The last stem segment may not be exactly 3-feet in length and the final stem diameter will be the 1” top).

**Appendix I**

**Randomized Branch Sampling Formulae**

The probability of selecting a jth branch from the kth node where j = 1, …, N

The procedure goes as follows:

Each potential sample branch is a path and has its own probability of being selected. To start each sample branch has the same probability. For each segment, you measure and record branch diameters and the segment end diameter. Each branch then has a probability that is equal to its diameter squared divided by the sum of all the diameters squared from that segment. From a list of random numbers (1 per sample branch) you compare each branch probability with each random number. If a given random number is less than a branch probability than that branch is selected as a sample branch and it is cut and weighed.

If only the segment end diameter is selected (no branches) than its probability is stored for any remaining sample branches and you move on to the next segment. This procedure continues up the bole until either all samples are collected or the user reaches a minimum bole diameter (1” for this example). The following example walks through 2 segments and the final expansion.

**Segment 1.**



For the example below, using the above random numbers, the only branch with a cumulative probability (cumlsum) greater than the random numbers is the segment end diameter. This means the segment end is the selected branch for each sample, its probability (pd2, 0.7) gets copied to all the branch probabilities (pbranch#) and you proceed to the next segment.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| d | d2 | pd2 | cumlsum | pbrnch1 | pbrnch2 | pbrnch3 | pbrnch4 | Pbrnch5 |
| 1 | 1 | 0.04 | 0.038 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 |
| 0.9 | 0.8 | 0.03 | 0.0688 |  |  |  |  |  |
| 0.9 | 0.8 | 0.03 | 0.0996 |  |  |  |  |  |
| 0.2 | 0 | 0 | 0.1011 |  |  |  |  |  |
| 0.8 | 0.6 | 0.02 | 0.1254 |  |  |  |  |  |
| 0.3 | 0.1 | 0 | 0.1288 |  |  |  |  |  |
| 0.9 | 0.8 | 0.03 | 0.1596 |  |  |  |  |  |
| 0.9 | 0.8 | 0.03 | 0.1904 |  |  |  |  |  |
| 1 | 1 | 0.04 | 0.2284 |  |  |  |  |  |
| 1 | 1 | 0.04 | 0.2664 |  |  |  |  |  |
| 0.9 | 0.8 | 0.03 | 0.2972 |  |  |  |  |  |
| 4.3 | 18 | 0.7 | 1 |  |  |  |  |  |

Segment end diameter ->

Figure 1. Table representation of first segment after measurement with no selections.

* d = diameter
* d2 = diameter squared
* pd2 = probability of branch being selected = (d2/Sum of d2’s)
* cumlsum = cumulative sum of pd2 (so we get a range from 0 to 1)
* pbrnch# = cumulative sample branch probability = inverse expansion factor

**Segment 2.**

All branch diameters and the segment end diameter are entered for the next segment. Random numbers are generated for each branch:



For this segment we get a hit for sample branch 1 since its random number (0.1587) is less than the 6th branch probability (0.2059). The branch probability is copied to the pbrnch probability for this branch and the segment probability (0.75) is copied over for all other samples. The branch is cut from the tree and weighed. The branch weight is entered and saved for later or the expansion can be computed using the technique described below.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| d | d2 | pd2 | cumlsum | pbrnch1 | pbrnch2 | pbrnch3 | pbrnch4 | Pbrnch5 |
| 0.5 | 0.3 | 0.01 | 0.0112 | 0.7 | 0.7 | 0.7 | 0.7 | 0.7 |
| 0.4 | 0.2 | 0.01 | 0.0184 | 0.08 | 0.75 | 0.75 | 0.75 | 0.75 |
| 0.8 | 0.6 | 0.03 | 0.0471 |  |  |  |  |  |
| 0.8 | 0.6 | 0.03 | 0.0758 |  |  |  |  |  |
| 1.1selected -> | 1.2 | 0.05 | 0.1301 |  |  |  |  |  |
| 1.3 | 1.7 | 0.08 | 0.2059 |  |  |  |  |  |
| 0.5 | 0.3 | 0.01 | 0.2171 |  |  |  |  |  |
| 0.8 | 0.6 | 0.03 | 0.2459 |  |  |  |  |  |
| 4.1 | 17 | 0.75 | 1 |  |  |  |  |  |

Figure 2. Table representation of 2nd segment after measurement with 1 selection.

* The probability of that branch getting selected is 0.08 which gets put in the pbrnch field for that sample branch.
* All other samples branches get the probability of selecting the segment end diameter, or 0.75.

**Remaining Segments.**

Data collection proceeds up the tree in the same fashion as the previous two segments until either 1) all samples branches are collected or, 2) you reach the designated (1” in this case) top diameter. If condition 2 occurs the current segment stops, usually short of 3’ (or whatever segment length you have selected), at the 1” top and the portion from 1” bole diameter up is your last branch.

In the following example sample 5 (segp5) gets the 1” tops probability (0.4) as its sample probability.



**Expansion Factors.**

Once a sample is collected the expansion factor is the inverse of the product of that samples probability. For instance, for sample branch 3 the expansion factor is the inverse of (0.7 \* 0.75 \* 0.99 \* 0.89 \* 0.01) = 1/0.006 = 166.7. To get the estimated weight of the crown biomass you multiply this expansion factor by the branch weight (collected earlier when the branch was selected); e.g., if the branch weighed 1.3 lbs we would get 166.7 \* 1.3 = 217 lbs of crown biomass.

This technique is then executed for each branch and the average of all the expanded weights is your final tree estimate.