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**Application of Randomized Branch Sampling to Conifer
Trees: Estimating Crown Biomass**

By

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B.Sc. (Forest Resource Management), University of Montana, 2009

A thesis submitted in partial fulfillment
of the requirements for the degree of

Master of Science

in

Forest Biometrics

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Forest Biometrics

Application of Randomized Branch Sampling to Conifer Trees: Estimating
Crown Biomass

Chairperson: David Affleck

Randomized branch sampling (RBS) is a sampling scheme which can be implemented to estimate many different attributes of an object displaying a branched or forked form. The aboveground structure of trees (stem and branches) lends itself naturally to this type of sampling design. RBS utilizes the branching form of the crown itself to draw probability samples and generate unbiased estimates. When implemented correctly, RBS can also greatly reduce the costs in time and labor of sampling when the purpose is estimating attributes borne within crown portions of trees. However, RBS was created for and has been implemented primarily in applications on trees with a decurrent crown structure. Considerations when applying RBS to excurrent crown structures, which are a common trait of conifer species, are examined in this thesis. The applications of several RBS schemes are examined within the context of sampling to estimate green crown biomass. The way branches are aggregated into groups for sampling along the main stem is the distinction between the proposed RBS schemes in this thesis. For estimating green crown mass, RBS was found to produce estimates with accuracy between that of simple random and list sampling methods. A sample size of five or six branches was sufficient to obtain standard errors within ten percent of the actual crown weight.

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Chapter 1

Introduction

Much effort and many studies have investigated models and equations designed to estimate the mass or volume present in the bole (stem) portion of trees. This focus can be attributed to the fact that the bole is typically the only portion of the tree which has economic value. From an economic perspective, branches and foliage have historically been viewed simply as the byproducts of logging operations, which are usually left on the site to either decay in place, or piled so they can be burned at some point in the future. Currently, little is known about the quantities and distribution of biomass present in the crown portion of trees, in part because even less is known about accurate and efficient methods to sample these attributes.

Biomass is a measure of the amount (weight) of matter contained in living or recently living tissues and organisms. Biomass is found in the forest in many forms, and each form exerts different influences on the natural processes and cycles within that forest. While the crown portion of trees represents only one of the pools of biomass present in a forest, having an

accurate measure of this would be a great benefit to modeling processes of forest growth, crown fire spread, or carbon storage for informing land management decisions. Providing a practical method of sampling to estimate crown biomass would allow for testing the validity of existing models, or for the development of new or regional models. Versions of these models could be utilized in applications across a wide range of forestry related sciences. Green-energy industries could use improved crown biomass models to assess the amount of bio-fuel in an area available for processing into other forms of energy. Increased accuracy of crown fuel inputs would benefit crown fire simulation models. Carbon and climate scientists could also use these models for greater accuracy in quantifying above ground carbon stocks within forests. The crowns also support all of the living foliage on a tree. The total amount of foliage on a tree is perhaps the primary factor which dictates how much photosynthesis (and thus growth) can take place over a given time period. A more thorough understanding of live foliage biomass distributions in tree crowns could lead to greater accuracy in individual tree and stand growth models.

Randomized branch sampling (RBS) was first proposed by Jessen (1955). It is a multi-stage unequal probability sampling method. The technique was designed to efficiently estimate the total number of fruit (oranges) found in the canopy of a tree while only having to count the fruit on select branches. With RBS, branches are selected from the tree by creating a pathway which starts at the base of the bole and travels upwards. Every time the path encounters a fork (branching), selection probabilities are calculated propor-

tional to the size¹ of each limb emanating from the fork. A random number is then generated to determine (select) the limb through which the path continues to travel along. This procedure is repeated up the tree until the path selects a terminal branch which is small enough that it becomes easy to measure the variable of interest. A tree level estimate is derived by combining the measure of interest from the terminal branch and the associated probability with which that particular branch was selected.

RBS is an advantageous sampling scheme in the field because it does not require the user to take measurements on, or to have prior knowledge of all branches in the crown. RBS was originally developed for estimating orange production but has since been used to estimate attributes on both hardwood and, to a lesser extent, conifer tree species (Evans and Gregoire 2006; Raulier *et al.* 2002; Hietz *et al.* 2010). Yet the excurrent branching architecture of the latter class of species (see Fig. 1.1) is distinctly different from the decurrent form of the orange tree crowns considered by Jessen (1955). Adjustments to the selection and estimation protocols of the original RBS procedure that exploit these structural crown characteristics may help produce more accurate and economical crown attribute estimators for coniferous species.

RBS was designed and has mostly been implemented in applications concerning trees which exhibit decurrent crown structures. Tree species which have decurrent crowns have a main stem that forks into major branches within a few meters of the stump. These major branches then each fork again into smaller branches, and so on until the most minor (terminal) branches are reached (Fig. 1.1A). For example, oak (*Quercus spp.*) or maple (*Acer*

¹Typically diameter or cross-sectional area is used as a measure of size.

spp.) trees exhibit decurrent crown structures. With these decurrent class species no distinction is made between the main stem and branches. In contrast to decurrent crowns most conifer tree species, for example Douglas-fir (*Pseudotsuga menziesii*) or western larch (*Larix occidentalis*), exhibit strong apical control, resulting in excurrent crown structures. The crowns of these species are dominated by one main stem which extends directly from the stump to the top of the tree. This main stem has many smaller (primary) branches attached directly to it (Fig. 1.1B). Main stem and primary branches are generally easily distinguished on conifers and attributes such as the number and diameters of the full set of primary branches are relatively easy to obtain.



Figure 1.1: Simplified branching diagrams highlighting the structural differences between A. Decurrent crown, and B. Excurrent crown.

Within the context of RBS, sampling decurrent crowns is fairly straightforward: every time a forking (decision node) is encountered selection probabilities are calculated for each branch emanating from the fork, a random number is generated to determine selection, and sampling continues along

the selected branch to the next forking. At each forking within a decurrent crown, the sizes of limbs emanating directly from it are fairly similar in size. And while the length of the path leading to a given terminal branch may differ, we would expect that the size of the segments which comprise each path to decrease gradually at a constant rate.

With the structure of excurrent crowns, optimal placement of RBS decision nodes becomes less apparent. There will be substantial differences between sizes of primary branches and the main stem at each forking (particularly low in the crown). The lengths of the paths to terminal branches differ substantially, being shorter for lower branches in the crown, and longer for the branches which are higher up. Segment diameter will decrease gradually along these paths only if a primary branch is selected from high in the crown. For the lower branches, segment diameter will decrease abruptly when the path diverges from the main stem.

To address these issues and furnish an efficient RBS protocol for use with excurrent crowned trees, several different methods could be employed to conceptually aggregate branches together into artificial whorls. The branches grouped together in these whorls are then considered jointly in the course of sampling (as if they all emanated from the same fork in a decurrent crowned tree). Utilizing some form of grouping might greatly increase the speed of sampling excurrent crowns with RBS in the field. This study was designed and undertaken to further investigate implementation of a few RBS strategies on excurrent species. The specific objectives are to:

1. Review previous uses of RBS in both decurrent and excurrent crowned

species.

2. Develop and implement different RBS selection strategies in excurrent tree species.
3. Evaluate the statistical and practical advantages or limitations of these different selection strategies.

Chapter 2 contains a review of RBS literature and addresses objective one. Objectives two and three will be addressed within the context of estimating the green crown mass of conifer trees and are covered in chapters 3 and 4.

Chapter 2

Randomized Branch Sampling

The purpose of this chapter is to provide the reader with knowledge of the mechanics, utility, and properties of RBS strategies. I will review the uses of RBS in previous scientific studies, and define some variables which are referred to throughout this thesis (Table 2.1). All equations from scientific articles will be expressed according to the standardized symbology presented below.

2.1 Foundations of RBS

The RBS method works by iteratively creating a sampling frame and one or more (m) selection paths through the tree. The starting point for the RBS pathway is the base (before the first branching occurs) of the object for which we wish to obtain an estimate. For example, if we wished to obtain an estimate of some attribute for a branch, the base of that branch

Table 2.1: Symbols used throughout this thesis.

Symbol	Description
M	Number of terminal branches, and number of possible RBS paths within a given tree.
m	Number of RBS paths specified within a given tree.
i	Refers to either terminal branch i of M , or RBS path i of m (when m RBS paths are present within a given tree).
Q	Unconditional branch selection probability.
q	Conditional branch selection probability.
R	Total number of segments within a given RBS path.
r	Refers to the r^{th} segment within a given RBS path.
K	Total number of RBS segments within a given tree.

would be the starting point of the RBS pathway. In order to extrapolate sampling results to the whole tree level, the path must begin at the base of the stem. This path continues upwards through the tree until a terminal branch is selected (Fig. 2.1).

For the purposes of RBS, a tree can be represented as collections of two distinct elements, segments and decision nodes. The segments are the sections of stem or branch which connect a network of decision nodes. While the decision nodes themselves are the points where a RBS path encounters a fork and one of the diverging segments emanating from that node must be selected to proceed along. This iterative process of selecting one segment at each successive node continues until a terminal branch is selected and the RBS path is fully specified. Once a RBS path has been fully determined, the attribute of interest needs only to be measured on each of the selected segments within the path. The total number of terminal branches in a tree (M) therefore also represents the number of possible RBS paths within that

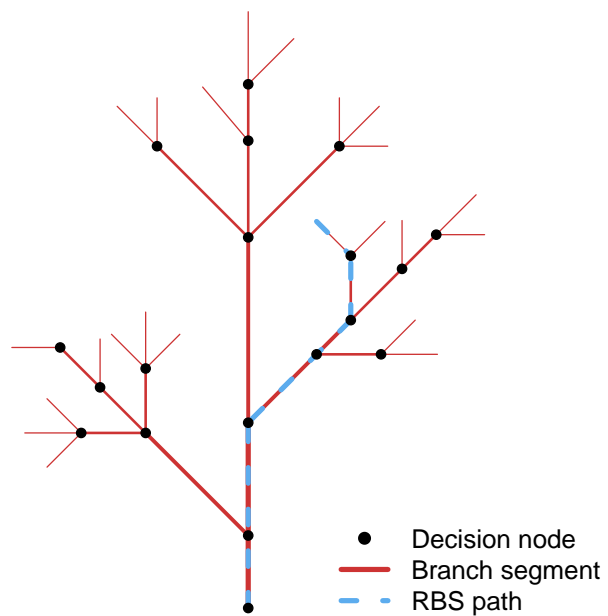


Figure 2.1: Simplified diagram of a tree showing one possible RBS path. There are $M = 23$ terminal branches in this diagram.

tree. The purpose of sampling with RBS can be to estimate some attribute which is typically borne only on the terminal branches (e.g. foliage mass or fruit count), some attribute which is present over the entire length of the path (e.g. volume, diameter, or total mass¹), or even a combination of both attribute types simultaneously.

The branch segment selected from any given decision node is chosen randomly, and typically with unequal probability. This probability is known as the conditional selection probability (q). The conditional probability assigned to each segment emanating from a particular node is arbitrary and can be calculated in several different fashions. However, to achieve the greatest precision possible these conditional probabilities should ideally be proportional to the quantities of interest borne by the respective branches emanating from the decision node (Gregoire *et al.* 1995). For example, if a single branch accounts for 1/10 of the portion of variable of interest emanating from a particular node, its conditional selection probability would also ideally be fixed at 1/10. Conditional probabilities will be denoted as q_r ($0 < q_r \leq 1$ for $r = 1, \dots, R$), for the r th of R segments which comprise a given path. The conditional selection probabilities of all segments emanating from any particular node must sum to one for RBS to produce unbiased estimates.

An unconditional selection probability (Q_r) is obtained from the conditional selection probability of the r^{th} segment when the probabilities of all prior selections to reach that point in the path are accounted for. To calculate Q_r , we take the product of the r^{th} segment's conditional selection

¹The aggregate of foliage, branch, and stem masses

probability, and of all conditional selection probabilities of the segments selected by the path below:

$$Q_r = \prod_{k=1}^r q_k \quad (2.1)$$

The variable of interest (x) is measured on each of the R segments within a specific RBS path. A Horvitz-Thompson estimator is then used to estimate the population (tree level) total of the variable of interest (X). The R measures taken from the selected segments are ‘blown up’ by the reciprocal of their associated unconditional selection probabilities, and summed to generate an overall estimate:

$$\hat{X} = \sum_{r=1}^R \frac{x_r}{Q_r} \quad (2.2)$$

where x_r is the variable of interest quantity on segment r . \hat{X} is an unbiased estimator of X , the population total of the variable of interest (Gregoire and Valentine 2008).

$$X = \sum_{k=1}^K x_k \quad (2.3)$$

In order to estimate variance of the estimator, there must be a minimum of two distinct selected paths ($m \geq 2$) within a tree. If \hat{X}_i is the estimate from path i for $i = 1 \dots m$ paths within a tree, then:

$$\hat{X} = \frac{1}{m} \sum_{i=1}^m \hat{X}_i \quad (2.4)$$

becomes the unbiased estimator of the tree level total of the variable of interest, and the variance of \hat{X} is unbiasedly estimated as:

$$\widehat{Var}(\hat{X}) = \frac{1}{m(m-1)} \sum_{i=1}^m (\hat{X}_i - \hat{X})^2 \quad (2.5)$$

2.2 Previous uses of RBS

In this section I will examine previous studies which have implemented RBS to estimate tree attributes. These have been classified according to whether the species of interest in the study have decurrent or excurrent crown structures.

2.2.1 Decurrent RBS applications

The idea for RBS first appeared in the literature with the publication of Jessen's paper in 1955. In this paper, Jessen lays down the ground work for conducting RBS illustrated with an example on one pineapple orange tree. Jessen states: "The object of sampling is to select some portion of a relatively large total which will represent that total reasonably well" (Jessen 1955). In the case of the orange tree, the 'portions' to be selected are the terminal branches upon which the fruit is typically borne. Jessen compares several different methods of calculating selection probabilities within the RBS framework. The first method discussed is uniform random selection of a branch. To achieve this uniform random selection, all potential sample branches must first be identified and numbered. Once this frame is iden-

tified, a pre-specified number of branches can be randomly selected with equal probabilities. Tree level estimates are derived by averaging the count of oranges across the selected branches and ‘blowing up’ this average by the total number of branches on the tree. This is equivalent to simple random sampling without replacement. While simple random sampling will produce unbiased estimates by design, the main issue here is that all branches must first be identified and counted, a time consuming and arduous task, particularly when sampling is conducted within the crowns of larger trees. To avoid complete identification of all potential sample branches and still provide the sampler with unbiased tree level estimates, Jessen proposes the use of RBS.

Jessen defines three methods of selecting paths within the RBS scheme. The first of these methods (discussed above) Jessen terms “probabilities equal”, and the unconditional probability of selecting any given terminal branch i is simply:

$$Q_i = \frac{1}{M} \tag{2.6}$$

The second method proposed was called “probabilities proportional to number”. Under this scheme, the numbers of branches emanating from a particular decision node are used to calculate conditional selection probabilities (e.g. if there are 3 branches originating from a given node, each branch’s conditional selection probability is 1/3). The product of the conditional probabilities at all R decision nodes within a path provides the unconditional selection probability for the terminal branch eqn. (2.1). This process of selecting branches will generally give rise to unequal unconditional selec-

tion probabilities for the M terminal branches.

The final method Jessen proposes is called “probabilities proportional to area”. Under this selection criterion, the squared circumference of each branch directly above the forking is used in determining branch selection probabilities. As with the second method, the product of all probabilities within a path provides the unconditional branch selection probability eqn. (2.1), but here the conditional probabilities are calculated as:

$$q_r = \frac{c_r^2}{\sum_{k=1}^{n_r} c_k^2} \quad (2.7)$$

where c_r is the branch circumference of the r^{th} segment in a RBS path, c_k is the branch circumferences of the n_r segments emanating from node r (c_r also being counted as one of the c_k).

Regardless of how branch selection probabilities are specified, an unbiased tree level estimate of total number of oranges (\hat{X}) is derived by taking the orange count (x) from selected terminal branch i and dividing by its corresponding unconditional selection probability (Q_i):

$$\hat{X} = \frac{x_i}{Q_i} \quad (2.8)$$

Jessen examines these three divergent methods of determining branch selection probabilities by implementing all three on a single orange tree. To compare the precision of the methods, Jessen uses the variances:

$$Var(\hat{X}) = \sum_{i=1}^M Q_i (\hat{X}_i - X)^2 \quad (2.9)$$

where \hat{X}_i is the estimate from terminal branch i , X is the actual number of oranges in the tree, and Q_i is the unconditional selection probability of branch i . In the instance of the particular orange tree measured for this study, the probability proportional to area selection method produced the smallest variability by a great margin.

Jessen also examines the efficiencies of defining branches of differing size as the terminal branches. This is essentially an attempt to see what is the cost in terms of precision between selecting a large terminal branch and counting many fruit on its many sub-terminal branchlets, versus selecting a smaller terminal branch and counting fewer fruit. Jessen uses three different classes of branch size as the definition of a terminal branch. Not unexpectedly, variance of the estimates increases as terminal branch size decreases. With smaller terminal branches we are effectively sampling smaller portions of the tree at a time. However, when $Var(\hat{X})$ is examined on a per counted fruit basis, the small branches taken with probability proportional to area became the most efficient method.

Jessen also discusses the assumption that all orange fruit is typically borne on terminal branches. This assumption is usually a simplification, and not very representative of actual orange trees. However Jessen provides a simple fix to this problem. Anytime a very small fruit bearing branch connected to a larger ‘main’ branch is encountered, instead of considering this small branch as an opportunity for the path to diverge, a fruit count (measurement) is performed on the small branch. This count is then considered as part of the segment that it is attached to and ‘blown up’ by the overall selection probability of that segment. This intermediate estimate is then

added to the overall estimate provided by the terminal branch the path ultimately selects. This procedure of skipping over the small branches in path selection can greatly reduce variability of the estimates. This is because by doing so we eliminate the possibility of taking samples with extremely small amounts of the variable of interest and with small selection probabilities (in circumstances when one is selecting branches with probability proportional to area). Jessen's article lays the foundation for implementing RBS: a method for sampling tree branches which does not require prior identification of all branches (when probability proportional to area or probability proportional to number selection methods are used), and provides the sampler with unbiased tree level estimates.

Two years after Jessen's article, Pearce and Holland published a critical account of the RBS method. They cited shortcomings of RBS such as difficulty in calculating selection probabilities and generating random numbers in the field. These obstacles are easily overcome with a programmable calculator or portable computer these days. One insightful criticism mentioned in their paper is Jessen's assumption that the number of fruit on a branch is proportional to the square of branch girth. Here, they note that the unconditional branch selection probability (Q) should ideally be proportional to the fraction of the tree's total fruit borne on that branch. Using the probabilities proportional to area method, three different exponents (branch diameter raised to the power of 2, 3, and 4) were used to calculate branch selection probabilities with the data from the same orange tree. Variance of the estimates was calculated as above with eqn. (2.9) as an indication of precision. Pearce and Holland found that increasing the

exponent always reduced the variability. They note: “Although [RBS] will be unbiased whatever power is used, it is desirable to adopt a value that is justified biologically and this will on average lead to the greatest accuracy” (Pearce and Holland 1957, page 128).

RBS was later used by Valentine and Hilton (1977) to estimate the number, surface area, and biomass of leaves on oak trees. They implemented a two phase sampling scheme. In the first phase, RBS was used to estimate the number of leaf clusters in a tree. In phase two, average number of leaves, dry weight, and surface area per leaf cluster was estimated with systematic sampling. Estimates from the two phases are then combined to generate tree level estimates of number of leaves, leaf dry mass, and leaf surface area. The RBS portion of sampling took place early in spring when the leaf clusters were small and easy to identify. Tree crowns were first stratified into major branches and RBS was implemented within each major branch. The estimates from each major branch stratum were summed to arrive at tree level estimates of the total number of leaf clusters. Conditional selection probabilities were determined by a climber’s visual estimate of leaf area on each segment emanating from a decision node. Since the number of leaf clusters is the variable of interest in the RBS phase, terminal segments were defined as the individual leaf clusters. An estimate of the total number of leaf clusters (within a main branch stratum) is therefore simply the inverse of a leaf cluster’s overall selection probability $\left(\frac{1}{Q_R}\right)$. Additionally, leaf clusters borne on small epicormic shoots need only be counted and included into the estimates as outlined by Jessen. In closing remarks, the authors note: “the precision of estimates depends largely on the probability assignments”

(Valentine and Hilton 1977). This statement further enforces the necessity of having a branch's unconditional selection probability be proportional to the fraction of the total it actually carries.

In 1984, Valentine, Tritton, and Furnival presented a sampling procedure for estimating the aboveground biomass, woody volume, and mineral content of a tree. RBS and importance sampling are both utilized by this procedure. The results of a field test in estimating tree green weight are reviewed. In this paper the authors provide a fairly in-depth review of RBS and add some new terminology which helps explain the RBS procedure in greater detail. The authors recommend assigning different conditional selection probabilities depending upon the purpose of the sampling. When sampling for woody biomass, volume, or total biomass, they recommend either the product of diameter squared and branch length, diameter cubed, or simply ocular estimates of volume or biomass to determine the conditional selection probabilities. When sampling for foliar biomass they suggest using branch diameter squared, or ocular estimates of foliar biomass to determine conditional selection probabilities.

To estimate the fresh weight of an entire tree from one path the authors use eqn. (2.2) adopting a segment's green weight as the x_r term. Here they note that it is also possible to estimate foliage weight simply by substituting foliage weight (f_r) for x_r in the same equation. It is simply the case that f_r is zero for the majority of the r segments which are not also terminal branches. The authors then describe how a disc can be selected from each segment using importance sampling to estimate dry weight, volume, and mineral content of each segment. Combining these importance sam-

pling estimates with the RBS probabilities provides tree level estimates of dry weight, volume, and mineral content. To test their proposed sampling scheme, eight trees were sampled in a mixed oak stand. Terminal branches were defined as limbs or portions of limbs with a diameter of 5 cm or less. One to four RBS paths were selected within each sample tree, and one disc was removed per path using importance sampling protocols. Sampling errors for the eight trees ranged from 5.6 to 14.4% of the actual fresh weights of the trees.

RBS was implemented in a sampling scheme to assess woody biomass of woodland stands in Burkina Faso and the Netherlands (de Gier and Kabore 1993). In this study no differentiation was made between trees and shrubs. RBS was used to select a path within the tree (or shrub) and proceeded until a terminal branch of 2.5 cm diameter was reached. Segment diameter raised to the power of 2.5 was used to calculate conditional selection probabilities. Procedures for removing and weighing a green disc from the selected path were followed according to Valentine *et al.* (1984). In the Netherlands 184 trees of 18 species were sampled. In Burkina Faso 118 trees from 37 species were sampled. The ultimate goal of this study was to create a regression equation so that biomass could be estimated in these stands without destructively sampling trees. To this end, the RBS biomass estimates from the 302 sampled trees were used in a weighted regression with stem diameter (DBH) as the only independent variable. The amount of time required to perform this type of sampling was also recorded. They found that for the majority of trees less than 2 man-hours were required per tree sampled. This was found to be a significant reduction in the time required to sample

as compared to other methods of estimating aboveground biomass. They also found no significant differences between trees of varying species when estimating woody biomass.

2.2.2 Excurrent RBS applications

Throughout my review of RBS literature, fewer applications to species with excurrent crowns were found. In one study (Valentine *et al.* 1994), which used RBS on excurrent species, the goal was to estimate foliar dry mass of loblolly pine (*Pinus taeda*). The overall purpose of this study was to examine relationships between foliar dry mass and either stem diameter at the base of the live crown or the product of DBH and a modified crown ratio (crown ratio above breast height). Data for this study were collected over the course of three non-consecutive years in various manners. The RBS procedure was only implemented in one of the three years, for a grand total of 30 trees sampled using RBS. These 30 trees first had their crowns stratified into thirds by length. Within each stratum RBS was used to select two branches. Conditional probabilities for branch selection were determined by using branch diameter squared. The RBS path continued along each selected branch to the branch tip. Foliage encountered along each selected segment was removed, dried, and weighed. Estimates were derived by multiplying the dry weight of foliage in a given segment by that segment's unconditional selection probability, and summing these estimates across a given path eqn. (2.2). Estimates are averaged within each strata to generate strata level estimates, and strata level estimates are then summed to arrive at tree level estimates.

Chapter 3

Methods

3.1 Proposed modifications to RBS protocol

To make RBS an efficient and accurate method to use in the field on conifer trees, we must evaluate different rules for how we are going to define the decision nodes. The definition of the decision node will dictate how and if branches are aggregated into groups while sampling. Limiting the sizes of these groups so that each node has a number of branches that is manageable to work with will facilitate sampling. This will reduce the amount of ancillary damage incurred by sample branches while the measurements are being collected. It will also make it easier to identify selected branches during sampling (e.g. finding which was branch 6 of 10 is much easier than finding branch 72 of 119).

As one works one's way through the crown, the stem area at the top of each grouping of branches is used to estimate the amount of branch area contained in the crown above. These groupings of branches will be referred to as

sections, the number of which (K) will depend on the particular tree being sampled and the RBS protocol that is implemented. It is very important that these stem segments at the top of each section be selected with probability which is as close as possible to the actual fraction of the variable of interest borne by the crown above. If not, branches sampled from higher sections will have sub-optimal unconditional selection probabilities since the probabilities of all branches incorporate stem selection probabilities from below (see eqn. (2.1)). If these stem selection probabilities are not proportional to the actual amounts of the variable of interest, the disparity in selection probability is carried through into the upper sections of the crown. Avoiding this effect will decrease variance of the estimator and is particularly important in the lower sections of the crown.

It is hypothesized that the length of each section which comprises a decision node should be of a length where the taper of stem cross-sectional area and branch basal area are similar to one another. If the intervals are too short, selection probabilities are subject to localized swelling of the main stem. Conversely, if the intervals are too long, any disparity between the taper of main stem and branch cross-sectional area may produce sub-optimal selection probabilities. The five different grouping methods for aggregating branches into decision nodes considered in this study are described below.

Individual branch (IB) Starting with the lowest live branch and working upwards, each time a live branch is encountered selection probabilities are calculated and either the stem or the branch is selected. Conditional selection probabilities are calculated using the branch diameter

and the stem diameter directly above the branch under consideration. This method is most equivalent to how RBS selection occurs within a decurrent type crown structure.

Five Branch (FB) Starting at the lowest live branch, branches are aggregated into groups of five. The diameters at the bases of the five branches and the diameter of the stem directly above the highest branch in the group are used to calculate conditional selection probabilities.

One Meter (OM) Starting from the height of the lowest live branch, one meter intervals are marked on the stem. All branches which fall within a given one meter length of stem are grouped together. The diameter at the bases of all branches within the segment and the stem diameter at the top of the segment are used in calculating conditional selection probabilities.

Crown thirds (CT) The crown is divided into three sections of equal length. All branches which fall within a given third of the crown are grouped together. Diameter of all branches within a section and stem diameter at the top of the section is used to calculate conditional selection probabilities.

Equal Basal Area (EA) Branches are iteratively added to a section until the total cross-sectional area of the branches is at least as great as the cross-sectional area of the stem directly above the highest branch in the section. All branch diameters in a section and the stem diameter

directly above the highest branch in the section are used in calculating conditional selection probabilities. This method fixes the stem's conditional selection probability at approximately 0.50 in each section.

These five selection methods can be classified by whether the number of branches and length of main stem included in each segment are fixed or variable (see Table 3.1). For all selection methods described above, anytime the stem is selected it means that no branch has been chosen from that section and RBS selection is continued on into the next highest section. In the topmost section, the leader (top portion of the main stem) is treated as a branch. Thus if sampling proceeds to this topmost section, a branch must be selected. When calculating selection probabilities, diameters of stems and branches are squared so these probabilities are proportional to branch or stem cross-sectional area.

Table 3.1: Differences of groupings between proposed RBS protocol.

Protocol	Number branches	Length of stem
IB	fixed	variable
FB	fixed	variable
OM	variable	fixed
CT	variable	fixed
EA	variable	variable

3.2 Study site

The trees measured for this project were located in Lubrecht Experimental Forest (LEF) ($46^{\circ} 54'N$, $113^{\circ} 27'W$). LEF is maintained and operated by

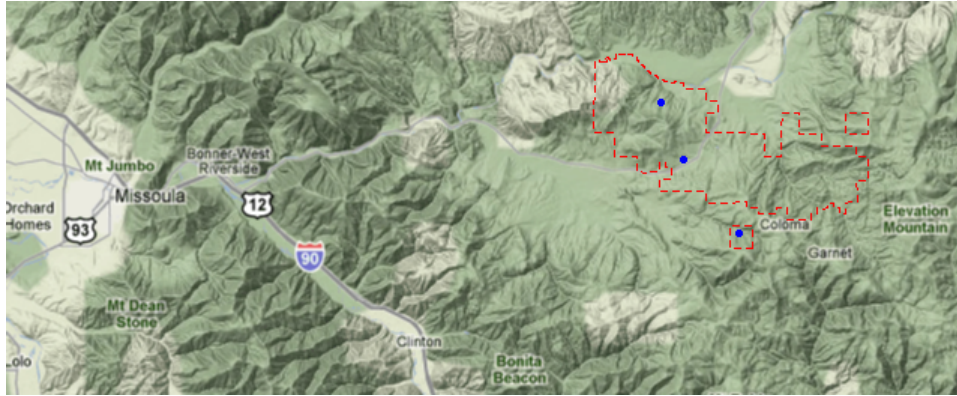


Figure 3.1: Map of Lubrecht Experimental Forest, boundary denoted by red lines. Stands where sample points were located are indicated by blue dots.

the University of Montana’s College of Forestry and Conservation, and is located approximately 50 km east of Missoula, Montana (Fig. 3.1). The majority of LEF falls into the Douglas-fir habitat type series (Pfister and Arno 1980). Elevation at LEF ranges from 1,097 m to 1,890 m. Mean annual precipitation averages approximately 50 cm, about half of which falls as snow during the winter months (Nimlos 1986). LEF is 11,330 hectares in size and was heavily logged in the late 1800s and early 1900s, while it was under the management of the Anaconda Copper Company. The current forest cover on LEF was established soon after that logging.

A total of twenty trees in 3 stands with excurrent crowns were destructively censused. Ten of the trees measured were Douglas-fir, and ten were western larch.

3.3 Stand and tree selection

Sample points were placed in mature stands in which both Douglas-fir and western larch occurred, points were located on a 100×100 m grid using local UTM coordinates and a Garmin model GPS 60 unit. At each sample point, a variable radius plot was established using a basal area factor of 2.3 m^2/ha . Sample trees were selected from those trees which fell within the variable radius plot. Additional criteria for selecting trees to be measured included:

1. Sample trees had to be of the species of interest (Douglas-fir or western larch);
2. Sample trees had to have diameter at breast height (DBH) within the range of 20 - 40 cm^1 ;
3. Sample trees had to have undamaged stems (no broken or multiple tops);
4. Sample tree crowns had to display no obvious sign of insect or disease damage.

Up to two trees were selected for measurement randomly from the pool of potential candidate trees at any given point. If only one tree met the qualifying criteria at a given point, only that tree was sampled. If no trees were present or none of the trees at the point met the qualifying criteria, nothing was sampled and a new point was established at a 100 m offset.

¹The first tree sampled, a Douglas-fir, had a smaller diameter than this specified range, to assess the workload.

3.4 Tree measurement

Once sample trees were selected, breast height (1.37 m) was measured and marked with paint on the bole. The tree was then directionally felled with a chainsaw in a manner so as to minimize crown breakage. The end of measuring tape was secured to the stem at breast height, and run along the length of the bole to the top of the tree. Working from the lowest live branch to the top of the tree, several measurements were taken every time a live branch with a diameter ≥ 0.5 cm at its base was encountered. Height of the branch was recorded. This height was simply where the branching from the main stem occurred. Branch diameter was measured using calipers at the base of the branch approximately 3 cm from the branching to avoid localized swelling. Stem diameter was measured with calipers directly above the branching. Each branch was then separated from the stem using pruning shears and weighed green, using an ADAM CBK 35a electronic scale, providing green weights for the complete set of all branches within the crown. A qualitative assessment (0-3) of the damage each branch incurred during felling was also recorded. These measurements were recorded for each live branch up to the location where the main stem tapered to a diameter of 5 cm. This point was considered the end of the stem and the remaining top of the tree was treated as an individual branch.

Stem diameter measurements were also taken at various heights along the bole where live branches did not necessarily occur. These additional stem diameter measurements were taken so RBS could be simulated under the differing branch selection criteria outlined in Section 3.1. Specifically,

stem diameter measurements were taken at 1 m intervals from the lowest live branch, and at heights which broke the crown into equal thirds (by length). The measurements taken in each tree allow for crown mass estimates to be derived from the five proposed RBS selection protocols for every live branch.

3.5 Crown mass estimation

First, actual crown mass was calculated from the census of branch weights for each tree. Then for all branch selection methods, total green crown mass was estimated using the inverse of each branch's unconditional selection probability, with eqn. (2.2) using the green weight of each branch as the x_r term. Selection probabilities of branches were calculated by using the cross-sectional areas of all branches (one to many depending on selection protocol), and the stem at the top of the section, with eqn. (2.7) using branch and stem diameters as the c_r and c_k terms. Because sample trees were censused (i.e. all branches were measured and weighed), I was able to calculate M crown mass estimates for each tree (one per live branch). I was also able to compute the actual variance of the estimates with eqn. (2.9), and the ideal unconditional probability with which each branch should be selected. This ideal selection probability is simply the fraction of total crown mass represented by each branch and is calculated as:

$$Q_{\text{ideal}} = \frac{\text{branch weight}_i}{\text{crown weight}} = \frac{x_i}{X} \quad (3.1)$$

for branch i ($i = 1, \dots, M$). With a minimal amount of rearranging it can be shown that if a branch is selected with the ideal unconditional probability, the estimate of crown mass derived from that branch will be equivalent to the actual crown mass:

$$\hat{X} = \frac{x_i}{Q_{\text{ideal}}} = \frac{x_i}{x_i/X} = X \quad (3.2)$$

A superior branch selection protocol will therefore select branches with probabilities which are as close as possible to their ideal unconditional selection probabilities.

3.6 Evaluation of RBS performance

To gauge the effectiveness of RBS in estimating crown mass, two well established sampling methods were used as benchmarks. These two comparison methods are simple random sampling, and list sampling. Under simple random sampling each branch is given an equal selection probability as in eqn. (2.6). To implement this type sampling scheme in the field requires a tally of all branches (to obtain M) before selection can take place. With list sampling, the selection probability for branch i is calculated as:

$$Q_i = q_i = \frac{c_i^2}{\sum_{i=1}^M c_i^2} \quad (3.3)$$

where c_i is the diameter measured at the base of branch i . This is equivalent to performing RBS with only one section throughout the entire tree (thus

$Q_i = q_i$). For list sampling, all branches must not only be tallied but have their diameters measured before selection takes place. One of the main differences between these two comparison sampling methods and the RBS methods is that RBS does not require collection of data on all branches within the crown prior to calculating selection probabilities.

Since all sampling methods (RBS and comparison) considered in this study produce unbiased estimates, I will use variance of estimates in percent standard error as a measure of the performance for a particular sampling method. For each tree and sampling method combination, variance of the estimates was calculated as:

$$\sigma^2 = Var(\hat{X}) = \sum_{i=1}^M Q_i (\hat{X}_i - X)^2 \quad (3.4)$$

where \hat{X}_i occurs with probability Q_i . To get units back into kilograms of mass (instead of kg^2), I will use the standard error ($\sigma = \sqrt{\sigma^2}$). Then, dividing the standard error by the actual crown mass (X) to work with these measures in percentage terms, I will define:

$$\sigma_{\%} = \frac{\sigma}{X} \times 100 \quad (3.5)$$

This tree specific percent standard error will effectively allow for comparison between trees of different size by giving a generalized measure of how well a particular sampling method performed.

I will also define Q_{ϵ} as being the ratio between the actual and ideal selection probabilities for branch i ($i = 1, \dots, M$) from a single tree. This is

calculated as:

$$Q_\epsilon = \log\left(\frac{Q_i}{Q_{\text{ideal}}}\right) \quad (3.6)$$

These Q_ϵ will serve as an additional measure of the performance of RBS. If all the Q_ϵ from a particular tree sampled under a specified RBS protocol are close to zero, the estimates (\hat{X}) will be close to the actual amount (X) and we can expect a high degree of accuracy from these estimates. Conversely, if all or some of the Q_ϵ are large, we can expect greater variation, and thus decreased accuracy, in the estimates. The log function is used so that the Q_i which are less than Q_{ideal} are not constrained to the range: $0 < Q_i < 1$.

With the measurements taken, it is also possible to calculate the expected height to which one would have to sample before selecting a branch within a given tree. This expected height is calculated as:

$$\mathbf{E}[\text{height}] = \sum_{i=1}^M h_i \times Q_i \quad (3.7)$$

where h_i is the height of branch i for a particular tree. Since sampling under most of the proposed RBS protocols takes place in sections, the length of which depend upon the particular sampling protocol implemented, the expected height equation above is only accurate for the individual branch selection method. To account for the grouping of branches into segments requires summing over K RBS sections for given tree and sampling method pair, as opposed to summing over the M individual branches. The h_i term is replaced with h_k , the height where the top of section k occurs. Likewise

the Q_i is replaced with Q_k , which is the sum of Q_i for all branches within section k :

$$Q_k = \sum_{i=1}^M Q_i \times d_i \quad (3.8)$$

where d_i is an indicator variable with value 1 if branch i is from section k , and 0 otherwise. For RBS protocols other than individual branch, the expected height is calculated as:

$$\mathbf{E}[\text{height}] = \sum_{k=1}^K h_k \times Q_k \quad (3.9)$$

Evaluating these expected sampling heights in relative ($h_{\%}$) terms:

$$h_{\%} = h_k/H \quad (3.10)$$

where H is total tree height, will allow for comparisons of expected sampling height between trees of different heights.

3.7 Sample size determination

Since we know that variance of the estimate will decrease with increasing sample size, and destructively sampling a tree to only sample one branch seems impractical, I will examine how the variances of these estimators scales with sample size. For the RBS and list sampling methods with a sample of

size m , the variance of \widehat{X} scales as:

$$\sigma_m^2 = \left(\frac{M-1}{M} \right) \frac{\sigma_{yz}^2}{m} \quad (3.11)$$

where σ_{yz}^2 is the variance of \widehat{X} based on a sample of one branch using method z . While for simple random sampling without replacement, for a sample of size m , the variance scales as:

$$\sigma_m^2 = \left(\frac{M-m}{M} \right) \frac{\sigma_{y,srs}^2}{m} \quad (3.12)$$

where $\sigma_{y,srs}^2$ is the variance of \widehat{X} for tree y under simple random sampling with a sample size of one branch.

Chapter 4

Results and Discussion

4.1 Sample tree characteristics

Dimensions of the selected trees are given in Table 4.1. Douglas-fir trees tended to be smaller in size (DBH, total height, and crown length) as compared to western larch trees of a similar crown mass (Fig. 4.1). That is, for a Douglas-fir and western larch of approximately the same size, the Douglas-fir crown will typically weigh far more than that of the western larch. This is consistent with results of previous studies such as Brown (1978). This is a species specific effect and is most likely due to the two species allocating mass differently as they grow. Western larch are deciduous, regrowing all of their foliage in spring at the beginning of each growing season, whereas with Douglas-fir, the foliage persists for several years and is replaced more gradually. Because the larch foliage is more intermittent, fewer resources may be allocated to the crown as the tree is growing. This could help explain why larch have lighter crowns than similar sized Douglas-firs.

Table 4.1: Summary measures of 20 trees censused for this study. Tree: 1-10: Douglas-fir, 11-20: western larch. DBH: diameter breast height (taken at height of 1.37m above the forest floor). Height: total tree height. Crown Mass: total green weight of all live branches. Branch Count: total number of live branches.

Tree	DBH (<i>cm</i>)	Height (<i>m</i>)	Crown Mass (<i>kg</i>)	Branch Count
1	34.7	20.83	150.6	136
2	12.9	9.22	40.0	70
3	21.7	9.99	97.9	65
4	22.0	15.82	77.4	112
5	24.2	13.61	145.1	110
6	37.5	22.37	316.8	145
7	38.5	18.90	273.5	112
8	27.6	17.43	144.5	92
9	36.3	18.74	276.2	129
10	31.7	17.26	241.2	116
11	28.5	20.64	144.6	172
12	37.2	24.00	104.8	83
13	23.8	14.97	52.7	77
14	36.6	24.00	179.6	214
15	39.3	21.10	207.7	128
16	23.2	18.72	46.5	74
17	22.9	21.62	49.0	99
18	22.5	18.30	44.1	58
19	33.7	24.42	125.7	123
20	30.8	19.60	155.6	135

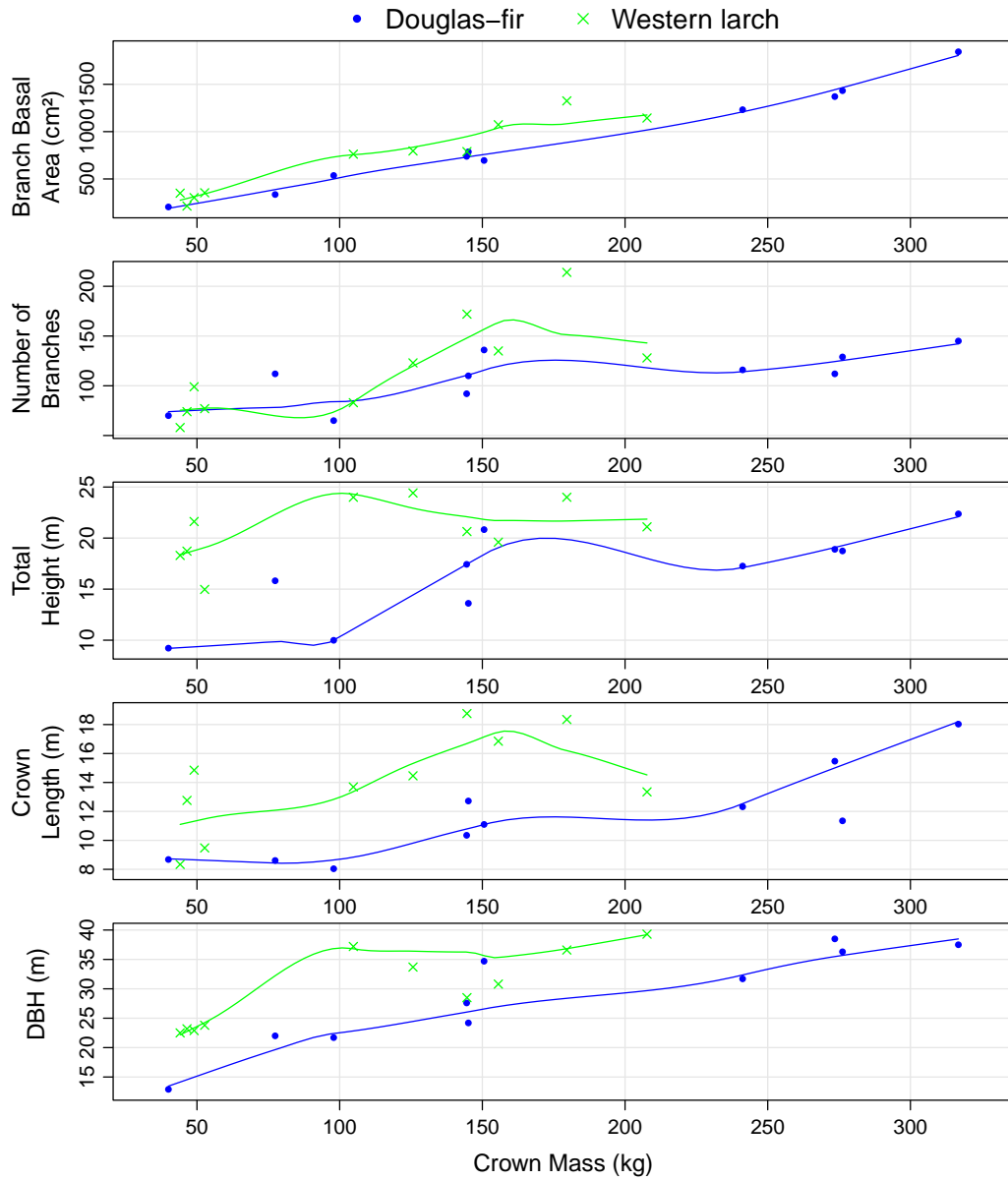


Figure 4.1: Crown mass plotted against diameter at breast height, crown length, total tree height, number of branches, and total branch basal area grouped by species for the twenty trees measured in this study. Solid lines represent smoothers run through the data.

A grand total of 2,250 branches were measured from the twenty trees censused. Green mass is plotted against diameter and basal area for each branch in Fig. 4.2. Branch mass appears to share a quadratic relationship with diameter, whereas with cross-sectional area the relationship becomes linear. This is broadly consistent with the pipe-model theory of Shinozaki *et al.* (1964), which posits that the size (area) of conductive tissue measured at any given point along the stem or on branches dictates the amount of biomass which can be supported in more distal regions.

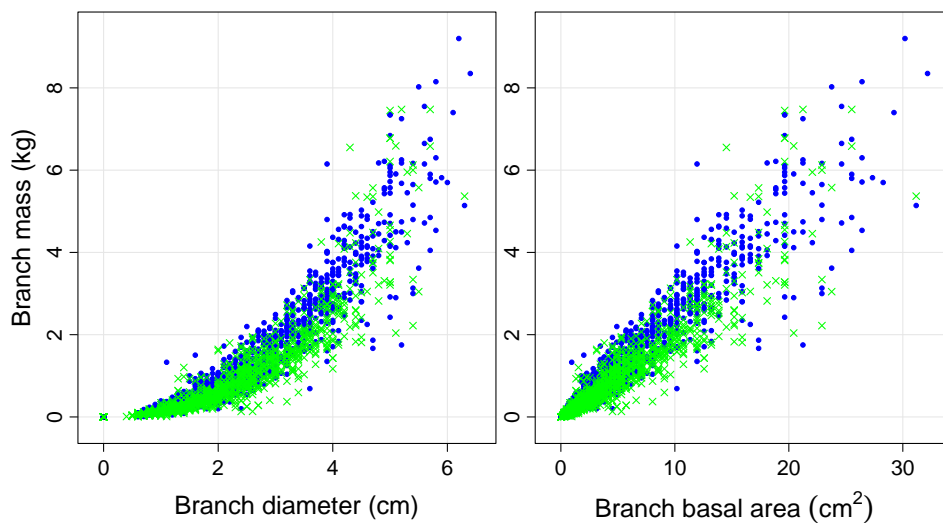


Figure 4.2: Relationship between branch mass and branch diameter (left), and branch basal area (right) for all 2,250 branches measured for this study. Douglas-fir is represented by blue dots and western larch by green x's.

The basis for pipe-model theory can be summarized as follows. The structure of stem and branches exists solely to maintain the photosynthetic tissues. This structure sustains the foliage both physically (supporting the canopy and extending to compete for sunlight) and by supplying the leaves

with liquid water, a vital ingredient of photosynthesis. Collectively the stem and branches can be viewed as a bundle of uniform diameter pipes, some actively functioning to supply water to foliage (sapwood), and some which are no longer in use (heartwood). Pipe-model theory regards these pipes as having equal diameter, so that each pipe is able to support photosynthesis for the same quantity of leaf matter. If this theory holds true, then we can think of the cross-sectional area of sapwood at a particular point along the stem or branch as a measure for how much water can be supplied to the leaves past this point. Thus, we would expect within a given species, a proportionality to exist between cross-sectional area (stem or branch) to the foliage quantity borne past the point where the measurement was taken. Furthermore, if the stem and branch are always supporting the maximum amount of foliage possible, the amount of support structure (stem and branches) present in more distal regions should also be proportional to cross-sectional area.

The relationship between mass and area for the branches in Figure 4.2 has a Pearson correlation coefficient (r value) of 0.9308 with both species combined. The r values are 0.9458 and 0.9253 individually for Douglas-fir and western larch respectively. While these branch variables are highly correlated, the individual tree totals of these variables are even more so (Fig. 4.1 upper panel). The r values of these relationships are 0.9907 and 0.9600 for Douglas-fir and western larch respectively. Because the branch mass and cross-sectional area variables are highly correlated at the individual branch and tree level, branch cross-sectional areas are suitable surrogate variables for branch mass. With highly correlated surrogate and response variables, if a RBS protocol selects branches with probability proportional

to the total of the surrogate (total branch area), these probabilities will also be proportional to the response variable (mass). This is important because branch diameters are much quicker and easier to collect in the field than are branch weights. Also, the more linear the relationship between surrogate and response variables, the easier it is to exploit that relationship for estimation of the response. Therefore, a higher correlation will result in greater estimate accuracy. Upon further examination of Fig. 4.2 we can also note a trend of increasing variance of branch weights with increasing branch diameter. This heteroscedasticity is not unexpected and is common when dealing with most types of biological data.

Attempting to determine the physical differences between individual trees which would affect the precision of RBS estimates of crown mass, I examined how stem area at a given point within the crown correlates to the amount of basal area remaining in branches above that point (Fig. 4.3). In the individual panels of Fig. 4.3 the top of the crown is located in the bottom left corner, while the lowest live branch is in the upper right. These measures always converge with a line of slope of one passing through the origin at the top of the tree due to how the branches and stem have been defined.

For all but three of the trees measured, the amount of branch basal area in the crown is greater than the stem cross-sectional area at the lowest live branch. In other words, the stem at the base of the crown is supporting cross-sectional area of branches which exceeds the stem area. This discrepancy between the cross-sectional area of the main stem and total branch area is

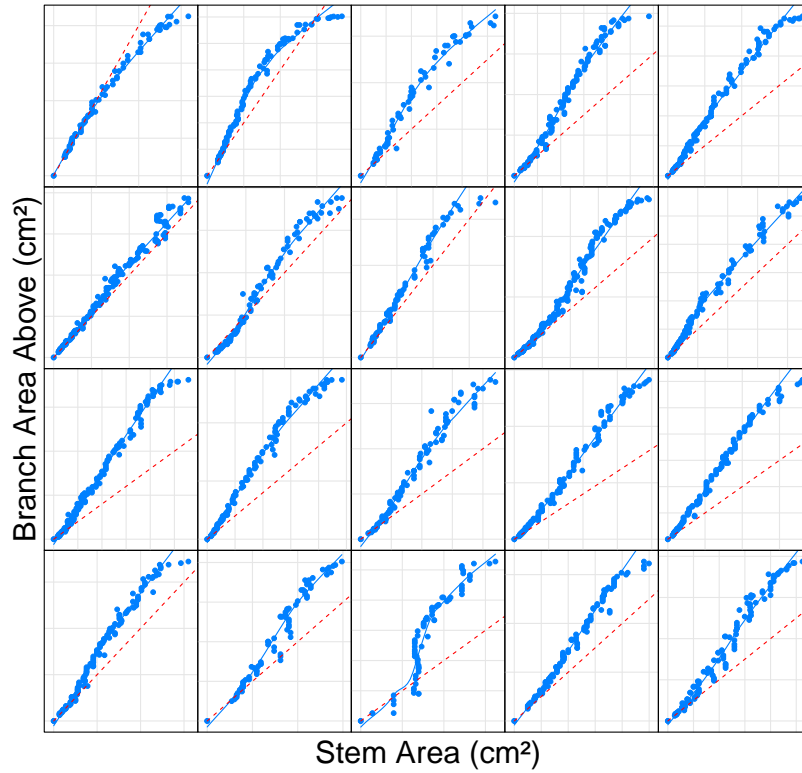


Figure 4.3: Branch area above plotted against stem area for sample all trees (tree number increasing left to right and bottom to top). The blue line represents a smoother run through the data, and the red dashed line is added for reference, it crosses the y-axis at zero and has a slope of one.

contrary to pipe-model theory, but may be explained in part by the presence of heartwood (non-functioning pipes) being present in the branches. Not only are these stem and branch area totals different at the base of the crown, but as one works their way higher into the crown, these variables taper at different rates. If the taper of these two variables were constant, they would form perfectly straight lines in Fig. 4.3, and the method employed to aggregate branches together into RBS sections would become arbitrary (as the stem would always provide a good estimate of the branch basal area in the crown above). However, because there is curvature present between the taper of stem and branch area above, RBS sections should be of a length where the relationship is approximately linear within each section. Doing so will produce branch selection probabilities which are close to Q_{ideal} and thus result a reduction of crown mass estimator variance.

To demonstrate the effects that taper between the surrogate and response variables has over RBS sections of different length, I have constructed Fig. 4.4. For this example I have chosen two trees, tree 6 which displays much curvature, and tree 11 which exhibits minimal curvature. The distance from ideal selection probability (Q_ϵ) is plotted against branch height for both the crown thirds and one meter RBS protocols. In this figure, we can see that the Q_ϵ are greatly reduced in magnitude for tree 6 as one moves from crown thirds to one meter RBS selection protocol. The reduction in magnitude of Q_ϵ , while still present, is not as great for tree 11 going from crown thirds to one meter RBS selection protocol.

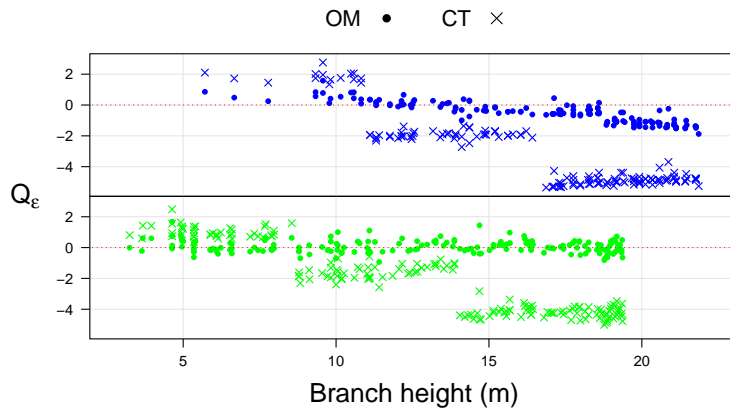


Figure 4.4: Distance from ideal selection probability for the branches on tree 6 (blue) and tree 11 (green) sampled under the crown thirds and one meter RBS protocol.

4.2 RBS estimation results

The variance of the crown mass estimates based on a sample size of one branch was calculated for all sample trees within the framework of each sampling protocol using eqn. (3.5). The variance was greatest for all sample trees when using the crown thirds RBS selection protocol (Fig. 4.5). These values of $\sigma_{\%}$ for all sample tree and sample method combinations is reported in Table 4.2.

The extremely high variance of the crown thirds method can be attributed to the fact that under this selection protocol, there are so many branches per section that the stem's conditional selection probability is dwarfed by the sum of all branch selection probabilities within the first section. Specifying RBS sections this long, and using the cross-sectional areas of branches and stem to calculate selection probabilities, the stem at the

Table 4.2: Percent standard error of estimates for proposed RBS protocol, simple random sampling, and list sampling for 20 censused trees, based on a sample size of one branch. Sampling methods, IB: Individual branch. FB: Five branch. OM: One meter. CT: Crown thirds. EA: Equal basal area. SR: Simple random sampling without replacement. LS: List sampling.

Tree	Sampling method						
	IB	FB	OM	CT	EA	SR	LS
1	36.78	33.73	30.80	515.68	32.09	77.02	24.58
2	52.40	51.52	49.37	322.26	35.20	150.21	27.59
3	52.73	50.96	51.62	504.72	45.81	67.90	28.66
4	56.06	54.28	49.70	425.27	43.55	106.94	24.70
5	56.93	52.96	63.30	626.76	48.67	77.74	19.72
6	64.45	58.62	62.53	623.11	42.11	97.21	29.41
7	70.84	62.28	55.54	617.48	48.45	79.83	20.69
8	79.76	77.98	57.21	629.43	63.98	76.55	26.53
9	86.95	80.20	70.71	731.66	57.61	70.59	22.41
10	92.30	81.52	69.29	740.18	68.61	62.13	25.65
11	34.27	35.37	34.13	496.08	37.14	116.79	33.05
12	34.37	31.69	32.24	377.47	31.98	83.82	30.07
13	35.97	37.71	36.32	382.61	33.12	97.50	29.31
14	41.77	39.64	39.39	528.56	34.88	95.31	24.47
15	44.33	42.31	31.18	472.87	40.79	121.12	30.48
16	46.97	45.15	34.32	224.08	44.98	132.21	30.77
17	55.51	53.38	50.77	296.47	48.17	162.65	31.79
18	75.00	70.72	46.45	413.35	63.08	97.73	30.82
19	88.16	77.97	64.01	567.50	68.21	77.24	33.02
20	92.04	84.56	60.68	571.28	67.71	96.05	27.37

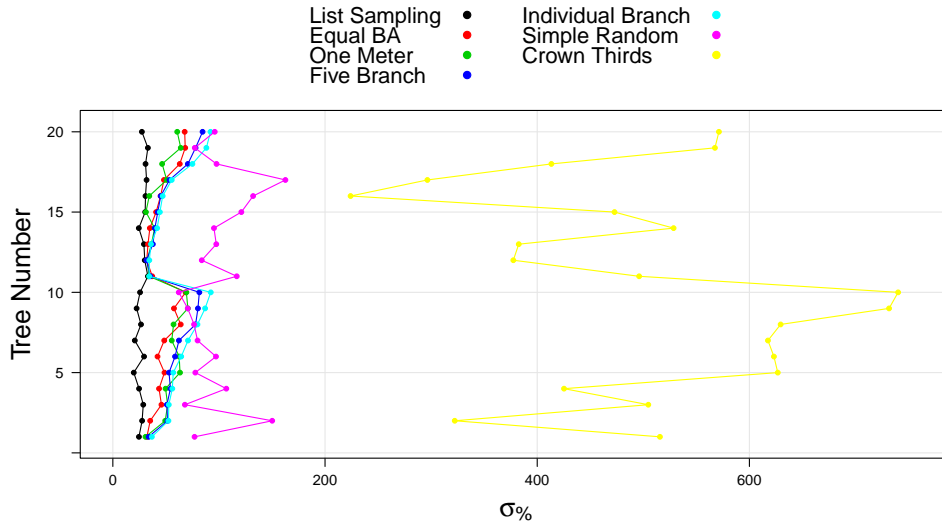


Figure 4.5: Percent standard error of estimates for each tree by selection method, based on sample size of one branch.

top of the first section becomes a poor surrogate measure for the amount of branch area remaining in the crown above. In the first section, if the stem is being selected with smaller than ideal unconditional probability, the branches are therefore (when considered jointly) selected with larger than ideal probabilities. Having been assigned a larger than ideal selection probability leads to underestimation of crown biomass. This disparity in selection probabilities is carried through into the upper sections where branches are selected with unconditional probabilities which are smaller than ideal probabilities, leading to overestimation.

A plot of Q_ϵ (the log ratio of actual to ideal selection probabilities) against the height and RBS section from which the estimate came is displayed in Fig. 4.6, for sample tree 11 (a western larch) under the crown

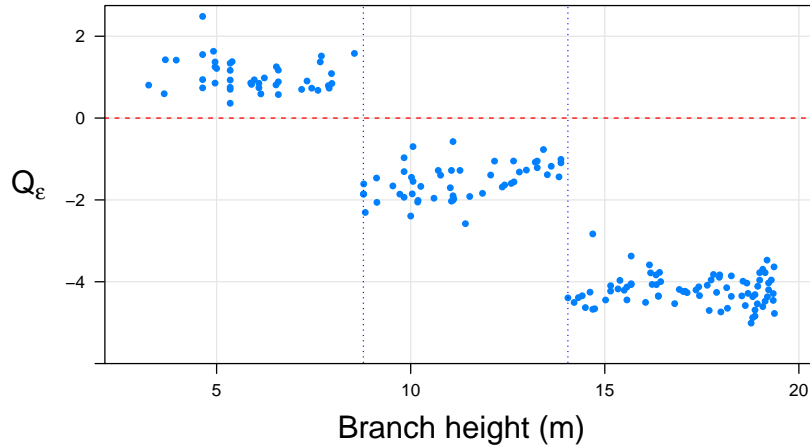


Figure 4.6: Distance from ideal selection probability for each branch on tree 11, sampled by the crown thirds RBS protocol. Blue dotted vertical lines represent the heights which mark the section boundaries under crown thirds RBS protocol.

thirds selection protocol. Figure 4.6 confirms the pattern of under- and over-estimation by section with the crown thirds method. One of the primary differences between crown thirds and the other four proposed RBS protocol is that under the other four RBS selection criteria, the stem segment typically has the largest selection probability (as compared to any one branch) within any given section. When the Q_ϵ values for the tree 11 branches sampled under the one meter selection protocol are examined (Fig. 4.7) we can still discern a pattern of under- and over-estimation but it is considerably less severe. For the one meter selection protocol, the magnitude of the Q_ϵ values has also been greatly reduced. Here, most branches are being selected with unconditional probabilities which are within one percent of their ideal selection probabilities.

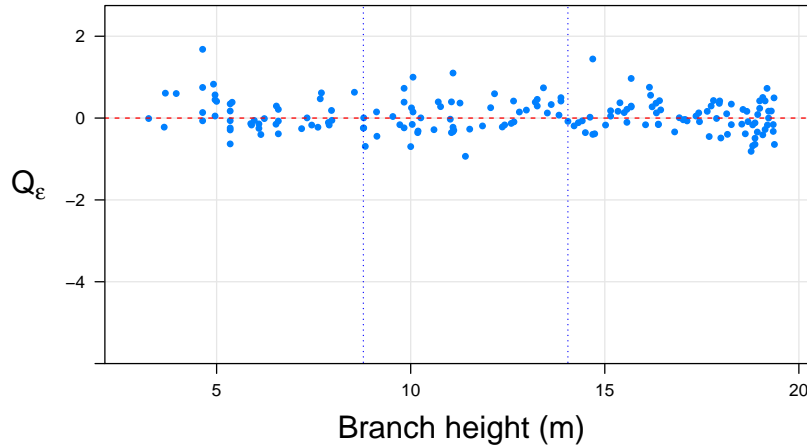


Figure 4.7: Distance from ideal selection probability for each branch on tree 11, sampled by the one meter RBS protocol. Blue dotted vertical lines represent the heights which mark the section boundaries under crown thirds RBS protocol (for reference with Fig. 4.6).

When the crown thirds method is not considered, we can see that the estimate variance of the other RBS sampling methods are more comparable to one another (Fig. 4.8). From this figure we can discern that the one meter and equal basal area RBS selection methods tend to perform slightly better than five branch and individual branch selection methods for the trees in this study. With regard to the benchmark methods, we can see that all of the RBS sampling methods, excluding crown thirds, typically tend to perform better than simple random sampling and worse than list sampling. Because the list sampling method treats the entire crown as one section, variance of the estimates arises only from the variation present between the surrogate variable (branch area) and the response variable (mass). With RBS methods, additional estimation variance is added by conceptually breaking the

crown into sections and using the cross-sectional area at the top of these sections as an estimate for the amount of branch basal area remaining in the crown above.

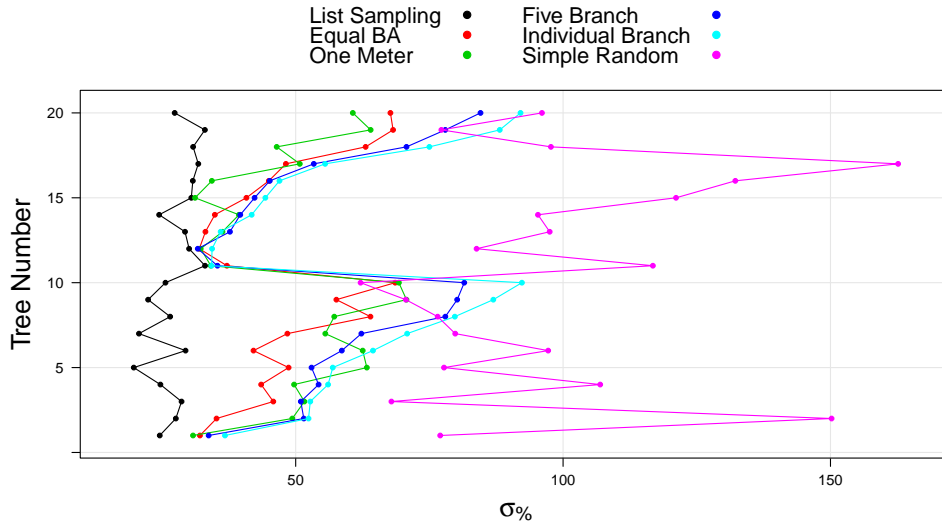


Figure 4.8: Percent standard error of estimates for each tree, based on samples of size one branch (crown thirds selection method omitted).

Expected relative height of sampling is plotted for each tree and RBS protocol pair in Fig. 4.9. While the expected relative sampling heights under the five RBS protocol range from approximately 30 to 80 percent of total tree height, the rankings from tree to tree remain quite similar. This ranking from low to high expected sampling heights is crown thirds, individual branch, five branch, one meter, and equal basal area. In other words, crown thirds protocol tends to select branches lower, and equal basal area higher, on the tree. Simple random sampling is not depicted in Fig. 4.9 but as with list sampling, it always requires sampling along the entire

length of the crown. Interestingly, for the RBS methods, a higher expected sampling height coincides with a reduction in estimate variance.

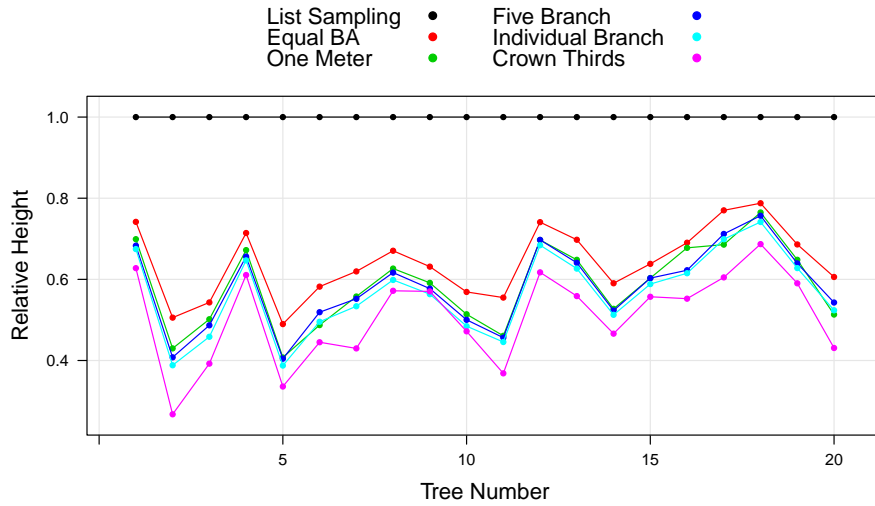


Figure 4.9: Expected height of sample branch selection by tree and selection method.

Measures of branch area above and stem area are plotted against height in Fig. 4.10 for sample trees 10 and 11. These two trees were chosen because RBS functioned particularly well on one (tree 11) and not as well for the other (tree 10). From this figure, it is apparent that stem area is a much better indicator of how much branch area remains in the crown above any given point for tree 11. When the taper profiles of these two variables agree well with one another, RBS essentially performs equivalent to list sampling. This is confirmed in Fig. 4.8 for tree 10, the percent standard error of the one meter RBS method is 170% greater than with list sampling, while for tree 11, it is only 3% greater than list sampling.

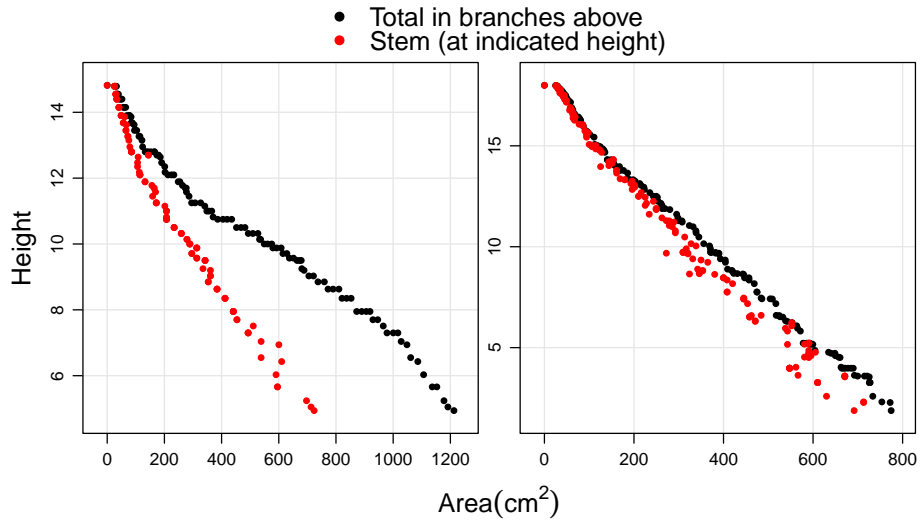


Figure 4.10: Branch area above and stem area taper plotted against height for sample trees ten (left) and eleven (right).

The average value of σ_m from twenty sample trees (for sample sizes of $m = 1, \dots, 10$ branches) is plotted for all sampling methods except crown thirds in Figure 4.11. From this figure, we can see that the RBS sampling methods occupy the middle ground between simple random and list sampling in terms of estimation accuracy. The percent standard error scales down to approximately ten percent for the RBS sampling methods with a sample size of around five or six branches. To reach this margin with simple random or list sampling requires, on average, sample of sizes of nine or three branches respectively.

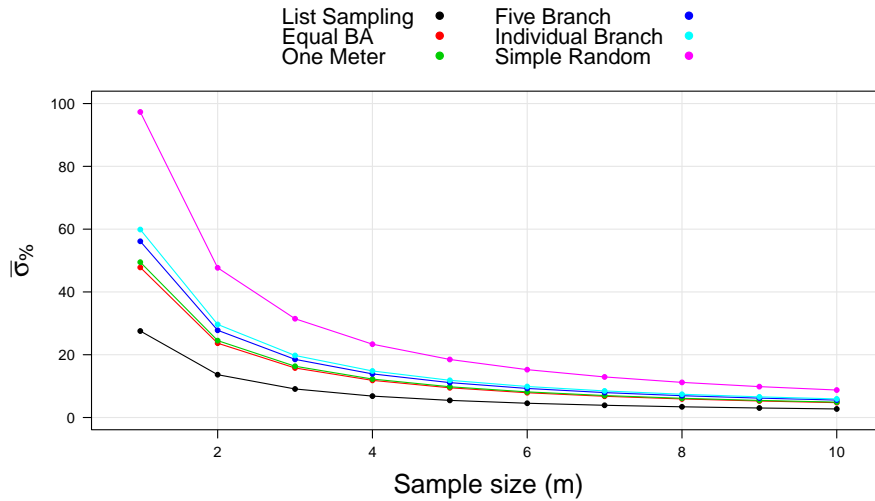


Figure 4.11: Scale of percent standard error of estimates with sample size for each sampling method. Where $\bar{\sigma}_{\%}$ is just $\sigma_{\%m}$ averaged over the twenty trees measured in this study.

4.3 Practical considerations

Statistical properties aside, to find a sampling method which is superior for estimating crown biomass, we must also consider the physical aspects and the ease with which these different methods can be applied to trees with excurrent crowns in the field. As mentioned above, one of the reasons RBS is a desirable sampling scheme is that it does not require the identification or measurement of all branches prior to beginning sampling. This is advantageous because potentially less time is spent enumerating and measuring branches. In the situation where RBS selects a branch from the last (top-most) section of a excurrent tree, sampling times may not differ from simple random or list sampling, but this is a rare event. However in this situation, RBS schemes still have the benefit of breaking the crown down into sections,

thus reducing the number of branches one is working with at any given time. Since these RBS sections have a smaller number of branches to keep track of, there is a reduced chance of incurring some type of non-sampling error, such as skipping over a branch entirely or mis-identifying a selected branch.

We can also evaluate the relative efficiencies (in general terms) of one RBS grouping method over the others. With individual branch RBS protocol, selection probabilities are calculated for each branch before potentially moving on to the next branch. Thus, a large amount of time would be spent going back and forth between measuring branches and calculating selection probabilities. Instead, it is probably more efficient to group more than one branch together before calculating the selection probabilities. Yet this is not true of the crown thirds selection protocol, as too many branches are included in one section and the same problems as with simple random and list sampling apply. The other methods of grouping within the RBS framework, (five branch, one meter, and equal basal area) are more similar to one another than the other two RBS methods in terms of the number of branches per section.

To distinguish between these three methods, let's examine how the groupings break the crown up into sections. Five branch groups the branches together by an absolute count of branches, one meter uses a specified length measured along stem, and equal basal area uses a measure of branch and stem cross-sectional areas. For the five branch and equal basal area selection methods the position of a branch relative to the other branches is important, whereas with one meter selection protocol, the position of the branch is only important relative to where the one meter RBS section marks are located.

When implementing RBS in the field, using the one meter approach would be the easiest to communicate to field crews. The one meter protocol also removes the complication of deciding which branch to add into a section. For example, say there are six branches in a whorl all at the same height on the stem. Under the five branch selection protocol, which of these branches should be grouped together and which one singled out and added into the next section?

With any of the RBS protocol, a portable computer or programmable calculator would be used to calculate selection probabilities and direct sampling. Writing programs for doing this would be simpler for the one meter protocol than for the equal basal area protocol (which would require running tallies of branch and stem areas). Also, with one meter sections, missed branch errors are easier to correct than they are with the other RBS methods where branch position relative to one another is critical.

4.4 Potential sources of non-sampling error

Anytime tree felling is necessary for sampling, we can expect that some of the branches are going to break, particularly on the bottom side of the tree (as it lays once felled). If these branches are detached from the stem but otherwise nearly undamaged, it is a relatively simple matter of identifying which branch came from where. If a branch is moderately damaged but it can still be pieced together, it should be reconstructed as best as possible and still considered for selection. When a branch is extremely damaged by felling

(buried into the ground, or shattered into too many pieces to reconstruct) then, if possible the branch diameter should be measured and included in the calculation of selection probabilities. However, if an extremely damaged branch is selected by RBS, it may be advisable to re-run random number generation and thus select another undamaged or less damaged branch.

When the objective of sampling is to measure the amount of some attribute borne by the branches, care must be taken to limit the amount of loss of that attribute between the time of selection and the time of measurement. This is particularly applicable to samples that require some sort of processing before measurement can take place. For example, say I was interested in obtaining the dry mass of the branches instead of just the green mass. The selected branches would therefore have to be transported, disassembled, and dried in ovens before weighing could take place. Depending upon the methods used in processing, each step presents opportunities for the branch to lose foliage, or even twigs before the measures of dry mass are taken. This loss, plus the fact that it is unlikely anything additional has been added to the sample, would make me view these measurements as a minimum value of what was originally on the branch.

When sampling small trees with RBS, a stopping point such as the 5 cm stem diameter used in this study may not be ideal. This is because the 5 cm top constitutes a larger portion of a small tree than it does of a larger tree. For small trees, it may be desirable to set a smaller stem diameter as the stopping point with RBS. Or more desirable still to just perform a census of the entire small tree, if time and financial constraints permit doing so.

Chapter 5

Conclusions

In the distribution of forest carbon, tree crowns can be thought of as one of several nested pools which would comprise a total measure of forest carbon. The crown biomass pool is part of the tree pool, which is part of the aboveground pool, which is then part of the total biomass pool. This total biomass pool incorporates all below ground (soil, roots) and aboveground material (tree, downed woody debris, duff, litter, and vegetation). If the purpose of sampling is to characterize this whole pool of carbon we expect sampling variability to be present in the measures of each individual pool.

Randomized branch sampling is an efficient and unbiased sampling strategy which can be used to estimate many attributes of trees which are borne within the crowns. By modifying the selection protocol RBS can easily be adapted and made more efficient for sampling trees with excurrent crowns. Five different modifications to the RBS selection protocol were considered in this thesis. Of these five protocols, the aggregation of all primary branches into 3 strata (crown thirds), was found to produce unsatisfactory estimates

because of the high degree of estimate variability. The remaining four selection methods resulted in crown biomass estimates with an accuracy somewhere between those generated by simple random sampling and list sampling for both species. The average ranking over 20 trees (order of increasing estimate variance) of these four RBS protocol is: equal basal area, one meter, five branch and individual branch. However due to practical considerations of implementing these protocols, I recommend using the one meter selection protocol wherein all primary branches within 1 m segments of main stem are aggregated.

When the purpose of sampling is to determine biomass contained in the crown, a sample size of five to six branches seems to be sufficiently large enough to generate standard errors within ten percent of the actual crown mass, this is true for both Douglas-fir and western larch. Because RBS can be performed quickly and has potential gains in time over using other unbiased sampling methods, RBS would be utilized best as a method applied to a large number of trees where the goal was to characterize biomass at a stand or landscape level. When used this way, the level of error should suffice as we would expect substantial inherent tree to tree variability in crown biomass to exist anyways.

When the goal of sampling tree crowns is to estimate the quantity of a variable of interest other than total biomass, I would recommend an initial calibration sampling phase. For this phase, a small number of trees should be censused as was done in this thesis for green crown biomass. With this information, the relationship between the surrogate and response variables can be examined. The procedure for calculating branch selection probabili-

ties can be established, and sample sizes which produce estimates within a reasonable amount of error found by simulated sampling. Once suitable RBS methods have been decided upon, a second less-intensive sampling phase can begin. In this second phase the assessment of individual trees can proceed at an increased pace.

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Appendix

Proof of the unbiasedness of RBS estimates follows.

RBS estimates are calculated as:

$$\hat{X}_i = \frac{x_i}{Q_i}$$

If \hat{X}_i is an unbiased estimate of X then:

$$E[\hat{X}_i] = X = \sum_{i=1}^M x_i$$

If we define \hat{X}_{Q_i} as:

$$\hat{X}_{Q_i} = \sum_{i=1}^M I_i \hat{X}_i$$

where:

$$I_i = \begin{cases} 1 & \text{if branch } i \text{ is sampled,} \\ 0 & \text{otherwise.} \end{cases}$$

Then:

$$E[\hat{X}_{Q_i}] = E\left[\sum_{i=1}^M I_i \hat{X}_i\right] = \sum_{i=1}^M E[I_i] \hat{X}_i$$

and since:

$$E[I_i] = [Q_i \times 1] + [(1 - Q_i) \times 0] = Q_i$$

Therefore:

$$E[\widehat{X}_{Q_i}] = \sum_{i=1}^M Q_i \widehat{X}_i = \sum_{i=1}^M Q_i \frac{x_i}{Q_i} = \sum_{i=1}^M x_i = X$$