Estimating lodgepole pine biomass

David Clarence Johnston

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ESTIMATING LODGEPOLE PINE BIOMASS

By

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ABSTRACT

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Biomass regression models predicting total live above-ground, bole wood, bole bark, live needle, live branch, cone, and live crown components were developed for lodgepole pine (Pinus contorta Dougl.) trees on two adjacent stands representing two habitat types in western Montana. A pseudo-random sampling scheme was employed, and regression models were developed separately for each stand. Crown component models were rather unreliable ($0.410 < R^2 < 0.830$); however, total wood, bark, and crown biomass models were very reliable ($0.820 < R^2 < 0.980$). Unit area biomass estimates were also obtained. Multivariate analyses indicated that lodgepole pine production potential was essentially the same on the two sites sampled.
AKNOWLEDGMENTS

I would like to extend my thanks and appreciation to my committee chairman, Dr. Hans R. Zuuring (Forestry), for his assistance and support throughout all phases of this study. I would also like to thank the other members of my committee, Dr. George M. Blake (Forestry), Dr. Don O. Loftsgaarden (Mathematics), and Dr. Robert D. Pfister (Forest Service) for their help and encouragement in the preparation of the study plan, the data analysis, and finally this paper. Special thanks go to Professor James L. Faurot (Forestry) for the time he donated during the data analysis. Without the assistance of two work study students, Mr. Keith Roskens and Mr. Dana Green, the laboratory portion of this study would have taken many months longer to complete, and their help is greatly appreciated. Although the graduate students who traded time with me during the field portion of this study are too numerous to name individually, their help is greatly valued. Financial support was provided by McIntire-Stennis Project B-29.
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CHAPTER I
INTRODUCTION

Throughout much of the twentieth century lodgepole pine (Pinus contorta Dougl.) has been regarded as a weed species because lodgepole pine stands are usually quite dense, and even in the more open grown stands, the trees are generally small. Compared to the much larger ponderosa pine (Pinus ponderosa Laws.) and Douglas-fir (Pseudotsuga menziesii (Mirb.) Franco) trees, the smaller sized lodgepole pine trees have not seemed worth the effort to manage.

Stand density is a basic problem of lodgepole pine management. As the species is both a prolific seeder and a fire species, large seed crops contained in serotinous cones often produce extremely dense stands, and seed crops upwards of 1 million seeds per acre are not uncommon in Montana.

In the past several years there has been an increase in the interest shown lodgepole pine. The species comprises the third largest timber type in the western United States with 14 million acres, and is surpassed only by ponderosa pine with 37 million acres, and Douglas-fir with 32 million acres. Much of the old-growth Douglas-fir and ponderosa pine stands have been cut, and there is
a general trend toward the utilization of smaller size classes. Today lodgepole pine is not as small a tree in comparison to trees of other species as it once was.

Early in this century some foresters began to realize that lodgepole pine has good quality wood. Lodgepole pine is one of the better western conifers. Lodgepole pine logs yield slightly more lumber than comparably sized ponderosa pine logs. In summary, lodgepole pine lumber compares very favorably with ponderosa pine lumber, and the two species are usually interchangeable.

In the northern Rocky Mountains the major portion of information relating to tree and stand production is in terms of volume. Nearly all the existing volume information for lodgepole pine is for the larger merchantable size classes. Very little volume information exists for trees 5 inches (12.7 cm) d.b.h. and smaller, and most of the volume information is concerned with the merchantable portion of the stem, neglecting the stump and top. This study was concerned with biomass, which may be more meaningful than volume when discussing land capabilities.

Since foresters are becoming interested in managing lodgepole pine, and since very little information about the species exists, a study was conducted to obtain biomass information for the smaller size classes of lodgepole pine.¹

¹Biomass refers to the oven-dry weight of tree material. Biomass may be found indirectly by multiplying an object's volume by its specific gravity.
CHAPTER II

OBJECTIVES

The study objectives were:

1. To obtain biomass estimates for small (1.0 cm to 13.0 cm (0.4 inch to 5.0 inches) d.b.h.) individual lodgepole pine trees from two contrasting sites on one area. Biomass estimates included total live above-ground, bole wood, bole bark, live branch, live needle, and cone components

2. To generate models predicting these various biomasses from simple tree measurement data

3. To determine if the lodgepole pine on the two sites is from the same population

4. To convert the individual tree biomass estimates to unit area biomass estimates

This study was concerned only with above-ground biomass as there was not enough time or money to excavate roots.
CHAPTER III
LITERATURE REVIEW

A large amount of biomass literature exists, but there is very little dealing with the biomass of Rocky Mountain species. A few biomass studies have been conducted in Canada, Colorado, and Montana, but the majority of North American studies have been conducted in the eastern United States. Researchers in Japan and Europe have also conducted many biomass studies.

In the United Kingdom Rutter (1955) conducted a study to determine the weights of Scots pine (*Pinus sylvestris* L.) and sitka spruce (*Picea sitchensis* (Bong.) Carr.) seedlings 6 years of age and younger. Rutter felt the rate of dry weight increase was the best indicator of a plant's success in its environment.

Landis and Mogren (1975) studied the biomass of Engelmann spruce (*Picea engelmannii* Parry) in Colorado. Tree height, d.b.h., stem diameter at the base of the live crown, crown length, and crown width were measured on each sample tree. Branchwood and foliage biomasses were determined by direct weighing. Tree wood and bark biomasses were determined by indirect methods, i.e. multiplying stem wood and bark volume estimates by respective specific gravity estimates. Prediction models were developed for
total tree, bole wood, bole bark, branchwood, and foliage biomasses. The measured tree parameters were used as independent variables. Equations involving diameter or its transformation resulted in the better models. Diameter squared multiplied by tree height used as the independent variable resulted in the best models, but for simplicity the published equations predicting both total and component biomasses were all parabolic with diameter squared as the independent variable. The $r^2$ values ranged between 0.88 and 0.98. The models were also used to estimate total tree and component biomasses on an area basis.

Dyer (1967) determined fresh and dry weights for northern white cedar (Thuja occidentalis L.). Regression equations were developed relating the diameter and height of each tree to total tree biomass and various component biomasses. The equations were all linear models in which the common logarithm of each variable was taken. The $R^2$ values for equations predicting dry weights of trees greater than 5.6 inches (14.2 cm) d.b.h. varied between 0.55 and 0.97. Equations of the same type were developed to predict dry weights of trees less than 5.6 inches d.b.h., and the $R^2$ values ranged between 0.89 and 0.96. Dyer also presented tables for total tree and component part fresh and dry weights. Young, Strand, and Altenburger (1964) also developed fresh and dry weight tables, including biomass information on seven Maine tree species.
Krumlik and Kimmins (1972) studied tree biomass of virgin stands in British Columbia. The tree species studied were two species of hemlock (*Tsuga mertensiana* (Bong.) Carr. and *Tsuga heterophylla* (Raf.) Sarg.) and Pacific silver fir (*Abies amabilis* (Dougl.) Forbes). Various tree parameters were measured on each sample tree, and biomass estimates were determined for tree branches, foliage, stem wood, stem bark, and total above-ground components. Diameter squared multiplied by tree height was the best independent variable for predicting bole wood biomass; diameter or basal area was the best independent variable for predicting bole bark biomass, and the prediction of crown component biomasses was best accomplished using diameter, height, crown length, or crown width. The prediction model, with each of the above tree parameters as independent variables, took the form of the logarithmic transformation of the allometric equation. This model using d.b.h. as the independent variable proved to be satisfactory for predicting any tree or component biomass.

Johnstone (1970; 1971) has conducted biomass research into lodgepole pine in Canada. Tree crown width, crown length, d.b.h. and height were used as independent variables for predicting tree total and various component biomasses. Crown component and stem wood and bark biomasses were determined by multiplying their fresh weights by their average moisture contents. The models predicting
total tree and component part biomasses were all logarithmic transformations of the allometric equation. Diameter squared multiplied by tree height was used as the independent variable in all the models, and the lowest $r^2$ value was 0.849.

Moir (1972) conducted a lodgepole pine productivity study in Colorado. As in other biomass studies, Moir determined biomass by indirect means. Moir determined that the productivity of the Colorado Front Range lodgepole pine stands is low, but efficiency in utilization could be increased 10 percent if live branches could be economically harvested.

Brown (1977) developed models predicting live and dead crown biomasses for eleven conifers in northern Idaho and western Montana. Brown developed both polynomial and exponential models using d.b.h., height, crown length, and crown ratio as independent variables. For all eleven species both the live crown and dead crown models' $R^2$ values ranged from 0.84 to 0.98. The polynomial and exponential models predicting lodgepole pine live crown biomass had $R^2$ values of 0.88.

Tree or component part biomasses may be estimated on an individual tree basis and converted to unit area biomass estimates. Two conversion methods are most commonly used, and both methods employ the use of regression models. The mean tree technique assumes trees of average dimensions have average biomasses. A few trees of
average dimension in the area of interest are measured. Their biomasses are determined from regression models, and the area biomass estimates are obtained by multiplying the sample estimates by the number of stems on the area. The every tree summation technique is different in that every tree on the area is measured. Biomass estimates are obtained with regression models, and the sum of the estimates is the area's biomass.

There is some debate as to which of these two methods yields the most reliable estimates. Crow (1971) compared the methods for estimating the biomass of a Jack pine (*Pinus banksiana* Lamb.) stand. The model used to estimate area biomass was the allometric equation with d.b.h. and other tree parameters as independent variables.

The actual biomass of the study area was not determined; it was estimated using the every tree summation technique. If area biomasses were determined by mean tree height, total area biomass was underestimated by 23.4 percent of the every tree summation estimate, and component biomasses were underestimated by 32.5 percent. Area biomass determined by mean tree d.b.h. or mean basal area resulted in underestimates of about 2.1 percent of the every tree summation estimates. Crow concluded that the mean tree technique should not be entirely discounted for estimating area biomass.

Madgwick (1971) also compared these two techniques of area biomass determination. His regression models were logarithmic
transformations of the allometric equation. Madgwick stated that there is little difference in predictive value between the two techniques, but comparisons are meaningless unless the actual biomass of the area is known. The two techniques merely compare each other's biomass estimates without really showing the actual biomass present.

Baskerville (1965) compared the mean tree technique and the every tree summation technique with allometric models; he found the percentages of tree branch and foliage biomasses increased as tree d.b.h. increased, that the percentage of stem wood biomass decreased as d.b.h. increased, and that the bark biomass percentage remained relatively constant as d.b.h. increased. Baskerville stated, therefore, that trees of average dimension would not necessarily have average biomasses, and the best method of obtaining an area biomass estimate would be the every tree summation technique.
CHAPTER IV
METHODS

Description of Study Area

The study was conducted on Lubrecht Experimental Forest, section 1, township 13 north, range 14 west, Montana principal meridian. The study area is composed of almost pure lodgepole pine, but there are a very few isolated western larch (Larix occidentalis Nutt.) and Douglas-fir trees which have survived past fires. A few isolated pockets of subalpine fir (Abies lasiocarpa (Hook.) Nutt.) and Engelmann spruce are found in the more moist draws. Casual observation indicates there is very little tree regeneration of any species.

The topography of the area is rather gentle. The eastern north-south section line runs along a ridgetop at approximately 1890 m in elevation. From this ridge a large spur ridge runs west nearly across the section about one third the distance from the southern section line to the northern. Hence, the majority of the section is divided between a northerly and southerly exposure.

Ten habitat types (as defined by Pfister et al. 1977) are found on the study area, and a partial habitat type map of the area is given (Map 1). Habitat types of the Douglas-fir series occupy
Partial habitat type map of study area.
Section 1, Township 13 north Range 14 west.
most of the southwestern portion of the section. The northwestern portion of the study area is nearly devoid of understory vegetation, apparently due to the extreme numbers of lodgepole pine per hectare. Isolated patches of *Menziesia ferruginea*, *Xerophyllum tenax*, and *Arnica* spp. may be found, but placing the area into one or more habitat types is very difficult. Habitat types of the subalpine fir series occupy the eastern half of the section.

Biomass estimates were obtained from two contrasting sites. The sites of interest were the *Abies lasiocarpa/Xerophyllum tenax* (Abla/Xete) stand and the *Abies lasiocarpa/Menziesia ferruginea* (Abla/Mefe) stand. The Abla/Xete stand is much drier than the Abla/Mefe stand, partly because their aspects differ. The Abla/Xete and Abla/Mefe stands were thought to contain separate populations of lodgepole pine.

These two stands appear to be representative of the Abla/Xete habitat type and the Abla/Mefe habitat type in general. The Abla/Xete stand understory union is dominated by *X. tenax* with varying amounts of *Vaccinium globulare* and *V. scoparium*, but no attempt was made to define the phases of the habitat type in this stand. Traces of *Linnaea borealis* and *M. ferruginea* may also be found, but these two species are confined mainly to ecotones.

The understory union of the Abla/Mefe stand is dominated by *M. ferruginea*.; *V. globulare*, *V. scoparium*, and *X. tenax* are also well represented. Traces of *Alnus sinuata*, *Viola* spp., and *Spirea betulifolia* may also be noted.
Tree regeneration is more abundant on the Abla/Mefe stand, apparently due to the moisture differences between the two stands. Being more moist, the Abla/Mefe stand has several pockets of residual Engelmann spruce and subalpine fir which act as a seed source. The site and community characteristics of these two stands have been quantified as discussed by Pfister (Table 1).

### TABLE 1
SITE AND COMMUNITY CHARACTERISTICS OF THE TWO SAMPLE STANDS

<table>
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<th>Site Characteristics</th>
<th>Abla/Xete Stand</th>
<th>Abla/Mefe Stand</th>
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<tbody>
<tr>
<td>elevation</td>
<td>1713 - 1908m</td>
<td>1664 - 1820m</td>
</tr>
<tr>
<td>slope</td>
<td>8 - 52%</td>
<td>21 - 50%</td>
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<tr>
<td>aspect</td>
<td>197 - 286°</td>
<td>275 - 12°</td>
</tr>
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</table>

<table>
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<th>Community Characteristics</th>
<th>Tree Species</th>
<th>Undergrowth species</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tree Species</td>
<td>(3) Pinus contorta (T) Pseudotsuga menziesii (T) Abies lasiocarpa (T) Larix occidentalis (T-2) Larix occidentalis (T-2) Abies lasiocarpa (T-1) Pseudotsuga menziesii (T) Picea engelmannii</td>
<td></td>
</tr>
<tr>
<td>Undergrowth species</td>
<td>(3) Xerophyllum tenax (2) Vaccinium globulare (2) Vaccinium scoparium (1) Viola spp. (+) Menziesia ferruginea (+) Linnaea borealis (+) Spirea betulifolia (+) Alnus sinuata</td>
<td></td>
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* Numbers and letters are coverage classes. See Appendix II.
Fire has played a major role in the present structure of the lodgepole pine. It appears that not one, but several fires have burned in the study area, as evidenced by the many distinct stands of lodgepole pine, all with different ages and stand densities. If the ages of the sample trees are any indication, the last fire burned about 50 years ago. The fires seem to have kept most of the typical forest pests out of the area; however, lodgepole pine dwarf mistletoe (*Arceuthobium americanum* Nuttall ex Engelmann) has invaded, but its presence is not noticeable to the casual observer.

**Field Procedure**

Total live above-ground biomass and each of the five component part biomasses have been defined specifically for this study, and the definitions are listed in Appendix I. In addition to defining each biomass component, three restrictions were placed on the two populations sampled. As the study was interested only in live biomass, no dead material, other than cones, was included in the samples. Trees with obvious bark voids, insect or pathogenic damage, or poor form (twists, bends, forked tops) were not sampled, and trees forked below d.b.h. also were not sampled.

The Abla/Xete and Abla/Mefe stands were sampled separately. A preliminary study was conducted to obtain a diameter class distribution for each stand and to quantify biomass variability on
each stand so that sample sizes could be obtained. Four diameter classes, each 2.9 cm in width, were defined for the sampling phase of this study. Class I contained trees 1.0 to 3.9 cm d.b.h.; class II included trees 4.0 to 6.9 cm d.b.h.; class III included trees 6.0 to 9.9 cm d.b.h., and class IV included trees 10.0 to 12.9 cm d.b.h. Sample sizes of 23 trees and 13 trees, respectively, were determined for the Abla/Xete and Abla/Mefe stands. Sampling within each stand was stratified by diameter class, and the number of trees sampled in each diameter class on each stand was proportional to the frequencies of each d.b.h. class on each stand.

The sampling scheme was pseudo-random. Points were located at random intervals along six parallel transects such that 23 points fell in the Abla/Xete stand and 13 points fell in the Abla/Mefe stand. At each point the d.b.h. of the nearest tree was measured. If the tree fell into one of the four diameter classes and met the criteria outlined above, the tree was sampled. If the tree was too large, too small, or did not meet the criteria outlined above, the diameter of the next closest tree was measured, and the tree included or excluded as a sample. The process was repeated at each point until a sample tree was located. A few of the diameter classes were filled with the requisite number of sample trees prior to all 36 sample points being located. When a new point was located with the nearest tree falling into a filled class, that sample point was abandoned and another randomly chosen.
At each sample point the elevation, aspect, slope, and tree density were recorded, and the habitat type visually checked against the map. Each sample tree was felled, and the d.b.h. (± 0.1 cm), height, crown length, crown width (± 0.01 m), age at ground level, and the stem diameter at the base of the live crown were measured.

Live branches were clipped and placed in labeled plastic bags. Any live needles or cones on the stem were also placed in these bags. The stem was cut into four sections of equal length, and the diameter outside bark was measured at both ends and the midpoint of each section. The diameter inside bark was measured at the same locations on each section. From the butt end of each section and from the tip of each tree, a 1 cm thick disk was cut and placed in a labeled plastic bag.

**Laboratory Procedure**

The crown material was taken to the laboratory, placed in labeled paper sacks, and allowed to air dry. The needles, cones, and branches of each tree were separated and oven-dried at 100°C for 24 hours. After oven-drying the material was weighed (± 0.01 gm) for direct biomass determination. Due to the vast amount of crown material involved, all material was oven-dried and weighed only once.

The five disks from each tree were placed in a water-filled dessicator, and soaked for 72 hours with a vacuum applied. Fresh
wood and bark volumes occur when the materials are at fiber saturation point, and since volumes do not increase above fiber saturation point, the disks were allowed to water-log.

Fresh volumes (+0.01 ml) were determined using the immersion technique (Krier, 1975). A pan of water was placed on a scale, and the weight of the water determined. A disk was completely immersed in the water, without touching the bottom or sides of the pan, and the additional weight recorded on the scale was the volume of the disk. Disk wood volume was determined in the same fashion once the inner and outer bark was removed, and disk bark volume was found by subtraction. After volume determination the disk wood and bark were air dried, then oven-dried at 100°C for 24 hours, and finally weighed (+0.01 gm). Disk wood and bark were oven-dried and weighed only once.

Biomass may be determined directly as was done with the crown material, or biomass may be calculated by multiplying an object's fresh volume by its specific gravity. The tree stem sections' fresh volumes were determined using Newton's formula,

\[
\text{fresh volume (cm}^3) = \frac{\pi/4(d_1^2 + 4d_2^2 + d_3^2)\cdot L}{6}, \quad (1)
\]
where \( d_1 \) and \( d_3 \) are the diameters in centimeters at each end of a section, and \( d_2 \) is the diameter at the midpoint of the section. \( L \) is the section length in centimeters. Section volumes were calculated using the outside bark diameters. Section wood volumes were determined using the inside bark diameters, and section bark volumes were found by subtraction.

Disk wood specific gravity was determined by dividing the disk wood oven-dry weight by its fresh volume. Disk bark specific gravity was determined in the same manner. Since bole wood and bark specific gravities vary along the stem, the average specific gravities for the wood and bark of each section had to be determined by averaging the wood and bark specific gravities of consecutive disks. The sections' wood and bark volumes were then multiplied by their respective average specific gravities to calculate stem section wood and bark biomasses. Summing for each tree resulted in tree bole wood and bark biomasses. Summation of all five components resulted in total live above-ground biomass.

**Statistical Analysis**

Each stand was analyzed separately by regression analysis. The dependent variables were total tree biomass and each of the five component biomasses, and the independent variables were chosen from the measured tree parameters. According to the literature, diameter,
diameter squared, and diameter squared multiplied by height are the best independent variables for predicting tree and component part biomasses, and consequently were of prime concern.

The developed models were used to predict individual tree biomass and biomass of individual tree components. By using the frequency distributions of the diameter classes on each stand and employing the every tree summation technique, the biomass per unit area was estimated for each stand.

An additional hypothesis: to discover if the two stands are markedly different in lodgepole pine production potential, was also considered. Statistical tests were conducted to determine whether the lodgepole pine from both stands came from the same population.
CHAPTER V
RESULTS

A summary of the field and laboratory portions of this study has been tabulated by listing the means, standard deviations, and ranges of all variables measured or estimated (Table 2). All statistical analyses were conducted at the $\alpha = 0.05$ significance level. The only significant variables in the regression analyses were tree d.b.h. (D), tree height (H), tree stem diameter at the base of the live crown ($D_c$), or combinations of these variables.

A summary of the regression models developed for the Abla/Xete stand is tabulated (Table 3). The graph and associated scatter diagram of the total biomass prediction model is given (Figure 1). The models predicting both total tree and tree wood biomasses are extremely reliable models, as the associated $r^2$ values are very high, and the standard errors are very low. Field application would be simple as the independent variable, $D^2H$, is easy to measure. The model predicting tree bark biomass is also quite reliable. The $r^2$ value is relatively high, and the standard error is low.

The models predicting needle, cone, and branch biomasses are all poor models. The $R^2$ values appear relatively high, but the
<table>
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<th>Variable</th>
<th>Mean</th>
<th>S.D.</th>
<th>Min.</th>
<th>Max.</th>
<th>Mean</th>
<th>S.D.</th>
<th>Min.</th>
<th>Max.</th>
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<td>Wood Biomass (Kg)</td>
<td>22.8475</td>
<td>12.4987</td>
<td>3.2178</td>
<td>43.7012</td>
<td>29.4049</td>
<td>14.8025</td>
<td>8.1220</td>
<td>55.4306</td>
</tr>
<tr>
<td>Bark Biomass (Kg)</td>
<td>1.8168</td>
<td>0.9506</td>
<td>0.3383</td>
<td>3.9882</td>
<td>2.1154</td>
<td>0.7686</td>
<td>0.9681</td>
<td>3.3417</td>
</tr>
<tr>
<td>Needle Biomass (Kg)</td>
<td>0.8621</td>
<td>0.5916</td>
<td>0.1038</td>
<td>2.4263</td>
<td>0.9362</td>
<td>0.4956</td>
<td>0.2468</td>
<td>1.8368</td>
</tr>
<tr>
<td>Cone Biomass (Kg)</td>
<td>0.2759</td>
<td>0.6135</td>
<td>0.0000</td>
<td>2.6856</td>
<td>0.0488</td>
<td>0.0572</td>
<td>0.0000</td>
<td>0.1770</td>
</tr>
<tr>
<td>Branch Biomass (Kg)</td>
<td>0.8455</td>
<td>0.4664</td>
<td>0.0857</td>
<td>2.0076</td>
<td>0.1834</td>
<td>0.7439</td>
<td>0.3965</td>
<td>2.6296</td>
</tr>
<tr>
<td>Tree d.b.h. (cm)</td>
<td>9.2478</td>
<td>2.1065</td>
<td>5.1000</td>
<td>17.7000</td>
<td>9.9385</td>
<td>2.0751</td>
<td>6.6000</td>
<td>12.7000</td>
</tr>
<tr>
<td>Tree height (m)</td>
<td>12.8170</td>
<td>3.1137</td>
<td>5.5500</td>
<td>17.5900</td>
<td>14.1015</td>
<td>3.0843</td>
<td>8.4400</td>
<td>18.4700</td>
</tr>
<tr>
<td>Stem Diameter - Base of Live crown (cm)</td>
<td>6.5348</td>
<td>1.5343</td>
<td>2.5000</td>
<td>9.1000</td>
<td>7.2154</td>
<td>1.2462</td>
<td>4.8000</td>
<td>9.1000</td>
</tr>
<tr>
<td>Tree Crown Length (m)</td>
<td>4.8496</td>
<td>1.4718</td>
<td>1.5800</td>
<td>7.5900</td>
<td>6.4262</td>
<td>1.3866</td>
<td>3.8100</td>
<td>8.4100</td>
</tr>
<tr>
<td>Tree Crown Width (m)</td>
<td>1.0643</td>
<td>0.3405</td>
<td>0.5200</td>
<td>1.5600</td>
<td>1.2538</td>
<td>0.3866</td>
<td>0.6400</td>
<td>1.7100</td>
</tr>
<tr>
<td>Tree Age</td>
<td>90.4783</td>
<td>14.9632</td>
<td>48.0000</td>
<td>104.000</td>
<td>94.2308</td>
<td>8.8803</td>
<td>76.0000</td>
<td>114.000</td>
</tr>
<tr>
<td>Basal Area at sample tree (m²/ha)</td>
<td>7.4783</td>
<td>1.8308</td>
<td>5.0000</td>
<td>12.0000</td>
<td>6.6932</td>
<td>1.4936</td>
<td>4.0000</td>
<td>9.0000</td>
</tr>
<tr>
<td>Stems per Hectare at sample tree</td>
<td>2763.9365</td>
<td>2020.0088</td>
<td>929.0000</td>
<td>10547.0000</td>
<td>1482.5385</td>
<td>349.1389</td>
<td>1017.0000</td>
<td>1977.0000</td>
</tr>
</tbody>
</table>
### TABLE 3
REGRESSION MODELS AND ASSOCIATED STATISTICS BY STAND

<table>
<thead>
<tr>
<th>Abla/Xete Stand $n_1 = 23$</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Dependent Variable</strong></td>
<td><strong>Equation</strong></td>
<td><strong>$R^2$</strong></td>
<td><strong>Standard Error of $y$</strong></td>
</tr>
<tr>
<td>Vegan:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$1.92718 + 0.0198085D^2H$</td>
<td>0.96914</td>
<td>2.53498</td>
</tr>
<tr>
<td>Wood</td>
<td>$1.33317 + 0.0172393D^2H$</td>
<td>0.97907</td>
<td>1.80836</td>
</tr>
<tr>
<td>Bark</td>
<td>$0.11396 + 0.00669656D_{2.45215}$</td>
<td>0.82933</td>
<td>0.39223</td>
</tr>
<tr>
<td>Needle</td>
<td>$-0.11614 + (0.05481D - 0.02839H)D_C$</td>
<td>0.82851</td>
<td>0.24499</td>
</tr>
<tr>
<td>Cone</td>
<td>$-0.35242 + (0.06146D - 0.03721H)D_C$</td>
<td>0.64786</td>
<td>0.36418</td>
</tr>
<tr>
<td>Branch</td>
<td>$0.13364 + (0.04178D - 0.02031H)D_C$</td>
<td>0.73127</td>
<td>0.24177</td>
</tr>
<tr>
<td>Crown</td>
<td>$9.37519 - 3.49819D + 0.28868H + C$</td>
<td>0.35016</td>
<td>0.50610</td>
</tr>
<tr>
<td></td>
<td>$0.35016D^2 - 0.00815198D^2H$</td>
<td>0.45065</td>
<td>0.24177</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Abla/Mefe Stand $n_2 = 13$</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Dependent Variable</strong></td>
<td><strong>Equation</strong></td>
<td><strong>$R^2$</strong></td>
<td><strong>Standard Error of $y$</strong></td>
</tr>
<tr>
<td>Vegan:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$4.22286 + 0.019866D^2H$</td>
<td>0.95299</td>
<td>3.35093</td>
</tr>
<tr>
<td>Wood</td>
<td>$2.23884 + 0.0175969D^2H$</td>
<td>0.97002</td>
<td>2.56290</td>
</tr>
<tr>
<td>Bark</td>
<td>$0.30520 + 0.0176178D^2$</td>
<td>0.82475</td>
<td>0.32178</td>
</tr>
<tr>
<td>Needle</td>
<td>$-0.12576 + 0.0198516D_C$</td>
<td>0.44644</td>
<td>0.36872</td>
</tr>
<tr>
<td>Cone</td>
<td>$-0.25054 + (0.061076 - 0.00405076D_C)D$</td>
<td>0.48062</td>
<td>0.41220</td>
</tr>
<tr>
<td>Branch</td>
<td>$-0.35742 + 0.288021D_C$</td>
<td>0.41115</td>
<td>0.57082</td>
</tr>
<tr>
<td>Crown</td>
<td>$-5.10409 + 1.23524D - 0.0344743DH$</td>
<td>0.51950</td>
<td>0.85553</td>
</tr>
</tbody>
</table>
TB = 1.92718 + 0.0198085D^2

$R^2 = 0.97907$

s.e. = 1.80836

Figure 1. Total Biomass by d.b.h. and Four Height Classes. *Abies lasiocarpa/Xerophyllum tenax* Stand.
standard errors are large, relative to the means of the dependent variables. Field application of these models is limited because of their poor reliability, and the fact that \( D_C \) is difficult to measure accurately. Needle, cone, and branch biomasses were combined to form crown biomass, and a reliable model predicting crown biomass was developed.

A summary of the regression models developed for the Abla/Mefe stand is also tabulated (Table 3), and the graph and associated scatter diagram of the total biomass prediction model is given (Figure 2). The models predicting tree total, wood, and bark biomasses are very reliable as the \( r^2 \) values are high, and the standard errors are low.

The models predicting needle, cone, and branch biomasses are all very poor models. Not only are the \( R^2 \) values very low, but the standard errors are extremely large relative to the means of the dependent variables. Each contains \( D_C \) as an independent variable; therefore, practical application is limited.

The model predicting crown biomass is also a poor model, as it has poor associated statistics. The model could have practical application as the independent variables are easy to measure, but the low \( R^2 \) value and high standard error indicate the model to be rather unreliable.
\[ \hat{T}_B = 4.22286 + 0.0190866D^2 H \]

\[ R^2 = 0.95299 \]

s.e. = 3.35093

Figure 2. Total Biomass by d.b.h. and Four Height Classes. *Abies lasiocarpa/Menziesia ferruginea* Stand.
It is interesting that the Abla/Mefe stand models predicting total, wood, bark, and crown biomasses are remarkably similar to the respective Abla/Xete stand models (Table 3). In contrast the Abla/Mefe stand models predicting needle, cone, and branch biomasses are remarkably dissimilar to the respective Abla/Xete stand prediction models.

The two stands were thought to belong to different populations of lodgepole pine, i.e. the lodgepole pine is not the same on both stands in terms of total tree and component biomasses. A multivariate two sample t-test was conducted. A multivariate normal distribution is defined by its mean vector $\mu$ and its variance-covariance matrix $\Sigma$. As with most parametric analyses of variance, homogeneity of variance between samples is either assumed or tested. The multivariate analog of Bartlett's test for homogeneous variance was used to test the sample based variance-covariance matrices for homogeneity. If homogeneous variance is found, the t-test may be conducted, and if the mean vectors are the same, the conclusion is the two samples come from a common distribution defined by $\mu$ and $\Sigma$. Since conducting the t-test is conditioned upon the outcome of the homogeneity of variance test, the significance levels of the two tests are not the same. Since the t-test was to be conducted at the $\alpha=0.05$ level, the variance test had to be conducted at $\alpha = 0.25$ (Bancroft, 1964).
Both the homogeneity of variance test and the t-test require the variance-covariance matrices to be non-singular. Testing for differences in component and total biomasses of the two stands in a single test results in a linear combination of variables and a singular matrix; hence, four separate hypotheses had to be tested. They were:

1. The lodgepole pine on the two stands is the same population in terms of total tree, wood, and bark biomasses; tree d.b.h., and tree height
2. The lodgepole pine on the two stands is the same population in terms of tree needle, cone, and branch biomasses; tree d.b.h., and tree height
3. The lodgepole pine on the two stands is the same population in terms of tree wood, bark, and crown biomasses
4. The lodgepole pine on the two stands is the same population in terms of tree crown biomass, tree d.b.h., and tree height

Hypotheses 1, 3, and 4 were accepted. In these cases the lodgepole pine populations have the same variance-covariance matrices and the same mean vectors. Hypothesis 2 was rejected. In this case the lodgepole pine populations have different variance-covariance matrices, so the t-test was not conducted. The calculated statistics
and the associated critical values are listed (Table 4); the $X^2$ statistics refer to the variance tests, and the $F$ statistics refer to the t-tests.

<table>
<thead>
<tr>
<th>Table 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>CALCULATED AND CRITICAL CHI SQUARE AND F STATISTICS FROM MULTIVARIATE ANALYSES</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>$H_1$</th>
<th>$X^2_c = 11.99$</th>
<th>$X^{2.75,15} = 18.25$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$F_c = 0.76$</td>
<td>$F.95;5,30 = 2.53$</td>
</tr>
<tr>
<td>$H_2$</td>
<td>$X^2_c = 102.23$</td>
<td>$X^{2.75,15} = 18.25$</td>
</tr>
<tr>
<td>$H_3$</td>
<td>$X^2_c = 7.32$</td>
<td>$X^{2.75,6} = 7.84$</td>
</tr>
<tr>
<td></td>
<td>$F_c = 0.81$</td>
<td>$F.95;3,32 = 2.90$</td>
</tr>
<tr>
<td>$H_4$</td>
<td>$X^2_c = 3.04$</td>
<td>$X^{2.75,6} = 7.84$</td>
</tr>
<tr>
<td></td>
<td>$F_c = 0.48$</td>
<td>$F.95;3,32 = 2.70$</td>
</tr>
</tbody>
</table>

The outcomes of these four tests reflect the differences and similarities of the regression models of the two stands. In terms of total, wood, bark, and crown biomasses, the two stands contain the same population of lodgepole pine, but in terms of needle, cone,
and branch biomasses, the two stands contain separate populations of lodgepole pine.

Acceptance of hypotheses 1, 3, and 4 allows pooling of the two samples, with respect to total, wood, bark, and crown biomasses. The regression analysis was repeated using a combined sample of all 36 observations. A summary of the regression models developed for the combined sample is tabulated (Table 5), and the graph and associated scatter diagram for the combined sample total biomass prediction model is given (Figure 3). The combined sample models predicting total, wood, bark, and crown biomasses have exactly the same form as the respective Abla/Xete stand models, and all four models have very good associated statistics.

The literature review discussed two widely used methods converting individual tree biomass estimates to unit area estimates (metric tons per hectare for this study). The method employed in this study is a combination of the mean tree and the very tree summation techniques. Diameter class frequency distributions for the Abla/Xete stand and the Abla/Mefe stand, respectively, are given (Figures 4 and 5).

Unit area biomass estimates were determined using the midpoint diameters of each d.b.h. class and their associated heights. Tree heights were computed from a combined sample tree height/d.b.h. regression model. The original model was quadratic in d.b.h., but
TABLE 5
COMBINED SAMPLE REGRESSION MODELS

\[ n_0 = n_1 + n_2 = 36 \]

<table>
<thead>
<tr>
<th>Dependent Variable</th>
<th>Equation</th>
<th>( R^2 )</th>
<th>Standard Error of ( \hat{y} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biomass: Total</td>
<td>( 2.55772 + 0.019658D^2H )</td>
<td>0.96384</td>
<td>2.89952</td>
</tr>
<tr>
<td>Wood</td>
<td>( 1.42383 + 0.0175609D^2H )</td>
<td>0.97475</td>
<td>2.15250</td>
</tr>
<tr>
<td>Bark</td>
<td>( 1.25263 + 0.0113944D^{2.22139} )</td>
<td>0.82733</td>
<td>0.36973</td>
</tr>
<tr>
<td>Crown</td>
<td>( 10.651607 - 4.13011D + 0.37999D^2 + 0.500352H - 0.00879356D^2H )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
\[
\hat{TB} = 2.5575 + 0.019658D^2H \\
R^2 = 0.96384 \\
s.e. = 2.89952
\]

Figure 3. Total Biomass by d.b.h. and Four Height Classes. Combined Sample
Figure 4. Diameter Class Frequency Distribution. Abies lasiocarpa/Xerophyllum tenax Stand.
Figure 5. Diameter Class Frequency Distribution. Abies lasiocarpa/Menziesia ferruginea Stand.
the maximum point of the curve fell within the range of the sample data. As this is not appropriate, a transformed linear model was developed,

$$H = 27.10181e^{-6.85034/D},$$  \hspace{1cm} (2)$$

where $H$ is tree height in meters, and $D$ is tree d.b.h. in centimeters.

This model was developed using the height and diameter data collected during the field work. Several trees with heights and diameters outside the range of the sample data were randomly selected and measured, insuring the model's appropriateness throughout the ranges of the lodgepole pine heights and diameters on the study area. No statistics are given as a logarithmic transformation was used; however, the model was rendered bias free through a technique described by Baskerville (1972).

The midpoint diameter was taken from each d.b.h. class on both stands. A corresponding tree height was obtained using equation (2), and the paired d.b.h. and height values were used with the combined sample regression models to obtain estimates of tree total, wood, bark, and crown biomasses.

For each stand the four biomass estimates of each diameter class were multiplied by the number of trees in that diameter class. Summing the biomass values resulted in per hectare estimates of total, wood, bark, and crown biomasses for each stand. A listing of unit
area tree and component part biomass estimates and their respective standard errors is given (Table 6). Unit area estimates of total tree and component part biomasses and their respective standard errors for trees whose diameters are within the range of the sample data are listed (Table 7).
### Table 6

**Total Tree Biomass (Metric Tons per Hectare) by Tree Component and Stand**

<table>
<thead>
<tr>
<th>Source of Biomass</th>
<th>Abla/Xete Stand</th>
<th>Abla/Mefe Stand</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Biomass</td>
<td>185.98 ± 0.22</td>
<td>189.09 ± 0.18</td>
</tr>
<tr>
<td>Wood</td>
<td>162.28 ± 0.16</td>
<td>166.95 ± 0.14</td>
</tr>
<tr>
<td>Bark</td>
<td>11.87 ± 0.03</td>
<td>11.44 ± 0.02</td>
</tr>
<tr>
<td>Crown</td>
<td>21.44 ± 0.09</td>
<td>23.69 ± 0.11</td>
</tr>
</tbody>
</table>

### Table 7

**Total Tree Biomass (Metric Tons per Hectare) by Tree Component and Stand for Trees Within the Range of the Sample Data**

<table>
<thead>
<tr>
<th>Source of Biomass</th>
<th>Abla/Xete Stand</th>
<th>Abla/Mefe Stand</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Biomass</td>
<td>82.66 ± 0.17</td>
<td>35.84 ± 0.09</td>
</tr>
<tr>
<td>Wood</td>
<td>71.01 ± 0.13</td>
<td>31.16 ± 0.07</td>
</tr>
<tr>
<td>Bark</td>
<td>5.70 ± 0.02</td>
<td>2.37 ± 0.01</td>
</tr>
<tr>
<td>Crown</td>
<td>5.38 ± 0.04</td>
<td>3.19 ± 0.02</td>
</tr>
</tbody>
</table>
Complete-tree utilization (using the entire tree from the root hairs to the foliage, consonant with the principles of forest ecology) is a concept which is becoming popular in the eastern United States and northern Europe. The first generation complete-tree harvesters should be in general commercial use by 1980 (Young 1968; 1974); however, complete-tree harvesters are currently being used in the southeastern United States (Jackson 1977). If this concept becomes wide spread, biomass may be the only practical means of quantifying forests and trees because of the extreme size and shape variability of components such as needles, branches, and roots (Young 1966). Biomass is not as dependent upon an object's size and shape as volume.

The amount of biomass present in trees and stands should be useful in forest ecology. The amounts of the various components not only influence the trees themselves, but other portions of the ecosystem. Foliage influences the amount and quality of sunlight and precipitation reaching the understory species and forest floor. Tree foliage influences evapo-transpiration rates of the understory species and the evaporation of water from the soil. Tree foliage
provides much litter fall, and also provides attacking sites for insects and pathogens (Kittredge 1944; Moir and Francis 1972). Photosynthetic rates are a function of the amount of foliage; hence crown biomass is closely related to forest productivity (Brown 1977). Cone biomass is related to the reproductive capacity of trees and stands, and cones provide a food source for birds and small mammals. Tree biomass information coupled with nutrient content information is needed to evaluate nutrient cycling in ecosystems.

Assuming intensified future forest management, tree component biomass measured in the field will be needed to insure efficient tree utilization. Branches of several eastern tree species have been used as a pulp source (Dyer 1967; Young and Chase 1965). While dyes, tannis and medicinals have been obtained from bark for centuries, the true potential of different barks is just now being discovered. Bark of several species has proven to be a very good mulch and erosion controller (Yocum 1972). Bark of the southern pines has displayed exceptional promise as an absorbing material for use on oil spills (Martin, Green, and Hodge 1972; Weldon 1972), and southern pine bark also completely absorbs mill odors from the Kraft pulping process (Martin and Crawford 1972). Barks of many species have made fair to good quality fiberboard (Brooks and Maloney 1972).
Of all tree components, other than bole wood, bole bark is the only component with well established uses. Knowing the amount of bark in a stand prior to harvest would be desirable since many of bark's uses depend upon its handling and processing.

Many times bark is measured after it has been laying around for long periods, and this changes many of bark's chemical and physical properties, not to mention its weight (Martin 1969). Bark is usually measured as weight per thousand board-feet of lumber, cubic-feet of bark per thousand board-feet of lumber, or as weight per cubic foot of volume. These measurements are not comparable without manipulation of log rules; weight is seldom measured as oven-dry, and the degree of compaction in volume measurements is not standardized (Williams 1969). Obviously, much variation and error are present in these measurements, and field biomass measurements may alleviate some of the problems.

Regression Analyses

According to the literature, one of the most common models used to predict tree and component part biomasses is the allometric equation,

\[ Y = AX^B, \quad (3) \]
where $A$ and $B$ are constants, and $Y$ and $X$ are the dependent and independent variables, respectively. Zar (1968) discussed in some detail the use of equation (3) as a biological model. Many researchers use the logarithmic transformation of equation (3),

$$\log Y = \log A + B \log X.$$  \hfill (4)

If data are in some curvilinear form, the transformation produces a linear relationship which is much easier to deal with than the nontransformed equation. While equations (3) and (4) are mathematically equivalent, they are not statistically equivalent. Least squares regression requires that the residuals be normally distributed with a constant variance. Obviously, if equation (3) satisfies these requirements, equation (4) will not; hence, the transformed equation would be inappropriate if used.

The error structure of the data must also be considered when using the allometric model. Most biological data have additive error rather than multiplicative error. If error is additive, the allometric model will be

$$Y = B_0 X^{B_1} + E,$$ or  \hfill (5)

$$\log Y = \log(B_0 X^{B_1} + E),$$ \hfill (6)
where $B_0$ and $B_1$ are population parameters to be estimated and $E$ is the error term. If error is multiplicative, the allometric model will be

$$Y = B_0 X^{B_1} E,$$

or

$$\log Y = \log B_0 + B_1 \log X + \log E.$$  

Clearly, equations (6) and (8) are not equivalent. If error is additive, the transformation is not appropriate as transformation implies multiplicative error.

Before the advent of the digital computer, fitting the allometric model without using the logarithmic transformation was very difficult and time consuming because of the nonlinear nature of the coefficients; the transformation was used as a matter of course. Due to the assumptions of least squares regression, this usually led to erroneous and misleading conclusions. Today there is no reason to use the transformation only for the sake of convenience; the use of one form of the model over the other should be decided upon according to the data's error structure and/or the distribution of residuals, and fitting equation (5) by nonlinear regression is a simple matter with today's computers. However, the distribution of the estimated population parameters obtained from nonlinear models is untabulated; therefore, no inferences about the model may be made.
The basic concern in the regression analyses was to generate simple, reliable, yet biologically sound models. To keep the models simple only linear models were developed. Nonlinear models of the allometric type may provide reliable, biologically sound models, but because of the statistical problems involved, nonlinear models and nonlinear regression were not used in this study.

Polynomial models are not always biologically sound when extended past the range of the sample data; however, a restriction requiring positive intercepts (where possible) was imposed upon all developed regression models. Since tree diameter is usually measured at breast height, a small amount of biomass exists when d.b.h. is zero. The minimum d.b.h. encountered on a sample tree was 5.1 cm; as such, the developed models may not be accurate as d.b.h. approaches zero, but requiring a positive intercept does give a certain amount of biological soundness throughout the height and diameter ranges on the study area.

Many of the original models had negative intercepts, and these models were changed where possible to obtain positive intercepts. These changes were cosmetic in nature, and did not significantly change the reliability of the models involved. The non-integer exponents of the Abla/Xete stand and the combined sample bark biomass models were obtained to give positive intercepts. The exponents were found by regressing the common logarithm of bark biomass
against the common logarithm of d.b.h. However, once the exponent was generated, traditional linear regression was conducted; no statistical bias should be associated with these models.

The scatter diagram and graph of the Abla/Xete stand crown biomass model is given (Figure 6). This model has two incongruities with regard to the other developed models. The first is apparent from Figure 6. The model suggests that if two trees have the same d.b.h. but different heights, the taller tree will have less crown biomass than the shorter tree. While tree genotype, tree age, and site quality probably relate to this phenomenon, the raw data indicate that stand density is also causing the anomaly.

Tree d.b.h. increases as tree height increases, but tree diameter growth is inversely related to stand density. If two sample trees are chosen, each with the same d.b.h., the taller of the two was almost invariably growing under more crowded conditions prior to removal. Since lodgepole pine needles cannot function at low light intensities, trees in dense stands should have smaller crowns than trees growing under more open conditions, and smaller crowns probably mean smaller biomasses.

The second incongruity of this model is associated with the independent variables of the model. All independent variables are significant at $\alpha = 0.05$, except $D^2H$. $D$ is significant at $\alpha = 0.05$, but only if $D^2H$ is already in the model. Deleting these
\[ \hat{CB} = 9.37519 - 3.49819D + 0.28868H + 0.35016D^2 - 0.0815198D^2H \] Total Height

\[ R^2 = 0.89365 \]
\[ \text{s.e.} = 0.50610 \]

Figure 6. Crown Biomass by d.b.h. and Four Height Classes. *Abies lasiocarpa/Xerophyllum tenax* Stand.
two variables results in a drastic reduction in reliability; hence, all four variables were kept.

If one studies the scatter diagram of Figure 6, it is seen that at around 8.5 cm d.b.h. there is a very constricted set of data points. This phenomenon is probably a function of the data and not of the population as a whole. Since the scatter diagram appears quadratic, $D^2$ entered the model first. $H$ entered the model second. If $H$ is held constant at various levels, a family of parallel curves may be drawn through the scatter diagram. Furthermore, all the curves will be symmetric with respect to the crown biomass axis.

$D^2H$ entered the model third, and now $H$ begins to influence the first derivative of the model; thus, the curves of the family are no longer parallel, but the curves are still symmetric with respect to the crown biomass axis so the curves do not intersect. The fact that $D^2H$ is not a significant contributor to the regression model may indicate that the variance of the scatter diagram is rather homogeneous.

$D$ entered the model last, and influenced the curves by shifting them to the right along the d.b.h. axis. Since $D^2H$ is already in the model and $H$ affects the first derivative, each curve in the family is shifted to the right by differing amounts, dependent upon
values of H. This causes each curve to be symmetric with respect to a different line; hence, the curves will intersect, reflecting the constricted data points of the scatter diagram.

D is an insignificant variable without $D^2H$ because if D entered the model prior to $D^2H$, H would not affect the first derivative. As such, D would shift to the right parallel curves, all symmetric to the same line; the curves would not intersect, and the constricted data points would not be reflected by the model.

The Abla/Mefe stand and the combined sample crown biomass models both show the same height, d.b.h., crown biomass anomaly as the Abla/Xete stand model; however, all independent variables are significant at $\alpha = 0.05$. That $D^2H$ should be significant in the combined sample model may indicate significant heterogeneity in the scatter diagram.

**Multivariate Analyses**

Since a habitat type is the sum of the physical environment expressed in terms of the climax plant association, one cannot define a habitat type using six variables measured from a successional stage in the development of that habitat type; hence, acceptance of hypotheses 1, 3, and 4 in no way implies that the Abla/Xete stand and the Abla/Mefe stand are the same. Acceptance of the hypotheses does imply that for this particular stage of succession, the lodgepole
pine trees on both stands do belong to the same population, in terms of the appropriate variables. A lodgepole pine management implication may be seen. Lodgepole pine d.b.h., height, and the interaction of these two variables are the same on both stands. Therefore, trees of the same dimension both stands should have the same biomasses. If the number of lodgepole pine stems per hectare and the diameter distributions are controlled such that they are the same on both stands, one should expect to harvest equal amounts of lodgepole pine fiber per hectare per diameter class from both stands.

There is one problem with accepting the three hypotheses. All calculated F values are less than one. If the null hypothesis is true, the expected value of F is one. As such it is disquieting that all calculated F values are less than one. Why this has occurred is not known, and acceptance of the hypotheses may be dangerous; however, acceptance will be considered correct. If combined sample scatter diagrams are made by plotting total, wood, bark, and crown biomasses against d.b.h., there is no data separation. All 36 sample points fall in the same band. Principle component analysis showed no data separation between stands.

**Biomass per Hectare**

Some irregularities exist for the data shown in Tables 6 and 7. As the diameters sampled in this study (5.0 cm < d.b.h. < 13.0 cm)
are a subset of the full d.b.h. range on the study area, the data
of Table 6 were acquired through extrapolation; this is usually not
appropriate. The data were developed strictly out of curiosity,
and no conclusions will be drawn. If the data are reasonably correct,
they may support the theory that unmanaged stands of the same species
do tend towards similar amounts of tree biomass. While the data of
Table 6 may be erroneous, it seems reasonable that the trend may be
correct. The diameter class distributions on the two stands appear
such that the larger number of large trees on the Abla/Mefe stand
balance out the larger number of small trees on the Abla/Xete stand.

Both Tables 6 and 7 illustrate that the predicted component
biomasses do not sum to the predicted total biomasses. The developed
models are not all of the same form. Multiplying the individual
tree biomass estimates by the number of stems in the diameter classes
also renders the predicted component biomasses nonadditive relative
to the predicted total biomasses.

The reported standard errors (Tables 6 and 7) also present
problems. Very little work has been conducted regarding the structure
of this type of standard error. In matrix notation, the formula
used to obtain the standard error is

\[ s_{Tj} = \sqrt{V(T_j)} = \sqrt{\sum_{i=1}^{14} n_i (s_j^2 + \frac{L_i}{(X'X)^{-1}} L_i^2)} \]  \( (9) \)
where \( V(T_j) \) is the error variance of the per hectare total tree, wood, bark, or crown biomass estimate; \( n_i \) is the number of stems per hectare in the \( i \)th d.b.h. class; \( s_j^2 \) is the estimated error variance of the combined sample total, wood, bark, or crown biomass model; \( L_j \) is a vector containing numerical values of the independent variables for the \( i \)th d.b.h. class, and \((X'X)^{-1} s_j^2 \) is the variance-covariance matrix of the regression coefficients for each of the combined sample models.

Independence between d.b.h. classes is assumed. This may be an incorrect assumption, but assuming dependence between classes requires knowledge of the covariances between classes. Quantifying these covariances is no trivial task.

One assumption of least squares regression is that the independent variables be known without error. Since the tree heights used to obtain per hectare biomass estimates were obtained through double sampling, the assumption is violated. The variances associated with the estimated height values were not considered in equation (9).

One other problem with these standard errors is that the tree count for each d.b.h. class is a random variable. The variance associated with the tree count is unknown and not considered in equation (9).

These problems indicate areas which need further investigation. As all the sources of variation were not considered in equation (9), little faith should be put in the reported standard errors. The
errors were reported because few other researchers even attempt to quantify the variance associated with total estimates, obtained by expanding individual estimates.

Comparisons with Other Studies

The results of this study may be compared to the results of other lodgepole pine biomass studies. Johnstone (1970; 1971) studied lodgepole pine trees considerably larger than the trees sampled in this study; however, the diameter ranges of the two studies do overlap slightly. Johnstone's prediction models contain $D^2H$ as the independent variable, and he reports no height data. Comparisons with his study are, therefore, somewhat difficult. Assuming that Johnstone's minimum reported biomass values correspond to the sample trees with diameters of 4 (10.2 cm) and 5 (12.7 cm) inches, all his reported minimum biomass estimates correspond fairly closely with the biomass estimates of this study obtained from trees 10 cm d.b.h. Johnstone's branch biomass estimates are much lower than those found in this study, however.

Moir (1972) conducted a lodgepole pine productivity study, and Brown (1977) developed crown biomass prediction models for lodgepole pine. The results of these two studies are compared with the results of this study (Table 8). Biomass estimates for this study were obtained using combined sample models and equation (2). Biomass
TABLE 8
COMPARISON OF REGRESSION BIOMASS ESTIMATES (Kg)
BETWEEN THREE STUDIES

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<th>d.b.h.</th>
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<td></td>
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<td>Crown Biomass</td>
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estimates for Brown's study were obtained using his polynomial crown model. This study's crown biomass estimates are directly comparable to Brown's estimates, but comparison of this study and Moir's study are not directly comparable as Moir used a logarithmic transformation
to develop his models, and Moir's total above-ground biomass estimates include dead branches and needles.

Moir's results and this study's results are quite different, and in every case Moir's estimates are the lower. Since Moir worked in the Colorado Front Range, and this study was conducted in the Garnet Mountains of Montana, one would not necessarily expect the biomass data to be similar. The Colorado Front Range is more xeric than the Garnet Mountains. This probably accounts for much of the difference between the data sets. Phenotypically, Colorado lodgepole pine is quite different from lodgepole pine found in west central Montana. Genetic differences in the two populations may explain some of the observed differences.

Brown's crown biomass estimates and this study's estimates do not agree well, and two reasons exist for the differences. Brown sampled over wider geographical and environmental ranges, and he sampled stands displaying greater variations in structure. As such all of Brown's models are much more generalized than the models developed in this study. While Brown sampled in a d.b.h. range from 3.0 to 45.0 cm, he was interested in a good fitting model only above 25 cm d.b.h.; therefore his polynomial crown biomass model may display a rather sloppy fit at the lower diameters.
CHAPTER VII
CONCLUSIONS AND SUMMARY

Reliable models predicting total live above-ground, bole wood, and bole bark biomasses were developed for both stands from relatively small sample sizes. While sample sizes of 23 and 13 trees appear rather small, sample sizes much larger could prove prohibitive in this type of research.

The models predicting needle, cone, and branch biomasses on both stands are poor models. With the collected data these are the best models obtainable with stepwise linear regression, but the models are unsuitable. For descriptive regression $D_c$ may be an appropriate variable, but measurement of $D_c$ is very difficult without climbing or falling the tree, so practical application of these models is limited. Several of these models have negative intercepts, making the models unsound.

Larger sample sizes might help improve these models by obtaining a better estimate of variation, but perhaps some other sampling scheme would be more appropriate. The lodgepole pine on both stands displays various amounts of stagnation which may cause much variation in crown configuration, and therefore, much variation in needle, cone, and branch biomasses. Perhaps stratifying samples
by crown position or some measure of tree crowding would be beneficial to the development of models predicting these three biomass components. Summing needle, cone, and branch biomasses, and developing a crown biomass prediction model gives much better results as much of the variation in needle, cone, and branch biomasses seems to be masked by the summation.

The crown biomass models for the Abla/Xete stand and the combined sample are both reliable models, but the crown biomass model for the Abla/Mefe stand is very unreliable. Perhaps there is less crown configuration variation on the Abla/Xete stand, or perhaps the larger sample sizes of the Abla/Xete stand and combined sample reduced the unexplained variation.

For this stage of succession, both sampled stands have the same population of lodgepole pine, in terms of total, wood, bark, and crown biomasses, but the two stands represent different populations in terms of needle, cone, and branch biomasses.

Several reasons may exist for the differences in these three biomass components. The interaction of the three variables may be different between the two stands. Disregarding covariance, the two stands are producing different amounts of needle, cone, and branch biomasses, and these differences could be caused by variations in stand densities, genetic differences, overall differences in stand vigor, or a myriad of environmental differences.
Under management these two stands should produce about the same amounts of lodgepole pine fiber per hectare, as tree height, d.b.h., and their interaction are the same on both stands.

In summary, the study was conducted to develop models predicting total live above-ground biomass and various component biomasses for lodgepole pine trees from two contrasting sites.

The sampling scheme was pseudo-random, and 23 trees were sampled from the Abla/Xete stand and 13 trees from the Abla/Mefe stand. In the laboratory crown component biomasses were determined by direct weighing, but stem wood and bark biomasses were determined through volume conversion.

Regression models were developed separately for each stand; however, the two stands were found to contain a single population of lodgepole pine in terms of selected variables. As such the two samples were combined, and the regression analysis was repeated. The combined sample models were used with diameter class frequency distributions to calculate total, wood, bark, and crown biomasses per hectare for both stands.
APPENDICES
APPENDIX I

DEFINITIONS OF BIOMASS COMPONENTS

1. Bole wood -- Bole wood is the wood of the stem from ground level to stem tip. Bole wood biomass is referred to simply as wood biomass.

2. Bole bark -- Bole bark is the inner and outer bark of the stem from ground level to stem tip. Bole bark biomass is called bark biomass.

3. Live branches -- Live branches are all wood and bark material of the living primary and secondary branches. All bud formations are also included in live branch biomass. To facilitate sampling branch wood and bark were not separated. Live branch biomass is called branch biomass.

4. Live needles -- Live needles are all needle and fascicle sheath material of all living needles on both the tree stem and all living branches. Live needle biomass is called needle biomass.

5. Cones -- Tree cones include all female fruiting material, both alive and dead, on both the tree stem and all branches, and seeds of serotinous cones. While dead
branches were ignored in this study, cones attached to dead branches were sampled as many of these cones were serotinous and therefore contained seed. Male cones were removed from the sample trees and discarded.  

6. Total tree -- The combination of the above five component biomasses is defined to be total live above-ground biomass. For convenience, this is referred to as total biomass.
APPENDIX II

COVERAGE CLASSES DEFINED BY PFISTER, ET AL. (1977)
FOR DEFINING HABITAT TYPES IN MONTANA

+ = present in stand but not in plot
T = 0 to 1% coverage in plot
1 = 1 to 5% coverage in plot
2 = 5 to 25% coverage in plot
3 = 25 to 50% coverage in plot
4 = 50 to 75% coverage in plot
5 = 75 to 95% coverage in plot
6 = 95 to 100% coverage in plot
LITERATURE CITED


