A test of alternative estimators for volume at time 1 from remeasured point samples

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Two estimators for volume at time 1 for use with permanent horizontal point samples are evaluated. One estimator, used traditionally, uses only the trees sampled at time 1, while the second estimator, originally presented by Roesch and coauthors (F.A. Roesch, Jr., E.J. Green, and C.T. Scott. 1989. For. Sci. **35**(2): 281-293), takes advantage of additional sample information that becomes available at time 2. In this test the Roesch *et al.* estimator was always lower in sum of squared differences and sum of absolute differences for board foot and cubic foot volume than the traditional estimator. In addition a simulation revealed no discernible bias for the Roesch *et al.* estimator over the traditional estimator.

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Deux estimateurs de volume au temps 1 utilisés pour des points-Cchantillons permanents horizontaux sont évalués. Un estimateur traditionnel utilise seulement les arbres-Cchantillons au temps 1 alors que le second, présenté originalement par Roesch *et al.* (F.A. Roesch, Jr., E.J. Green, and C.T. Scott. 1989. For. Sci. **35**(2): 281-293) prend avantage de l'information Cchantillonale additionnelle qui devient disponible au temps 2. Dans ce test, l'estimateur de Roesch *et al.* Ctait plus bas dans la somme des carrés des différences et la somme des differences absolues pour le pied de planche et le volume en pieds cubes que l'estimateur traditionnel. De plus, une simulation n'a révélé aucun biais mesurable entre l'estimateur de Roesch et al. et l'estimateur traditionnel.

[Traduit par la redaction]

Introduction

Perhaps the most important question to foresters is How is the forest changing? In an effort to answer this question much energy has been committed to taking the same measurements at the same places over a long period of time. Usually this results in the most efficient way to estimate change. A familiar representation of net change in a forest is found in the components of growth equation presented by Meyer (1953):

$$[1] \quad V_2 - V_1 = S + I - M - C$$

where

V_i is the volume at time i

S is survivor growth

I is ingrowth

M is mortality

C is cut

Equation 1 partitions the change in volume from time 1 to time 2 into four mutually exclusive components. Roesch et al. (1989) presented new compatible groupings of estimators for these components for use with remeasured horizontal point samples.

Thousands of permanent horizontal point samples have been established worldwide. This use of horizontal point samples for permanent forest inventories has been challenged lately (e.g., see Green 1992). The arguments usually center around the increased complexity of point samples over fixed-area plot samples. One might question the value of introducing this increased complexity to attain increased efficiency for only those variables that are proportional to tree basal area. This paper is not intended to defend or criticize the use of permanent point samples; we simply acknowledge the need for efficient estimators when this sample design is used for a continuous inventory.

Compatibility of the estimators of the components is both desirable and logical; volume at time 1 plus net change does equal volume at time 2, so it seems this relationship should also hold for the estimators. Very often, estimators of these components that were chosen because of their desirable statistical qualities (i.e. unbiasedness and low variance) were not compatible. Practitioners, who encountered a situation in which the "best" estimates of the components did not sum to the "best" estimate of net change, understandably questioned the validity of the estimates. The compatible grouping of estimators originally presented in Roesch *et al.* (1989) and given below relied on an estimator of time 1 volume that utilized information not available until time 2 to maintain compatibility, although the analysis in that article had been limited to the growth estimators. The implicit assumption was
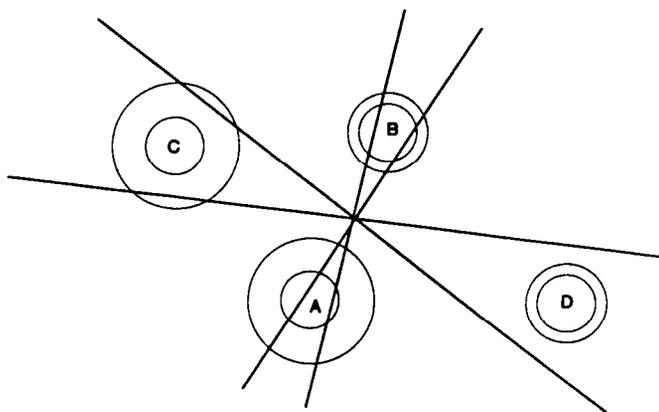
FIG.1. Basal areas of four trees at times 1 and 2 in close proximity to a sample point. The inner circles represent basal area at time 1, and the outer circles represent basal area at time 2. The four trees were an equal size at time 1. Trees B and D have the same basal area at time 2, while the basal area of trees A and C are greater and equal to each other at time 2. Trees A and B are distance X from the point center, while trees C and D are a farther distance (Y) from the point center. The small angles are all equal and represent the sampling angle.

that if the estimator of each component of growth is either improved or unchanged, then the time 1 estimator of instantaneous volume must also be improved since the two groups of estimators are complementary. We now present an analysis of the time 1 volume estimator presented in that work which shows that this is indeed the case.

Definitions

We will use the following definitions of Martin (1982) for the six sample categories encountered in remeasured point samples:

o	The sample of trees that were below minimum DBH (nonmerchantable) and not sampled (out) at the first measurement but above minimum DBH (merchantable) and sampled (in) at the second measurement
n	The sample of trees that were above minimum DBH and out at the first measurement but grew sufficiently to be in at the second measurement
i	The sample of trees that were below minimum DBH and in at the first measurement but above minimum DBH by the second measurement
s	The sample of trees that were in and above minimum DBH at both measurements
m	The sample of trees that were in and above minimum DBH at the first measurement but die before the second measurement
c	The sample of trees harvested between measurements and otherwise analogous to mortality trees

Then and *s* samples are drawn from the population of survivor trees, while the *o* and *i* samples are drawn from the population of ingrowth trees. The *n* and o samples are confounded and initially indistinguishable. One must infer the population from which each sample tree was drawn.

In Martin (1982) notation utilizing these definitions appears. We will use that notation as it was later augmented in Roesch *et al.* (1989). The estimator is obtained by multi-

plying a constant K with the sum of the volume (or any other tree attribute) to basal area ratios (VBAR) constructed in each case as described below:

i	Estimate obtained when the time 2 (final) volumes are divided by the final basal areas of trees in the i sample
i'	Estimate obtained when the final volumes are divided by the time 1 (initial) basal areas of trees in the i sample
o	Estimate obtained when the final volumes are divided by the final basal areas of trees in the *o* sample
n_2	Estimate obtained when the final volumes are divided by the final basal areas of trees in the *n* sample
n_1'	Estimate obtained when the initial volumes are divided by the final basal areas of trees in the *n* sample
s_2	Estimate obtained when the final volumes are divided by the final basal areas of trees in the *s* sample
s_1'	Estimate obtained when the initial volumes are divided by the final basal areas of trees in the *s* sample
s_1	Estimate obtained when the initial volumes are divided by the initial basal areas of trees in the *s* sample
m	Estimate obtained when the initial volumes are divided by the initial basal areas of mortality trees
c	Estimate obtained when the initial volumes are divided by the initial basal areas of cut trees

Van Deusen *et al.* (1986) showed that the published estimators for survivor growth (including the one that they present) and ingrowth differed by the placement of an error term

$$[2] \quad \xi = s_2 - s_2' + n_2$$

Roesch *et al.* (1989) proposed estimators for S, *I*, and V_1 and showed how one compatible grouping of estimators

$$[3] \quad \hat{V}_2 - V_1^{**} = \hat{V}_2 - (\hat{V}_1 + \xi_1)$$

$$= s_2 - s_1 + i + 0 + n_2 - m - c - \xi_1$$

$$= \hat{I}_P + s^{**} - m - c$$

where $\hat{I}_P = i + o$ and $S^{**} = s_2 - s_1' + n_2 - n_1'$, subdivides ξ into a time 1 yield component

$$[4] \quad \xi_1 = s_1' - s_1 + n_1'$$

and a growth component

$$[5] \quad \xi_G = (s_2 - s_1') - (s_2' - s_1) + (n_2 - n_1')$$

This compatible grouping of estimators assigns each error term to its respective component. This grouping was shown by Roesch *et al.* (1989) to be unbiased if the estimator of

$v_1(n_i)$, where $v_t(z_i)$ is the volume at time t of the ith tree in the z sample, is unbiased and will remain compatible regardless of bias because the estimators are complementary.

The growth estimators were then compared empirically in Roesch *et al.* (1989), using point samples of varying basal area factor (BAF) drawn from one-fifth acre (1 acre = 0.40 ha) plot data. In that paper, we used the known rather than the estimated values of $v_1(n_i)$ with the justification that the intent was not to determine the best method of estimating the values of $v_1(n_i)$. In this paper we demonstrate that once the problem of obtaining unbiased estimates of $v_1(n_i)$ is conquered, improved estimates of V_1 are obtainable. We compare the Roesch *et al.* (1989) estimator of the volume at time 1

$$[6] \quad V_1^{**} = (\hat{V}_1 + \xi_1)$$
$$= s_1' + n_1' + m + c$$

with the traditional estimator of volume at time 1

$$[7] \quad \hat{V}_1 = s_1 + m + c$$

If we wish to estimate previous volume, ignoring mortality and cut, we have two levels of information on survivor trees available from remeasured horizontal point samples, the s sample and the n sample. We have measured previous volume on only the trees in the s sample, while those trees in the n sample improve our estimate of the number of trees present at time 1. Since the s sample is usually large, it seems the relationship between $v_1(s_i)$ and $v_2(s_i)$ should be easily established.

However, one difficulty that should not be ignored while using V_1^{**} is that sampling of the survivor trees by n is biased toward faster growing trees. This occurs because the "new" sample (e.g., those trees not measured until time 2) selects trees proportional to basal area growth ($(b_2 - b_1)/b_2$, where b_t is the basal area at time t), while the "old" sample (those trees measured both times) selects trees proportional to basal area at time 1 (b_1/b_2). Therefore, naive application of a prediction based on the growth of trees in the old sample to trees in the new sample will result in underprediction of the growth on trees in the new sample or overprediction of $v_1(n_i)$ and $v_1(o_j)$. This selection of the new sample is shown by the example in Fig. 1.

All four trees in Fig. 1 are exactly the same size at time 1 and live at least until time 2. Trees B and D are growing slowly and at the same rate. Tree B is distance X from the point center and sampled at time 1, while tree D is a farther distance (Y) from the point center and not sampled. Trees A and C are growing faster than trees B and D and at the same rate as each other. Tree A is distance X from the point center, while tree C is distance Y. Both trees at distance X (A and B) will be included in the old sample. The faster growing tree at distance Y (tree C) will be included in the new sample and the slower growing tree (D) will not be sampled at all. Therefore, in a given time 2 DBH class, the faster growing trees are sampled more heavily in the new sample than the slower growing trees. Lappi and Bailey (1987) provide a thorough introduction to this problem after noting an observation by Van Deusen (1986) that the point sampling distribution of diameter is obtained by weighting the original distribution.

The severity of this bias is dependent upon the variance of survivor growth since time 1 of trees of a particular size at time 2, because as the variance of growth increases so will the difference between trees in the s sample and the n sample. Therefore this bias would increase as time between inventories and the heterogeneity of trees in the population increase.

There are a few approaches to control this bias. For example, if a time 1 volume prediction is made for a tree in the n sample that is greater than the volume corresponding to a borderline tree (i.e., one that would just be in the point sample), the volume could be set to that of a borderline tree because we know the tree was smaller than borderline at time 1 by the definition of n. Using this method, overprediction would still occur; however, it would be reduced without excessive effort.

Roesch (1988) presented an algorithm designed to eliminate this bias; however, it was somewhat convoluted. A formal development of the weighting necessary to predict the basal area at time 1 for trees measured for the first time at time 2 using trees measured both times appears in Roesch and Van Deusen (1992). Only a slight modification of this development is needed to predict the time 1 volume/time 2 basal area ratio (V1BAR) for trees not measured at time 1. The results will show that this weighting was extremely successful in that no bias is detectable in the time 1 estimator which relies on these predictions.

Estimator evaluation

Data description
The data were the same as those used in Roesch *et al.* (1989). Fifty-three circular, concentric one-tenth acre pulpwood plots and one-fifth acre sawlog plots were established in 1968 and remeasured in 1981 in Hancock County, Maine, by the USDA Forest Service Northeastern Forest Experiment Station. All trees that were at least 5 in. (1 in. = 2.54 cm) DBH were measured on the inner tenth acre, while trees of sawlog size (at least 9 in. DBH for softwoods and at least 11 in. DBH for hardwoods) were measured on the outer tenth acre. Table 1 shows the diameter distribution of the measured trees at each point in time. Cubic foot and board foot volumes were calculated using individual tree volume equations developed by Scott (1979, 1981). The fifth acre plots were expanded to determine per acre values for sawlog-sized trees, while the tenth acre plots were expanded for per-acre values of pulpwood-sized trees.

The position of cut and mortality trees had previously been deleted from the data set, so we randomly placed these trees on the plots. Since it was known whether each tree had been on the inner or the outer tenth-acre plot, we randomly placed the trees accordingly. There were also seven trees that had been missed at time 1. Values for volumes and basal areas at time 1 for these trees were assumed to be equal to the median of the respective values for trees of similar characteristics at time 2; i.e., the time 1 median DBH of all trees within ±0.1 in. DBH at time 2, the time 1 median cubic foot volume of all trees within f0.2 ft^3 (1 ft^3 = 0.03 m^3) at time 2, and the time 1 board foot volume of all trees within ±1 board ft (1 board ft = 2.4 dm^3) at time 2.

Methods
Point samples were drawn from the plot data in a manner described in Roesch *et al.* (1989). We took a point sample

TABLE 1. The diameter distribution of trees measured in 1968 (time 1) and 1981 (time 2) on the 53 plots in Hancock County, Maine, given as number of trees per acre (N), percent of total (%), and cumulative percent (Cum. %)

	Time 1				Time 2		
DBH	N	%	Cum.	%	N	%	Cum. %
5	42.5	17.7	17.7		40.2	14.8	14.8
6	57.6	24.2	41.9		61.0	22.5	37.3
7	37.6	15.8	57.7		43.3	15.9	53.2
8	28.1	11.8	69.5		30.5	11.2	64.4
9	22.2	9.3	78.9		28.2	10.4	74.8
10	17.1	7.2	86.0		18.7	6.9	81.7
11	11.7	4.9	90.9		15.9	5.8	87.5
12	6.6	2.8	93.7		11.7	4.3	91.8
13	6.5	2.7	96.5		6.7	2.5	94.3
14	2.8	1.2	97.5		5.9	2.2	96.5
15	2.5	1.0	98.7		2.1	0.8	97.2
16	1.6	0.7	99.3		2.7	1.0	98.2
17	0.7	0.3	99.6		2.1	0.8	99.0
18	0.1	0.0	99.6		1.2	0.4	99.4
19	0.2	0.1	99.7		0.8	0.3	99.7
20	0.2	0.1	99.8		0.0	0.0	99.7
21	0.1	0.0	99.8		0.1	0.0	99.7
22	0.2	0.1	99.9		0.2	0.1	99.8
23	0.0	0.0	99.9		0.1	0.0	99.8
24	0.0	0.0	99.9		0.2	0.1	99.9
26	0.1	0.0	99.9		0.0	0.0	99.9
27	0.2	0.1	100.0		0.0	0.0	99.9
29	0.0	0.0	100.0		0.3	0.1	100.0

from plot center, varying the basal area factor (in increments of 5) from 10 to 50 ft^2/acre. We assumed that the expanded plot values were the true board foot and cubic foot volumes per acre for the area around each plot.

The squared differences, absolute differences, and arithmetic differences' between the estimate from each estimator and the "truth" on each plot were summed over the 53 plots for each BAF considered and will be referred to as the SSD, SAD, and SD, respectively. The SD gives an indication of the bias of an estimator. The SAD and SSD include a bias component and a precision component.

Because of the loss of primary information, the exact locations of cut and mortality trees were not known. It was known that a tree was somewhere on the inner tenth acre if it was sampled and it was smaller than sawlog size. This problem could be dealt with in a number of ways. First, mortality and cut could be ignored completely in the evaluation of the estimators for V_1. This is reasonable because mortality and cut trees play the exact same role in both estimators, although a small effect would be seen in the sum of squared error (i.e., differences would be slightly exaggerated, although the order should not change). Because of this effect and because mortality and cut trees can represent a large part of the information available about a forest, we did not choose this approach. Another approach would have been to locate gaps within the plots at time 2 and randomly locate the mortality and cut trees within these gaps. We did not use this approach because it seemed too subjective and distracting for this study.

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'Difference = plot value − estimate; therefore a positive difference indicates underprediction.

Instead, we placed the trees in a random location on the inner or outer tenth acre plots, according to which they were known to be on. In reality, cut trees are never randomly located on a plot and mortality trees are seldom randomly located. Both of these components of growth are more likely to display clumped spatial distributions. However, they could possibly be located a random distance from point center, since trees are not chosen for harvest by their proximity to a sample point. As we mentioned above, regardless of where the mortality and cut trees are located, the mortality and cut trees will be used in the same way by each estimator of V_1 at a particular BAF. The effect on the judgement of the estimators should therefore be minimal and much smaller than the effect of ignoring these trees.

A slight modification of Roesch and Van Deusen (1992) shows us that to estimate the time 1 VBAR of trees in the new sample, the regression of interest is the expected value of v_1/b_2 given v_2/b_2 under the sample domain. Given the large sample of all trees of a particular merchantability class measured at time 2, the probability that a particular tree was not measured at time 1 (i.e., it is in the new sample) is equal to $(b_2 - b_1)/b_2$. So the expected value of VlBAR for trees of a particular VBAR at time 2 in the new sample (e.g., the regression of VlBAR on VBAR at time 2) can be determined using the fundamental properties of conditional expectation:

$$[8] \quad E_{\text{new}}\left[\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right] = E\left[\left[\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right] \,\middle|\, \text{new}\right]$$

which is equal to the expectation of v_1/b_2 given v_2/b_2 and being in the new sample divided by the expected value of being in the new sample:

$$[9] \quad E_{\text{new}}\left[\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right] = \frac{E\left[\left[\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right], \text{new}\right]}{E[\text{new}]}$$

Therefore, by the definition of expected value

$$[10] \quad E_{\text{new}}\left[\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right] = \frac{\int_0^\infty \frac{v_1}{b_2}\left(\frac{(b_2 - b_1)}{b_2}\right) f\left(\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right) d\left(\frac{v_1}{b_2}\right)}{\int_0^\infty \left(\frac{(b_2 - b_1)}{b_2}\right) f\left(\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right) d\left(\frac{v_1}{b_2}\right)}$$

$$= \frac{E\left[\frac{v_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right] - E\left[\frac{v_1 b_1}{b_2^2} \,\middle|\, \frac{v_2}{b_2}\right]}{1 - E\left[\frac{b_1}{b_2} \,\middle|\, \frac{v_2}{b_2}\right]}$$

Note that E_i indicates the expected value in sample domain i, and if E is unsubscripted, the expectation is over the entire population. In [10] we have obtained the regression line of interest through a linear combination of three easily obtained regression lines. To separate the o and n samples we also need to predict the time 1 basal areas of the new sample from a
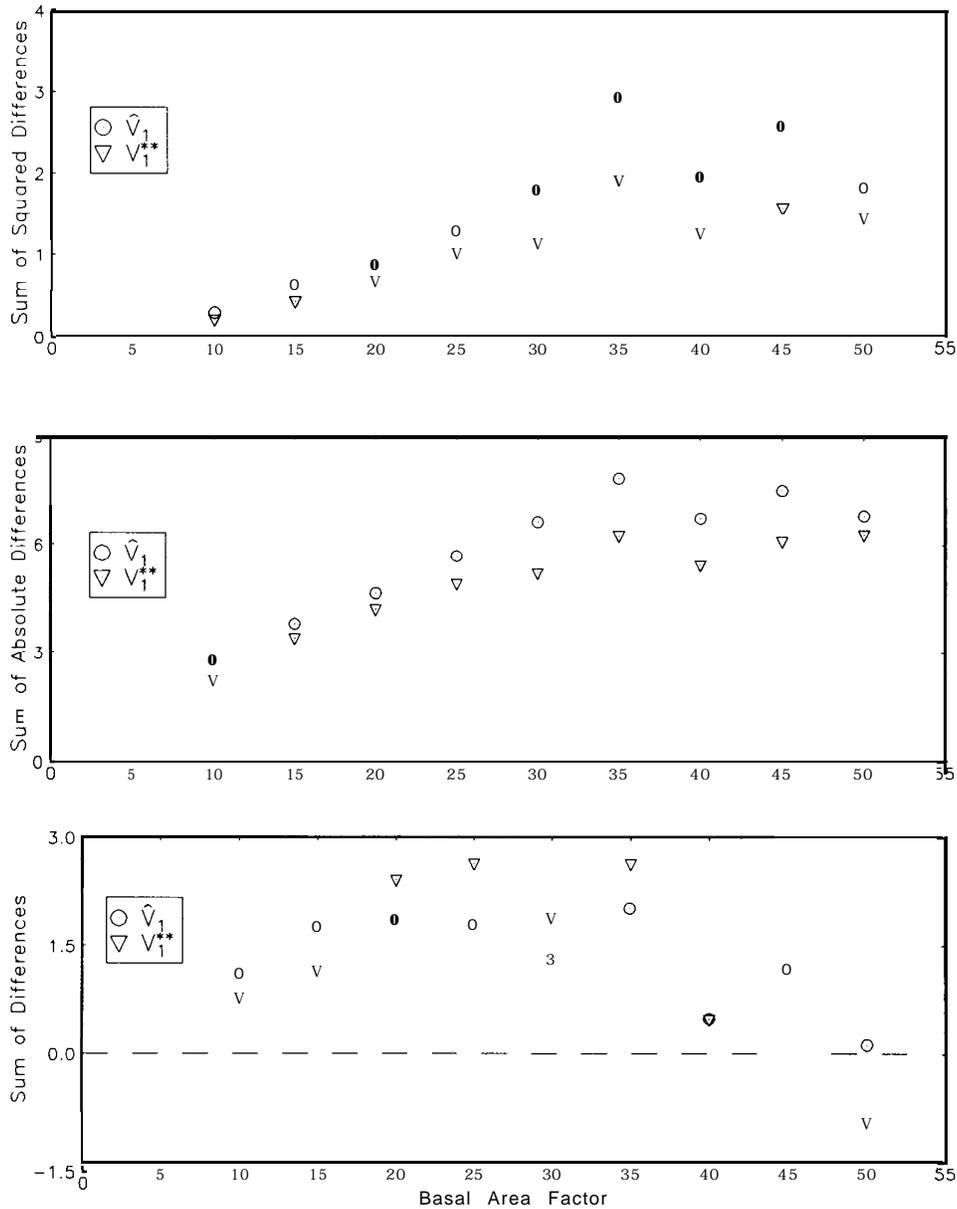
FIG. 2. The sums of squared differences ($\times 10^{-8}$), absolute differences ($\times 10^{-4}$), and differences ($\times 10^{-4}$) between the estimators of board foot volume of sawlog-sized trees at time 1 and the fixed area plot values versus basal area factor.

regression involving the old sample. Roesch and Van Deusen (1992) showed

$$[11] \quad E_{\text{new}}[b_1 \mid b_2] = \frac{b_2 E[b_1 \mid b_2] - E[b_1 \mid b_2] E_{\text{old}}[b_1 \mid b_2]}{b_2 - E[b_1 \mid b_2]}$$

$$= \frac{E[b_1 \mid b_2] \, (b_2 - E_{\text{old}}[b_1 \mid b_2])}{b_2 - E[b_1 \mid b_2]}$$

Equation 11 gives us the expected value of basal area at time 1 given basal area at time 2 for a tree in the new sample in terms of the same expected values for the population and the old sample. The expected value of b_1 given b_2 for the population is determined by a weighted regression over the trees in the old sample with the weights being the inverse probability of selection (i.e., multiply each observation by b_2/b_1).

In summary we used [11] to separate the new sample into the *o* and *n* samples and then we used [IO] to predict the V1BAR values for the *n* sample to use with $V_1{}^{**}$.

Results

Figures 2 through 4 show the results for $\hat{V}_1$ and $V_1{}^{**}$ for board foot volumes of sawlog-sized trees, cubic foot volumes of pulpwood-sized trees, and cubic foot volume of all trees, respectively. These figures show that, as expected, $V_1{}^{**}$ is less than $\hat{V}_1$ in SSD and SAD over all BAF values. $V_1{}^{**}$ gives better estimates than $\hat{V}_1$ because of the additional information provided by the trees first measured at time 2.

For board foot volume, Fig. 2 shows that $V_1{}^{**}$ is consistently lower in SAD and SSD than $\hat{V}_1$. The SD plots show that there is no more detectable bias in $V_1{}^{**}$ than there is in $\hat{V}_1$. This indicates that no bias has been introduced by the
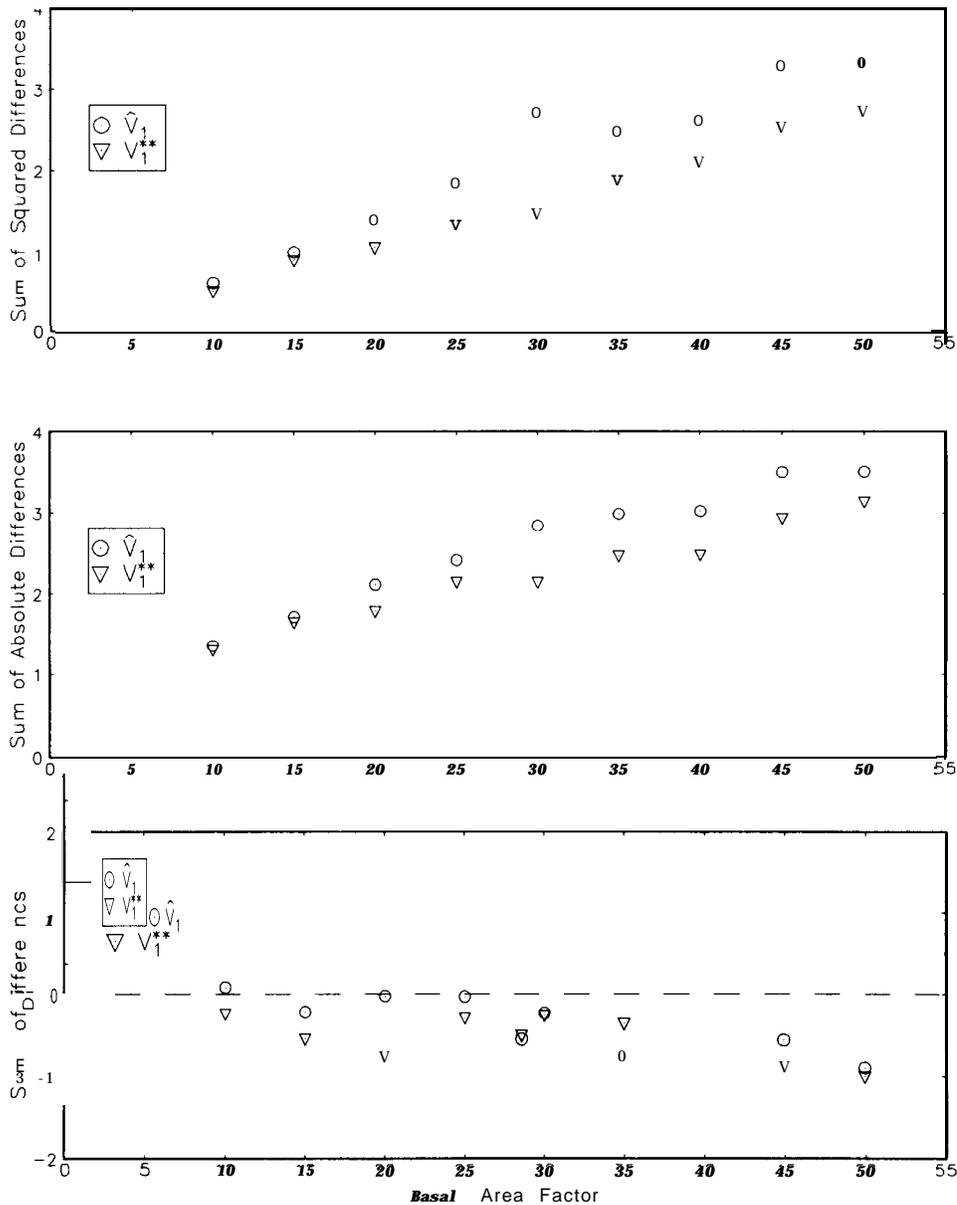
F[IG]. 3. The sums of squared differences ($\times 10^{-7}$), absolute differences ($\times 10^{-4}$), and differences ($\times 10^{-4}$) between the estimators of cubic foot volume of pulpwood-sized trees at time 1 and the fixed area plot values versus basal area factor.

method used to predict the V1BAR for n. The SSD of V_1** is 50–75% of that of $\hat{V}_1$ over most of the BAF values owing solely to the additional new sample. Also, as expected, V_1** enjoys a roughly increasing reduction in error over V_1 as BAF increases, until BAF becomes large enough to drastically reduce the number of trees in the old sample, making previous predictions for the new sample very difficult. Our study has only revealed this problem at BAF 50 for the sawlog-sized trees (Fig. 2). Even in this case there is still some small improvement by these criteria for V_1** over $\hat{V}_1$.

In Fig. 3 V_1** and $\hat{V}_1$ show little empirical bias for prediction of cubic foot volume of pulpwood-sized trees. This figure also shows the roughly increasing advantage of V_1** over V_1 at the higher BAF values in terms of both SAD and SSD owing to the additional information from the n sample. The inability of V_1** to greatly improve upon V_1 at these lower

BAF values for cubic foot volumes is not surprising, since the number of trees in the s samples were quite large at these lower BAF values, and the extra information advantage was too small to contribute much of an improvement. One would also reach the same conclusions in the case of cubic foot volume of all trees after examining Fig. 4.

Conclusion

The best of these two estimators will depend largely on the ratio of total basal area at time 2 to total basal area at time 1 (B_2/B_1) in the population. The larger this ratio becomes, the larger the new sample will be relative to the old sample. So the faster the rate of growth and the longer the remeasurement interval relative to the age of the forest are, the greater will be the contribution of the new sample. And the greater the contribution of the new sample is, the greater will be the advantages
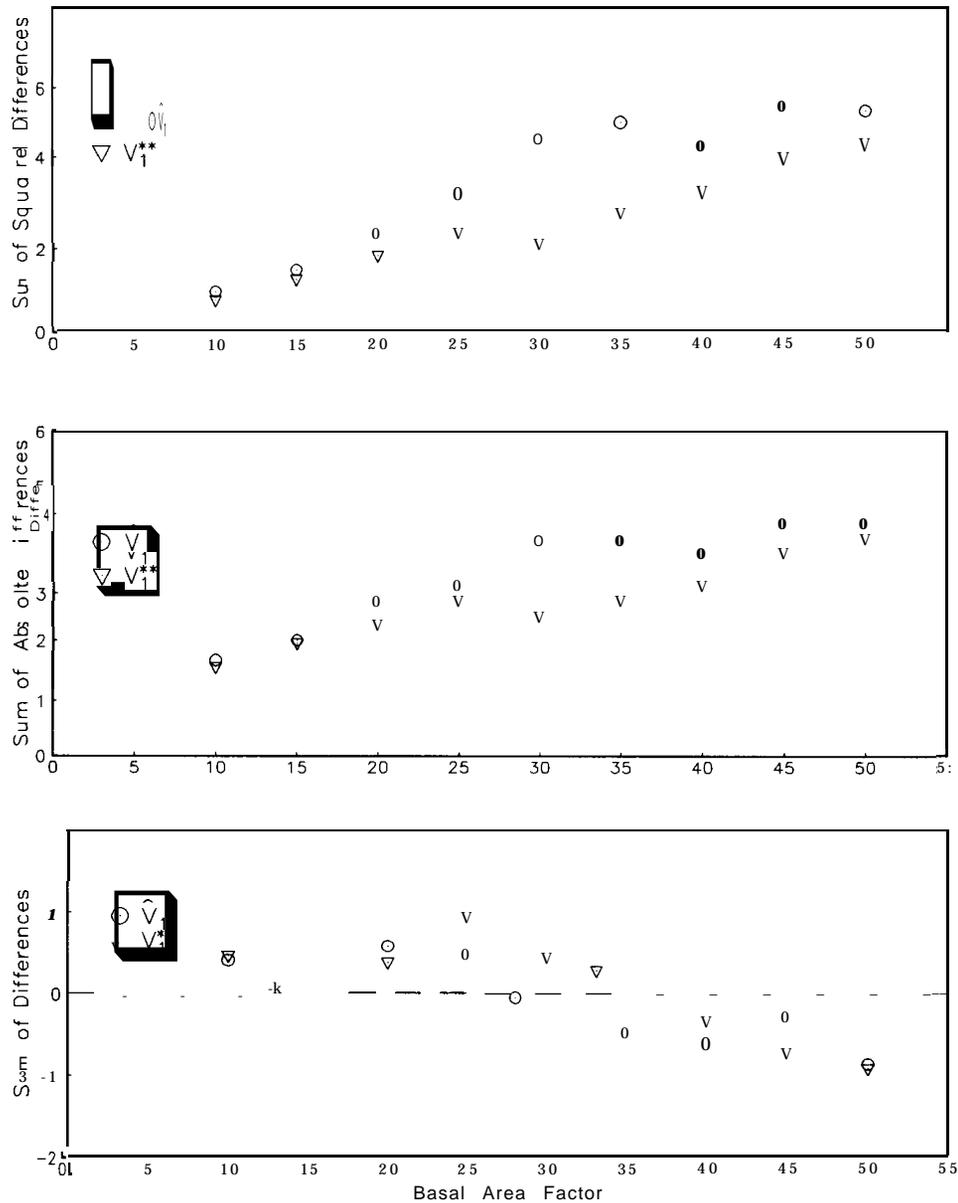
FIG. 4. The sums of squared differences ($\times 10^{-7}$), absolute differences ($\times 10^{-4}$), and differences ($\times 10^{-4}$) between the estimators of cubic foot volume of all trees at time 1 and the fixed area plot values versus basal area factor.

of utilizing the information available from this sample. However, predictions of v_1 will contain more error, the magnitude of which depends on the variance of the growth of the survivor trees. So recognition of both the relative times of measurement in the life of the stands and the homogeneity of the populations present are vital with respect to the choice of compatible estimators of growth and yield from remeasured point samples.

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