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Compatible Basal Area and Number of Trees Estimators from Remeasured Horizontal Point Samples

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ABSTRACT. Compatible groups of estimators for total value at time 1 (V_1), survivor growth (S), and ingrowth (I) for use with permanent horizontal point samples are evaluated for the special cases of estimating the change in both the number of trees and basal area. Caveats which should be observed before any one compatible grouping of estimators is chosen for a particular application are given. FOR. SCI. 37(1):136–145.

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THIS WORK EXAMINES THE ATTRIBUTES of the compatible estimators discussed in Roesch et al. (1989) for survivor growth (S), ingrowth (I) and total value at time 1 (V_1) when used to provide estimates for change in basal area and the number of trees. Survivor growth occurs on trees which were above some minimum merchantability limit at both times 1 and 2, while ingrowth is due to trees which were below the merchantability limit at time 1 and above the limit by time 2. In this paper we consider only one merchantability limit at a time and deliberately ignore the possibility of a tree growing out of one merchantability class into a larger merchantability class.

Martin (1982) stated, explicitly, the six sample categories of trees possible on remeasured point samples. Two categories, "o" and "n", consist of trees which were "out" (not sampled) at the first measurement and alive, and "in" (sampled) at the second measurement. Trees in the "o" category were below the minimum diameter at breast height (dbh), for their time 2 size class, at time 1 and are, therefore, ingrowth trees, while trees in the "n" category were above this minimum dbh and are, therefore, survivor trees. The other four categories included trees which were "in' the point sample at time 1. Ingrowth and survivor trees which were measured at both times fall into the "i" and "s" categories, respectively. Trees which were "in' and above minimum dbh at the first measurement but die or are cut before the second measurement are sampled as "m" or "c," respectively. To avoid ambiguity, we will not attach names to these samples (i.e., "ongrowth," "ingrowth," "nongrowth," etc.), as was customary in the past (see, for example, Martin 1982, Iles and Beers 1983).

The notation we will use follows that of Martin (1982), as augmented in Roesch et al. (1989). Using the characteristic sampling terminology of Oderwald (1981), in which the estimation characteristic (C_e) is the quantity of interest measured on each sample unit and the sampling characteristic (C_s) is the attribute by which the unit is selected for inclusion in the sample, we define:

i = estimate obtained using the **final** values of C_e and the **final** values of C_s for trees in the "i" sample;

i' = estimate obtained using the **final** values of C_e and the **initial** values of C_s for trees in the "i" sample;

o = estimate obtained using the **final** values of C_e and the **final** values of C_s for trees in the "0" sample;

s_2 = estimate obtained using the **final** values of C_e and the **final** values of C_s for trees in the "s" sample;

s_2' = estimate obtained using the **final values** of C_e and the **initial values** of C_s for trees in the "s" sample;

s_1 = estimate obtained using the **initial** values of C_e and the **initial** values of C_s for trees in the "s" sample;

s_1' = estimate obtained using the **initial** values of C_e and the **final** values of C_s for trees in the "s" sample;

n_2 = estimate obtained using the **final** values of C_e and the **final** values of C_s for trees in the "n" sample;

n_1 = estimate obtained using the **initial** values of C_e and the **initial values** of C_s for trees in the "n" sample;

n_1' = estimate obtained using the **initial** values of C_e and the **final** values of C_s for trees in the "n" sample;

m = estimate obtained using the **initial** values of C_e and the **initial** values of C_s for trees in the "m" sample;

c = estimate obtained using the **initial** values of C_e and the **initial** values of C_s for trees in the "c" sample.

Note that a prime (′) indicates that the C_s divisor in the C_e/C_s ratio is from the time period other than that subscripted (or that obvious from the context as in the case of "i" and "o"). Of course, in the specific case of horizontal point sampling, C_s is tree basal area.

To be compatible, the estimators for each component of growth on the right hand side of the equation (Meyer 1953),

$$V_2 - V_1 = S + I - M - C \tag{1}$$

must sum to the difference of the estimators of the left hand values. In (1)

V_i = the total value at time i,
S = survivor growth,
Z = ingrowth,
M = mortality, and
c = cut.

In particular, we will discuss the estimators presented in Table 1.

TABLE 1.

The estimators of the components of growth and instantaneous volume calculated from remeasured horizontal point samples.

The estimators for survivor growth:	
$\hat{S} = s_2' - s_1$	The Grosenbaugh (1958) estimator as reviewed by Martin (1982).
$\tilde{S} = s_2 - s_1 + n_2$	The estimator developed by Van Deusen et al. (1986).
.s** $= s_2 - s_1' + n_2 - n_1'$	An unbiased estimator which subtracts the time 1 values of trees in the "n" sample, discussed in Roesch et al. (1989).
The estimators for ingrowth:	
$\hat{I}_A = i + 0 + n_2 + s_2 - s_2'$	Martin's compatible estimator.
$\hat{I}_p = i + 0$	The "revised" Purdue estimator.
The estimators for the total value at time 1:	
$\hat{V}_1 = s_1 + m + c$	The traditional estimator.
$V_1^{**} = s_1' + n_1' + m + c$	The Roesch et al. estimator.

Martin (1982) presented an ingrowth estimator,

$$\hat{I}_A = i + o + n_2 + s_2 - s_2', \tag{2}$$

which is compatible with the Grosenbaugh (1958) estimator for survivor growth:

$$\hat{S} = s_2' - s_1. \tag{3}$$

Van Deusen et al. (1986) developed the following unbiased estimator for S:

$$\tilde{S} = s_2 - s_1 + n_2. \tag{4}$$

They also showed the compatibility of $\tilde{S}$ with the "revised Purdue" estimator for ingrowth (Beers and Miller 1964):

$$\hat{I}_p = i + o. \tag{5}$$

Another estimator for survivor growth',

$$S^{**} = s_2 - s_1' + n_2 - n_1', \tag{6}$$

will be unbiased if the estimator of the time 1 values of the trees in the "n" sample is unbiased. Roesch et al. (1989) showed that S^{**} is also compatible with *I,,, if* used with an updated estimator of the total value at time 1:

$$V_1^{**} = s_1' + \text{n,'} + \boldsymbol{m} + \boldsymbol{c}.$$

For now, we will ignore the estimators of $V_2, M,$ and C and discuss only the estimators of $S, I,$ and V_1 *in* the three compatible groupings:

$$\hat{V}_2 - \hat{V}_1 = \hat{S} + \hat{I}_A + \hat{M} + \hat{C} \tag{7}$$

$$\hat{V}_2 - \hat{V}_1 = \tilde{S} + \hat{I}_p + \hat{M} + \hat{C} \tag{8}$$

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[1] The use of the estimated growth on the "new" trees seems to have been originally proposed when the USDA Forest Service Survey units first began remeasuring lo-point clusters in the early 1970s. The earliest documentation of this idea that we've found to date is in the form of an intra-office memorandum from Donald R. Gedney to Melvin E. Metcalf both of the Pacific Northwest Forest and Range Experiment Station dated July 30, 1973.

$$\hat{V}_2 - \hat{V}_1^{**} = S^{**} + \hat{I}_p + \hat{M} + \hat{C} \tag{9}$$

for estimation of basal area and number of trees.

Van Deusen et al. (1986) showed that the first two groupings differed by the placement of an error term:

$$\epsilon = s_2 - s_2' + n_2,$$

which has an expected value of zero. Roesch et al. (1989) showed that Equation (9) splits ϵ into 2 parts:

$$\epsilon_1 = \{s_1' - s_1 + n_1'\}$$

and

$$\bullet \quad \text{G} = \{(s_2 - s_1') - (s_2' - s_1) + (n_2 - n_1')\},$$

each with an expected value of zero, and applies ● 1 to V_1^{**} and ϵ_G to S**. As shown in Mood et al. (1974),

$$\text{var}[ES_1 \pm \epsilon_A] = \text{var}[ES_1] + \text{var}[\epsilon_A] \pm 2\text{cov}[ES_1,\epsilon_A],$$

where ES_1 is an estimator of interest and ● A is any of the above error terms. If we let

$$ES_2 = ES, -\beta\epsilon_A$$

where *ES,* is a second estimator of interest and β is 1 or − 1. The variance of *ES, will* be lower than that of *ES, if*

$$2\beta\text{cov}[ES_1,\epsilon_A] > \text{var}[\epsilon_A].$$

This result will be used later for variance comparisons because any of the estimators above can be written as the combination of at least one of the other estimators and one of the error terms.

ESTIMATION OF BASAL AREA GROWTH

In this section C_e will be basal area. Also, the subscript *B* appended to the growth estimators will refer to basal area and *BA will* replace *V* for the time 1 estimators.

We can expect the advantages and disadvantages of $S, \tilde{S},$ and S** to be somewhat different when basal area is the characteristic of interest than when volume was the estimation characteristic in Roesch et al. (1989). S_B uses only the "s" sample, ignoring the information in the new sample ("*n*"):

$$\hat{S}_B = s_{2B}' - s_{1B} = \frac{FL}{m}\sum_{j=1}^{m}\sum_{i\epsilon A}\left[Y_{ij}\left[\frac{b_{2i} - b_{1i}}{b_{1i}}\right]\right]$$

where

$$Y_{ij} = \begin{cases} 1 \text{ if tree } i \text{ is included in the "s" sample from point } j, \\ 0 \text{ otherwise;} \end{cases}$$

b_{ki} = *the* basal area of tree i at time k;

$\hat{b}_{ki}$ = the estimated basal area of tree i at time k;

F = *the* basal area factor;

L = the land area of the forest;

m = the number of sample points;

A = the population of trees alive and merchantable at both times (survivor trees).

Similarly, we define for later use:

$$X_{ij} = \begin{cases} 1 \text{ if tree } i \text{ is included in the “n” sample from point } j, \\ 0 \text{ otherwise;} \end{cases}$$

$$Z_{ij} = \begin{cases} 1 \text{ if tree } i \text{ is included in either the “i” sample or the “o” sample from} \\ \quad \text{point j,} \\ 0 \text{ otherwise;} \end{cases}$$

$$W_{ij} = \begin{cases} 1 \text{ if tree } i \text{ is included in either the “m” sample or the “c” sample from} \\ \quad \text{point } j, \\ 0 \text{ otherwise;} \end{cases}$$

D = the population of trees which die or are cut between times 1 and 2;

N = the population of trees merchantable at time 2 which were not merchantable at time 1 (ingrowth trees).

Because the “s” sample is usually large, $\hat{S}_B$ will normally be a very good, low variance estimator of the basal area growth of survivor trees, despite the fact that it ignores information. Unfortunately, the ingrowth estimator shown by Martin (1982) to be compatible with S_B,I_{AB}, will often have a higher variance than I_{pB}. $\hat{I}_{AB}$ will have less variance than $\hat{I}_{pB}$ when

$$-\,2\mathrm{cov}[\hat{I}_{pB}, \epsilon_B] > \mathrm{var}[\epsilon_B].$$

This condition will exist only when there is a relatively strong negative correlation between I_{pB} and ϵ_B. We would not expect this to be true, in general. Rather, we would expect these terms to be poorly correlated because ϵ_B contains only terms from the sampled survivor trees and has an expected value of zero and I_{pB} contains only terms from the sampled ingrowth trees. However, as bias in our time 1 basal area estimates for trees in the new sample (“o” and “n”) increases, this strong negative correlation is more likely to occur, because, polarized bias will occur between I_{pB} and ϵ_B. By polarized bias we mean that every unit of negative (positive) bias in I_{pB} creates a unit of positive (negative) bias in ϵ_B. At the same time, this bias, which is affecting $\hat{I}_{pB}$, ***will*** not increase the bias of $\hat{I}_{AB}$ because the distinction between “o” and “n” does not have to be made.

As mentioned in Van Deusen et al. (1986), only the “n” sample is used in $\tilde{S}$ when basal area growth is of interest:

$$\begin{aligned}
\tilde{S}_B &= s_{2B} - s_{1B} + n_{2B} \\
&= \frac{FL}{m} \sum_{j=1}^{m} \sum_{i \epsilon A} \left[Y_{ij} \left[\frac{b_{2i}}{b_{2i}}\right] - Y_{ij} \left[\frac{b_{1i}}{b_{1i}}\right] + X_{ij} \left[\frac{b_{2i}}{b_{2i}}\right] \right] \\
&= \frac{FL}{m} \sum_{j=1}^{m} \sum_{i \epsilon A} [X_{ij}] \\
&= n_{2B}.
\end{aligned}$$

Therefore, $\tilde{S}_B$ could also be viewed as ignoring information because the sample trees which were measured for any change in basal area ("s") are eliminated from the estimator. When using S_B the opportunities for measurement error are greatly reduced, since each sample tree used ("*n*") is measured only once and there are potentially few of them. Sampling and prediction errors become extremely important however. Since each tree in the "n" sample represents a large amount of basal area growth, missing a tree at either time which should have been sampled or including a tree at either time which should not have been included at that time will contribute a large error to the estimator. Also, prediction of the previous basal area of each tree new to the sample at time 2 is necessary to determine if it is an ingrowth tree or a survivor tree and should be included in the "o" or "n" sample respectively. Any bias in this classification could have a profound effect on $\tilde{S}_B$.

$\tilde{S}_B$ will have less variance than $\hat{S}_B$ when

$$-2\text{cov}[\hat{S}_B, \epsilon_B] > \text{var}[\epsilon_B].$$

Similar to the comparison of the ingrowth estimators above, this condition will only exist when there is a somewhat strong negative covariance between S_B and ϵ_B. By the definition of covariance, we can see that the satisfaction of this condition will depend upon the heterogeneity in both growth and spatial distribution as well as the relative length of the measurement interval and sampling angle chosen.

$S_B{}^{**}$ is a possible alternative which uses the predicted time 1 basal areas of the "n" trees for more than simple sample classification. Roesch et al. (1989) contend that these predictions should be sufficiently precise when volume is of interest; however, Roesch (1988) does demonstrate the need to exercise caution when making these predictions to avoid the introduction of bias. Specifically, as shown in Van Deusen et al. (1986), "s" samples survivor trees proportional to basal area at time 1 while "n" samples survivor trees proportional to basal area growth. Therefore, weighted regressions of b_2 on b_1 are in order if results from the "s" sample are to be applied to trees in the "n" sample. Now

$$\begin{aligned} S_{B^{**}} &= (s_{2B} - s_{1B}') + (n_{2B} - n_{1B}') \\ &= \frac{FL}{\text{m}} \sum_{j=1}^{m} \sum_{i \epsilon A} \left[Y_{ij} \left[\frac{b_{2i} - b_{1i}}{b_{2i}} \right] + X_{ij} \left[\frac{b_{2i} - \hat{b}_{1i}}{b_{2i}} \right] \right] \\ &= \tilde{S}_B - \epsilon_{1B}. \end{aligned}$$

$S_B{}^{**}$ will have less variance than $\tilde{S}_B$ when

$$2\text{cov}[\tilde{S}_B, \epsilon_{1B}] > \text{var}[\epsilon_{1B}]. \qquad (10)$$

A positive covariance between $\tilde{S}_B$ and ● m is a prerequisite for the above to be true and is, under certain conditions, to be expected. That this positive covariance is possible is supported by the observation that if survivor trees do not shrink, then whenever ● m is positive, $\tilde{S}_B$ is positive and ϵ_{1B} must be negative (or zero) when S_B is zero. The results of simulations presented by Roesch[2] show that (10)

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[2] Roesch, F.A., Jr. 1989. Growth from variable-radius plots: Solutions revisited. Paper presented at the meeting of the Association of Southern University Biometricians, Mountain Lake, VA.

does occur under realistic conditions. The time 1 estimator compatible with S_B^{**} and $\hat{I}_{pB}$ is

$$BA_1^{**} = s_{1B}' + n_{1B}' + m_B + c_B$$

$$= \frac{FL}{m} \sum_{j=1}^{m} \left[\sum_{i\epsilon A} \left[Y_{ij} \left[\frac{b_{1i}}{b_{2i}} \right] + X_{ij} \left[\frac{\hat{b}_{1i}}{b_{2i}} \right] \right] + \sum_{i\epsilon D} W_{ij} \left[\frac{b_{1i}}{b_{1i}} \right] \right].$$

BA_1^{**} ***will*** sometimes have a lower variance than the traditional estimator of time 1 basal area due to the additional information provided by the "n" sample. The magnitude of this reduction in variance will depend on both the number of trees in the "n" sample representing additional information and the accuracy with which the time 1 basal areas of the these trees are predicted. This accuracy is especially important in the boundary area between merchantable and nonmercharitable, because, if less (more) trees are misclassified as "n" than misclassified as "o," the time 1 predictions of basal area will be too low (high) and they will also be applied to too few (many) trees. If the population of trees is varied, and those falling close to this boundary are only a small part of the population of interest, then this two-fold effect of bias is likely to be unimportant. Suppose instead that the forests of interest are roughly even-aged and the basal areas of the trees are clustered about the merchantability limit at time 1. In this latter case, a biased estimator of individual tree time 1 basal area could have a significant effect on the estimate of the total time 1 basal area. Note also, however, that the latter, more homogeneous forest provides conditions under which the individual tree basal areas at time 1 would be easier to predict. Since

$$BA_1^{**} = BA, + \bullet \quad m,$$

a variance reduction will be realized for BA_1^{**} over $\widehat{BA}_1$ if:

$$-2 \ \mathrm{Cov}(\widehat{BA}_1, \epsilon_{1B}) > \mathrm{Var}(\epsilon_{1B}). \tag{11}$$

Results in Roesch (1988) when total and merchantable volume were the characteristics of interest show variance reduction under ideal circumstances. Whether (11) occurs in most inventory situations remains to be investigated.

ESTIMATION OF CHANGE IN NUMBER OF TREES

When the objective is to estimate the components of the change in number of trees, the value of C_e for a tree is 1 if it is present and 0 otherwise, so the change in number of survivor trees:

$$S_N = s_{2N} - s_{1N} + n_{2N}$$

$$= \frac{FL}{m} \sum_{j=1}^{m} \sum_{i\epsilon A} \left[Y_{ij} \left[\frac{1}{b_{2i}} \right] - Y_{ij} \left[\frac{1}{b_{1i}} \right] + X_{ij} \left[\frac{1}{b_{2i}} \right] \right]$$

$$= \frac{FL}{m} \sum_{j=1}^{m} \sum_{i\epsilon A} \left[Y_{ij} \left[\frac{b_{1i} - b_{2i}}{(b_{2i})(b_{1i})} \right] + X_{ij} \left[\frac{1}{b_{2i}} \right] \right] \neq 0, \text{ in general.}$$

Although the expected value of $\tilde{S}_N$ is zero, in a particular inventory this estimator will almost never be zero. Therefore, the survivor growth estimator is included in the equation of change in number of trees:

$$\hat{N}_2 - \hat{N}_1 = \tilde{S}_N + i_N + o_N - m_N - c_N.$$

This is intuitively unappealing because the change in number of survivor trees is zero by definition. In other words if we use S_N to estimate S in (1), we've chosen to substitute the known value of S (zero) for an estimate which we know will be wrong most of the time, and therefore will have variance while the true value does not.

The (**) estimators do not possess this disadvantage. In the case of change in number of trees, the estimators use the point sample components in what might be considered the most logical manner. The estimators for the number of trees at times 1 and 2 are, respectively:

$$\begin{aligned} N_1^{**} &= s_{1N}' + n_{1N}' + m_N + c_N \\ &= \frac{FL}{m} \sum_{j=1}^{m} \left[\sum_{i \epsilon A} \left[Y_{ij} \left[\frac{1}{b_{2i}}\right] + X_{ij} \left[\frac{1}{b_{2i}}\right]\right] + \sum_{i \epsilon D} W_{ij} \left[\frac{1}{b_{1i}}\right]\right] \end{aligned}$$

and

$$\begin{aligned} \hat{N}_2 &= s_{2N} + n_{2N} + i_N + o_N \\ &= \frac{FL}{m} \sum_{j=1}^{m} \left[\sum_{i \epsilon A} \left[Y_{ij} \left[\frac{1}{b_{2i}}\right] + X_{ij} \left[\frac{1}{b_{2i}}\right]\right] + \sum_{i \epsilon N} Z_{ij} \left[\frac{1}{b_{2i}}\right]\right]. \end{aligned}$$

Therefore, the estimator for change in number of trees reduces to:

$$\begin{aligned} \hat{N}_2 - N_1^{**} &= \frac{FL}{m} \sum_{j=1}^{m} \left[\sum_{i \epsilon N} Z_{ij} \left[\frac{1}{b_{2i}}\right] - \sum_{i \epsilon D} W_{ij} \left[\frac{1}{b_{1i}}\right]\right] \\ &= i_N + o_N - m_N - c_N. \end{aligned}$$

This claim is true because:

$$\begin{aligned} S_N^{**} &= s_{2N} - s_{1N}' + n_{2N} - n_{1N}' \\ &= \frac{FL}{m} \sum_{j=1}^{m} \sum_{i \epsilon A} \left[Y_{ij} \left[\frac{1}{b_{2i}}\right] - Y_{ij} \left[\frac{1}{b_{2i}}\right] + X_{ij} \left[\frac{1}{b_{2i}}\right] - X_{ij} \left[\frac{1}{b_{2i}}\right]\right] \\ &= 0. \end{aligned}$$

This result is significant because estimates are only made for the components which actually need to be estimated and the samples are only used for estimates of the populations from which they are thought to have been drawn. We can see that S_N^{**} always equals zero as it should, giving it zero variance and zero bias. In addition, N_1^{**} uses all of the sample trees known or predicted to have been in the size category at time 1 and the estimate for change in number of trees includes only sample trees known or predicted to have contributed to that change. The accuracy of the estimates of the number of ingrowth trees and the number of trees present at time 1 does depend, however, on an unbiased separation of the "o" and "n" samples. The $(\hat{I}_{pN}, \tilde{S}_N, \hat{N}_1)$ compatible grouping retains this separation problem in the estimators of change I_{pN} and S_N while the $(\hat{I}_{AN}, \tilde{S}_N, N_1)$ compatible grouping provides the desirable estimate of zero for survivor growth:

$$\hat{S}_N = s_{2N}' - s_{1N} = \frac{FL}{m} \sum_{j=1}^{m} \sum_{i \epsilon A} \left[Y_{ij} \left[\frac{1}{b_{1i}} \right] - Y_{ij} \left[\frac{1}{b_{1i}} \right] \right] = 0.$$

and also does not require the separation of "o" from "n". However, the estimator of ingrowth $(\hat{I}_{AN})$ illogically uses the samples of survivor trees in order to ensure compatibility. The new compatible grouping of estimators could be more precise, in some cases, to the previously developed estimators of the change in number of trees from remeasured horizontal point samples. There would, however, be very little difference between the three groupings of estimators when the number of survivor trees is small.

CONCLUSIONS

In this paper we have examined the idea of a more logical use of the "n" trees proposed in Roesch et al. (1989) for the specific cases of basal area and number of trees. Van Deusen et al. (1986) established the sampling relationship between "n" and "s" and used the "n" sample in the estimator S. Roesch et al. (1989) developed the compatible S^{**} and V_1^{**}, which assign the two components of "n" to the proposed "proper" places, analogous to the traditional treatment of the "s" sample. The costs of this placement are the necessity to estimate the time 1 values of C_e and basal area for the trees in the samples new at time 2 and to update the time 1 estimate of the total characteristic of interest (i.e., $V_1 \rightarrow V_1^{**}$).

The estimates of the individual tree time 1 attributes play two roles. First, the time 1 basal area estimates are used to assign each new tree to either the "o" or the "n" sample. Second, the time 1 estimates of C_e are used for the "n" trees in S** and V_1^{**}. We see that any error in the first step will be reflected in both the $(\hat{I}_p, S^{**}, V_1^{**})$ and the $(\hat{I}_p, \tilde{S}, \hat{V}_1)$ compatible groupings, but not in the $(\hat{I}_A, \hat{S}, V_1)$ grouping. The second step affects only the $(\hat{I}_p, S^{**}, V_1^{**})$ grouping. In the case of basal area, the error associated with the first role of these predictions is somewhat counterbalanced by the error associated with the second role in S_B^{**}. That is, if too few trees are classified as "n" it is because the time 1 basal area predictions were too low and basal area growth predictions were too high. In S_B^{**}, more growth is applied to fewer trees, thereby_ adjusting somewhat for the misclassification. No such mechanism is utilized by S_B. In both groupings ((Î,,, S_B^{**}, BA_1^{**}) and (I_{pB}, S_B, BA_1)) however, $\hat{I}_{pB}$ suffers from the extra trees in the "o" sample. BA_1^{**} absorbs the error in the former grouping because less time 1 basal area is applied to fewer trees in the "n" sample. This effect on predictions of other characteristics of interests will vary by how closely correlated the time 1 predictions of basal area and the C_e are. Whether the time 1 estimate of the total C_e should share the risk of poor time 1 predictions with the estimates of survivor growth and ingrowth is a decision that will have to be made by the inventory specialist. Surely, as the relative length of the growth interval shortens the greater would be the temptation to allow some of this risk to be borne by the time

1 estimator because the risk would become small while the size of the time 1 estimate becomes large relative to that of the survivor growth estimate. If reliable time 1 estimates of the individual tree characteristics cannot be made, then neither the (I_p, S^{**}, V_1^{**}) nor the $(I_p, \bar{S}, \hat{V}_1)$ compatible groupings should be used. The conditions affecting the choice of compatible groupings can be summarized for both basal area growth and change in number of trees as dependent upon the relative length of the measurement interval, the spatial distribution of the trees in the respective size classes, the variance of growth since time 1 within each size class at say time 2, and the interrelationships of these conditions as defined by the growth curve and sampling angle chosen.

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