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RELATIVE EFFICIENCY OF POINT SAMPLING CHANGE ESTIMATORS

Guillaume Thérien
Consultant, 2399 7e Avenue, Trois-Rivières, Quebec, G8Z 3E2, Canada

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Abstract. Concerns about the efficiency and the reliability of point sampling to estimate change in forest growth variables have been expressed ever since point sampling appeared in the literature more than 60 years ago. Change estimators for point samples based on point-to-tree distance in variable-radius plots were introduced about 30 years ago but are rarely implemented despite easy access to point-to-tree distance. The statistical efficiency and bias of these newer estimators were compared to traditional fixed-area plot estimators using stem-mapped permanent sample plots. Methods using variable-radius plots and point-to-tree distance were more efficient to estimate volume and basal area while fixed-area plots were more efficient to estimate trees/ha. Compatible and time-additive estimators are examined for estimating survivor, mortality, and ingrowth change using point samples. These estimators are unbiased under unrestrictive conditions.

Keywords: variable-radius plots, fixed-area plots, change estimation

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1 Introduction

Basal area is the simplest and most widely used measure of stand density (Spurr 1952, p. 276). Bitterlich (1947) introduced angle-count sampling (*winkelzhlprobe* in German) as a new sampling method to estimate basal area. The method has become known in English under various other names such as plotless sampling (*e.g.*, Grosenbaugh 1952), variable plot sampling (*e.g.*, Bell and Alexander 1957), Bitterlich method (*e.g.*, Afanasiev 1958), point sampling (*e.g.*, Grosenbaugh 1958), prism cruising (*e.g.*, Bruce 1961), and horizontal point sampling (*e.g.*, Husch et al. 1983, p. 220).

Point sampling is a clever sampling method to select trees proportional to their cross-sectional area and estimate basal area with minimal effort using variable-radius plots. Grosenbaugh (1958) laid out the statistical foundations of point sampling and expanded the sampling method beyond basal area to all stand-level attributes of interest. Grosenbaugh (1958) also addressed the use of variable-radius plots for estimating change.

Despite Grosenbaugh's explanations, many foresters considered estimating change using variable-radius plots a problem due mainly to the trees expanding inclusion zone over time. The main concern was that change estimators were deemed "incompatible" when applied to variable-radius plots (Flewelling 1981, Gregoire 1993). This means that *i*) the change estimate between the beginning and the end of the growth period (Time 1 and 2) added to the point estimate at Time 1 can be different from the point estimate at Time 2

$$\hat{V}_2 \neq \hat{V}_1 + \hat{\Delta}_{2-1} \tag{1}$$

where $\hat{V}_t$ is an attribute estimate at time t and $\hat{\Delta}_{v-t}$ is the change estimate between Time t and v, and *ii*) change estimates are not time-additive, that is the sum of the change estimates between Time 1 and 2 and between 2 and 3 is different from the change estimate between Time 1 and 3:

$$\hat{\Delta}_{3-1} \neq \hat{\Delta}_{2-1} + \hat{\Delta}_{3-2} \tag{2}$$

The incompatibility problem is not unique to variable-radius plots since the same problem occurs with fixed-area plots when a plot is reduced in size when the number of trees in the plot gets too large or when multiple plot sizes are used for different diameter at breast-height (DBH) classes. The incompatibility issue associated with fixed-area plots, however, has not generated the same level of interest and debate among forest statisticians when applied to variable-radius plots.

Over the last 50 years, a large body of literature has been devoted to tackling the incompatibility issue (Beers and Miller 1964, Ericksson 1995, Flewelling 1981, Grosenbaugh 1958, Iles 1981, Iles and Carter 2007, Martin 1982, Roesch et al. 1989, Van Deusen et al. 1986, among others), but fixed-area plots are still used more commonly for estimating change (Scott 1998).

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Iles (1981) suggested that any volume to basal area ratio (VBAR) function decreasing from the tree position to the edge of the tree inclusion zone, with an expected value of VBAR, could provide an efficient estimate of change for stand volume. Bitterlich (1984, p. 240) referred to it as "Iles' method". Iles and Carter (2007) expanded the volume estimates of Iles (1981) to any variables using, as an example, the function describing a cone because it was a very simple function compared to the actual tree form (Iles 1981) and was easy to implement. Flewelling (1981), working independently from Iles, suggested using a function describing a truncated neiloid that had some of the basic properties mentioned by Iles (1981) which adjusted the basal area estimate, and implicitly, the other estimates. This estimator is referred to as Flewelling's method hereafter.

The relative efficiency of both Iles' and Flewelling's methods for estimating change has never been compared to traditional fixed-area plot estimators using real data. Numerous studies (see Scott and Alegria 1990 for an exhaustive list; Hradetzky 1995) have investigated the efficiency of change estimators based on fixed-area and variable-radius plots, but none of those comparisons has used a distance-dependent estimator, probably because point-to-tree distance, the distance between plot centre and an included tree, was seldom recorded in the field at the time. Using simulated data, Carter (2007) found that the cone implementation of Iles' method was an efficient volume change estimator. In this paper, the relative efficiency of net change using Iles' and Flewelling's methods were compared to the net change estimator computed from fixed-area plots using stem-mapped permanent sample plots. The comparisons were made for the overall net change and for the basic net change components: survivor, ingrowth, cut and mortality.

Estimators for change components have been proposed in the past (*e.g.*, Ericksson 1995, Roesch et al. 1989, Van Deusen et al. 1986) but these estimators required prediction of unknown information at Time 1 or when a tree "grows onto" a point, which likely introduces bias in the estimators. The methodology proposed by Iles and Carter (2007) warrants revisiting the change components problem with a fresh approach.

2 MATERIAL

Two data sources were used in this study. One was provided by the British Columbia (BC) Ministry of Forests and Range Forest Inventory and Analysis Branch (BC data), while the second was from the Huai Kha Khaeng Wildlife Sanctuary in Thailand and was provided by the Thai National Parks, Wildlife, and Plant Conservation Department (HKK data) (Table 1). The BC data allowed testing the estimators under a range of stand conditions, while the HKK data allowed simulating the sampling of a population with a large number of repetitions.

Table 1: Population net change estimates in British Columbia (BC) and Thai (HKK) data sets.

Component	Trees/ha	Basal Area m^2/ha	Volume m^3/ha
	BC (152 plots)		
Survivor	0.0	5.3	68.7
Mortality	-132.2	-2.6	-23.5
Ingrowth	158.2	1.4	7.8
Overall	25.9	4.1	53.0
	HKK (1 plot)		
Survivor	0.0	3.1	
Mortality	-369.6	-4.8	
Ingrowth	710.5	0.2	
Overall	340.9	-1.5	

2.1 BC Data: The BC data included 152 large stem-mapped, fixed-area permanent sample plots containing 20,807 trees. The plots were located throughout the BC interior (49°–57°N, 114°–124°W), covering a wide range of ecological and climatic conditions. The plot radii were either 12.65 m (20 plots), 16.06 m (106 plots), or 17.98 m (26 plots). Only the last growth period of each plot was kept for analysis. Growth periods were either 9 years (86 plots) or 10 years (66 plots). The DBH tagging limit was 9.1 cm. DBH at the beginning of the growth period ranged from 9.1 to 77.6 cm with a median of 14.3 cm.

2.2 HKK Data: The HKK data was obtained from a 1,000 m by 500 m (50 ha) permanent sample plot located at 15°40′N, 99°10′E containing 120,804 stem-mapped trees. The plot was measured three times (in 1994, 1999, and 2004), but only the last growth period (1999-2004) was used for analysis. The DBH tagging limit was 1.0 cm. DBH at the beginning of the growth period ranged from 1.0 to 402.5 cm with a median of 4.3 cm. Volume was not available for this data set.

2.3 Tree Classification: Trees were classified into four categories:

1. Live-and-in (L) trees were live, in the sample plot, and above the DBH tagging limit at the beginning (Time 1) and at the end (Time 2) of the growth period.
2. Mortality (M) trees were live, in the sample plot,

and above the DBH tagging limit at Time 1 and dead at Time 2.

3. Cut (C) trees were live, in the sample plot, and above the DBH tagging limit at Time 1 and removed before Time 2.

4. Recruitment trees (R) were not in the sample plot at Time 1 and live, in the sample plot, and above the DBH tagging limit at Time 2.

L trees are usually called survivor trees in the point sampling literature, which is a misnomer because some of the R trees are also trees that survived throughout the growth period. R trees are often split into more classes such as ingrowth, ongrowth, or nongrowth, but these sub-classes require knowing the DBH of the trees at Time 1.

3 TERMINOLOGY

Beers (1962) identified five different definitions of "growth". For this paper, the definition of interest was net change (or "net increase" in Beers' terminology), defined as:

$$\begin{aligned}\Delta_{2-1} &= V_2 - V_1 && (3)\\ &= \Delta^S + V_2^I - V_1^M - V_1^C && (4)\end{aligned}$$

where Δ_{2-1} is the overall net change between Time 1 and Time 2; V_1 and V_2 are the stand-level live attributes at Time 1 and Time 2, respectively; Δ^S is the survivor change between Time 1 and Time 2; V_2^I is the stand-level attribute on ingrowth trees at Time 2; V_1^M is the stand-level attribute on Mortality trees at Time 1; and V_1^C is the stand-level attribute on Cut trees at Time 1. Survivor change is the change on trees that were live at Time 2 and above the DBH tagging limit at Time 1. Ingrowth trees are live and above the DBH tagging limit at Time 2 and below the DBH tagging limit at Time 1. Two common assumptions usually made when estimating net change were also used for this study. Growth on Cut and Mortality trees between Time 1 and the time they were cut or died is ignored. Growth on trees that were below the DBH tagging limit at Time 1 and dead by Time 2 is also ignored.

4 METHODS

The attributes investigated in this paper were number of trees/ha, basal area, and, for the BC data only, gross whole-stem volume/ha. Net change in each attribute was estimated using three methods:

1. Fixed-area plots;

2. Variable-radius plots and Flewelling's method; and

3. Variable-radius plots and the cone implementation of Iles' method.

The same sample trees are included with Flewelling's and Iles' methods, only the change estimators are different. The basal area factor (BAF) for the two methods based on variable-radius plots was selected individually for each permanent sample plot by taking the basal area of the full-size permanent sample plot at Time 1 divided by 6, rounded to the largest integer in order to have a variable plot with about 6 trees. BAF varied between 1 and 27 m^2/hain the BC data with an average of 7 m^2/ha. BAF was 6 m^2/ha for all sample plots used in the HKK data.

The relative efficiency of different sampling designs or estimators can be expressed as the relative monetary cost to achieve a certain precision or relative precision for a certain monetary cost. The latter expression was employed in this paper, following a similar study in which the sampling cost was fixed by selecting a plot radius and basal area factor (BAF) to yield a constant number of trees in each plot (Banyard 1976). The radius of the fixed-area plot was therefore reduced to match the cost of the two point sample-based methods so that their efficiencies could be compared. The fixed-area plot radius (3.30 m for the BC data and 2.90 m for the HKK data) was iteratively computed to provide an average number of sample trees per measurement similar to the one obtained using variable-radius plots.

The attributes of interest at a point in time were computed using:

$$\hat{V}_{it}^k = \left[\sum_{j=1}^{s_{it}} y_{ijt}\right] \times \mathrm{phf}_{ijt}^k \qquad (5)$$

where $\hat{V}_{it}^k$ is the estimator for the stand-level attribute of interest on plot i at time t using method k, y_{ijt} is the attribute of interest on tree j; phf_{ijt}^k is the number of trees/ha each tree represents, and s_{it} is the number of live trees in the sample plot.

The quantity phf_{ijt}^k can be estimated for each method using the following formulae:

$$\begin{aligned}\mathrm{phf}_{ijt}^{\mathrm{FP}} &= \frac{10,000}{\pi R_i^2} && (6)\\ \mathrm{phf}_{ijt}^{\mathrm{IC}} &= 3 \times \left[\frac{D_{ijt} - d_{ij}}{D_{ijt}}\right] \times \frac{\mathrm{BAF}_{it}}{g_{ijt}} && (7)\\ \mathrm{phf}_{ijt}^{\mathrm{F}} &= \frac{1}{g_{ijt}} \times \left[\frac{10,000}{4 - 8\ln(p)}\right] \times \\ &\quad \left[\left(\frac{\mathrm{DBH}_{ijt}}{100 d_{ij}}\right)^2 I_t^+ + \left(\frac{\mathrm{DBH}_{ijt}}{p100D_{ijt}}\right)^2 I_t^-\right] && (8)\end{aligned}$$

where FP=fixed-area plots, IC=cone implementation of the Iles' method, and F=Flewelling's method; R_i is the fixed-area plot radius (m); g_{ijt} is the tree basal area (m^2/ha); D_{ijt} is the variable plot radius (m); d_{ij} is the distance (m) between the plot centre and the tree; p is the proportion of the variable plot radius where the tree-level BAF starts to decrease; DBH is the DBH (cm), I_t^+ is an indicator variable that takes the following values:

$$\begin{aligned} I_t^+ &= 1 \quad \text{if} \quad 0.4D_{ijt} < d_{ij} \le D_{ijt} \\ &= 0 \quad \text{if} \quad 0 \le d_{ij} \le 0.4D_{ijt} \end{aligned} \tag{9}$$

and I_t^- is $1 - I_t^+$.

The coefficient 3 in Equation (7) is the coefficient for a cone. The cone was used for this paper but other shapes having different coefficients are also possible. Flewelling (1981) was not specific about the relative distance where the BAF starts to decrease, other than recommending a value between 0.3 and 0.6. After examining his Figure 3, the value 0.4 ($p = 0.4$) was selected because it appeared to be an adequate choice for the range of growth rates shown in the figure (5%, 10%, 20%, and 40%).

Using Equations (4) and (5), Cut and Mortality change estimators can be defined as:

$$\hat{V}_{i1}^{kM} = \left[\sum_{j=1}^{m_{i1}^k} y_{ij1}\right] \times \mathrm{phf}_{ij1}^k \tag{10}$$

$$\hat{V}_{i1}^{kC} = \left[\sum_{j=1}^{c_{i1}^k} y_{ij1}\right] \times \mathrm{phf}_{ij1}^k \tag{11}$$

where $\hat{V}_{i1}^{kM}$ and $\hat{V}_{i1}^{kC}$ are the attribute estimators for the Cut and Mortality components, respectively, and m_{i1}^k and c_{i1}^k are the number of M or C trees, respectively. Since M and C trees behave similarly and there were no C trees in the BC data, both groups are reported as a single group under Mortality in the Results section.

Various estimators for the survivor and ingrowth components have been proposed in the past. An unbiased estimate of the sum of the survivor and ingrowth components can be defined as:

$$\begin{aligned} \hat{\Delta}_i^{kS+I} = & \sum_{j=1}^{l_i^k} \left[\left(y_{ij2} \times \mathrm{phf}_{ij2}^k\right) - \left(y_{ij1} \times \mathrm{phf}_{ij1}^k\right)\right] + \\ & \sum_{j=1}^{r_i^k} y_{ij2} \times \mathrm{phf}_{ij2}^k \end{aligned} \tag{12}$$

where $\hat{\Delta}_i^{kS+I}$ is the estimate of the sum of the survivor and ingrowth components, l_i^k is the number of L trees, and r_i^k is the number of R trees. Equation (12), however, cannot easily be split into survivor and ingrowth components. While all L trees should be added within the survivor change component estimate, R trees should be added to either the survivor or the ingrowth component estimate, but it is generally impossible to tell which trees belong to each component without additional information.

If the DBH tagging limit was 0, or if DBH on borderline trees outside the plot were recorded at Time 1, or if R trees were cored, unbiased estimates of the survivor and ingrowth components would be possible:

$$\begin{aligned} \hat{\Delta}_i^{kS} = & \sum_{j=1}^{l_i^k} \left[\left(y_{ij2} \times \mathrm{phf}_{ij2}^k\right) - \left(y_{ij1} \times \mathrm{phf}_{ij1}^k\right)\right] + \\ & \sum_{j=1}^{r_i^k} y_{ij2} \times \mathrm{phf}_{ij2}^k I_{ij}^+ \end{aligned} \tag{13}$$

$$\hat{V}_{i2}^{kI} = \sum_{j=1}^{r_i^k} y_{ij2} \times \mathrm{phf}_{ij2}^k (1 - I_{ij}^+) \tag{14}$$

where $\hat{\Delta}_i^{kS}$ and $\hat{V}_{i2}^{kI}$ are unbiased estimators of the survivor change (Δ^S) and the ingrowth component (V_2^I) respectively using method k, and I_{ij}^+ is an indicator variable (1 if DBH was above the tagging limit at Time 1, 0 otherwise). In most situations, I_{ij}^+ are unknown. One obvious biased option is to use a model to predict the unknown indicator variables. Bias is then introduced by the wrong predictions of the indicator variable. Grosenbaugh (1958) proposed an unbiased survivor component estimator:

$$\hat{\Delta}_i^{GS} = \sum_{j=1}^{l_i^k} (y_{ij2} - y_{ij1}) \times \mathrm{phf}_{ij1}^k \tag{15}$$

where $\hat{\Delta}_i^{GS}$ is Grosenbaugh's net survivor change estimator, but this estimator can be larger then the unbiased estimate for the sum of the survivor and ingrowth components (Equation 12), leading to an inconsistency because the estimate for ingrowth would then be negative to maintain additivity. Grosenbaugh, in a personal communication to Tim Gregoire, suggested rescaling $\hat{\Delta}_i^{GS}$ to avoid negative ingrowth estimates (Gregoire 1993).

Rather than re-scaling $\hat{\Delta}_i^{GS}$, the estimator can be constrained between known lower and upper bounds. The indicator variable I_{ij}^+ in Equations (13) and (14) is not unknown for all trees. Trees that are at a distance less than the maximum radius of a tree with the DBH tagging limit have obviously an indicator variable of 0 since they would have been included if their DBH had been at or above the DBH tagging limit. Some trees have obviously an indicator variable of 1 for biological reasons; their DBH could not have been below the DBH tagging limit at Time 1. If we call B trees those trees whose indicator variable is obviously 1, and W trees those trees whose indicator variable is truly unknown, the estimated lower and upper bounds of the survivor component are:

$$\begin{aligned}\hat{L}_i^k &= \sum_{j=1}^{l_i^k} \left[\left(y_{ij2} \times \text{phf}_{ij2}^k \right) - \left(y_{ij1} \times \text{phf}_{ij1}^k \right) \right] + \\ &\quad \sum_{j=1}^{b_i^k} y_{ij2} \times \text{phf}_{ij2}^k \qquad (16)\\ \hat{U}_i^k &= \hat{L}_i^k + \sum_{j=1}^{w_i^k} y_{ij2} \times \text{phf}_{ij2}^k \qquad (17)\end{aligned}$$

where $\hat{L}_i^k$ and $\hat{U}_i^k$ are the estimated lower and upper bounds of the survivor component, respectively; b_i^k is the number of B trees; and w_i^k is the number of W trees. We then define the survivor net change component estimator as:

$$\hat{\Delta}_i^{kS} = MIN(\hat{U}_i^k, MAX(\hat{L}_i^k, \hat{\Delta}_i^{GS})) \qquad (18)$$

and the estimator for the ingrowth component as:

$$\hat{V}_{i2}^{kI} = \hat{\Delta}_i^{kS+I} - \hat{\Delta}_i^{kS} \qquad (19)$$

For the HKK data set, 2,000 repetitions of a 50-point sample were simulated. Each sample followed a systematic sampling design with a random start. The initial point was randomly selected within the coordinates [(0 m, 100 m), (0 m, 100 m)] and subsequent plots were located with 100 m offset in both the x- and y-axes. The walkthrough method (Ducey et al. 2004) was applied to boundary overlap situations. The regularly shaped rectangle used as boundary of the HKK data set meets the formal requirement for unbiasedness of the walkthrough method as stated by Ducey et al. (2004). The mean estimate of each sample was considered as a single observation (sample size of 2,000).

Relative efficiency was defined as the ratio of the variation of the plot estimate around the population parameter:

$$RE_{k/l} = 100 \times \frac{\sum_{i=1}^{n} (\hat{y}_i^k - \mu)}{\sum_{i=1}^{n} (\hat{y}_i^l - \mu)} \qquad (20)$$

where $RE_{k/l}$ is the relative efficiency of method k with respect to method l, $\hat{y}_i^k$ is either the plot-level change estimate on plot i (BC data) or the mean plot-level change estimate in sample i (HKK data) using method k; n is the number of observations (152 in the BC data and 2,000 in the HKK data); and μ is the population parameter. The population parameter μ was the true average change for the 152 plots in the BC data and the true change between 1999 (Time 1) and 2004 (Time 2) for the HKK data. RE greater than 100% indicates estimator l is more efficient or the opposite if less than 100%. Note that survivor change for trees/ha when using fixed-area plots is 0 by definition; relative efficiency based on that estimate is meaningless and doesn't need to be calculated.

The bias of the change estimators was also computed using:

$$\text{Bias}^k = \frac{1}{n} \sum_{i=1}^{n} \hat{y}_i^k - \mu \qquad (21)$$

where Bias^k is the bias due to estimator k.

All computations and simulations were completed within the statistical software R (R Development Core Team 2008).

5 RESULTS

5.1 Relative Efficiency: Iles' method was most efficient for estimating overall net change in basal area and volume while the fixed-area plot estimator was most efficient for estimating overall net change in trees/ha (Table 2). Flewelling's method was less efficient than Iles' method for basal area and volume while it was slightly better for trees/ha. The difference in efficiency was larger in the HKK data than in the BC data.

The results for the net change components were similar to the overall estimates, except that fixed-area plots were more efficient to estimate all ingrowth attributes. Ingrowth trees contribute little to basal area and are selected less frequently in point samples. This was particularly the case in the HKK data where DBH ranged between 1 and 400 cm. More ingrowth trees would have been selected if two BAFs would have been used at each point. For instance, a BAF of 1 m^2/ha for trees less than 10 cm and the regular BAF for trees bigger than 10 cm could have been used. This strategy would have increased the probability of selection of trees less than 10 cm in point samples.

5.2 Bias: Both Iles' and Flewelling's methods showed less bias than the fixed-area plot method in the BC data (Table 3). BC data results showed bias because the sampling point was not random and the stand conditions around the sampling point were not necessarily similar to the entire plot, not because of biases in the procedures. The smaller bias with the two methods based on variable-radius plots indicates that these methods provided estimates that were more representative of the full-size permanent sample plots than the small-size fixed-area plots. The bias results for the HKK data set are more indicative of the true potential for bias because each of the 2,000 samples was based on a systematic design with a different random starting point. There was very little bias associated with basal area in the HKK data set. Only Flewelling's method showed some

Table 2: Relative efficiency (%) of net change estimates in the BC and HKK data sets.

Methods	BC			HKK	
	Trees/ha	Basal Area m^2/ha	Volume m^3/ha	Trees/ha	Basal Area m^2/ha
			Survivor		
FP/IC		260	184		1998
FP/F		249	190		199
F/IC	79	105	97	95	1005
			Mortality		
FP/IC	44	164	204	2	1748
FP/F	42	156	186	2	1799
F/IC	105	105	110	96	97
			Ingrowth		
FP/IC	26	43	50	2	4
FP/F	30	49	53	2	5
F/IC	86	88	95	96	96
			Overall		
FP/IC	31	148	211	2	1571
FP/F	33	142	191	2	798
F/IC	94	105	110	96	197

bias when estimating survivor basal area. The observed bias associated with ingrowth and overall net change for trees/ha with Iles' and Flewelling's methods is more likely due to random variation because the proposed estimators are theoretically unbiased for trees/ha. Ingrowth trees were all less than 4 cm DBH in the HKK data. This translates into a maximum plot size of about 2 m^2 when using a BAF of 6 m^2/ha. Given the small plot areas surrounding ingrowth trees, it appears that 100,000 plots (2,000 samples of 50 plots) were not close enough to infinity to provide the theoretical answer, given the size of the population (50 ha).

6 Discussion

Furnival (1979) related his difficulties in convincing people that change can be estimated using point samples. Husch *et al.* (1983, pp. 315–317) discussed common concerns among foresters about estimating change using point samples. They dismissed most of the concerns but the compatibility issue remained (because they looked at only the Grosenbaugh (1958) estimator). Scott (1998) does not recommend point samples for permanent sample plots, mainly because of problems with estimating the change components and that he did not consider the newer methods to estimate change in variable-radius plots.

As in many complex questions, the debate over fixed-area plots or point samples to estimate change should not be settled by a definite statistical answer. There are practical pros and cons to both plot layouts and it is important to take these pros and cons into consideration when deciding what plot layout is best. Organizations wondering if they can re-measure existing point samples to estimate change should be told it can be done, and that it is more efficient for volume and basal area. A network of existing point samples should not be dismissed outright for change estimation because the past literature preferred fixed-area plots.

When only overall net change is needed (that is, no change component is required), variable-radius plots and Iles' method should be considered. Iles' method was more efficient at estimating overall change for basal area and volume than either fixed-area plots or Flewelling's method and less efficient for trees/ha. Thus, whenever estimating change in basal area and volume are more important than change in trees/ha, variable-radius plots and Iles' method would be an appropriate choice.

In the rare situations when estimates of change components are needed, the best option is not as clear. Practical solutions for the perceived compatibility problem associated with variable-radius plots exist. Unbiased, compatible, and time-additive estimators for survivor

Table 3: Bias in net change estimates in British Columbia (BC) and Thai (HKK) data sets

Methods	BC Trees/ha	BC Basal Area m^2/ha	BC Volume m^3/ha	HKK Trees/ha	HKK Basal Area m^2/ha
		Fixed-Area			
Survivor	0.0	0.5	7.5	0.0	0.0
Mortality	-46.6	-2.7	-29.9	-2.7	0.2
Ingrowth	-19.7	-0.2	-1.3	-4.1	0.0
Overall	-66.3	-2.4	-23.6	-6.8	0.2
		Iles			
Survivor	0.0	0.3	4.8	0.0	0.0
Mortality	-35.0	-1.9	-19.9	3.7	0.0
Ingrowth	-8.8	-0.3	-1.6	18.8	0.0
Overall	-43.8	-1.9	-16.6	22.4	0.0
		Flewelling			
Survivor	0.0	0.0	3.0	0.0	0.5
Mortality	-43.8	-2.0	-21.2	2.1	0.0
Ingrowth	-16.4	-0.1	-0.1	16.8	0.0
Overall	-60.2	2.1	-18.2	18.9	0.5

and ingrowth change can be obtained with minimal efforts (Equations 13 and 14). There was, on average, only 1 and 0.5 R trees per plot in the BC and HKK data, respectively. If estimating ingrowth change is an important aspect of the permanent sample plot program, borderline trees outside the plot should be measured for distance and DBH, and eliminated from the compilation by the compilation software. The only measurement required on these borderline trees outside the plot is DBH to be able to determine if they were above or below the tagging limit at the previous measurement. Modifying the compilation software to flag these trees should not be onerous.

A constrained version of the Grosenbaugh (1958) survivor estimator can be used to estimate survivor change. The ingrowth estimator derived from Equation (12) and the constrained Grosenbaugh estimator (Equation 18) is always positive. The potential for bias can be drastically reduced by reducing the number of W trees (trees where the status above or below the DBH tagging limit is truly unknown). A careful review of the R trees and available information (site index, relative DBH growth on L trees, etc.) should help reduce the number of W trees. In the two data sets used for this paper, W trees were present on only 24% and 3% of the plots in the BC and HKK data sets, respectively. The bias will never be eliminated using this estimator, but it could be made practically insignificant.

Fixed-area plots were more efficient for estimating change in all ingrowth attributes and trees/ha, while Iles' method was more efficient for estimating change in volume and basal area for the survivor and mortality components. Variable-radius plots are inefficient for quantifying ingrowth of small trees simply because those trees are sampled at a lower frequency than survivor trees. Whenever ingrowth is an important attribute requiring a change estimate, fixed-area plots are the most efficient plot layout. It is also possible to use both fixed-area plots for trees under a certain size and variable-radius plots for larger trees. Using multiple plot layouts centered at one sampling point is an efficient sampling strategy when sampling for different resources. The same idea can be applied when estimating change for ingrowth and survivor trees.

One major drawback with variable-radius plots is the difficulty of extracting inter-tree spatial interactions. Large, fixed-area plots provide the most information for this purpose simply because more spatial interactions can be investigated at a single point. Inter-tree spatial interactions are usually not an operational concern but research organizations are well justified to use fixed-area permanent sample plots simply for that reason. The main advantage variable-radius plots have over fixed-area plots is their statistical efficiency for important variables as shown by the results of this study. Statistical efficiency, however, is usually not an important concern for establishing a network of permanent sample plots for research purposes.

Finally, the importance of recording in the field the distance between the sampling point and the trees in variable-radius plots must be emphasized. Range finders and lasers now make this task very simple. Stem-mapping should become a standard inventory practice to facilitate future use of variable-radius plots. The extra time in the field to record the information is minimal, changes to the database to store the information are simple, and modifications to the data compilation software are straightforward and will allow the software to compute change. Organizations with stem-mapped permanent sample plots can easily test Iles' method over multiple measurements and various forest types and compare the results to their traditional estimators.

7 Conclusions

Foresters have refrained from using variable-radius plots for estimating change over concerns about the statistical efficiency and compatibility of change estimates. The new change estimator proposed by Iles and Carter (2007) was shown to be more efficient than the fixed-area plot estimator for basal area and volume for overall net change. Compatibility and time additivity are no longer an issue undermining the credibility of change estimates based on point samples. The perceived complexity due to the expanding inclusion zone is no longer a problem. Iles' method can be retro-fitted on existing stem-mapped fixed-area permanent sample plots (after checking for possible large trees outside the plots) and its accuracy compared to traditional change estimates. Change component estimators for point samples exist and can be unbiased under certain unrestrictive conditions (tagging limit is 0, or DBH of borderline trees is recorded, or recruitment trees are cored). Point-to-tree distance is now a simple measurement that should be recorded in all forest management inventories. Finally, forestry students should be taught that point samples can be used efficiently to estimate change.

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