

Field efficiency and bias of snag inventory methods

Robert S. Kenning, Mark J. Ducey, John C. Brissette, and Jeffrey H. Gove

Abstract: Snags and cavity trees are important components of forests, but can be difficult to inventory precisely and are not always included in inventories because of limited resources. We tested the application of N -tree distance sampling as a time-saving snag sampling method and compared N -tree distance sampling to fixed-area sampling and modified horizontal line sampling in mixed pine–hardwood forests of southern Maine and New Hampshire. We also present a novel modification of N -tree distance sampling that limits the distance from plot center that an observer must search to find tally trees. A field test shows N -tree to be quick, but generally biased and characterized by high variability. Distance-limited N -tree sampling mitigates these problems, but not completely. We give recommendations for operational snag inventory in similar forest types.

Résumé : Les chicots et les arbres avec des cavités sont des composantes importantes de la forêt. Par contre, ils peuvent être difficiles à inventorier avec précision et ils ne sont pas toujours inclus dans les inventaires à cause des ressources limitées. Cette étude teste l'application de l'échantillonnage de N arbres selon la distance comme méthode d'échantillonnage des chicots qui permet d'économiser du temps. Les auteurs comparent l'échantillonnage de N arbres selon la distance à l'échantillonnage par placettes circulaires à rayon fixe et à l'échantillonnage en ligne horizontale modifié dans les forêts mélangées de pin et de feuillus dans le sud du Maine et du New Hampshire. Une modification originale de l'échantillonnage de N arbres selon la distance visant à réduire la distance à partir du centre de la placette sur laquelle l'observateur doit chercher pour trouver les arbres à considérer est aussi présentée. Un test sur le terrain montre que l'échantillonnage de N arbres selon la distance est rapide, mais il est généralement biaisé et caractérisé par une forte variabilité. L'échantillonnage modifié de N arbres selon la distance corrige ces problèmes, mais pas complètement. Des recommandations sont fournies pour l'inventaire de chicots dans les types de forêt similaires.

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Introduction

With increasing attention being paid to nontimber aspects of forest management (e.g., New Hampshire Forest Sustainability Standards Work Team 1997), foresters are occasionally called on to inventory nontraditional aspects of forest structure, including snags. Snags are important to a variety of wildlife species in northern forest types (DeGraaf et al. 1992), and Forest Stewardship Council guidelines call for maintenance of snag abundance to support “natural cycles that affect the productivity of the forest ecosystem” (Forest Stewardship Council 2002, p. 19). Snags are rarely the sole or primary focus of forest inventories, however, so a sampling regime that does not add much extra time while preserving acceptable confidence limits would be ideal. Unfortunately, snags are notoriously difficult to inventory, in part because they are often sparsely distributed (Bull et al. 1990), and there is little to guide the practitioner in choosing an appropriate sampling method.

Most current inventory methods for snags are modifications of methods for live trees and focus on design-unbiased approaches. These methods include strip cruising, sampling with fixed-area plots, and horizontal point sampling (prism

sampling). However, such methods typically encounter very few snags, with high point-to-point variability, and as a result confidence limits can be poor despite considerable time investment (Bull et al. 1990). Recently, Ducey et al. (2002) proposed a method that can be considered a hybrid of horizontal point and horizontal line sampling. This modified horizontal line sampling (MHLS) approach produces larger tallies than horizontal point sampling, without the visibility problems that would occur simply through changing the basal area (BA) factor in horizontal point sampling. It was competitive with horizontal point sampling in their limited field trial in terms of efficiency, where efficiency is defined in terms of the relationship between time spent sampling and width of the resulting confidence limits.

Recently, renewed attention has focused on N -tree distance sampling for live tree inventories. N -Tree distance sampling is done by measuring characteristics of interest on a specified number of trees (N) closest to the sample point (Moore 1954, Cottam and Curtis 1956). Distance to the furthest (N th) tree forms the radius of an imaginary circular plot at each sample location. For example, if $N = 3$ (three-tree distance sampling), the third closest tree would be located and its distance from plot center measured. This method often requires

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Table 1. Site description for the six study compartments.

Compartment name	Code	No. sample points	Area (ha)	BA (m ² /ha) ^a	QMD ^b (cm)	Dominant species	Description
East Foss Farm	EFF	31	7	27	24	<i>Pinus strobus</i> , <i>Acer rubrum</i> , <i>Quercus rubra</i>	Complex of managed stands
West Foss Farm	WFF	18	12	21	20	<i>Pinus strobus</i> , <i>Populus grandidentata</i> , <i>Acer rubrum</i>	Young, managed stand
College Woods A	CWA	16	10	32	33	<i>Pinus strobus</i> , <i>Tsuga canadensis</i>	Late-successional reserve
Massabesic S2	MEF2	59	40	21	19	<i>Pinus strobus</i> , <i>Acer rubrum</i> , <i>Quercus rubra</i>	Young stand, burned in 1947 fires
Massabesic S3	MEF3	56	135	40	29	<i>Pinus strobus</i> , <i>Tsuga canadensis</i> , <i>Acer rubrum</i>	Old stand, not burned in 1947 fires
Massabesic S4	MEF4	33	22	26	16	<i>Pinus strobus</i> , <i>Quercus rubra</i> , <i>Tsuga canadensis</i>	Two-cohort stand, partially burned in 1947

^aBA, basal area.^bQMD, quadratic mean diameter.

less time than traditional methods and is simple to implement. However, unlike fixed-area plots or horizontal point sampling, which are design-unbiased, that is, theoretically unbiased regardless of the spatial pattern of trees (Palley and Horwitz 1961), *N*-tree distance sampling makes specific assumptions about tree distribution and will be biased if those assumptions are violated (Pielou 1969). Hence, *N*-tree distance sampling is only model-unbiased (see, e.g., Gregoire 1998). *N*-Tree distance sampling was compared to fixed-radius plots and horizontal point sampling by Lessard et al. (1994) in several lake state forest types; their results suggested *N*-tree distance sampling might be cost-effective for rapid inventories. Other recent studies (Jonsson et al. (1992) in Scandinavia; Lynch and Rusydi (1999) in Indonesian teak plantations) have also shown promising results for live overstory inventories. However, no field test of *N*-tree distance sampling has been published for snag or cavity trees.

One challenge with *N*-tree distance sampling, especially when applied to sparse populations such as snags, is that the *N*th tree may be quite far from the sample point. This can dramatically increase search times and may lead to trees that should have been tallied being missed. A useful modification of *N*-tree distance sampling would limit the distance an observer must travel to locate the *N*th tree to some predetermined maximum distance, preferably one within which the search would be rapid and failsafe. Batcheler and Bell (1970) present just such a modification for the simple case of one-tree sampling. In this study, we developed a method that generalizes the Batcheler and Bell (1970) approach to distance-limited *N*-tree sampling.

We conducted a field study to compare the field performance, including bias, variability, and time efficiency, of *N*-tree distance sampling, distance-limited *N*-tree sampling, MHLS (Ducey et al. 2002), and fixed-area plot sampling. Fixed-area plot sampling was used as the "gold standard", as it is a commonly used technique, familiar to field foresters and ecologists, theoretically unbiased, and presents few opportunities to introduce bias through field errors.

Methods

Study site description

A snag inventory was completed in six management compartments from June to August 2002. Though each compart-

ment typically contained several stands, the general forest structure and age remained similar throughout a compartment. Three compartments were located on University of New Hampshire properties in Durham, New Hampshire, and three were in the Massabesic Experimental Forest in Alfred, Maine. A full floristic description of the Massabesic Experimental Forest is given by Dibble et al. (2004). The compartments span a range of structural and developmental characteristics associated with the transition hardwood forests of central New England (Table 1).

Compartments CWA and MEF3 were selected to represent mature conditions. Both compartments are dominated by large white pine (*Pinus strobus* L.) and eastern hemlock (*Tsuga canadensis* (Raf.) Sarg.), where individuals frequently have DBH >25 cm and have not experienced any major disturbances in recent history.

Compartments MEF2 and MEF4 were heavily burned by a severe fire in 1947 and were selected to represent younger, unmanaged forest conditions. The compartments are in the stem-exclusion stage, and an abundance of small snags is obvious upon visual inspection.

Compartments EFF and WFF represent middle-aged, mixed forest of white pine, oak (primarily *Quercus rubra* L.), aspen (both *Populus tremuloides* Michx. and *Populus grandidentata* Michx.), and red maple (*Acer rubrum* L.). Most trees are of pole to small sawtimber size class, but quadratic mean diameter is 41 and 43 cm, respectively, because of scattered individuals with DBH >64 cm.

Field methods

A timed field trial was performed to compare variance, bias in implementation, and efficiency between several snag sampling methods. We hypothesized that the small per-point sample size associated with *N*-tree sampling might yield a high variance, but that it might show comparable or better time efficiency compared to other methods because of reduced time requirements. Similarly, we hypothesized that both fixed setup costs and a large per-point sample in MHLS would lead to high time requirements, but that the payoff (in terms of design-unbiasedness and sampling larger snags with greater probability) might lead to even larger reductions in variance.

Each compartment was assigned a systematic array of plot centers (number of plots is indicated in Table 1), and eight sampling methods were used at each sampling location. The order of the methods was rotated systematically between points. Only the first method applied at each point was timed, since a foreknowledge of a sample tree's characteristics and location would underestimate time requirements for subsequent methods. In each method, all snags with DBH of 7.5 cm were tallied. To be considered a snag, the tree must be completely dead and taller than 1.37 m. Characteristics recorded were species, DBH, height by ocular estimation, presence or absence of cavities (defined as any visible hollowing of the stem at least 2.5 cm in diameter and depth, and excluding small insect holes), and decay according to the five-class system following Thomas et al. (1979). Though not presented in this paper, species, cavities, and decay class were recorded to simulate time requirements of an actual inventory. All methods were timed with both one-person and two-person crews.

It is important to note that all distances were measured with an electronic distance measurer (Haglof DME; Haglof, Inc., Madison, Mississippi). This saved considerable time on methods highly dependent on proximity, such as fixed-area sampling. Had we used a traditional tape measure, time requirements for these methods would be significantly higher and the efficiency ranking for each method might be different.

We used the following eight methods.

Method 1

We tallied all snags on an 0.02 ha, 8.03 m radius (1/20th acre, 26.33 ft radius) fixed-area circular plot. Distances to all borderline snags were measured using the electronic distance measurer. Choice of plot size was motivated by three major factors: anticipated variability, nonsampling error, and time cost. Of these, nonsampling error was most critical for the purposes of this study; for fixed-area plots to provide unbiased estimates, it was important that field errors, such as missing small snags, be minimized. Variability is less important, because in operational inventories it can be controlled by changing the number of plots used. We know of no time-cost study evaluating varying plot sizes for snag inventory, but efficiency studies in live tree inventory report relatively small efficiency changes when plot size varies over a reasonable range (Zeide 1980; Gambill et al. 1985). The plot size used here is slightly larger than the 0.017 ha plot used by the USDA Forest Service Forest Inventory and Analysis program (USDA Forest Service 2005).

Method 2

We performed MHLS using a 40.23 m (132 ft) transect centered on the sample point and a prism with a BA factor of 4.59 m²/ha (20 ft²/acre). In MHLS, all trees that appear "in" using the prism along the transect are tallied, creating a variable-width strip. In addition, the prism is used in a half-sweep around each end of the transect, capping the variable-width strip with half of a variable-radius plot on each end. The result is a sausage-shaped inclusion zone, the size of which is a linear function of DBH and DBH² for each snag. Theory for the method, including estimators for snags per unit area and BA per unit area, is presented in Ducey et al. (2002). The transect was laid out using the electronic distance measurer and a hand compass and marked visibly with

pin flagging to facilitate checking borderline trees. Measurement time for this method included removal of flagging.

Methods 3, 4, and 5

We conducted ordinary N -tree distance sampling, tallying only snags and ignoring live trees. We conducted sampling with $N = 1$ (simple nearest-neighbor sampling), $N = 2$, and $N = 3$. After an initial field reconnaissance, we judged that locating more than three snags would require an impractically large search area in most stands. Suppose there are n sample points, and let $r_{i,N}$ be the distance (in m) from the sample point to the N th tree on the i th point. Then a bias-adjusted maximum likelihood estimator of the number of snags per hectare, λ , is (Pollard 1971)

$$[1] \quad \hat{\lambda}_P = \frac{10000(Nn - 1)}{\pi \sum_{i=1}^n r_{i,N}^2}$$

and the corresponding estimator of BA (Jonsson et al. 1992) is

$$[2] \quad \hat{B} = \bar{B} \hat{\lambda}_P$$

where \bar{B} is the average BA (in m²) of the tallied snags. Note that eq. 1 differs from the estimator presented by Lessard et al. (1994), who formed an estimate for each point and then averaged those estimates. Equations 1 and 2 provide unbiased estimates if snags are randomly distributed in space without regard to size or the position of other snags, but may lead to biased estimates if snags are clumped or distributed in a regular fashion (like trees in a plantation).

Methods 6, 7, and 8

We conducted distance-limited N -tree sampling with $N = 1$, $N = 2$, and $N = 3$ and a maximum search distance of 8.03 m (26.33 ft). In distance-limited N -tree sampling, if the maximum search distance is reached before the N th tree is found, the search for additional trees is terminated. In other words, the field procedure is exactly like N -tree sampling, except the search is confined to a small circular plot.

Using the same notation as for N -tree sampling, let r_{\max} be the maximum search distance and let $q_{i,N}$ be the lesser of $r_{i,N}$ and r_{\max} . In other words, if $r_{i,N}$ is reached before r_{\max} , then $q_{i,N} = r_{i,N}$; otherwise, $q_{i,N} = r_{\max}$. Furthermore, let m_i be the number of snags reached within search distance $q_{i,N}$; note $m_i \leq N$. Then, assuming a Poisson (completely random) distribution of snags, the maximum likelihood estimator of λ is

$$[3] \quad \hat{\lambda}_{ML} = \frac{10000 \sum_{i=1}^n m_i}{\pi \sum_{i=1}^n q_{i,N}^2}$$

However, this estimator is slightly biased. Unfortunately, the integrals necessary to evaluate an exact bias correction are intractable. Through simulations, we found that a correction factor, incorporating the number of plots n_{\max} at which $m_{i,N} = N$,

$$[4] \quad c = \frac{Nn - n_{\max}/n}{Nn}$$

leading to an adjusted estimator

$$[5] \quad \hat{\lambda}_{DL} = c\hat{\lambda}_{ML}$$

provided nearly unbiased estimates for reasonable sample sizes when the Poisson assumption was satisfied. Derivations, and results of the simulations, are presented in Appendix A.

Statistical analysis

Basic estimates of snags per hectare and snag BA per hectare were calculated using the usual estimators for fixed-area sampling, the estimators presented in Ducey et al. (2002) for MHLS, and the estimators given above for *N*-tree and distance limited *N*-tree. To evaluate whether snags were clumped in each compartment, we performed a variance ratio test using the fixed-area plot data. Under the Poisson assumption, note that the variance of the number of snags tallied on each plot (*x*) should equal the average plot tally (λ). The variance:mean ratio

$$[6] \quad v = \frac{s_x^2}{x}$$

is distributed as χ^2 with *n* – 1 degrees of freedom (Fisher et al. 1922; Pielou 1969). While the variance ratio *v* may fail to detect many departures from Poisson, and has inadequacies as a general measure of spatial pattern (Hurlbert 1990), it serves our purposes as a weak test and description of the clumping of snags in each compartment (e.g., Pielou 1969, p. 91).

Variance estimates for fixed-area plots and for MHLS were calculated using the usual estimators as the variances of the estimates from individual points (e.g., Husch et al. 2003, p. 36; Ducey et al. 2002). However, because the *N*-tree and distance-limited *N*-tree estimators do not rely on probability sampling, the variances cannot be computed in that fashion. Instead, we used a simple bootstrap resampling procedure (Efron and Tibshirani 1993) to calculate the variances of the estimates for each of these methods. In the bootstrap procedure, points (rather than trees) are resampled from the original data set with replacement; we used 10 000 bootstrap repetitions, which is far more than is necessary for variance estimation but was useful for hypothesis testing (detailed in next paragraph). For comparative purposes, we also calculated an equivalent coefficient of variation as

$$[7] \quad CV_z = 100 \frac{\sqrt{nS_z^2}}{\hat{z}}$$

where *z* is either snags per unit area or BA per unit area. This calculation assumes that the variance of the estimate for *N*-tree and distance-limited *N*-tree is proportional to n^{-1} , which is approximately true under the Poisson assumption (Pollard 1971).

An ideal test of the bias of the methods would require complete knowledge of the population, that is, a 100% tally of the snags in each compartment. Such a tally is extremely time consuming (Bull et al. 1990). Instead, we used the fixed-area plot estimates as a “gold standard”, because the method is familiar to practitioners, design-unbiased, and pres-

ents relatively few opportunities for field error. To test whether the estimate for a particular method differed from the fixed-area plot estimate, we used a bootstrap procedure (Efron and Tibshirani 1993). For each repetition of the bootstrap, a synthetic data set with the same number of plots as the original was generated by resampling the original plots with replacement. The appropriate estimators and snag density and BA were employed for each method. We used 10 000 repetitions to build up a bootstrap distribution for the difference between the fixed-area plot estimate and the estimates for the other methods, and a percentile test was used to evaluate the statistical significance of the observed difference. Note that a paired-sample *t* test could have been used to evaluate the differences between fixed-area plots and MHLS, but the extreme non-normality of the differences violated a key assumption of the test. A paired sample *t* test would have been inappropriate for the *N*-tree and distance-limited *N*-tree estimates, because those estimates are not the mean of the individual plot estimates.

To estimate time requirements for each method, using crew sizes of one or two, at all points, we used a regression approach. In fixed-area sampling and MHLS, the number of snags tallied can have a strong influence on time requirements. We modeled time requirement for these methods as

$$[8] \quad t_i = \beta_0 + \beta_1 x_i + \varepsilon$$

where *t_i* is the time required at a point, *x_i* is the number of snags tallied, ε is an error term, and β_0 and β_1 are fitted coefficients. By contrast, in *N*-tree sampling, the number of snags tallied per point is fixed, but the area searched can vary widely; we modeled time requirement as

$$[9] \quad t_i = \beta_0 + \beta_2 \pi(r_{i,N})^2 + \varepsilon$$

In distance-limited *N*-tree sampling, both the number of snags tallied and the search area can vary; our model was

$$[10] \quad t_i = \beta_0 + \beta_2 x_i + \beta_2 \pi(q_{i,N})^2 + \varepsilon$$

Equations 8, 9, and 10 were fit to the data pooled across compartments, but treating crew size separately, using non-negative least squares. The resulting equations were then used to estimate the time requirement for each method and crew size for every point.

We calculated efficiency of each method as

$$[11] \quad e = \frac{CV_z^2 \sum_i \hat{t}_i}{CV_{z,FA}^2 \sum_i \hat{t}_{i,FA}}$$

where *z* is either snags per unit area or BA per unit area and FA denotes fixed-area plots. When *e* > 1, a method is less efficient than fixed-area plots; when *e* < 1, the method is more efficient. By definition, the efficiency of fixed-area sampling is one. Comparison of efficiencies using eq. 11 involves two assumptions: first, that the bias of a method can safely be ignored, and second, that the variance of the estimate is proportional to n^{-1} . The second assumption is true exactly for MHLS and is nearly exact for *N*-tree and distance-limited *N*-tree sampling except when *n* is very small.

Table 2. Summary of results from fixed-area sampling, and variance ratio tests for randomness.

Stand ^a	No. snags/ha	Snag BA ^b (m ² /ha)	Snag QMD ^c (cm)	Variance ratio	<i>p</i>
EFF	100.4 ± 17.8	2.34±0.49	17	1.98	0.002
WFF	148.3 ± 35.3	2.59±0.76	15	3.06	<0.001
CWA	68.0 ± 17.4	1.54±0.54	17	1.44	0.235
MEF2	216.9 ± 15.8	2.43±0.21	12	1.37	0.001
MEF3	132.4 ± 18.7	3.99±0.71	20	3.00	0.061
MEF4	194.7 ± 24.1	2.89±0.54	14	2.00	<0.001

Note: Estimates are shown as mean ± 1 SE.

^aStand codes are defined in Table 1.

^bBA, basal area.

^cQMD, quadratic mean diameter.

Table 3. Sampling method time requirements by stand for crew sizes of one or two persons.

Stand ^a	Time (min) ^b							
	FAS	MHLS	One-tree	Two-tree	Three-tree	DL one-tree	DL two-tree	DL three-tree
One-person crew								
EFF	3.8	9.9	1.5	4.7	5.8	1.8	2.7	3.3
WFF	4.9	10.4	1.3	3.9	4.7	1.6	2.7	3.6
CWA	3.2	8.5	1.6	5.0	6.4	2.0	2.7	3.2
MEF2	6.3	11.6	1.3	3.6	4.1	1.5	3.1	4.4
MEF3	3.3	8.3	1.4	4.8	6.0	1.9	2.5	3.0
MEF4	5.8	10.8	1.3	3.8	4.3	1.6	2.8	3.9
Two-person crew								
EFF	2.6	6.0	1.4	3.7	4.6	0.9	1.8	2.0
WFF	3.3	6.3	1.1	2.5	3.6	0.7	1.8	2.2
CWA	2.1	5.2	1.4	4.2	5.1	1.1	1.8	1.9
MEF2	4.2	7.0	1.1	2.1	3.1	0.6	1.8	2.7
MEF3	2.2	5.1	1.2	3.9	4.7	1.0	1.8	2.4
MEF4	3.9	6.5	1.1	2.3	3.3	0.7	1.8	2.4

^aStand codes are defined in Table 1.

^bTo obtain person-minutes, multiply time requirements for a two-person crew by two.

Results and discussion

Table 2 summarizes the results of the fixed-area sample for each of the study compartments. Snag number and BA were poorly related with the developmental stage in each compartment, although mean snag diameter was weakly related to mean diameter of the existing overstory trees. All six study compartments showed variance:mean ratios greater than one, although in two compartments the ratio was not statistically significant. Nonetheless, there is a strong tendency for snags to be clumped in most of the study compartments. In several compartments, this was at least partly due to the abundance of dead stump sprouts of *Acer rubrum*.

The design of the study offers an opportunity to examine whether the selected plot size (0.04 ha) is sufficiently small to avoid nonsampling error, because the area around the plot center is searched multiple times as each sampling method is conducted in sequence. Over the course of the study, 11 snags (or 1.9% of those within the plot radius) were missed during the initial fixed-area sample and were only discovered later when another method was employed. The missed snags tended to be smaller (quadratic mean diameter of 9.8 cm) than most snags tallied (quadratic mean diameter of 14.4 cm).

The result would be a very small bias in estimates of snags per hectare and an even smaller bias in BA per hectare; however, these results suggest that even with a relatively small plot, there is some danger of nondetection bias. Use of a larger fixed-area plot in these conditions seems certain to aggravate this difficulty.

Time requirements for each method are shown in Table 3. As expected, MHLS required the most time per point of any method. All the methods required substantially less time with a two-person crew than with a one-person crew, and this was especially true of MHLS.

Estimates of snags per hectare by method are shown in Fig. 1. Fixed-area sampling and MHLS gave similar estimates in every compartment, and field bias was never statistically significant. This is not surprising, since both methods are design-unbiased. By contrast, all of the *N*-tree methods, including distance-limited methods, were significantly biased in at least one compartment, with two-tree and three-tree sampling showing a significant downward bias in the majority of compartments. The lack of statistically significant bias for one-tree sampling in some compartments is almost certainly due to the high inherent variability of one-tree sampling and hence low power. Even when the bias was not

Fig. 1. Estimates for number of snags per hectare for each method and stand. Statistically significant bias is evaluated using a bootstrap paired-sample test (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$).

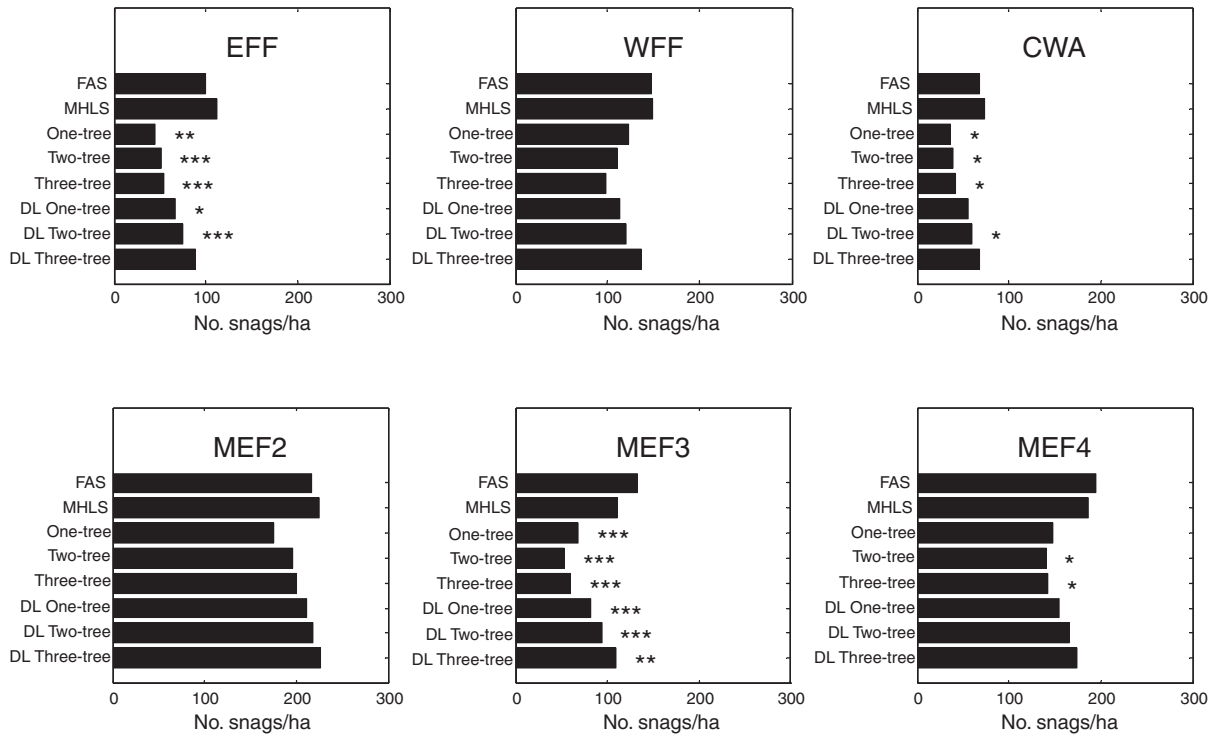
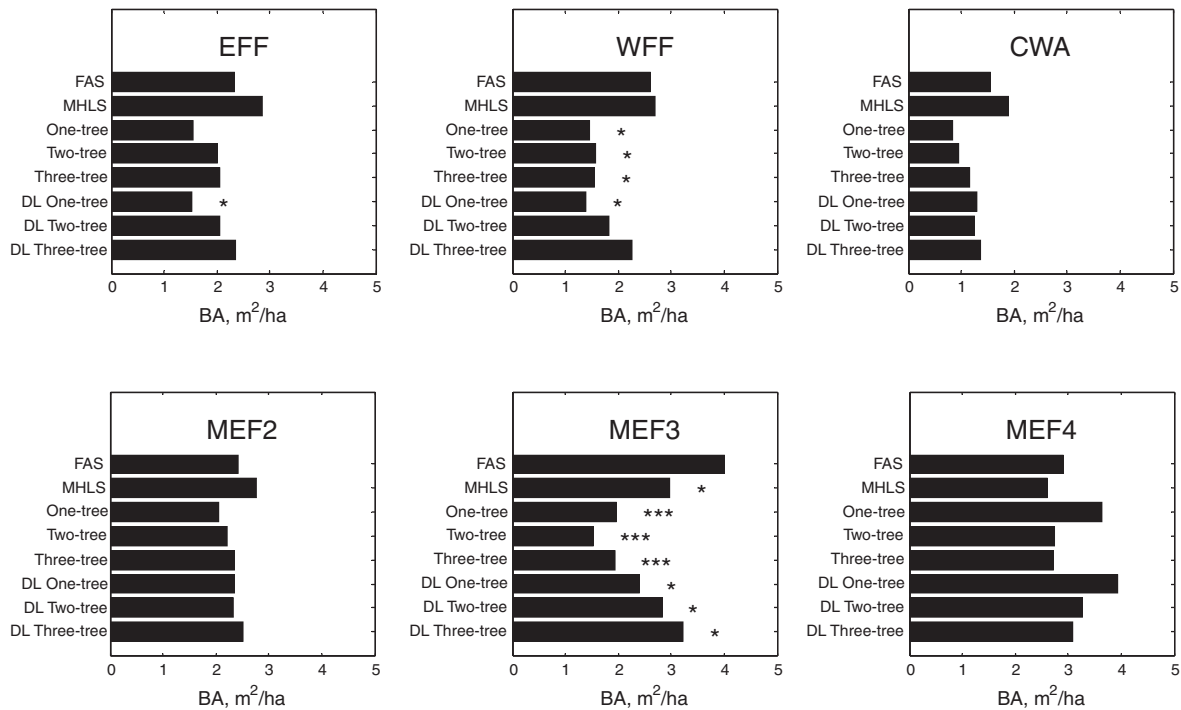


Fig. 2. Estimates for snag basal area per hectare for each method and stand. Statistically significant bias is evaluated using a bootstrap paired-sample test (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$).



statistically significant, a broad general trend in the estimates is apparent: the lowest estimates are given by the regular N -tree methods, followed by the distance-limited N -tree methods in order of increasing N , followed by the design-

unbiased methods. Bias using the N -tree methods is occasionally quite severe.

Estimates for snag BA are shown in Fig. 2. In some compartments, the pattern for BA is similar to that for snags per

Table 4. Effective coefficients of variation (CV) by stand and method for number of snags and snag basal area (BA).

Stand ^a	CV (%)							
	FAS	MHLS	One-tree	Two-tree	Three-tree	DL one-tree	DL two-tree	DL three-tree
No. snags/ha								
EFF	99	83	174	113	107	139	104	103
WFF	101	63	109	111	104	132	124	108
CWA	102	108	166	119	94	101	96	93
MEF2	56	56	189	116	97	109	81	69
MEF3	106	100	135	181	162	130	98	96
MEF4	71	67	137	115	105	134	108	89
Snag BA (m²/ha)								
EFF	117	73	143	122	109	162	143	135
WFF	124	66	157	139	137	171	149	139
CWA	141	95	256	185	127	231	147	139
MEF2	68	49	172	99	93	128	96	88
MEF3	134	85	223	211	181	244	165	149
MEF4	107	56	289	195	141	275	205	165

^aStand codes are defined in Table 1.

hectare, although statistical significance of the biases is generally weaker. MHLS gave a significantly lower estimate in only one compartment (MEF3). This may be due to an operational tendency to miss large snags. MEF3 had the highest live overstory BA of any compartment, and the BA factor employed in this study is slightly below the range that would be recommended in such a stand using typical rules of thumb calling for five to eight tally trees per point. MEF3 also contained large snags. Large snags can be located relatively far from the MHLS transect and might be hidden by live trees (Ducey et al. 2002). Alternatively, the result may simply be a false positive. Figures 1 and 2 jointly contain 84 significance tests for bias. Using $\alpha = 0.05$, one would expect approximately four false rejections of the null merely by chance. Note that a similar bias was not apparent in CWA, which also had large snags, albeit enmeshed in a live overstory with lower BA.

The bias results reported here for *N*-tree sampling are similar in pattern, if not in magnitude, to those found in other studies. For example, Jonsson et al. (1992) found underestimates of live tree number and volume in a simulation study, while Lessard et al. (1994) found underestimates in clumped stands and overestimates in a plantation. The underestimates were of much smaller degree in those studies, however. For example, Lessard et al. (1994) report underestimates of only up to 10%, while underestimates exceeded 50% in this study in several instances. A key difference may be in the value of *N*; the sparsity of snags forces a small value of *N* unless search distances can be allowed to grow very large. We considered the possibility that the difference was due to the estimator used in this study and that used by Lessard et al. (1994, 2002); however, use of the alternative estimator did not materially affect the bias and in some cases greatly increased the variance of estimates.

The distance-limited *N*-tree approach showed less bias overall than traditional *N*-tree methods. In a sense, this occurs because as snag abundance falls, distance-limited *N*-tree sampling behaves similarly to fixed-area plot. When the plot center falls in a "void" of a clumped stand, the observer is less likely to search a large treeless area; this impacts not only the search time, but also the estimates produced.

Effective coefficients of variation for each method are shown in Table 4. As expected, the heavy time investment in MHLS is partially compensated by lower variation, while the fast implementation at a single point of *N*-tree and distance-limited *N*-tree is often offset by higher variability. The combination of cost and variability in terms of efficiency is shown in Table 5 for snags per hectare. Regardless of crew size, fixed-area sampling is more efficient than either MHLS or *N*-tree sampling when snags per hectare is the primary variable of concern. For MHLS, this is not surprising, because from a design-based perspective, sampling is almost always most efficient when it is conducted with probability proportional to the variable of interest (e.g., Thompson 1992). Fixed-area sampling operates with probability proportional to frequency, so its properties should be nearly optimal for snags per hectare. The negative result for *N*-tree sampling was surprising, because model-based theoretical considerations have suggested that *N*-tree sampling might be more efficient (Lessard et al. 2002). Yet distance-limited *N*-tree sampling was more efficient than any other method, especially when a crew size of two was used. This efficiency should be considered skeptically, as the efficiency criterion used here does not account for bias; distance-limited *N*-tree sampling is not design-unbiased and did show significant downward bias in some compartments, especially with $N = 1$ and $N = 2$.

Efficiencies for BA are shown in Table 6. Here, a different pattern emerges. MHLS is almost always more efficient than fixed-area sampling with a crew size of two and is usually competitive even when the crew size is one. Again, design-based considerations explain the result: MHLS does not tally trees with probability proportional to BA, but it does place extra weight on large trees (Ducey et al. 2002). Traditional *N*-tree sampling is almost always worse than both fixed-area sampling and MHLS, and in some cases its performance is dismal, even without accounting for bias. The performance of distance-limited *N*-tree sampling is inconsistent from compartment to compartment.

Another way of looking at the relative performance of the different methods is to examine the time required to achieve a specified set of confidence limits on a target variable, as

Table 5. Efficiency of snag inventory methods relative to fixed area sampling for number of snags.

Stand ^a	No. snags/ha						
	MHLS	One-tree	Two-tree	Three-tree	DL one-tree	DL two-tree	DL three-tree
One-person crew							
EFF	1.83	1.22	1.61	1.78	0.93*	0.78*	0.94*
WFF	0.83*	0.31*	0.96*	1.02	0.56*	0.83*	0.84*
CWA	2.98	1.32	2.13	1.70	0.61*	0.75*	0.83*
MEF2	1.84	2.35	2.45	1.95	0.90*	1.03	1.06
MEF3	2.24	0.69*	4.24	4.25	0.87*	0.65*	0.75*
MEF4	1.66	0.83*	1.72	1.62	0.98*	1.12	1.06
Two-person crew							
EFF	1.62	1.66	1.85	2.07	0.68*	0.76*	0.83*
WFF	0.74*	0.39*	0.92*	1.16	0.36*	0.82*	0.76*
CWA	2.78	1.77	2.72	2.06	0.51*	0.76*	0.75*
MEF2	1.67	2.98	2.15	2.21	0.54*	0.90*	0.98*
MEF3	2.06	0.88*	5.17	4.99	0.68*	0.70*	0.89*
MEF4	1.48	1.05	1.55	1.85	0.64*	1.07	0.97*

Note: Where efficiency is >1, the method is less efficient than fixed-area sampling; where efficiency is <1, the method is more efficient. The efficiency of fixed-area sampling is, by definition, 1. Note that this efficiency measure does not include bias, which is an important consideration for *N*-tree and distance-limited *N*-tree methods. An asterisk indicates that the method is significantly more (efficiency <1) or less (efficiency >1) efficient than fixed-area sampling.

^aStand codes are defined in Table 1.

Table 6. Efficiency of snag inventory methods relative to fixed-area sampling for snag basal area (BA).

Stand ^a	Snag BA (m ² /ha)						
	MHLS	One-tree	Two-tree	Three-tree	DL one-tree	DL two-tree	DL three-tree
One-person crew							
EFF	1.01	0.59	1.34	1.32	0.91*	1.06	1.16
WFF	0.60*	0.43*	1.00	1.17	0.62*	0.80*	0.92*
CWA	1.21	1.65	2.69	1.62	1.68	0.92*	0.97*
MEF2	0.96*	1.32	1.21	1.22	0.84*	0.98*	1.17
MEF3	1.01	1.17	3.61	3.32	1.91	1.15	1.12
MEF4	0.51	1.64	2.18	1.29	1.82	1.77	1.60
Two-person crew							
EFF	0.90*	0.80*	1.55	1.54	0.66*	1.03	1.02
WFF	0.54*	0.53*	0.95	1.33	0.40*	0.79*	0.84*
CWA	1.12	2.20	3.44	1.97	1.41	0.93*	0.88*
MEF2	0.87*	1.68	1.06	1.38	0.51*	0.85*	1.08
MEF3	0.93*	1.51	4.40	3.90	1.51	1.24	1.35
MEF4	0.46*	2.06	1.96	1.47	1.19	1.69	1.46

Note: Where efficiency is >1, the method is less efficient than fixed area sampling; where efficiency is <1, the method is more efficient. The efficiency of fixed area sampling is, by definition, 1. Note that this efficiency measure does not include bias, which is an important consideration for *N*-tree and distance-limited *N*-tree methods. An asterisk indicates that the method is significantly more (efficiency <1) or less (efficiency >1) efficient than fixed-area sampling.

^aStand codes are defined in Table 1.

calculated directly from the time costs per point (Table 3), effective coefficients of variation (Table 4), and the usual formulae for simple random sampling (e.g., Thompson 1992). Results, calculated separately for each compartment and then averaged, are shown in Table 7. Ranking of the methods is similar to that seen in the efficiency calculations (Tables 5 and 6). Again, these results do not incorporate bias, so the apparent efficiency of *N*-tree sampling, or distance-limited *N*-tree sampling with small *N*, should be questioned. Note, furthermore, that achieving 95% confidence limits of ±20% requires a large number of sample points. Translating the fixed-area sampling results from number of points to area

sampled, approximately 1.6–2.6 ha of plots would be required to meet those inventory goals. This is far from the 100% tally suggested by Bull et al. (1990), unless the compartment is very small, but it still represents a substantial effort.

Conclusions and recommendations

The design-unbiased methods studied here, fixed-area sampling and MHLS, performed well and in keeping with the expectations outlined in typical sampling theory. Fixed-area sampling is most efficient for snags per hectare, while MHLS is most efficient for BA, especially when two persons are

Table 7. Number of plots and time required to achieve an allowable error of 20% in an average stand for number of snags and snag basal area (BA).

	FAS	MHLS	One-tree	Two-tree	Three-tree	DL one-tree	DL two-tree	DL three-tree
No. snags/ha								
<i>n</i>	80	64	228	158	125	150	101	85
Time (h), crew of one	5.5	10.0	5.4	11.6	11.1	4.3	4.6	4.9
Time (h), crew of two	3.7	6.1	4.7	8.6	8.7	2.1	3.0	3.1
Snag BA (m ² /ha)								
<i>n</i>	133	50	438	257	173	417	228	182
Time (h), crew of one	9.2	7.9	10.3	18.9	15.4	12.3	10.3	10.6
Time (h), crew of two	6.2	4.8	8.8	14.1	12.0	6.0	6.9	6.8

Note: Calculation of time required to achieve error of 20% ignores potential bias. Time costs include only the measurement time at each sample point, not travel time between sample points.

Table 8. A key to sampling situations, with recommendations for the most effective snag sampling strategy.

1. Is the most important variable in the inventory snags per hectare or is it a variable related to basal area, such as biomass or volume?
 - a. Snags per hectare — go to 2.
 - b. Basal area — go to 4.
2. Is it feasible to sample at a large number of locations in the compartment?
 - a. Yes — go to 3.
 - b. No — use MHLS.
3. Is design-unbiasedness an important criterion?
 - a. Yes — use fixed-area sampling with small plots.
 - b. No — use distance-limited three-tree sampling.
4. Is it feasible to sample at a large number of locations in the compartment?
 - a. Yes — go to 5.
 - b. No — use MHLS.
5. Is there only one crew member or is snags per hectare an important secondary variable in the inventory? (Only one must apply.)
 - a. Yes — use fixed-area sampling with small plots.
 - b. No — use MHLS.

available to implement the method. In general, traditional *N*-tree methods were poor performers in this study and offered little to compensate for the loss of design-unbiasedness. The novel distance-limited methods did show some improvement when snags per hectare was the most important variable, but showed inconsistent results for BA.

We have summarized the results of this study as recommendations in a dichotomous key (Table 8). Ecologists and foresters wishing to conduct a snag inventory should know whether snags per hectare or snag BA is a more important variable to their management or scientific questions and should also be prepared to address basic questions about the nature of the inventory (crew size and number of sample points). It is also important to understand whether design-unbiasedness is an important criterion for the inventory. Design-unbiasedness would be most important when results will be compared as absolute numbers, when comparisons are to be made across stands with widely varying spatial patterns of snags, or when defensibility of absolute results is important. Design-unbiasedness might be less important if all that is needed is a rapid comparison of relative snag abundance across stands with similar spatial structure.

This key should be interpreted as preliminary, as it depends on a field trial within one ecological type. For example, part of the poor performance of *N*-tree methods in this study may be due to the abundance of dead clumps of stump sprouts. It may be that *N*-tree methods would be more competitive in forests dominated by conifers or that distance-limited *N*-tree

methods would be even more competitive. Furthermore, the applicability of the results reported here depend on the equipment used. In particular, this study used electronic distance measurement. We did not time a traditional approach using a tape, but the unanimous opinion of the field crew members was that fixed-area sampling and all the *N*-tree methods would be significantly disadvantaged with a tape, perhaps making MHLS the dominant method, even when snags per hectare was the most important variable for inventory design.

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Appendix A. Estimators for distance-limited *N*-tree sampling

We take a maximum likelihood approach to estimation in the distance-limited *N*-tree case, following Pollard's (1971) lead for the traditional case. Our approach generalizes the case for $N = 1$, as proposed by Batcheler and Bell (1970) and Batcheler (1971). Suppose we conduct sampling at n points, and at each point $i = 1, 2, \dots, n$, we record the distance from the point to the N th nearest tree, $r_{i,N}$. Let the true density of trees be λ , and let the trees be distributed according to the Poisson assumption. It is straightforward to show that $2\pi\lambda(r_{i,N})^2$ is distributed as χ^2 with $2N$ degrees of freedom (Skellam 1952; Thompson 1956). By the usual properties of the χ^2 distribution, $\sum_i 2\pi\lambda(r_{i,N})^2$ is distributed as χ^2 with $2Nn$ degrees of freedom; equivalently, $\lambda\sum_i \pi(r_{i,N})^2$ is distributed as $\gamma(1, Nn)$. A maximum likelihood estimator of λ is

$$[A1] \hat{\lambda} = \frac{10000(Nn - 1)}{\pi \sum_i (r_{i,N})^2}$$

where the factor 10 000 converts from the units of r^2 (in our case, m^2) to units of area (ha). However, this estimator is biased. The adjusted maximum likelihood estimator is (Pollard 1971) (cf. eq. 1)

$$[A2] \hat{\lambda}_P = \frac{Nn - 1}{Nn} \hat{\lambda}_{ML}$$

Now, suppose that values of $r_{i,N}$ greater than some cutoff r_{max} cannot be observed, so that we record $q_{i,N} = r_{i,N}$ if $r_{i,N} < r_{max}$, and $q_{i,N} = r_{max}$ otherwise. Let $m_i \leq N$ be the number of trees within $q_{i,N}$ of the sample point. Now, conditional on $m_i = N$, the log-likelihood of the datum $q_{i,N}$ taken at point i is

$$[A3] \ln_{i|m_i=N} = N \ln \lambda + (N - 1) \ln(\pi q_{i,N}^2) - Yq_{i,N}^2 - \ln \Gamma(N)$$

Conditional on $m_i < N$ (or equivalently, on $q_{i,N}^2 < r_{max}^2$), the log-likelihood of the datum m_i taken at point i is

$$[A4] \ln_{i|m_i=N} = m_i \ln \lambda + m_i \ln(\pi q_{i,N}^2) - \lambda q_{i,N}^2 - \ln \Gamma(m_i + 1)$$

Noting that the two conditions are mutually exclusive, and that the combined log-likelihood of the n samples is the sum of their log-likelihoods,

$$[A5] \ln L = \sum_i \{m_{i,N} [\ln \lambda + \ln(\pi q_{i,N}^2)] - \lambda \pi q_{i,N}^2 - \ln \Gamma(m_{i,N} + 1)\} + \sum_{i|m_i=N} [\ln(\pi q_{i,N}^2) + \ln N]$$

Differentiation with respect to λ yields

$$[A6] \frac{\partial \ln L}{\partial \lambda} = \frac{1}{\lambda} \sum_i m_{i,N} - \sum_i \pi q_{i,N}^2 = 0$$

so the maximum likelihood estimator is (cf. eq. 3)

$$[A7] \hat{\lambda}_{ML} = \frac{10000 \sum_{i=1}^n m_i}{\pi \sum_{i=1}^n q_{i,N}^2}$$

Unfortunately, the integrals required to evaluate the bias of [A7] are intractable, even for the simple case of $N = 1$, although simulation clearly establishes that bias is present.

Now, intuitively, as r_{\max} grows very large, the distance limitation will become irrelevant, so one would expect the bias to approach $Nn/(Nn-1)$, and a corrected equation similar to [A2] with a correction factor $(Nn-1)/Nn$ would seem appropriate. Conversely, as r_{\max} becomes small, the distance limitation will become inevitable, so that the distance-limited sample will act like a fixed-radius sample and [A7] should be unbiased, so the correction factor should approach $Nn/Nn = 1$. After testing and rejecting a variety of correction factors with this property, we found that

$$[A8] \quad \hat{\lambda}_{DL} = \frac{Nn - n_{\max}/n}{Nn} \hat{\lambda}_{ML}$$

performed well across a range of n , N , and r_{\max} . Table A1 shows the relative bias of $\hat{\lambda}_{DL}$ for $N = 1, 2$, and 3 , at three different sample sizes and three values of λ , with $r_{\max} = 8$. For each combination, 6400 simulated inventories were conducted, and bias was evaluated as the difference between the mean of the estimates and the actual density. Statistical significance of the bias was assessed using a Bonferroni-adjusted t test. All simulations were conducted using MATLAB release 12.1 (Mathworks, Inc., Natick, Massachusetts). Simulated bias is everywhere less than 0.5% and is nowhere statistically significant.

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Table A1. Evaluation of the relative bias (bias/true density) of $\hat{\lambda}_{DL}$ using Monte Carlo simulation (6400 inventories at each combination).

	$\lambda = 50$	$\lambda = 100$	$\lambda = 200$
$N = 1$			
$n = 8$	-0.004	0.002	0.001
$n = 16$	0.005	-0.001	-0.003
$n = 32$	0.003	-0.004	-0.003
$N = 2$			
$n = 8$	-0.004	-0.003	-0.005
$n = 16$	0.000	-0.005	0.000
$n = 32$	0.001	0.002	0.000
$N = 3$			
$n = 8$	0.001	-0.001	-0.001
$n = 16$	0.001	0.002	-0.003
$n = 32$	-0.004	0.003	-0.002

Note: Nowhere is the bias statistically significant at $\alpha = 0.05$, using a Bonferroni-adjusted t test.

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