

# Auxiliary Network Sampling for Multi-Objective National Forest Inventories: A Practical Examination of Search Distances

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## ABSTRACT

Building upon the work of Roesch and McWilliams (2007), this paper discusses additional examples of an auxiliary sampling strategy that allows National Forest Inventory (NFI) practitioners to efficiently estimate the attributes of rare events or species. When the rare event is immediately identifiable in the field, such as the tree species itself, a trivial simplification of theory is evident, that being that clusters of networks of trees (of that species) are being sampled by the area-based plot, rather than clusters of individual trees. When this is the case one does not have to think of the design as adaptive but rather as simply auxiliary. This can be of some help in the presentation of a large, multi-objective inventory. This paper focuses on a practical examination of network search distances for this special case of an auxiliary mechanism for NFIs such as the Forest Inventory and Analysis (FIA) sample design in the United States.

**Keywords:** Auxiliary, FIA, rarity, sampling, spatial.

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## INTRODUCTION

National Forest Inventories (NFIs) are designed to address small-scale problems such as estimating the level of an attribute over a very large area such as a State or province. However, rare, large-scale events are also of interest, which highlights the need for an efficient auxiliary mechanism for adapting these inventories to large-scale problems. Roesch and McWilliams (2007), partially following theory found in Roesch (1993, 1994), investigated a few alternative approaches to detecting and estimating rare events. They found adaptive cluster sampling to be useful for the extremely rare distribution of American chestnut (*Castanea dentata*). The networks of rare trees were formed by their proximity to each other, defined by a fixed limiting distance to the nearest member. In adaptive cluster sampling, auxiliary observations are made when a predefined rare event is encountered. In the earlier work, Roesch (1993, 1994) showed how to do this for unequal-probability samples, in which unique networks of trees are sampled rather than individual trees.

Adaptive designs are usually described as having two stages, the first being a probability sample of units in a population, and the second being the selection of additional units near those units that display a specific condition of interest during the first stage. In this paper, as was explained in previous work, we view the same procedure as a single stage. That is, each rare event of interest (such as the presence of a particular species) defines its own population of networks. These populations are then sampled simultaneously with the remaining population of trees by the inventory's first stage, un-adapted sample design. In field practice, if a sample tree is a member of one of these special populations, a predefined area is searched for other trees in its network. This is repeated for every new network tree found. The practical goal is to choose a search area that would define a population of reasonably-sized networks. These networks would be large enough to increase the support for sample estimates at a reasonable cost and small enough to not become unmanageable. In this work, we show how adequate existing data can be used to find the range of search areas (or distances) that could be used for any species (or subspecies), and then we apply the method in an attempt to find practical search distances for 43 species (and 1 subspecies).

To review the theory, assume that there are  $N$  trees with labels  $1, 2, \dots, N$ . Associated with the  $N$  trees are values of interest  $\mathbf{y} = \{y_1, y_2, \dots, y_N\}$  and characteristics of interest  $\mathbf{C} = \{C_1, C_2, \dots, C_N\}$  (Roesch 1993). If the species itself is the characteristic of interest and tree  $i$  is a member of the rare species,  $C_i = 1$ , otherwise  $C_i = 0$ . Let  $x_i = C_i y_i$ , so if tree  $i$  is the rare species,  $x_i = C_i y_i = 1 * y_i$ . If tree  $i$  is not a member of the rare species, then  $x_i = 0$ . The selection of any tree within the network leads to the discovery of every other tree in the network. That is, only the trees for which  $C_i = 1$  are sought as a result of the discovery of a network member. This simplified special case of adaptive cluster sampling can be viewed as a single stage, which we will call Auxiliary Network Sampling (ANS).

ANS maps the population of  $N$  trees into a population of  $M$  networks, conditioned on the species  $S$ , and each network is sampled with known probability. The probability ( $p_i$ ) of including a particular tree  $i$  is equal to the union of the selection areas of each tree in its network, divided by the area of the forest ( $L_F$ ). Thompson (1990) showed that an unbiased estimator can be formed for adaptive cluster sampling using the Horvitz-Thompson estimator (Horvitz and Thompson 1952). Unlike the more general case considered by Thompson (1990), in the special case being considered here, all probabilities of being included in the sample are known because only other members of the same network are included as a result of the first network member being discovered (as opposed to having to include and then examine every tree within the search area for the occurrence of a particular characteristic). Observations on trees of non-networked species are included only when they are sampled by the initial design. The probability of tree  $k$ , in network  $K$ , being included in the sample during ANS from at least one of  $m$  plots is equal to 1 minus its probability of not being included:

$$\alpha_k = \alpha_K = 1 - \left( 1 - \frac{a_k}{L_F} \right)^m$$

where

$L_F$  = the total land area (usually of the forest)

$a_k$  = union of the initial sample's inclusion areas for the trees in network  $K$  to which tree  $k$  belongs

$\alpha_k$  = the probability of tree  $k$  being included in the sample, and

$\alpha_K$  = the probability of network  $K$  being included in the sample.

The network inclusion probabilities can then be used in any subsequent estimator. For instance, for species  $S$ , substitute  $S$  for  $C$ , and sum over the  $v$  distinct species trees in the sample to obtain the  $HT$  estimator of the population total:

$$t_{S(HT)} = \sum_{k=1}^v \left( \frac{S_k y_k}{\alpha_k} \right).$$

The statistical properties of  $t_{S(HT)}$  and other potential estimators are discussed in Roesch (1993).

## METHODS

To illustrate the factors that must be considered when choosing a search distance, a population was built from data obtained by the USDA Forest Service's Forest Inventory and Analysis (FIA) Program. The simulated population was constructed using the measured plot data from the Eastern United States collected through the years 1998 to 2016, available in the Forest Inventory and Analysis Database (FIADB) at [https://apps.fs.usda.gov/fia/datamart/CSV/datamart\\_csv.html](https://apps.fs.usda.gov/fia/datamart/CSV/datamart_csv.html). The stem-mapped data from each FIA cluster plot observation were expanded to create a square population element of approximately 1.075926 hectares (2.65867 acres). This population element was intended to represent the area immediately surrounding the ground plot using the information observed on the plot while minimizing the assumptions made about how what was not observed might be different from what was observed. We accomplish this in two steps.

In step 1, each circular subplot is reshaped into a square of the same size by randomly relocating observations (trees) occurring in the slivers of the circle outside of a centrally co-located square of the same size into the corners of the co-located square (outside of the circle) by each of the four quadrants (see fig. 1), while keeping all observations that were common to both the circle and the square in their original locations. This method preserved all of the tree information available on the subplots, while also preserving most of the spatial location information. We did not restrict the random relocation of the trees from the slivers into the corners with respect to the location of any other trees for a number of reasons. First, our analysis considers one rare species at a time and there would be a very low probability of two trees of the rare species being relocated into the same corner of a particular subplot square, in excessively close proximity to each other. Each corner (and sliver) is approximately 0.0226 of the subplot

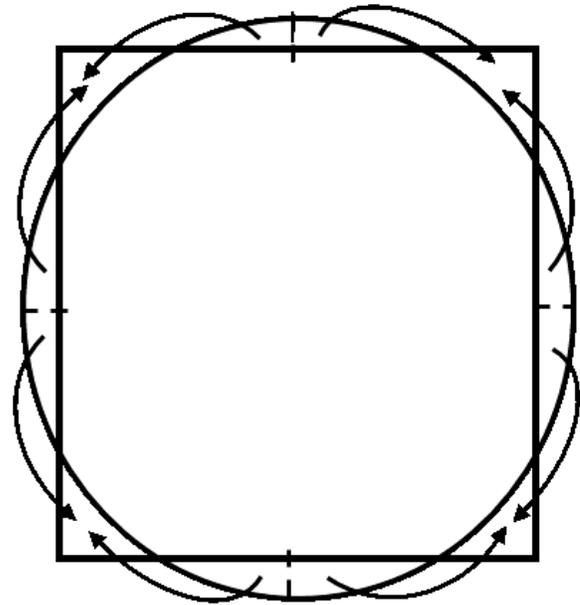


Figure 1—Converting each circular subplot from figure 3 into a square of the same size. Each subplot has a radius of 24 feet, while the square of an equal area has a side length of approximately 42.54 feet. Trees located in the area common to both the circle and square are left in place. Trees located in the slivers of the circle outside of the square, of each quadrant, are randomly relocated into the same quadrant's corner of the square.

area. Therefore, each subplot would have to have about 44 rare trees before you would expect 1 in each sliver. Second, trees being located very close to each other do occur in nature, so it is unclear what restriction, if any, would be appropriate. Third, a restriction of  $<5$  feet would have no effect on the current investigation, because the minimum search distance that we consider for network inclusion is 5 feet.

In step 2, the four subplot squares for each plot are grown into the larger (1.075926 hectare) square population element (16× larger than the informing plot cluster), arranged in the pattern shown in figure 2. The goal was to create a population element that maintained most of the spatial relationships observed between and within subplots. Therefore, we did not effect further randomization of tree locations within subplot squares or between subplot squares. We chose this pattern because it is simple and comes close to mimicking the pattern of observation of the original subplots, as shown in figure 3, thereby closely maintaining the spatial relationships between subplots. Many other choices might have been made, although most others would have lost more of the observed spatial relationships between subplots. We note that this deterministic pattern, as well as any other,

2	2	2	2	2	2	2	2
2	2	2	2	2	2	2	2
1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1
4	4	4	4	3	3	3	3
4	4	4	4	3	3	3	3
4	4	4	4	3	3	3	3
4	4	4	4	3	3	3	3

Figure 2—The square subplot pattern arrangement for each “plot” square. Sixteen copies of each of the four (squared) subplots (1 to 4) are placed into an 8 × 8 grid in the pattern above.

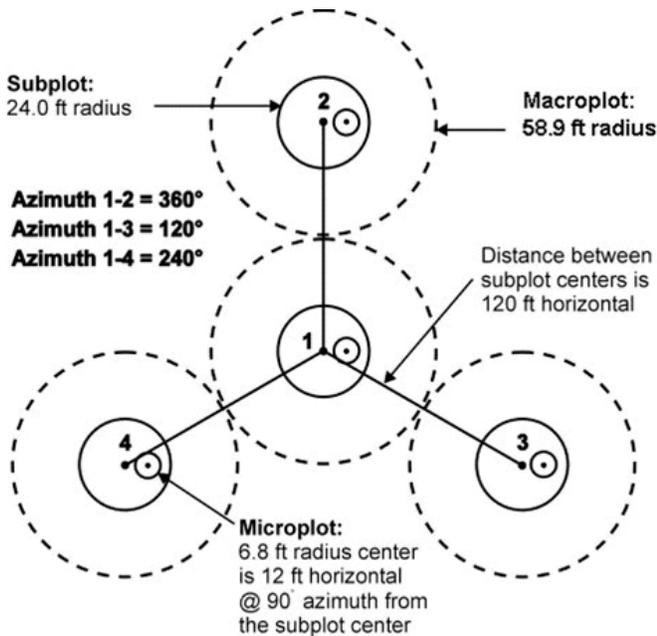


Figure 3—The FIA plot design. All trees > 5.0 inches in d.b.h. are measured on the subplot. Although not used in this paper, trees > 1.0 inch in d.b.h. are measured on the microplot. The macroplot is an optional feature currently used in the Pacific Northwest as an auxiliary sample for large trees (Bechtold and Patterson 2005).

will have an obvious potential for chaining together tree locations from neighboring squares. A one-tree example will show the reader that this could occur all at once between the 16 adjacent squares at search distances exceeding the length of the side of a square (42.5 feet). Note that if only one tree is present on a subplot, then no actual within-subplot spatial distribution has been observed. This is one reason that we didn't consider search distances that large in this study. When more than one tree occurs on a subplot square, this threshold distance will be lower; however, it will also be highly dependent on the spatial relationships between the trees observed on the subplots. If we had rather randomized the spatial locations of trees on each of the 16 subplot squares, different connections between the squares would be made; however they would no longer depend on the spatial relationships observed on the subplots.

In order to create the simulated population, the population elements described above were ordered by latitude, longitude, and then measurement year (when multiple measurement years were available) in a list. There were enough population elements to fill a square of 497 elements on a side. Therefore, the first ( $497^2 = 247,009$ ) of these population elements were used to build the square population tree map. Each cell of the population square was filled with a population element square starting from the bottom left, across each row and then up to the top right of the square. The intent was to create a population that would have local qualities very much like those that would be present in a temporally collapsed realization of the collection of annually sampled populations. One major assumption is that the resulting simulated population reasonably represents a wide diversity of local spatial distributions. This leads to another major assumption, which is that an auxiliary sampling scenario that works well in this simulated population (and species-specific subsets of it), and can be argued to be practical, should work well for any NFI over a wide range of existing species distributions.

In this paper we focus on one of the most practical problems mentioned in Roesch (1994). That paper points out the additional monetary cost of the adaptive strategy for a particular application depends on relative network sizes and their spatial distribution in the sample—factors that can be predicted given adequate previous knowledge of the populations of interest. In the example in Roesch (1994), the additional cost of including extra trees

was shown to be controllable by the distance examined. As search distance increases, the probability of creating excessively large networks also increases. For any specific attribute, such as species or subspecies, we want to select a minimally sized search area relative to the local spatial distribution of the target trees. Here we attempt to find a set of practical search distances for 44 tree species and subspecies. These search distances should serve as useful

starting points for FIA and many other NFIs. This list of interesting species is not exhaustive but rather is intended to represent local distributions of many special interest species including rare, semi-rare, invasive, and high-value species. To give the reader an idea of the relative coarse-scale distributions of each of the 44 (sub) species within the overall population, each is plotted over the population in figure 4.

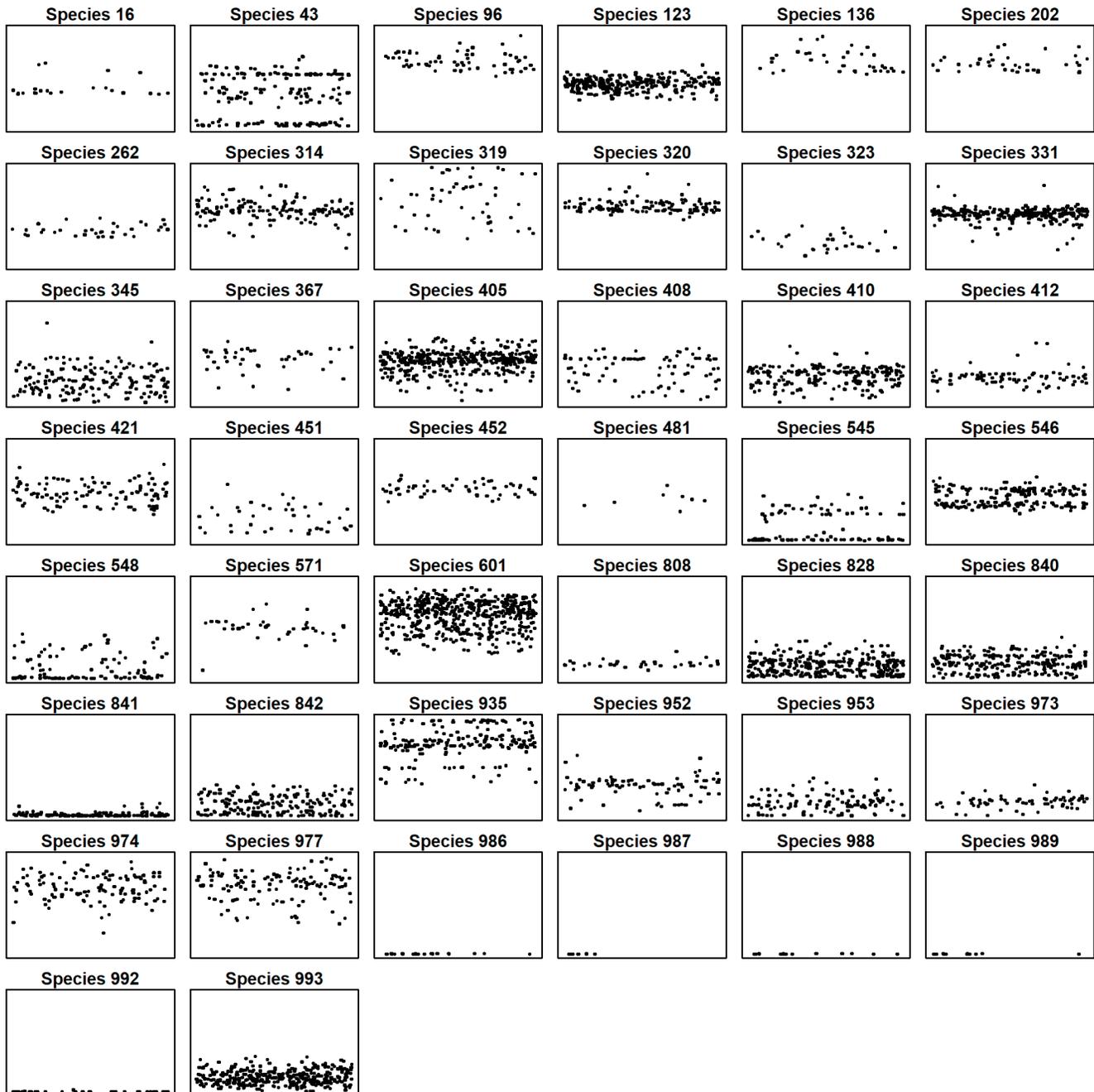


Figure 4—The global distribution map of each of the 43 species and 1 subspecies over the population space.

We proceed in this investigation by building the networks for each species at a series of search distances and then examining the maximum size of network for each search distance. Once an excessively large network was found, larger search distances were dropped from consideration.

Although we cannot fully judge how large of a network would be impractical without giving some consideration to the initial sample design, we do build the networks independently of any specific sample design. With the FIA cluster plot (fig. 3) in mind as an initial design, certainly if the maximum network size exceeded 30 trees, the search distance is becoming too large to be advantageous, because the networks have a higher probability of being observed by multiple subplots. A maximum network size of <10 trees may indicate a network size distribution that would not have an advantage over the FIA cluster plot, unless perhaps for a very rare and valuable species that requires a search distance which is quite large. Search distances that are too small would form many networks of trees that would have already been observed on the initial cluster plot and may not be helpful.

## RESULTS

Table 1 is intended to show the reader the practical limits of possible search distances (in feet) for each species. Some impractical results are included when they help define the limit. For example, the first species listed in the table (*Abies fraseri*, species code 16) has results listed for search distances of 8, 9, and 10 feet. Clearly, the maximum network size of 230 found for a search distance of 10 feet is far too high, while the results for 8 and 9 feet both show promise. Although not the focus here, a simulation as described in Roesch (1993) could be used to determine which one is best under any given initial sample design. The table also shows that as declared in previous publications, different species can have quite different optimal search distances. For instance, *Tsuga caroliniana*, *Acer spicatum*, and *Acer leucoderme* (species codes 262, 319, and 323, respectively) all appear to have quite high optimal search distances relative to *Abies fraseri* (species code 16) and *Chamaecyparis thyoides* (species code 43). Very often in the table we see a difference of only 1 foot between a reasonable maximum network size result and a very unreasonable result.

**Table 1—The maximum network sizes resulting from a selection of search distances for each species (or subspecies) in the study**

Species code	Species (or subspecies)	Common name	Number of trees	Search distance (ft.)	Maximum network size
16	<i>Abies fraseri</i>	Fraser fir	5,504	8	11
				9	25
				10	230
43	<i>Chamaecyparis thyoides</i>	Atlantic white-cedar	53,584	5	12
				6	19
				7	29
96	<i>Picea pungens</i>	Blue spruce	8,944	5	6
				6	11
				7	31
123	<i>Pinus pungens</i>	Table Mountain pine	43,216	8	12
				9	125
136	<i>Pinus nigra</i>	Austrian pine	9,552	6	5
				7	45
				8	45
202	<i>Pseudotsuga menziesii</i>	Douglas-fir	6,336	6	6
				7	19
				8	51
262	<i>Tsuga caroliniana</i>	Carolina hemlock	1,776	20	5
				22	5
				23	21
				24	21
				25	50
314	<i>Acer nigrum</i>	Black maple	11,312	10	6
				12	6
				13	6
				14	8
				15	28
				16	28

(continued)

**Table 1 (continued)—The maximum network sizes resulting from a selection of search distances for each species (or subspecies) in the study**

Species code	Species (or subspecies)	Common name	Number of trees	Search distance (ft.)	Maximum network size
319	<i>Acer spicatum</i>	Mountain maple	1,440	27	16
				35	19
				36	32
320	<i>Acer platanoides</i>	Norway maple	6,960	10	13
				11	13
				12	149
323	<i>Acer leucoderme</i>	Chalk maple	1,056	24	12
				30	12
				31	12
				32	24
331	<i>Aesculus glabra</i>	Ohio buckeye	23,248	15	14
				17	19
				18	73
				12	16
345	<i>Albizia julibrissin</i>	Mimosa	8,032	15	16
				18	16
				19	20
				20	20
				21	20
				22	20
				23	64
367	<i>Asimina triloba</i>	Pawpaw	1,552	24	8
				25	8
				26	8
				27	64
405	<i>Carya laciniosa</i>	Shellbark hickory	25,088	15	9
				16	21
				17	30
408	<i>Carya texana</i>	Black hickory	4,016	15	7
				16	15
				17	116
410	<i>Carya pallida</i>	Sand hickory	14,496	17	7
				18	144
412	<i>Carya ovalis</i>	Red hickory	4,272	16	8
				17	32
421	<i>Castanea dentata</i>	American chestnut	4,512	19	6
				20	20
451	<i>Catalpa bignonioides</i>	Southern catalpa	1,936	21	80
				18	8
452	<i>Catalpa speciosa</i>	Northern catalpa	4,032	19	24
				8	15
				9	30
481	<i>Cladrastis kentukea</i>	Yellowwood	496	10	34
				20	4
				21	24
				22	24
545	<i>Fraxinus profunda</i>	Pumpkin ash	21,984	25	24
				11	14
				12	20
546	<i>Fraxinus quadrangulata</i>	Blue ash	16,816	13	110
				13	15
				14	20
				15	40

(continued)

**Table 1 (continued)—The maximum network sizes resulting from a selection of search distances for each species (or subspecies) in the study**

Species code	Species (or subspecies)	Common name	Number of trees	Search distance (ft.)	Maximum network size
548	<i>Fraxinus caroliniana</i>	Carolina ash	17,040	9	11
				10	13
				11	28
571	<i>Gymnocladus dioicus</i>	Kentucky coffeetree	2368	14	10
				15	76
601	<i>Juglans cinerea</i>	Butternut	25,104	10	6
				11	6
				12	6
				13	6
808	<i>Quercus sinuata</i>	Durand oak	2,112	14	28
				12	13
				18	13
				20	13
				22	13
828	<i>Quercus texana</i>	Texas red oak	24,896	23	24
				24	24
				25	48
				9	9
				10	9
840	<i>Quercus margarettiae</i>	Dwarf post oak	25,008	11	11
				15	19
				16	28
841	<i>Quercus minima</i>	Dwarf live oak	21,584	8	26
				9	27
				10	27
842	<i>Quercus incana</i>	Bluejack oak	8,688	15	12
				16	13
				17	13
				18	15
				19	40
935	<i>Sorbus americana</i>	American mountain-ash	13,232	12	13
				13	14
				14	28
952	<i>Tilia americana (heterophylla)</i>	White basswood	6,864	15	28
				15	9
				16	20
				17	20
				18	20
953	<i>Tilia americana (caroliniana)</i>	Carolina basswood	7,312	19	48
				20	8
				21	24
973	<i>Ulmus crassifolia</i>	Cedar elm	4,144	16	16
				18	16
				19	48
974	<i>Ulmus pumila</i>	Siberian elm	8,768	12	15
				13	15
				14	219
977	<i>Ulmus thomasi</i>	Rock elm	5,888	15	16
				17	16
				19	21

(continued)

**Table 1 (continued)—The maximum network sizes resulting from a selection of search distances for each species (or subspecies) in the study**

Species code	Species (or subspecies)	Common name	Number of trees	Search distance (ft.)	Maximum network size
986	<i>Avicennia germinans</i>	Black mangrove	2,768	10	13
				11	18
				12	20
				13	20
				14	43
987	<i>Conocarpus erectus</i>	Buttonwood mangrove	1,568	7	13
				8	22
				9	33
988	<i>Laguncularia racemosa</i>	White mangrove	2,720	11	7
989	<i>Rhizophora mangle</i>	American mangrove	1,792	15	9
				16	37
992	<i>Melaleuca quinquenervia</i>	Melaleuca	9,328	5	18
				6	25
				7	28
993	<i>Melia azedarach</i>	Chinaberry	29,376	5	56

Sometimes there is only a 1-foot difference between a result that is probably too low to be useful and one that is unreasonably high, such as shown in the results for four species (species codes 136, 367, 410, and 988). In these cases, although less practical, one might consider a search distance between the two integer values, after further investigation.

The final species on the list (*Melia azedarach*, species code 993) shows that at a search distance of only 5 feet, at least one network with 56 member trees was formed. The conclusion we would draw from this observation is that the estimation of this species' attributes would not benefit from this type of auxiliary sample design.

Subsequent to a filtering of search distances by maximum network size, further examination of the network size distributions could be helpful, especially when multiple search distances yield the same maximum network size, as is the case for species code 481 (*Cladrastis kentukea*) in table 1. While a search distance of 20 feet yields a maximum network size of only 4, the search distances of 21, 22, and 25 feet all yield a maximum network size of 24. We show the distributions of these three search

distances in table 2 and note that there is an advantage to each increase of search distance in this range for this species. At a search distance of 22 feet, 12 networks of size 1, and 12 networks of size 3 found at a search distance of 21 feet have been replaced by 12 networks of size 4. A further, reasonable consolidation of networks is seen as the search distance is increased from 22 to 25 feet.

**Table 2—The number of networks for each network size for three search distances for species code 481 (*Cladrastis kentukea*)**

Network size	Search distance		
	21 ft.	22 ft.	25 ft.
1	212	200	192
2	52	52	32
3	12	—	—
4	24	36	—
16	—	—	12
24	2	2	2
Sum	302	290	238

— = No networks of that size for the specified search distance.

## DISCUSSION

Systematic areal-based designs ensure a thorough dispersion of the sample plots through the population. This special case of an adaptive sampling design used in conjunction with an areal-based design could improve the estimation of a rare event (or species) subsequent to the mapping of the individual tree species distribution into a distribution of networks of those same trees. In most inventory efforts, relative cost is the major concern when choosing between sampling strategies. Much of this cost comes in the form of planning and travel to the observation sites. The additional cost of this auxiliary design depends on the relative network sizes. This paper shows that this factor can be predicted given adequate previous knowledge of a population of interest. The existing data in the FIADB can be used to gain that knowledge. In the example in Roesch (1994), using a small dataset, the additional cost of including extra trees was shown to be controllable by the distance examined. The size of the search area determines the size of the networks of interest found. ANS provides a way for NFI efforts to monitor rare events at a relatively small cost. Here, we have provided the practical guidance left for further research in previous publications. Table 1 gives guidance to those who are interested in the species listed, in the Eastern United States, and elsewhere, if that species has a similar local spatial distribution to that of the Eastern United States.

The way that this simulated population was built did have some effect on the results because we assumed that what was not observed in the vicinity of the observed subplots was like what was observed on the subplots. There are many other ways this might have been accomplished, and each would have resulted in somewhat different sets of networks being formed; however they should have not been substantially different. In cases in which our

approach formed a very large network, at a particular search distance, any other approach that relies on the same assumption of local similarity should also form a very large network. Therefore, the same conclusions about optimal search distances would most likely be drawn from any one of those other approaches. The approach to finding reasonable search distances that we used here could also be used to make a similar determination anywhere, for any rare species, especially when a similar preponderance of data is available.

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