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Systematic adaptive cluster sampling for the assessment of rare tree species in Nepal

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Abstract

Sampling to assess rare tree species poses methodic problems, because they may cluster and many plots with no such trees are to be expected. We used systematic adaptive cluster sampling (SACS) to sample three rare tree species in a forest area of about 40 ha in Nepal. We checked its applicability and efficiency and compared it to conventional systematic sampling. Comparison of SACS to conventional systematic sampling showed that efficiency for density estimation increased 500% for the clustered *Schima wallichii*, but reduced 40% for the unclustered *Daphniphyllum himalayense*. The method was found to be more efficient for larger groups of individuals of a rare species than for extremely small groups. SACS may also be used to establish relationships with spatially referenced variables, but data availability was a constraint. SACS is a promising design for resource managers and survey specialists dealing with rare and endangered species in the context of biodiversity and sustainable forest management. © 2000 Elsevier Science B.V. All rights reserved.

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1. Introduction

Rare and endangered plant species present special problems for conservation, since they reflect characteristic differences from common plants in their biology, pattern of threat and resources available for conservation management. Rare and sought after species form an even more endangered category. Selective cutting may turn once common forest tree species

into rare ones, and bring rare species even to extinction. Forest degradation, whether caused by selective logging, or fires, overgrazing, introduction of new species or economic incentives, leads to species rarity and to loss of biological biodiversity in general (UNEP, 1992).

Assessing occurrence and spatial distribution of rare species meets with problems when applying conventional sampling designs, such as simple random sampling or grid sampling (Cochran, 1977; Schreuder et al., in press). Their application would result in a small probability of selecting a sampling unit in which the desired rare species occurs. Consequently, there will be many plots without such trees, making the design inefficient.

If a species is known, or can be expected to cluster, i.e., growing in groups, more efficient adaptive

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sampling designs are available (Thompson, 1992; Roesch, 1993). In adaptive sampling the procedure for selecting units to be included in the sample depends on the value of the variable of interest, as observed during the survey of an initial sample. The main purpose of adaptive sampling is to exploit the clustering characteristic of the population units, to obtain more precise population estimates for a given sample size or cost. Simply adding sampling units, however, might result in biased estimators and variances. Estimators are, therefore, required that do not depend on assumptions about the population, but depend on the way the sample is selected.

This paper focuses on the application of systematic adaptive cluster sampling (SACS) and on determining its suitability to estimate the density and distribution of three rare tree species: *Schima wallichii* Choisy (vernacular name *Chilaune*), *Michelia kisopa* Buch.-Ham. ex DC (vernacular name *Champ*), and *Daphniphyllum himalayense* Muell. Arg. (vernacular name *Raktachandan*). These species are rare or even endangered in Nepal (Acharya, 1994; Shrestha and Joshi, 1996). SACS is compared with systematic sampling in terms of efficiency and assessment performance.

1.1. Study area

The study area, 37.8 ha in size, is part of the Shivapuri Watershed and Wildlife Reserve, about 12 km north of Kathmandu, capital of Nepal. The area was declared a reserve in 1985 and occupies a total area of about 97 km². It is the major source of drinking water to Kathmandu. The Shivapuri area has national importance as a reserve for biodiversity and watershed protection. Logging and agriculture are no longer permitted, with very few exceptions. A boundary wall, approximately 1.5 m high, surrounds the entire reserve, while the area is guarded against intruders. The area is also important for tourism and for religious purposes. The altitudinal range is between 1360 and 2732 m a.s.l. The climate is sub-tropical to warm temperate, with a marked rainy season between June and September. In the rainy season, 84% of the mean annual precipitation of about 2700 mm falls. The warmest months are June till August. The topography is steep mountainous with about half the area having slopes between 30 and 60%, and about one-third steeper than 60%. The natural forest on the

southern slopes was under heavy pressure until 1985, because of commercial harvest of timber and fuelwood, and intensive grazing and crop production. Because of planting and natural regeneration, about 70% of the area is now classified as dense forest. The subtropical forest consists of species of the genera *Alnus*, *Schima*, *Castanopsis* and *Pinus*, while in the higher and warm temperate forest *Quercus semecarpifolia* dominates. Despite current regulations, the local population is still using a number of tree species of the reserve. *S. wallichii* and *D. himalayense* are both used for fuelwood and small timber, and *M. kisopa* for furniture. Over the years, these tree species have been selectively removed, which caused them to become rare. They are, therefore, well suited for the present study.

1.2. Adaptive cluster sampling

The adaptive sampling design consists of two steps. In the first step systematic sampling is applied, yielding an initial set of M sampling units (plots). In each plot, the presence of at least one tree (dbh \geq 12 cm) of the rare species concerned is determined. If at least one such tree is present, the second step adds neighboring plots to this plot (and thus to the sample). The presence of at least one rare tree of the species in each one of these added plots is determined. If positive, further neighboring plots are added. Plots are added repeatedly until no additional plots contain the rare tree species anymore. A major difference with conventional designs is, therefore, that the procedure for selection in adaptive designs depends upon population values observed in the field.

The area, in which systematic adaptive cluster sampling is to be applied, consists of a set of contiguous square blocks of the same size. Each block is divided into an equal number of non-overlapping square plots. To select the initial systematic sample, a plot is selected randomly in the first block. Its location in the block defines the systematically arranged plots in all other blocks. This set of plots forms a primary unit, whereas the plots themselves are the secondary units. More than one primary unit may be randomly selected. A primary unit is a projection of a possible collection of initial sampling units to such a block, for example the first block. Secondary units (plots) are the sampling units included in the sampling after selection of a primary unit.

Plots are denoted by u_{ij} , with index $i, i = 1, \dots, N$ denoting the primary unit, and $j, j = 1, \dots, M_i$ the secondary unit. The neighborhood of a plot is a contiguous set of surrounding plots, consisting of itself plus its four adjacent plots, depending only upon physical proximity. Plots containing a rare tree species are positive plots. After selection of a primary unit, the plots are sampled. When a rare tree species is observed, the total neighborhood is sampled. If a neighborhood plot contains again a rare tree species, then the neighborhood of that plot is sampled again, and so on.

Under the design, a group is defined as a set of one or more adjacent plots, containing the rare tree species. Detecting one single rare tree of a group, will, therefore, result in the inclusion of the whole group of that rare tree species. A consequence of this procedure is that a group is defined by trees that are no more than the plot diameter apart. Plot size thus influences group size.

One feature of adaptive sampling is that the sample size is not known beforehand. The effective sample size is the expected number of adaptively added plots in the final sampling, i.e. the average number of adaptively added plots, for a given initial sample size of population. The effective sample size $E(v)$ is computed as the sum of inclusion probabilities π_{ij} :

$$E(v) = \frac{1}{M} \sum_{i=1}^N \sum_{j=1}^{M_i} \pi_{ij} \tag{1}$$

and π_{ij} is:

$$\pi_{ij} = 1 - \frac{\binom{N - m_{ij} - a_{ij}}{n}}{\binom{N}{n}} \tag{2}$$

where n is the number of initial primary units, m_{ij} the number of primary units intersecting the group containing plot u_{ij} and a_{ij} the number of primary units not intersecting the group of u_{ij} but intersect the group of one or more units containing a rare tree species in the neighborhood of plot u_{ij} . For a plot containing a rare tree species, $a_{ij} = 0$, whereas for a plot not containing a rare tree species, $m_{ij} = 1$ (Thompson, 1992).

Three unbiased estimators for the mean number of trees and their variances will be used and compared in this study (Table 1). A suitable estimator for use in adaptive cluster sampling is derived from the Hansen–

Hurwitz (HH) estimator ($\hat{\mu}_1$) which divides the observed number of rare trees (the y and value) by its associated selection probability and multiplies it by the number of times the plot is selected. It is an unbiased estimator of the population mean, based on partial selection probabilities (Cochran, 1977; Thompson, 1992). For sampling with replacement, the HH-estimator is often appropriate as it uses the probability that a plot is selected. In a population without sufficient information on location and variation of rare trees, however, it is difficult to determine the selection probability of each rare tree. A modified HH-estimator suits populations in which the location and amount of individuals are unknown before the survey (Thompson, 1992). Notice that for any plot in the k th group, $m_{ij} = x_k$, where m_{ij} equals the number of primary units intersecting this group and x_k equals the number of primary units in the population that intersects it. This estimator utilizes the y -values (observed number of trees) in the group as often as there are primary units in the initial sampling intersecting it.

A second estimator is the Horvitz–Thompson (HT) estimator. The HT-estimator ($\hat{\mu}_2$) uses partial inclusion probabilities of plots included in the sample. In adaptive cluster sampling, however, the inclusion probabilities of plots are unknown because the number of primary units not intersecting the group hit by plot u_{ij} but intersecting one or more plots containing rare tree species in its neighborhood may be unknown. Therefore, a modified HT-estimator is based upon the partial knowledge of the inclusion probabilities obtainable from the data (Thompson, 1991, 1992; Thompson and Seber, 1996). The weight an observation receives in the estimator does not depend (as it does with the estimator based on partial selection probabilities) on the number of intersecting primary units selected, as long as at least one of them is included in the initial sampling.

Finally, an unbiased estimator of the population mean (μ) is the initial sample mean ($\hat{\mu}_0$), obtained by ignoring all adaptively added plots to the sample. It offers the basis for comparison with adaptive and non-adaptive strategies.

The condition for adding adjacent sampling plots was based upon the occurrence of a tree (dbh ≥ 12 cm) of any of the three species: if $y_{ij} > 0$ for any j , then the neighborhood was extended. The number of plots that are adaptively added to the

Table 1
Estimators used in the applied sampling designs^a

| Estimator | Mean | Variance |
|------------------|--|---|
| Initial sample | $\hat{\mu}_0 = (1/Mn) \sum_{i=1}^n y_i$ | $\text{var}(\hat{\mu}_0) = (N-n)/(M^2 Nn) s_0^2$ |
| Hansen–Hurwitz | $\hat{\mu}_1 = (1/n) \sum_{i=1}^n w_i$ | $\text{var}(\hat{\mu}_1) = (N-n)/(Nn) s_w^2$ |
| Horvitz–Thompson | $\hat{\mu}_2 = (1/MN) \sum_{k=1}^K (y_k z_k / \alpha_k)$ | $\text{var}(\hat{\mu}_2) = (1/M^2 N^2) \sum_{k=1}^K \sum_{j=1}^K (y_k y_j z_k z_j) / (\alpha_{kj}) ((\alpha_{kj} / \alpha_k \alpha_j) - 1)$ |

^a y_i : the total number of rare trees in the i th primary unit; M : the number of secondary units; N : the number of primary units; n : the number of initial systematic sampling units; $s_0^2 = (1/(N-1)) \sum_{i=1}^N (y_i - M\hat{\mu}_0)^2$; $s_w^2 = (1/(n-1)) \sum_{i=1}^n (w_i - \hat{\mu}_1)^2$; $w_i = (1/M) \sum_{k=1}^K ((y_k I_{ik}) / x_k)$; K : the total number of groups in the population, $K = \sum_{i=1}^N k_{ik}$ with $y_k =$ total of y -values (rare trees) in the k th group; I_{ik} : an indicator variable ($I_{ik} = 1$ if the i th primary unit intersects the k th group and $I_{ik} = 0$ otherwise); $x_k =$ the number of primary units in the population that intersects the k th group that is, $x_k = \sum_{i=1}^N I_{ik}$; α_k : the intersection probability of the k th group

$$\alpha_k = 1 - \frac{\binom{N-x_k}{n}}{\binom{N}{n}}$$

α_{kj} : the probability that the k th and the j th group have atleast one unit in common:

$$\alpha_{kj} = 1 - \frac{\binom{N-x_k}{n} + \binom{N-x_j}{n} - \binom{N-x_k-x_j+x_{kj}}{n}}{\binom{N}{n}}$$

z_k : an indicator variable with $z_k = 1$ if one or more of the primary units that intersect group k are included in the initial sample and $z_k = 0$ otherwise.

sample, influences the efficiency of ACS. Many adaptively added plots will yield a large cluster size.

1.3. Procedures

Slope-corrected rectangular plots of 400 m² were used as initial and adaptively added plots. Plot size was based upon species-area curves developed in a previous study in the same area (Acharya, 1996). The same study yielded an inter-plot distance of 300 m, on the basis of a geostatistical analysis. The rectangular study area (Fig. 1) consisted of $N = 225$ (15×15) primary units, each one with $M = 42$ secondary units (plots), i.e., there are 42 blocks, each consisting of 225 square plots. The total population consists of 9450 plots (37.8 ha). Two primary units were randomly selected without replacement (Bhattarai, 1997).

From the starting point, compass and tape were used to locate the plots in the field. Cross checking with existing landmarks was done frequently to contain location errors. The corners of all field plots were

marked. Plot data were collected only for the species concerned and included the number of trees, diameter at breast height (≥ 12 cm) and basal area (cm²). Plot characteristics like elevation and slope were recorded as well. Adaptively adding plots was done separately for each rare species. No plots were encountered with different rare species growing together.

Sample means, sample variances, standard deviations and estimated populations in the study area at the 95% confidence interval were calculated. Estimated population sizes in the study area equal $T = NM(\hat{\mu}_i)$ where $\hat{\mu}_i$ refers to the calculated means from the different methods. The confidence intervals ($p = 0.05$) were calculated as $T \pm t_{0.05} \cdot \text{sd}(\hat{\mu}_i) \cdot NM$ where $\text{sd}(\hat{\mu}_i)$ equals the sample standard deviation of the mean and $t_{0.05}$ Student's t -value for $p = 0.05$.

2. Results

In our data set the number of primary units N was equal to 225, the number of secondary units (plots per

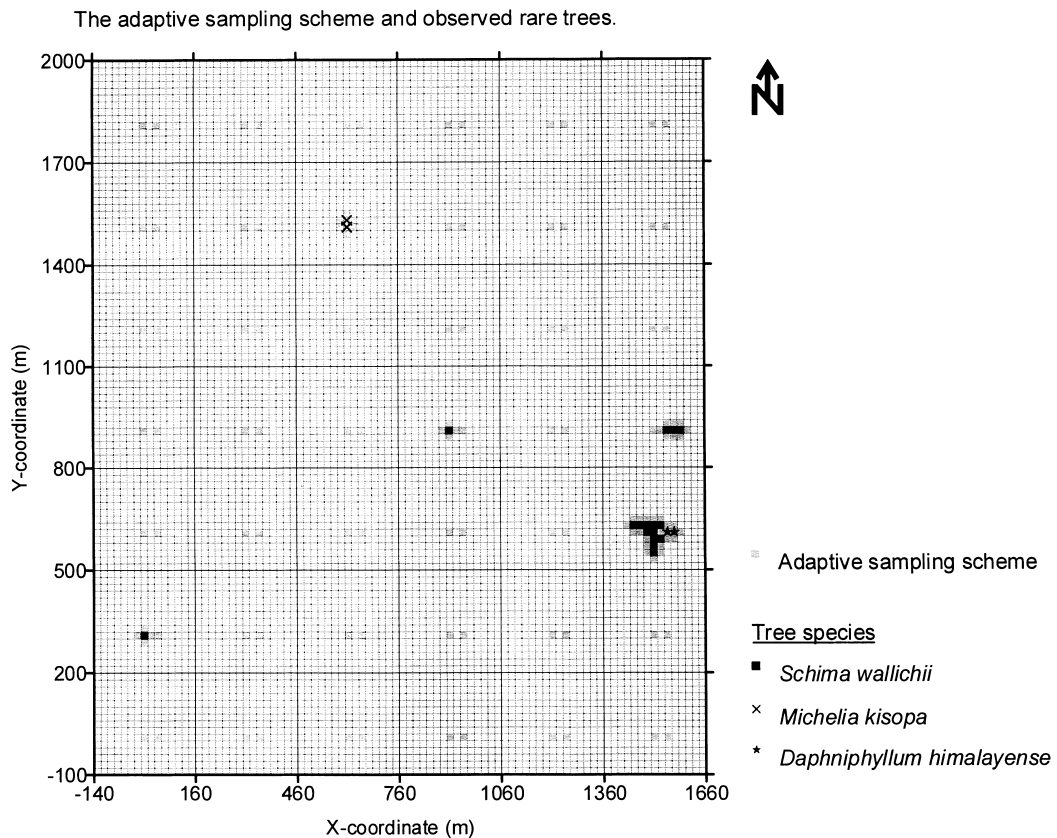


Fig. 1. Layout of the adaptive sampling design area with primary and secondary plots.

primary unit) M was 42, and the number of initial primary units n was 2. Hence, the number of initially sampled detection plots was equal to $Mn = 84$. Out of these 84 initial detection plots, 4 plots were found to be located in a group of *S. wallichii*; one plot in a group of *D. himalayense* and one plot in a group of *M. kisopa* (Table 2). The size of a group affects selection and inclusion probabilities to be included in the sample. The average number of trees observed per group was small for all the selected species. For *S. wallichii* 45 plots were added adaptively. In 16 out of 49 ($= 4 + 45$) plots, at least one tree was observed, yielding a total of 26 trees. The remaining 36 plots were edge plots. The total sampled area for this species was the area of the 84 initial detection plots plus the area of the 45 adaptively added plots, totaling 51 600 m², or 1.365% of the study area. The largest group intersected by *S. wallichii* contained 27 plots added adaptively and one detection plot, the smallest

one five plots. The average cluster size for this species was 12 plots with on the average 4 plots containing the species and 8 being edge plots. Corresponding values for *D. himalayense* and *M. kisopa* were 2 and 6, respectively. The cluster size ranged from 0.2 to 1.08 ha, with an average for *S. wallichii* of 0.48 and 0.4 ha for both *D. himalayense* and *M. kisopa*.

For each rare tree species, estimators and their variances were computed, using the estimators $\hat{\mu}_1$, $\hat{\mu}_2$ and $\hat{\mu}_0$. Table 3 shows the different sample variances for different estimators. Variance was lowest for the HT-estimator $\hat{\mu}_2$ and highest for the initial sample mean $\hat{\mu}_0$. For $\hat{\mu}_0$, the within-sample variance is influenced only by the number of trees observed in the initial systematic primary units, as it does not consider the units, which were added adaptively. On the other hand, the number of trees per group and the number of plots per group influence the variance of $\hat{\mu}_1$, as $\hat{\mu}_1$ considers the number of plots added adaptively.

Table 2
Descriptive statistics for the three tree species in different groups

| | Groups ^a | NT _k | m _{ij} | a _{ij} | y _k | y _k /m _{ij} |
|----------------------------------|---------------------|-----------------|-----------------|-----------------|----------------|---------------------------------|
| <i>Schima wallichii</i> | 1 (12A) | 1 | 1 | 4 | 1 | 1 |
| | 2 (18A) | 5 | 11 | 17 | 21 | 1.909 |
| | 3 (21A) | 1 | 1 | 4 | 1 | 1 |
| | Total of A | 7 | 13 | 25 | 23 | 3.909 |
| | 4 (19B) | 1 | 3 | 8 | 3 | 1 |
| | Total of (A + B) | 8 | 16 | 33 | 26 | 5.1 |
| <i>Daphniphyllum himalayense</i> | 1 (18B) | 2 | 2 | 6 | 5 | 2.5 |
| | Total | 2 | 2 | 6 | 5 | 2.5 |
| <i>Michelia kisopa</i> | 1 (34A) | 1 | 2 | 6 | 2 | 1 |
| | Total | 1 | 2 | 6 | 2 | 1 |

^a Group: the serial number of the group and the code of the initial detection plot for that group (1A, 1B, 2A, 2B, ..., 42A or 42B, i.e., a total of 84 plots); NT_k: the number of trees in the initial primary unit; m_{ij}: the number of plots per group; a_{ij}: the number of edge plots for each group; y_k the number of trees per group.

Unlike the other two methods, $\hat{\mu}_2$ uses the inclusion probabilities of the given group to be included in the sample. The larger the group, the larger is the inclusion probability and vice versa. Therefore, its sample variance is smaller than for the other two methods.

For *M. kisopa* only two plots formed a group, each consisting of a single tree. This means that for $\hat{\mu}_1$ the value (number of trees observed divided by the number of plots in the group) equals the one observed tree in the detection plot, i.e. the y-value for initial sample mean method. Therefore, variance and standard deviation are the same for the three estimators. Single trees of the species *D. himalayense* were observed in two different plots. Three additional trees were observed in the adaptively added plots. Therefore, the larger number of trees divided by the smaller values of selection

and inclusion probabilities has given higher variances (0.00088) when compared to the initial sample mean method (0.00056).

For a large cluster (*S. wallichii*), the estimated population size is lower as obtained by adaptive procedures than obtained by the initial sample mean, whereas it increases for *D. himalayense* when adaptive procedures are applied. The adaptive procedures account for the number of adaptively added plots and observed mean values in the plots. Hence, when only two positive plots are observed and observations in the added plots are found to be higher than the initial plot, it will yield a higher value for the estimate. For *M. kisopa* the mean number of trees per group is one and only one tree means a single detection plot. Thus, the estimated value is the same for the three methods.

Table 3
Calculated values (for trees) by the initial sampling design (1), the partial selection probability design (2) and the partial inclusion probability design (3)

| Species | Estimation method | Mean ($\hat{\mu}$) | Variance | Est. number \pm 95% confidence interval |
|----------------------------------|-------------------|----------------------|----------|---|
| <i>Schima wallichii</i> | 1 | 0.0952 | 0.00506 | 900 \pm 147 |
| | 2 | 0.0584 | 0.00119 | 552 \pm 57 |
| | 3 | 0.0590 | 0.00091 | 558 \pm 50 |
| <i>Daphniphyllum himalayense</i> | 1 | 0.0238 | 0.00056 | 225 \pm 49 |
| | 2 | 0.0298 | 0.00088 | 281 \pm 59 |
| | 3 | 0.0298 | 0.00088 | 281 \pm 58 |
| <i>Michelia kisopa</i> | 1 | 0.0119 | 0.00014 | 113 \pm 24 |
| | 2 | 0.0119 | 0.00014 | 113 \pm 23 |
| | 3 | 0.0119 | 0.00014 | 113 \pm 23 |

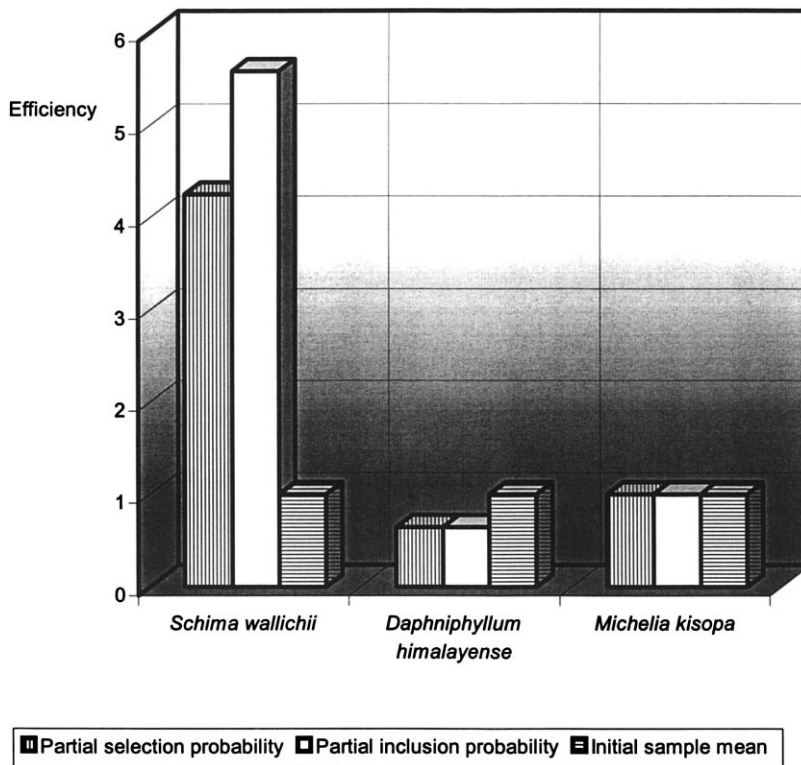


Fig. 2. Efficiency of different estimators for the three rare tree species.

The calculated sample variances were used to compare the efficiency for the three different methods, taking the initial sample mean as the standard (Fig. 2). The variance from the initial sample mean was divided by the variance from the adaptive procedures. When the number of clusters was larger than one (*S. wallichii*) the adaptive procedure appeared more efficient than the initial sample mean. For *M. kisopa*, however, observed in one single cluster only and with a low number of trees per sampling plot, the calculated efficiency was the same. For *D. himalayense* with few plots in the group but a higher number of trees in those plots, the adaptive procedure was found to be less efficient. This might be explained by the partial selection and inclusion probabilities of the groups. It can be concluded that the adaptive procedure is apparently becomes more efficient (in terms of sample variances) than the initial systematic sampling design, if the intersected groups are larger.

3. Discussion

Systematic adaptive cluster sampling is a more efficient design than systematic sampling, under the assumption that the concerned species cluster. The outcome shows that this is certainly true for *S. wallichii*. For the other two species, however, the study found a more dispersed pattern, possibly caused by the very low number of these trees in the study area. Similar investigations in larger areas and with different cluster sizes should bring more clarity here. Because plot size also influences group size, the effect of this should be studied as well.

The question when SACS is more efficient than the initial design can tentatively be answered. From the data in Table 3 overall efficiencies, as calculated above, can be derived and compared between the designs and for different average group sizes and species. Average group size in our study is species

dependent, and is 4 for *S. wallichii*, 2 for *D. himalayense*, and 1 for *M. kisopa*. For group size 1, the designs are equally efficient (1.00), which may not necessarily be correct. For group size 2 the efficiency reduces for all three, but for group size 4, efficiency is highest (1.39) for SACS-HT, followed by 1.06 for SACS-HH and 0.25 for the initial design. An increase in group size, therefore, appears to increase efficiency of SACS, as was anticipated. It can further be expected that there will be an optimal group size in respect of survey efficiency, because when groups get too large, SACS becomes equivalent to (near) full enumeration. Survey cost will therefore have to be taken into consideration as well to arrive at a complete picture. Further research is needed on these issues. Comparing the designs for all group sizes and species reveals that systematic sampling has the lowest overall efficiency (0.58). SACS, using the HT estimators, is highest with 0.90, and using the HH estimators it is 0.79. These differences can mainly be ascribed to the effects of largest group, as a large group increases SACS and reduces initial design efficiency.

Of interest would be to find a predictive model for the geographic location of rare trees. We, therefore, investigated relations between tree species and spatially referenced variables like the coordinates, elevation, aspect and slope. Using a stepwise regression procedure we only found a significant explanatory model for *S. wallichii*:

$$\text{Trees} = 0.191 + 0.00025 \cdot xc - 0.00509 \cdot \text{slope} \\ \times (R^2 = 0.096)$$

where,

Trees are the number of trees, xc is the *x*-coordinate, expressed in m, and slope is the plot slope, expressed in percent.

The R^2 value is too low to draw detailed specific scientific inferences. We might tentatively surmise that the highest probability of encountering a specimen of *S. wallichii* is at the relatively flat areas in the eastern part of the study area, but this is because of the occurrence of a relatively large cluster there.

4. Conclusions

1. Systematic adaptive cluster sampling was found more effective and efficient than systematic

sampling in estimating the density of rare tree species that cluster and form groups, that are larger than the area of one sampling plot. Larger groups appear more efficient to estimate than smaller ones. The initial design of primary units detected only 11 rare trees; SACS discovered a total of 45 trees. Moreover, SACS found that *S. wallichii* is a species that indeed occurs in groups.

2. SACS may also be used to establish relationships between rare species abundance and spatially referenced variables, but data availability will have to be considered. In this study, significant relationships were not found because of this, but also because possibly related variables would have to be considered as well.
3. Systematic adaptive cluster sampling is a promising design for resource managers and survey specialists who need information on forest species that are rare.

We conclude that this study has particular relevance to assess the effects of human induced activities in the forest, that increase species rarity. Several of these species, however, need to be conserved for purposes of biodiversity conservation or sustainable forest management.

References

- Acharya, B., 1994. A geostatistical approach for biodiversity study in Nepal. M.Sc. thesis. Forest Science Division, International Institute for Aerospace Survey and Earth Sciences (ITC), Enschede, The Netherlands.
- Acharya, B., 1996. Pilot survey report of Shivapuri Watershed and Wildlife Reserve. Forest Science Division, International Institute for Aerospace Survey and Earth Sciences (ITC), Enschede, The Netherlands, unpublished.
- Bhattarai, G.P., 1997. Systematic adaptive cluster sampling for assessing density and distribution of rare tree species in Shivapuri Watershed and Wildlife Reserve, Nepal. M.Sc. thesis. Forest Science Division, International Institute for Aerospace Survey and Earth Sciences (ITC), Enschede, The Netherlands.
- Cochran, W.G., 1977. Sampling Techniques. Wiley, New York.
- Roesch, F.A., 1993. Adaptive cluster sampling for forest inventories. For. Sci. 39, 655–669.
- Schreuder, H.T., Czaplewski, R., Bailey, R.G. Combining mapped and statistical data in forest ecological inventory and monitoring – supplementing an existing system. Journal of Environmental Monitoring and Assessment, in press.

- Shrestha, T.B., Joshi, R.M., 1996. Rare, endemic and endangered plants of Nepal. WWF Nepal Program, Kathmandu, Nepal.
- Thompson, S.K., 1991. Adaptive cluster sampling: design with primary and secondary units. *Biometrics* 47, 1103–1115.
- Thompson, S.K., 1992. *Sampling*. Wiley, New York.
- Thompson, S.K., Seber, G.A.F., 1996. *Adaptive Sampling*. Wiley, New York.
- UNEP, 1992. Agenda 21, Chapter 11: Combating deforestation. Report of the United Nations Conference on Environment and Development, Rio de Janeiro, 3–14 June 1992.