

GEORG-AUGUST UNIVERSITÄT GÖTTINGEN

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Göttingen, 2011

**New adaptive plot designs
for sampling rare and clustered populations**

A dissertation to obtain degree of Doctor

At the Faculty of Forest Sciences and Forest Ecology of
GEORG-AUGUST UNIVERSITÄT GÖTTINGEN

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Date of oral exam: November 28, 2011

Acknowledgements

I would like first to express my greatest gratitude to my supervisor, Prof. Dr. Christoph Kleinn for his inspiration, encouragement, tireless support, and sufficient trust and great patience given to me throughout the course of the project application and the study. This dissertation would not have been possible without his innovative ideas, extensive expertise, insightful advice and excellent supervision.

I extend my heartfelt thanks to Prof. Dr. Alparslan Akça and Prof. Dr. Klaus von Gadow for their constant kindness, encouragement and generosity in allowing me to share their experience.

My sincere thanks are due to my friendly research fellows, Dr. František Vilčko, Dr. Hans Fuchs, Dr. Lutz Fehrmann, Dr. Nils Tremer, Axel Buschmann, Hamid Reza Riyahi, Paul Magdon, Tim Exner, Sebastian Schnell, Christoph Fischer, Philip Beckschäfer, Henning Aberle, Torsten Sprenger, Mauricio Vega-Araya, Aura Yorlene Cárdenas and Chaw Chaw Sein for their valuable tips, constructive comments and kind helps during my study. I owe my special thanks to my senior colleagues, Ms. Ulrike Docktor, Mr. Hendrik Heydecke and Mr. Reinhard Schlote for their active and effective administrative and technical support.

I would like to thank Prof. Dr. Shouzheng Tang, Prof. Dr. Yuancai Lei and Dr. Guangyu Zhu at the Institute of Forest Resources Information Techniques, Chinese Academy of Forestry for their friendly reception and support to my study visits and cooperative assistance with the field work at Experimental Center of Desert Forestry CAF in northwest China.

I am grateful to Prof. Dr. Timothy G. Gregoire at the School of Forestry & Environmental Studies, Yale University for his gracious reception, liberal hospitality and considerate arrangement during our visit to his school.

This work was funded jointly by the German Research Foundation (DFG) through grant KL894/10-1 and the National Natural Science Foundation of China (NSFC). I highly appreciate their financial support.

I am deeply indebted to my parents, parents in law, my wife and my siblings for their full understanding and constant support. I would like to thank my lovely sons for bringing me so much joy and taking me out of stress sometimes during preparation of this dissertation.

Sincerely thanks to all,

HaijunYang

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LIST OF ABBREVIATIONS AND ACRONYMS

ACDS	Adaptive cluster double sampling
ACS	Adaptive cluster sampling
ACS _{ord}	Adaptive cluster sampling based on order statistics
ACS _{PPSS}	Adaptive cluster sampling with probability proportional to Strip sizes
ACS _{WORC}	Adaptive cluster sampling without replacement of clusters
ACS _{WORN}	Adaptive cluster sampling without replacement of networks
ATSS	Adaptive two-stage sequential sampling
BAF	Basal area factor
CIACS	Constrained inverse adaptive cluster sampling
CrV	Critical value
DBH	Diameter at breast height
DSS	Double sampling for stratification
EF	Expansion Factor
HH	Hansen-Hurwitz
HHM	Modified Hansen-Hurwitz
HT	Horvitz-Thompson
PSF	Plot size factor
RACS	Restricted adaptive cluster sampling
RB	Rao-Blackwell
RMSE	Root Mean Square Error
RSS	Ranked set sampling
SRS	Simple random sampling
SRS _{WOR}	Simple random sampling without replacement
TSRACS	Two-stage restricted adaptive cluster sampling
TSS	Two-stage sequential sampling
UMVUE	Uniformly minimum variance unbiased estimator

1 INTRODUCTION

1.1 BACKGROUND

Forest inventories and ecological surveys are common and essential tools of data collection to support decision making in forest management and conservation. Statistical sampling based forest inventories date back to around a century ago. With the changing and growing needs of various users for statistically sound data, a wide range of statistical sampling strategies and techniques aiming at improving sampling efficiency have been developed, evaluated and translated accordingly into sampling designs, especially over the past decades. There are numerous sampling designs available for application to obtain precise and reliable information on populations of interest for a variety of purposes in forest inventories and ecological surveys, such as natural resources assessment, biodiversity monitoring, and management planning.

In sample based forest inventories or ecological surveys, sampling design, response design and estimation design are three basic design elements to be taken into account. Sampling design refers to the procedure by which the sample of units is selected from the population of interest for estimating characteristics of that population, and a set of rules/protocol for all possible occasions needs to be explicitly specified for its appropriate implementation. The response design defines the sample units and the observations to make on them. In the context of forest inventories, response design is usually known as plot design or observation design, where sample plots are commonly used as sample units and described in terms of plot shape and plot size. The estimation design addresses what statistical estimation procedures and in particular what estimators will be applied to make inferences or extrapolations from the sample to the population. Normally the last element needs to be in compatibility with the first two, and thus an appropriate sampling design together with response design is integral and crucial to the sampling efficiency. For the convenient choice of the most effective sampling and plot design for the population of interest, Thompson and Seber (1996) differentiated all available sampling and response designs into three types: conventional designs (e.g. stratified random sampling and two-stage sampling), adaptive designs (e.g. inverse sampling and adaptive cluster sampling) and nonstandard designs (e.g. ranked set sampling).

In conventional designs, neither sampling design nor response design depends on any observation of the variable of interest. It is implied that a fixed size sample of units selected prior to an inventory or survey for data collection is unchangeably used as such throughout

that inventory or survey, and no modification to sampling design or plot design is allowable to be triggered by any observation. Simple random sampling (SRS), stratified random sampling, systematic sampling, cluster sampling, multistage sampling and relascope sampling are common conventional designs.

In adaptive designs, the sample selection or plot design may depend on the observed values from the sample units, and the final number of sample units remains unknown to the sampler until the completion of a sampling mission. The development of the adaptive designs is motivated by the important challenge of sampling “rare events” (Thompson, 2004). Rare events are target objects such as plants that occur in very low density. Frequently, the abundance of rare species is of a particular interest for conservation and biodiversity monitoring. Accurate information about rare objects is difficult to achieve with conventional designs. The simple and intuitive philosophy underlying adaptive sampling, known also as informative sampling sometimes, is that more precise estimates of population parameters are expected to be obtained by adaptively adding more objects of interest to the sample. The adaptive approaches are suggested to be preferable in situations where nonadaptive designs are proven to be notoriously inefficient, especially when rare, clustered, unpredictable, elusive, spatially and temporally uneven, and hard to detect populations are of interest. A typical example is “inverse sampling” (Haldane, 1945; Cochran, 1977), in which a sample unit is sequentially selected into the sample until a prefixed number of sample units with the characteristic of interest are observed. Whether the addition of an extra sample unit continues or not is judged following the observations made upon the current sample.

In nonstandard designs, the selection of sample units is influenced by the observed values of the target variable for the units outside the sample or by unknown parameter values, which can be seen clearly from an example given in Thompson and Seber (1996) and ranked set sampling (RSS) (Dell and Clutter, 1972; Chen et al., 2004). In RSS, the ranking of potential sampling units on the target variable using judgment or an ancillary variable is required for the sample selection. Nonstandard designs are much less well known and their use needs serious caution in comparison with the other two types of designs owing to the complicated inference problem arising from the unknowns involved in designs.

The overall performance of a sampling design depends on a variety of factors such as design settings, population structure, degree of homogeneity of the target variable, physical conditions of the inventory region for example accessibility, and available budget. A

comprehensive consideration of those factors is required to determine which design is suitable or optimal.

In ecological systems, rare species outnumber common species (Cao et al., 1998; Magurran and Henderson, 2003) and have great importance to biodiversity conservation (Raphael and Molina, 2007). Many of them, such as palms, shrubs, trees, and medicinal and aromatic plants, are not only rare in number, but also clustered in patches over a region. For such populations, the efficiency of nonadaptive designs tends to be even much worse in terms of relative standard error, including the conventional cluster sampling. The reason is that a vast majority of sample plots are empty and eventually the estimates of population characteristics are derived from the observations of the objects of interest within very few sample plots. A technique referred to as adaptive cluster sampling (ACS) was introduced and suggested by Thompson (1990) in this context.

The principal strategy of ACS is to take the advantage of spatial clustering of individuals to focus the sampling effort on the locations where the target individuals concentrate so that the sampling precision and efficiency can be improved. From a probabilistic point of view, it is to assign a higher probability to be included in the sample to the individuals with more neighbors than those with fewer or even no neighbors in the adjacent area.

According to the definition of ACS given by Thompson (1990), under the design of ACS, an initial set of units (initial sample) is selected by an ordinary probability sample e.g. by simple random sampling or systematic sampling, and whenever the variable of interest of a selected unit satisfies a predefined criterion or condition C (for instance, the presence of at least one object of interest in a sample plot), all units in its neighborhood not already in the sample are added to the sample; if an additional unit meets C once again, then further sampling of its unsampled neighbors is needed. The iterative sampling process continues until C is not satisfied any more. The condition C is often expressed in terms of a critical value (CrV), the minimum value to trigger the adaptive addition of neighbors, and the neighborhood can be defined in a variety of ways such as first-order neighborhood and second-order neighborhood (Christman, 2000). At the completion of ACS, a set of clusters of different sizes is finally formed when it is area-based. “Area-based” (Cochran, 1977) implies that the region where the target objects occur is completely tessellated into squares (referred to as plots in forestry and quadrats in ecology) as usual. That region and the plots within it are subsequently defined as the population of interest and population units respectively. In the case that the condition C of ACS is the presence of at least one target object, as seen in Figure 1.1, a non-empty

initial sample plot is step by step enlarged by adding more and more plots and becomes an irregularly shaped cluster of subplots. Eventually the cluster will contain the entire group of target objects intersected by the initial sample plot. Thus, the cluster plot adapts in size and shape to the group of target objects encountered at a sample location. If no target object is found on the initial sample plot, then the cluster consists of the initial sample plot only.

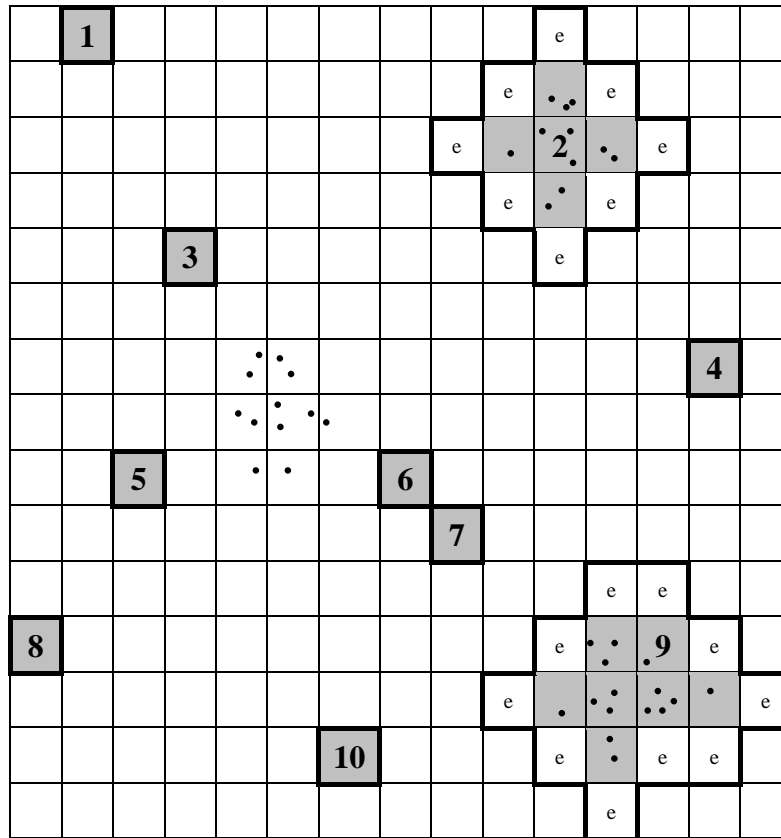


Figure 1.1 An adaptive cluster sample with an initial simple random sample of 10 units numbered from 1 to 10. The black dots denote the objects of interest. Each resultant cluster is outlined in bold with its network consisting of units satisfying C highlighted in shade and edge units labeled with e. The neighbors of a unit are defined to consist of four adjacent units sharing a common boundary line with it. The condition for adaptive addition of neighboring units is: the presence of at least one object of interest in the quadrat.

In the context of ACS, a cluster, as seen in Figure 1.1 above, is the set of all sampled units resulting from the selection of an initial sample unit, and a network is such an aggregate of units that the selection of any of its units leads to the inclusion of all its other units in a sample. Any unit in a cluster not satisfying C but in the neighborhood of one that does is called an edge unit (Thompson, 1990). There exist two types of networks: single-unit network and multi-unit network. A single-unit network consists of only one unit if that unit either simply

fails to fulfill C, or does fulfill C but its contiguous neighbors cannot. Apparently, a multi-unit network comprises at least two adjacent units and all units within it satisfy C. By definition, an edge unit is actually a single-unit network, namely, a network of size 1. If the same condition C is applied to classify all plots in a region into networks, then a certain number of mutually exclusive and completely exhaustive networks of various sizes will be developed. Then a population of interest can be uniquely partitioned into distinct, nonoverlapping networks. A network is also described to be a cluster with its edge units removed, if any. The estimation design of ACS in the original work of Thompson (1990) was based on the attributes of the resultant networks rather than clusters, which justifies/accounts for the introduction of the term “network” into ACS in addition to the term cluster. It is very obvious that ACS as a specific adaptive design is a technique of sampling with unequal probabilities from the set of networks. However, neither Horvitz-Thompson (HT) estimator (Horvitz and Thompson, 1952) nor Hansen-Hurwitz (HH) estimator (Hansen and Hurwitz, 1943) can be directly applied to ACS as usual because the inclusion probability or the draw-by-draw selection probability of each sampled edge unit cannot be derived unless all clusters it belongs to are sampled. As an alternative, the modified HT and HH estimators were developed by excluding the sampled edge units of clusters from the estimation process. As a result, the modified HT estimators use the probability that the initial sample intersects a network, while the modified HH estimators use the number of units in the initial sample which intersect or fall in a network. Both of them are design unbiased, i.e. without any assumption about the population of interest.

ACS is claimed to be superior to conventional sampling techniques when the objects of interest are rare and geographically clustered in that it may provide more precise estimates with additional gain in information on the spatial distribution pattern of the population of interest with an equivalent amount of sampling effort (Thompson, 1990). However, it has not yet been used on a routine basis in field surveys for forest inventory and biodiversity monitoring as there are also practical difficulties in field implementation. Under the design of ACS, the final number of sampled units is a random variable, and thus the total sampling effort is not precisely predictable.

Depending on the structure of the population and the plot design, the challenge may arise during the survey that the adaptive clusters become excessively large and the sampling work there turns out to be impractical and too costly. Furthermore, there are numerous factors influencing the efficiency of ACS (Thompson, 1994), and the relationship between the

sampling efficiency of ACS and those factors is not straightforward (Brown, 2003) so that there is no explicit and workable definition about how to configure an efficient ACS design but some general principles from Thompson and Seber (1996) and a rule of thumb given by Brown (2003): the final sample size, which is the number of subplots in strict sense, should not be excessively larger than the initial sample size and networks should not be so small that the within-network variance is very low. ACS is not uniformly better than the conventional designs in terms of precision, and it may be found even less efficient than simple random sampling without appropriate settings of design factors in the case of equivalent amount of sampling effort. Therefore, further research is necessary on how to reach the promising potential of ACS in a more practical manner without restriction from the noted drawbacks.

1.2 OBJECTIVES

In this methodological study with the focus on practicability of implementation, three new adaptive plot designs will be introduced. The main objectives of the study are:

- Introduction and detailed elaboration of three new adaptive plot designs including their sampling procedure, design factors and their difference from the conventional ACS design
- Developing estimation designs for the researched adaptive plot designs based on the inclusion zone approach
- Evaluation of the statistical performance as well as cost efficiency of the studied adaptive plot designs based on their efficiency relative to the nonadaptive designs in various sampling situations in one real and eleven artificial populations
- Suggestion for the appropriate choice of design parameters to improve the efficiency of the new plot designs

2 LITERATURE REVIEW

2.1 BRIEF INTRODUCTION TO THE STUDIES ON ACS

ACS attracts general interest and is widely considered to be a preferable technique for sampling rare and geographically clustered populations since it was introduced in the foundational research work of Thompson (1990). There, a comprehensive description on ACS accompanied by illustrative examples is available and one can obtain a general and fundamental insight into ACS, such as justification, definition of elementary concepts, sampling design, estimator development, and comparative efficiency relative to simple random sampling. The efficiency of ACS is influenced by a number of factors, and how to fill the gap between the theoretical potential and actual performance is still a major concern. Many methodological and applied studies have been carried out for a variety of purposes; some of them are regularly published and some are available as gray literature. The methodological studies focus mainly on adapting sampling and plot designs, as well as designing estimators with satisfactory properties.

2.2 VARIATIONS OF ADAPTING SAMPLING AND PLOT DESIGN

An ACS design can be considered to consist of two sampling components: one defines the selection of the initial sample, and the other defines the adaptive addition of extra sampling units at an initial sample unit satisfying the condition of interest, which is referred to as extra sampling or additional sampling. According to the definition of ACS (Thompson, 1990) any sampling design can be used to select the initial sample theoretically, and thus there are various ACS designs available depending on how its initial sample is selected. The overall gain in precision of one form relative to another has two sources, of which one is contributed by the initial design component and the other by the incorporated adaptive component. Which component accounts more varies considerably from one sampling situation to another. Hence, the choice of initial sampling design is very crucial to the best yield of sampling efficiency.

Conventional ACS

The ACS (see Figure 1.1) first introduced in Thompson (1990) is often referred to as classical, conventional, standard or ordinary ACS in order to differentiate it from the other types of ACS designs. Throughout this dissertation, it is consistently referred to as conventional ACS

to avoid confusion. A comprehensive description on conventional ACS including justification, elementary concepts and basic terminologies can also be found in Thompson (1992) and Thompson and Seber (1996). The principle of conventional ACS was illustrated for quadrat-based sampling, where the study area is usually partitioned into nonoverlapping quadrats for sample selection. Its initial sample is designed to be selected by SRS of fixed size either with or without replacement. However, no matter what it is, possible repeated observations of networks and their associated clusters are unavoidable as more than one initial sample unit may fall into a network. The larger the size of a network is, the higher its probability of repeated observation. Throughout the sampling procedure including initial sampling and extra sampling, the same sampling units, quadrats, are employed. It is natural that this design is also applicable in theory to other shapes of sampling units in area sampling than quadrats.

The conventional ACS is neighborhood-based since the extra sampling units to be adaptively added into the sample are confined to the neighboring units of the sampled ones. In addition, its condition to adapt or CrV is predefined in some way prior to the initial sampling and holds for the entire sampling process unlike the ACS based on order statistics (Thompson, 1996), in which the CrV is determined at the completion of initial sampling. The design-unbiased total and variance estimators were developed as well as their Rao-Blackwell versions (Lehmann and Casella, 1998). It was noted that neither of the HT and HH estimator is uniformly better than the other although in the small example in Thompson (1990) the adaptive HT estimator performed clearly better than its HH counterpart. For a more realistic comparison as seen in classical cluster sampling, a reasonable cost function was also presented for the conventional ACS with a brief explanation. It was concluded that the conventional ACS is a promising sampling technique in comparison with the conventional sampling strategies. As mentioned before, the main drawback of this design is that it is impossible to put the final sample size under control.

The overall efficiency of the conventional ACS depends not only on its design configuration, but also on many other factors. Those factors were identified in Thompson (1994), including within-network variation, sample size, cost issue, and the degree of rarity and clustering of the population of interest. Some general guidelines to follow for a better efficiency were elaborated there. Christman (2000) notes explicitly that for the rare and clustered populations, quadrat-based stratified sampling is more efficient than conventional ACS when population stratification is possible. In Brown (2003), it was found that the design factors such as critical

value and neighborhood definition interact with each other and the relationships between them are not straightforward by analyzing in detail how they influence the efficiency.

Dryver (2003) studied the conventional ACS in a multivariate setting where several variables are of interest and pointed out: a better efficiency can be achieved when the variables of interest are highly correlated, otherwise a function of the variables rather than a value of the main variable should be used as the condition to adapt.

Tout (2007) stressed that the placement of grid and the size of the grid cells are also two vital factors influencing the efficiency of the conventional ACS because they affect the geographical clustering of the population of interest, e.g. a population is geographically clustered when it is tessellated with a small grid cell size, but may not any longer with a large enough grid cell size. These factors attracted surprisingly little attention, and should be taken into consideration during the evaluation of comparative efficiency.

ACS without replacement of networks

ACS without replacement of networks (ACS_{WORN}) (Salehi and Seber, 1997a) is a modification of the conventional ACS. Its selection of networks without replacement is realized by excluding the already sampled network units from the selection of the next initial sample unit. It follows that the repeat observation under this design can still possibly occur, but only to edge units. The sampled networks are excluded from the selection of the next initial sample unit. The design unbiased estimators including Raj's estimator (Raj, 1956), Murthy's estimator (Murthy, 1957), and their Rao-Blackwell versions were presented. Murthy's estimator is a modified version of Raj's estimator and always found to be more efficient than Raj's estimator. However, it requires substantial computation, especially when initial sample size is large. Without considering the Rao-Blackwell versions of HH and HT presented by Thompson (1990), ACS_{WORN} using Raj's estimator and Murthy's estimator is found to be more efficient than the conventional ACS in two examples. Salehi and Seber (1997a) believe that the ACS_{WORN} using Murthy's estimator is more efficient than the conventional ACS using HH or HT estimators for most but not all populations, and consider that further comparative studies are needed to confirm it. It was claimed that ACS_{WORN} has an obvious practical advantage over the conventional ACS when there exists a cost restriction and the main sampling expense is the travel cost between the sites of initial sample units, since the final number of networks to be sampled is fixed under the former design but variable under the latter design. However, from a practical point of view, this design will pose

difficulty to the fieldwork organization because only the location of the first initial sample unit can be known prior to fieldwork and other initial sample units cannot be selected until the sampling of all units in the cluster associated with the preceding initial sample unit is completed. When ancillary information is available to rapidly identify all units at low cost in a cluster to which an initial sample unit belongs but population stratification is still impossible, ACS_{WORN} design is then preferable to the conventional ACS as its sequential selection of initial sample units can be easily completed in advance of fieldwork.

ACS without replacement of clusters

ACS without replacement of clusters (ACS_{WORC}) (Dryver and Thompson, 2007) is an improvement of ACS_{WORN} . They differ from each other in the sequential selection of the initial sample. The former excludes any previously sampled clusters i.e. all sampled units rather than merely networks as in the latter from the selection of the next initial sample unit. Repeat observation is hence avoided in ACS_{WORC} in comparison with ACS_{WORN} where repeat observation upon edge units is allowable by design. Two types of design-unbiased estimators including variance estimators were developed. One is the modified Raj estimator and the other is the modified Murthy estimator. The simulation study demonstrated that in the univariate case ACS_{WORC} produced a modest gain in efficiency relative to ACS_{WORN} with the critical value being equal to 1. According to Dryver (2003) and Dryver and Thompson (2005), ACS_{WORC} may be also noticeably more efficient than ACS_{WORN} in the case of large CrVs or in a multivariate setting (i.e. more than one variable are of interest). ACS_{WORC} shares a common drawback with ACS_{WORN} due to their sequential selection of initial sample units as mentioned above when no ancillary information is available for the rapid identification of cluster units. ACS_{WORC} is only considered to be practical and advantageous when sampling is very costly and thus repeated observations are undesirable.

ACS with primary and secondary units

Thompson (1991a) introduced the ACS designs in which the sampling units used in the initial sampling are different from those in the extra sampling and the initial sample is selected by simple random sampling without replacement. The sampling units used in the initial sampling and the extra sampling are referred to as primary units and secondary units, respectively. Each primary unit is actually a collection or cluster of an equal number of secondary units. All secondary units in a selected primary unit are required to be observed and whenever the

observation in a secondary unit satisfies condition C, then the extra sampling will be invoked and conducted so that a cluster of secondary units is eventually sampled. The extra sampling is allowed only at the secondary unit level (Turk and Borkowski, 2005), and hence the associated condition to adapt and neighborhood definition are secondary unit oriented. It implies that no extra primary unit as a whole is designed to be adaptively added into the sample during the survey and the boundaries of primary units impose no geographical restriction on the extra sampling. The secondary units in the unselected primary units may be involved in the extra sampling according to the given definition of neighborhood. Thompson (1991a) presented two types of primary units according to the spatial arrangements of secondary units within a primary unit, and correspondingly two specific ACS designs as seen in Figure 2.1. One design is called strip ACS, in which a primary unit consists of a long thin strip of contiguous secondary units, and the other is called systematic ACS (Acharya et al., 2000; Christman, 2000), in which a primary unit consists of a set of systematically selected secondary units with a single random starting point and usually at least two primary units resulting from two random points to be initially sampled to ensure the design-unbiased error variance estimation. However, in normal practice, we select systematic sample with only one random starting point rather than two in order to save sampling effort, especially in large forest inventories due to the advantages of systematic sampling over SRS (Cochran, 1977). Unfortunately, how to approximate the error variance for systematic ACS with one single random starting point was not addressed (Christman, 2000).

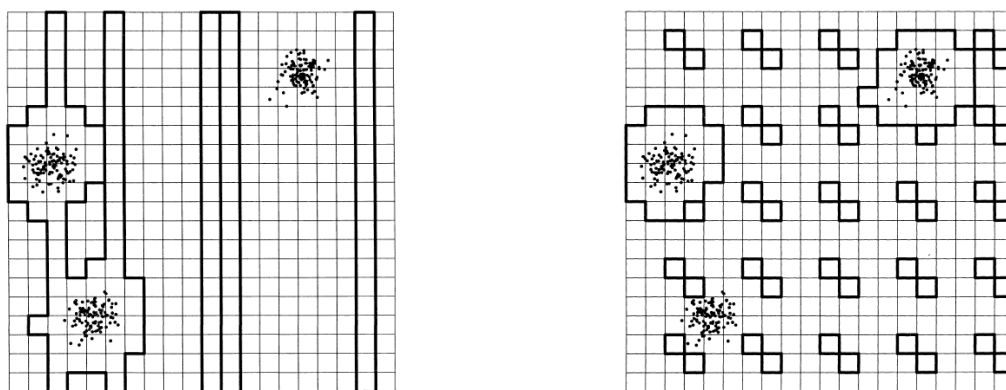


Figure 2.1 Illustration of strip ACS with initial random selection of five strip plots (primary units) (left) and systematic ACS with initial random selection of two systematic samples (right). The condition to adapt for both designs is the presence of at least one object of interest in a secondary unit, and the neighbors of a unit are defined to consist of four adjacent units sharing a common boundary line with it. The final sample obtained on each side is outlined (from Thompson, 1991a).

PPS strip ACS

PPS strip ACS (ACS_{PPSS}) (Pontius, 1997) with replacement described the strip ACS design where the primary units have different numbers of secondary units and the initial sample of primary units is selected with probabilities proportional to the sizes of primary units (see Figure 2.2). The PPS with replacement is achieved by dropping random points to the area of interest. A primary unit is selected once a random point hits onto it. Stratified ACS_{PPSS} is a further development of ACS_{PPSS} with all its primary units being stratified into strata. It is independently performed in each stratum. ACS_{PPSS} is suitable for sampling situations where the site of interest is not ideally a rectangle and thus equal sized strips cannot be realized as expected.

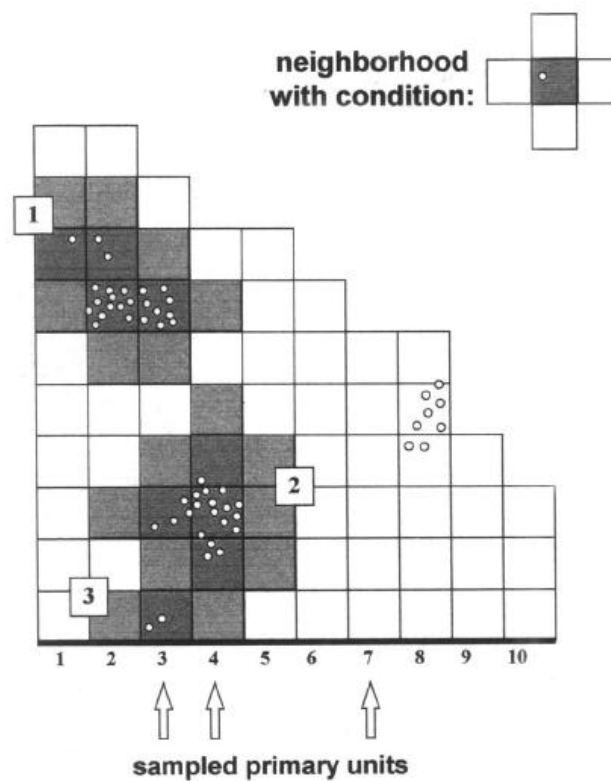


Figure 2.2 Illustration of ACS_{PPSS} . The primary units are of different sizes, and the open circles represent the locations of plants. There are four networks but only the three numbered ones are sampled through the selection of primary unit 3, 4 and 7. The sampled networks and the edge units associated with them are highlighted with the darker shading and the lighter shading, respectively. The condition to adapt is the presence of at least one plant in a secondary unit (from Pontius, 1997).

Adaptive simple Latin square sampling +1

Adaptive simple Latin square sampling + 1 (Munholland and Borkowski, 1993; Borkowski, 1999) as illustrated in Figure 2.3 refers to the ACS design in which the selection of the initial sample follows the so called simple Latin square sampling +1 (Munholland and Borkowski, 1996) approach or SLSS+1. This initial sampling approach combines simple Latin square sampling (SLSS) with random sampling for the selection of 1 additional sample unit from the remaining unsampled units after SLSS.

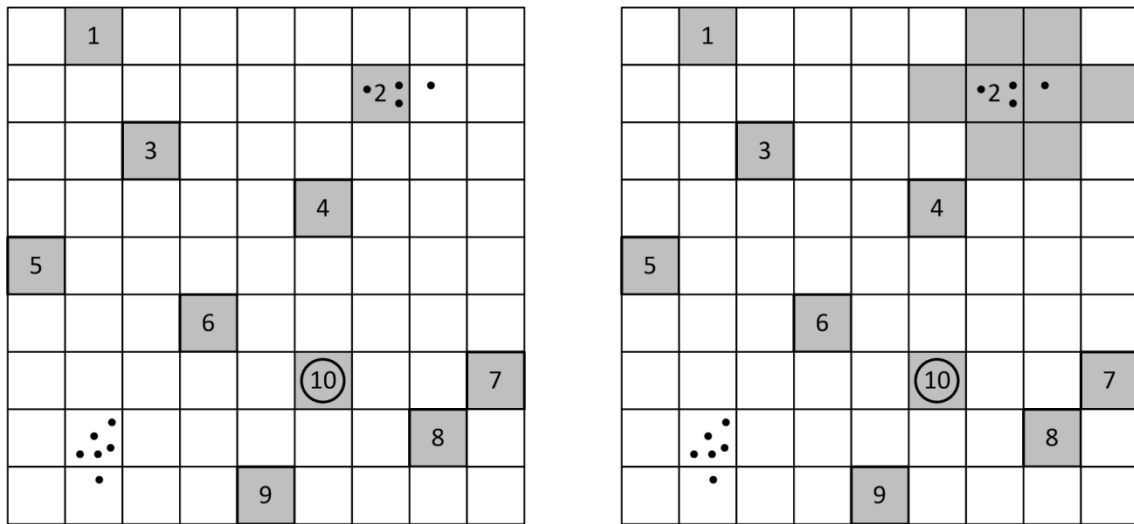


Figure 2.3 Illustration of adaptive SLSS+1 design. Left: the region of a tree population denoted by black dots is tessellated into a 9×9 simple Latin square, and the initial sample contains 9 simple Latin square sample plots numbered from 1 to 9 and one randomly selected plot with the number 10 in the circle. Right: The plots in the final sample are light-shaded for $CrV=1$.

The simple Latin square sample consists of units selected in such ways to ensure that exactly one single unit is sampled from each of the rows and columns of a Latin square, for an instance, with a generated random permutation of rows or columns. That Latin square for the sample size of n can be created by tessellating the inventory region into a $n \times n$ grid of equisized quadrats. The SLSS is characterized by a good spatial coverage comparable to or even better than the initial systematic sampling as used in systematic ACS. Furthermore, it outperforms systematic sampling in general in the presence of positive spatial autocorrelation (Munholland and Borkowski, 1996) or periodic variation in the population of interest. The additional random sample of size one subsequent to SLSS is designed deliberately to enable the variance estimation. In the sense of the preceding two aspects, this design can be seen as a modification of systematic ACS with a single random start. However, from the practical

perspective, its potential applications are constrained by some drawbacks. First, it lacks flexibility in the choice of initial sample size since the initial sample size for a study or survey region with a given quadrat size is automatically determined following the principle of SLSS. Second, it requires a survey region to be a square of rectangular quadrats due to its implicit assumption, which is apparently not realistic especially for the forest inventories where most inventory regions are irregular in shape or where a grid of hexagons rather than quadrats are used. Borkowski (2003) extended the SLSS+1 to $SLSS \pm k$ to allow an arbitrary choice of sample size. It is likely to expect that the adaptive counterpart of $SLSS \pm k$ will provide another viable alternative for sampling rare and clustered populations.

Stratified ACS

Stratified ACS (Thompson, 1991b) (see Figure 2.4) described another class of ACS designs with an initial stratified random sample without replacement and proposed them for the sampling situations where the prior information for population stratification is available, whereas the locations and shapes of the population clusters are either unknown or unpredictable. As in its nonadaptive counterpart, the partition of the population of interest into strata and allocation of sample size into each stratum influence the final gain in precision in stratified ACS. The stratification and allocation strategies in conventional stratified sampling are still do hold also for stratified ACS. However, it may take place that a natural cluster prior to the stratification lies across more than one stratum after the stratification. When a network unit of such a cluster is selected in a stratum, a confusing argument will arise whether the entire cluster or just those cluster units in that stratum should be adaptively sampled. As a solution, two specific designs were presented. One ignores the stratum boundaries and the extra sampling can be conducted as if the population of interest were not stratified, namely it allows the adaptive addition of extra sample units through crossing stratum boundaries, whereas the other restricts the extra sampling within the same stratum where it is triggered by truncating clusters lying across strata at the stratum boundaries. The sampling in different strata under the former design is not completely independent as under the latter one, and thus the corresponding estimators should be appropriately chosen with caution for each design. Turk and Borkowski (2005) noted that the first design is preferable to the second one in terms of efficiency simply because it allows the clusters that straddle stratum boundaries to be enumerated and thereby more target objects can be observed. This justification was supported only by the example given in the work of Thompson (1991b)

without analytic comparison, and thus not convincing enough. Additional comparative studies are needed to confirm whether the first design always outperforms the second one.

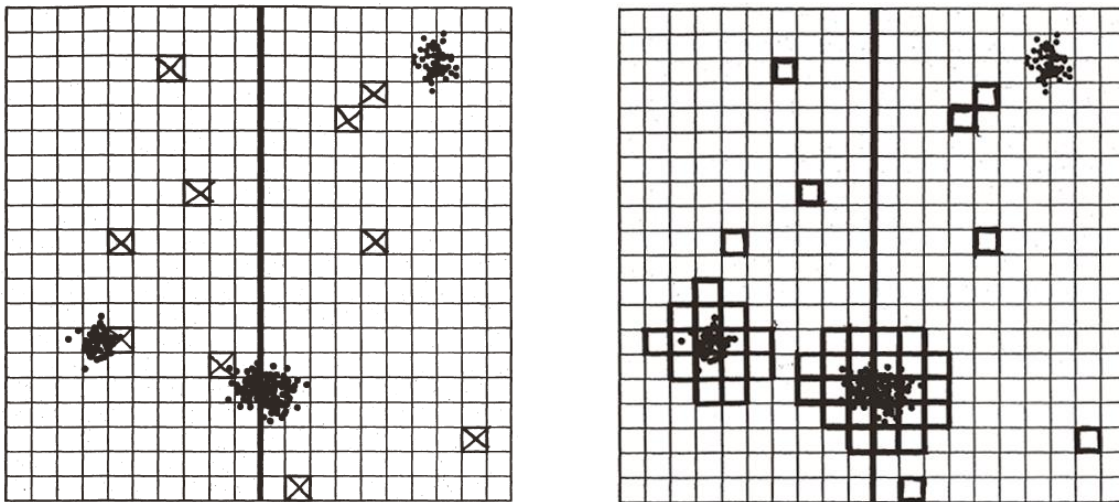


Figure 2.4 Illustration of stratified ACS. On the left side, an initial stratified random sample of five units with a cross inside is taken from each of the two strata. On the right side is the final sample of the stratified ACS (modified from Thompson, 1991b).

Two-stage ACS

Two-stage ACS (Salehi and Seber, 1997b) (see Figure 2.5) was developed by integrating the adaptive component of ACS into conventional two-stage sampling or subsampling with units of equal size (Cochran, 1977). The selection of the initial sample for two-stage ACS follows the same sampling procedure as in its nonadaptive counterpart, conventional two-stage sampling: in the first stage, selecting a fixed number of primary units by simple random sampling without replacement, and in the second stage, selecting a fixed number of secondary units in each selected primary unit also by simple random sampling without replacement. All selected secondary units then serve as seeds. The extra sampling in this design can be triggered exclusively at the secondary unit level. It implies that the condition to adapt and neighborhood are defined in terms of secondary units rather than primary units. During the extra sampling, it may happen that a secondary-unit-based cluster lies across the boundary of a primary unit. For such situations, two variations of this design were therefore prompted in order to avoid possible arguments or confusions, following a similar way as seen in the stratified ACS (Thompson, 1991b). One is called overlapping scheme, where a secondary unit based cluster is allowed to grow across primary unit boundaries; the other is called nonoverlapping scheme, where clusters lying across primary units are truncated at the

boundaries of primary units. The selected scheme should be applied consistently throughout the sampling, and no arbitrary shifting between the two schemes is allowed during the survey. It is apparent that under the nonoverlapping scheme, the probability of such a cluster lying across primary units to be sampled is lower than that under the overlapping scheme. However, the nonoverlapping design has an advantage over the overlapping one in that it can readily lend itself to a cost analysis based on a pilot survey aiming at a better configuration of design factors. The reason is that the number of the primary units in the final sample is fixed to the initial sample size under the nonoverlapping scheme, but varies under the overlapping scheme. No definite conclusion about which of the two schemes is preferable in terms of estimation efficiency was given by the authors, possibly because a variety of influencing factors should be taken into account in necessary comparative studies. From the perspective of the sampling procedure, two-stage ACS can be virtually conceived as a special type of ACS with primary and secondary units with its selected primary units being sampled but not fully surveyed or enumerated when the primary units are defined to consist of spatially contiguous secondary units.

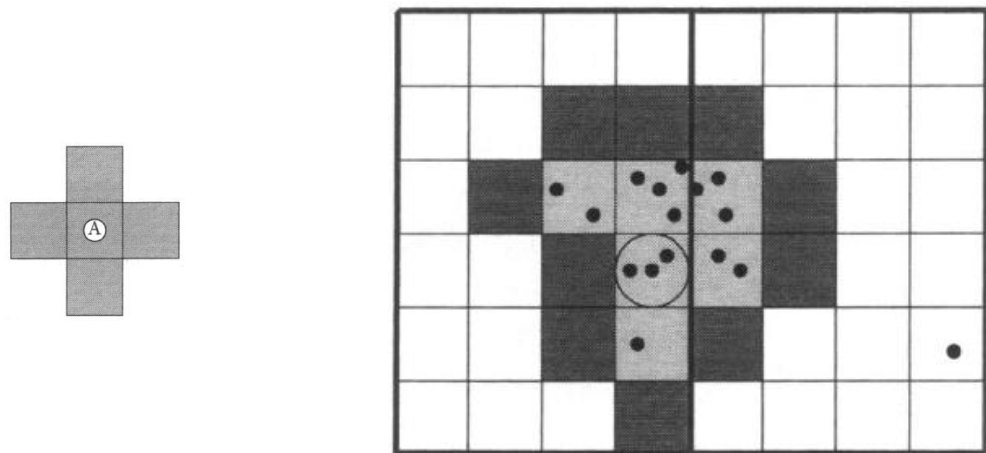


Figure 2.5 Illustration of two-stage ACS with a secondary-unit-based neighborhood of unit A (left). A secondary unit containing a circle is initially sampled from the selected one of two primary units. The single cluster straddles the primary unit boundary (right). The condition to adapt is the presence of at least one dot in a secondary unit. The adaptively added secondary units in the network and edge units in the cluster are light-shaded and dark-shaded respectively (from Salehi and Seber, 1997b).

Two-stage ACS with encounter sampling strategy

Naddeo and Pisani (2005) proposed another form of two-stage ACS to address the problem of handling the special case of imperfect detectability in conventional ACS by using a pure

design-based approach. The selection of its initial primary units follows the same approach as seen in the preceding two-stage adaptive designs. But within each selected primary unit, an encounter sampling strategy (Barnett, 2004), where the encounter procedure such as line transect needs to be replicated for a prespecified number of times, is applied. Whenever the estimated abundance in a selected primary unit by replicated counts satisfies a predefined condition, e.g. larger than a given value, then its neighboring primary units will be adaptively added to the sample. The adaptive addition of neighboring primary units continues until no more selected primary units meet the condition to adapt as usual. That is, its extra sampling is designed only for the primary unit level rather than the secondary unit level as seen before. The design-unbiased mean and variance estimators were presented. The results of empirical comparison based on some Monte Carlo simulations with an artificial population showed that the proposed sampling method was dramatically less efficient than the conventional ACS even with an equal final sample size in terms of the area effectively sampled. The poor relative statistical performance of the proposed design was interpreted to originate from the imperfect detectability due to the use of the encounter sampling. As a consequence, some network units may not be included in the final sample even though the network itself is intercepted by the initial sample. It was remarked that the assumption of perfect detectability may be fairly unrealistic even for conventional ACS when sampling an elusive population. Naddeo and Pisani (2005) suggested that the possible imperfect detectability should be taken into consideration in order to avoid the serious underestimation of sampling variance.

Adaptive two-stage one-per-stratum sampling

Adaptive two-stage one-per-stratum sampling (Christman, 2003) refers to ACS designs in which the initial sample is taken according to a Markov chain one-per-stratum design (Breidt, 1995; Gruijter et al., 2006). The Markov chain one-per-stratum sampling, which was further developed from Markov sampling (Chandra et al., 1992), is not straightforwardly understandable. For the better understanding of its adaptive counterpart, a brief and general introduction to it in plain language is given here. Systematic sampling is the most widely used sampling technique in forest inventory sampling since it is easy to implement in the field and much more efficient than SRS on a comparable basis for positively autocorrelated populations without systematic features like trends and periodicities, although its error variance can only be approximated but not estimated. However, it is disastrously inefficient in the presence of systematic features (Cochran, 1977; Bellhouse, 1988); stratified simple random sampling may be more efficient for the non-autocorrelated populations with systematic features than

systematic sampling. It is then self-explanatory that neither of them is efficient for the populations with positive autocorrelation plus systematic features. Markov chain one-per-stratum sampling was devised for sampling such populations, and found to be more efficient than either of them if appropriately defined with a vector of initial selection probabilities and a stochastic transition probability matrix. For simplicity, the Markov chain one-per-stratum sampling can be perceived as a compromise or trade-off between strict systematic sampling with a single random start and stratified simple random sampling with one sample unit per stratum (Thompson, 2003). Strict systematic sampling itself can be interpreted to be a specific case of stratified sampling with one sample unit per stratum, and thus this sampling technique refers indeed to a broad class of designs for one-per-stratum selection from a finite population. In this class, conventional systematic sampling, stratified simple random sampling with one sample unit per stratum and balanced systematic sampling (Murthy, 1967; Bellhouse and Rao, 1975) are three specific cases, of which the former two are both opposite extremes. The Markov chain one-per-stratum sampling is not so commonly used in forest inventories, which might be owing to its complications in the selection of sample units following a Markov process. The 1992 National Resources Inventory (NRI) in Alaska offered an example of its implementation (Breidt, 1995).

Adaptive two-stage one-per-stratum sampling, as its name indicates, requires first partitioning the population of interest into equal-sized strata and in turn each of those strata into substrata of equal size. Its designs are neighborhood-free and have a non-adaptive extra sampling i.e. the designs adapt to the observations of interest not by the means of iterative addition of unsampled neighboring units into the sample until no more sampled units meet the condition C and thus the entire cluster is completely enumerated, as seen in those neighborhood-based ACS designs. Instead, when an initially sampled unit satisfies the given condition C for adaptive sampling, then a single additional Markov chain one-per-stratum subsample of a fixed size will be selected in the stratum to which the initially sampled unit belongs for observation, and the sampling in that stratum ends immediately thereafter. In other words, an adaptively added subsample is non-adaptable to any observation and the sampling in a stratum terminates at an initially sampled unit not satisfying the condition C or otherwise a single adaptively added subsample in that stratum. Such appealing characteristics make this adaptive sampling easier to implement and thus more practical. Furthermore, the final sample size becomes controllable to some degree although it is still random, which will substantially facilitate sampling planning and may also contribute eventually to sample efficiency (Brown, 2003). One disadvantage of adaptive two-stage one-per-stratum sampling is that there exists

no design-unbiased variance estimator due to its one-per-stratum selection as in conventional systematic sampling (Cochran, 1977; Wolter, 2007). As an alternative, some biased alternative estimators (Christman, 2003), such as SRS variance estimator, have to be used.

Adaptive two-stage systematic sampling as a specific case of adaptive two-stage one-per-stratum sampling was described in detail as example by Christman (2003). It has two response designs: one uses single random-start systematic sampling for both the initial sampling and the extra sampling, while the other uses a single random-start systematic sample in the initial sampling and a single predefined systematic subsample within each stratum (namely a single predefined secondary systematic sample) for the possible extra sampling there. The latter design and its non-adaptive counterpart were empirically compared with three small artificial populations for which adaptive sampling is appropriate by employing several approximate variance estimators constructed upon all sampled units but not just those satisfying the condition for extra sampling. The finding is that the bias of the HT variance estimator is usually very small and thus it is not unreasonable to use it although the best variance estimator is population-dependent. But the usual approaches to the construction of confidence intervals based on the asymptotic normality of the point estimates is not appropriate for adaptive two-stage systematic sampling due to the highly skewed sampling distribution (Cochran, 1977; Thompson, 1992), especially when the initial sample size is small like in the empirical study in Christman (2003) where the initial sample size of 10 was used. In Christman (2003), it has not been mentioned how to improve the confidence interval so that it can cover the true value of a population parameter.

Two-stage-sequential sampling

Two-stage sequential sampling (TSS) (Salehi and Seber, 2005) (see Figure 2.6) is another class of neighborhood-free adaptive sampling designs. It can be understood as a neighborhood-free version of two-stage ACS (Salehi and Seber, 1997b). In the course of its initial sampling, simple random sampling without replacement is used to select both the first-stage sample of size m and the second-stage sample of initial size n_{i1} ($i=1, 2 \dots m$) in the selected primary unit i . When at least one unit of the second-stage sample in the selected primary unit i satisfies the condition for extra sampling, then a predetermined fixed number of randomly selected secondary units, n_{i2} , are added for observation and terminate the sampling in that primary unit. Thereby the second-stage sample has a final size of $n_{i1} + n_{i2}$ adapted from its initial size of n_{i1} . The extra sampling is designed to be performed only at the secondary

unit level and confined to each selected primary unit where it is launched. The design-unbiased estimators for this adaptive sampling strategy were developed based on the Murthy's estimator (Murthy, 1957), which is a RB improvement of Raj's estimator (Raj, 1956) and a trivial unbiased estimator (Salehi and Seber, 2001).

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Figure 2.6 Illustration of TSS with the numbers of blue-winged teal as given by Smith et al. (1995). Eight primary units are labeled along the left and right margins with numbers from 1 to 8. A simple random sample of four primary units (1, 3, 5 and 6) is selected. The two initially selected secondary units from each selected primary unit without replacement are shaded with light gray, and the four secondary units added randomly without replacement are shaded with dark gray. The condition for the additional sequential sampling is at least 10 blue-winged teals found in a secondary unit (from Salehi and Seber, 2005).

TSS has two attractive advantages. One is that it can restrain the final or effective sample size to some degree because the size of the second-stage sample is either n_{i1} or $n_{i1} + n_{i2}$ in each selected primary unit and the maximum of total sampling effort is predictable, which will ease the work to plan sampling for the best sampling efficiency, especially sampling with a given budget constraint; the other is that it can be more easily implemented and is thus more practical than those neighborhood-based designs where the adaptive addition of neighboring units might be fairly cumbersome and susceptible to mistake. The sampling simulation with two real biological populations and one artificial population with different degrees of rarity and clustering demonstrated that given the same effective sampling effort, TSS is not uniformly, but in most cases more efficient relative to SRS, conventional two-stage sampling

and two-stage adaptive sampling with nonoverlapping scheme for which the modified HH and HT estimators were used. In particular, this sampling scheme had little or no efficiency loss compared to conventional two-stage sampling for the rare populations lacking clustering, for which the neighborhood-based designs such as conventional ACS and two-stage ACS turn out to be unsuitable. It implies that it can be applied to a wider range of populations than conventional ACS. The selection of values for n_{i1} and n_{i2} influences the efficiency of TSS. Accordingly, the general guidelines were provided and elaborated by the authors for the choice of appropriate or optimal values of n_{i1} and n_{i2} in various sampling situations, where the degree of rarity and clustering of the target population, availability of a priori information, and possibility of stratification are taken into account. It is suggested to choose a moderate or larger values of n_{i1} and relatively small values of n_{i2} to ensure some amount of gain in efficiency when no information about the degree of rarity and clustering is available.

Adaptive two-stage sequential sampling

Adaptive two-stage sequential sampling (ATSS) (Brown et al., 2008) is a modification of two-stage sequential sampling (TSS) introduced by Salehi and Seber (2005). It differs merely in the allocation of extra second-stage sampling units to the selected primary units when the extra sampling is triggered there. The number of extra second-stage sample units, n_{i2} , is a predefined fixed number in TSS, but varies with the number of initial second-stage sample units satisfying the condition for extra sampling, denoted with g_i . In ATSS, it is defined to be a function of g_i as follows: $n_{i2} = g_i \times \lambda$, where λ is a predefined value. Various factors need to be taken into account for the choice of an appropriate value for λ , especially the primary unit size since the extra sampling cannot be carried out with a n_{i2} larger than it. In comparison with the equal allocation of extra second-stage sampling units in TSS, the proportional allocation strategy in ATSS can direct more extra sampling effort to the primary units with a high concentration of target objects. The direct or analytical comparison between ATSS and TSS was too difficult to be conducted due to an unfeasibly large number of possible design combinations. The comparative simulation study with the data from the count of an extremely clustered population of blue-winged teal (Smith et al., 1995) showed that in general TSS was far more efficient than ordinary two-stage sampling and ATSS was marginally superior to TSS. However, the planning of survey under ATS is more difficult than that under TSS because the total survey effort in terms of the final sample size is unknown prior to sampling. Two general rules for designing an efficient ATS were recommended to follow. One is the

use of a small initial sample size within a primary unit, and the other is the choice of a large CrV, which was also suggested but with caution for conventional ACS (Brown, 2003; Smith et al., 2004).

Adjusted two-stage ACS of Muttalak and Khan

Muttalak and Khan (2002) proposed an alternative to the conventional ACS for the sampling situations where an easy-to-observed auxiliary variable is available for the rapid assessment of a network size in the rare and clustered populations and the target variable is relatively costly and time-consuming to observe. The initial sample of this design is selected as in conventional ACS. Unlike in conventional ACS, a rapid assessment of the network size associated with an initial sample unit precedes the sampling in its neighborhood under this design. The network definition used in this design is identical to that in conventional ACS. If the size of a network is assessed to be larger than a given value k , then a random subsample of size j needs to be taken without replacement from that network. The given values of k and j hold unchanged throughout the sampling. Otherwise, the network should be completely enumerated. This design can be interpreted to be a mixture of single-stage and two-stage sampling when a network is considered as a primary unit. One advantage of this design over the conventional ACS is that it is more practical since it overcomes the difficulty of sampling excessively large clusters encountered in the conventional ACS by subsampling within each large network and excluding all less informative edge units from sampling. In addition, the final sample size in this design is somehow better controllable than that in the conventional ACS. The major problem of this design is that auxiliary information for rapid assessment of network sizes is often unavailable. Design-unbiased mean and variance estimators were developed and presented. A small comparative example from a blue-winged teal population given by Smith et al. (1995) reported that the conventional ACS was substantially more efficient than simple random sampling but only marginally more efficient than this design, given an equal sample size. However, some comprehensive comparative studies are necessary to obtain more insights into its performance.

Adaptive cluster double sampling (ACDS)

ACDS introduced by (Félix-Medina and Thompson, 2004) is an adaptive version of multi-phase sampling and considered to be appropriate for sampling rare and clustered populations when a cheap and easy-to-measure auxiliary variable highly correlated with the expensive and

difficult-to-measure target variable is available. The auxiliary variable can be defined to be one of different variable types, e.g. metric, ordinal or Boolean, as seen in ordinary double or multiphase sampling (Schreuder et al., 1993). The realizations of a Boolean auxiliary variable are often determined by a preliminary assessment of presence or absence of the objects of interest, or by a rapid assessment of the target variable with a given threshold. The value of 1 will be assigned to the auxiliary variable in the presence of at least one object of interest or when the threshold is exceeded, and 0 otherwise. The sample in the first phase of ACDS is selected by using the conventional ACS with the condition for extra sampling defined in terms of the auxiliary variable; in the second phase, a set of networks will be selected from the resulting networks in the first phase; and in the third phase, a subsample of units will be selected from each selected network in the second phase. The subsamples in the last two phases are selected by conventional, namely, nonadaptive sampling. The regression-type estimators and the design-unbiased HT-type estimators were presented. Three practical variants from a wide variety of ACDS designs were described in detail, and designated by ACDS-I, ACDS-II and ACDS-III respectively. In the first two variants, each sampled network in the first phase should be subsampled, with a given sampling fraction for ACDS-I and a specified upper bound for the maximum number of measurements of target variable for ACDS-II. The advantage of ACDS-I is that the second-phase sampling within a sampled network can start once the first-phase sampling there is completed. Thereby, the travelling cost incurred from revisiting the same sampled network can be avoided, but the number of measurements of the more expensive target variable is not controllable. The situation is reversed for ACDS-II compared with ACDS-I. In ACDS-III, not every initially sampled network is designed for subsampling. Only those initially sampled networks of size larger than 1 are included with probability equal to 1 for subsampling when they account for not less than one half of the sampled networks. Otherwise, some initially sampled networks of size 1 are needed to be additionally selected by simple random sampling without replacement to ensure that one half of the initially sampled networks can be subsampled. The number of measurements of target variable is restricted with a given upper bound as seen in ACDS-II. ACDS-III has the same advantage and disadvantage as ACDS-II.

In the comprehensive simulation study with two artificial finite populations, of which one is more clustered than the other, SRS, conventional ACS, conventional double sampling, and three aforementioned variants of ACDS were compared on the basis of approximately equal expected total cost by taking different factors into consideration, such as the type of auxiliary variable, ratio of costs of measuring target variable and auxiliary variable, and type of

estimators. The simulation results demonstrated that ACDS-III outperformed all other designs considered in the simulation study, and the performances of three ACDS variants improved as the cost ratio or degree of correlation between target variable and auxiliary variable increased, and also as the degree of population clustering decreased. The regression-type estimator and the HT-type estimator both provided satisfactory estimates, but the former one was more efficient than the latter one. It was noted that the evaluation of the considered designs in the study could be very different in the real sampling situations where the travelling costs between the random sample locations, which was not considered in the simulation, should be inevitably taken into account. In addition, it was confirmed that the conventional ACS is an appropriate sampling technique only for the populations with high level of spatial clustering, and turned out to be inefficient when a population's network sizes are relatively large and the within network variances of the target variable are small.

Inverse adaptive cluster sampling

Inverse ACS is a form of ACS with its initial sample selected by inverse sampling (Haldane, 1945; Cochran, 1977; Espejo et al., 2008) either with or without replacement to ensure the presence of a certain number of units satisfying a defined condition in the initial sample. It differs from the conventional ACS merely in that its initial sampling is also adaptive.

Christman and Lan (2001) presented three inverse ACS designs where the condition defined to be satisfied by a prespecified number of units in the initial inverse sampling and the condition to trigger the additional sampling of clustered units are identical. These three designs are associated with the following three stopping rules respectively for the selection of their initial samples: (i) the initial sampling continues until a given number of units satisfying the condition, say k ($k > 1$), are selected; (ii) the initial sampling starts with SRS of fixed sample size n_0 . It stops if at least one unit in n_0 satisfies the condition, and otherwise continues sequentially until totally k units satisfying the condition are sampled; (iii) the initial sampling starts with SRS of fixed size n_0 . It terminates once at least k sampled units in n_0 satisfy the condition, and otherwise continues until k units satisfying the condition are sampled. The initial designs using stopping rule (i) is referred to commonly as ordinary sampling, and those using stopping rule (ii) and (iii) are referred to as modified or mixed inverse sampling, which are actually a hybrid of fixed-size random sampling (nonsequential sampling) and ordinary inverse sampling (sequential sampling).

The extra sampling in the vicinity of each selected initial sample unit satisfying the condition to adapt follows the procedure described in Thompson (1990).

The design-unbiased estimators for totals were developed for the two designs using stopping rule (i) and (iii) whereas a biased one was presented for the design associated with (ii). However, no variance estimators for these designs were derived. Instead, some bounds based on Mikulski and Smith (1976) were provided to approximate the standard error with a reasonable underestimation in comparison with the true value in Lan (1999). The Monte Carlo simulation with four populations, three real and one artificial, of different degrees of spatial clustering and degrees of rarity demonstrated that the presented inverse ACS designs associated with (i) and (iii) statistically outperformed the nonadaptive inverse sampling designs only at the cost of a slight increase in final sample size for rare and clustered populations, and the inverse ACS design (iii) is the best in terms of having the smallest variance as mentioned by the authors. It was noted that for the rare and clustered populations the sampling error of the design using stopping rule (iii) depends mainly on the selected k value for the initial inverse sampling rather than the initial sample size n_0 . The simulation results confirmed that the proposed designs as a form of ACS designs is not suited for only rare but geographically not clustered populations.

Salehi and Seber (2004) derived the design-unbiased total and variance estimators for all these three designs using Murthy's estimator (Murthy, 1957). However, the variance calculated from the estimators for the two designs (ii) and (iii) tend to be excessively large and thus unacceptable for someone who prefers a biased estimator but with a smaller mean square error.

The challenge posed by these inverse ACS designs to the sampler is the selection of an appropriate value for k . When the value of k is set to be too large relative to the number of units satisfying the condition in the population of interest, it might occur that the budget, which is usually limited, cannot afford sampling an unfeasibly large number of units or even a complete census; when it is too small, then maximally only k objects of interest can be sampled, which will result in a large sampling error.

Furthermore, the final initial sample size is unpredictable and the locations of the initial sample units are therefore unknown prior to the sampling due the sequential selection of the initial sample units. This makes planning of the sampling effort extremely difficult and designing an efficient route to travel between those locations impossible.

General inverse adaptive cluster sampling

Salehi and Seber (2004) proposed an ACS design with its initial sample being selected by general inverse sampling, and it differs from the conventional ACS only in the selection of the initial sample. General inverse sampling starts with a SRS of size n_0 and stops at its completion if n_0 contains at least k units of interest. Otherwise, a further sampling initiates and continues in a sequential manner until either exactly k ($k > 1$) units of interest are selected or a given number of units, say n_2 , are sampled in total. General inverse sampling is believed to be more practical than the above mentioned ordinary inverse sampling or mixed inverse sampling in that it makes the sampling process more controllable because we can stop our sampling once the resources run out. It covers the inverse sampling designs using stopping rule (i) and (iii) in (Christman and Lan, 2001) and SRS as its special cases.

The total and variance estimators of general inverse ACS were developed from Murthy's estimator (Murthy, 1957). A small numerical example and the simulation study with the same populations as used by Christman and Lan (2001) were employed to investigate the influences of the design factors k , n_0 and n_2 on sampling efficiency. The results illustrated that the coefficient of variation (CV) depends largely on n_2 and moderately on k for the most rare population, which is consistent with Christman and Lan (2001), and a substantial improvement in sampling efficiency can be achieved by using general inverse ACS even with considering the final sample size during the comparison.

Constrained inverse adaptive cluster sampling

Rocco (2003) proposed two ACS designs and referred to them as constrained inverse ACS (CIACS). In CIACS, two inverse sampling designs are used for initial sampling. One starts the initial sampling with SRS of fixed size n_0 . The initial sampling terminates once at least two sampled units in n_0 satisfy the condition, and otherwise continues until two units satisfying the condition are sampled. It is actually a specific case of $k=2$ for the initial sampling design (iii) in Christman and Lan (2001). The other initial inverse sampling design is slightly different in that it excludes the last sequentially selected initial sample unit satisfying the condition in the first one from its initial sample. Once the initial sample is selected, the extra sampling proceeds in the same manner as in conventional ACS.

It is found from the simulation study that the design including all selected initial units is generally less efficient even though it needs more sampling effort based on the developed design-unbiased total and variance estimators.

Adaptive cluster sampling based on an initial relascope sample

Relascope sampling (Bitterlich, 1948; Grosenbaugh, 1952; Palley and Horwitz, 1961), known as a variety of names such as Bitterlich sampling, angle-count or angle-gauge sampling, plotless sampling, point sampling, horizontal point sampling, variable plot/radius plot sampling and prism sampling, is commonly used in forest inventories with a long history. For the purpose of consistency and clarity, the term relascope sampling is used throughout this dissertation in contrast to plot sampling. Relascope sampling is a sampling with unequal selection probability or more exactly with selection probability proportional to size (PPS), and it is particularly effective in obtaining precise estimates of tree basal area.

The ACS design with its initial sample selected by relascope sampling put forth by Roesch (1993) for forest inventories is a combination of relascope sampling and fixed-area circular plot sampling (see Figure 2.7). At the beginning of its initial sampling, a fixed number of randomly placed points are selected. And then at each selected point, relascope sampling is implemented with relascope, prism or bottle-opener dendrometer to select individual trees into the initial sample. Whenever an initial sample tree, say tree i , exhibits the rare characteristic of interest, then a fixed-area circular plot sampling with the plot center at it is triggered, and all unsampled trees within the circular plot, referred to as search area by Roesch, will be selected and observed. This fixed-area circular plot sampling as performed for tree i continues to be launched by each adaptively added sample tree until no more sampled trees with the characteristics of interest are found. In addition, during the field work, measuring the diameter at breast height (DBH) and recording the location of each sampled tree with the characteristic of interest are necessary for producing estimates of sampling errors and statistical inference. The term cluster in this design refers to the set of all trees included in the sample resulting from a randomly placed sampling point, and a network is a subset of trees possessing the characteristic of interest in a cluster.

Three types of design-unbiased total and variance estimators were developed for this adaptive design: HH, modified HH (referred to as HHM), and HT estimators. In HH estimators, each network selected by a randomly placed point is counted only once regardless of the number of its network trees, which implies that the selection probability of a network used in the estimators is proportional to the union of the selection areas (Roesch, 1993) of all network trees, whereas in HHM estimators, each network selected by a random sampling point is counted as many times as the number of its network trees, which implies that the selection

probability of a network used in the estimators is proportional to the sum of selection probabilities of all trees inside it.

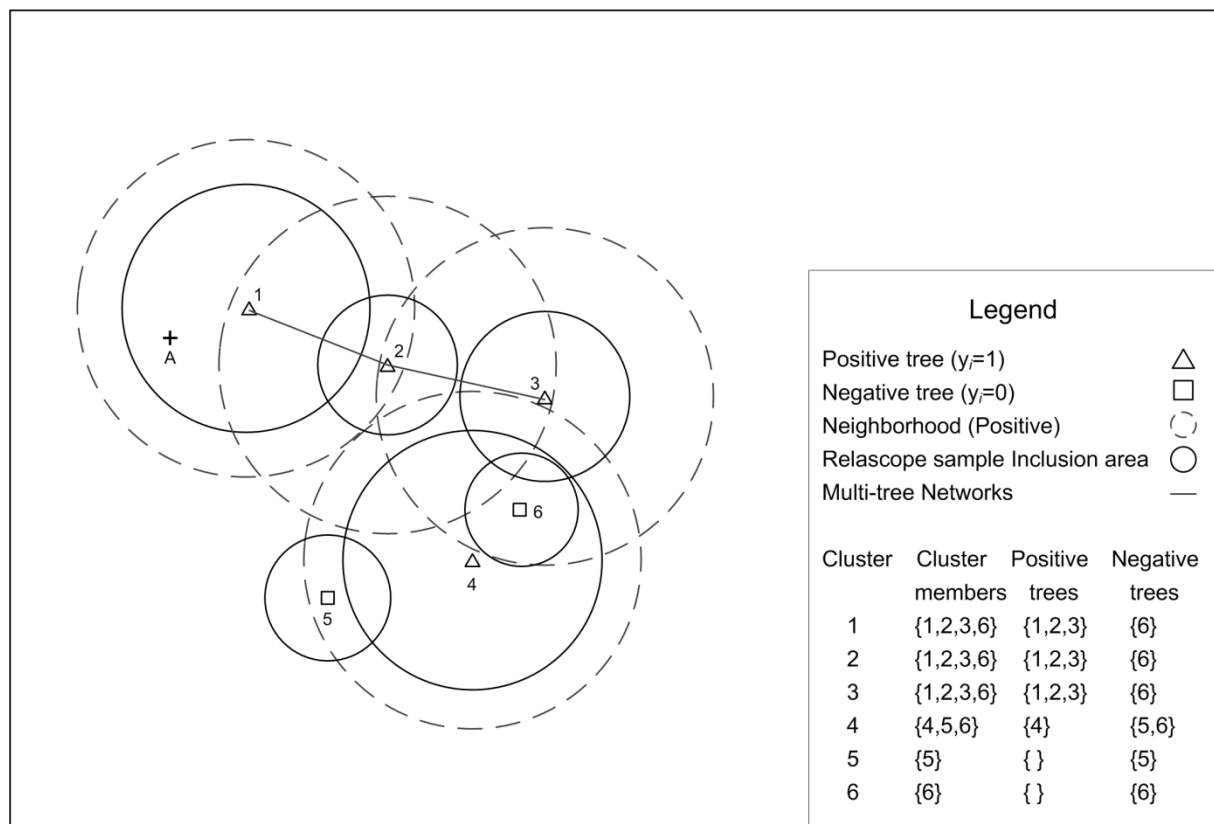


Figure 2.7 ACS based on an initial relascope sample for a group of six trees in a population. The condition to adapt is the possession of a predefined characteristic, e.g. damage. A tree is a positive tree if it possesses that characteristic, otherwise a negative tree. One randomly placed point can select the following initial samples: { }, {1}, {2}, {3}, {4}, {5}, {1, 2}, {3, 4}, {3, 4, 6}, {4, 5}, and {4, 6}. The random sample point A falls in the inclusion area of tree 1, and thus it is selected as an initial sample tree. A fixed-area circular plot (dashed circle) is installed around it for further sampling because it has the predefined characteristic. The sampling continues and stops at tree 6, a negative tree. As a result, tree 1, 2, 3, and 6 are finally sampled for sample point A (cross) (modified from Roesch, 1993).

The sampling simulation results based on a basal area factor (BAF) of $10\text{ft}^2/\text{ac}$ showed that the statistical performance of the proposed adaptive design depends on the size of the fixed-area circular plot and is better than its nonadaptive counterpart, the ordinary relascope sampling, for the estimation of number of rare clustered tree species. The HT estimators are superior to the other types of estimators, and HHM estimators yield the poorest statistical performance. The simulation results confirmed that the adaptive sampling scheme is only statistically efficient for rare clustered species.

The influence of the size of the basal area factor (BAF), misidentification of rare characteristic of interest on design efficiency, and the cost incurred by the adaptive sampling work was not addressed. However, the author claimed that the adaptive sampling scheme is only applicable to those rare, clustered populations with their characteristics that can be identified with complete confidence. In addition, the calculation of selection area of an individual tree for a given BAF was not explained, and the readers who are unfamiliar with it may refer to Gregoire and Valentine (2008) for detailed descriptions of the calculation.

ACS based on order statistics

ACS based on order statistics (David and Nagaraja, 2003) (ACSord) is a special form of ACS design suggested by Thompson (1996) (see Figure 2.8). It differs uniquely from the conventional ACS in the determination of the CrV, the formulation of the condition for adaptive sampling. In conventional ACS, the CrV is determined prior to the initial sampling in some way, for instance using prior knowledge, previous studies or survey, or a pilot survey, and holds until the end of the entire sampling, whereas in ACSord, the CrV is determined at the completion of the initial sampling, and equals the k^{th} order statistic (David and Nagaraja, 2003) of the initial sample, i.e. the k^{th} smallest observed value in the initial sample ($1 \leq k \leq n$, n denotes the initial sample size). It is apparent that in ACSord, the CrV varies from sample to sample and this complicates the estimation process since the network structure of the population of interest changes accordingly.

The design-unbiased estimators including their Rao-Blackwell version were provided for ACSord. However the design-unbiased variance estimators pose computational difficulty and may take on negative values in some cases. As a result, a biased but inevitably non-negative and easily computable ordinary variance estimator as well as a so-called combined estimator was proposed as an alternative. The combined variance estimator applies the design-unbiased variance estimators when the resulting estimates are non-negative, and otherwise the ordinary variance estimator, to avoid negative variance estimates.

The advantage of ACSord over conventional ACS is that it allows concentrating sampling efforts in a fairly controllable and thus flexible manner on those hot-spots with high values of interest if there are any in an initial sample. As a result, some possible undesirable situations in conventional ACS can be avoided, such as all or none of initial sample units satisfies the condition for extra sampling according to the prespecified but inappropriate CrV. ACSord is considered to be recommendable when the interest of a survey is not only in estimating the

population parameters, such as population mean and total, but also in seeking high values for some purpose specific to a field of study.

It is clear that in ACSord, those initial sample units with their observed values larger than the CrV should be revisited after the completion of its initial sampling. Thus, ACSord is not preferable in sampling situations where travel between initial sample units is very costly, such as forest inventories, especially large-area forest inventories. In addition, locating those initial sample units for revisit can be time-consuming and might involve some error.

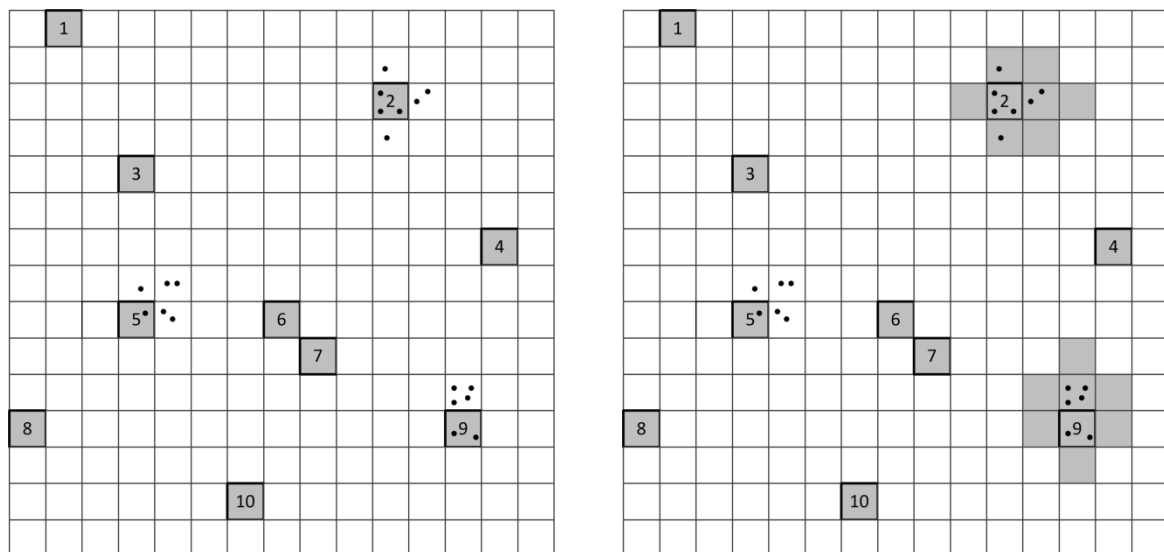


Figure 2.8 Illustration of ACSord. In the initial sampling, ten plots numbered from 1 to 10 are selected from the population (left). The number of trees denoted by black dots is the target variable. The second order statistic of the initial sample equals 2 and is used as the CrV for the adaptive sampling. All sampled units with the CrV of 2 are light-shaded (right). The initial sample plot 5 cannot trigger the adaptive sampling, although there is one tree inside it.

Restricted Adaptive cluster sampling

In unrestricted ACS, the number of units in the final sample is a random variable and remains unknown until the completion of the entire sampling since no stopping rule is introduced to regulate it. It might occur that a sampling cannot be carried out as planned before the resources available for it run out when the final sample size is excessively large. In order to overcome this difficulty, Brown and Manly (1998) suggested a restricted version of conventional ACS (see Figure 2.9), termed restricted ACS (RACS), with a hope to predict the final sample size of ACS with more certainty and thereby ease the survey planning. In RACS, a limit L used to restrict the variability of the final sample size (total number of

subplots) is specified prior to sampling, and accordingly an initial sample is selected sequentially i.e. one after another rather than nonsequentially as seen in unrestricted/conventional ACS. The sequential selection of an additional unit into the initial sample will not stop as long as the cumulative number of sampled units is smaller than L . The adaptive sampling in the vicinity of a selected initial sample unit satisfying the condition follows the same procedure as in conventional ACS. It implies that the sampling of RACS continues until the number of sampled units reaches or first exceeded L . As a result, the final sample size equals or fluctuates more or less above the given limit L .

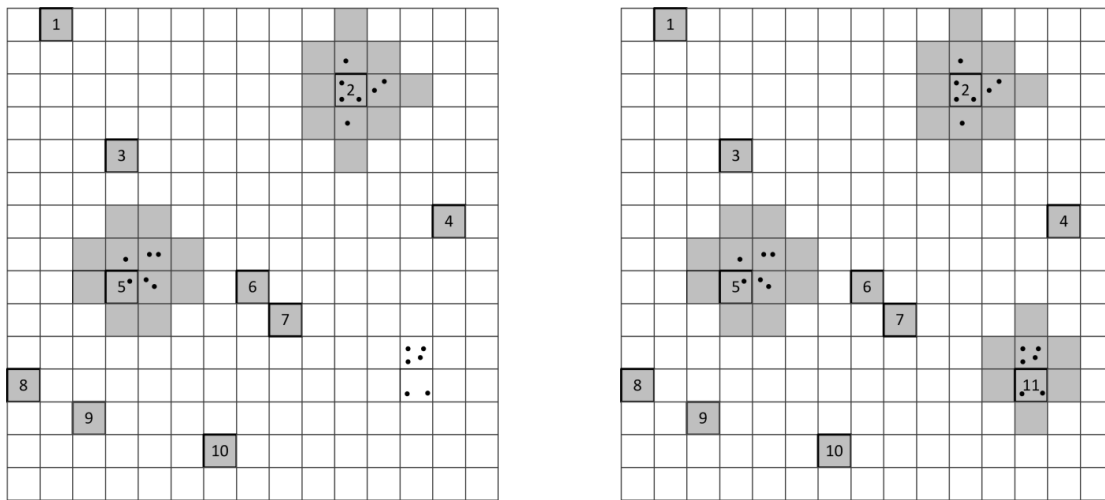


Figure 2.9 Illustration of RACS. The predetermined limit L is 35 and CrV is set to 1. The sampled plots are light-shaded. The cumulative number of all sampled subplots from 10 sequentially selected initial sample plots numbered from 1 to 10 reaches 32 (left) but is still smaller than L , and thus the sample plot numbered 11 (right) is randomly selected and results in 40 sample subplots, which is larger than L , and the entire sampling process comes to the end.

As shown in the simulation with a range of populations, RACS can put its number of units in the final sample under better control, although at the cost of precision of estimation, compared with its unrestricted counterpart. The variability in final sample size and estimated variance under RACS increases with a decreasing level of clustering of a population. According to Brown and Manly (1998), RACS is preferable to its unrestricted counterpart in any of the following cases: (i) the level of clustering of a population is unknown prior to the sampling; (ii) additional sampling effort over a certain limit will become very costly or even impossible due to some severe logistical constraints, such as aviation fuel constraint in aerial surveys; (iii) a prediction of likely sampling effort is necessary or required. For those populations

consisting of very compact clusters, the final sample sizes in unrestricted ACS are generally very close to their corresponding initial sample sizes, to the given limit L in RACS or the initial sample sizes in unrestricted ACS. It follows that RACS is not superior or even inferior to its unrestricted counterpart for them when their high level of clustering is known prior to the sampling.

The following are some challenges arising from RACS. The initial sample size in RACS is random due to the sequential selection of its initial sample, and thus it is impossible to make an efficient plan for the travels between sampling locations. This may be a severe problem, especially when the travels are difficult and/or costly. In addition, the choice of an appropriate restricting limit based on the resources available for sampling is very crucial and needs prior knowledge of the clustering level of a population, which is very often not available. RACS with a small restricting limit for a population of large size clusters may run into the risk that finally only one cluster can be fully enumerated and in consequence the variance estimation is impossible.

In Brown and Manly (1998) the design-unbiased HH and HT estimators for conventional ACS were used for RACS and found to be biased in a similar degree. The smallest bias occurs to those populations consisting of small and compact clusters. The bias was demonstrated to be satisfactorily reduced in many cases using an easy-to-compute non-parametric bootstrapping approach (Efron and Tibshirani, 1993). The design-unbiased total and variance estimators for RACS with a better performance than those biased ones in Brown and Manly (1998) were then developed and introduced by Salehi and Seber (2002) based on the estimators proposed by Murthy (1957).

Two-stage restricted adaptive cluster sampling

Two-stage restricted ACS (TSRACS) (Rocco, 2008) can be considered as a restricted version of ordinary two-stage ACS with a nonoverlapping scheme (Salehi and Seber, 1997b), or a combined version of ordinary two-stage ACS and RACS. It starts first with an ordinary two-stage ACS, where SRS_{WOR} of fixed size is used to select initially m primary units of size N and n secondary units in each of them ($m, n \geq 2$). At the completion of the sampling in all initially selected primary units, the total number of all sampled secondary units, saying v , will be compared with a restricting limit l defined prior to the sampling. If v is larger than l , then TSRACS stops here, and otherwise it continues by selecting some number of additional primary units at random in a sequential manner until v equals exactly l or first exceeds l . the

design-unbiased total and variance estimators were developed from Murthy's estimators (Murthy, 1957).

The remarkable advantage of TSRACS from a practical point of view is that the upper limit of its final sample size, although still variable, becomes easily predictable, which is equal to $\max(m \times N, v + N - 1)$. Moreover, the variability in final sample size and variance of estimates in TSRACS are smaller than those in RACS and ordinary two-stage ACS. However, it is pointed out that the better performance of TSRACS depends on the patchiness of the population of interest and appropriate sizes of primary and secondary units and it can be less efficient when inappropriately designed or applied. One disadvantage of TSRACS as seen in RACS is that the possible sequentially selected primary units cannot be located prior to the sampling and thus it is impossible to optimize the travel route.

Incomplete adaptive cluster sampling

For avoidance of a complete enumeration of prohibitively large clusters in conventional ACS, a different restricted version of ACS referred to as incomplete ACS was introduced by Chao and Thompson (1999). In incomplete ACS, a restriction is imposed on the number of neighborhood levels beyond each unit satisfying the condition in an initial sample of fixed size (Su and Quinn II, 2003), rather than on final sample size as seen in the version of Brown and Manly (1998), and accordingly its neighborhood definition is not symmetric, unlike in most ACS designs. All neighbors of the initial sample units satisfying the condition are on the first neighborhood level, and in turn all neighbors to be added based on those units on the first neighborhood level are then considered to be on the second neighborhood level, and so on. In brief words, a cluster defined in conventional ACS is allowed to be truncated in a predetermined distance to the initial sample unit intersecting it under incomplete ACS. However no design-unbiased total or variance estimators were presented except insights into the derivation of the inclusion probabilities required for construction of design-unbiased estimators were offered.

Su and Quinn II (2003) and Lo et.al (1997) incorporated the component of incomplete ACS into the extra sampling phase of ACSord (Thompson, 1996) and stratified ACS (Thompson, 1991b) as a stopping rule respectively and thus two new ACS designs were produced. In the former one, an unbiased HH estimator and a biased HT estimator were given, and in the latter one, only biased estimators were available.

The attractive feature of these designs is that it can be easily implemented since the locations of its initial sample units and the maximum sampling effort are known prior to sampling. However, the truncation of encountered clusters in these designs may lead to the loss in efficiency compared to the complete versions, i.e. conventional ACS designs in some cases, although their performances were positively evaluated.

Chaudhuri et al. (2005) proposed a so-called size-constrained adaptive sampling design. This design can be considered a mixture of restricted ACS (Brown and Manly, 1998) and Adjusted two-stage ACS (Muttalak and Khan, 2002). It imposes a restriction on final sample size as restricted ACS, but the restriction is realized by using subsampling selected networks, as in adjusted two-stage ACS, where only those selected large size networks need subsampling. Under this design, when the size of a selected network becomes known in some way, for instance, by rapid assessment using auxiliary variable, a subset of units will be drawn by SRS_{WOR} . The cardinality of a subset is determined by the predefined restricting limit on the final sample size. The unbiased estimators were given by the authors. It is very obvious that this design is applicable only when the rapid assessment of the sizes of the selected networks is possible.

2.3 DEVELOPMENT AND IMPROVEMENT OF ESTIMATORS FOR ACS DESIGNS

There are a variety of ACS designs available for our choice, but their common core is conventional ACS presented in Thompson (1990) as the other designs are its further developments by incorporating it into the existing designs, and thus the work relevant to estimation designs including the development of new estimators and improvement on existing estimators was mainly focused on conventional ACS. In Thompson (1990), the modified design-unbiased HH and HT estimators, which exclude the sample edge units from the estimation process, were first developed and referred to as conventional ACS estimators from here on. However neither of them is a function of the minimal sufficient statistic (Thompson, 1990; Thompson and Seber, 1996; Lehmann and Casella, 1998), the unordered set of distinct, labeled sample observations in the context of finite population sampling setting because both of them depend on the order of selection (Christman and Pontius, 2000). According to the Rao-Blackwell (RB) theorem (Rao, 1945; Blackwell, 1947; Thompson and Seber, 1996), they can be improved by applying Rao-Blackwellization to them. That means: the information contained in the original sampling data is not fully utilized by the two ordinary estimators, for

instance, the information carried by the observations upon sample edge units is not used by them. Rao-Blackwellization enables the efficient use of sampling data for a reliable statistical inference. As a result, the RB estimators may have smaller but never larger variances than their original counterparts, the conventional ACS estimators.

The RB estimators presented by Thompson (1990) can integrate the data collected from sample edge units into the estimation process and do outperform their original counterparts. However, their computation is very difficult due to the lack of a suitable method or an efficient algorithm for the full enumeration of all ordered samples given an unordered sample. Salehi (1999) worked out an easy-to-compute closed form for the RB version of the conventional ACS estimators and compared them. He found that the RB version of the HH estimator has a larger variance reduction than that of the HT estimator.

It was noted in Thompson (1990) that neither of the two ordinary estimators is a uniformly minimum variance unbiased estimator (UMVUE), namely, neither of them is uniformly better than the other, and further study is necessary to obtain a comprehensive insight into their performances and to find out in what circumstances which one of them is preferable. Salehi (2003) analytically compared the properties of these two estimators, and strongly recommended practitioners to use the modified HT estimator, which has generally smaller variances, although the modified HH estimator is comparatively easier to calculate. However, he mentioned in the end that some comprehensive study is still needed for a clear choice of an appropriate estimator.

Dryver and Thompson (2005) developed two improved estimators for the conventional ACS, which are also design-unbiased, by applying the RB theorem to make use of the information from sampled edge units. The two improved estimators were derived by conditioning on the sufficient but not necessarily minimal statistic. It was shown that they are more efficient than, but as easy-to-compute as, the ordinary estimators, although they are less efficient than the fully Rao-Blackwellized estimators in Thompson (1990), i.e. the RB estimators based on the minimal sufficient statistic.

The asymptotic normality and consistency of the conventional ACS estimators under the ACS designs with their initial sample selected by SRS_{WOR} or by unequal probability sampling with replacement were studied by Félix-Medina (2003) under an asymptotic framework where the number of units in the initial sample, as well as the number of units and networks in the population of interest tend to infinity. It was proved that both ordinary estimators are design-

consistent and asymptotically normally distributed, and the estimators of their variances are also design-consistent.

Christman and Pontius (2000) found that the sampling distribution (namely finite-sample distribution) of a rare and clustered population derived from a small sample size and the ordinary estimators is often highly skewed and discrete and the confidence intervals based on the asymptotic normal theory (Cochran, 1977) may be inappropriate. Hence, for the purpose of constructing ACS confidence intervals, they studied the following four nonparametric, finite population bootstrap methods: Sitter's mirror-match method (Sitter, 1992a, b), Gross's method (Gross, 1980), Rao and Wu's Rescaling method (Rao and Wu, 1988), and McCarthy and Snowden's Bootstrap with-replacement method (McCarthy and Snowden, 1985). The third method with percentile intervals was recommended when the modified HH estimator is employed for conventional ACS. Salehi et.al (2010) tried to derive the confidence intervals for the population mean based on two pseudo empirical likelihood functions, and found that the obtained confidence intervals are as good as or better than those from the bootstrap methods of Christman and Pontius (2000) in terms of coverage rate.

Dryver and Chao (2007) suggested two ratio estimators for conventional ACS, only one of which is design-unbiased. The two ratio estimators were compared with conventional ratio estimators for SRS_{WOR} and existing design-unbiased ACS estimators in terms of sampling efficiency. It was noted that they can be robust alternatives to the conventional estimators, especially in the case that the correlation between the target variable and the auxiliary variable is not high enough for the conventional estimators to exhibit a satisfactory performance. In addition, in the two ACS ratio estimators, the sample edge units provide no information for the estimation. Further study is expected to improve the efficiency of the two ratio estimators by means of Rao-Blackwellization.

In the dissertation of Dryver (1999), various ACS estimators associated with a range of ACS designs were described in detail, including a modified jackknife estimator for variance estimation.

2.4 APPLIED STUDIES ON ACS

ACS has been applied in a range of fields including forestry since its introduction, and the reported performances turn out to be diverse, despite its appeal from most of the aforementioned methodological or theoretical research work.

Acharya et al. (2000) employed the systematic ACS with two random starting points to assess rare tree species in Nepal, and his finding is that systematic ACS outperformed systematic sampling and was more efficient for the larger groups of individuals of a rare species than for extremely small groups. Talvitie et al. (2006) applied almost the same method for the inventory of sparse forest populations and found that it was considerably more effective than SRS. Phillipi (2005) used an conventional ACS design for estimation of abundance with local populations of low-abundance plants and a noticeable success was achieved. Bih (2007) implemented ACS, under which the CrV was determined based on a pilot inventory, for the assessment of non-timber forest products in off-reserve forest in Ghana. He concluded that ACS is more efficient than the compared design, as considered generally. Zhu et al. (2010) carried out a comparative study, where overlapping and nonoverlapping schemes of stratified ACS, conventional ACS and their nonadaptive counterparts were applied to estimate the density of a shrub species in a desertified area. The nonoverlapping scheme of stratified ACS together with modified HT estimator exhibited to be most efficient.

In some applied studies, ACS is positively evaluated in part or non-negatively evaluated. Sullivan et al. (2008) conducted the conventional ACS for the purpose of estimating density of spatially autocorrelated larvae of the sea lamprey, and the results demonstrated that ACS is not always more efficient but never less efficient than SRS. Smith et al. (1995) used the conventional ACS and its ordinary estimator to estimate density of three species of waterfowl and found that it was not uniformly more efficient than SRS as theoretically expected. He applied it later again to low-density populations of fresh mussels (Smith et al., 2003), but obtained no gain over SRS in precision of estimation at all. He also tried single and two-stage ACS designs together with their nonadaptive counterparts (Smith et al., 2009) to estimate density and abundance of freshwater mussels in a large river, and noticed that all considered designs performed similarly in terms of precision. Hanselman et al. (2003) and Noon et al. (2006) used ACS to estimate national deforestation rates and to sample Alaska rockfish respectively. In their studies, the gains of ACS in precision were offset by the additional cost incurred by the adaptively sampled units.

In the application of ACS for estimation of abundance of rare subtidal macroalgae in the southern coast of Australia and for detection of terrestrial herpetofauna in a tropical rainforest, ACS failed to provide more precise estimates.

3 METHODS AND MATERIALS

3.1 STATISTICAL METHODS

3.1.1 Adaptive plot designs

In this study, the following three new adaptive plot designs are proposed. Plot design I and II are proposed for fixed-area plot sampling and plot design III for relascope sampling. The principles of conditional plot expansion under plot design I and II are actually applicable to any fixed-area plot shape. For simplicity, only circular plots are singled out deliberately in the study as an example to illustrate those principles since they are very commonly used in forest inventories. As in conventional relascope sampling, plot design III uses exclusively virtual or imaginary variable-radius circular plots, i.e. relascope plots, and the choice of a plot shape is not an issue to consider for it.

3.1.1.1 Plot design I

Plot design I uses a simple and thus very practical “conditional isotropic expansion of initial plots” approach with only two pre-defined plot sizes: (1) a common initial plot and (2) a larger (adapted) but fixed sized plot whenever a predefined condition to adapt is satisfied. For example, a standard initial plot size of 500m² is installed at each sample point; and if the condition “at least one tree on the initial plot” is fulfilled, then the initial 500m² plot is expanded to a 1500m² plot. The principle of the conditional expansion of initial plots is schematically illustrated in Figure 3.1.

The conditional expansion of initial plots under plot design I is determined by the condition for expansion as its name indicates, and the geometry of the expansion defined by the prespecified final plot size i.e. the size of the expanded plot. In the example given in Figure 3.1, the condition to expand an initial plot is stated in terms of the number of target trees found on it. The minimum number needed to trigger an expansion is defined as CrV. The plot size factor (PSF) defines how much larger the expanded plot area is in relation to the initial plot: a plot size factor of two indicates that the final plot size is a doubling of the initial plot area.

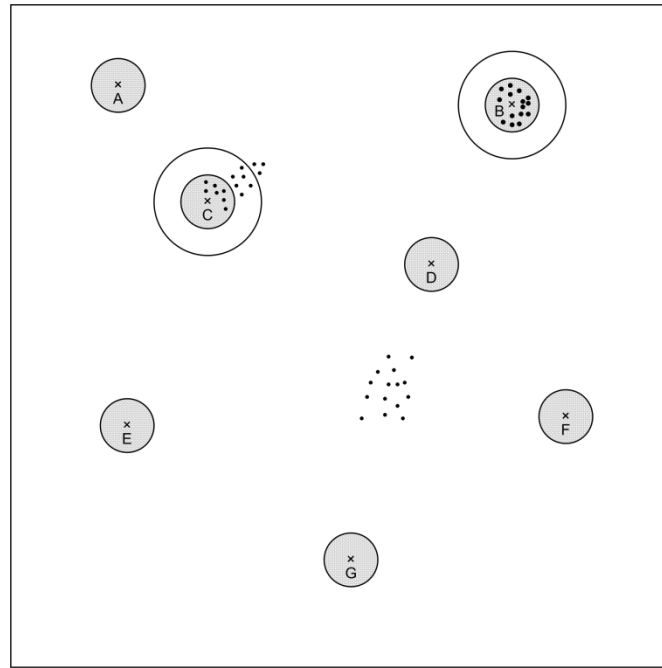


Figure 3.1 An example of plot design I: an initial sample plot of a defined size (gray shaded) is established at each sample point (crosses A to G). When the condition: the initial plot contains at least one tree (black dot) - is met, the plot is expanded to a fixed larger size (shown for two initial plots at sample point B and C). The final plot size is the same for all expanded plots (from Yang et al., 2009).

The advantage of this plot design is that it can overcome the practical issues of differently sized, gradually growing and possibly very, even excessively large clusters of sub-plots inherent in the conventional ACS, and its field implementation is much easier in comparison with the conventional ACS as the same predefined simple plot expansion rule holds during a sampling survey for all initial plots and the adaptation process needs not to be done in a time-consuming and error-prone sequential fashion. Meanwhile, more trees are likely to be included into the sample for observation with plot design I rather than with a non-adaptive design. However, in contrast to the conventional ACS, plot design I cannot ensure a full capture of all trees in an isolated cluster intercepted by an initial plot. The cluster here refers not to a natural cluster, but to a cluster in the sense of conventional ACS. For a natural cluster intercepted by an initial sample plot, the number of trees adaptively added into the sample from it depends only on the CrV in conventional ACS, and both CrV and PSF in sampling with this plot design.

3.1.1.2 Plot design II

In plot design II, an initial sample of single compact fixed-area plots is installed. If the observed value from the initial plot at a sample point meets the condition to adapt, then a fixed-area cluster plot of a predefined type, which includes the initial sample plot as a subplot, will be installed there. In principle, any type of cluster plots can be used in this design. In this study, just one type of cluster plots is used uniformly as an example to explore the performance of this design. As seen in Figure 3.2, a cluster plot of this type consists of totally five compact subplots: an initial sample plot and four additional plots installed at four points in a prespecified distance (referred to as subplot distance) and directions from the initial sample point. For example, an initial single compact plot of 500m² is installed at each sample point; and if the condition “at least one tree on the initial sample plot” is fulfilled, then the initial 500m² compact plot is directionally expanded to a 2500m² cluster plot consisting of 5 subplots. Plot design II can be considered as a variant of plot design I in that plot design I turns to plot design II when a uniformly expanded plot in plot design I is replaced with a fixed-area cluster. The example in Figure 3.3 demonstrates the principle of plot design II.

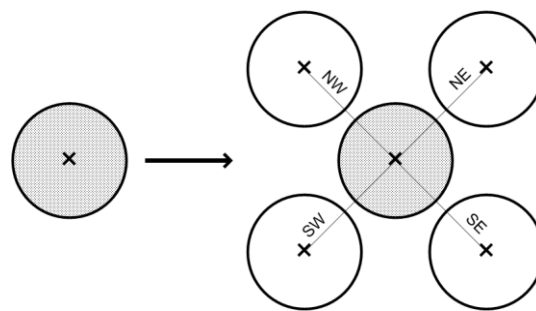


Figure 3.2 The plot expansion process at a sample point under plot design II. On the left hand side is an initial plot installed at a sample point (cross) where the condition to adapt is satisfied, and on the right hand side is the cluster plot at that sample point and the four adaptively added subplots are in the NW, NE, SW and SE direction of the sample point.

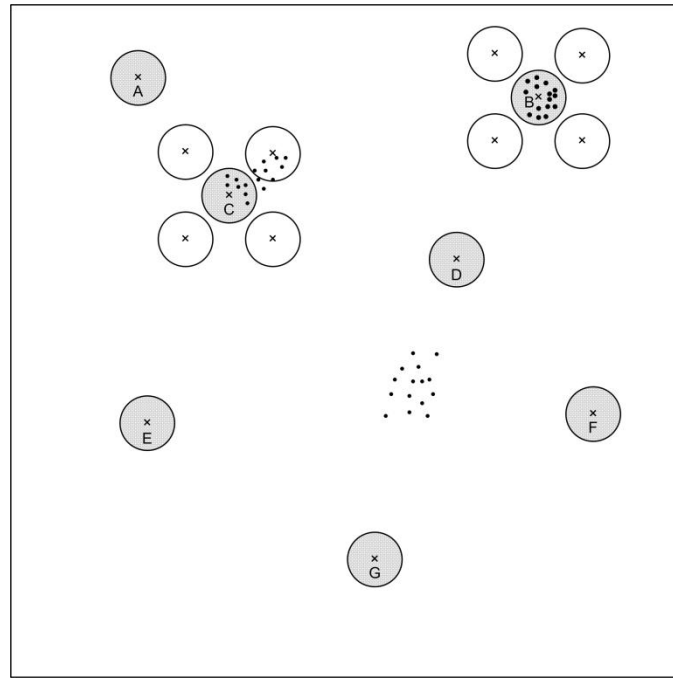


Figure 3.3 An example of plot design II: an initial single compact sample plot of a defined size (gray shaded) is established at each sample point (crosses A to G). When the condition: the initial plot contains at least one tree (black dot) - is met, then a fixed-area cluster plot of the predefined type is installed, as seen at sample point B and C.

The performance of plot design II will be determined by the CrV, the subplot distance, and other factors known also from the ordinary (nonadaptive) cluster sampling, such as the spatial autocorrelation of the population of interest and intracluster correlation, which is partly influenced by the geometric spatial arrangement of subplots.

Plot design II shares the common practical advantages with plot design I. However, the choice between plot design I and II is an issue of the trade-off between costs and efficiency, and hence varies from situation to situation. From a practical point of view, the field implementation of plot design II is not as easy as that of plot design I and causes additional costs because of the inevitable need to locate subplots of a cluster plot. But from an ordinary viewpoint of spatial statistics, plot design II is likely to be more efficient than plot design I on a sound comparative base because it better tackles the issue of spatial autocorrelation.

3.1.1.3 Plot design III

Plot design III is an adaptive version of relascope sampling. In conventional relascope sampling, a constant BAF is applied at every sample point. In plot design III, two BAFs, one

large and the other small, need to be predefined prior to sampling in addition to the condition to adapt. They are denoted by k as initial BAF and by k' as final BAF. Sampling starts with the large BAF, namely with small initial plots. Whenever the condition to adapt is met, then a predefined smaller BAF k' is used. The change of BAF in plot design III is actually an expansion of the imaginary circular plots in relascope sampling. It is known that the imaginary circular plot for a tree with DBH of d_i has an area of $\pi \frac{2500}{k} d_i$ and $\pi \frac{2500}{k'} d_i$ for the BAF k and k' respectively. According to the definition of PSF given in plot design I, $\frac{k}{k'}$ is then the PSF corresponding to the adaptive change of BAF from k and k' . Therefore, plot design III shares the sample principle of plot expansion as plot design I and II. The concept of plot design III is illustrated in Figure 3.4.

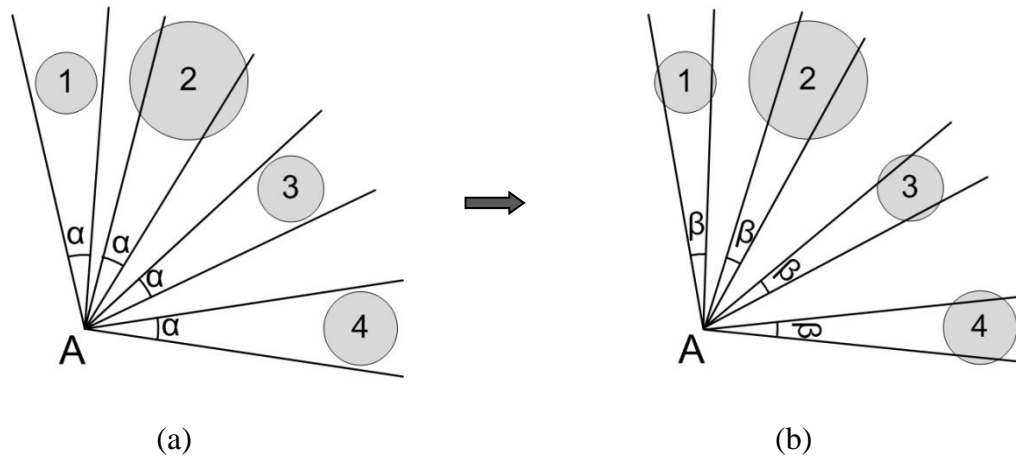


Figure 3.4 An example of plot design III. A cluster of trees around sample point A are labeled with numbers from 1 to 4. Tree 2 is tallied with the initial BAF corresponding to the critical angle of α in (a). When the condition that at least one tree is tallied at a sample point is met, then a small BAF corresponding to the critical angle of β ($\beta < \alpha$) is used. As a result, four trees in the cluster are tallied as shown in (b).

3.1.2 Unequal probability sampling

Plot design I, II and III are proposed based on the strategy of unequal probability sampling. In unequal probability sampling, the population units have different probabilities to be selected or included into the sample, and thereby a better efficiency relative to equal probability sampling is expected to be possible under certain conditions. The statistical performance of an unequal probability sampling design depends very much on its capability of imposing

reasonably high probabilities on the important units of a population. The important units are the units containing more information on the population parameter to be estimated than the others, for example, the trees with large DBH in a forest stand in the case of estimating the stand basal area. There are various unequal probability sampling methods being used and found to be efficient in forest inventories, such as relascope sampling, randomized branch sampling (Jessen, 1955; Pearce and Holland, 1957), importance sampling (Gregoire and Valentine, 2008) and probability proportional to prediction sampling (3P sampling) (Grosenbaugh, 1963; Van Laar and Akça, 2007).

It is usually much more challenging to develop estimators for unequal probability sampling than for equal probability sampling, but fortunately there are two general unbiased estimators of finite population total available for unequal probability sampling, one is the Hansen-Hurwitz (HH) estimator (Hansen and Hurwitz, 1943), and the other is the Horvitz-Thompson (HT) estimator (Horvitz and Thompson, 1952). The HH estimator of population total $\hat{\tau}_p$ is:

$$\hat{\tau}_p = \frac{1}{n} \sum_{i=1}^n \frac{y_i}{p_i}$$

And the HT estimator of population total $\hat{\tau}_\pi$ is

$$\hat{\tau}_\pi = \sum_{i=1}^v \frac{y_i}{\pi_i}$$

where:

y_i =value of interest for unit i ,

p_i =selection probability of unit i ,

n = the sample size,

v = the effective sample size (the number of distinct units in the sample of size n), and

π_i =inclusion probability of unit i .

The HH estimator is restricted to random sampling with replacement, while the HT estimator is applicable for random sampling with or without replacement. As we can see, the primary difference between HH estimator and HT estimator is that the former uses the selection probability, the probability of a unit being selected on each draw, and the latter uses the inclusion probability, the probability of a unit being eventually included into the sample. For a given with replacement sampling scheme, if the selection probability of unit i is p_i , then its

inclusion probability for a sample size of n is $\pi_i = 1 - (1 - p_i)^n$. The elaboration of difference between selection probability and inclusion probability based on an example can be found in (Gregoire and Valentine, 2008). Their secondary difference, which exists only in the case of with-replacement sampling, is that the HH estimator utilizes the value of unit i as many times as it is selected in the sample, whereas the HT estimator does not and each sample unit is utilized only once in the HT estimator regardless of how many times it has been selected into the sample (Thompson, 1992). If the sampling is without replacement, then the HH estimator is inapplicable, and the effective sample size v in the HT estimator equals the sample size n since it is impossible for a unit to appear more than once in the sample. These two estimators indicate that an unequal probability sampling design can be more efficient than an equal probability sampling design only when either the selection probabilities or the inclusion probabilities are approximately proportional to the target variable. Otherwise, it may turn out to be even less efficient than its counterpart. In theory, zero variance results if the probabilities are set perfectly proportional to the variable of interest. In this study, an infinite population approach is employed to derive estimators for the three proposed plot designs.

3.1.3 Infinite population approach

The standard technique used in fixed-area plot sampling to extrapolate the per-plot observations to per-hectare values cannot be applied to adaptive plot designs because it requires equal inclusion probability for all trees at a given sample point. In the proposed three adaptive plot designs, the inclusion probability of each population unit is obviously not constant but variable: a tree with other trees nearby has a higher inclusion probability than an isolated tree or a tree with fewer neighbors, because the selection of a neighboring tree in an initial plot may lead to the selection of that particular tree finally in the sample.

The estimation design in this study adopts the infinite population paradigm which considers the dimensionless points in the area of interest as sampling elements (Eriksson, 1995). The paradigm is described in, for example, Gregoire and Valentine (2008) and Mandallaz (2008). Construction of design-unbiased estimators for various plot designs is straightforward under this paradigm, for example fixed count sampling (Kleinn and Vilčko, 2006), because it analytically determines the inclusion probability for each sample tree. Once inclusion probabilities of sample units are known, the HT estimator framework can be applied directly. A probabilistic sampling design for selection of the initial sample points is a prerequisite; in this study, the attention is restricted uniformly to SRS.

The inclusion probability of a particular tree can be derived from its inclusion zone constructed geometrically as the horizontal area around it that leads to its inclusion if a sample point falls within it. The area of its inclusion zone divided by the domain area of the population is a geometrical measure of that particular tree's inclusion probability.

The basic question becomes how to construct an inclusion zone and determine its area for a given sample tree under plot design I, II and III. For the conveniences of description and understanding, the following three new terms are introduced: relevant tree, relevant tree identification circle and relevant tree search circle. A relevant tree of a particular tree is a tree whose selection leads to the inclusion of that tree in the case of $CrV=1$. It implies that a tree is always its own relevant tree. The relevant tree identification circle or circles of a particular tree serves to identify its relevant neighbors and subsequent geometry operations involved in the inclusion zone construction. A neighboring tree is judged to be its relevant tree only when the initial-plot based inclusion zone of that neighbor overlaps its relevant tree identification circle. The relevant tree search circle or circles around a sample point demarcate the maximal area in the field to be searched for all relevant trees of all sample trees there. These definitions hold throughout the dissertation.

In plot design I, the inclusion zone of a tree varies with the factors that define the plot design (initial plot size, PSF, and CrV) and the number and spatial arrangement of trees. Figure 3.5 schematically illustrates an example for a center tree and for a fixed PSF but two $CrVs$ (left: “at least one tree in the initial plot” and right: “at least two trees in the initial plot”). All sample points falling inside the gray filled inclusion zone leads to an inclusion of the center tree in the sample. The gray filled area is a direct measure of its inclusion probability. For a CrV of 1 (Figure 3.5, left), the center tree (target tree) is included if it is either directly inside an initial plot or if at least one of its neighboring trees are within an initial sample plot which would trigger an initial plot expansion that subsequently includes the focus tree. The two inclusion paths for a tree translate into the shown inclusion zones $CrVs$ of 1 and 2 (Figure 3.5).

To determine the inclusion zone of a tree, only that particular tree and its neighbors whose initial-plot based inclusion zones overlap the big dashed circle centered at it are relevant. The big dashed circle is of the same size as an expanded plot and serves as the relevant tree identification circle. For $CrV=1$ the inclusion zone of the centered target tree is then constructed from the intersection between the relevant tree identification circle and the union of the initial-plot based inclusion zones of all relevant trees. For $CrV=2$ the inclusion zone of the center tree can be depicted from the intersection of the union of the initial-plot based joint

inclusion zones of all relevant neighbors and the initial-plot based inclusion zone of the center tree with the big circle. Joint inclusion zone (Gregoire and Valentine, 2008) is the region of the overlap between the inclusion zones of two trees, and a sample point falling in it will lead to the inclusion of those two trees in the sample.

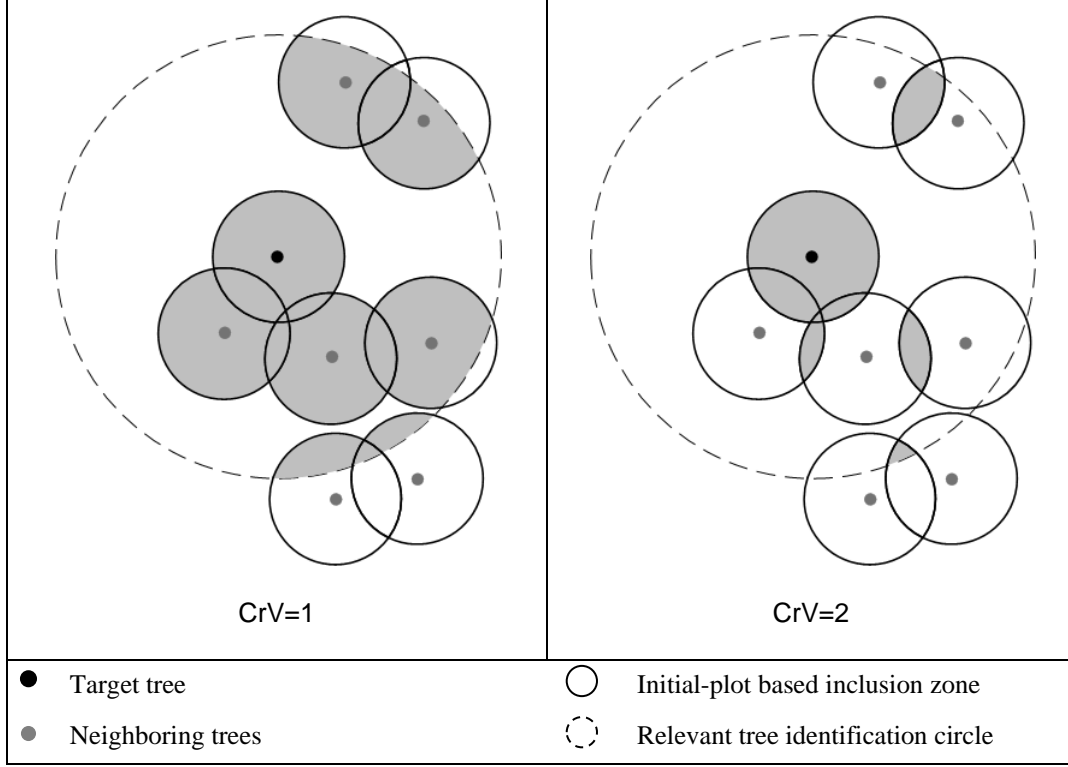


Figure 3.5 Two examples of inclusion zones for the center tree under plot design I. For explanation of the construction principles see text (from Yang et al., 2009).

Obviously, as can be seen from Figure 3.5, the determination of an actual inclusion zone for a particular tree requires the coordinates of all trees up to a distance that equals the sum of radii of the expanded plot and the initial plot. In consequence, a maximal circular area of $(2\sqrt{PSF} + 1)^2$ times the size of the initial plot around a sample point has to be observed for coordinates when a plot is expanded. At sample point locations where the initial plot contains target objects but the predefined condition is not satisfied (their number is smaller than the defined CrV), at most a circular area of $(\sqrt{PSF} + 2)^2$ times the initial plot size have to be checked. The collection of coordinates relative to the sample point causes additional efforts, and is indispensable unless more straightforward approaches or tools are developed to determine the inclusion probability or appropriate proxies.

In plot design II, the inclusion zone of a tree depends also on the type of cluster plot being used including the number and geometric spatial layout of subplots. Figure 3.6 illustrates the inclusion zones of a target tree under plot design II where the condition to adapt is defined to be the presence of at least one tree (left) and two trees (right) respectively in the initial sample plot. As seen in Figure 3.6, there are four relevant tree identification circles associated with the target tree. They are centered at four crosses in a prespecified distance, say D , apart from the target tree along the four primary intercardinal directions (NE, SE, SW, and NW) respectively, and share the same radius as the initial sample plot.

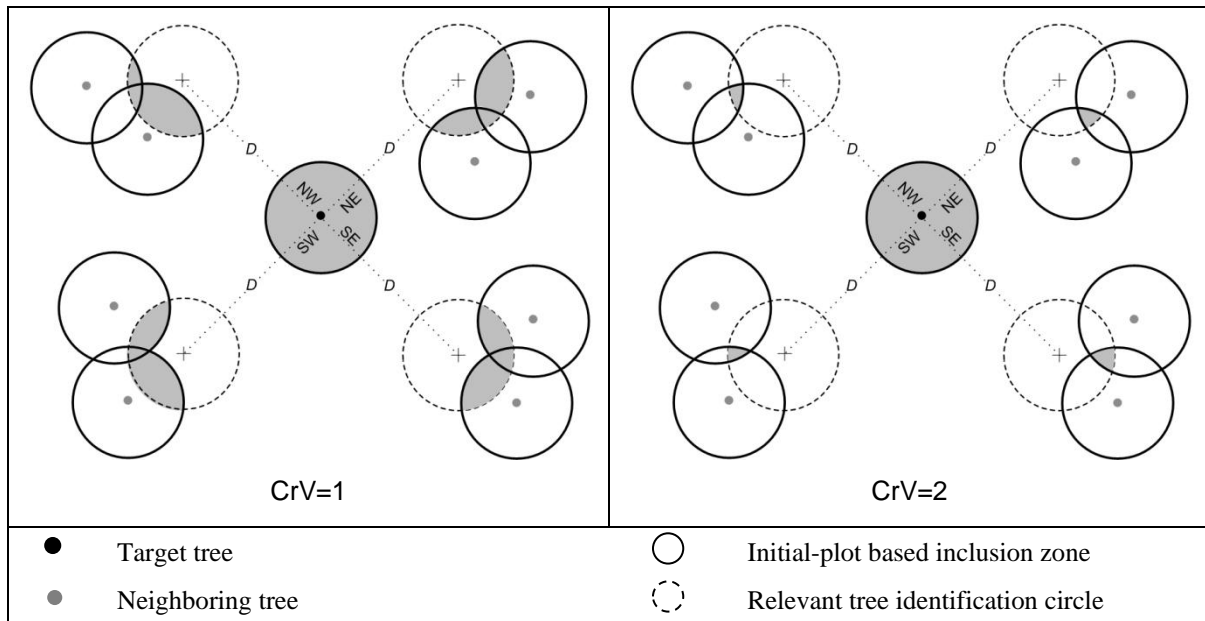


Figure 3.6 Two examples of inclusion zones for the target tree under plot design II with a subplot distance of D . The inclusion zones of the target tree are filled in gray color.

The inclusion zone of the centered target tree in the case of $CrV=1$ can then be delineated from the intersection between the four relevant tree identification circles and the union of the initial-plot based inclusion zones of all relevant trees. In the case of $CrV=2$, the inclusion zone of the target tree results from the intersection of the union of its initial-plot based inclusion zone and the initial-plot based joint inclusion zones of all its relevant neighbors with the four relevant tree identification circle.

Accordingly, a certain number of relevant tree search circles placed around the initial sample point as shown in Figure 3.7 need to be searched in order to collect the coordinates of all relevant trees of the sampled trees. The relevant tree search circles are of the same size with a radius three times that of an initial plot. As seen in Figure 3.7, a total of thirteen relevant tree

search circles are required to be searched in the field around a sample point when the condition to adapt is satisfied there (left), otherwise only five (right).

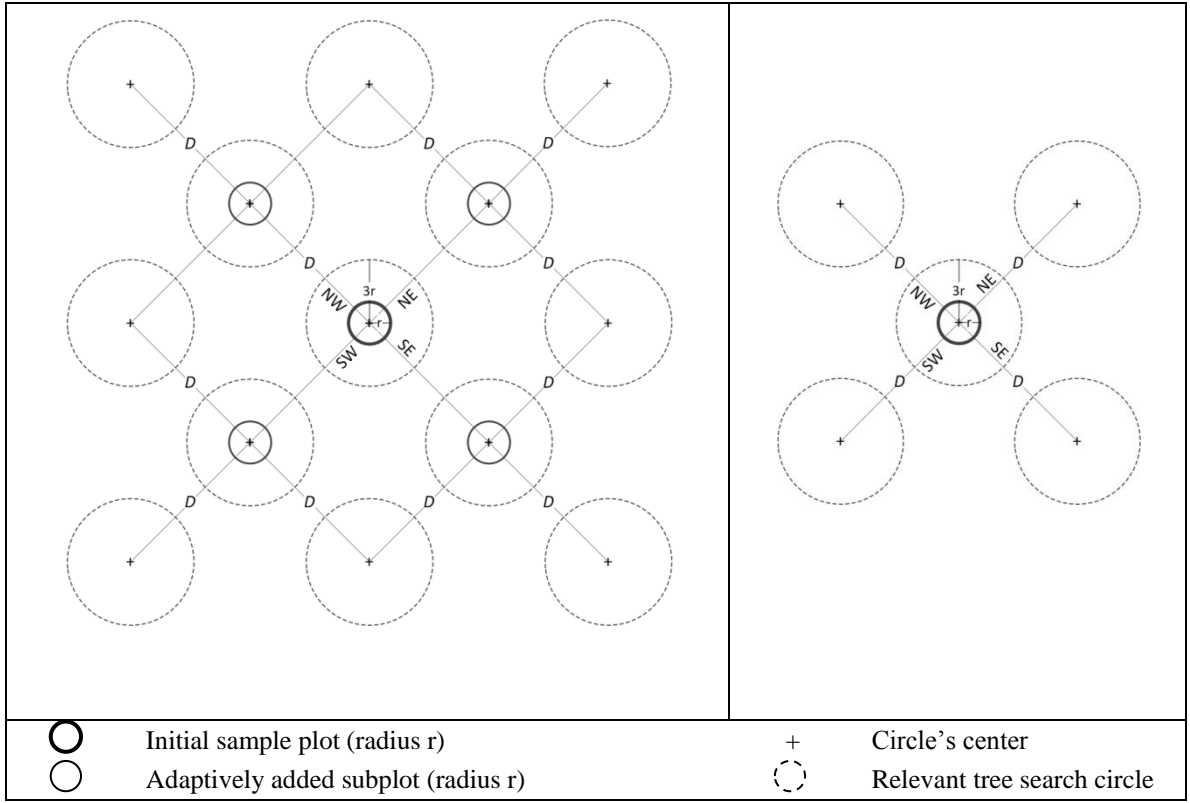


Figure 3.7 The spatial layout of relevant tree search circles under plot design II around a sample point in the center when the condition to adapt is satisfied (left) and not (right). The subplot distance for the design is D .

In plot design III, BAF and CrV determine the final inclusion zone of a tree, together with its DBH and the spatial distribution of its neighboring trees. For a tree with a DBH of d , its initial inclusion zone (i.e. initial-BAF based inclusion zone) and relevant tree search circle are centered at it, and have a radius of $c_i d$ and $c_f d$ respectively. Here c_i and c_f are the plot radius factor corresponding to the predefined initial BAF and final BAF respectively. Two examples are given in Figure 3.8 to illustrate how the inclusion zone of a tree is constructed on two different occasions. The inclusion zone of the centered target tree in the case of CrV=1 (namely at least one tree is tallied) is obtained from the intersection between its relevant tree identification circle and the union of the initial-BAF based inclusion zones of all relevant trees. In the case of CrV=2 (namely at least two trees are tallied), the inclusion zone of the target tree is derived from the intersection of the union of its initial-BAF based inclusion zone and the initial-BAF based joint inclusion zones of all its relevant neighbors with its relevant tree identification circle.

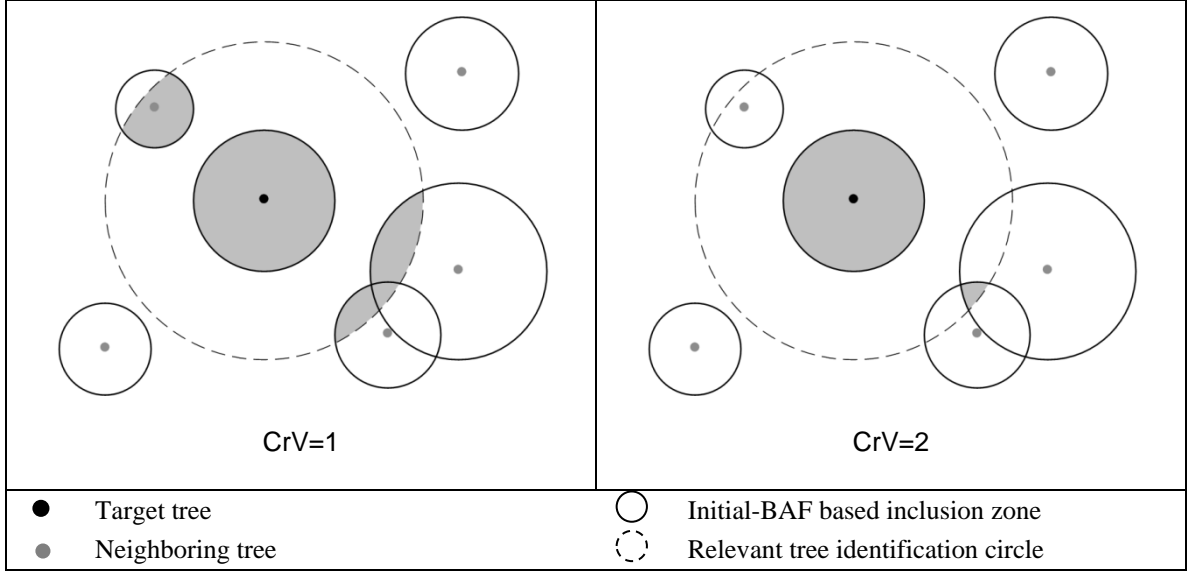


Figure 3.8 Two examples of inclusion zones for the center tree under plot design III. The inclusion zones of the target tree are filled in gray color.

It is straightforward under plot design I and II to determine in the field whether a tree is a relevant tree of the sampled trees based only on its distance to a reference point, such as a sample point and the center of a relevant tree search circle. However, such a determination under plot design III is remarkably complicated by the nature of plot design III: the initial-BAF based inclusion zone and the relevant tree identification circle of a tree both vary with its DBH. As a consequence, the procedure below needs to be followed in the field to determine whether a tree is a relevant tree of a tallied tree or not: (a) measure the distance D between them, and the DBH of the possible relevant tree, d_p and the tallied tree, d_t ; (b) calculate $c_f d_t + c_i d_p$, (c_i and c_f are the plot radius factor corresponding to the predefined initial BAF and final BAF respectively); (c) compare D with $c_f d_t + c_i d_p$. If $D \geq c_f d_t + c_i d_p$, then the tree in question is a relevant tree of the tallied tree, otherwise not. This procedure needs to be repeated not only for each tallied tree, but also for the trees around it, until all relevant trees of the sampled trees are determined for the collection of coordinates.

Once the inclusion zones of all sampled trees have been analytically determined and their areas calculated, the Horvitz-Thompson estimator applies for the estimation of the total of any obtained tree characteristic.

Following largely the notation in Valentine et al. (2001), the estimate for the total \hat{T}_k for the inventory region of size A_T derived from the observations at sample point k is then:

$$\dot{T}_k = \sum_{i=1}^N \frac{Y_i}{A_i / A_T} Z_{ki}$$

with

N = total number of trees in the inventory area,

A_i = inclusion area of tree i ,

Y_i = observed value of the target variable at tree i ,

$$Z_{ki} = \begin{cases} 1, & \text{if sample point } k \text{ falls into the inclusion zone of tree } i \\ 0, & \text{otherwise.} \end{cases}$$

From the individual observations as produced at each sample point, the estimators for the total \hat{T} and its variance $\hat{\text{var}}(\hat{T})$ from n sample points are, respectively,

$$\hat{T} = \frac{\sum_{k=1}^n \dot{T}_k}{n} \quad \text{and} \quad \hat{\text{var}}(\hat{T}) = \frac{\sum_{k=1}^n (\dot{T}_k - \hat{T})^2}{n(n-1)},$$

and this applies to totals of any tree variable. In the sampling simulation, estimating the number of stems per ha (N/ha) under plot design I and II, and basal area per ha (G/ha) under plot design III in the inventory regions is taken as an example.

According to Valentine et al. (2001), the above mentioned estimator can be interpreted or derived by the integral geometric approach widely used in the applications of sampling continuous populations, such as importance sampling and crude Monte Carlo. That approach, called a Monte Carlo integration approach to areal sampling in Gregoire and Valentine (2008), is being elaborated in what follows.

At each randomly selected sample point (here the basic situation of simple random sampling of sample points is exclusively dealt with), one observation Y_k of the target variable is derived from all the measurements taken at the set of observed sample trees (for example number of stems or tree basal area per plot). The algorithm how to calculate that per-plot observation Y_k for plot k (the plot at sample point k) is specific for the plot design used. This calculation here is carried out from the inclusion zone approach and follows largely the notation in Valentine et al. (2001) as well. In order to start the calculation, each per-tree value of the target variable observed from the discrete population of individual trees needs to be re-expressed as the volume of an imaginary solid disc. That disc uses the inclusion zone of a tree as its bottom

surface and has a uniform height of $\frac{Y_i}{A_i}$, which results from the value of the target variable Y_i of that particular tree. That is, each per-tree value is imagined to be evenly prorated over its corresponding inclusion zone. For example, if the target variable is “number of trees”, then, the observation for each tree is $Y_i=1$, and consequently the height of all discs is $\frac{1}{A_i}$. Discs of neighboring trees do, of course, overlap so that in a particular inventory area a complex “virtual landscape” is generated. The volume of this landscape of all piled up overlapping discs in the inventory region is then the total of that particular variable for the inventory region. The task is now to estimate this total. The total area A_T of the inventory region is known so that only the average height of the “virtual landscape” needs to be estimated to produce an estimate of the total. At any sample point, a sample observation for the mean height is straightforwardly produced for any variable by measuring the height of the m overlapping discs. Actually, these m discs at one particular sample point do belong to the m sample trees included into the plot established at that particular sample point.

This geometric approach to forest sampling is applicable to various plot designs for which an unambiguous rule can be defined how to include the sample trees from a particular sample point: For fixed area circular plots, the rule is defined by a constant maximum distance, for relascope sampling it is a maximum distance which depends on the trees’ DBH and for fixed count sampling it is the maximum number of neighboring trees. Figure 3.9 illustrates the approach. A stem map is given (top) together with the overlapping inclusion circles per tree (middle) and then the virtual landscape of “piled-up” discs (bottom). The example in Figure 3.9 refers to a simple case of fixed area circular plots (that is: all inclusion zones have the same shape and size) for the estimation of density (that is: all trees have the same value 1 and, therefore, all discs have the same height). It can be observed that in those areas of the “inventory area” where the tree density is high, the elevation of the landscape is higher because many inclusion zones do overlap and pile up to a higher “elevation” that leads to higher observed values at these points. In this example, the issue of edge effects (plots overlapping the population boundary) is eliminated. The inclusion zones do not straddle the forest boundary.

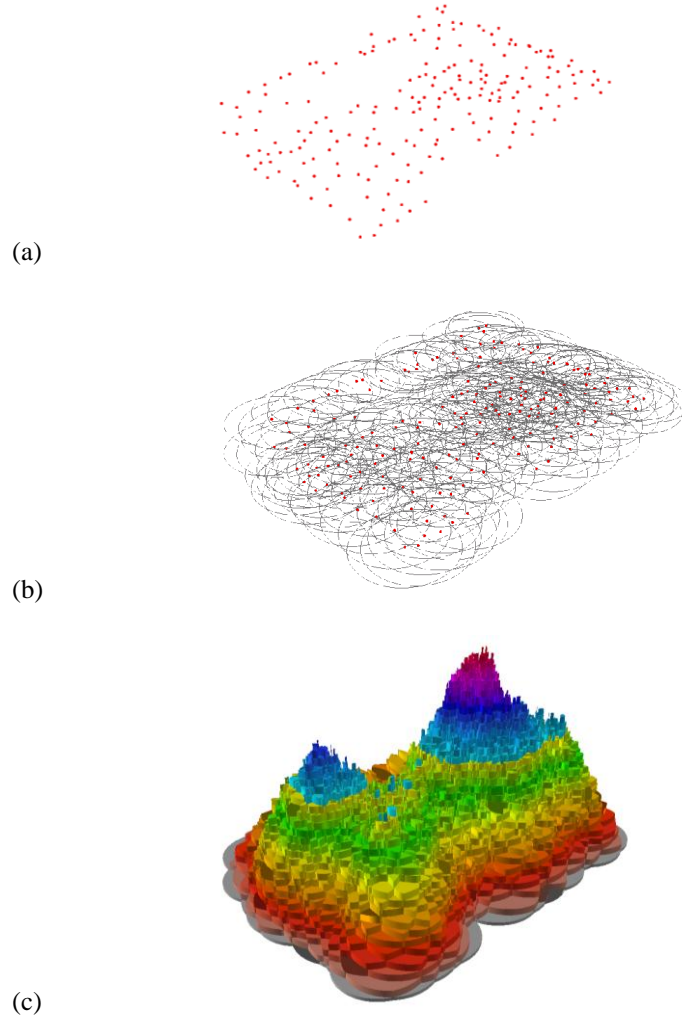


Figure 3.9 Graphical illustration of the geometric approach to estimation from the inclusion zone concept for fixed area circle plots. The target variable is density (that is, number of trees per area) and each tree carries the same value of observation 1; (a) gives the positions of the trees and (b) all the overlapping circular inclusion zones; (c) depicts the virtual landscape whose volume corresponds to the total of the target variable to be estimated. This figure is prepared by Dr. Lutz Fehrmann and its use is with his permission.

The estimate of the mean height of this landscape of overlapping discs is the sum of the m disc heights at this particular sample point. In order to generalize, a 0/1 indicator variable Z_{ki} is introduced to indicate whether tree i of the population of N trees is included for sample point k or not as before. The observation of the height H_k at the k th sample point is then

$$H_k = \sum_{i=1}^N \frac{Y_i}{A_i} Z_{ki}$$

The estimate for the total \hat{T}_k for the inventory region of size A_T from the observations at the k th sample point becomes:

$$\dot{T}_k = \sum_{i=1}^N \frac{Y_i}{A_i / A_T} Z_{ki}$$

From the individual observations as produced at each sample point, the estimators for the total \hat{T} and its variance $\hat{\text{var}}(\hat{T})$ from n sample points (Valentine et al., 2001) are, respectively:

$$\hat{T} = \frac{\sum_{k=1}^n \dot{T}_k}{n} \quad \text{and} \quad \hat{\text{var}}(\hat{T}) = \frac{\sum_{k=1}^n (\dot{T}_k - \hat{T})^2}{n(n-1)},$$

and this applies to totals of any tree variable. It can be seen that these estimators from the integral geometric approach are identical to those from the non-geometric approach.

In this study, the sample points are assumed to be constrained to fall only within the population boundary, i.e. inventory region. For each tree whose inclusion zone slops over the population boundary, the method of direct measurement of inclusion area (Gregoire and Valentine, 2008) is used for the edge effect correction to ensure the unbiasedness of the estimators. That method allows only the portion of the inclusion zone within the population boundary to be involved in the estimation, and thus needs an operation of geometry intersection between the inclusion zone of each tree and the inventory region.

3.1.4 Estimation approach in double sampling for stratification

In addition to the above described infinite population approach, the standard estimator for double sampling for stratification (DSS) (Cochran, 1977; Chojnacky, 1998; Van Laar and Akça, 2007; Lam et al., 2010) was tried and investigated only for the random sampling with plot design I, despite the fact that the sampling with plot design I is essentially different from DSS. DSS is a variant of standard double sampling or namely two-phase sampling (Neyman, 1938; Cochran, 1977) and they share a common feature: a large sample is selected in the first phase for the observation of a cheap-to-measure auxiliary variable and a small subsample is taken from the first phase sample for that of the target variable. DSS is found to be a sampling strategy suitable for the situations where the population of interest is heterogeneous but a clear prestratification is hardly possible or feasible for some reason although conducive to sampling efficiency. Such situations are very common in sampling rare and geographically clustered populations. In DSS, the strata sizes need to be estimated from the observed values of an auxiliary variable acquired by sampling, unlike in stratified sampling or post-stratified sampling (Van Laar and Akça, 2007), where they are assumed to be known prior or posterior to sampling.

Let

L = number of strata,

n' = total number of sample units in the first phase sample,

n'_h = number of sample units in the first phase sample falling in stratum h ,

w_h = weight of stratum h estimated from the first phase sample, and

\bar{y}_h = estimated mean of target variable Y in stratum h .

Then the unbiased estimator of the population mean from DSS is

$$\bar{y}_{dss} = \sum_{h=1}^L w_h \bar{y}_h$$

where $w_h = \frac{n'_h}{n'}$.

The standard DSS estimator is applied for random sampling with plot design I in this study in the following manner. The initial sample under plot design I is considered as the first phase sample in DSS and stratified into two strata according to the criterion whether the observed value of target variable on an initial sample plot is larger than the predefined CrV. If not, then that initial sample plot is stratified into stratum 1, otherwise stratum 2. The weights of two strata can be estimated respectively as follows:

$$w_1 = \frac{n_{01}}{n_0}$$

$$w_2 = \frac{n_{02}}{n_0}$$

where:

n_0 = Initial sample size (number of initial sample plots),

n_{01} = Number of initial sample plots not satisfying the condition to adapt,

n_{02} = Number of initial sample plots satisfying the condition to adapt, and

$$n_0 = n_{01} + n_{02}$$

Then, the n_{01} nonexpanded initial sample plots and the n_{02} expanded ones are used as the second phase sample plots in stratum 1 and stratum 2 respectively, and the SRS mean estimator is employed to calculate \bar{y}_h , the estimated mean of target variable Y in stratum h .

The estimated population mean is derived by substituting the right hand side of the DSS estimator as follows:

$$\bar{y}_{dss} = \frac{n_{01}}{n_0} \times \frac{\sum_{i=1}^{n_{01}} y_{1i}}{n_{01}} + \frac{n_{02}}{n_0} \times \frac{\sum_{j=1}^{n_{02}} y_{2j}}{n_{02}} = \frac{1}{n_0} \times \left(\sum_{i=1}^{n_{01}} y_{1i} + \sum_{j=1}^{n_{02}} y_{2j} \right)$$

where:

y_{1i} = value of the target variable observed on the i th sample plot in the stratum 1, and

y_{2j} = value of the target variable observed on the j th expanded plot in the stratum 2.

Both y_{1i} and y_{2j} are calculated by means of plot-size-dependent expansion factors EF, which converts the per-plot observations to per-ha observation. The sizes of the initial sample plots and the expanded plots are used to derive the EF for y_{1i} and y_{2j} respectively.

In order to eliminate the edge effect for the DSS estimator, the mirage method (Gregoire, 1982; Gregoire and Valentine, 2008) is employed. But for the convenience of the sampling simulation programming, it is implemented by generating mirage populations, instead of installing mirage plots across the population boundary as seen in its field applications. Figure 3.10 illustrates the idea how to mirage a tree population. The original mapped population is enclosed in the rectangle $ABCD$. The tree u_1 , denoted by a black dot, is mirrored across the four boundary lines AB , BC , CD , and AD , and reflected 180° across the four square corners respectively. Thereby eight mirage trees from m_1 to m_8 denoted by eight gray dots are generated from the tree u_1 and finally eight mirage populations are generated when the population mirage approach is applied to each tree in the population. As a result, the sampling in a boundary plot can be carried out simply by tallying all trees including the mirage trees within it as in a non-boundary plot. However, the performance of edge effect correction of the mirage method remains unaffected.

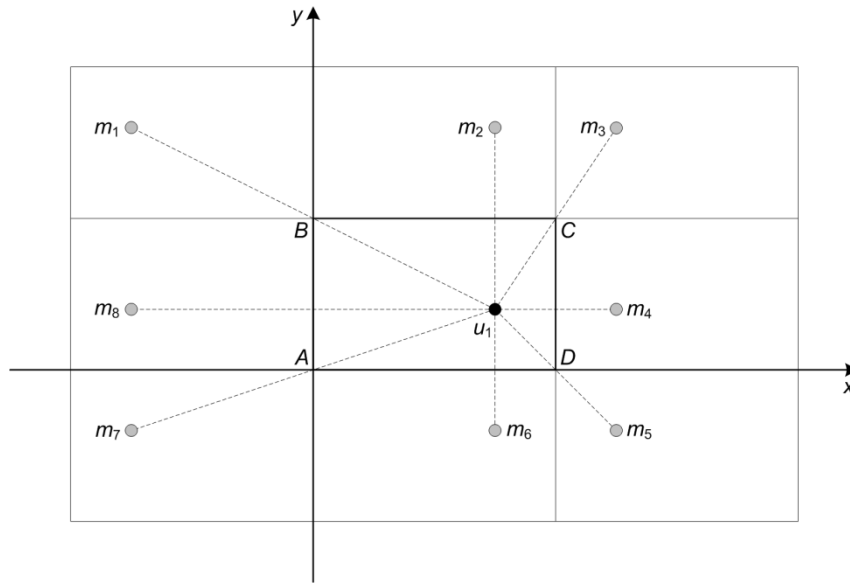


Figure 3.10 Implementation of mirage method by generating mirage population units.

3.2 COST FUNCTION

In this study, the comparisons of the proposed plot design I, II and III with their nonadaptive counterparts based solely on their statistical performances without considering costs. Adaptive plot designs demand more time in the field and thus cause higher cost than fixed-area plot designs for a given sample size. But in reality, the main concern in forest inventories especially large area forest inventories is quite often which sampling strategy can produce an estimate of the best precision for a given cost. A sampling strategy which is superior for a given number of elements in the sample may yield a less precise estimate for a given cost. In other words, it may not be cost efficient. One typical relevant example is SRS and conventional random cluster sampling. For a given number of elements in the sample, SRS is usually known to have a better statistical performance than conventional cluster sampling, but for a given cost a more precise estimate may be obtained with conventional cluster sampling under certain conditions (Cochran, 1977; Matérn, 1986; Thompson and Seber, 1996) since travelling to a new random sample point in an inventory region is generally much more time-consuming than the observations on a cluster of subplots installed at an existing sample point in cluster sampling. Thus, in practice overall efficiency, which takes costs into account, is mostly the decisive factor for the choice of sampling strategy. For this reason, the overall efficiencies of the three proposed adaptive plot designs need still to be compared for their practical application, although they are akin to conventional cluster sampling in nature and the

results obtained in this study are positive for them. A comparison of overall efficiency requires cost functions based on the assumptions about the additional field effort.

The cost functions here are developed from the modification of a cost function for SRS which is simplified from Scheuber and Köhl (2003). All costs involved in the following cost functions are expressed in terms of time, not money. The notations in all cost functions are used consistently. The cost function for SRS is:

$$C_T = C_0 + nC_1 + nC_2$$

where:

C_T = total cost in terms of time,

C_0 = average time requirement of the round travel between the camp and the inventory region,

C_1 = average time requirement to travel to next sample point,

C_2 = average time requirement for field observation within a sample plot, and

n = sample size.

3.2.1 Plot design I

The cost function for plot design I depends not only on its design factors but also on the estimator for it. When the estimator presented in this study is used, the collection of the coordinates of all sampled trees as well as their relevant trees and its cost must be accordingly added into the cost function as a new cost item. The cost function for plot design I modified from C_T is then:

$$C'_T = C_0 + nC_1 + [(n - m_i) + m_i\sqrt{PSF}]C_2 + [(m_1 - m_i)(\sqrt{PSF} + 2)^2 + m_i(2\sqrt{PSF} + 1)^2]C_3$$

where:

C'_T = total cost in terms of time for plot design I,

C_0 = average time requirement of the round travel between the camp and the inventory region,

C_1 = average requirement to travel to next sample point,

C_2 = average time requirement for field observation of the target variable per initial sample plot area,

C_3 = average time requirement for collection of coordinates of relevant trees of the sampled trees per initial sample plot area,

n = sample size or number of initial sample plots,

m_1 = expected value of the number of initial plots with the presence of at least one tree,

m_i = expected value of the number of initial plots with the presence of at least i trees ($i \geq 1$),

i = CrV (critical value set for the design), and

PSF = plot size factor

The values of m_1 and m_i can be calculated as follows:

$$m_1 = np_1, \text{ and } m_i = np_i$$

where:

p_1 = the average percentage of expanded plots for CrV of 1, and

p_i = the average percentage of expanded plots for CrV of i .

This cost function will be greatly simplified by removing the last cost item from it when an alternative estimator without need for tree coordinate collection becomes available.

3.2.2 Plot design II

Following the same way as above, the cost function for plot design II with the estimator used in this study is developed according to the number of relevant tree search circles, which is 5 for an initial sample plot satisfying the condition to adapt and 13 otherwise, and the size of a relevant tree search circle, which is 9 times larger than the area of the initial sample plot as shown in Figure 3.7. It is presented as follows:

$$\begin{aligned} C_T'' &= C_0 + nC_1 + (n + 4m_i)C_2 + [(m_1 - m_i) \times 5 \times 9 + m_i \times 13 \times 9]C_3 \\ &= C_0 + nC_1 + (n + 4m_i)C_2 + (45m_1 + 72m_i)C_3 \end{aligned}$$

where:

C_T'' = total cost in terms of time for plot design II,

C_0 = average time requirement of the round travel between the camp and the inventory region,

C_1 = average time requirement to travel to next sample point,

C_2 = average time requirement for field observation of the target variable per initial sample plot area,

C_3 = average time requirement for collection of coordinates of relevant trees of the sampled trees per initial sample plot area,

n = sample size or number of initial sample plots,

m_1 = expected value of the number of initial plots with the presence of at least one tree,

m_i = expected value of the number of initial plots with the presence of at least i trees ($i \geq 1$),
and

i = CrV (critical value set for the plot design)

The calculation of m_1 and m_i can be done with the formula given for plot design I.

The cost for the travel between subplots and relevant tree search circles is not taken into account as it is normally very small in comparison with the cost for travels from sample point to sample point.

If an alternative estimator without need for tree coordinate collection comes into existence in the future, then the last cost item can be simple dropped.

3.2.3 Plot design III

The cost function composed for plot design III is:

$$C_T''' = C_0 + nC_1 + nC_{IBAF} + m'_i C_{FBAF} + (m'_1 - m'_i)C'_3$$

where

C_T''' = total cost in terms of time for plot design III,

C_0 = average time requirement of the round travel between the camp and the inventory region,

C_1 = average time requirement to travel to next sample point,

C_{IBAF} = average time requirement for field observation using initial BAF at a sample point,

C_{FBAF} = time requirement for field observation using final BAF at a sample point where the condition to adapt is met,

C'_3 = average time requirement for collection of coordinates of relevant trees of the sampled trees at a sample point,

n = sample size or number of sample points,

m'_1 = expected value of the number of sample points with at least one tree tallied with an initial BAF,

m'_i = expected value of the number of sample points with at least i ($i \geq 1$) trees tallied with an initial BAF, and

i = CrV (critical value set for the plot design)

The values of m'_1 and m'_i can be calculated as follows:

$$m'_1 = np'_1, \text{ and } m'_i = np'_i$$

where:

p'_1 = the average percentage of adapted sample points for CrV of 1, and

p'_i = the average percentage of adapted sample points for CrV of i .

Unlike C_3 in plot design I and II, C'_3 in the last cost item of the cost function for plot design III cannot be fixed as the relevant tree search circle for a sampled tree has a variable size as mentioned before. This will bring some difficulty for the comparison of overall efficiency.

3.3 MATERIALS

3.3.1 Real population

A real population referred to as TR was used to evaluate the statistical performance of the proposed new plot designs. It consists of 268 individuals of the shrub species *Tamarix ramosissima* mapped on a rectangular study site of 500m×100m. The study site (lat 40°15'57.6"N, long 106°56'24"E) is located at the northeast edge of the Ulan Buh Desert in Dengkou County of north China's Inner Mongolia Autonomous Region as seen in Figure 3.11. It has spare desert vegetation under a typical temperate arid and semi-arid climate, which is controlled by the dry, cold northwesterly monsoon in winter and by warm, moist southeasterly monsoon in summer. The surface temperature recorded from 1955 to 1985 had a maximum of 67.0°C and a minimum of -37.2°C. From 1955 to 2003, the mean annual air temperature was 8.6°; the mean annual precipitation was only 107.8mm whereas the annual evaporation reached 2956.8mm and was more than 27 times than the annual precipitation, and 80% of the precipitation was concentrated in the four months from June to September. The common tree, shrub and subshrub species on the study site are *Elaeagnus angustifolia*, *Haloxylon ammodendron*, *Nitraria tangulorum*, *Hedysarum scoparium* and *Artemisia arenaria* in addition to *Tamarix ramosissima*. Like many other desert plant species, these species have various morphological and physiological traits to survive under harsh

environmental conditions in the arid and semi-arid zones in China (Chun et al., 2008), such as unusually strong tolerance to drought, high salinity, extreme temperature and strong wind (Tobe et al., 2001). They provide crucial environmental and ecological functions in the control and prevention of desertification and the restoration of desert ecosystem (Gao et al., 2002), such as fixation of sand dunes, preservation of underground water table and in particular protection of the desert margin areas. China is one of the countries severely threatened by desertification and has devoted tremendous efforts and resources to combating desertification over the past several decades (Chen and Tang, 2005), including a variety of scientific and technical research in support of desert rehabilitation, e.g. this study jointly funded by DFG and NSFC.

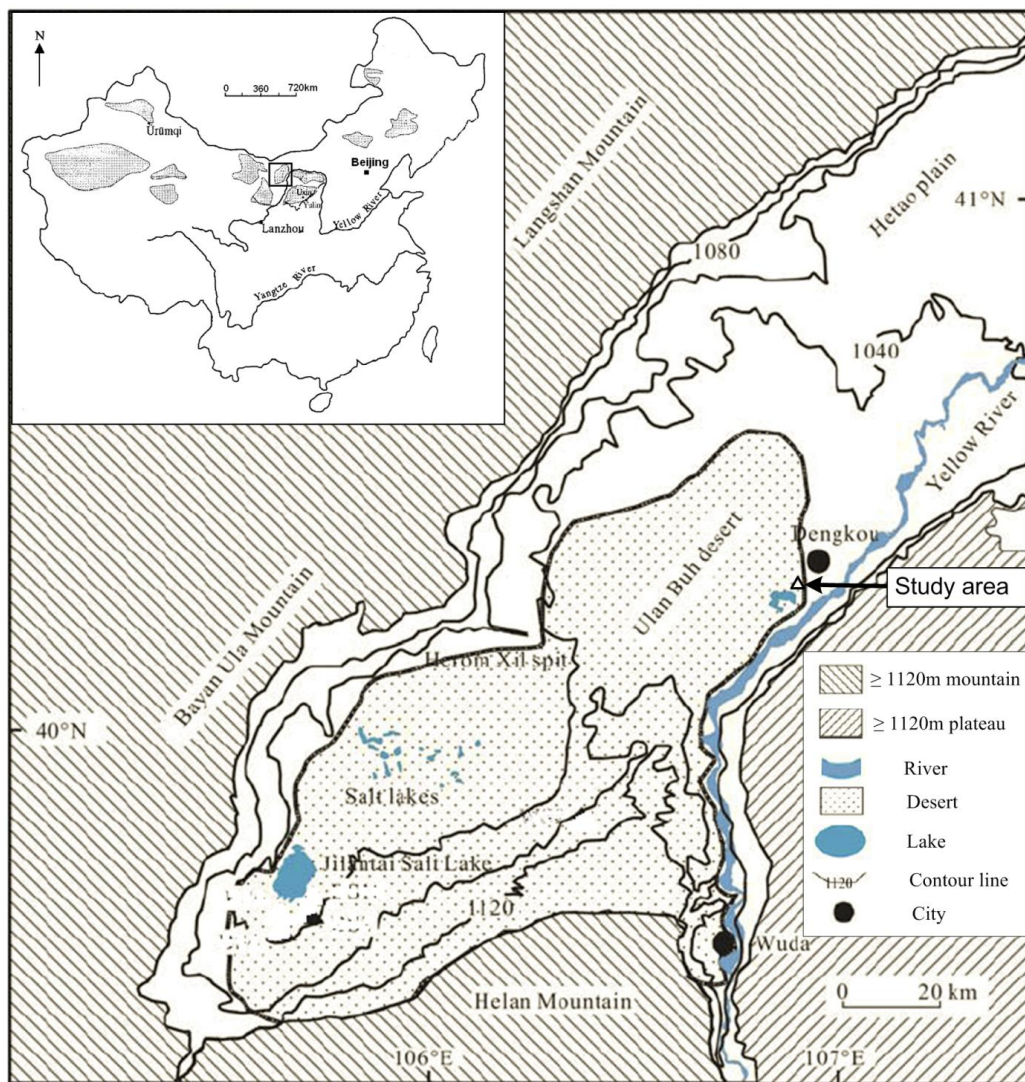


Figure 3.11 Location of study area in Ulan Buh desert, inner Mongolia, China (modified from Zha and Gao, 1997; Chun et al., 2008).

Field data were collected in September 2007. As seen in Figure 3.12, TR is geographically clustered as many other desert plant species, which is considered as their adaptation to the adverse desert environment (Wright and Howe, 1987; Eccles et al., 1999; Malkinson et al., 2003). For sampling such populations, the proposed adaptive plot designs are suspected to be exclusively suitable if they are appropriately configured.

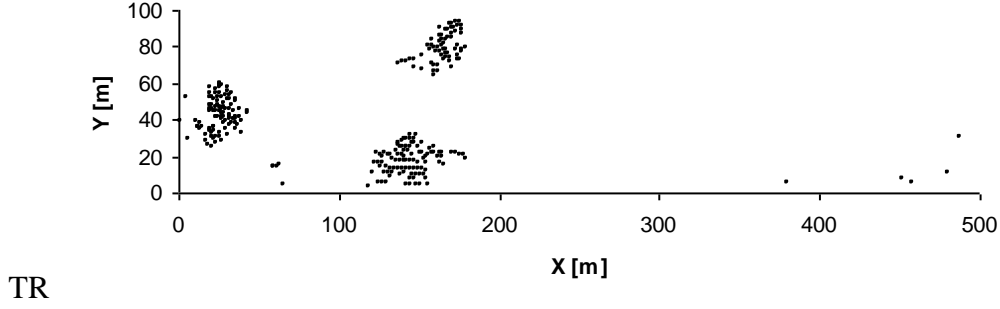


Figure 3.12 The map of the real population TR of *Tamarix ramosissima* in Inner Mongolia, China (from Yang et al., 2009).

3.3.2 Simulated populations

In addition to the real population TR, eleven artificial populations were also used for comparison and further analysis. They are referred to as SIM_{dss} , SIM_{rnd} , SIM_{uni1} , SIM_{uni2} , SIM_{cl} , and SIM1 to SIM6 respectively. The generation of these artificial populations is intended to: (1) find whether the proposed adaptive plot designs are superior exclusively for the clustered populations as expected, and (2) examine whether the degree of clustering of a clustered population strongly affects their statistical performances as in conventional ACS (Smith et al., 2003).

SIM_{dss} populates a square area of 500m×500m with 620 trees in clusters and was employed to check the applicability of DSS estimator for plot design I.

As depicted in Figure 3.13, SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} each have 184 individuals arranged over an area of 300m×300m but in four different spatial patterns: one random (SIM_{rnd}), two uniform (SIM_{uni1} , SIM_{uni2}) and one clustered (SIM_{cl}). They served to investigate whether the proposed designs are specifically efficient for geographically clustered populations or not. The DBHs of the trees in each of the four populations except SIM_{uni2} were generated independently from a normal population with a mean of 50cm and a standard deviation of 20cm. SIM_{uni2} shares the same set of DBHs with SIM_{uni1} .

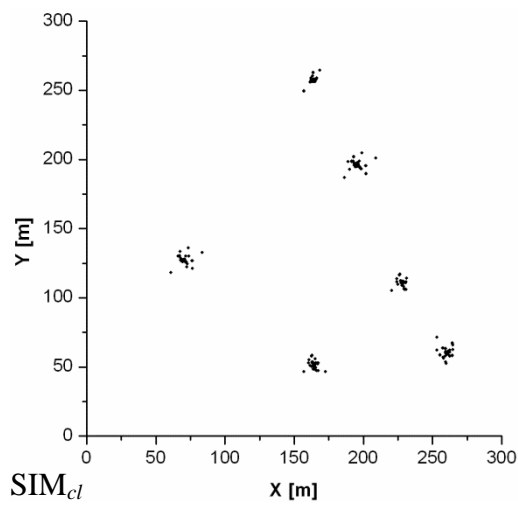
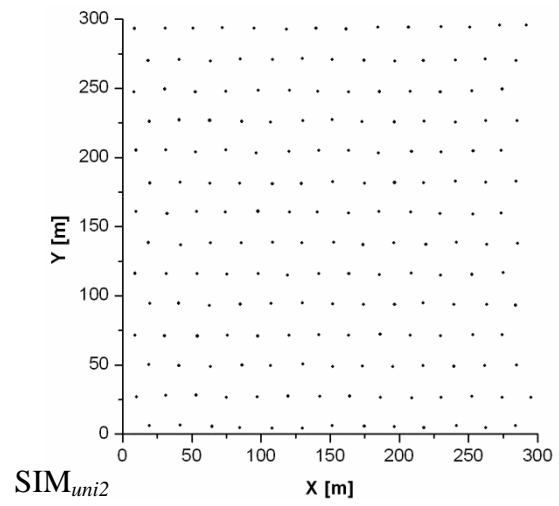
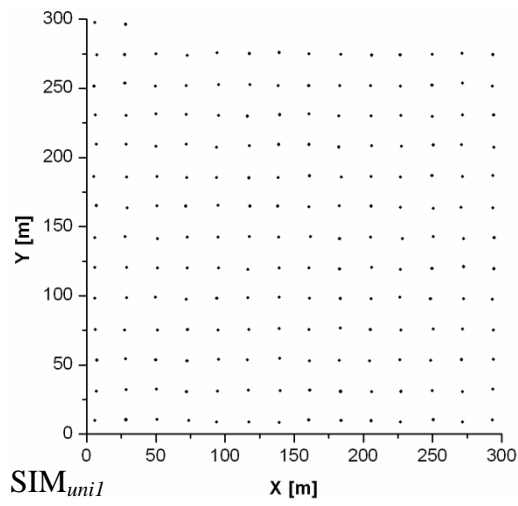
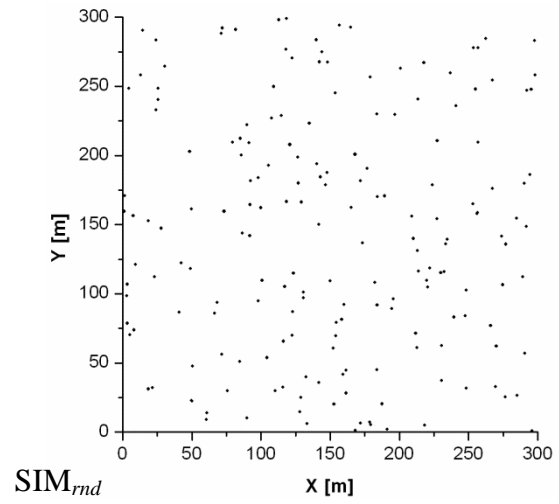
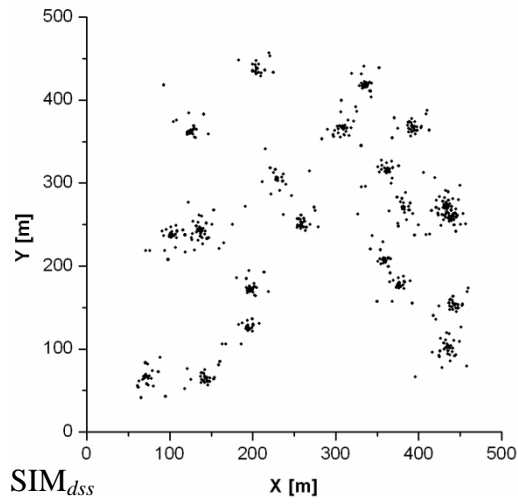


Figure 3.13 Maps of artificially generated populations with different spatial patterns for simulation: SIM_{dss} , SIM_{rnd} , SIM_{uni1} , SIM_{uni2} , SIM_{cl} .

Each population from SIM1 to SIM6 is geographically clustered as shown in Figure 3.14 and has the same spatial domain and number of individuals as TR— only the plant locations are varied. These seven populations are used to investigate how the statistical performances of the proposed designs vary with the degree of clustering of a population.

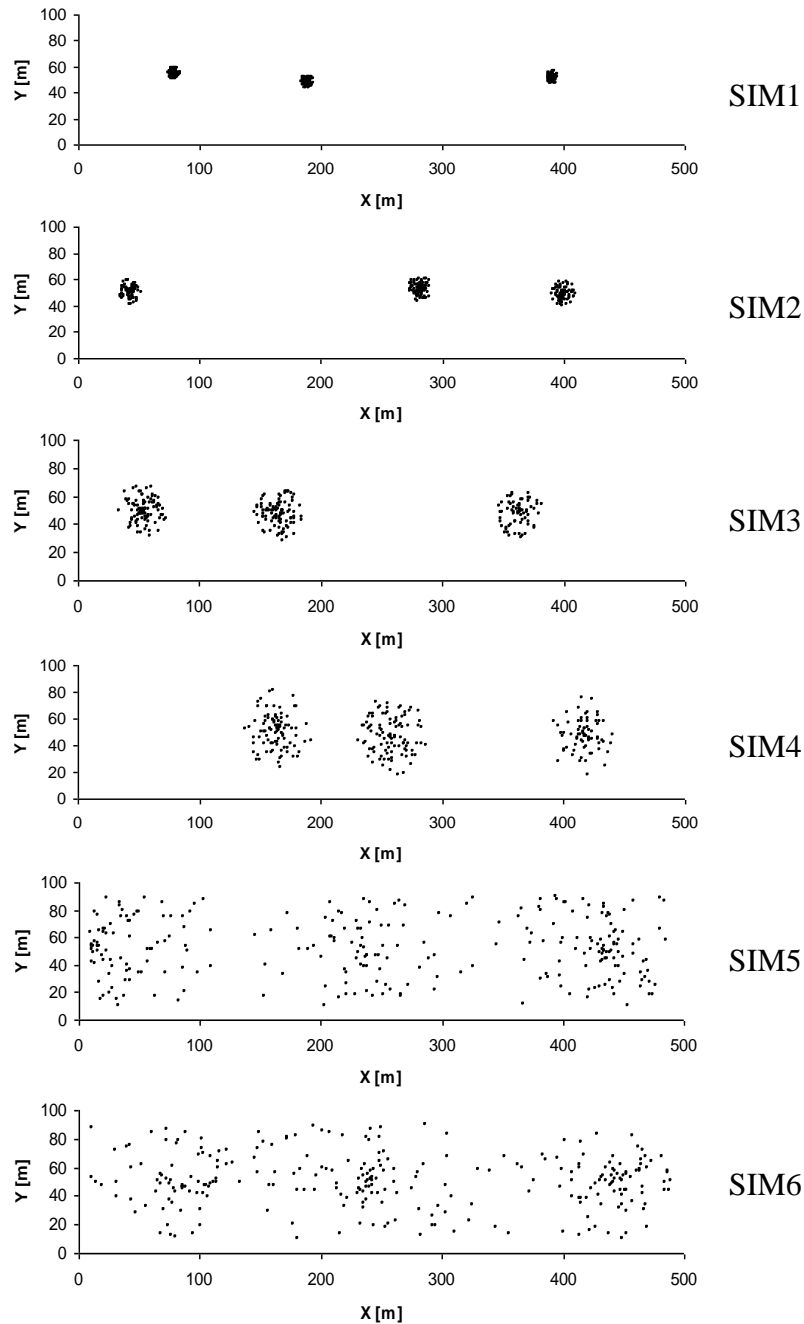


Figure 3.14 Maps of the six artificial populations SIM1 - SIM6. All maps have 268 trees as in the real population TR; the artificially generated populations SIM1 to SIM6 are arranged in three major clusters of different size characterized by the scale parameter λ : SIM1 ($\lambda=5\text{m}$), SIM2 ($\lambda=10\text{m}$), SIM3 ($\lambda=20\text{m}$) and SIM4 ($\lambda=30\text{m}$), SIM5 ($\lambda=100\text{m}$), SIM6 ($\lambda=100\text{m}$). (From Yang et al., 2009).

The eight clustered artificial populations including SIM_{dss} , SIM_{cl} , and $SIM1$ to $SIM6$ were generated from a variation of a Poisson cluster process (Diggle, 2003). In each of them, the number of clusters and the number of individuals per cluster were generated at random from two Poisson distributions with respective means of 30 and 30 for SIM_{dss} , 5 and 3 for SIM_{cl} , and 3 and 90 for $SIM1$ to $SIM6$. The coordinates of each cluster center were generated randomly. In addition, the spatial extension of the clusters varied. The position of a tree within a cluster is then determined relative to its cluster center by a random azimuth and distance. The random azimuths were drawn from a uniform distribution between 0° and 360° ; the random distances were generated from an exponential distribution with a mean of 10 and 3 for SIM_{dss} and SIM_{cl} respectively and from a continuous uniform distribution with a location parameter 0 and a scale parameter λ for $SIM1$ to $SIM6$. The λ values used for $SIM1$ to $SIM6$ were 5m, 10m, 20m 30m and 100m (with two different spatial arrangements) respectively. The resulting spatial distributions of $SIM1$ to $SIM6$ are mapped in Figure 3.14.

3.4 DESCRIPTION OF ANALYSIS

In order to compare the performance of the proposed adaptive plot designs, it is necessary to know for each of the inventory regions the variance of the estimates derived from the per-plot observations of the target variable for both the adaptive and the non-adaptive approach. As all points in the inventory area are potential sample plot centers, this population is infinite and the sought population characteristics are traditionally approximated by Monte-Carlo simulations of a large number of random samples. However, Roesch et al. (1993) introduced a direct approach to calculate these characteristics by finding the selection probabilities for each distinct set of sample trees as defined by the plot design, the so-called jigsaw-puzzle approach, based on the concept of inclusion zone. In this study, both approaches were used.

The jigsaw puzzle approach is illustrated in Figure 3.15 and is used in this study to calculate rather than approximate the true variance of estimates of N/ha for plot design I and II, and the true variance of estimates of G/ha for plot design III.

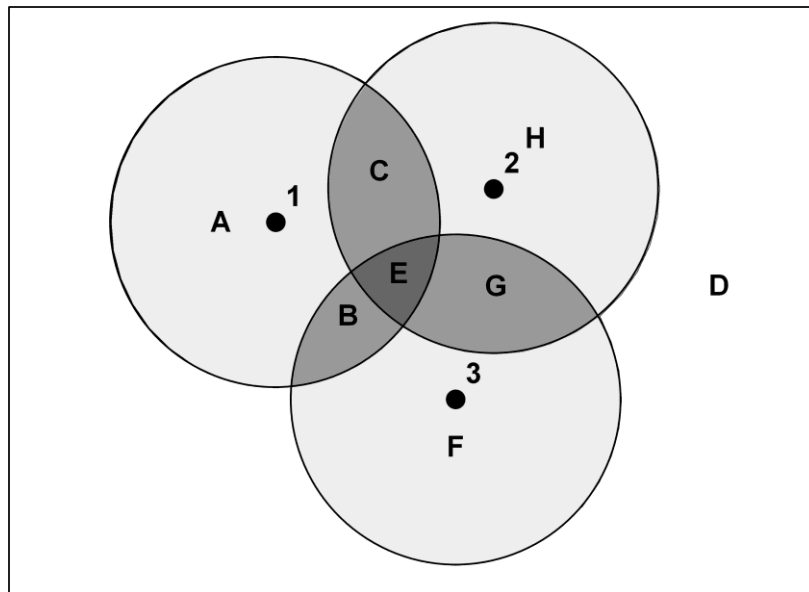


Figure 3.15 Illustration of the jigsaw puzzle approach as introduced by Roesch et al. (1993), applied to fixed area circular sample plots. Around each tree there is a circular inclusion zone. Inclusion zones of neighbouring trees can overlap and the resulting tessellation in non-overlapping pieces is akin to a “jigsaw puzzle” that covers the entire area without any gaps. All sample points within one specific ‘jigsaw’ piece (A, B, C, D, E, F, G or H) lead to the selection of exactly the same set of trees. That is, the probability of any possible set of sample trees to be selected by simple random sampling with a given plot design is defined by the area of one particular piece of this jigsaw puzzle (from Yang et al., 2009).

In this study, the jigsaw puzzle for the non-adaptive plot design and for the adaptive plot design for all possible level-combinations of design relevant factors was solved by calling the geoprocessing functions of ArcObjects from a self-written MS Visual Basic program. However, the jigsaw puzzle can be easily created with standard GIS techniques, such as ArcGIS Desktop without any programming effort once the inclusion zones are determined. The design relevant factors are initial plot size, CrV and PSF for plot design I, initial plot size, CrV and distance of the adaptive subplots to initial sample point for plot design II, and Initial BAF, final BAF and CrV for plot design III. From this tessellation, the selection probabilities of all possible sample trees are known and parametric values of the per-plot-observations can be directly calculated and need not to be approximated by Monte-Carlo simulation any more. The resulting inclusion probabilities for both the adaptive and the non-adaptive plots are design-unbiased and the populations are identical with respect to the parametric value. Therefore, the statistical performance for any sample size can be directly compared by means of any measure of variability of sample plot observations. Here, the relative standard error in percentage (SE%) was used.

According to Roesch et al. (1993), the variance $V(\hat{Y})$ of \hat{Y} is:

$$V(\hat{Y}) = \left(\frac{1}{nA_T}\right) \sum_{j=1}^M a_j \left(\frac{A_T y_j}{a_j} - Y\right)^2$$

where:

n = sample size/the number of randomly placed sample points,

A_T = the total area of the inventory region,

M = the total number of jigsaw puzzle pieces,

a_j = the area of jigsaw puzzle piece j ,

y_j = the value of the target variable for jigsaw puzzle piece j , and

Y = the total of the target variable

$$\hat{Y} = \frac{A_T}{n} \sum_{j=1}^n \frac{y_j}{a_j} \text{ (the estimator for the total of the target variable)}$$

The value of the target variable for jigsaw puzzle piece j is:

$$y_j = \sum_{i=1}^N \left(\frac{a_j}{A_i}\right) z_{ij} y_i$$

where:

A_i = the inclusion area of tree i ,

y_i = the observed value of the target variable at tree i , and

$$z_{ij} = \begin{cases} 1 & \text{if jigsaw puzzle piece } j \text{ is part of the inclusion zone of tree } i \\ 0 & \text{otherwise} \end{cases}$$

The relative standard error in percentage, SE%, is:

$$SE\% = \frac{\sqrt{V(\hat{Y})}}{Y} \times 100$$

In this study, the target variable to be estimated is N/ha for plot design I and II, and G/ha for plot design III. Therefore, the observed value of the target variable y_i equals 1 under design I and II, and equals the basal area of tree i under plot design III.

In addition, the average percentage of expanded plots, EP%, for each adaptive design can be derived also from a jigsaw puzzle:

$$EP\% = \frac{\sum_{j=1}^M a_j z_j}{A_T} \times 100$$

$$z_j = \begin{cases} 1 & \text{if jigsaw puzzle piece } j \text{ is part of the inclusion zones of at least } \gamma \text{ trees (} \gamma = CrV \text{)} \\ 0 & \text{otherwise} \end{cases}$$

The EP% will be used for the computation of comparative efficiencies of the nonadaptive designs.

The major procedures involved in the process of data analysis for all three proposed adaptive designs and their nonadaptive counterparts for comparison based on the jigsaw puzzle approach are represented in Figure 3.16. The steps from a mapped population to the parametric SE% for given sample size n are executed in a self-written MS Visual Basic program running on Windows XP Pro SP3. The control from a trial version of the ESRI Mapobjects-Windows Edition 2.4 and the libraries from the ESRI ArcObjects software development kit 9.3 are integrated into that program. The former is used for the inclusion zone construction, and the latter for the jigsaw puzzle creation.

At the beginning of the inclusion zone construction, a mapped population is converted into a points object of Mapobjects, i.e. a collection of point objects. The initial-plot based inclusion zone and relevant neighbor search circle of a population unit is delineated by applying the buffer method to the corresponding point in the points object and then stored as polygon objects for subsequent geometry operations and determination of the topological relationship between an inclusion zone and each jigsaw puzzle piece. The relevant neighbor search circle acts as a cookie-cutter for the inclusion zone construction.

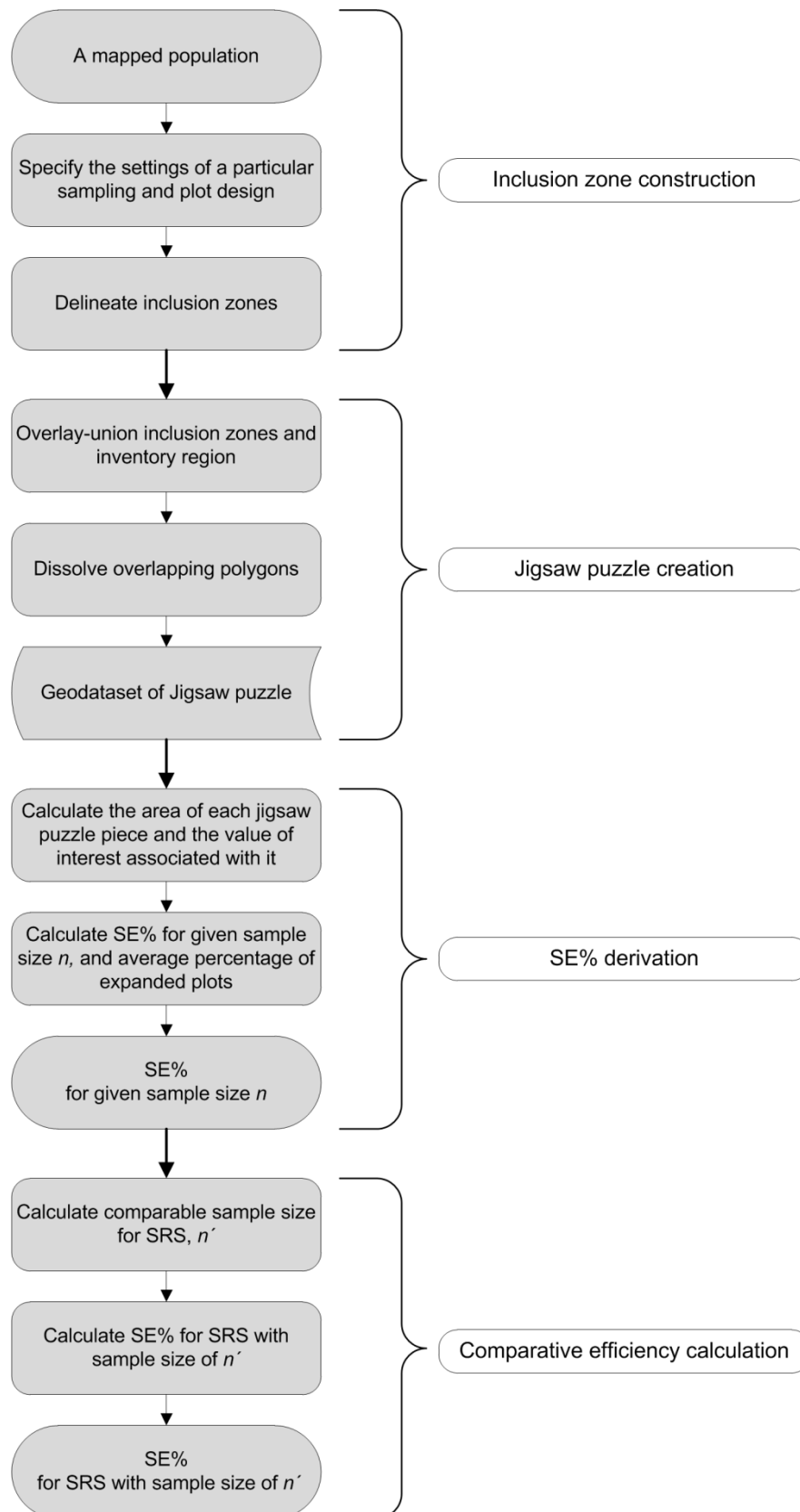


Figure 3.16 Data analysis flowchart of the jigsaw puzzle approach. All steps are classified into four groups: inclusion zone construction, jigsaw puzzle creation, SE% derivation and comparative efficiency calculation.

The built-in method of DistanceTo is used to identify the relevant neighbors of each target unit. An odometer function was written to construct the inclusion zones for $CrV > 1$, and served to enumerate all possible combinations of a corresponding number of relevant neighbors of each target unit, aiming to depict the necessary initial-plot based joint (second order) or higher order inclusion zones.

The geoprocessing operation of overlay-union on the resultant inclusion zones provides us a jigsaw puzzle, but with the overlapping parts duplicated. Those duplicates are deleted by the operation of Dissolve based on the coordinates of the centroids of the jigsaw puzzle pieces.

In order to have a comprehensive insight into plot design I and II, plot design I and II are also compared with their nonadaptive counterparts on the basis of an equivalent sampling effort in addition to an equivalent sample size of $n=20$. The sampling effort in this study is measured in terms of the total area of sample plots. For a given sample size n , the sampling effort of either is a variable, but never less than that of its nonadaptive counterpart, and therefore its expected value is used as the baseline for comparison. The sample size of SRS with an equivalent sampling effort is referred to as comparable sample size for SRS and denoted by n' .

For a given sample size n and a plot size of F , the expected sampling effort under plot design I E_I and under plot design II E_{II} and their respective comparable sample size for SRS n'_I and n'_{II} are given as follows:

$$E_I = n \times (1 - EP\%) \times F + n \times EP\% \times PSF \times F = [n + n \times (PSF - 1) \times EP\%] \times F,$$

$$n'_I = n + n \times (PSF - 1) \times EP\%,$$

$$E_{II} = [n + 4 \times n \times EP\%] \times F, \text{ and}$$

$$n'_{II} = n + 4 \times n \times EP\%.$$

The value of SE% from SRS with the comparable sample size n' , $SE(n')\%$, can be derived from $SE(n)\%$, the one with sample size of n :

$$SE(n')\% = \sqrt{\frac{n}{n'}} \times SE(n)\%$$

The traditional and commonly used approach of Monte Carlo sampling simulation was applied only for the purpose of investigating the suitability of the DSS estimator for plot design I in comparison with the SRS estimator for its nonadaptive counterpart (SRS). In each run of the simulation program written in MS visual basic 6, the sampling under the adaptive design and its nonadaptive counterpart was replicated 5000 times in parallel based on an

identical set of randomly placed sample points for the possible convenience of the subsequent analysis. The result of each replication was stored for analysis. In addition to simulation mean, another useful statistic for comparison, RMSE (Root Mean Square Error) was also calculated. The RMSE equals the standard error when an estimator is unbiased. The major steps of Monte Carlo sampling simulation and analysis are given in Figure 3.17.

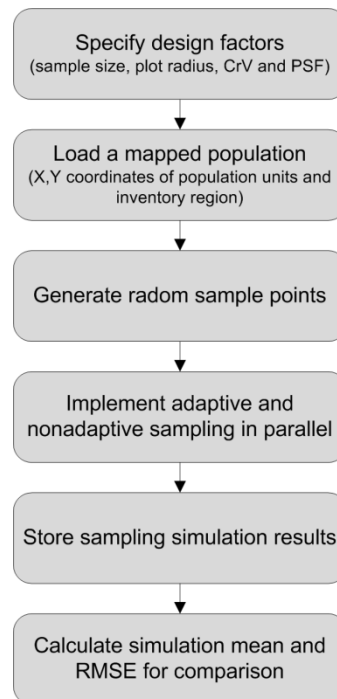


Figure 3.17 Flowchart of sampling simulation and analysis of the DSS estimator for plot design I.

4 RESULTS

4.1 RESULTS FROM PLOT DESIGN I

4.1.1 Double sampling for stratification estimator

The results of Monte Carlo simulation with the population SIM_{dss} for the adaptive designs of plot design I using DSS estimator to estimate stem density are presented in Figure 4.1.

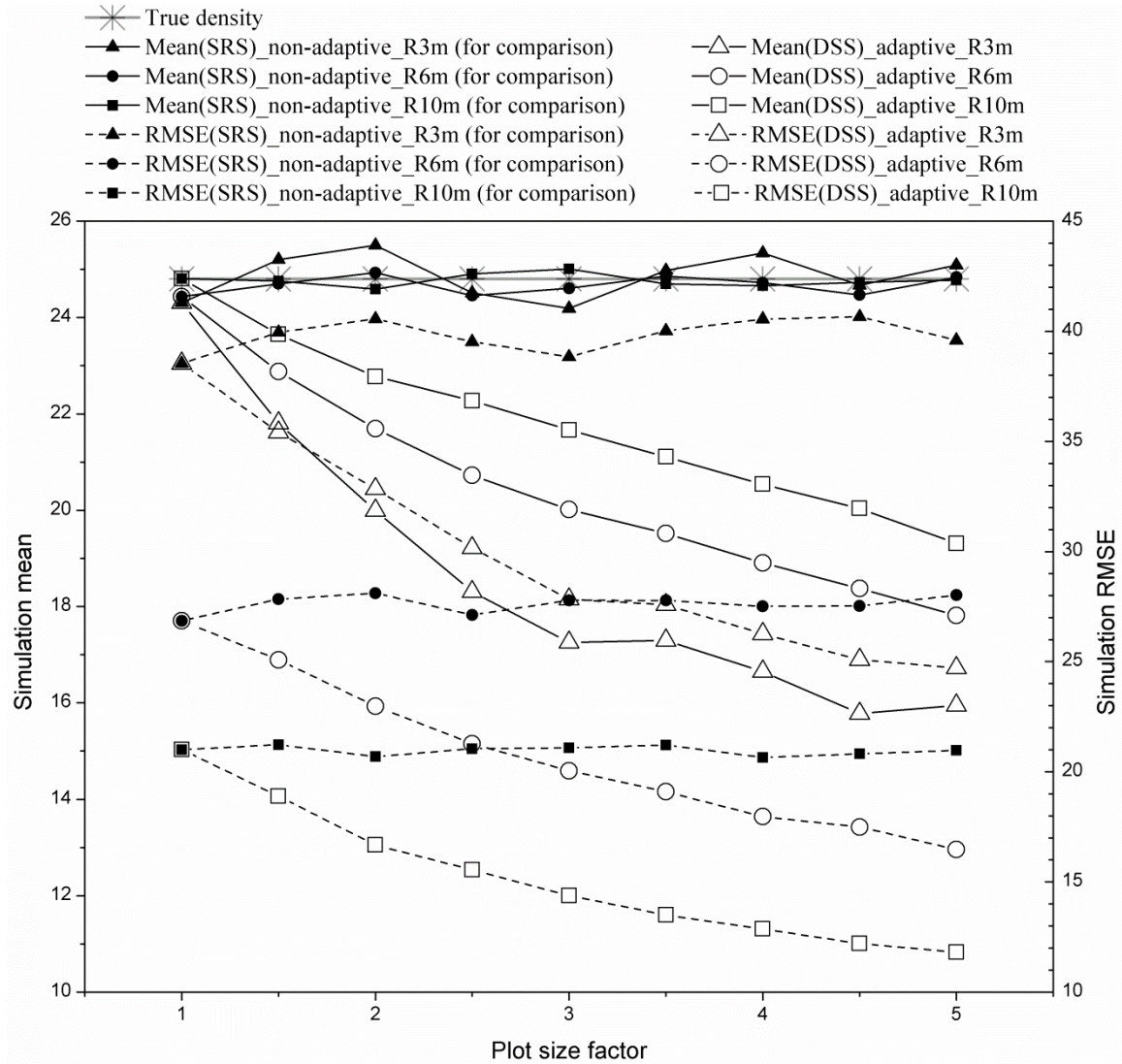


Figure 4.1 Simulation means and RMSEs based on the DSS estimator for the adaptive designs with $CrV=1$, PSF ranging from 1 to 5 and the initial circular plot radius R set to 3m, 6m and 10m respectively. The sample size for all simulated designs is 20. Each simulated nonadaptive design shares the same size of circular plot with its adaptive counterpart.

All of the simulation means of the estimates from the DSS estimator for the adaptive designs with PSF greater than 1 were lower than not only the true density, but also those from their corresponding nonadaptive designs using the design-unbiased estimator (SRS estimator), which fluctuated around the true density. Their differences from the true density became larger with increased PSF and decreased size of the initial circular sample plot. The RMSEs from the non-adaptive designs are actually the estimated standard errors as the SRS estimator is design-unbiased for those designs and varied only slightly for a specific sample plot size. All of the RMSEs from the adaptive designs were consistently smaller than the estimated standard errors from their nonadaptive counterparts, and decreased with increased PSF and size of initial circular sample plot.

The simulation results from the adaptive designs using the DSS estimator for a fixed CrV of 1, PSF of 2 and sample size of 20, but varying initial sample plot radii from 1m to 20m are drawn in Figure 4.2 and Figure 4.3.

Figure 4.2 shows the mean numbers of the initial sample plots for each of the two strata. With increased initial sample plot radii, the average numbers of initial sample plots in stratum 1, into which an initial sample plot not satisfying the condition to adapt is classified, decrease, while those in stratum 2 increase.

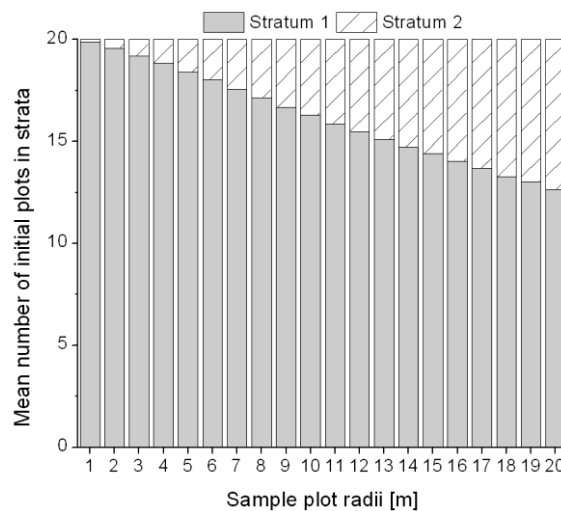


Figure 4.2 Mean numbers of the initial sample plots in each of the two strata from the adaptive plot designs for the population SIM_{dss} with the sample plot radii ranging from 1m to 20m. The sample size, CrV and PSF for all designs were fixed to 20, 1 and 2 respectively.

As seen in Figure 4.3, all of the simulation means of estimates from the DSS estimator for the adaptive plot design increased toward the true density with the increased initial sample plot

radii, but were consistently smaller than the true density and the simulation means of SRS estimates. Their differences from the true density became smaller with increased initial sample plot radii.

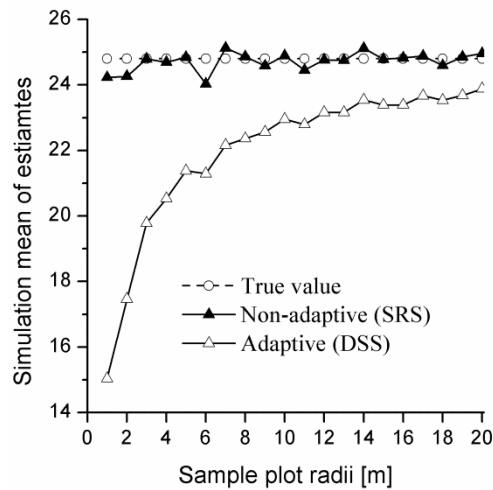


Figure 4.3 Simulation means of estimates from the DSS estimator for the adaptive plot designs with a fixed CrV of 1 and PSF of 2, but varying initial sample plot radii from 1 to 20m.

4.1.2 HT and HH estimator

4.1.2.1 Comparison among different spatial patterns

The results using the HT estimator from an equivalent sample size of $n=20$ are presented in Figure 4.4.

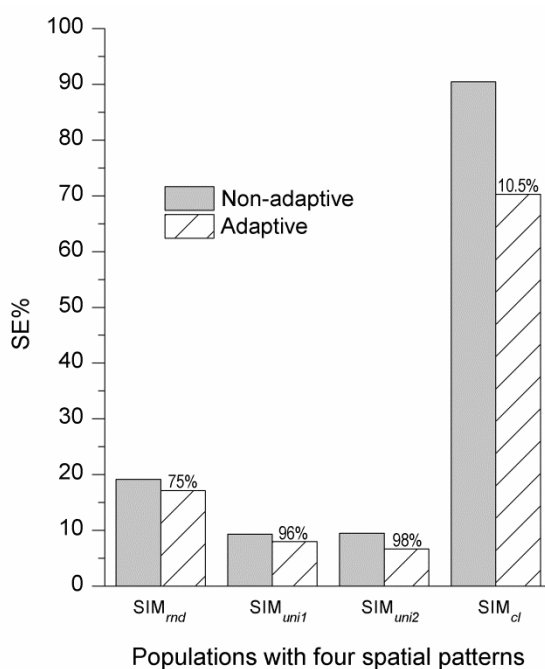


Figure 4.4 SE% of the N/ha estimates under plot design I with an initial sample plot radius of $R=15m$, CrV of 1 and PSF of 2 for four populations with different spatial patterns: SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} respectively. The average percentages of expanded plots from the adaptive design are noted on the figure.

In comparison with its nonadaptive counterpart, the SE% derived from the adaptive design is much lower for the clustered population SIM_{cl} with a fairly small average percentage of expanded plots of 10.5%, and only slightly lower for the other three populations but with a very high average percentage of expanded plots, which reaches 75% for SIM_{rnd} , 96% for SIM_{uni1} and 98% for SIM_{uni2} . These high average percentages of expanded plots imply that the vast majority of the initial sample plots need to be expanded if the adaptive plot design is applied to a random or especially a uniform population, which will incur a large amount of cost for the additional observations on the expanded plots.

The results from an equivalent sampling effort are illustrated in Figure 4.5. It is seen that the SE% from the adaptive plot design is noticeably higher for SIM_{rnd} and SIM_{uni1} , and very slightly lower for SIM_{uni2} , but much lower for the clustered population, SIM_{cl} , in comparison with that from its nonadaptive counterparts. As shown in Table 4.1, the population SIM_{cl} has the smallest comparable sample size for SRS among the four considered populations.

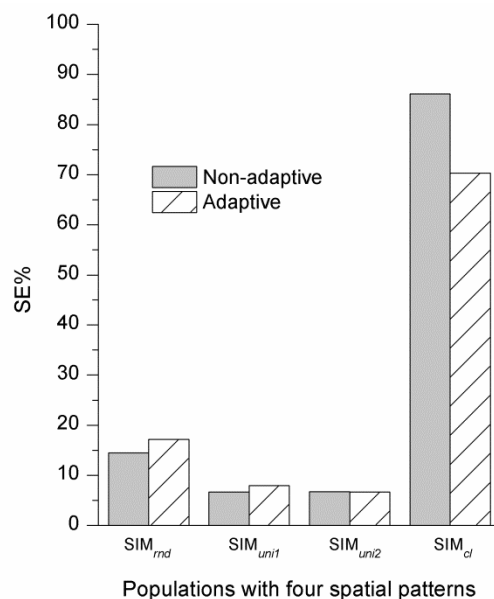


Figure 4.5 SE% of the N/ha estimates under plot design I from equivalent sampling efforts for four populations with different spatial patterns: SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} respectively. The adaptive plot design has an initial sample plot radius of $R=15m$, CrV of 1 and PSF of 2.

Table 4.1 The comparable sample size for SRS from the adaptive plot design with $n=20$, CrV=1, PSF=2 and plot radius of $R=15m$.

Populations	Comparable sample size for SRS
SIM_{rnd}	35
SIM_{uni1}	39.2
SIM_{uni2}	39.6
SIM_{cl}	22.1

4.1.2.2 Sample size

The variability of the population SE% as a function of sample size is shown in Figure 4.6. For all populations, the SE% from the adaptive design is smaller than that from the nonadaptive counterparts, although they both displayed the same trend that is well-known in the field of nonadaptive random sampling: the SE% decreases with increasing sample size and levels off at a certain sample size, which varies from population to population. The difference in SE% between the two plot designs decreases with increasing sample size for each considered population. At a particular sample size, a large difference in SE% is observed from the populations SIM1 to SIM3, which have smaller cluster sizes in comparison with the other four populations.

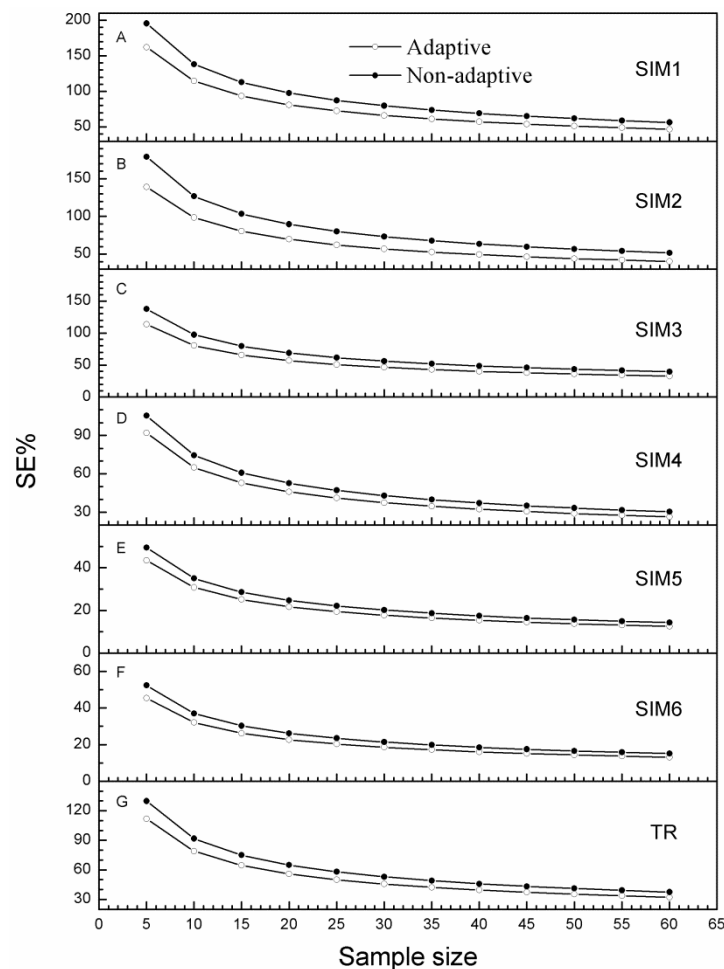


Figure 4.6 SE% of the N/ha estimates under plot design I as a function of sample size for the seven populations: SIM1 to SIM6 and TR. The settings for plot design I are: initial sample plot radius=15, CrV=1 and PSF=2.

4.1.2.3 Plot size factor and initial plot size

The results for the role of the PSFs from an equivalent sample size of $n=20$ are given in Figure 4.7.

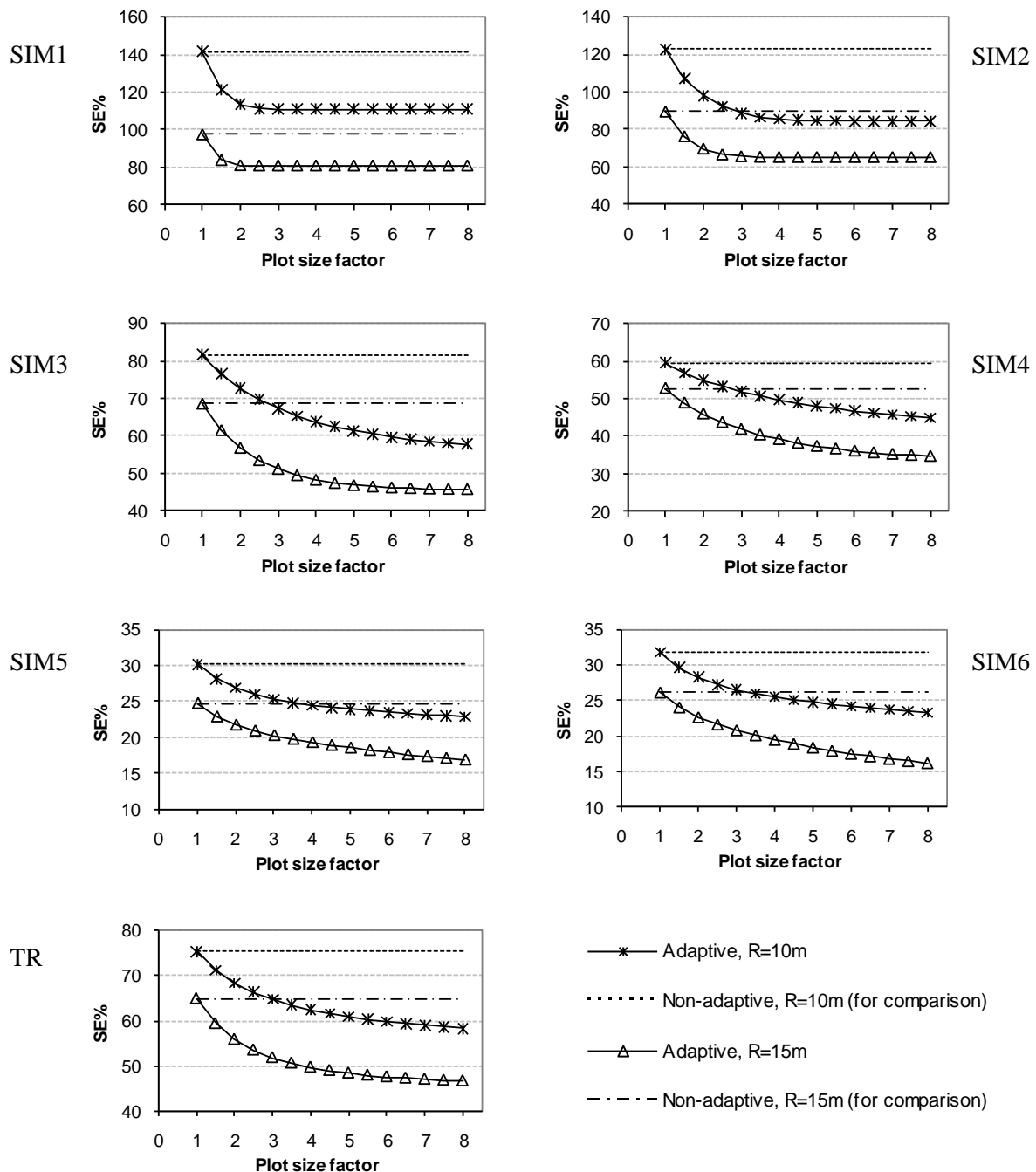


Figure 4.7 SE% of the N/ha estimates under plot design I on the basis of an equivalent sample size as a function of PSF for the populations SIM1-SIM6 and TR. The SE% values of SRS are depicted as dotted and dashed horizontal line for the non-adaptive circular sample plots of 10m and 15m radius, respectively. The critical value of each adaptive design is CrV=1 (from Yang et al., 2009).

General trends are: (1) a larger initial plot size produces less variability, as expected; (2) the adaptive plot design lowers the variability in density estimates for all PSFs greater than 1, (3) the values of SE% decrease with increasing PSF but at diminishing rates of decline as PSF gets larger. This point of leveling-off occurs slightly earlier for the larger initial plot size $R=15\text{m}$ for all maps. The PSF value beyond which the decline in SE% is small (Figure 4.7) was for population SIM1 about 2.5 and 2 for initial sample plot radius 10m and 15m, respectively, about 5 and 3 for population SIM2, and about 7 and 5 for population SIM3 and about 8 for both initial plot sizes in SIM4. For the other study populations the point of level-off did not appear in the considered range of PSF. The differences in performance can be explained by the different size of clusters. In SIM1 a relatively small PSF-value can lead to capture of an entire cluster. In other populations a larger PSF is needed to accomplish the same (e.g. SIM4 and TR). However, in SIM5 and SIM6 where neighboring clusters may overlap, a very large PSF is needed to achieve a comparable reduction of SE%.

Figure 4.8 shows the results from an equivalent sample effort, from which the following can be seen: (1) for all populations, the values of SE% for both adaptive and nonadaptive designs decrease but at different rates with increasing PSFs, on which the comparable sample sizes for SRS depend as seen in Table 4.2; (2) for the compactly clustered populations SIM1 to SIM3, and the real population TR, the adaptive design lowers the SE% at diminishing rates in a certain lower range of PSF and thereafter at growing rates, but with exception that the SE% from the adaptive design becomes larger from a certain PSF on for the populations SIM1 and SIM3 with the initial plot radius of $R=15\text{m}$, and for the population TR ; (3) for the populations with large sizes of clusters SIM4 to SIM6, the SE% from the nonadaptive design is smaller than that from the adaptive design.

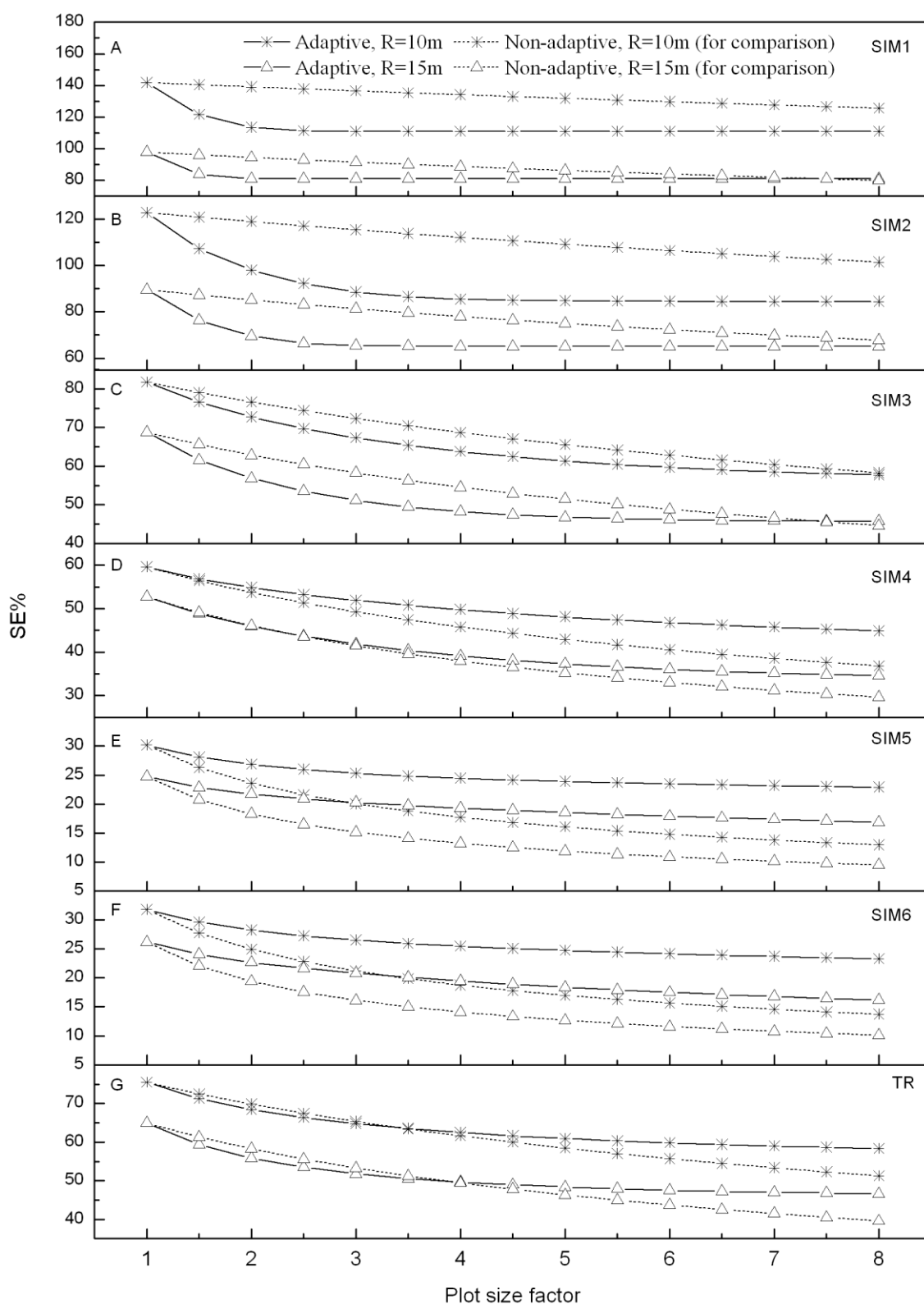


Figure 4.8 SE% of the N/ha estimates under plot design I on the basis of equivalent sampling efforts as a function of PSF for the seven study populations SIM1-SIM6 and TR. The critical value for the adaptive designs is CrV=1.

Table 4.2 Comparable sample size for SRS from the adaptive plot designs with the PSFs ranging from 1 to 6 and CrV=1 for two initial plot radii , $R=10\text{m}$ and $R=15\text{m}$, for the populations SIM1-SIM6 and TR.

Comparable sample size for SRS														
PSF	R=10m							R=15m						
	SIM1	SIM2	SIM3	SIM4	SIM5	SIM6	TR	SIM1	SIM2	SIM3	SIM4	SIM5	SIM6	TR
1.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0
1.5	20.4	20.7	21.4	22.3	26.3	26.3	21.7	20.7	21.1	22.0	23.1	28.3	28.2	22.4
2.0	20.8	21.3	22.8	24.6	32.7	32.5	23.3	21.4	22.1	23.9	26.2	36.7	36.3	24.8
2.5	21.2	22.0	24.2	27.0	39.0	38.8	25.0	22.1	23.2	25.9	29.3	45.0	44.5	27.2
3.0	21.6	22.7	25.5	29.3	45.4	45.1	26.7	22.9	24.3	27.9	32.4	53.3	52.7	29.6
3.5	22.0	23.3	26.9	31.6	51.7	51.3	28.3	23.6	25.4	29.8	35.5	61.6	60.9	32.1
4.0	22.4	24.0	28.3	33.9	58.1	57.6	30.0	24.3	26.4	31.8	38.6	70.0	69.0	34.5
4.5	22.7	24.7	29.7	36.3	64.4	63.9	31.7	25.0	27.5	33.8	41.7	78.3	77.2	36.9
5.0	23.1	25.3	31.1	38.6	70.7	70.1	33.3	25.7	28.6	35.7	44.8	86.6	85.4	39.3
5.5	23.5	26.0	32.5	40.9	77.1	76.4	35.0	26.4	29.6	37.7	47.9	94.9	93.5	41.7
6.0	23.9	26.7	33.9	43.2	83.4	82.7	36.7	27.1	30.7	39.6	51.0	103.3	101.7	44.1
6.5	24.3	27.3	35.2	45.5	89.8	88.9	38.3	27.8	31.8	41.6	54.1	111.6	109.9	46.5
7.0	24.7	28.0	36.6	47.9	96.1	95.2	40.0	28.6	32.9	43.6	57.2	119.9	118.0	48.9
7.5	25.1	28.6	38.0	50.2	102.5	101.5	41.7	29.3	33.9	45.5	60.3	128.2	126.2	51.3
8.0	25.5	29.3	39.4	52.5	108.8	107.7	43.4	30.0	35.0	47.5	63.4	136.6	134.4	53.7

4.1.2.4 Critical value

Figure 4.9 illustrates the interaction between CrV and PSF with respect to their effect on the statistical performance of the different plot designs with an equivalent sample size: (1) the SE% for the adaptive designs is less than that for non-adaptive designs (horizontal line in Figure 4.9); and (2) the SE% increases (slightly) with increasing CrV. The latter rests on the fact that a CrV of 1 triggers the largest number of plots to be expanded. Table 4.3 gives the proportion of expanded plots for the different designs in Figure 4.9.

The proportions of expanded plots depend on the spatial distribution of trees. SIM1 with its compact clusters has the lowest proportion of expanded plots. As well, the percentage of expanded clusters is smaller for larger CrVs. For population SIM1, for example, with CrVs =1, 2 or 3, the SE% is pretty much constant across levels of PSF. An explanation is again in the spatial pattern: if an initial plot intersects a compact and dense cluster, there is likely more

than one captured object which, everything else equal, tends to make results with CrV =1, 2 and 3 similar. For some populations, the effect of CrV is stronger and interacts with PSF. Examples of this are TR, SIM3 and SIM4 which exhibit fairly similar spatial patterns (c.f. Figure 3.14).

The absolute gain in precision of estimated density from the adaptive plot design is highest for the compactly clustered populations SIM1 and SIM2, and lowest for the scattered clusters in population SIM5 and SIM6. For the statistical performance, the choice of PSF is generally much more critical than the choice of CrV, the one exception is SIM1 with very compact clusters.

Table 4.3 Average percentage of expanded plots in the seven study populations SIM1-SIM6 and TR. The initial plot radius is 15m (from Yang et al., 2009).

CrV	Percentages of expanded plots						TR: Mapped real population of <i>Tamarix ramosissima</i>
	SIM1 $\lambda=5\text{m}$	SIM2 $\lambda=10\text{m}$	SIM3 $\lambda=20\text{m}$	SIM4 $\lambda=30\text{m}$	SIM5 $\lambda=100\text{m}$	SIM6 $\lambda=100\text{m}$	
1	7.13	10.72	19.65	31.00	83.25	81.70	24.10
2	6.91	10.07	17.90	26.76	65.64	64.74	19.16
3	6.74	9.52	16.56	23.67	48.61	50.90	16.83

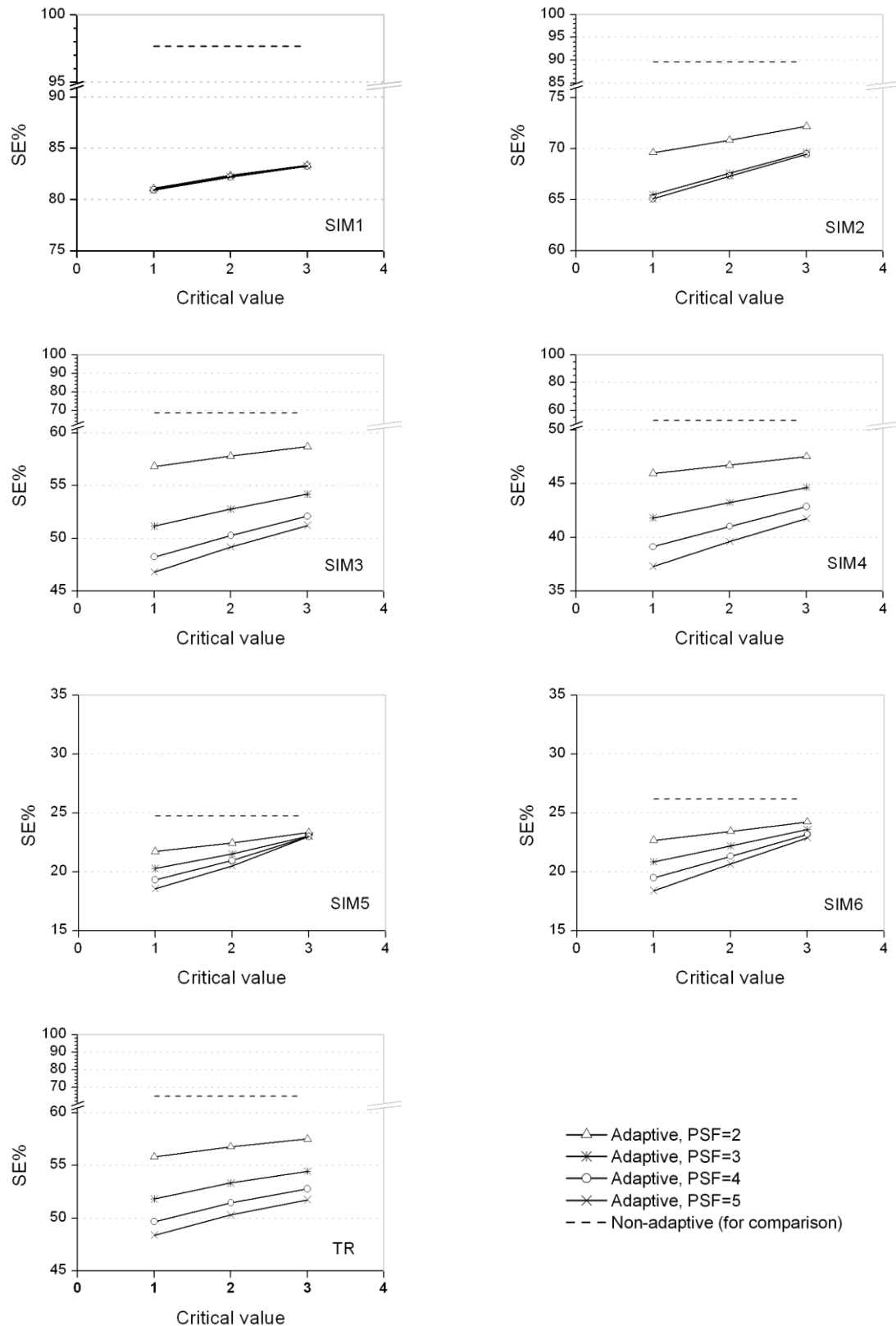


Figure 4.9 SE% of the N/ha estimates under plot design I on the basis of an equivalent sample size for the seven study populations SIM1-SIM6 and TR for CrVs between 1 and 3 and PSFs from 2 to 5. Initial sample plot radius was $R=15\text{m}$. For comparison, results for non-expanded initial plots are given as a horizontal dashed line (from Yang et al., 2009).

The results on the basis of equivalent sampling efforts are illustrated in Figure 4.10. It is found that: (1) the adaptive designs still lowers the SE% for the compactly clustered populations SIM1-SIM3 and the real population TR, and their absolute gain in reducing the SE% decreases with increasing CrV and is higher for SIM1 and SIM2 than for SIM3 and TR; and (2) the SE% for the nonadaptive plot designs is smaller in general for the population SIM4-SIM6.

As expected, the comparable sample sizes for SRS decrease with increasing CrV, as seen in Table 4.4. The CrV has a stronger effect on the comparable sample size for SRS for the populations with large clusters, e.g. SIM5 and SIM6 than for those with small clusters. That gives the reason why the nonadaptive designs with comparable sample sizes turn out to be more statistically efficient than their adaptive counterparts.

Table 4.4 Comparable sample sizes for SRS from the adaptive plot designs with the CrV in the range of 1 to 3 for the PSFs from 2 to 5 for the populations SIM1-SIM6 and TR.

PSF	CrV	Comparable sample size for SRS						
		SIM1	SIM2	SIM3	SIM4	SIM5	SIM6	TR
2	1	21.43	22.14	23.93	26.20	36.65	36.34	24.82
	2	21.38	22.01	23.58	25.35	33.13	32.95	23.83
	3	21.35	21.90	23.31	24.73	29.72	30.18	23.37
3	1	22.85	24.29	27.86	32.40	53.30	52.68	29.64
	2	22.76	24.03	27.16	30.70	46.26	45.90	27.66
	3	22.69	23.81	26.63	29.47	39.45	40.36	26.73
4	1	24.28	26.43	31.79	38.60	69.95	69.02	34.46
	2	24.14	26.04	30.74	36.05	59.39	58.84	31.50
	3	24.04	25.71	29.94	34.20	49.17	50.54	30.10
5	1	25.70	28.57	35.72	44.80	86.60	85.36	39.28
	2	25.52	28.06	34.32	41.40	72.51	71.79	35.33
	3	25.39	27.61	33.25	38.94	58.89	60.72	33.46

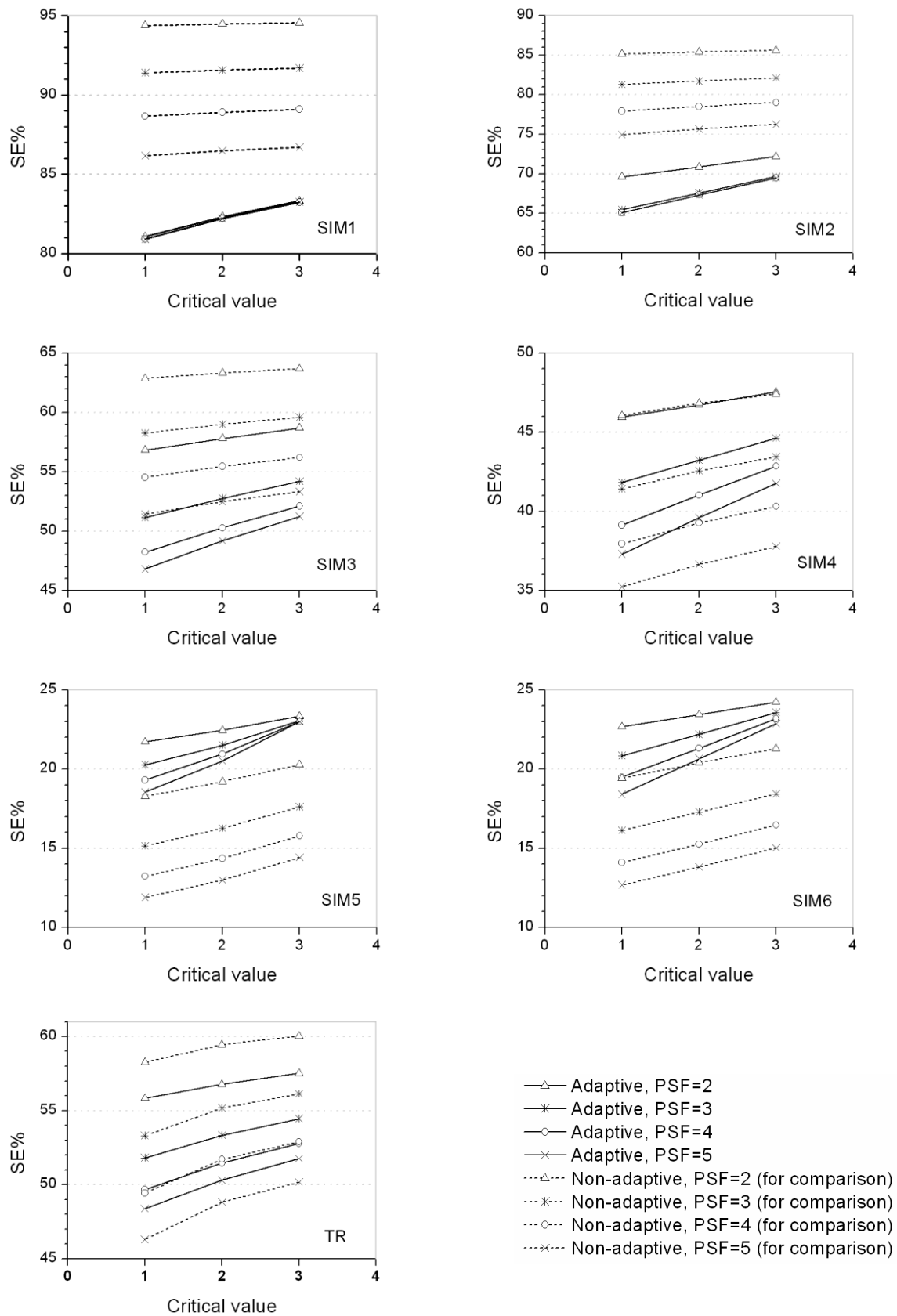


Figure 4.10 SE% of the N/ha estimates under plot design I on the basis of equivalent sample efforts for the seven study populations SIM1-SIM6 and TR for CrVs between 1 and 3 and PSFs from 2 to 5. Initial sample plot radius was $R=15m$.

4.2 RESULTS FROM PLOT DESIGN II

4.2.1 Comparison among different spatial patterns

The results from an equivalent sample size for the four populations with distinct spatial patterns SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} are presented in Figure 4.11, which demonstrates: (1) the adaptive plot design lowers the variability of SE% greatly only for the clustered

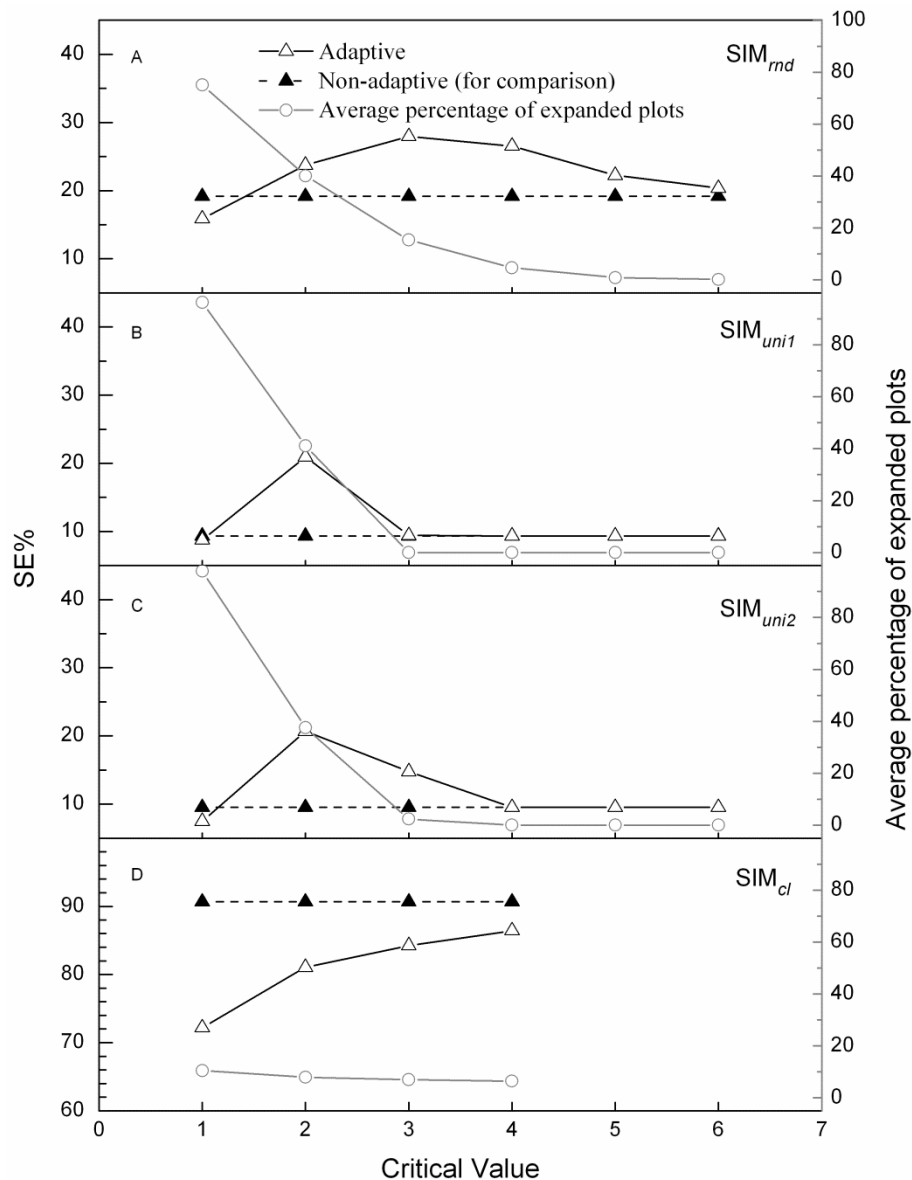


Figure 4.11 SE% of the N/ha estimates and average percentages of expanded plot under plot design II for four study populations with different spatial patterns on the basis of an equivalent sample size of $n=20$: SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} . The initial plot radius $R=15m$, and the subplot distance $D=30m$.

population SIM_{cl} in the entire considered range of CrV from 1 to 4 but with a low and slightly varying average percentage of expanded plots; (2) the adaptive plot design lowers the variability of SE% very slightly only at the CrV of 1 but with a very high average percentage of expanded plots for the three nonclustered populations, SIM_{rnd} , SIM_{uni1} and SIM_{uni2} , especially for the last two, where the average percentage of expanded plot is nearly 100%; (3) a sharp increase and subsequent decrease in SE% occurred to the two uniform populations accompanies a sharp decrease in the average percentage of expanded plots in the lower range of CrV around 2 ; (4) the average percentage of expanded plots under the adaptive plot design decreases to zero at the CrV of 3 and 4 for the two uniform populations, SIM_{uni1} and SIM_{uni2} respectively, which implies that the adaptive design is reduced to the nonadaptive design there as the condition to expand the plot was not fulfilled at any plot location. However, the zero average percentage of expanded plots is not found in the presented range of CrV from the random population SIM_{rnd} , and the clustered population SIM_{cl} , although at the CrV of 6, the observed average percentage of expanded plots is slightly higher than zero; (5) the variability of the average percentage of expanded plots under the adaptive plot design with CrV observed from the clustered population SIM_{cl} is substantially lower than that from the three nonclustered populations.

For the population SIM_{cl} , the values of SE% under the adaptive plot design for the CrV of 5 and 6 is not available simply because their computation turned out to be too time-consuming with the algorithm in use and finally had to be given up.

The results on the basis of equivalent sampling efforts are given Figure 4.12 : (1) the SE% for the nonadaptive plot designs gets larger with increasing CrV, which reflects the decrease of the comparable sample sizes with increasing CrV as well, as shown in Table 4.5; (2) for the three nonclustered populations, the SE% for the adaptive designs is never smaller than that for the nonadaptive designs in the considered range of CrV; (3) no difference in SE% among plot designs exists any more from a certain level of CrV for the two uniform populations SIM_{uni1} and SIM_{uni2} ; and (4) for the clustered population SIM_{cl} , adaptive design lowers the SE% only at the CrV of 1 and thereafter its loss in estimation precision occurs, and gets heavier with increasing CrV. However, the loss is very slight at the CrV of 2.

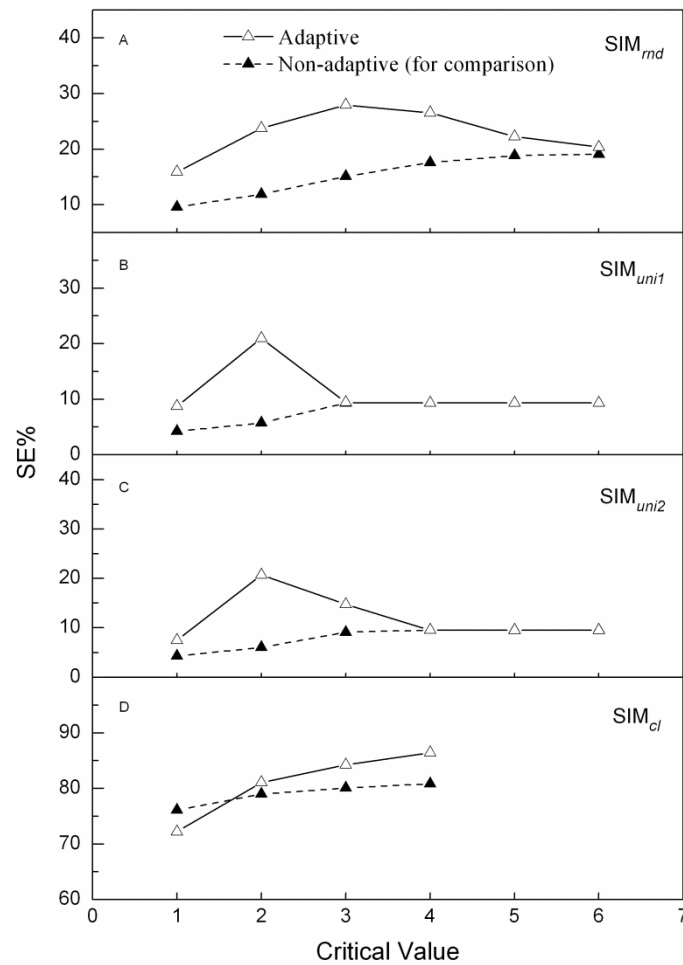


Figure 4.12 SE% of the N/ha estimates under plot design II on the basis of equivalent sampling efforts for four study populations with different spatial patterns: SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} . The initial plot radius $R=15m$, and the subplot distance $D=30m$. The sample size given to all adaptive designs is $n=20$.

Table 4.5 Comparable sample sizes for SRS from the adaptive plot designs with CrV ranging from 1 to 6 for the populations SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} .

CrV	Comparable sample size for SRS			
	SIM_{rnd}	SIM_{uni1}	SIM_{uni2}	SIM_{cl}
1	80	97.0	98.3	28.4
2	52.1	52.9	50.0	26.36
3	32.3	20.0	21.9	25.7
4	23.8	20.0	20	25.2
5	20.7	20	20	--
6	20.1	20	20	--

4.2.2 Subplot distance

The results from an equivalent sample size for the subplot distance D are given in Figure 4.13. It can be seen: (1) the adaptive plot design lowers the values of SE% for all the considered populations, but in different manners as the subplot distance D became larger; (2) the SE% under the adaptive plot design gets higher with increasing distances at a diminishing rate for SIM1 and SIM2, but at a slightly growing rate for SIM3, SIM4 and TR. But it decreases with increasing distances at a very slightly diminishing rate for SIM5 and SIM6; (3) for SIM1 and SIM2, it levels off at the distance of 40m and 45m respectively, where the difference in SE% from both considered designs vanishes or almost vanishes. Such a levelling off is not found from the other clustered populations, where the SE% from the adaptive plot design is always smaller than that from the nonadaptive plot design; and (4) the average percentage of expanded plots is independent of the distance between a subplot centre and its associated initial sample point for a particular population. It is remarkably lower for SIM1-SIM4 and TR than that for SIM5 and SIM6, which have an average percentage of expanded plots higher than 80%.

The results from equivalent sampling efforts are depicted in Figure 4.14: (1) for the most compactly clustered population SIM1, the real population TR and the three loosely clustered populations SIM4-SIM6, the SE% for the adaptive designs is higher than that for the nonadaptive designs over the considered range of the subplot distance. The differences in SE% remain constantly obvious for SIM5 and SIM6 over the entire range of the subplot distance D , but very slight for the non-loosely cluster populations SIM1, SIM4 and TR at the smallest subplot distance of $D=30\text{m}$; (2) for the populations SIM2 and SIM3, the SE% from the adaptive designs is smaller in a certain lower range of the subplot distance D , and gets gradually equal to and then larger than that from the nonadaptive designs, with increasing subplot distance.

The comparable sample sizes for SRS from the adaptive plot designs do not depend on the subplot distance D , as seen in Table 4.6.

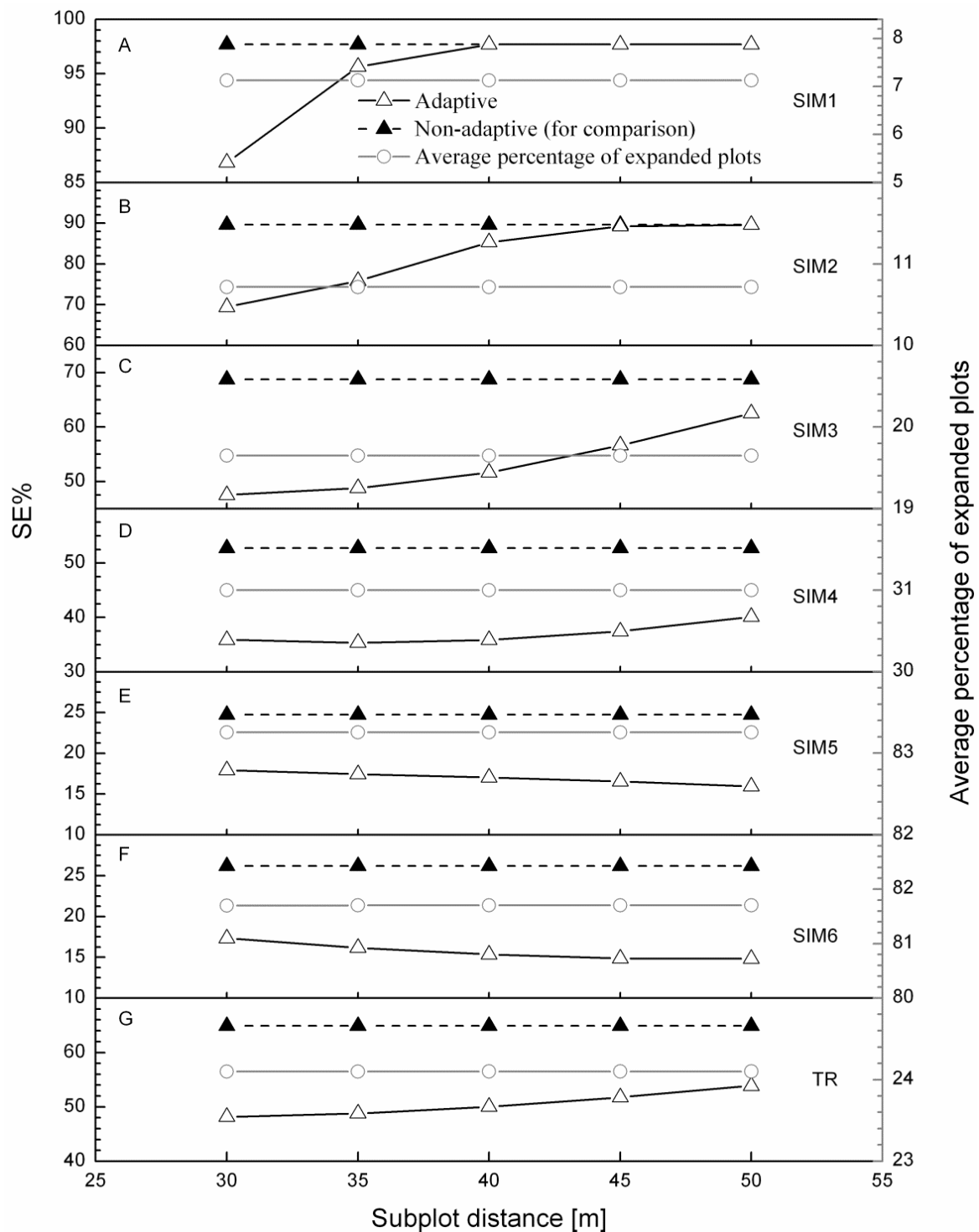


Figure 4.13 SE% of the N/ha estimates and averaged percentages of expanded plots on the basis of an equivalent sample size for the seven study populations SIM1-SIM6 and TR. The initial sample plot radius was $R=15\text{m}$ and the CrV was 1.

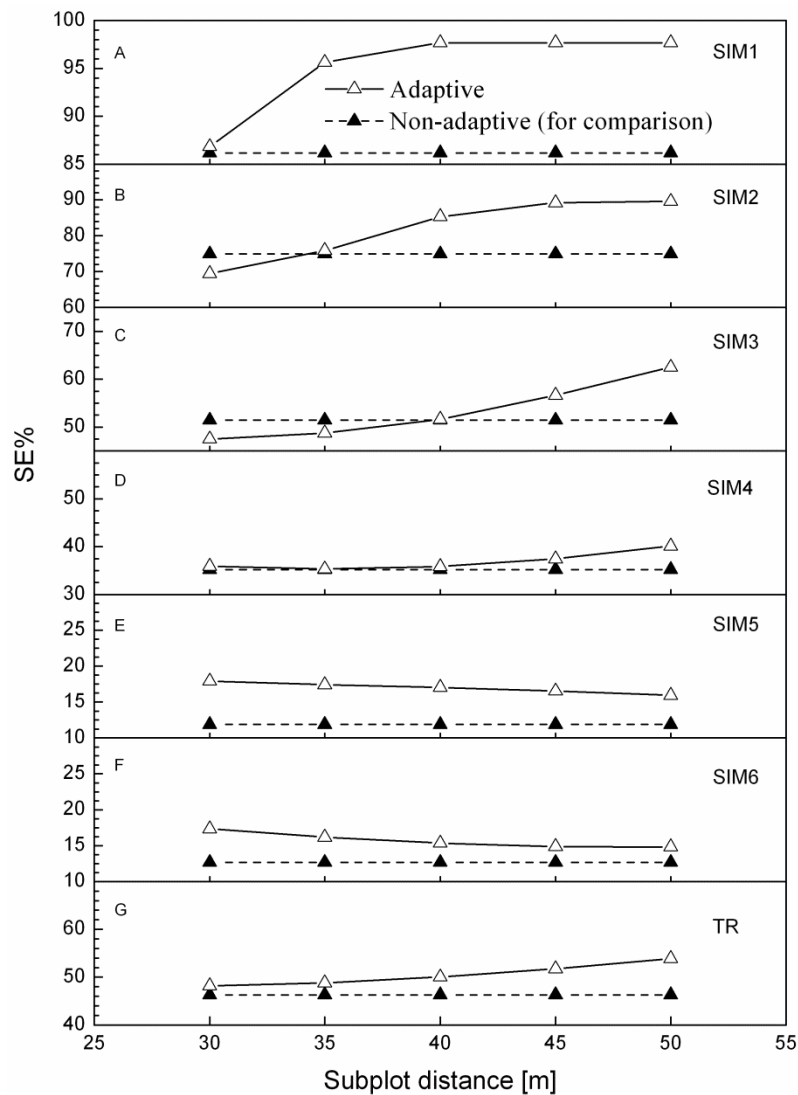


Figure 4.14 SE% of the N/ha estimates under plot design II on the basis of equivalent sampling efforts for the seven populations SIM1-SIM6 and TR. The initial sample plot radius was $R=15\text{m}$ and the CrV was 1.

Table 4.6 Comparable sample sizes for SRS for the populations SIM1-SIM6 and TR. The settings for the adaptive designs are the same as seen in Figure 4.13.

Populations	Comparable sample size for SRS
SIM1	25.7
SIM2	28.6
SIM3	35.7
SIM4	44.8
SIM5	86.6
SIM6	85.4
TR	39.3

4.2.3 Critical value

The SE% and average percentage of expanded plots with CrV ranging from 1 to 3 for four predefined subplot distances for the real population is illustrated in Figure 4.15. The results from an equivalent sample size illustrate: (1) the SE% under the adaptive plot designs is lower than that under their nonadaptive counterparts (horizontal line in Figure 4.15); (2) the SE% increases slightly with increasing CrV for each of the four given distances D ; (3) the distance D has stronger effect on the SE% than CrV when D is high enough, for instance, when D is increased from 30m to 50m; and (4) the average percentage of expanded plots under each adaptive plot design is not related to the subplot distance D , but depends on the CrV. It decreases with increasing CrV at a slightly diminishing rate.

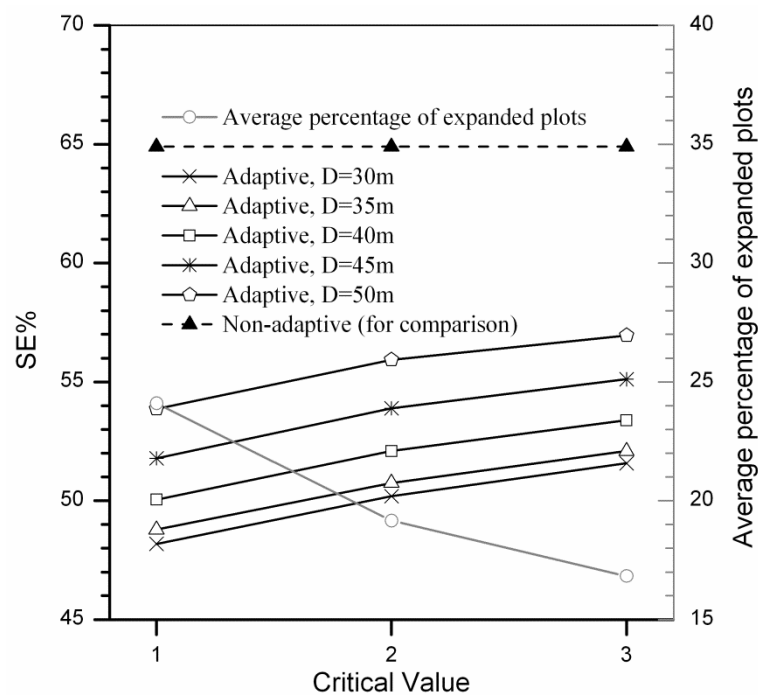


Figure 4.15 SE% of the N/ha estimates under plot design II for the plot designs with an equivalent sample size for the real population, TR. The initial sample plot radius is $R=15m$, and the subplot distance is $D=30m$.

Figure 4.16 shows the results from equivalent sampling efforts. It can be found that: (1) the SE% for nonadaptive designs is constantly lower than that from the adaptive designs over the entire considered range of CrV; (2) the SE% for the nonadaptive designs gets higher with increasing CrV, which is very similar to the trends observed from the adaptive designs. The comparable sample sizes related to the CrVs are given in Table 4.7.

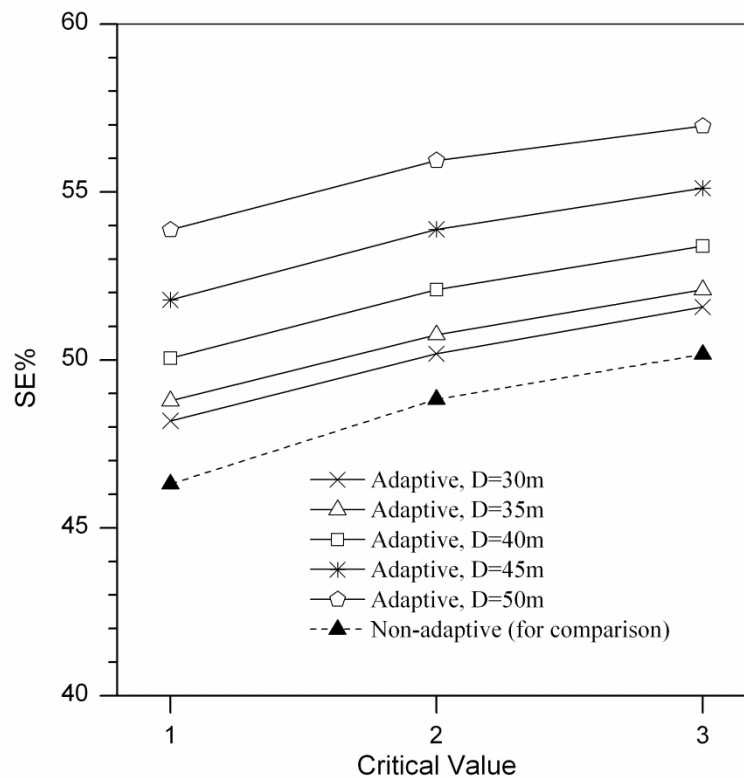


Figure 4.16 SE% of the N/ha estimates under plot design II on the basis of equivalent sampling efforts for the real population TR, for sample size $n=20$. The initial plot radius $R=15\text{m}$, and the subplot distance $D=30\text{m}$

Table 4.7 Comparable sample sizes for SRS from the adaptive plot designs with CrV ranging from 1 to 3 for the real population TR. The initial sample plot radius is $R=15\text{m}$ and the subplot distance is $D=30\text{m}$.

CrV	Comparable sample size for SRS for the population TR
1	39.28
2	35.33
3	33.46

4.3 RESULTS FROM PLOT DESIGN III

4.3.1 Comparison among different spatial patterns and critical value

The results for the four populations with distinct spatial patterns SIM_{rnd} , SIM_{uni1} , SIM_{uni2} and SIM_{cl} , to which plot design III is applied to estimate the basal area per ha, are presented in Figure 4.17.

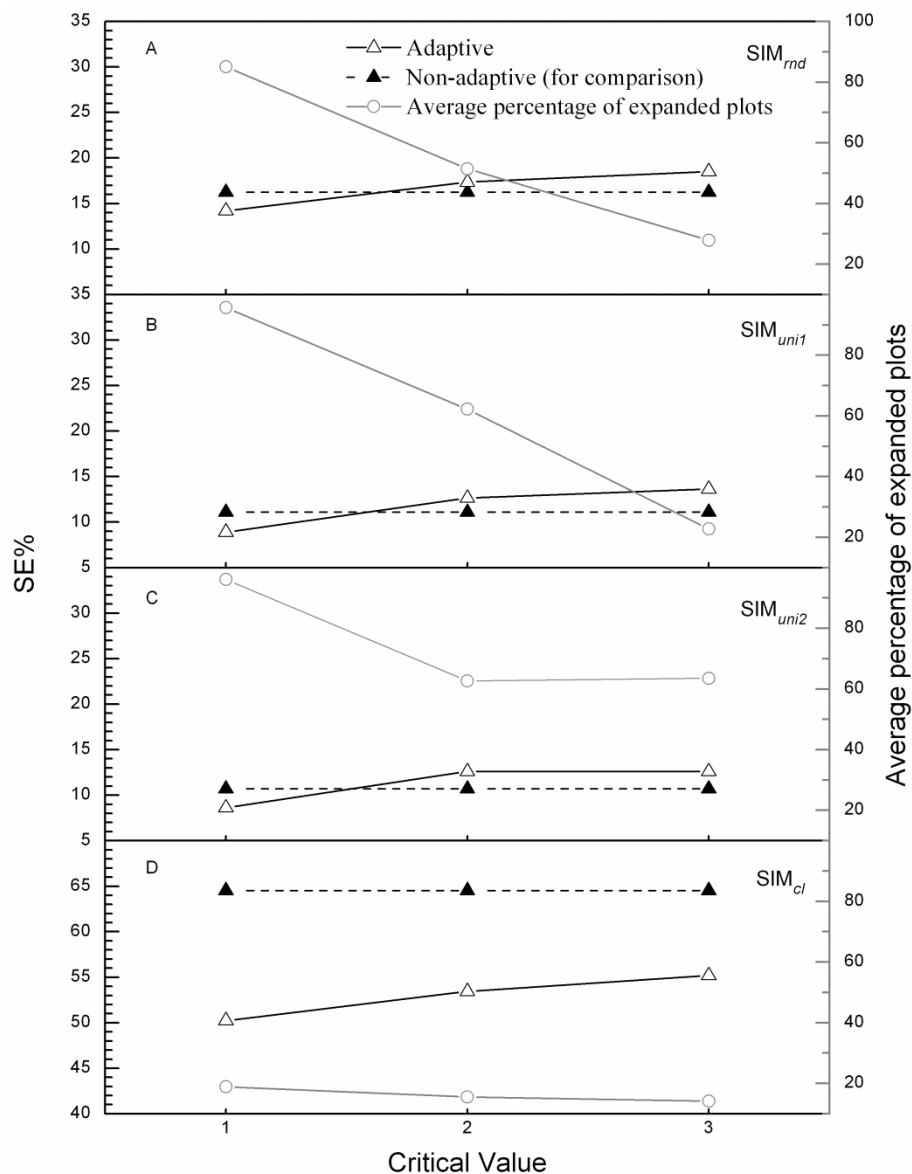


Figure 4.17 SE% of the G/ha estimates under plot design III on the basis of an equivalent sample size and averaged percentages of expanded plots for the four populations with distinct spatial patterns, SIM_{rnd} , SIM_{uni1} , SIM_{uni2} , and SIM_{cl} . The initial BAF was 2 and the final BAF was 1, and $n=20$.

It is found: (1) the adaptive plot design reduces the variability of SE% greatly only for the clustered population SIM_{cl} in the range of CrV from 1 to 3, but with a very low and slightly varying average percentage of expanded plots; and (2) the adaptive plot design reduces the SE% very slightly only at the CrV of 1 but with a very high average percentage of expanded plots for the three nonclustered populations, which is 85% for SIM_{rnd} , 96% for SIM_{uni1} and SIM_{uni2} . But at the CrV larger than 1, the SE% from the adaptive plot design exceeds that from its nonadaptive counterpart with a considerably large drop of the average percentage of expanded plots. In order to be consistent with the expressions used for plot design I and II, the term “average percentage of expanded plots” continues to be used for plot design III, but means actually the average percentage of adapted initial BAF.

4.3.2 Plot size factor and initial BAF

The results for the role of the PSF are illustrated in Figure 4.18, from which the following is

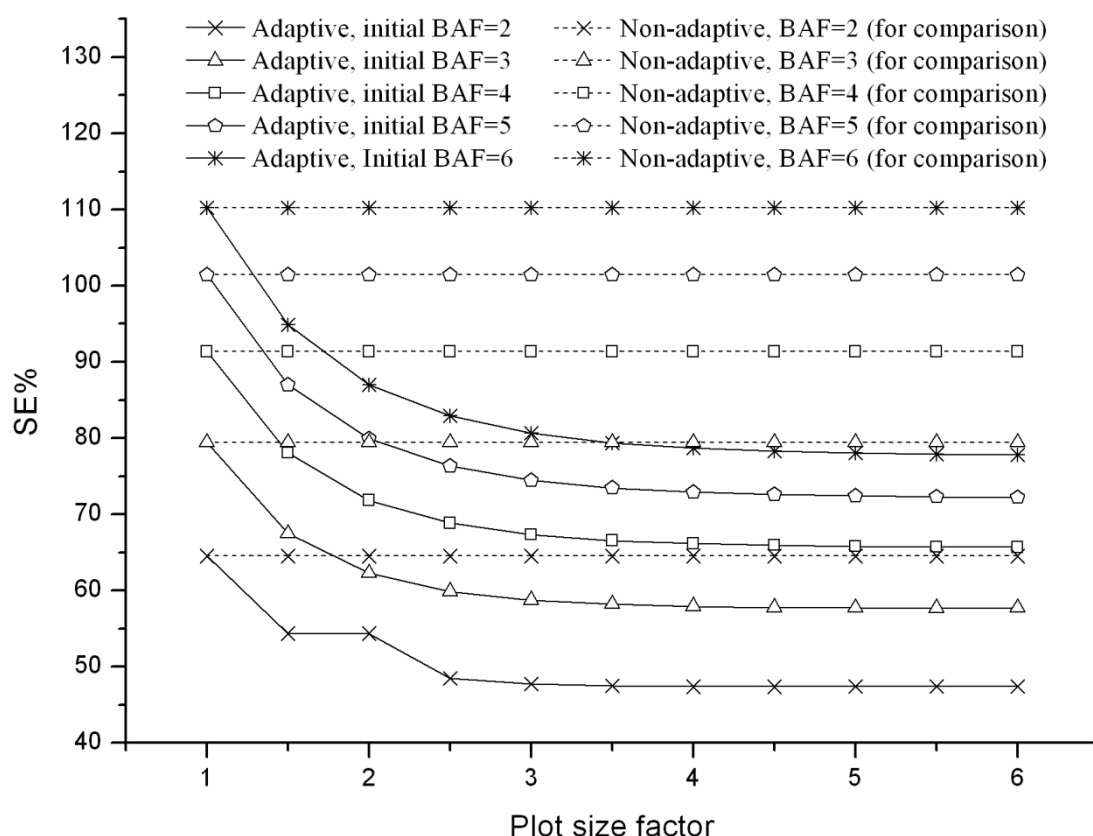


Figure 4.18 SE% of the G/ha under plot design III as a function of PSF for different initial BAFs in the case of CrV=1 for the population SIM_{cl} . The sample size is $n=20$.

found: (1) the small initial BAFs produce more precise estimates of G/ha as expected; (2) the adaptive designs reduce the variability in G/ha estimates for all PSFs larger than 1; (3) the values of the SE% decrease at diminishing rates with increasing PSF. The bigger the initial BAFs are, the lower is the SE% levels off. The PSF values at the leveling-off points of SE% are about 2.5, 3.5, 4, 4.5 and 5 for the initial BAFs of 2, 3, 4, 5 and 6 respectively and their corresponding final PSFs are 1.25, 1.17, 1, 0.9 and 0.83.

4.4 RESULTS FROM COMPARING PLOT DESIGN I AND II

Figure 4.19 shows the results of comparison between plot design I and plot design II on the common basis that both designs have the same sample size of $n=20$, the same initial sample plot radius of 15m, the same CrV of 1 and the same size of adapted initial sample plot ensured by defining the PSF for Plot design I to be 5. The subplot distance is set to 30m for plot design II because at that distance the populations under consideration except SIM5 and SIM6 have the lowest SE% as seen in Figure 4.13.

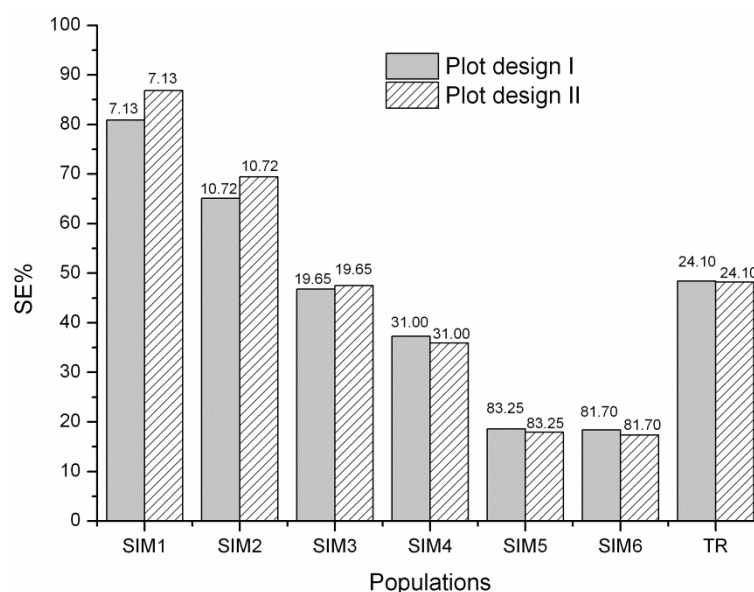


Figure 4.19 Comparison between plot design I and II. PSF for plot design I is 5, and the subplot distance D is set to 30m for plot design II. The average percentages of adapted initial sample plots from both designs for populations SIM1-SIM6 and TR are noted on the top of each column.

From Figure 4.19, it is observed that: (1) plot design I provides a noticeable lower SE% for the two compactly clustered populations SIM1 and SIM2 and a slightly lower SE% for the less compactly clustered population SIM3; (2) the SE% from plot design I is slightly larger than that from plot design II for the scattered or widely scattered populations SIM4-SIM6, and hardly larger for population TR; (3) both designs exhibit no difference in the average percentage of adapted initial sample plots for each considered populations here as they have the same size of initial sample plot and an equal CrV of 1.

5 DISCUSSION

Over the past several decades, a variety of adaptive sampling strategies have been developed. In this study, three easy-to-implement adaptive plot designs are proposed and their statistical performances are comparatively evaluated. The results demonstrate that the proposed plot designs are promising in general.

In this study, stratification of the test populations is assumed impossible for two reasons: (1) stratification of rare and geographically clustered populations is usually impossible and (2) if it is possible, conventional stratified random sampling is more efficient than conventional ACS (Christman, 2000). The results of the Monte Carlo simulation for plot design I with DSS mean estimator indicates that for a geographically clustered population the DSS mean estimator is negatively biased for plot design I. The magnitude of bias depends on PSF and initial plot size. The DSS mean estimator is a design-unbiased estimator. It implies that the unbiasedness of the DSS estimator depends not on the spatial pattern in a population to be sampled at all, but on the strict implementation of the DSS sampling procedure. Bias can be introduced even into any design-unbiased estimators by edge effect (Gregoire, 1982) if it is not or not appropriately corrected.

However, in this study, the edge effect across the population boundaries is believed to be appropriately corrected by the mirage method because the boundaries of the simulated population SIM_{dss} are straight with square corners, and definitely not a source of bias. That is confirmed by the unbiased mean estimates from the SRS estimator for the nonadaptive designs as seen in Figure 4.1. In addition, a slopover of some plots into neighboring strata in the stratified sampling will introduce bias if it is not correctly addressed. But it is not an issue for DSS at all as explicitly mentioned in Lam et al. (2010). All these suggest that the bias originates from the difference of plot design I from DSS in the sampling procedures.

From a DSS point of view, the initial sampling under plot design I serves the same purpose of estimating strata weights as the first-phase-sampling in DSS. The only difference between them is that the target variable rather than an ancillary variable is used to estimate the strata weights for plot design I. But that will not constitute a principal problem because the target variable can be imagined to be an ancillary variable sharing the same values with it. In essence, the initial sampling under plot design I is equivalent to the first-phase-sampling of DSS in terms of sampling design, plot design and estimation design as seen in Lam et al.

(2010), Chojnacky (1998), and Williams (2001). It is impossible that the bias is from the initial sampling for the estimation of the strata weights.

The standard sampling procedure in the second-phase of DSS is taking a subsample of the first-phase sample plots to observe the target variable for the derivation of strata estimates. The “subsample” here implies that the sizes of the first-phase-plots and the second-phase-plots, which is referred to as a support region (Williams, 2001) or a reference area (Lam et al., 2010) to derive the value of a point in an infinite/continuous population, should not be different to ensure the unbiasedness of the DSS estimators. However, the implied principle for the unbiasedness is obviously violated by the expanded plots under plot design I. The size difference issue between the plots of two phases was discussed with respect to the misclassification but not the bias in Lam et al. (2010), where the second-phase-plots for two strata are smaller than but still within the first-phase-plots.

The bias of the DSS estimator for plot design I can also be interpreted from the viewpoint of inclusion probability. In this study, the standard DSS estimator is used, which implies that all trees in the same stratum are assumed to have an equal inclusion probability. As a matter of fact, the inclusion probabilities of the trees under plot design I are different even for the trees in the same stratum, which can be seen very clearly from the inclusion zone concept illustrated in Figure 3.5.

The RMSEs from plot design I with the DSS estimator is systematically smaller than the standard error derived from SRS and decrease with increasing PSFs. But on the other hand, the bias increases with increasing PSFs as well. That can also be easily explained using the HT estimator based on the inclusion zone concept illustrated in Figure 3.5, where it can be seen directly that the area of the inclusion zone of a tree in a rare and geographically clustered population is mostly smaller than but seldom equal to that of the expanded plots. In the simulation with the population SIM_{dss} , the CrV for plot design I is set to 1. That means, the mean estimate for the stratum where the condition to adapt is not met equals always zero simply because no tree is found there. The mean estimate for the stratum with the condition to adapt satisfied is derived from the SRS mean estimator based on the expanded plots. That implies the area of the inclusion zone of a tree is assumed to equal that of the expanded plots. It is then clear that the assumed inclusion probabilities of most trees in the population are more or less larger than their actual inclusion probabilities under plot design I. As a consequence, the negative bias occurs. To be more specific, the replacement of the actual inclusion probabilities with the assumed inclusion probabilities introduces the bias, and the

cause for the bias to be negative is that the assumed inclusion probabilities are mostly larger but never smaller than the actual inclusion probability.

The increase of the bias with increasing PSFs is because the assumed inclusion probabilities have a higher rate of increase with increasing PSFs than the actual inclusion probabilities.

The comparison based on the inclusion zone concept for HT estimator and the jigsaw puzzle approach for plot design I shows that plot design I is superior to sampling with the non-expanded initial plots on the basis of an equivalent sample size in all considered cases, especially for the clustered populations as demonstrated in Figure 4.4. Yet the relative performance for a clustered population depends (1) on the PSF, (2) on the CrV and above all (3) on the degree of clustering of the target objects in the study populations, as demonstrated in Figure 4.9: for more widely scattered clusters, as in populations SIM5 and SIM6, the precision of sampling with nonadapted initial plots is only slightly less than for the adaptive plot design. However, in compactly clustered populations the adaptive design suggests a potential of improvements in precision without encumbering field work by complex, impractical and time-consuming plot-expansion rules as typically seen in conventional ACS designs (Smith et al., 2003; Su and Quinn II, 2003; Turk and Borkowski, 2005), but at the cost of measuring positions of all sampled trees and their relevant neighbors.

The number of expanded plots under plot design I can be controlled, to a certain extent, by the choice of CrV: a higher CrV triggers fewer expansions (Table 4.3). Taking into account that the loss in precision by using a CrV of 2 or 3 is expected to be minor (Figure 4.9), one might choose a CrV larger than 1. Choosing a suitable CrV is also a strategic issue for the classic adaptive plot design (Brown, 2003).

The comparison made between plot design II and its nonadaptive counterpart on the basis of an equivalent sample size demonstrates that plot design II outperforms its nonadaptive counterpart, but only for the spatially clustered populations as seen in Figure 4.11 and Figure 4.13. The sharp increases of SE% occurred to the populations SIM_{uni1} and SIM_{uni2} with CrV varied from 1 to 2 are resulted from the sharp decreases in the average percentage of expanded plots due to the larger CrV. The sharp decreases in the average percentage of expanded plots implies that only a smaller proportion of trees have their inclusion probabilities increased and the others not. That is to say, the ratios used in the HT estimator remain unchanged for most trees, but decrease for the trees with its inclusion probabilities still increased with the CrV of 2. Hence, the variabilities in terms of SE% increase.

As shown in Figure 4.13 and Figure 4.15, for a clustered population, its comparative performance is affected by: (1) the subplot distance D ; (2) the CrV and in particular, and (3) the degree of clustering of the target objects in the populations of interest. For the compactly clustered populations, the distance D of two times the initial plot radius is recommended. As a result, the four adaptively added subplots are tangent with the initial sample plot. For the populations with widely scattered clusters as SIM5 and SIM6, an increase in distance D to have distant adaptive subplots brings very limited gain in precision with a side effect of more travel time to the adaptive subplots. Plot design II is rather similar to plot design I in the influencing of the CrV and the degree of clustering on sampling precision as well as the fashion to control the number of expanded plots.

From a geostatistical point of view, it may be better to have subplots of a cluster plot settled far away from each other for a better precision with respect to spatial autocorrelation. It follows that design II would be expected to be more efficient than design I, since the expanded plots under plot design I are still single compact plots unlike the cluster plots under plot design II. However the comparison made between plot design I and II as seen in Figure 4.19 shows, interestingly, for the compactly clustered populations, plot design I turns out to be statistically more efficient. For the less compactly clustered population, plot design I produces only slightly more precise estimates. Even for the populations with widely scattered clusters, plot design I is only slightly less efficient than plot design II. Furthermore, from a practical point of view, the field installation of the adaptively expanded plots under plot design I is much easier than that of the adaptive cluster plots under plot design II since the positioning of the centers of subplots and relevant tree search circles costs additional time. Therefore, plot design I is preferable to plot design II for sampling rare and geographically clustered populations.

The comparison made for plot design III on the basis of an equivalent sample size demonstrates that plot design III is statistically more efficient only for sampling rare and spatially clustered populations than its nonadaptive version and its performance depends on the CrV and the PSF as seen in Figure 4.17 and Figure 4.18. As in plot design I and II, the CrV serves to control the average percentage of adapted sample points. The choice of CrV among 1, 2 and 3 is actually an issue of trade-off between more sampling effort and more gain in precision. However, this needs to be confirmed with more clustered populations in addition to SIM_{cl}.

The adaptation under plot design I, II and III means that more time is needed for making additional field observations; time that could be equally devoted to a larger nonadaptive sample size, namely a comparable sample size on the basis of an equivalent sampling effort as seen in the tables from Table 4.1 to Table 4.7. The comparison made for plot design I and II on the basis of equivalent sampling efforts as seen in Figure 4.5, Figure 4.8, Figure 4.10, Figure 4.12, Figure 4.14, and Figure 4.16 provides another insight into their statistical performances, which shows clearly that plot design I and II are efficient exclusively for sampling the clustered populations. However, in most forest inventories especially large area forest inventories, considerable time is spent in moving between sample locations. If a modest increase in the time spent on a single sample location is necessary to complete an expanded plot, the increase in total inventory time may not be a concern. The results obtained from this study only allow a rough estimation of the additional efforts: If determination of the coordinates of an object takes a fixed amount of time, and the number of objects to measure is proportional to the observed area, the additional time requirement can be obtained from the percentage of expanded plots as seen in the presented cost functions.

For any complex plot design that derives inclusion probabilities from inclusion zones (e.g. Kleinn and Vilčko, 2006) the challenge is to find an efficient and fast numerical procedure that is geometrically correct. Determination of inclusion zones may, for example, be made easier by survey techniques that allow a rapid mapping of tree positions or models that can predict the inclusion zones from easy and rapidly observable features in a field plot. In this study the actual inclusion probabilities are derived analytically in a GIS environment, so that field work is restricted to the determination of polar coordinates of relevant trees. The determination of relevant trees is relatively easy under plot design I and II, but conspicuously difficult under plot design III because it is impossible to define a fixed relevant tree search area.

This study provides some insights to three new easy-to-implement adaptive plot designs for sampling sparse yet spatially clustered populations. They can be expected to be a viable alternative to the conventional ACS if it conserves most of the statistical efficiency attributed to ACS, as a cumbersome open-ended field work is excluded. It is obvious that overall efficiencies of these designs and the conventional ACS design vary from case to case, and thus a direct analytic comparison between them simply based on the variance estimator is impossible. Which plot design is preferable depends on the actual conditions and cannot be answered in general.

6 CONCLUSION

The standard DSS estimator for the mean as used for plot design I in the manner presented in this study is negatively biased.

The proposed three adaptive plot designs are superior to their nonadaptive counterparts in sampling rare and geographically clustered populations. However, effort for estimation is problematic. Their statistical performances depend on the degree of clustering the population of interest and the settings of their design factors including initial plot size, CrV, PSF (only for plot design I and III), and subplot distance (only for plot design II). The subplot distance equal to the sample plot diameter produces the best performances for the rare and spatially clustered populations.

Plot design I is preferable to plot design II in terms of sampling efficiency, flexibility in the choice of final sample plot size and easy field implementation for sampling rare and geographically clustered populations.

Further simulation studies with populations of different degrees of spatial clustering are needed for plot design III to have a comprehensive insight into the influences of clustering on its performance.

7 SUMMARY

In ecological systems, rare species have great importance to biodiversity monitoring and conservation. Many of them are not only numerically rare, but also geographically clustered, and do not allow statistically meaningful stratification. For such populations, the efficiency of nonadaptive designs with a predefined number of n sample plots is low because of many “empty plots”.

Adaptive cluster sampling (ACS) was introduced as a strategy to address that challenge and is generally considered to be superior to conventional sampling techniques. Many studies on it have been carried out, ranging from the development of ACS designs to the appropriate configuration of design factors and their practical application. The major developments and related key issues in ACS since its introduction are reviewed in chapter two of this dissertation for reference in choosing an appropriate ACS design and estimators.

ACS has not yet been used on a routine basis in field surveys due to its disadvantages leading to practical difficulties in field survey design and implementation. In this methodological study, three new and more practical adaptive plot designs, referred to as plot design I, II and III, are introduced and compared with their nonadaptive counterparts with an overall objective to improve the efficiency of sampling rare and geographically clustered populations in forest inventories and ecological surveys. The proposed designs are based on a simple and practical approach of “conditional one-off expansion of initial plots”; thereby their adaptation processes need not to be conducted in a time-consuming and error-prone sequential fashion as seen in the conventional ACS design. For simplicity, only circular plots are used in the study as an example.

In plot design I, two plot sizes need to be predetermined, one small for the initial plots and the other large but fixed sized for the expanded plots whenever a predefined condition to adapt is satisfied. The size of the expanded plots is expressed in terms of a plot size factor (PSF), which indicates how much larger the area of an expanded plot is in relation to that of an initial plot.

In plot design II, an initial sample of single compact and fixed-area plots is installed, and each initial plot expands to a fixed-area cluster plot whenever the condition to adapt is met. Each cluster plot consists of five compact subplots: an initial sample plot and four additional plots installed at a predefined subplot distance in the NW, NE, SW and SE direction of the initial sample plot respectively.

Plot design III is an adaptive version of relascope sampling, and a PSF for the imaginary plots are predefined alternatively in terms of a final basal area factor (BAF) larger than a predefined initial BAF. Under plot design III, an initial relascope sample is selected with the initial BAF, and the final BAF will be used to repeat the relascope sampling once more at each sample point where the condition to adapt is satisfied.

The three plot designs are proposed based on the strategy of unequal probability sampling. Under them, a population unit with other units nearby has a higher inclusion probability than an isolated unit or a unit with fewer neighbors since the selection of a neighboring unit in an initial plot may lead to the selection of that particular unit finally in the sample. Therefore, the standard technique used in fixed-area plot sampling to extrapolate the per-plot observations to per-hectare values is inappropriate for them to produce design-unbiased estimates.

In this study, the estimation design adopts the infinite population approach, which considers the dimensionless points in the area of interest as sampling elements. Under this approach, the construction of design-unbiased estimators for various plot designs is straightforward, so that the Horvitz-Thompson (HT) estimator framework can be applied directly once the inclusion probabilities of sample units are computed. The inclusion probability of a population unit is derived from its inclusion zone, which depends on the initial plot size, PSF (for plot design I and III), subplot distance (for plot design II), the condition to adapt in terms of a critical value (CrV), and the degree of clustering of that population. In addition, the initial sample points are selected by simple random sampling (SRS) in order to meet the prerequisite of a probabilistic sampling.

In addition to the HT estimator for the population total, the mean estimator for double sampling for stratification (DSS) is also tried, but only for plot design I. The initial sample, which serves the same purpose as the first-phase sample in DSS, is stratified into two strata, one where the observations of the target variable are less than the CrV (stratum 1) and the other where they are not (stratum 2). The estimated means for stratum 1 and stratum 2 are derived using the SRS mean estimator from the initial plots in stratum 1 and the expanded plots respectively.

The cost function for each adaptive plot design is developed from a cost function for SRS. All costs are expressed in terms of time and broken down into three categories: average time requirement for the round trip between the camp and the inventory region, for the field

measurement of the target variable, and for the collection of the relevant neighbors of the sample units.

The traditional Monte-Carlo simulation of a large number of random samples and the jigsaw-puzzle approach based on the concept of inclusion zones are employed for the evaluation of the statistical performances of the considered adaptive plot designs and their nonadaptive counterparts. The former is used for the approximation of the root mean square error (RMSE) of the estimates from plot design I with the DSS mean estimator, the latter for the direct computation of parametric relative standard error (SE%) of the estimates from all three plot designs with the HT estimator. The parameter to be estimated is the number of stems per hectare (N/ha) for plot design I and II, and the basal area per hectare (G/ha) for plot design III.

One real and eleven artificial populations are used to reveal whether the proposed designs are exclusively more efficient for sampling rare and geographically clustered populations than their nonadaptive counterparts as expected and investigate the effects of the adaptive design factors and the degree of clustering of the population on the statistical performances of different adaptive plot designs. The simulated clustered populations are generated from a variation of a Poisson cluster process.

The results from the traditional Monte-Carlo simulation for plot design I show: (1) the simulation means of the estimates from the DSS mean estimator for the adaptive designs with $CrV=1$ decrease with increasing PSFs ($PSF \geq 1.5$) for a particular initial plot size and increase with growing initial plot size for the given $PSF=2$, but are always lower than the parametric value and those from their nonadaptive counterparts; (2) the RMSEs from the adaptive designs are consistently smaller than the estimated standard error from their nonadaptive counterparts.

The results from the jigsaw-puzzle approach on the basis of an equivalent sample size of $n=20$ demonstrate that the adaptive designs lower the SE% considerably with the low average percentages of expanded plots for the clustered populations, and only slightly for the random and uniform populations but with the high average percentages of expanded plots. For the considered clustered populations, it is also shown for the adaptive designs that (1) a larger initial plot size produces less variability as expected; (2) the SE% increases with growing CrV ; (3) the SE% is reduced when PSFs larger than 1 for plot design I and III. It decreases with increasing PSF and levels off at a certain point in general; (3) for plot design II, the SE% in the case of $CrV=1$ increases with growing subplot distance, and the point of leveling-off occurs only to the two compactly clustered populations; (4) on a comparable basis, plot

design I produces a noticeable lower SE% than plot design II with its subplot distance equal to the diameter of the initial sample plot for the two compactly clustered populations. Only slight differences in SE% are observed for the other considered populations.

The adaptation under plot design I, II and III means that more sampling effort is needed for making additional field observations. The results from the jigsaw-puzzle approach on the basis of an equivalent sample effort measured in terms of the total area of sample plots for plot design I with its PSF larger than 1 and plot design II with its subplot distance equal to the initial plot diameter illustrate that the SE% from either of them is mostly lower and seldom slightly higher for the populations with their clusters not widely scattered. The comparable sample size for SRS depends on the initial plot size and CrV, and on PSF for plot design I as well.

It is concluded from this study that: (1) the DSS mean estimator used for plot design I in the manner of this study is negatively biased. The reason is that the objects in the population of interest have unequal probabilities to be included in the sample, but the SRS mean estimator is used to derive the strata mean estimates for the estimation of the population parameter; (2) the proposed three adaptive plot designs are superior to their nonadaptive counterparts in sampling rare and geographically populations, and their statistical performances depend on the degree of clustering the population of interest and the settings of their design factors including initial plot size, CrV, PSF (only for plot design I and III), and subplot distance (only for plot design II); (3) the subplot distance equal to the sample plot diameter for plot design II produces the best performances for the rare and spatially clustered populations; (4) plot design I is preferable to plot design II in terms of sampling efficiency, flexibility in the choice of final sample plot size and easy field implementation; (5) further simulation studies with populations of different degrees of spatial clustering are needed for plot design III to have a comprehensive insight into the influences of clustering on its performance.

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