DETERMINATION OF AN EFFICIENT SAMPLING DESIGN FOR RARE AND CLUSTERED POPULATION USING DESIGN BASED ESTIMATORS

MWANGI CHARLES WAMBUGU

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DECLARATION AND RECOMMENDATION

DECLARATION

This thesis is my original work and has not been submitted or presented for examination in any institution.

Signature: ____________________ **Date:__________________**

Mr. Mwangi Charles Wambugu
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RECOMMENDATION

This thesis has been submitted for examination with our approval as university supervisors.

Signature: ____________________ **Date: __________________**

Prof. Ali Islam
Department of mathematics
Egerton University

Signature: ____________________ **Date: __________________**

Dr. LukeOrawo
Department of mathematics
Egerton University

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DEDICATION

This work is dedicated to my dear parents Mr. and Mrs. JamesMwangi and my wife Janet.

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ABSTRACT

A sampling design that provides estimates of population mean and abundance with small variance is important to researchers. Estimates that are accurate even with minimal sampling efforts allow researchers to easily and confidently investigate rare populations. In the determination of efficient sampling design for rare and clustered population, mean square errors have been applied in many previous research works. However, this method only captures the variability of the estimator and fails to capture their reliability. This study obtained the interval estimates based on the design based estimators, the HT and HH estimators. The study examined the behavior of the Horvitz Thompson (HT) and Hansen Hurwitz (HH) estimators under the ordinary adaptive cluster sampling design (ACS) and adaptive cluster sampling with data driven stopping rule (ACS') design using artificial population that is designed to have all the characteristics of a rare and clustered population and another population that does not have those characteristics. The efficiency of HT and HH estimators were used to determine the most efficient design in estimation of population mean in rare and clustered population. The coverage probability confidence intervals of population mean based on HT estimators and the HH estimators were examined. Results of the simulated data show that the adaptive cluster sampling with stopping rule is the more efficient sampling design for estimation of rare and clustered population than ordinary adaptive cluster sampling.

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LIST OF ABBREVIATIONSAND ACRONYMS

ACS	Adaptive Cluster Sampling
ACS’	Adaptive Cluster Sampling with stopping rule
HH	Hansen Hurwitz
HT	Horvitz-Thompson
SRS	Simple Random Sampling
LL	Lower limit
UL	Upper limit
Neighborhood	The unit itself with adjacent units to the north, east, west and south
Rare	A characteristics that is not easy to reach
Clustered	Characteristics that occurs in groups

CHAPTER ONE

INTRODUCTION

1.1Background information

In research, efficiently sampling rare species is a challenging task. Conventional sampling designs may require substantial effort in order to achieve even moderate precision (Evans and Viengkham, 2001). Accurate estimates of abundance are often most needed for rare species. Adaptive cluster sampling is attractive because it can perform more efficiently than conventional designs for geographically rare, clustered populations (Gattone and Batista, 2010;Esha and Jesse, 2012). Adaptive cluster sampling is a sampling design that can be used to estimate the population parameters of interest for rare, clustered and endangered populations (Thompson, 1990).The sampling design is termed as adaptive if the samplingprocedure depends on the selection rather than the assumption of the population. The basic idea behind this sampling plan is to decide on an initial sample from a defined population by some probability sampling method such as simple random sampling and to keep on sampling within the vicinity of the units that satisfy the conditions that are defined. The requisites of adaptive cluster sampling design comprise of an initial selection of units, a condition that determines when additional units should be added to the sample from the neighborhood of that unit and a clear definition of the neighborhood of every unit.

There is an increase in sampling efficiency under Adaptive cluster sampling design (ACS) resulting in more precise estimates of the population mean. Adaptive cluster sampling leads to an increase in the number of observations of the target species that may result in more reliable estimates of other population parameters such as species richness in information, population composition and relative abundance (Smith *et al.,* 2003). These advantages are more evident in rare and clustered populations (Noon *et al.,* 2006).

The major disadvantage of adaptive cluster sampling in estimation of population parameters is the uncertainty of the final sample size. Much attention has been focused to limit the size of the final sample in ACS (Brown, 2003).However, prior knowledge of the population is required to limit the final sample size (Turki and Barkowski, 2005).

A restrictive adaptive cluster sampling was proposed to control sample size prior to sampling (Brown and Marley, 1998). ACS with stopping rule that determine when the sampling process is ended once an optimal sample size is obtained was proposed.Such a sampling criterion based on the data makes adaptive sampling more realistic by ensuring that neither too many nor too few adaptive units are sampled since the criterion for adaptive sampling changes at every stage of adaptive sampling (Su and Quinn,2003). Another ACS with stopping rule was proposed where the prior knowledge of the population is not required (Gattone and Battista, 2010).

If all units in the realized adaptive sample received equal weight, classical equal probability abundance estimators would be positively biased. Similarly under the classical based inferential approach, the unbiased estimators do not utilize all the information provided by the final sample of the design. The modified versions of the Horvitz-Thompson and Hansen-Hurwitz estimators could account for the unequal probabilities of selection imposed by the adaptive design (Thompson, 1990). These estimators are design-unbiased (they are unbiased without relying on any assumptions about the population). Although these estimators are unbiased they are not the best since they are not functions of sufficient statistics.

Better estimators, can be derived through the Rao-blackwell idea of taking conditional expectation of the estimator given the minimal sufficient statistics.Thompson did not present analytical expression for the Rao-blackwell estimator but only used the averages of the estimators over all the initial samples giving rise tothe obtained final sample. Various researchers have come up with different analytical expressions of the Rao-blackwell estimators. Another alternative mathematical formula for the two Rao-blackwell estimators derived by taking expected value of the usual estimators given sufficient statistics was provided by Dryver and Thompson (2005).

Efficiency of ACS is dependent upon the spatial distribution patterns of a given population being studied (Weigand*et al.,* 2007).According to him, efficiency of ACS of species that exhibit clustering in multiple spatial scales is dependent on the distribution pattern of the population.

1.2 Statement of the problem

Establishing an efficient sampling scheme for a rare and clustered population is a challenging task. Adaptive cluster sampling design has been shown to be an important design in sampling theory and estimation of parameters of rare, endangered and clustered population. Most researchers have determined the efficiency of adaptive cluster sampling designs and classical sampling designs by use of mean square errors of the estimators of population parameters obtained from either of the sampling designs. The mean square error just measure the variability and hence no indication of how likely it is that the value is close to the true population parameter. For a complete estimation of the population attribute of interest, confidence intervals are always recommended as they areable to present some indication of reliability of the estimators associated with confidence level. This study computed the estimates of population mean and constructed the confidence intervals using the samples obtained through ordinary adaptive cluster sampling design, and adaptive cluster sampling with data driven stopping rule design. The study also obtained the coverage probability of the confidence intervals on HT estimator and the HH estimators. The study compared the most efficient estimate of population mean and also the best sampling design for rare and clustered population.

1.3 Objectives

1.3.1 General objective

The purpose of this study was to determine the efficiency of adaptive cluster sampling designs and simple random sampling design in estimation of population mean from rare and clustered population.

1.3.2 Specific objectives

1. To estimate the population mean by simple random sample mean, modified Hansen Hurwitz estimator and modified Horvitz-Thompson estimator
2. To construct the confidence interval of population mean based on; simple random samplemean, modified Hansen-Hurwitz estimator and modified Horvitz-Thompson estimator.
3. To determine the most efficient estimate of population mean for different populations

   byMonte Carlo simulation

1.4 Assumptions of the study

1. The criterion of additional sampling was tocontinue sampling in the neighborhood ofevery unit in the initial sample if there is at least one unit in the initial unit.
2. Initial sample was selected using simple random sampling without replacement.
3. The neighborhood of any units was defined as the unit itself with adjacent units to thenorth, east, west and south.

1.5 Justification

There has been considerable investment in the designing of a sampling scheme that is effective for estimating population parameters from rare and clustered populations.Adaptive cluster sampling designs have been found to be more efficient than classical sampling designs in the estimation of parameters of rare and clustered populations. The adaptive design increases the efficiency thus leading to precise estimates of population parameters and high number of species of interest. The biggest drawbackof this design is the uncertainty and inability to control the final sample size. Different approaches that require the knowledge of prior information have been taken into consideration to limit the final sample size. The prior information is not always available. Another form of adaptive design the ACS', was proposed to limit the final sample.

CHAPTER TWO
LITERATURE REVIEW

2.1 Sampling

A sample is a subset of the populationbeing studied. It represents the larger population and is used to draw inferences about that population. Sampling is a research technique used as a way to gather information about a population without having to measure the entire population. There are several different ways of choosing a sample from a population, ranging from simple to complex.

2.2 Simple random sampling

Simple random sampling is the basis of all other sampling designs. In simple random sampling, the estimator of population mean (μ) given a random sample of n primary units from N total units is the average of the y-values associated with each unit i included in the sample. In this case the y-values will represent the number of individuals within each sampling unit. Under the simple random sampling each unit has equal chance of being included, the inclusion probability π_i is the same for all units and is equivalent to the fraction of the total sample space being sampled. The SRS estimate of the population mean can be expressed as

$$\hat{\mu}_{srs} = \frac{1}{n}\sum_{i=1}^{n} y_i \qquad (1)$$

The sample variance of this estimator can be expressed as;

$$var(\hat{\mu}_{srs}) = \frac{(N-n)}{nN} \times \frac{1}{N-1}\sum_{i=1}^{N}(y_i - \hat{\mu})^2 \qquad (2)$$

where, μ is the population mean, or the average number of individuals per unit

$$\mu = \frac{1}{N}\sum_{i=1}^{N} Y_i \qquad (3)$$

Since inclusion probabilities are not equal for every unit selected in the adaptive cluster sample, classical estimators such as $\mu_{srs}$are biased. Two design-unbiased estimators the Horvitz-Thompson and Hansen-Hurwitz estimators were proposed for estimation of population mean (Thompson, 1990).

2.3 Adaptive cluster sampling design

Sampling scheme is said to be adaptive if the sample selection procedure depends on the values of the variable of interest observed in the sample rather than the assumption of the population (Thompson, 1990). The basic idea behind this sampling design is to take an initial sample from a defined population by some probability sampling procedure such as simple random sampling and to continue sampling within the neighborhood of the units that satisfy the conditions that are defined previously. The basic essentials of adaptive cluster sampling design consist of an initial selection of units, a condition that determines when additional units should be added to the sample from the neighborhood of the unit selected in the initial sample and a clear definition of the neighborhood of every unit. This design was introduced for estimation of population mean of rare and clustered populations (Thompson, 1990). Since the introduction of this design many researchers have had a lot of interest in the use of this design in estimation of parameters of highly clustered and rare populations (Smith, *et. al.,* 2004,Gattone and Battista, 2010). It then operates under the rule that if any of these initially selected units satisfies a certain condition of interest, *C*, additional units in the neighborhood of that unit will be added to the sample. In area-based sampling, neighborhoods are usually defined based on spatial proximity, such as all units sharing an edge with the initially selected unit. In sampling biological populations, the condition to include additional units in a sample (*C*) is usually based on the count of individuals of the target population within the initial sample of units. Thus, any initially sampled units containing enough individuals to satisfy the condition *C* will cause additional units in their neighborhood to be added to the sample. If any of these additional units also satisfy *C*, further sampling of their neighborhoods occurs as well. This process continues until no further neighborhood units satisfy *C*. Through this process, ACS takes advantage of clustering within a population to make units containing interesting information more likely to be included in the sample.The main objective of ACS is to increase accuracy of estimators of population mean or total of rare and clustered populations (Thompson and Seber, 1996).

The ways of forming the criterion for selection of additional neighboring units, depends on the nature of study (Thompson, 1990). The criterion is either interval or says a set Cin the range of the variable of interest. Thus a unit i is said to satisfy the condition for additional neighboring units if $y_i \in C$.For each population unit, the neighborhood of a unit i is identified as a set of units which includes unit i such that the relationship of the neighborhood is symmetrical, that is, if unit*j*is in the neighborhood of unit *i* then unit *i* is in the neighborhood of unit *j*.The neighborhoods do not depend on thepopulation values. The set of all units that are observed under the design as a result ofinitial selection of unit *i*is termed as a cluster. A unit that does not satisfy the inclusion condition is referred to as an edge unit. A cluster whose all its edge unit are excluded is referred to as a network. This therefore defines a unit not satisfying the criteria C, a network of size one.

An ACS in which the initial sample is selected by simple random sampling, with or without replacement was defined to increase the precision of the estimator (Thompson, 1990). In other ACS designsdescribed in the literature the initial sample is selected by unequal probability with replacement and applied in determination of efficiency of ACS in estimating density of winter waterfowl (Smith *et al*, 1995).ACS in which initial sample is selected by systematic and cluster sampling and where the initial sample is selected by stratified sampling design was proposed when the population has a defined pattern (Thompson, 1991a, 1991b). ACS with networks selected without replacement where the ACS is modified by ensuring that networks are sampled once in the estimation of forest population(Salehi and Seber,1997a).

After introduction of ACS in 1990, much applications have been performed in biological settings. In addition, some recent studies have found ACS to live up well to its promising potential, the majority of studies have had either mixed or fully negative results regarding the applicability of ACS to real biological systems. Acharya et al. (2000) sampled rare tree species in Nepal and found ACS to work well for some but not for others, concluding that the applicability had to do with distribution characteristics of the different species (some were more clustered than others). When ACS was used to sample rockfish off Alaska it provided more precise estimates, but these gains in precision were offset by increasing costs due to adaptively adding sampling units, especially edge units (Hanselman et al, 2003). ACS has performed poorly for other researchers. A study of comparing sampling designs with an aggregated winter annual plant, led them to conclude that the population’s distribution was simply inappropriate for ACS (Morrison et al. 2008). ACS was better at detecting a higher fraction of individuals within the population, but found that it uniformly failed to provide more precise estimates of population size (Smith et al. 2003, Noon et al. 2006, and Goldberg et al. 2007).

The specific problems that samplers have had with ACS are in general due to either excessive realized sample sizes, a disproportionately high fraction of the sample being edge units, or bias of estimates resulting from the use of devices to curb excessive sample sizes. These general problems have been for the most part anticipated or duly noted by theoreticians over the years, and a number of articles have been published offering modifications of either the original basic design or estimators. Because the final size of the realized adaptive sample is unknown, it can be difficult to control the total sampling effort and accurately plan the cost of a survey in advance. Thompson (1996) discussed a design that allows researchers to control the number of units added to a sample by ordering the values of the completed initial sample and using a certain percentile to choose the condition to further add units to the sample. Unfortunately, it is not always possible in real-world situations to completely finish the initial sample before adding units adaptively. Another downside of the ACS design is that the information from edge units is not incorporated into estimators unless they are encountered in the initial sample. Thus the ratio of edge units to network units can have a strong effect on the efficiency of ACS.

While most applications of ACS have been ineffective in some way, there have also been multiple examples of success. In an inventory of sparse forest populations, Talvitie et al. (2006) found ACS to be “considerably more effective” than SRS. In estimating the abundance of local populations of low abundance plants,(Philippi,2005) successfully used ACS, Skibo et al. (2008) employed a modified ACS design to efficiently sample red sea urchin populations and Sullivan et al. (2008) found ACS to work well for a large proportion of the sea lamprey populations they examined. These successes were predicted in multiple simulation studies by (Christman 1997, Christman& Pontius, 2000). In these examples, performance has typically been based on the precision of estimates provided by ACS relative to those from other, more conventional designs given an equal effort. Regardless of the precision of estimates, a frequently acknowledged benefit provided by ACS is its tendency to sample a higher fraction of occupied sample units, allowing additional information to be collected concurrent to the sample (Lo et al. 1997, Noon et al. 2006, Smith et al. 2003). This can be especially useful when studying rare or endangered species for which such additional information is frequently lacking.

Overall there seems to be a gap between the theoretical potential of ACS and its realized performance in the field. In part, this is due to a characteristic of the ACS design that can be considered both an advantage and disadvantage. While ACS is in general recommended for rare, clustered populations, samplers have a considerable degree of flexibility in constructing a specific sample, potentially allowing it to be tailored to a wide variety of different situations and distributions. At the same time, it is the existence of so many different options that makes determining an optimal strategy so difficult.

There are multiple alternatives for neighborhood type, the condition *C*, the size of the initial sample, the initial method of selecting the sample, the size of the basic sampling unit, and the estimator that utilizes the collected information. There have been several neighborhood definitions described for ACS (Christman, 2000) but the most common definition used in grid-based sampling is the first-order neighborhood, which includes the four immediately adjacent quadrats. Setting an appropriate *C* can be very important in designing an efficient adaptive cluster sample. If more restrictive *C* is used substantially less sampling with very little loss of estimation precision would be achieved (Hanselman et al., 2003). The initial sample size (*n1*) must be set high enough to ensure the inclusion of some networks, but if set too high it may lead to excessive sizes of the realized adaptive sample. There are also a number of different options for selection of the initial sample, such as simple random sampling with or without replacement (Thompson, 1990), strip sampling, systematic sampling (Thompson, 1991a), stratified sampling (Thompson, 1991b) and simple Latin square sampling (Borkowski, 1999). Both the modified Hansen-Hurwitz and Horvitz-Thompson estimators suggested by Thompson (1990) have seen use in applied situations, and both have had advantages and disadvantages identified with them (Phillipi 2005, Salehi 2003).

Researchers have also consistently noted that the efficiency of ACS is dependant upon the spatial distribution patterns of the particular population being studied, but surprisingly little attention has been paid to sample design parameters that are fully under the control of samplers and significantly affect the distribution of point populations across grid-based sampling universes. In particular, White (2004) showed that for members of the *Astragalus*genus, an herbaceous member of the plant family *Fabaceae*, distributions in a grid-based setting can be highly influenced by both the placement of the grid and the size of the grid cells. Thus by coordinating the size of the basic sampling unit with the scale of clustering within the target population researchers can have a great deal of control over the effectiveness of ACS.

A restrictive adaptive cluster sampling was proposed to control sample size prior to sampling and units are selected consecutively for the initial sample size (Brown and Marley, 1998). Ratio estimators in ACS were proposed by Chao and Dryver (2007) while Chao *et al.* (2008) described improved ratio estimators under ACS. Model-based inference from ACS where knowledge of the population is used to inform both the sampling design and inference was described by Rapley and Welsh (2008). The final sample size depending on the choice of the criterion for additional neighboring units is important(Talvitie*et al.*,2006). Inappropriate selection of criterion will lead to selection of higher number of edge units and the final sample size will be excessively large (Brown, 2003).

The major disadvantage of adaptive cluster sampling in estimation of population parameters is the uncertainty of the final sample size.The biggest challenge to limit the final sample size is that Prior knowledge of the population is required (Turki and Barkowski, 2005). This prior knowledge is not always available. Much attention has been focused to limit the size of the final sample in ACS (Brown, 2003).

A stopping rule that is fixed in advance defining a stopping level S where the sampling process is terminated at the S^{th} step of the neighboring unit search was developed(Su and Quinn, 2003). However, the best choice of the stopping rule requires some prior knowledge about the population structure. A data driven stopping rule that changes at each step of the `aggregative procedure and for each unit in the initial sample was developed by Gattone and Battista (2010). This procedure controlled the final sample size and it does not require prior knowledge of the population structure.

2.3.1 Adaptive cluster sampling with data driven stopping rule

Let $n_1=\{1,2,\ldots, n\}$ be an initial sample of size n . For each unit $i\in n$, (Gattone and Battista, 2010) described ACS' design as a set of steps. The initial step $K = 0$ is composed of the initial sampleand if unit i in the initial sample satisfies the condition C, adaptive sampling procedure is carried out in the neighborhood of that unit. In the second step $K= 1$ adaptive sampling procedure is carried out in the neighborhood of the units added at step $K= 0$. Thus at step $K= 1$ there is just the ordinary ACS. In the second step, neighboring units satisfying the condition C at step K= 1 are added to the sample forming units for step K= 2. The procedure continues until there are no units satisfying condition C but, from step K= 2, units in the network associated with unit i will be sampled if and only if

$$S_i^k = \left\{ \frac{s_i^{2(K)}}{s_i^{(k-1)}} \frac{1-\frac{1}{m_1^{(k-1)}}}{1-\frac{1}{m_i^{(k)}}} \right\} > 1 \qquad (4)$$

where $s_i^{2(K)}$ is the within network variance estimate for the K^{th} step for the i^{th} initial unit and $m_i^{(k)}$ is the cardinality of the set of units adaptively sampled after the k^{th} step(Gattone and Battista, 2010).

2.4 Estimator

In this section, the design based estimators will be reviewed. These estimators are design based, that is, their biasedness depends on the selection of sample rather than the assumption of the population.

2.4.1 Hansen- Hurwitz estimator

The Hansen-Hurwitz estimator is based on draw-by-draw selection probability of selecting a primary sampling unit on any given draw. Since draw-by-draw selection probability cannot be known for all primary units in the sample but can be established for the networks that are encountered (Thompson, 1990). The modified Hansen-Hurwitz estimator is expressed as

$$\mu_{HH} = \frac{1}{n_1}\sum_{i=1}^{n_1} v_i \qquad (5)$$

where v_i is the average of the $y_i$values in the network (A_i) that include the i^{th} unit of the initial sample of size n_1 and $m_i$is the number of units in that network given as;

$$v_i = \frac{1}{m_i}\sum_{i\in A_i} y_i \qquad (6)$$

the sampling variance of the Hansen-Hurwitz estimator is expressed as

$$Var(\mu_{HH}) = \left(\frac{N(N-n_1)}{n_1}\right)\sigma^2 \qquad (7)$$

where, $\sigma^2 = \left(\frac{1}{n_1 - 1}\right)\sum_{i=1}^{N}(v_i - \mu)^2$ (8)

2.4.2 Horvitz-Thompson estimator

The Horvitz-Thompson estimator is based on inclusion probabilities (π_i), but on application of ACS the inclusion probabilities for every sampling unit selected in the sample cannot be established. Nevertheless, it is possible to establish the probability of including a network in the sample selected. A network is a subset of distinct units within a cluster, such that selection of any unit within the network would lead to the inclusion of all other units in the network. Units that fail to satisfy C but are in the neighborhood of one that satisfy are referred to as edge units. Thus, all units selected in the initial sample and fail to satisfy C will be considered to be networks of size one (Thompson, 1990). On partitioning the adaptive cluster sample into distinct networks rather than basic sampling units, the HT estimators for the population mean can be expressed as

$$\mu_{HH} = \frac{1}{N}\sum_{k=1}^{N} y^{*}_{k} \tag{9}$$

where y_k* is total number of individuals in the kthnetwork, k is the number of distinct networks in the sample, and the π_k is the probability of including any unit in the network k. If there are m_k units in the kth network, then the inclusion probability can be expressed as

$$\pi_k = 1 - \binom{N-m_k}{n_1} / \binom{N}{n_1} \tag{10}$$

and the sampling variance of the HT estimator is expressed as

$$Var(\mu_{HT}) = \frac{1}{N^2}\sum_{k=1}^{N}\sum_{h=1}^{N} y_k y_h (\pi_{kh} - \pi_k \pi_h) / \pi_k \pi_h \tag{11}$$

where π_{kh} is the probability of including both network k and h in the adaptive sample and is expressed as

$$\pi_{kh} = 1 - \left\{\binom{N-m_h}{n_1} + \binom{N-m_k}{n_1} - \binom{N-m_k-m_h}{n_1}\right\} / \binom{N}{n_1} \tag{12}$$

2.5 Improvement of the estimators by Rao-blackwell method

Although the three estimators, $\mu_{HH,}$ $\mu_{HT,}$ and $\mu_{srs}$are unbiased they are not function of minimal sufficient statistics, and hence each may be improved by Rao-Blackwell theorem by taking conditional expectation of each of the given minimal sufficient statistic. The minimal sufficient statistic D is the unordered set of distinct, labeled observations, that is

$$D=\{(k,y_k);\ k \in s\} \tag{13}$$

Let 't' be any of the unbiased estimator , then $t_{RB} = E(t|D)$ is also unbiased estimator and a function of minimal sufficient statistics (Basu, 1969).

Let n_1 denote a number of distinct units in the final adaptive sample n. If the initial sample n_1 is selected without replacement, we define $G=\binom{n}{n_1}$, the number of possible combinations are indexed in an arbitrary way by the label g (g=1, 2,…,G). Let t_g denote the value of t when n_1 consist of combination g and let var_g (t) denote the value of unbiased estimator var (t), when computed using the g^{th} combination. An initial sample that gives rise through the design to the given value D of the minimal sufficient statistic is compatible with D. Let the g^{th}indicator variable (I_g) takes the value 1 if the g^{th}combination could give rise to D (i.e., is compatible with D), and 0 otherwise. The number of compatible combinations is therefore given as

$$\xi = \sum_{g=1}^{G} I_g \tag{14}$$

But the estimator t may be improved using Rao-Blackwell theorem and is the average of the values of t obtained over all those initial samples that are compatible with D. The improved estimator t_{RB} is given as

$$t_{RB} = \frac{1}{\xi}\sum_{g=1}^{G} t_g I_g \tag{15}$$

and its variance is given by

$$\text{var}(t_{RB}) = \text{var}(t) - E[\text{var}(t \mid D)] \tag{16}$$

The unbiased estimator of the variance of t_{RB} is given by

$$\text{var}(t_{RB}) = \frac{1}{\xi}\sum_{g=1}^{G} (\text{var}(t_g) - (t_g - t_{RB})^2) I_g \tag{17}$$

2.6 Confidence interval

Confidence interval is an interval estimate of population parameter and is used to indicate the reliability of an estimate. An estimator that is consistent and asymptotically normal can be used to construct asymptotic confidence interval. The greatest factor that determines the length of the confidence interval is the sample size.

In ACS design, the design based unbiased estimators; HT estimator and HH estimator based on small sample have skewed distribution thus provide interval estimates with very low coverage probability. In this case the asymptotic normalityapproximation is used for all large samplesestimators always tend to have same characteristics as the normal distribution. Thus, $z = \left(\frac{(t_n-\mu)\sqrt{n}}{s_n}\right)$has approximate normal distribution standard and we may write.

$$\Pr(|Z| < c) = \gamma \tag{18}$$

where, γ is the desired confidence level and c is the critical value.

Then if t_n is a consistence sequence of estimators of sample mean then the desired confidence interval is given as

$$t_n - \mathrm{c}\frac{\mathrm{s_n}}{\sqrt{\mathrm{n}}} < \mu < t_n + c\frac{s_n}{\sqrt{n}} \qquad (19)$$

where, s_n is the asymptotic standard deviation of t_n and n is the sample size.

2.7 Summary

Most research work have dealt with the efficiency of adaptive cluster sampling designs and classical sampling designs by use of mean square errors of the estimators of population parameters obtained from either of the sampling designs. The mean square error just measure the variability and hence no indication of how likely it is that the value is close to the true population parameter. Confidence intervals are always recommended as they are able to present some indication of reliability of the estimators associated with confidence level. This study will construct the confidence interval under adaptive cluster sampling.

CHAPTER THREE

MATERIALS AND METHODS

3.1Source of data

The described study was conducted on artificial population (simulated population) that was generated from a Poisson cluster process as described by Diggle (1983). The Poisson cluster process is such that for any population the realization is from a Poisson process with parameter μ_1. Under Poisson cluster process, the parents are randomly located within the study area. For every parent, the number of children was generated according to a Poisson random variable with mean μ_2. The children are placed around their parents at a random angle uniformly distributed between 0 and 360 degrees and at a distance taken from an exponential distribution with mean λ. The parameters of the Poisson model are as follows:

$\mu_1 -$ mean number of the parents (clusters)

$\mu_2 -$ mean number of offspring of the cluster (children)

λ -mean of the exponential distribution.

In this study, the parameters in population 1 are $\mu_1 = 3, \mu_2 = 40, \lambda = 0.9$ and in population 2are $\mu_1 = 3, \mu_2 = 60, \lambda = 0.1$. The study area will be divided into $40 \times 40 = N$ units. For control of the edge effect of Poisson cluster process a 20×20 units was selected as the study area. Each population was sampled 180 times with SRS, ordinary ACS and ACS with data driven stopping rule. The ACS and ACS' designs were carried out by using an initial sample size of $n_1 = 3$. The condition of adaptive sampling was set to be:

$c = \{y_i \geq 1\}$, that is, at least one of the offspring is observed in the initial sample.

The estimators' were computed using the statistical package R version 2.13.0 (Smith *et. al,* 2010), while Poisson clustered population be simulated by MATLAB version (2010) Service Pack 1.

3.2 Data analysis

The confidence interval of population mean based on; modified Hansen-Hurwitzestimator, Horvitz-Thompson estimator and simple random sample estimator willbe constructed. The efficiency of the adaptive designs was analyzed using two approaches. First, relative efficiency of the estimates of the population mean from both ACS and ACS'. The relative efficiency was obtained as follows $R.E_{ACS} = \frac{MSE_{ACS}}{MSE_{SRS}}$ and $R.E_{acs'} = \frac{MSE_{ACS'}}{MSE_{SRS}}$. Secondly, bycomparing the confidence intervals computed based on estimatesof the population mean for both the ACS and ACS’ by evaluating their coverage probabilities.

CHAPTER FOUR

RESULTS AND DISCUSSIONS

4.0 Introduction

In this section, the population of the rare and clustered which is in the figure one and the population that is not rare and clustered this is population two.

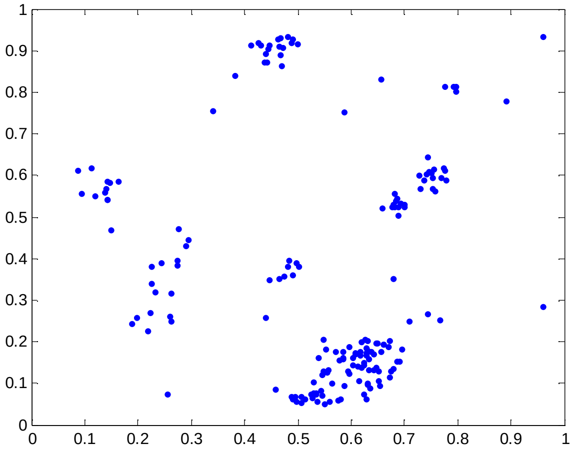

Figure 1: The spatial point pattern for a rare and clustered population with parameters μ_1=3,μ_2=45,λ=0.9

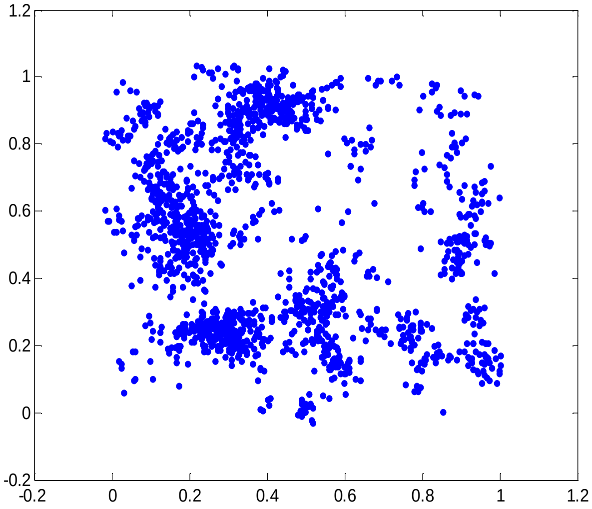

Figure 2: The spatial point pattern for general population that is not rare and clustered with parameters μ_1=3,μ_2=60,λ=0.1

4.1 The relative efficiency

The results of relative efficiency of the design based HT and HH estimators for population 1 and population 2 are represented in table 1 and table 2 respectively. For rare and clustered population 1 the relative efficiency of the HT and HH estimator was better under the ACS' design than under ordinary ACS design. Under the ordinary ACS, the HT estimator had a higher efficiency than the HH estimator. Thus, under the ordinary ACS the HT estimator is a better estimate of the population mean of rare and clustered population. Under the ACS', the HT estimator had a higher efficiency than the HH estimator. Thus, under the ACS' the HT estimator is a better estimate of mean of rare and clustered population than the HH estimator.

When the final sample size is increased, the relative efficiency of the HT estimator and HH estimator increases. The increase in relative efficiency of the HT estimator and the HH estimator was much significant under the ACS' design.

For the two populations examined (figure 1 and 2) in this study there were multiple conditions under which one or both design based estimators were relatively more efficient than the classical estimator given an equal final sample size. The Hansen-Hurwitz estimator performed uniformly worse than the Horvitz-Thompson estimator and rarely better than the SRS mean. Complete tables of the relative efficiencies of both the HT and HH estimators under all conditions are presented in table 1 and 2.

As the final sample size increased, some interesting characteristics were observed. The efficiency of both adaptive cluster sampling estimators in ACS and ACS' increased as the final sample size increased. Interestingly, the HT estimators showed intense increase in efficiency with only modest increase in the sample size. For example the efficiency of the HT estimator at sampling of the population 1, from results in table 1 increases by 0.1413 folds for ACS and by 0.0505 for ACS' as the final sample size increases from 20 to 90. The above results are caused by the increase of the final sample size as the probability of including the large networks increases and hence resulting into low variances.

As the rarity and the clustering of the population decreases, the efficiency of design based estimators (HT and HH estimators) relative to classical estimator (SRS mean) reduces. The results of the efficiency of the HT and HH estimators from population 2 as shown in table 2 indicate a reduction in efficiency. This indicates that the design based estimators are only efficient for population that is rare and clustered. The classical estimator perform better than the design base estimators (HT and HH estimators) for population 2 which was not rare and clustered.These findings are consistent with the findings of Esha and Jesse (2012).

Table 1:Relative efficiency for rare and clustered population

N	ACS		ACS’	
	R.E$_{HT}$ =$\frac{mse(HT)}{mse(SRS)}$	R.E$_{HH}$ =$\frac{mse(HH)}{mse(SRS)}$	R.E$_{HT}$ =$\frac{mse(HT)}{mse(SRS)}$	R.E$_{HH}$ = $\frac{mse(HH)}{mse(SRS)}$
20	0.2780	0.8034	0.0963	0.3635
30	0.2683	0.5435	0.1642	0.3246
40	0.2242	0.4206	0.1478	0.2412
50	0.2163	0.2946	0.1326	0.1466
60	0.1733	0.1509	0.0867	0.1211
70	0.1633	0.1372	0.0739	0.1088
80	0.1592	0.1093	0.0604	0.0662
90	0.1367	0.0851	0.0458	0.0838

Table 2: Relative efficiency for a general population that is not rare and clustered

N	ACS		ACS’	
	R.E$_{HT}$ =$\frac{mse(HT)}{mse(SRS)}$	R.E$_{HH}$ =$\frac{mse(HH)}{mse(SRS)}$	R.E$_{HT}$ =$\frac{mse(HT)}{mse(SRS)}$	R.E$_{HH}$ = $\frac{mse(HH)}{mse(SRS)}$
20	2.1604	1.6723	2.781	2.6636
30	2.7464	1.9659	2.4570	2.4736
40	2.3546	2.0001	2.3622	2.3339
50	3.6010	3.5232	2.1110	2.1954
60	3.9401	2.4648	2.2970	2.2682
70	3.6765	3.7524	1.948	1.9059
80	3.4817	3.9153	1.8689	1.7907
90	4.8170	4.1216	1.6294	1.7907

4.2 Variance

Results of variance of the estimators are given in table 3 and 4. From the tables, a great reduction in variance of the HT estimator and HH estimator when they were computed from samples obtained under a rare and clustered population 1 was observed.

For the rare and clustered population, the HT estimator had the smallest variance than HH estimator and the SRS mean under the ACS design and the ACS' design. However, the HH estimator had a smaller variance than the SRS mean. This indicates that, the design based estimators are better than the classical estimators in estimation of population mean of a rare and clustered population.

When the variance of the two adaptive design estimators are evaluated, the variance of HT estimator is smaller than the variance of HH estimator under both ACS design and ACS' design. However, the variances of HT estimator and HH estimator under the ACS' were smaller than under the ACS design.

When the design based estimator are applied on the population that is not rare and clustered, it was observed that the classical estimator, that is, the simple random sample mean had a smaller variance than the design based estimators, the HT estimator and the HH estimators. for example when the final sample size is 20 the SRS mean had a variance of 2.585, while under ACS' the HT estimator had a variance of 7.1889 and HH estimator had a variance of 6.8854. When the sample size increases to 70, the SRS mean had a variance of 0.8554, while under ACS' the HT estimator had a variance of 1.6978 and HH estimator had a variance of 1.6303. This indicates that the SRS mean is more efficient than HT estimator and HH estimator in estimation of population mean under a population 2 (figure 2) that is not rare and clustered which is consistent with the findings of Gattone and Batista (2010).

Table 3: Results of variance of the estimators under the population that is rare and clustered

N	ACS			ACS’	
	Var(HT)	Var(HH)	Var(SRS)	Var(HT)	Var(HH)
20	0.7509	2.1701	2.7011	0.1872	0.9818
30	0.5656	1.1457	2.108	0.3461	0.6843
40	0.4397	0.8247	1.9610	0.2898	0.4730
50	0.2676	0.3644	1.2370	0.1640	0.1813
60	.01440	01254	0.8312	0.0721	0.1007
70	0.1197	0.1006	0.7331	0.0542	0.0798

Table 4: Results of variance of the estimators under the population that is not rare and clustered

N	ACS		ACS’		
	Var(HT)	Var(HH)	Var(HT)	Var(HH)	Var(SRS)
20	5.5846	4.3229	7.1889	6.8854	2.585
30	5.7158	4.0914	5.1135	5.1481	2.0812
40	3.9181	3.3282	3.9307	3.8836	1.6640
50	5.0126	4.9043	2.9385	3.0560	1.3920
60	3.8897	2.4332	2.2676	2.2392	0.9872
70	3.1449	3.2098	1.6978	1.6303	0.8554

4.3 Confidence interval and coverage probability

In this section, we are focusing on the properties of confidence intervals of population mean based on the HT estimator, HH estimator, and SRS mean. The results of confidence intervals are given in table 5, table 6, table 7, table 8, table 9, and table 10. The results of confidence interval of population mean under the population that is not rare and clustered are given in Table 5, table 6, and table 7. From these results, we observe that the both HT estimator and HH estimator under the ACS and ACS’ have larger width than the SRS mean. This implies that estimator under classical sampling is better than the design based estimators for a population that is not rare and clustered. For example, under ACS design, when the final sample is 20, the width of confidence interval of population mean based on HT estimator is 9.2636, the width of

HH estimator is 8.1503, while the width of the SRS mean is 6.3026. Under the ACS’, the width of confidence interval of HT estimator is 10.5104, and the width of HH estimator is 10.2861. When the final sample is.60, the width of confidence interval of population mean based on HT estimator is 7.7312, the width of HH estimator is 6.1147, while the width of the SRS mean is 3.8948. Under the ACS’, the width of confidence interval of population mean based on HT estimator is 5.8514, and the width of HH estimator is 8.8659.This indicates that the confidence interval of population mean based on SRS mean has the smallest width than the confidence interval of population mean based on HT estimator and HH estimator.Despite that, in comparison of the design based estimators, the HH estimator has a narrow width than the HT estimator in a population that is not rare and clustered. This indicates that the HH estimator is better than the HT estimator under a population that is not rare and clustered. As the final sample size increases, the width of the confidence interval also decreases. Table 8, table 9 and table 10 give the results of confidence interval of HT estimator, HH estimator and SRS mean under the population that is rare and clustered. From the results, the HT estimator and the HH estimator have smaller confidence width than SRS mean in all situations. This implies that the ACS design and ACS’ design sampling is better than Simple random sampling. For example, under ACS design, when the final sample is 20, the width of confidence interval of population mean based on HT estimator is 3.3969, the width of HH estimator is 5.7747, while the width of the SRS mean is 6.4425. Under the ACS’, the width of confidence interval of population mean based on HT estimator is 1.6961, and the width of HH estimator is 3.8842. When the final sample is60, the width of confidence interval of population mean based on HT estimator is 0.4704, the width of HH estimator is 1.2433, while the width of the SRS mean is 3.5739. Under the ACS’, the width of confidence interval of population mean based on HT estimator is 1.0526, and the width of HH estimator is 1.2439.This indicates that the confidence interval of population mean based onHT estimator has the lowest confidence width than HH estimator in both ACS design and ACS’ design. This implies that the HT estimator is a better estimator than HH estimator in sampling a rare and clustered population.

Table 5: Confidence interval for HT estimator, HH estimator under a population that is not rare and clustered considering the adaptive cluster sampling

	ACS					
	HT			HH		
N	L.L	U.L	Width	L.L	U.L	Width
20	-1.7318	7.5318	9.2636	-1.1752	6.9752	8.1503
30	-1.7859	7.5859	9.3718	-1.0645	6.8645	7.9291
40	-0.9797	6.7797	7.7593	-0.6757	6.4757	7.1514
50	-1.4882	7.2882	8.7764	-1.4405	7.2405	8.6811
60	-0.9656	6.7656	7.7312	-0.1573	5.9573	6.1147

Table 6: Confidence interval for SRS mean under a population that is not rare and clustered

	SRS		
N	L.L	U.L	Width
20	-0.2513	6.0513	6.3026
30	0.0724	5.7276	5.6551
40	0.3717	5.4283	5.0566
50	0.5875	5.2125	4.6249
60	0.9526	4.8474	3.8948

Table 7: Confidence interval for HT estimator, and HH estimator under a population that is not rare and clustered considering the adaptive cluster sampling with stopping rule

	ACS’					
		HT		HH		
N	L.L	U.L	Width	L.L	U.L	width
20	-2.3552	8.1552	10.5104	-2.2430	8.0430	10.2861
30	-1.5322	7.3322	8.8643	-1.5471	7.3471	8.8943
40	-0.9859	6.7859	7.7718	-0.9625	6.7625	7.7251
50	-0.4598	6.2598	6.7197	-0.5264	6.3264	6.8527
60	-0.0515	5.8515	5.9030	-0.0329	5.8329	5.8659

Table 8: Confidence interval of HT estimator, HH estimator and under a population that is rare and clustered

	ACS’					
	HT			HH		
N	L.L	U.L	Width	L.L	U.L	Width
20	1.2016	4.5984	3.3969	0.0127	5.7873	5.7747
30	1.4260	4.3740	2.9481	0.8021	4.9979	4.1959
40	1.6003	4.1997	2.5993	1.1201	4.6799	3.5599
50	1.8861	3.9139	2.0278	1.7168	4.0832	2.3663
60	2.6648	3.1352	0.4704	2.2783	3.5217	1.2433

Table 9: Confidence interval for SRS mean under a population that is rare and clustered

	SRS		
N	L.L	U.L	Width
20	-0.3213	6.1213	6.4425
30	0.0543	5.7457	5.6914
40	0.1553	5.6447	5.4894
50	0.7201	5.0799	4.3598
60	1.1131	4.6869	3.5739

Table 10: Confidence interval of HT estimator, HH estimator and SRS mean under a population that is rare and clustered

	ACS					
	HT			HH		
N	L.L	U.L	Width	L.L	U.L	width
20	2.0520	3.7480	1.6961	0.9579	4.8421	3.8842
30	1.7469	4.0531	2.3061	1.2786	4.5214	3.2427
40	1.8449	3.9551	2.1103	1.5520	4.2480	2.6960
50	2.1063	3.6937	1.5875	2.0654	3.7346	1.6691
60	2.3737	3.4263	1.0526	2.2780	3.5220	1.2439

Results of the coverage probabilities are given in tables 11 and 12. From these results, the coverage probability performance of confidence interval of HT estimator and HH estimator under adaptive designs was investigated. The confidence intervals of population mean based on HT estimator under ordinary ACS and ACS’ performed better than the HH estimator based on their coverage probabilities. As observed from table 11, increasing the final sample size caused the coverage probability of the confidence intervals to go up gradually for the two estimators. The coverage probability performance of the confidence intervals HT estimator and HH estimator under the ordinary ACS in population 1 that is rare and clustered indicated that the HT estimator performed better than the HH estimator in the same population.

Interestingly, the coverage probability of confidence interval ofpopulation mean based on HT estimator in the two designs and in both population appeared to perform better than the coverage probability of confidence interval ofpopulation mean based on HH estimator in both the design. For example, when the final sample size was 20 in table 11, the coverage probability of confidence interval ofpopulation mean based on HT estimator and HH estimator were 0.9238 and 0.9142 respectively under the ordinary ACS. Under the ACS', when the final sample size was 20 in table 11, the coverage probability of confidence interval of population mean HT estimator and HH estimator 0.9488 and 0.9392 respectively. From this example, the coverage probability of confidence interval of population mean based on HT estimator was better under the ACS and ACS' than the coverage probability of HH estimator in both designs. When the final sample size was raised to 60 in table 11, the coverage probability of confidence interval of population mean based on HT estimator and the HH estimator raised to 0.9397 and 0.9338 respectively under the ordinary ACS. When the final sample size was raised to 60 in table 11, the coverage probability of confidence interval of population mean based on HT estimator and the HH estimator raised to 0.9511 and 0.9477 respectively under the ACS'. From the observation of the coverage probability in table 11, both the HT estimator and the HH estimator were performing better under the ACS' than ordinary ACS.

When degree of rarity and clustering of the population decreases, the performance of the coverage probability decreases in both ACS' and ordinary ACS. For example, when the final sample size is equal to 20, the coverage probability of confidence interval ofpopulation mean based on HT estimator changes from 0.9238 to 0.8901 in population1 that is rare and clustered to population 2 which is not rare and clustered under ordinary ACS. The coverage probability of confidence intervalof population mean based on HH estimator also changes from 0.9142 to 0.8869 in population 1 that is rare and clustered to population 2 which is not rare and clustered under ordinary ACS. From above observation of the two populations, the coverage probability is better under the rare and clustered population than a population that is not rare and clustered. When the ACS' is used, the coverage probability of confidence interval ofpopulation mean based on HT estimator changes from 0.9488 to 0.9016 from population 1 that is rare and clustered to population 2 which is not rare and clustered, while the coverage probability of confidence interval ofpopulation mean based on HH estimator also changes from 0.9392 to 0.8864 from population 1 that is rare and clustered to population 2 which is not rare and clustered.

From the results below, the coverage probability of confidence interval ofpopulation mean based on HT estimator and HH estimator is uniformly better under the population 1 as show in table 11 than inpopulation 2 as show in table 12. The results of coverage probability of confidence interval of population mean based on HT estimator and the HH estimator indicate that the two estimators perform better in a rare and clustered population. The coverage probability of confidence interval of population mean based on HT and HH estimators also indicate that the ACS' is a better design in sampling of a rare and clustered population than the ordinary cluster sampling.

Table 11: Coverage probability for a general population that is not rare and clustered

N	ACS		ACS'		
	(HT)	(HH)	(HT)	(HH)	SRS
20	0.8901	0.8863	0.9016	0.8864	0.7118
30	0.8928	0.8869	0.9068	0.8859	0.7910
40	0.8986	0.8864	0.9035	0.8928	0.7993
50	0.8989	0.8918	0.9043	0.8986	0.7976
60	0.9100	0.9012	0.9039	0.8992	0.7958

Table 12: Coverage probability for a population that is rare and clustered

	ACS		ACS'		
N	(HT)	(HH)	(HH)	(HT)	SRS
20	0.9238	0.9142	0.9392	0.9488	0.8845
30	0.9278	0.9194	0.9423	0.9492	0.8870
40	0.9345	0.9221	0.9415	0.9495	0.8952
50	0.9393	0.9232	0.9474	0.9508	0.8926
60	0.9397	0.9338	0.9477	0.9511	0.8908

When the population is not rare and clustered, we observe that the coverage probability reduces. In both the population, sampling is based on the network. Unlike the design based estimator that uses the inclusion probability and the draw by draw probabilities that are based on the network, the SRS mean uses theprobability that are based on the assumption of the population. In this study, since the sampling is done based on the networks, the sample size of the population species that is used in simple random is actually higher than the final sample size achieved when sampling using the network. The large sample size of the population species under the simple random sample causes the standard error of the SRS mean to be small hence leading to small confidence width. When the confidence width is smaller, most of the confidence intervals could not contain the true value of the population mean. This effect of the large sample size under the simple random sample causes the coverage probability to reduce.

CHAPTER FIVE

CONCLUSIONS AND RECOMMENDATIONS

5.1 Conclusion

It clear that efficiency of adaptive cluster sampling designs is influenced by a number of factors. Good results of efficiency are achieved when the within-network variance has a large proportion of the total variance as well as when the final sample size is slightly higher than the initial sample size (Smith *et al.* 1995, Thompson&Seber 1996, Brown 2003, Christman, 1997),but achieving a condition when the final sample size is slightly higher than the initial sample size and within network variance has a large proportion of total variance is difficult at the same time. The efficiency of an adaptive cluster sample is a function of the interaction between the within-network variance and final sample size and ultimately depends upon the spatial distribution of the target population (Smith *et al.* 2004). The results of this study show thatthe design based estimators (HT estimator and HH estimator) are better than the classical estimators like SRS mean in estimation of population mean of rare and clustered population.From the results obtained, the HT estimator and the HH estimator did better for the population that was rare and clustered than the SRS mean. In comparison of the performance of the two designs based estimators under the ACS design and the ACS' design, the HT estimator performed better than the HH estimator. The ACS' design is better than the ACS design since it was able to minimize the within network variance as the final sample since increased.We thus conclude that the ACS' design is a better design in estimation of population parameter of rare and clustered population.

5.2 Recommendation and further research

Most of research work uses the design based estimators that are based on the networks rather that the entire population. These design based estimators are sensitive to size of the final sample and the within-network variance.Applications of these estimators in adaptive cluster sampling (ACS) have had inconsistent results in real-world settings, leading to increasing scrutiny of the factors that influence the efficiency of this design. Much more work still needs to be done in order to provide samplers with the knowledge of when adaptive cluster sampling design is appropriate and how to maximize its effectiveness.Further research work is recommended;

1. Determination of design based estimators that are based on the entire population rather than the networks.
2. Determination of design based estimators that are not sensitive to both final sample size and the within network variance

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