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Bootstrap interval estimation of wildlife population sizes from multiple surveys

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Chapter 1

Introduction

Knowledge about the sizes of populations of different species in a game reserve is crucial for implementing policy decisions such as the introduction or removal of animals, depending on the carrying capacity of the reserve. Relocation of animals and protection of endangered species is influenced by the knowledge of population sizes of the different species. There are many methods that are used in practice for estimating wildlife population sizes. These methods include a census and methods based on various sampling approaches. Aerial surveys are a practical means of estimating the number of large animals inhabiting an extensive area. However estimates are often biased and have large variances (Seber, 1982). They may be biased undercounts of the true population size because of tree cover, and the extent of the bias can differ from one census to another depending on conditions. Sampling methods have been used in recent times to estimate the population sizes of the white and black rhinoceros (*Ceratotherium simum and Diceros bicornis*) and other wildlife species in the Hluhluwe-Umfolozi Park in KwaZulu Natal, South Africa. Sampling methods are generally much cheaper than aerial surveys.

The Hluhluwe-Umfolozi Park is one of South Africa's major game reserves, which is particularly important for its population of white and black rhinoceros. The rhinoceros is a large primitive looking mammal that dates to the Miocene era. In recent decades rhinos have been relentlessly hunted to the point of extinction. Since 1970 the world rhino population has declined by 90%, with five species remaining in the world today, all of which are endangered. The white rhino's (*Ceratotherium simum*) name derives from the Dutch word "wijd," meaning wide, a reference to its wide, square muzzle adapted for grazing. The black, or hooked-lipped rhino (*Diceros bicornis*), along with all other rhino species, is an odd-toed ungulate (three toes on each foot). It has a thick, hairless, grey hide.

The method used to conduct the survey for the white rhino was based on observations taken along line transects passing through different sections of the park, using a distance based methodology to account for the decreasing detection rate with increasing distance between the observer and the animal (Buckland et al., 1993). In contrast, this methodology is said to be inappropriate for the black rhino with its shy habits, and instead a "mark-recapture" method (Seber, 1982) is used to estimate its population size. Between 1973 and 1996 eight surveys of the white rhino population were undertaken whereas seven surveys were conducted for the black rhino between 1990 and 1996.

1.1 Motivation

Estimates of living populations are required for many purposes in wildlife management and they are essential in policy making for the protection of species. Techniques for the estimation of absolute abundance of wildlife populations have received a lot of attention in recent years. Knowledge of the population size of wildlife helps in the protection of endangered species. Significance of wildlife to the country has also stimulated research on the population sizes of wildlife in recent years. The sudden decrease in numbers of white rhino between the 1994 and 1996 surveys in Hluhluwe-Umfolozi Park triggered concern about the estimation of the population sizes, as there was no explanation for the apparent sudden decrease. These factors and others mentioned above have been the motivation for this research on the estimation of population sizes for the white and black rhino in Hluhluwe-Umfolozi Park.

1.2 Aim of the study

This research aims to provide bootstrap interval estimates of wildlife population sizes from multiple surveys. The estimates will be based on the model proposed by Fatti et al., (2002). This model does not depend on the particular method used in the surveys. The method is applied separately to the white and black rhino populations in the Hluhluwe-Umfolozi Park.

1.3 Objectives

The objectives of the research are:

1. Using the bootstrap, to obtain improved estimates of the true population size at each of the surveys based on the model proposed by Fatti et al. (2002). Estimates are obtained for each of the time points.
2. To obtain the bootstrap estimate of the natural annual rate of increase in the population also based on the Fatti et al. (2002) model for both the white and black rhino.
3. To construct the confidence intervals for the bootstrap estimates obtained in 1 and 2 above at each of the time points, using the percentile confidence interval and standard confidence interval methods for both the white and black rhino. (See Chapter 2 for a full description of the confidence interval methods.)
4. To compare the confidence interval results obtained from the percentile and the standard method.
5. To assess the coverage probability of the confidence intervals for the bootstrap estimates in 3 above using a simulation study.
6. To obtain the Jackknife estimates and standard errors based on the model proposed by Fatti et al. (2002).
7. To compare the bootstrap method with the jackknife method.

1.4 Project layout

The layout of this report is as follows: Chapter 1 consists of the introduction, motivation, aim and objectives of the research. Chapter 2 reviews the literature relevant to the study. In Chapter 3 the methods used to achieve the aim and objectives for the study are discussed. Chapters 4 and 5 focus on the results obtained and discussion of the results. Conclusions and recommendations are given in Chapter 6.

C h a p t e r 2

L i t e r a t u r e R e v i e w

This chapter gives a review of the literature involved in the study of bootstrap interval estimation of wildlife population sizes from multiple surveys. The basic concepts associated with the analysis of wildlife data and some important definitions are also reviewed.

2.1 Definitions

Definition 2.1 Confidence interval
A confidence interval for a parameter is a random interval constructed from data in such a way that the probability that the interval contains the true value of the parameter can be specified.

Definition 2.2 Coverage probability
Coverage probability of a procedure for constructing confidence intervals is the chance that the procedure produces an interval that covers the true parameter value.

Definition 2.3 Random sampling
Random sampling is the probabilistic selection of a sub-element from a larger population, with the aim of approximating a representative picture of the whole. It is a way of obtaining information about a large group by examining a smaller, randomly chosen selection (the sample) of group members. If the sampling is conducted correctly, the results will be representative of the group as a whole.

Definition 2.4 Sample Estimate
Sample estimate from this study will refer to the estimates of the true population obtained from fitting the model.

Definition 2.5 Survey Estimate

Survey estimate from this study refers to the estimates of the population of the white and black rhino obtained from Hluhluwe Umfoloz Park which are indicated in Appendix A.

Definition 2.6 Bootstrap Estimate

Bootstrap estimate in this study refers to the estimates of the true population obtained from implementing the bootstrap procedure.

2.2 Estimating animal abundance

This section describes and presents a literature review on the methods that have been specifically used for estimating the white and black rhino population at the Hluhluwe-Umfolozi Park.

2.1.1 Line transect sampling

Line transect surveys are an efficient and widely used means of estimating abundance of wildlife populations. Buckland et al. (1993) provide a comprehensive treatment of convential line transect model theory and practice. Line transect sampling involves the observation of individuals along transects located over the range of a populations of interest. It is a specific type of distance sampling in which the sample consists of one or more lines, which are traversed by observers on foot, vehicle or other means. Observers count individuals detected from the line and measure the distance from each individual to the line. The distance data are then used to estimate detection rates and thus to adjust the count to obtain an estimate of the true density (Williams et al., 2002). In line transect sampling, the observer travels along the centreline of the strip and records the perpendicular distance x of each detected animal (or group of animals) from the line. Borchers et al. (2002) contends that it is easier to record the detection radial distance r and angle θ from which $x = r \operatorname{Sin} \theta$. Line transect sampling is a useful method for estimating the abundance of a wide range of objects, including the density of immobile objects such as trees in a forest.

A comprehensive overview of survey design and data recording requirements in the context of line transect sampling is given by Buckland et al. (1993). According to them, line transect sampling can be used to derive unbiased estimates of local site densities provided the key assumptions are met.

Marques (2004) investigated the effect of error measurement on line transect estimates. He also produced confidence intervals for the corrected estimates using a bootstrap variance estimate. He further presented a multiplicative error model and proposed a simple way of correcting estimates based on knowledge of the error distribution.

Melville and Welsh (2001) considered an approach to line transect sampling using a separate calibration study to estimate the detection function. They presented a simulation study, contrasting their results with the traditional 'Buckland' estimator.
Fewster et al. (2005) later showed that the traditional 'Buckland' methods perform to expectation when applied correctly.

Adaptive line transect sampling offers the potential of improved population density estimation efficiency over conventional line transect sampling when populations are spatially clustered. In adaptive sampling survey effort is increased when areas of high animal density are located, thereby increasing the number of observations. Pollard et al. (2002) mentioned that the adaptive line transect sampling has a disadvantage in that the survey effort required is not known in advance. They developed an adaptive line transect methodology which allows total effort to be fixed at the design stage.

Hiby and Krishna (2001) argued that existing paths or game trails may be suitable as transects for line transect sampling even though they will not usually run straight. They say the use of existing paths carries the risk of bias resulting from unrepresentative sampling of available habitats, and this must be weighted against the increase in coverage available.

Chen et al (2002) considered using sequential procedures to determine the amount of survey effort required in a line transect survey in order to achieve a certain precision level in estimating the abundance of a biological population. The criterion used to derive the stopping rules was the width of the confidence interval for the animal abundance and the stopping rules were developed based on the asymptotic distributions and the bootstrap.
According to Burnham et al., 1980, the basic principles of line transect sampling are:

1. The objects to be sampled in an area are distributed in accordance with a stochastic process with a constant density per unit area.
2. A line of known length is randomly located and traversed. Objects detected on either side of the line are recorded including either:
    a) perpendicular distance or
    b) sighting distance and angle for each detected object.

Usually several randomly placed lines are used. As long as the transect lines are randomly located it is not necessary to assume that the objects are randomly or even independently distributed. The particular method used for the white rhino at the Hluhluwe-Umfolozi Park was the sighting distance.

The mathematical foundation of line transect sampling was developed by Burnham and Anderson (1976), and further refined by Buckland (1982, 1985), Buckland et al. (1993), Gates (1981), Gates et al. (1985), Johnson and Routledge (1985), Pollock (1978), Pollock and Kendell (1987), Quinn and Gallucci (1980), Quinn (1985) and Quang (1990). Drummer and McDonald (1987) using parametric models and Quang (1991) using non-parametric models extended line transect theory to account for size biased sampling.

a) Sampling scheme and modelling approach

In line transect sampling, the locations of individuals on either side of one or more transects are recorded, and used as a basis for estimating the effective area that is sampled and hence the population density. We will assume that the transects of specified length L are located at random within the range of a population of interest. Each transect is

traversed systematically, starting at one end of the transect line and proceeding along the line at a constant pace. Locations of individuals are described either as distance x_i perpendicular to the transect or radial distance r_i from the observer, along with the angle θ_i of incidence to the transect. It is especially important that all individuals located directly on the transect line are observed and recorded. The figure below illustrates the basic layout of a line transect sample.

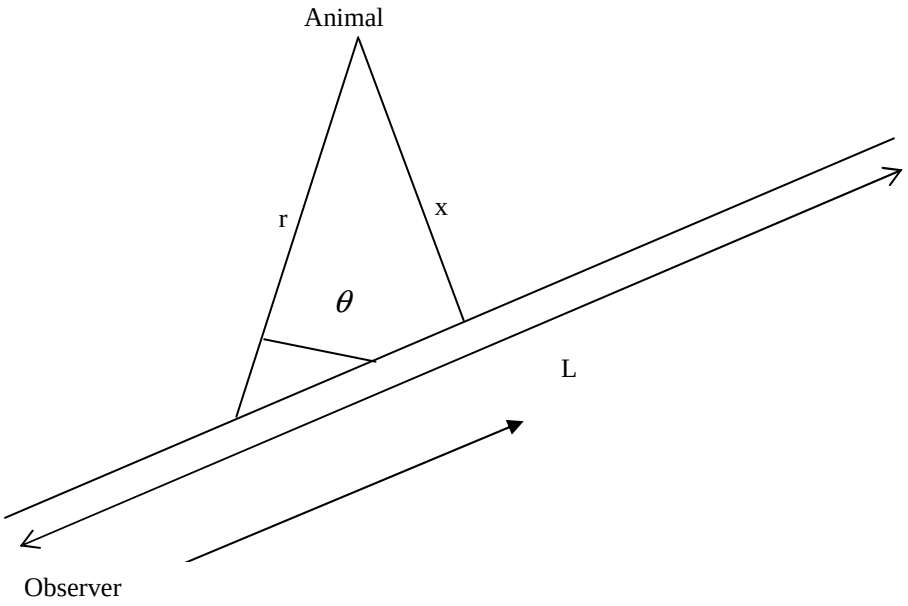


Figure 2.1: Example of line transect sampling and measurement

The arrow indicates the direction of travel, r is the observer to object distance, x is the perpendicular distance to the transect line, L is the transect length. On completion of the field work, the distances of individuals from the transects are used to determine density. Assuming complete observability, an estimate of density is given by:

$$\hat{D} = \frac{n}{2wL}$$

where n is the number of animals observed, L is the transect length, and w is the estimated effective half width (Williams et al. 2002).

b) Abundance estimation

To estimate density accurately it is necessary to introduce a detection function that expresses the probability of detecting an animal as a function of distance x from a transect line:

$$g(x) = \mathrm{P}(\text{animal is detected}|x).$$

The probability of detection is assumed to decrease with distance. For animals directly on a transect line the probability of detection is one: $g(0) = 1$. We assume that N animals within the transect area are distributed such that N_x are at a distance x from the transect line; thus on average $N_x g(x)$ of those animals are observed. The expected number of observations over the whole width of the transect is then given by:

$$\begin{aligned} E(n) &= NP_a \\ &= \int_0^w \left(N_x g(x)\right) dx \end{aligned}$$

N is the total number of animals in the transect area

P_a is an average detection probability: $P_a = \int_0^w (N_x \mid N)\, g(x)\, dx$

It follows that:

$$E\left(\frac{n}{P_a}\right) = \frac{E(n)}{P_a} = \frac{N}{P_a}\int_0^w \left(\frac{N_x}{N}\right) g(x)\, dx = N$$

and $\hat{N} = \dfrac{n}{P_a}$ is an unbiased estimate of N.

On assumption the animals are randomly located with respect to transect position, the average detection probability simplifies to:

$$P_a = \int_0^w g(x)\, dx / w$$

This assumption is assured by the random positioning of transects in the study area. The unbiased estimator for the actual density will then be given by:

$$\tilde{D} = \left(\frac{n}{P_a}\right)\left(\frac{1}{2Lw}\right)$$
$$= \frac{n}{2L\left(wP_a\right)}$$

but the effective strip width is given by:

$$\tilde{w} = wP_a = \int_0^w g\left(x\right)dx$$

substituting in the expression for actual density we have

$$\tilde{D} = \frac{n}{2L\left(wP_a\right)} = \frac{n}{2L\tilde{w}}$$

The relationship between strip width and detectability can be formalised in terms of the probability density function of observed distances. We let x be the distance of animals from transect line thus,

$$f\left(x\right) = \frac{g\left(x\right)}{\int_0^w g\left(x\right)dx}.$$

In particular, the probability that an observed animal is directly on the transect line is:

$$f\left(0\right) = \frac{g\left(0\right)}{\int_0^w g\left(x\right)dx} = \frac{1}{\int_0^w g\left(x\right)dx} = \frac{1}{\tilde{w}}$$

substituting in the expression of density we have:

$$\tilde{D} = \frac{n}{2L\tilde{w}} = \frac{nf\left(0\right)}{2L} \quad \tilde{D} = \frac{n}{2L\tilde{w}} = \frac{nf\left(0\right)}{2L}$$

Since $f\left(0\right)$ must be estimated from the data, the density estimator is more properly expressed as $\hat{D} = \frac{n\hat{f}\left(0\right)}{2L}$

If the samples are taken from an area of known size A, then the abundance can be estimated by:

$$\hat{N} = \hat{D}A$$

In particular, if the sampling is stratified, each stratum having an area A_j, then the estimate of overall abundance is obtained as:

$$\hat{N} = \sum_{j=1}^{J} A_j \hat{D}_j$$

c) Assumptions

Buckland et al. (1993) states that to develop a statistical model for line transect sampling it is necessary to make assumptions about random sampling and field sampling.

Random sampling

Transect lines are assumed to be randomly positioned with respect to the distribution of objects. This assumption is automatically met if individuals are randomly located over their range, irrespective of placements of the transect lines. If individuals are not randomly distributed, then the transect lines must be randomly located over the population range. For details of sampling designs see Buckland et al. (1993).

Field sampling

There are three assumptions pertaining to field sampling which are critical to reliable density estimation. These are:

1. Individuals directly on a transect line are certain to be observed, thus the probability of detection for individuals on a transect is one.
2. Objects are detected at their initial locations and the locations of individuals are not influenced by observation, thus individuals do not move prior to detection in response to sampling disturbance. If this assumption does not hold then large biases may occur in the resulting estimates. Also, any movement after initial detection does not result in individuals being counted more than once.
3. Distances and angles are measured accurately, thus neither measurement errors nor rounding errors occur. This assumption can only be met by accurate field methods and careful data recording.

Buckland et al. (1993) considers the three assumptions on field sampling to be essential for reliable estimation of density from line transect surveys. In addition to these assumptions, the statistical models for line transect sampling require assumptions about the nature of the data collection and the underlying detection model. Of particular importance is the assumption that individual sightings are independent events. Buckland et al. (2001) suggest that this assumption can be relaxed if robust procedures of variance estimation are adopted. More critical to estimation are assumptions about the shape of the detectability function, especially on or near the transect line. Failure of any of the three assumptions above can cause substantial bias. The effect of violating the first two assumptions and ways to deal with them, have been the subject of recent work (Laake, 1978; Buckland & Turnock, 1992; Quang & Becker, 1997; Borchers et al., 1998a,b). The third assumption has received less emphasis.

2.1.2 Mark-recapture methods

This is sometimes known as *capture-recapture sampling.* The method involves randomly selecting organisms and marking them. The marking of individuals is done in a variety of ways. It is usually designed to satisfy the unique identification of the animals under study in the environment in which they reside. The marked individuals are then mixed back with the rest of the animals. The animals are then sampled again making note of the number of marked animals 'caught' a second time. The concept of ratio and proportion based on the Hypergeometric distribution are then used to estimate the total number of objects.

Primarily, the objective of a mark-recapture method is to obtain an estimate of the number of individuals in an animal population (*abundance*). At the same time animals are marked, other characteristics are usually measured, such as length, weight, sex and general health condition, and this is true only when animals are physically captured. As for the black rhino, the animal was not physically captured. The marked black rhino are those that are recognisable by the natural markings on them for example, a visible cut on the ear, a damaged horn or a particular pattern of natural markings on the body. These characteristics are then re-examined for each marked individual recaptured in subsequent

samples. These data allow the investigator to estimate not just population size but population health and constitution.

Steps in carrying out the method:

- A set of randomly selected (captured) individuals is marked and then released back into their original population (environment).
- These marked individuals are assumed to mix freely with unmarked individuals in the population.
- One or more follow up samples of randomly chosen individuals are selected and examined.
- The ratio of marked to unmarked individuals in the sample is used to estimate abundance.

The more follow-up samples taken, the better the estimate of animal abundance. Mark-recapture methods are one approach to animal abundance estimation in a broader class of *change-in-ratio techniques*. Mark-recapture technique makes certain *assumptions*. Making assumptions is an essential step in all research. Change-in-ratio technique is a useful practical procedure for estimation of fish and wildlife population sizes. It requires pre and post removal "type" ratios such as size and sex and that the number of removals of each type be known. Change-in ratio methods estimate population abundance based on changes in the composition of populations before and after interventions, such as hunter harvest. They offer a cost-effective and efficient alternative to population analysis because the data can be obtained easily (Skalski and Millspaugh, 2006). Despite a long history of use and several quantitative advancements, computational requirements have limited the interest and opportunity to use more informative and precise change-in ratio techniques.

Assumptions made in mark-recapture sampling:

1. Assume that every organism in the population has an equal chance of being captured. Thus, both individuals and follow up samples must be *random* samples.
2. Assume that there is no change in the ratio between marked and unmarked organisms during the interval between samplings. This means, for example, that the marking technique does not make an organism more likely to be eaten by a predator. It is acceptable if some of the organisms in the population emigrate or die, as long as there is no difference between marked and unmarked animals.
3. Assume that the marked animals, when they are released back into the wild, distribute themselves randomly. If all the marked organisms were to remain near the trap or place of observation (as was the case with the black rhino), then they might be more likely to be caught in the second sample. This would affect the estimate, as the proportion of marked animals will be large.
4. Finally, assume that there is no increase in the size of the population between samplings as a result of births or immigration of unmarked animals. This also would change the ratio of marked to unmarked animals.

Thus samplings must be random, and the time between samplings must be long enough to allow for thorough mixing of marked animals, but not so long as to allow for an increase by immigration or reproduction. The estimation for the mark-recapture method depends on the nature of the data collected and the assumptions. A number of models are available for the different situations. For details of the models see Buckland et al. (1993), Borchers et al. (2002), Williams et al. (2002).

Bell et al. (2003) developed a mark-recapture approach to estimate population density from continuous trapping data. The method incorporates flexibility to allow for sampling difficulties encountered in real field experiments. They described a short-term mark-recapture experiment, which was aimed at estimating density of edible crabs (*Cancer pagurus).* They further used bootstrapping to show that temporal variation is much more important than spatial variation as a component of uncertainty in density estimates.

Zwane and Van der Heijden (2003) also presented an algorithm for the parametric bootstrap that can be used when there are continuous covariates. The parametric bootstrap was used for variance estimation for mark recapture estimates.

Zwane and Van der Heijden (2004) further developed a flexible method for modelling capture-recapture data with continuous covariates that describe heterogeneous catchability.

Link and Barker (2005) presented a hierarchical extension of the Cormack-Jolly-Seber (CJS) (Cormack, 1964; Jolly, 1965; Seber, 1965) model for open population capture recapture data. They modeled first the capture of animals and then the losses on capture. The procedure was illustrated using mark recapture data for the moth *Gonodontis bidentata.*

Harrington et al. (2001) conducted mark-release-recapture studies in Puerto Rico and Thailand to determine whether estimated daily survival rates between two different age cohorts of the dengue vector Aedes aegypti (L.) were the same. Survivorship was estimated with non-linear regression analysis using bootstrapping to obtain estimates of errors.

Minta and Mangel (1989) proposed a bootstrap estimator based upon the frequency of resightings of marked individuals and the total sightings of unmarked individuals (some of which may be spotted more than once). A bootstrap procedure was also used to determine the variance and 95% confidence interval for each population estimate. An estimate of the population was obtained from the bootstrap method. The Minta and Mangel (1989) method was based on Monte Carlo simulation. The percentage values associated with the population estimates represented the percentage of times that the bootstrap procedure calculated a larger or smaller value for the population. Variance estimates were based on 1000 iterations of the bootstrap procedure.

2.1.3 Brief review of State Space Models of population abundance

Model choice is an important issue within any analysis of wildlife populations, since the different models represent different competing hypotheses for the underlying dynamics of the system. Morgan et al. (2002) provide an integrated stochastic analysis of separate data sets relating to survival and reproduction. Their approach centres on a state space model for survey data, which is combined with a model for mark recapture data. The work is illustrated by application to ring–recovery data. They also unify capture-recapture methodology and Leslie matrix population modelling.

Newman (1998) also uses state-space modelling to describe the annual movements and mortalities of Pacific coho salmon (*Oncorhynchus ksutch*) populations over time. The Kalman filtering algorithm was used in this case to estimate and predict parameters. Animal survival and migration was approached at the individual animal level with decomposition into the three components of initial location, survival and movement. Newman (1998) used stochastic models for both the unobservable fish movements and their mortalities.

Besbeas et al. (2002) show how a state space model for census data in combination with the usual multinomial based models for ring recovery data provide estimates of productivity not available from either type of data. Also Besbeas et al. (2005) describe an approach, which centres on a state space model for abundance data which is combined with a capture-recapture model and probabilistic modelling of fecundity data. Their procedure provides a way of assessing animal population dynamics and can be applied to avian, fish and mammal populations.

Buckland et al. (2004) developed a unified framework for jointly defining population dynamics models and measurements taken on a population. The framework was a state-space model where the population processes were modelled by the state process and measurements were based on the observation process. The method they developed was fully flexible for allowing stochastic variation in the processes.

Hosn (1999) investigated behavioural sequences of juvenile brook trout (*Salvelinus fontinalis)* by time-lapse video recording in the laboratory. He then introduced a state space model using the estimated time dependent probabilities to capture the temporal structure of the fish behaviour.

Other models, which have been used to analyse multiple animal surveys, include the stochastic diffusion model originally proposed by Dennis et al. (1991). Some other models for estimating animal abundancy are mentioned in Fatti et al. (2002). The model proposed by Fatti et al. (2002) is much simpler than most of the models given above. The motivation of the model was the principle of parsimony, particularly in view of the relatively small number of surveys which have been conducted in the Hluhluwe-Umfolozi Park. The model proposed by Fatti et al (2002) does not distinguish between estimation of juveniles and adults. A full description of the model is given in Chapter 3.

2.3 Resampling

Resampling is a procedure in which inference is based upon repeated sampling within the same sample. Resampling is a revolutionary methodology because it does not necessarily require distributional assumptions about the data. It is a process for estimating probabilities by conducting vast numbers of numerical experiments. Resampling techniques generally rely on the computer to generate data sets from the original data. The techniques differ, however, as to how they generate the datasets. Resampling techniques allow us to base the analysis of a study solely on the design of that study, rather than on a possible poorly fitting model.

Diaconis and Efron (1983) argued that resampling frees researchers from two limitations of conventional statistics:

1. Assumption that the data conform to a normal distribution.
2. The need to focus on statistical measures whose theoretical properties can be analysed mathematically.

Peterson (1991) defined resampling as an approach that addresses a key problem in statistics, that is, how to infer the 'truth' from a sample of data that may be incomplete or drawn from ill-defined population. According to Simon and Bruce (1991), resampling prevents researchers from simply taking the formula for some test without understanding why they use the test.

The difference between resampling methods is the nature of the resamples. For example, some are conducted with replacement while others are conducted without replacement. There are at least four major types of resampling, and these are:

- Randomisation exact testing
- Cross validation
- Jackknife
- Bootstrap.

2.3.1 Randomisation exact testing

This is also known as the permutation test. R.A Fisher (1935/1960), one of founders of classical statistical testing, developed the test. The randomisation exact test is a test procedure in which data are re-assigned so that an exact p-value is calculated based on the permuted data. It is normally treated as a different approach to resampling because it exhausts all possible outcomes. The lack of computers in Fisher's early years required him to automate such a laborious method and as a result he lost interest in the permutation method.

The randomisation procedure starts with the original data and draws samples without replacement. These procedures systematically reorder (shuffle) the data many times and calculate the appropriate test statistic on each reordering, then compare actual test statistic against the randomisation distribution of test statistic. Since shuffling data amounts to sampling without replacement, the issue of replacement is one distinction between bootstrapping and randomisation.

2.3.2 Cross validation

Cross validation involves using part of the available observations to fit the model and a different part to test the fit of the model. The focus of cross validation is prediction rather than on the model parameters. The original objective of cross validation was to verify replicability of results. As with hypothesis testing the goal is to find out if the result is replicable or just a matter of random chance. Cross validation and bootstrapping are both methods for estimating error based on resampling. Cross validation can also be used for parameter estimation by choosing the parameter value which minimises the prediction error. This is a powerful method widely used in statistics.

Cross validation is classified into several categories, namely simple cross validation, double cross validation and multicross validation. Simple cross validation was proposed by Kurtz (1948). Moiser (1951) developed double cross validation which was later extended to multi-cross validation by Krus and Fuller (1982).

a) Simple cross validation

The method works by dividing the data set into two groups one for training and the other for testing. The parameters β are estimated on the training data set, where the β coefficients are the standardized coefficients obtained from fitting the model. Cross validation prediction standard error is computed using the test sample.

b) Double cross validation

Models are generated on both sub-samples and then both models are used to generate cross validation standard errors. With double cross validation we do cross validation using "Sample A" as training sample and "Sample B" as testing sample, then repeat cross validation using "Sample B" as training sample and "Sample A" as testing sample.

c) Multicross validation

This is an extension of double cross validation. The procedure involves repeating the double cross validation procedures many times by randomly selecting sub-samples from the data.

d) K-fold cross validation

This is one of the ways to improve the simple cross validation method. The data set is divided into *k* subsets, and the simple cross validation method is repeated *k* times. Each time, one of the *k* subsets is used as the test set and the other *k-1* subsets are put together to form a training set. The error variance across all *k* trials is then computed. The advantage of this method is that it matters less how the data are divided. Every data point is used in a test set exactly once, and is used in a training set *k-1* times. The disadvantage of this method is that the training algorithm has to be rerun from scratch *k* times, which means it takes *k* times as much computation to make an evaluation. A variant of this method is to randomly divide the data into a test and training sets *k* different times. The advantage of doing this is that the researcher is able to independently choose how large each test set is and the average number of trials. For small data sets it will be best to use 'leave-one-out' cross validation where $k = n$. The general procedure of 'leave-one-out' cross validation is to hold out one observation from the data set, to fit the model on the remaining observations and evaluate that fit on the item that was left out (Hubert & Engelen, 2004). The one observation left out is used as the validation set with the remainder of the data being the training set. A prediction is made for that point left out and the average error is computed and used to evaluate the model. This procedure is more like the jackknife procedure.

The principal difference between cross validation and the bootstrap is that the bootstrap re-samples the available data with replacement, whereas cross validation does it without replacement. Stone (1974, 1977) was the first to give clearly stated accounts on cross validation. According to Shtatland et al. (2003) "cross validation is not the ultimate answer to model selection. It only works well in a few situations, because it has bad asymptotic properties. That is why we need additional techniques such as the bootstrap". According to Efron (1983), bootstrapping seems to work better than cross validation in many cases.

2.3.3 Jackknife

This tool is also known as the Quenouille-Tukey Jackknife and was invented by Quenouille (1949) and later developed by Tukey (1958). Tukey (1958) attempted to use the Jackknife to explore how a model is influenced by subsets of observations when outliers are present. Jackknife is a step beyond cross validation. In the Jackknife the same test is repeated by leaving one subject out each time, thus the technique is also known as 'leave-one-out'; this is a special case of the jackknife. The more general case of the jackknife is the 'leave-k-out' where the test is repeated by leaving k subjects out each time. This procedure is especially useful when the dispersion of the distribution is wide or extreme scores are present in the data set. The jackknife was first introduced to reduce bias by Quenouille (1949). The method was introduced to estimate bias and variance of a statistic and to test whether the statistic has pre-specified mean.

A jackknife estimator is a kind of non-parametric estimator for a regression function. It is a linear combination of kernel estimators with different window widths. Jackknife estimators have higher variance but less bias than the kernel estimators. A jackknife creates a series of statistics, usually a parameter estimate from a single data set, by generating that statistic repeatedly on the data set leaving one data value out each time. This produces a mean estimate of the parameter and a standard deviation of the estimates of the parameter. The jackknife is a method that allows one to judge the uncertainties of estimators derived from small samples without assumptions about the underlying probability distributions. For each of the samples generated from the jackknife the estimator under study can be calculated and the probability distribution of the estimator obtained will allow a researcher to draw conclusions about the estimator's sensitivity to individual observations.

The jackknife as applied in this research consists of two steps:

1. Forming systematic groups from the full sample by leaving out one observation at a time.
2. Computing the estimate of variance for the parameter of interest.

The jackknife has been used both to estimate and compensate for bias in statistical estimates and to derive robust confidence intervals. It assesses the variability of a statistic by examining the variation within the different jackknife estimates rather than through the use of parametric assumptions. The jackknife is primarily used for making inferences in cases of complex sampling and for identifying outlying data points. The jackknife is also used for bias reduction and estimation of standard error of estimates. Given a data set $\mathrm{x} = (x_1, x_2, ..., x_n)$ and an estimator $\hat{\theta} = s(x)$. We wish to estimate the bias and standard error of $\hat{\theta}$. The ith jackknife sample x_i is defined to be x with the ith data point removed, $x_i = (x_1, x_2, ..., x_{i-1}, x_{i+1}, ..., x_n)$ for $i = 1, 2, ..., n$. Let $\hat{\theta}_{(i)} = s(x_{(i)})$ for $i = 1, 2, ..., n$ be the ith jackknife replication of $\hat{\theta}$

The jackknife estimate of bias is then defined by:

$$Bias_{jack} = (n-1)\left(\hat{\theta}_{(\cdot)} - \hat{\theta}\right)$$

Where $\hat{\theta}_{(\cdot)} = \dfrac{\sum_{i=1}^{n} \hat{\theta}_{(i)}}{n}$. The jackknife estimate of standard error will then be defined by:

$$\hat{se}_{jack} = \left[\frac{n-1}{n}\sum\left(\hat{\theta}_{(i)} - \hat{\theta}_{(\cdot)}\right)^2\right]^{\frac{1}{2}}$$

You and Chen (2003) proposed the jackknife estimator for reducing bias in partially linear regression models. They compared the jackknife estimator to the semi- parametric least squares estimator (SLSE). The simulated results showed that the confidence interval estimation based on the jackknife estimator had better coverage probability than that based on the SLSE.

Kezdi and Solon (2001) proposed a jackknife minimum distance estimator designed to reduce the finite bias of the optimal minimum distance estimator. Their Monte Carlo results indicated that their jackknife minimum distance estimator is a promising alternative to existing minimum distance procedures.

Biswal et al. (2001) used the jackknife to determine the reliability and the confidence intervals of task activated functional MRI (fMRI) parameters. In their research they concluded that the jackknife resampling technique for data analysis produced reliable distributions and statistical parameters. It was shown that the jackknife estimates were stable even for small sample sizes.

Consideration on the jackknife

The major motivation for the jackknife estimates is that they reduce bias. The jackknife can fail, however, if the statistic $\hat{\theta}$ is not smooth (that is, small changes in data cause large changes in the statistic). Some examples of non-smooth statistics for which the jackknife works badly are the median and quantiles. Jackknife resampling has the drawback that the sub-replicates are of a smaller size than the original data set which may change the statistical properties of the samples. For this reason, the jackknife has largely been replaced by the bootstrap. Best results for the jackknife are obtained with statistics that are linear functions of the data. For highly non-linear statistics the jackknife can be inaccurate.

2.3.4 The bootstrap method

The term bootstrap is derived from the phase "*to pull oneself up by one's bootstraps"*. Davison and Hinkley (1997) suggest that the bootstrap was so called because "to use the data to generate more data seems analogous to a trick used by the fictional Baron Munchausen, who when he found himself at the bottom of a lake got out by pulling himself up by his bootstraps. Bootstrap is a computer based resampling method for assigning measures of accuracy to statistical estimates. In statistics bootstrapping can be defined as a method for estimating the sampling distribution of an estimator of a

parameter (vector) by resampling with replacement from the original sample. Bootstrapping is a process of randomly sampling n times with replacement from the original data points and the process is repeated a large number of times, say B independently. The process yields a standard error and confidence interval for the unknown parameter (vector), which is a function of the original data.

The bootstrap technique was invented by Efron (1979, 1981, 1982) and further developed by Efron and Tibshirani (1993). Efron (1981, 1982) developed bootstrap with inferential purposes. Bickel and Freedman (1981) formulated conditions for consistency of the bootstrap. Work by Bickel and Freedman (1981) resulted in further extensions of Efron's methodology (bootstrap) to a broad range of standard applications, including regression and stratified sampling. Efron's bootstrap is a Monte Carlo simulation that requires no distributional assumptions about the underlying population from which the data are drawn.

The bootstrap method is a computationally intensive statistical method that can require a large number of iterations and hence usually requires the use of the computer. Since the early work of Efron other forms of the bootstrap and methods of implementation have emerged. Meeker and Escobar (1998) used bootstrapping to estimate percentiles.

Boos (2003) gives his own opinion on bootstrapping. He contends that 'the real reason the bootstrap was so path-breaking and has remained so popular is that Efron described it mainly in terms of creating a 'bootstrap world, where the data analyst knows everything'. He further described the bootstrap as a technique that has made a fundamental impact on how we carry out statistical inference in problems without analytical solutions.

Chatterjee and Bose (2005) introduced a generalised bootstrap technique for estimators obtained by solving estimating equations; some special cases of this generalised bootstrap were the classical bootstrap of Efron, the delete-*d* jackknife and variations of the Bayesian bootstrap. They established distributional consistency of the method and an asymptotic representation of the resampling variance estimator was obtained.

Herwartz and Neumann (2004) analysed OLS based tests of long run relationships, weak exogeneity and short run dynamics in conditional error correction models. In their Monte Carlo studies they revealed that in small samples the bootstrap outperforms first order asymptotic approximations in terms of the empirical size even if the asymptotic distribution of the test statistic does not depend on nuisance parameters.

Serneels and Espen (2005) showed that the bootstrap is a successful technique to obtain confidence limits for estimates where it is theoretically impossible to establish an exact expression for them. They applied the bootstrap to trilinear partial least squares regression and revealed that the bootstrap confidence intervals have a desirable coverage.

Bootstrapping (Efron & Tibshirani, 1993) is now extensively used for simulating samples from a real data set, evaluating bias, estimating variances, and constructing confidence limits. Bootstrapping is also used for incorporating model uncertainty into estimation.

Norris and Pollock (1996b) discuss a bootstrap approach for estimating the population sizes in closed populations which takes into account the fact that the model is unknown. They also make some recommendations for open populations.

Carlson et al. (1998) developed a bootstrap technique for quantifying estimation precision, provide a procedure for determining sample size and present a method of estimating short term mark survival. The method was applied to sockeye salmon (*Oncorhynchus nerka*) smolts. The bootstrap was also used to derive the variance and confidence intervals for the estimates.

Reeves (2005) used both the parametric and non-parametric bootstrap to construct prediction intervals for autoregressive conditional heteroskedasticity, and on comparing the prediction intervals to traditional asymptotic prediction intervals they found that the bootstrap leads to improved accuracy.

Davison et al. (2003) stated that the bootstrap has provided both a powerful set of solutions for practical statisticians and a rich source of theoretical and methodological problems for statistics since its introduction. In the same article they explained that when the data are independent but not identically distributed, the key step in applying the bootstrap is to identify exchangeable components to which resampling can be applied and suggested that residuals can often be these components.

Beran (2003) gave three points that he considered were brought about by bootstrap procedures and he further developed the first two points which are:

1. Bootstrap algorithms provide an effective and intuitive way to realise certain programs in statistics. These include the construction of (possibly simultaneous) confidence sets, test and prediction regions in classical models for which exact or asymptotic distribution theory is intractable.
2. Success of the bootstrap, in the sense of doing what is expected under a probability model for data, is not universal, and modifications to Efron's (1979) definition of the bootstrap are needed to make the idea work for estimators that are not classically regular.

Lahiri (2003) suggested that 'the bootstrap is probably the most flexible and efficient method of analysing survey data since it can be used to solve a variety of challenging statistical problems (for example, variance estimation, imputation, small area estimation) for complex surveys involving both smooth and non-smooth statistics'. 'Survey sampling is a fascinating field and is constantly offering practical problems that are theoretically challenging'. The flexibility of the bootstrap and its straightforward implementation in a complex environment will certainly make the method suitable for handling new problems in the field of survey sampling.

According to Politis (2003), the two main reasons for the immense success and popularity of the independent and identically distributed (iid) bootstrap of Efron (1979) are:

1. The bootstrap was shown to give valid estimates of distribution and standard error in 'difficult' situations; a prime example is the median of iid data for which the

(delete 1) jackknife was known to fail and the asymptotic distribution is quite cumbersome.

2. In 'easy' cases where easy-to-construct alternative distribution estimators exist, for example the regular sample mean with its normal large sample distribution, the (studentized) bootstrap was shown to outperform those alternatives, that is, to possess 'second order accuracy'.

The bootstrap was first introduced in an attempt to give some new perspective to an old and established statistical procedure, the jackknife. Unlike jackknifing, which is mostly concerned with calculating standard errors of statistics of interest and for reducing bias, the bootstrap has been set to achieve the more ambitious goal of estimating not only the standard error but also the distribution of a statistic. The bootstrap employs sampling with replacement which is more accurate than sampling without replacement in terms of simulating chance. The bootstrap method has the advantage of modelling the impacts of the actual sample size (Fan & Wang, 1996) unlike cross validation and jackknife where n in the sub-sample is smaller than that in the original sample. Bootstrapping can also be used to obtain precision estimates for structural equation models or for regression trees.

The bootstrap procedures are widely used, particularly in cases where no analytical methods exist for determining the sampling distribution of a statistic. The statistical method of bootstrapping is based on the assumption that the statistical properties of a sample should be similar to the statistical properties of the population from which the sample was drawn. The larger the sample the more representative it should be of the population. Conversely, if the original sample was large enough, it should also be possible to take smaller samples from the larger sample and expect that the smaller samples also retain most of the statistical properties of the original population.

The bootstrap is often used to find:

1. Standard errors for estimators
2. Confidence intervals for unknown parameters
3. p values for test statistics under a null hypothesis.

The bootstrap is easy to implement and flexible. Its principle can be adapted to virtually all the problems encountered in statistics; however, bootstrap is a computer intensive procedure and it is not a panacea. For example, bootstrapping sparse or messy data does not make it more informative or well behaved.

In this research expectation, variance and probability calculated with respect to a simulation distribution are written with an asterisk * as, $E_*(\cdot)$, $Var_*(\cdot)$ and $P_*(\cdot)$, respectively, to show that they are obtained from a bootstrap analog.

a) The bootstrap estimate of standard error

We let $\mathbf{x} = \{x_1, x_2, ..., x_n\}$ be a single, homogeneous sample of data. The sample values are thought of as the outcomes of independent and identically distributed random variables $X_1, X_2, ..., X_n$ whose probability density function (PDF) and cumulative distribution function (CDF) will be denoted by f and F, respectively. The sample is to be used to make inferences about a population characteristic, generally denoted by θ using a statistic S whose value in the sample is s. The bootstrap method makes inferences about $\theta = s(F)$ from $\hat{\theta} = s(\hat{F})$, which is a characteristic of the sample. Focus is made on the probability distribution of $\hat{\theta}$, its bias, its standard error, its quantiles and its confidence values.

In the bootstrapping method there are two situations to distinguish, the parametric and the non-parametric. The parametric situation is when there is a particular mathematical model with adjustable constants or parameters that fully determine f. The statistical methods based on this model are parametric methods. When there is no mathematical model used, the statistical analysis is non-parametric and uses only the fact that the random variables X_j are independent and identically distributed. Even if there is a plausible parametric model, a non-parametric analysis can still be useful to assess the robustness of conclusions drawn from a parametric analysis (Davison & Hinkley, 1997).

The empirical distribution plays an important role in non-parametric analysis as it puts equal probabilities n^{-1} at each sample value x_j. The empirical distribution function (EDF) denoted by $\hat{F}$ is the estimate of F (CDF).

The bootstrap estimate of standard errors requires no theoretical calculations and is available no matter how mathematically complicated the estimator $\hat{\theta}$ may be. The method is based on the plug in principle. A plug in estimator is one that uses the same formula to compute an estimate from a sample that is used to compute a parameter from the population.

The bootstrap method depends on the notion of a bootstrap sample. A bootstrap sample is defined to be a random sample of size n drawn from $\hat{F}$ say, $\mathbf{x}^* = \{x_1^*, x_2^*, ..., x_n^*\}$, $\hat{F} \to \{x_1^*, x_2^*, ..., x_n^*\}$ (Efron & Tibshirani,1993), where $\mathbf{x}^*$ is a randomised or resampled version of $\mathbf{x}$. The bootstrap data points $x_1^*, x_2^*, ..., x_n^*$ are a random sample of size n drawn with replacement from $\mathbf{x} = \{x_1, x_2, ..., x_n\}$. Thus the bootstrap data set $\{x_1^*, x_2^*, ..., x_n^*\}$ consists of members of the original data set $\{x_1, x_2, ..., x_n\}$, some appearing zero times, some appearing once, some appearing twice and so on. For each bootstrap data set $\mathbf{x}^*$ there corresponds a bootstrap replication of $\hat{\theta}$:

$$\hat{\theta}^* = s(\mathbf{x}^*)$$

The quantity $s(\mathbf{x}^*)$ is a result of applying the same function $s(\cdot)$ to $\mathbf{x}^*$ as applied to $\mathbf{x}$. If $s(\mathbf{x})$ is the sample mean $\bar{x}$ then $s(\mathbf{x}^*)$ is the mean of the bootstrap data set $\bar{x}^* = \frac{1}{n}\sum_{i=1}^{n} x^*$.

The bootstrap estimate of $se_F(\hat{\theta})$ defined by $se_{\hat{F}}(\hat{\theta}^*)$ is called the ideal bootstrap estimate of standard error of $\hat{\theta}$ and it is the standard error of $\hat{\theta}$ for the datasets of size n randomly sampled from $\hat{F}$. A computational way of obtaining a good approximation to the numerical value of $se_{\hat{F}}(\hat{\theta}^*)$ is by using the bootstrap algorithm which is described in the next section.

b) The bootstrap algorithm for estimating standard errors (Efron & Tibshirani, 1993)

1. Select B independent bootstrap samples $\mathbf{x}^{*1}, \mathbf{x}^{*2}, \ldots, \mathbf{x}^{*B}$, each consisting of n data values drawn with replacement from $\mathbf{x}$.
2. Evaluate the bootstrap replication corresponding to each bootstrap sample:

$$\hat{\theta}^*(b) = s(\mathbf{x}^{*b}) \qquad b = 1,2,\ldots,B$$

3. Estimate the standard error $se_F(\hat{\theta})$ by the sample standard deviation of the B replications

$$\widehat{se}_B = \left\{ \frac{1}{B-1} \sum_{b=1}^{B} \left(\hat{\theta}^*(b) - \hat{\theta}^*(\cdot) \right)^2 \right\}^{\frac{1}{2}}$$

where

$$\hat{\theta}^*(\cdot) = \frac{1}{B} \sum_{b=1}^{B} \hat{\theta}^*(b)$$

The bootstrap algorithm works by drawing many independent bootstrap samples, evaluating the corresponding bootstrap replications and estimating the standard error of $\hat{\theta}$ by the empirical standard deviation of the replications. The result is called the bootstrap estimate of standard error denoted by $\widehat{se}_B$, where B is the number of bootstrap samples used. The algorithm given above is referred to as the Monte Carlo Algorithm (Efron, 1982). The ideal bootstrap estimate $se_{\hat{F}}(\hat{\theta}^*)$ and its approximation $\widehat{se}_B$ are called non-parametric bootstrap estimates because they are based on $\hat{F}$. The parametric bootstrap uses a different estimate of F.

c) The number of bootstrap replications B

Determining the number of replications is a complicated matter and depends on the statistic of interest and the unknown bootstrap distribution. In variance and bias calculations the number of replications required is less than when computing confidence limits. The amount of computer time depends mainly on how long it takes to evaluate

each bootstrap replication. The time increases linearly with B. Time constraints may dictate a small value of B if $\hat{\theta} = s(\mathbf{x})$ is a complicated function of $\mathbf{x}$. An approximate, but quite satisfactory answer can be phrased in terms of the coefficient of variation of $\widehat{se}_B$. The increased variability as a result of stopping after B bootstrap replications, rather than going on to infinity, is reflected in an increased coefficient of variation,

$$cv(\hat{se}_B) = \frac{Var(\hat{se}_B)^{\frac{1}{2}}}{E(\hat{se}_B)}$$

$$cv\left(\widehat{se}_B\right) \approx \left\{ cv\left(\widehat{se}_\infty\right)^2 + \frac{E(\Delta)+2}{4B} \right\}^{\frac{1}{2}}$$

where E(Δ) is the parameter that measures how long tailed the distribution of $\hat{\theta}^*$ is. Δ is zero for the normal distribution, it ranges from -2 for the shortest tailed distribution to arbitrarily large values when F is long tailed (Efron & Tibshirani, 1993). The rule of thumb, gathered by Efron and Tibshirani (1993) experimentation is:

1. Even a small number of bootstrap replications, say B=25, is usually informative. B=50 is often enough to give a good estimate of $se_F\left(\hat{\theta}\right)$.
2. Very seldom are more than B=200 replications needed for estimating a standard error. Much bigger values of B are required for bootstrap confidence intervals.

According to Gould and Pitblado (2001), the key to choosing the right number of replications is:

1. Choose a large but tolerable number of replications. Obtain the bootstrap estimates.
2. Change the random number seed. Obtain the bootstrap estimates again, using the same number of replications.
3. Repeat step 2 and compare the results. Try a larger number and if the results are similar enough, you probably have a large enough number.

Efron and Tibshirani (1993) suggest that for confidence intervals we use bootstrap replications of 1000. Davison and Hinkley (1997) also reported that 1000 replications are sufficient for many applications. In determining the evolutionary potential of a gene, Hall and Malik (1998) also considered 1000 replications to be the best.

d) The parametric bootstrap

The parametric bootstrap estimate of standard error is defined as:

$$se_{\hat{F}_{par}}\left(\hat{\theta}^{*}\right)$$

where $\hat{F}_{par}$ is an estimate of F derived from a parametric model for the data. Instead of sampling from the data, we draw *B* samples of size *n* from the parametric estimate of the population $\hat{F}_{par}$. The parametric bootstrap is useful in problems where some knowledge about the form of the underlying population is available, and for comparison with non-parametric analysis.

The parametric bootstrap involves sampling from a known distribution with estimated CDF $\hat{F}_{par}$ and the CDF is a member of some prescribed parametric family, whereas the non-parametric bootstrap sampling is sampling at random with replacement from the known sample. The non-parametric bootstrap relies on consideration of the empirical distribution generated by the random sample. The non-parametric method is used more often since it does not require information about the underlying distribution.

Performing bootstrapping with the "correct" parametric model and performing non-parametric bootstrap are asymptotically equivalent (Davison & Hinkley, 1997). In practice, the Empirical Distribution Function (EDF) produces results close to those of the nearest parametric model. In situations where each bootstrapping cycle incurs a considerable computational cost, the non-parametric bootstrap can aid the choice of a parametric model. For more details about the parametric bootstrap see Efron and Tibshirani (1993) and Davison and Hinkley (1997).

e) Bootstrapping in Regression Models

Regression analysis is one of the most important and frequently used types of statistical analysis, in which we study the effects of explanatory variables or covariates on a response variable. We consider a standard linear regression model:

$$\mathbf{Y} = \mathbf{X}\beta + \varepsilon$$

where $\mathbf{X}$ is an $(n \text{ x } k)$ matrix of exogenous variables, β is a $(k \text{ x } 1)$ vector of regression coefficients and $\mathbf{Y}$ is an $(n \text{ x } 1)$ vector of response variables. ε is an $(n \text{ x } 1)$ vector of error terms, that is random fluctuations of Y about its true expected value $X\beta$. For a simple linear regression with one exogenous variable we have:

$$Y_j = \beta_0 + \beta_1 x_j + \varepsilon_j \qquad\qquad j = 1,\ldots,n$$

The simplest analysis of the model is by Ordinary Least Squares method (OLS) and the OLS estimates of β are:

$$\hat{\beta}_1 = \frac{\sum_{j=1}^{n}\left(x_j - \bar{x}\right)y_j}{\sum_{j=1}^{n}\left(x_j - \bar{x}\right)}$$

where $\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_j$ and $\hat{\beta}_0 = \bar{y} - \hat{\beta}_1\bar{x}$

In the regression context bootstrapping can be performed in two ways: resampling the pairs (regressor variables, response) that is, resampling the entire cases of the data or resampling the observed errors/residuals. These are effectively the non-parametric approaches. The two types of non-parametric bootstrapping, which are resampling the data and resampling the residuals, are asymptotically equivalent, but Efron and Tibshirani (1986) noted that the schemes can perform differently in small sample situations. The problem with the former resampling method is that it ignores the error structure of regression model (Freedman 1981, 1984). The whole point of resampling is to mimic the random component of the process. The classic regression model holds that the regressors are fixed constants and that the response is a function of the fixed constants and a random error term (Draper & Smith, 1981). The only random aspect of the process is the error

term, ε_j and therefore it should be the quantity that is resampled in bootstrapping. Efron and Tibshirani (1993) noted that bootstrapping pairs is less sensitive to assumptions than bootstrapping residuals.

Efron (1982) prefers working with centred residuals in regression context. He notes that resampling the residuals may yield misleading results if a vastly over-parameterised model is considered, in which case resampling the data points appears to give reasonable answers (Efron, 1982). Hall (1992) applies a more pragmatic viewpoint, arguing that regression is inherently concerned with inference on the design points and thus the residuals and not the pairs should be sampled. Bootstrapping of regression models is discussed at a deeper mathematical level by Freedman (1981) and Bickel and Freedman (1983). Efron (1991) discussed the estimation of regression percentiles.

f) Bayesian bootstrap

Bayesian bootstrap is a variation proposed by Rubin (1981) where different observations in the sample may have different chances of being selected in the resample. When the data are grouped or extreme observations are present in the sample or sampling units are of unequal size, it is more appropriate to assign unequal probabilities of selection to each observation in the original sample to get the resampled observations. The other use of the Bayesian bootstrap was the imputation when data are missing rather than inference for θ per se. Rubin (1981) introduced this variation in the bootstrap with a Bayesian justification. The Bayesian bootstrap was first developed for simple random sampling with replacement (with sample size n).

If the data consists of random sample $x_1, x_2, ..., x_k$, let the data vector x assume at most K distinct values and let $d = (d_1, d_2, ..., d_K)$ be a vector of these distinct values. Let f_i counts how many x_i equal to d_j. Define the vector of probabilities $\alpha = (\alpha_1, \alpha_2, ..., \alpha_K)$ by:

$$\Pr(x_i = d_k \mid \alpha) = \alpha_k, \qquad \sum \alpha_k = 1$$

The probability of the observed data given the values of α_j is proportional to $\prod_{j=1}^{k} \alpha_j^{f_i}$. If the prior information regarding the d_j is summarized in the prior density $\pi(\alpha_1, \alpha_2, ..., \alpha_k)$ the joint posterior density of α_j given the data is proportional to

$$\pi(\alpha_1, \alpha_2, ..., \alpha_k) \prod_{j=1}^{k} \alpha_j^{f_i}$$

and this induces a posterior density for θ. If π is the Dirichlet density the prior and posterior densities are respectively proportional to

$$\prod_{j=1}^{k} \alpha_j^{a_i}, \quad \prod_{j=1}^{k} \alpha_j^{a_j + f_i}$$

In practice with continuous data we have $f_j \equiv 1$. The simplest version of the simulation puts $a_j = -1$, corresponding to an improper prior distribution with support on $x_1, x_2, ..., x_k$; the G_j are exponential.

Rubin (1981) showed that the Bayesian bootstrap procedure is equivalent to assuming that the prior distribution of α is the (improper) distribution:

$$\Pr(\alpha) = \prod_{k=1}^{K} \alpha_k^{-1} \qquad \textit{where } \sum \alpha_k = 1$$

The posterior distribution of α, is, by Bayes Theorem, proportional to its prior distribution multiplied by the likelihood, and turns out to be:

$$\Pr(\alpha \mid x) \propto \prod_{k=1}^{K} \alpha_k^{n_k - 1}$$

where the n_k are the number of x_i equal to d_k for $i = 1, 2, ..., n : \sum n_k = n,$ and $\sum \alpha_k = 1$.

According to Rubin (1987), Bayesian bootstrap sample x^{*b} is selected by a two-step procedure as follows:

Step1: Draw uniform random numbers between 0 and 1 and let their ordered values be $a_1, a_2, ..., a_{n-1}$, also let $a_0 = 0$ and $a_n = 1$.

Step 2: Draw each of the n values in $X^{*b} = \left(x_1^{*b}, x_2^{*b}, ..., x_n^{*b}\right)$ by drawing from $x_1, x_2, ..., x_n$ with probabilities $(a_1 - a_0)$, $(a_2 - a_1), ..., (1 - a_{n-1})$, that is independently n times, draw a uniform number u and select x_i if $a_{i-1} < u < a_i$

Heckelei and Mittelhammer (2002) presented a Bayesian Bootstrap Multivariate Regression (BBMR) procedure that allows robust Bayesian posterior analysis of traditional multivariate regression models. Their Monte Carlo study they performed provided evidence on the accuracy and robustness of the approach in representing posterior distributions even under the application of highly non-linear mappings.

Lo (1987) showed that the Bayesian bootstrap has the same desirable large sample properties as Efron's bootstrap.

Kim and Lee (2003) proposed two Bayesian bootstrap extensions, the binomial and the Poisson forms for proportional hazards models. They mention that the advantage of the proposed Bayesian bootstrap procedures over the standard Bayesian analysis is conceptual and computational simplicity.

Horowitz (2004) conducted a Monte Carlo study to evaluate the Bayesian bootstrap performance when estimating the population mean. She considered different sampling distributions and concluded that the Bayesian method performs best for symmetric sampling distributions.

The Bayesian bootstrap was not used in this research.

g) Confidence intervals

Confidence intervals are important for assessing the uncertainty of parameter values. Confidence regions all focus on the same target properties. The first is that a confidence region with specified coverage probability γ should be a set $C_\gamma(y)$ of parameter values which depends only upon the data y and which satisfies

$$\Pr\{\theta \in C_\gamma(y)\} = \gamma$$

where γ, the confidence coefficient or coverage probability, is the relative frequency with which the confidence region would include or cover the true parameter value θ in repetitions of the process that produced the data y. The second important property of a confidence region is its shape. The general principle is that any parameter value inside C_γ should be more likely than all values outside C_γ. A $100(1-2\alpha)\%$ confidence interval will be defined by limits $\hat{\theta}_\alpha$ and $\hat{\theta}_{1-\alpha}$ such that for any α,

$$\Pr\left(\theta < \hat{\theta}_\alpha\right) = \alpha \text{ and } \Pr\left(\theta > \hat{\theta}_{1-\alpha}\right) = \alpha$$

Standard bootstrap confidence limits are based on the assumption that the estimator $\hat{\theta}$ is normally distributed with mean θ and variance σ^2, where the variance is obtained by maximum likelihood estimation. A more direct approach for constructing a $100(1-\alpha)\%$ confidence interval is to use the upper and lower $\frac{\alpha}{2}$ values of the bootstrap distribution of $\hat{\theta}$.

Chernick (1999) described different methods for constructing bootstrap confidence intervals. These included the standard, percentile and bootstrap-t, accelerated percentile, bias corrected and the iterated bootstrap. DiCiccio and Efron (1996) provided a useful survey of many such intervals. The focus was to improve by an order of magnitude upon the accuracy of standard intervals in a way that allows routine application even to very complicated problems.

Singh (1981) and Davison et al. (2003) realised that the bootstrap could deliver higher order accuracy for confidence intervals, equivalent to Edgeworth correction of classical normal intervals, but less painful and less liable to errors and hence more reliable in practice.

1. Standard confidence interval

The bootstrap standard confidence interval is by far the easiest method to implement. It is also known as the normal approximation bootstrap confidence interval. The interval is based on the asymptotic result:

$$z = \frac{\hat{\theta} - \theta}{se_{\hat{\theta}}} : \; N(0,1)$$

The confidence interval is therefore given by:

$$\left[\hat{\theta} - z_{\frac{\alpha}{2}} se_{\hat{\theta}}, \;\; \hat{\theta} + z_{1-\frac{\alpha}{2}} se_{\hat{\theta}} \right]$$

Where $se_{\hat{\theta}}$ is the standard deviation of the bootstrap estimate of θ and $z_{\frac{\alpha}{2}}$ is the $\frac{\alpha}{2}$-quantile of the standard normal distribution. According to Efron and Tibshirani (1993), this method is only an approximation in most problems, though a very useful one in an large variety of situations. The interval can be used when asymptotic normality is valid.

As mentioned earlier expectation, variance and probability calculated with respect to a simulation distribution are written with an asterisk * as, $E_*(\cdot)$, $Var_*(\cdot)$ and $P_*(\cdot)$, respectively, to show that they are obtained from a bootstrap analog.

2. Percentile bootstrap confidence interval

We let $\hat{r}$ be an estimator of r and r^* be its bootstrap analog based on $x_1^*, x_2^*, \ldots, x_n^*$ and define

$$K_{BOOT}(x) = P_*(r^* \le x)$$

The bootstrap percentile method (Efron 1981a) gives the following lower confidence bound for r

$$r_{(lower)} = K_{BOOT}^{-1}\left(\frac{\alpha}{2}\right)$$

The name percentile comes from the fact that $K_{BOOT}^{-1}\left(\frac{\alpha}{2}\right)$ is a percentile of the bootstrap distribution. Thus the $1-\alpha$ percentile confidence interval is defined by the $\frac{\alpha}{2}$ and $1-\frac{\alpha}{2}$ percentile of K_{BOOT}:

$$\left[K_{BOOT}^{-1}\left(\frac{\alpha}{2}\right),\ K_{BOOT}^{-1}\left(1-\frac{\alpha}{2}\right)\right]$$

$K_{Boot}^{-1}\left(\frac{\alpha}{2}\right)$ is obtained by arranging in ascending order the B values of r_b^*, $b = 1,2,\ldots,B$ and considering the $B\left(\frac{\alpha}{2}\right)$ value of r_b^*, and similarly for $K_{BOOT}^{-1}\left(1-\frac{\alpha}{2}\right)$ we consider $B\left(1-\frac{\alpha}{2}\right)$.

If $B\left(\frac{\alpha}{2}\right)$ is not an integer the following procedure by Efron and Tibshirani (1993) can be used.

Assume $\alpha \le 0.5$, let $k = \left[(B+1)\frac{\alpha}{2}\right]$, the largest integer $\le (B+1)\frac{\alpha}{2}$. Then we define the empirical $\frac{\alpha}{2}$ and $1-\frac{\alpha}{2}$ quantiles by the k$^{\text{th}}$ largest and $(B+1-k)^{th}$ largest values of $Z^*(b)$, respectively, where $Z^*(b)$ is computed for each bootstrap sample and is given by:

$$Z^*(b) = \frac{\hat{r}^*(b) - \hat{r}}{\widehat{se}^*(b)}.$$

If the bootstrap distribution of $\hat{r}^*$ is roughly normal, then the standard normal and percentile intervals will nearly agree, since by the central limit theorem as $n \to \infty$ the bootstrap histogram will become normal shaped.

Polansky (1999) showed that bootstrap confidence intervals constructed using the percentile methods have bounds on their finite sample coverage probabilities. It is said that the bounds are valid even for methods that are asymptotically second order accurate.

Martinez and Martinez (2002) and Efron and Tibishirani (1993) maintained that this technique has the benefit of being more stable than the bootstrap-t and it also enjoys better theoretical coverage properties.

Chernick (1999) pointed out that "in the case of small samples the percentile method does not work well. The standard bootstrap percentile intervals are first order accurate (error goes to zero at a rate of $n^{-\frac{1}{2}}$), thus the probability that a one sided interval with nominal level $1-\alpha$ contains θ is $1-\alpha+0\left(n^{-\frac{1}{2}}\right)$, which means that the error getting exactly desired $\frac{\alpha}{2}$ probability is an order of magnitude greater than that of the bootstrap-t intervals which are second order accurate.

It is generally recommended that the number of bootstrap replications should be equal to or greater than 1000 for the method to produce accurate results.

To obtain the percentile confidence intervals the following steps are used:

1. Given a random sample, $\mathbf{x} = (x_1, ..., x_n)$, calculate $\hat{\theta}$.
2. Sample with replacement from the original sample to get $\mathbf{x}^{*b} = (x_1^{*b}, ..., x_n^{*b})$.
3. Calculate the same statistic using the sample in step 2 to get the bootstrap replicate, $\hat{\theta}^{*b}$.

4. Repeat steps 2 through 3, B times where $B \geq 1000$.
5. Order the $\hat{\theta}^{*b}$ from smallest to largest.
6. Calculate $B \cdot \alpha$ and $B \cdot (1-\alpha)$.
7. The lower endpoint of the interval is given by the bootstrap replicate that is in the $B \cdot \alpha$-th position of ordered $\hat{\theta}^{*b}$, and the upper endpoint is given by the bootstrap replicate that is in the $B \cdot (1-\alpha)$-th position of the same ordered list. Alternatively using quantile notation, the lower endpoint is the estimated quantile $\hat{q}_{\alpha}$ and the upper endpoint is the estimated quantile $\hat{q}_{1-\alpha}$, where the estimates are taken from the bootstrap replicates.

3. Other types of confidence intervals

One of the commonly used confidence intervals is the bootstrap-t method. The bootstrap-t confidence intervals are second order accurate (error goes to zero at a rate of 1/n) thus the probability that a one sided interval with nominal level $1-\alpha$ contains θ is $1-\alpha+0\left(n^{-1}\right)$, which makes it a popular choice in practice. Efron and Tibishirani (1993) warned that the method can give erratic results and can be heavily influenced by a few outlying points. Polansky (2000) investigated two methods for stabilising the endpoints of bootstrap-t intervals in the case of small samples. Martinez and Martinez (2002) pointed out that the bootstrap-t interval has good coverage probabilities but does not perform well in practice.

The bootstrap-t method (Efron, 1982) is based on a given studentized "pivot":

$$\Re_t = \frac{\hat{r} - r}{\hat{\sigma}}$$

where $\hat{r}$ is an estimator of r and $\hat{\sigma}^2$ is a variance estimator for $\hat{r}$. If the distribution G_t of $\Re_t$ is unknown, then it is estimated by the bootstrap estimator G_{BOOT} defined by

$$G_{BOOT}(x) = P_*\left\{\Re_t^* \le x\right\}$$

where $\Re_t^* = \dfrac{\hat{r}^* - \hat{r}}{\hat{\sigma}^*}$ and $\hat{r}^*$ and $\hat{\sigma}^*$ are bootstrap analogs of $\hat{r}$ and $\hat{\sigma}$, respectively. The resulting bootstrap-t confidence interval for ε_t is:

$$\left[\hat{r} - \hat{\sigma} G_{BOOT}^{-1}(1-\alpha)\ ,\ \hat{r} - \hat{\sigma} G_{BOOT}^{-1}(\alpha)\right]$$

If $B(\alpha)$ is not an integer, we use the convention given in the percentile method.

The bootstrap-t confidence interval requires the estimation of $\hat{\sigma}$ for each survey estimate as well as $\hat{\sigma}^*$. With the white and black rhino data sets we are only able to obtain $\hat{\sigma}^*$, hence it is impossible in this research to construct the bootstrap-t confidence intervals.

For detailed discussions of the bootstrap-t confidence intervals and other types of confidence intervals, see Davison and Hinkley (1997), Efron and Tibshirani (1993) and Shao and Tu (1995).

Besides the standard, percentile and bootstrap-t confidence interval, there are other types of confidence intervals used in bootstrapping. These include accelerated percentile bias corrected and the iterated bootstrap, but these will not be discussed in this report.

h) Monte Carlo simulation evaluation of the bootstrap

Monte Carlo simulation is a method of evaluating substantive hypotheses and statistical estimators by developing a computer algorithm to simulate a population, drawing multiple samples from pseudo random samples and evaluating estimates obtained from these samples. Both bootstrap and Monte Carlo simulation are based on repetitive sampling and direct examination of the results. The big difference between the methods, however, is that bootstrapping uses the original initial sample as the population from which to resample, while Monte Carlo simulation is based on setting up a data generation process (with known values of the parameters). In that sense Monte Carlo simulation is very similar to the parametric bootstrap except that with the parametric bootstrap the

parameters are obtained from the data. Monte Carlo simulations may be adversely affected by the random number generators, seeds used for these generators and the number of random drawings or correlations between simulations. These problems also affect the bootstrap method. When repeated for many scenarios, the average solution will give an approximate answer to the problem. The accuracy of the Monte Carlo simulation is proportional to the square root of the number of scenarios used.

Monte Carlo simulation is advantageous because it is a 'brute force' approach, that is, it is able to solve problems for which no other solutions exist. This means it is a computer intensive procedure and should be avoided if simpler solutions are possible. The method is useful for obtaining numerical solutions to problems which are too complicated to solve analytically.

In 1946, Ulam invented the Monte Carlo method. He invented the Monte Carlo simulation while pondering the probabilities of winning a card game of solitaire. The Monte Carlo method as it is understood today encompasses any technique of statistical sampling employed to approximate solutions to quantitative problems. Later in 1946 Ulam described the idea to John von Neumann and they began to plan actual calculations. Working with John von Neumann and Nicholas Metropolis, Ulam developed an algorithm for computer implementations and also explored means of transforming non random problems into random forms that would facilitate their solution via statistical sampling. This work transformed statistical sampling from a mathematical curiosity to a formal methodology applicable to a wide variety of problems. It was Metropolis who named the new methodology after the casinos of Monte Carlo. Ulam and Metropolis published the first paper on the Monte Carlo method in 1949 (Metropolis & Ulam 1949).

According to Beran (2003) Monte Carlo algorithms for approximating bootstrap distributions offered a remarkably intuitive way to estimate complex sampling distributions that depend on unknown parameters. He further explained that the Monte Carlo technique reflected the growing role of algorithms and computational experiments in statistics.

Let $\hat{P}_n$ be an estimated model using data $X_1,...,X_n$. In the case where $X_1,...,X_n$ are i.i.d from a distribution F, $\hat{P}_n = \hat{F}$, an estimator of F. If $\hat{F}$ is the empirical distribution then $\left\{X_{1,}^{*b},...,X_n^{*b}\right\}$ is a simple random sample from $\{X_1,...,X_n\}$. The bootstrap bias, variance, and distribution estimators are, respectively,

$$b_{BOOT} = E_*\left[\Re_n\left(X_{1,}^*,...,X_m^*,\hat{P}_n\right)\right] \tag{2.1}$$

$$v_{BOOT} = \mathrm{var}_*\left[\Re_n\left(X_{1,}^*,...,X_m^*,\hat{P}_n\right)\right] \tag{2.2}$$

and

$$H_{BOOT}(x) = P_*\left\{\Re_n\left(X_{1,}^*,...,X_m^*,\hat{P}_n\right) \le x\right\} \tag{2.3}$$

where $\left\{X_{1,}^*,...,X_m^*\right\}$ is a sample from $\hat{P}_n$, $\Re_n(\cdot,\cdot)$, is an appropriately defined functional and E_*, var_* and P_* are conditional expectation, variance and probability, respectively, for given $X_1,...,X_n$. In general m is not necessarily the same as n.

To apply the Monte Carlo method for computing the bootstrap estimators in equations 2.1, 2.2 and 2.3, the researcher begins with a generation of B independent samples $\left\{X_{1,}^{*b},...,X_n^{*b}\right\}$, $b=1,...,B$ from the estimated model $\hat{P}_n$, then calculate $\Re_n^{*b} = \Re_n\left(X_{1,}^{*b},...,X_n^{*b},\hat{P}_n\right)$ for $b=1,...,B$, and approximate $b_{BOOT}^{(B)}$, $v_{BOOT}^{(B)}$ and $H_{BOOT}^{(B)}$ by respectively,

$$b_{BOOT}^{(B)} = \frac{1}{B}\sum_{b=1}^{B}\Re_n^{*b}$$

$$v_{BOOT}^{(B)} = \frac{1}{B}\sum_{b=1}^{B}\left(\Re_n^{*b} - \frac{1}{B}\sum_{b=1}^{B}\Re_n^{*b}\right)^2$$

$$H_{BOOT}^{(B)} = \frac{1}{B}\sum_{b=1}^{B} I\left\{\Re_n^{*b} \le x\right\}.$$

where the indicator function

$$I\left\{\Re_n^{*b} \le x\right\} = \begin{cases} 1 & \text{if } \Re_n^{*b} \le x \text{ is true} \\ 0 & \text{otherwise} \end{cases}$$

i) Limitations of the bootstrap

As with any statistical method, the bootstrap has its limitations. It is contended that "unless certain basic ideas are understood it is all too easy to produce a solution to the wrong problem or a bad solution to the right problem". Beran (2003) emphasised that "success of the bootstrap is not universal. Modification to Efron's definition of the bootstrap is needed to make the idea work for modern procedures that are not classically regular". Ghosh et al. (1984) gave helpful insights and comments on limitations of the bootstrap.

Meeker and Escobar (1998) contend that "justification for the bootstrap is based on large sample theory. Even with large samples, however, there can be difficulties in the tails of the sample". The sample size plays a key role in the accuracy of the bootstrap methods.

When might the bootstrap fail?

The bootstrap may fail when there are

a) incomplete data (survival data, missing data)
b) dependent data (for example correlated time series)
c) dirty Data (data which include outliers).

j) Errors in resampling methods

The error in resampling methods is generally a combination of statistical error and simulation error. Statistical error is a result of the difference between the underlying distribution F and the empirical distribution F. The magnitude of this error depends on the choice of $t(F)$. The use of rough statistics $t(F)$, such as sample quantiles and the median can make resampling approach behave wildly. The simulation error is a result of the use of empirical (Bootstrap) properties of $t(F)$ rather than exact properties. Simulation error decreases by increasing the number B of the bootstrap replications.

Chapter 3

Methodology

This section describes the methods used to analyse the data for the study. The method is based on a simple State Space model, which provides a framework for estimating and predicting animal abundance given partial or inexact information. Bootstrap interval estimation was carried out and these confidence intervals were assessed using Monte Carlo simulations. The source and nature of data are also discussed.

3.1 Source and nature of the data

The data used in the research was obtained from Fatti et al. (2002). The data were obtained from surveys conducted at Hluhluwe-Umfolosi Park. Eight surveys were conducted for the white rhino population in the 24 year period between 1973 and 1996. The method used to estimate the sizes of the populations for the white rhino was based on observations taken along line transects passing through different sections of the Park, using a distance based methodology to account for the decreasing detection rate, with increasing distance between the observer and the animal (Buckland et al., 1993). For the black rhino seven surveys were conducted from 1990 to 1996. In contrast to the white rhino the method was said to be inappropriate for the black rhino with its shy habits and instead a 'mark-recapture' method (Seber, 1982) was used to estimate its population size.

3.2 Proposed model

To combine the data from the eight surveys, which were conducted in the 24 year period between 1973 and 1996, a model is required which will take into account the various known and unknown factors that have affected the rhino population over this time period. A simple discrete time state space model was used in this research.

The model was proposed by Fatti et al. (2002) and it describes the dynamics of the population over time across successive surveys. The model was developed because it takes into account the various known and unknown factors which have affected the rhino population over this time period. The factors which affected the rhino population over the period, are:

Known factors

1) Number of animals relocated and introduced from and to the Park at different times between surveys.
2) Number of mortalities in the Park.

Unknown Factors

1) Natural rate of increase in the population.
2) Error in each of the surveys.

The model consists of two components:

1. Deterministic process

   This component describes the change in the (unknown) true population from one survey to the next, taking into account the species' natural rate of increase as well as the relocations, introductions and mortalities, which occurred in between.

2. Simple stochastic error model

   The second component describes the relationship between the survey estimates and the corresponding true population sizes.

The same notation as used in Fatti et al., (2002) was used:

y_t = population estimate at survey t

μ_t = true population size at survey t (*unknown*)

l_t = nett losses $(\text{removals} + \text{mortalities} - \text{introductions})$ between survey t and $t+1$ (*assumed known*)

r = natural annual rate of increase in the population, excluding mortalities (*unknown*)

s_t = number of years between survey t and $t+1$

n = the total number of surveys over the period .

Assuming that the losses occur uniformly over time between successive surveys and that the natural rate of increase r is constant over the whole period, in the deterministic process the true population size at the time of survey $t+1$ is related to that at survey t by the following formula:

$$\begin{aligned}\mu_{t+1} &= \mu_t e^{rs_t} - \int_0^{s_t} \frac{l_t}{s_t} e^{rx} dx \\ &= \mu_t e^{rs_t} - l_t \left(\frac{e^{rs_t} - 1}{rs_t} \right)\end{aligned} \qquad 3.1$$

The formula takes into account the natural growth in the population and the losses (including the growth which would have accrued from these animals had they not died or been removed). We assume that the estimate y_t at survey t is an unbiased estimator of the true population size but that there is an unknown, random observation error. The model for the estimate at survey t takes the following simple form:

$$y_t = \mu_t + \varepsilon_t$$

where ε_t is a random error term which has zero expectation (since y_t is unbiased) and variance σ^2.

Therefore at survey $t+1$:

$$\begin{aligned}y_{t+1} &= \mu_{t+1} + \varepsilon_{t+1} \\ &= \mu_t e^{rs_t} - l_t \left(\frac{e^{rs_t} - 1}{rs_t} \right) + \varepsilon_{t+1} \\ &= (y_t - \varepsilon_t) e^{rs_t} - l_t \left(\frac{e^{rs_t} - 1}{rs_t} \right) + \varepsilon_{t+1}\end{aligned} \qquad 3.2$$

The relationship between the error at survey $t+1$ and that at the previous survey is therefore given by:

$$\varepsilon_{t+1} = y_{t+1} - (y_t - \varepsilon_t) e^{rs_t} + l_t \left(\frac{e^{rs_t} - 1}{rs_t} \right) \qquad 3.3$$

To fit the model the following algorithm was specified by Fatti et al. (2002):

3.2.1 Algorithm 3.1

1. Start at $t = 1$. Assign initial values to ε_1 and r.
2. Now generate the error terms $\varepsilon_2, \ldots, \varepsilon_n$ successively from equation 3.3:

$$\varepsilon_2 = y_2 - (y_1 - \varepsilon_1)e^{rs_1} + l_1\left(\frac{e^{rs_1} - 1}{rs_1}\right)$$

$$\varepsilon_3 = y_3 - (y_2 - \varepsilon_2)e^{rs_2} + l_2\left(\frac{e^{rs_2} - 1}{rs_2}\right)$$

.
.

$$\varepsilon_n = y_n - (y_{n-1} - \varepsilon_{n-1})e^{rs_{n-1}} + l_{n-1}\left(\frac{e^{rs_{n-1}} - 1}{rs_{n-1}}\right) \qquad 3.4$$

3. Estimate ε_1 and r via least squares, that is, find those values of ε_1 and r that minimize $\sum_{t=1}^{n} \varepsilon_t^2$, using a nonlinear minimisation procedure. An estimate of the standard error of the survey estimates σ is:

$$\hat{\sigma} = \sqrt{\frac{1}{n-2}\sum_{t=1}^{n} \varepsilon_t^2} \qquad 3.5$$

taking into account the loss in degrees of freedom because of the estimation of two parameters ε_1 and r.

4. Finally, given the estimated $\hat{\varepsilon}_1$ and $\hat{r}$, successively compute the estimated true population size at each survey:

$$\hat{\mu}_1 = y_1 - \hat{\varepsilon}_1$$

$$\hat{\mu}_2 = y_2 - \hat{\varepsilon}_2$$

$$= (y_1 - \hat{\varepsilon}_1)e^{\hat{r}s_1} - l_1\left(\frac{e^{\hat{r}s_1} - 1}{\hat{r}s_1}\right)$$

$$\hat{\mu}_2 = \hat{\mu}_1 e^{\hat{r}s_1} - l_1\left(\frac{e^{\hat{r}s_1} - 1}{\hat{r}s_1}\right)$$

.

.

$$\hat{\mu}_n = \hat{\mu}_{n-1} e^{\hat{r}s_{n-1}} - l_{n-1}\left(\frac{e^{\hat{r}s_{n-1}} - 1}{\hat{r}s_{n-1}}\right) \qquad 3.6$$

In addition to the obvious utility of the population estimates $\hat{\mu}_i$, the estimated annual growth rate in the population, $\hat{r}$, is also of scientific interest. According to Fatti et al. (2002), the least squares solution was shown to be insensitive over a wide range of initial values for ε_1 and r. The initial values $\varepsilon_1 = 0$ and $r = 0.1$ have been found to yield quick convergence.

The program used in Matlab (http://www.mathworks.com/products/matlab/) for fitting the model using algorithm 3.1 is shown in Appendix B. For minimisation purposes the function $\sum_{t=1}^{n} \varepsilon_t^2$ was written as follows:

$$\sum_{t=1}^{n} \varepsilon_t^2 = \varepsilon_1^2 + \sum_{t=2}^{n} \varepsilon_t^2$$

and each of the error terms was written as a function of y, ε_1, l, and s:

$$\varepsilon_2 = y_2 - (y_1 - \varepsilon_1) e^{rs_1} + l_1\left(\frac{e^{rs_1} - 1}{rs_1}\right)$$

$$\varepsilon_3 = y_3 - (y_1 - \varepsilon_1) e^{r(s_1+s_2)} + l_1\left(\frac{e^{rs_1} - 1}{rs_1}\right) e^{rs_2} + l_2\left(\frac{e^{rs_2} - 1}{rs_2}\right)$$

$$\varepsilon_4 = y_4 - (y_1 - \varepsilon_1) e^{r(s_1+s_2+s_3)} + l_1\left(\frac{e^{rs_1} - 1}{rs_1}\right) e^{r(s_2+s_3)} + l_2\left(\frac{e^{rs_2} - 1}{rs_2}\right) e^{rs_3} + l_3\left(\frac{e^{rs_3} - 1}{rs_3}\right)$$

.

.

and so on.

a) Assumptions of the proposed model

1. The losses occur uniformly over time between successive surveys and that the natural rate of increase r is constant over the whole period.
2. The estimate y_t at survey t, is an unbiased estimator of the true population size, but there is an unknown, random observation error, ε_t.
3. The random error term, ε_t has zero expectation since y_t is unbiased and variance σ^2. That is $\varepsilon_t \sim G(0, \sigma^2)$ where $G(\cdot)$ denotes some distribution, possibly normal.
4. The change in the population size from one survey to the next is deterministic (effectively assume that the randomness in this process is much smaller than that of the observation process and that it can be subsumed in the latter).

Note that the assumption of constant error variance σ^2 does not hold for distance based sampling estimates, as this variance is a function of the true population density (Buckland et al., 1993). However, unless the variation of the population density is considerable, this assumption should be acceptable within the general accuracy of the approach (Fatti et al., 2002).

3.3 Bootstrap application

Fatti et al. (2002) proposed the jackknife method for obtaining standard errors for the estimated population sizes at each survey, but in the spirit of the modern methods described as "computer intensive" by Diaconis and Efron (1983), researchers use the bootstrap method. Mooney and Duval (1993) suggested that jackknife is of largely historical interest today. Through simulations Fan and Wang (1996) found that the bootstrap technique provides less biased and more consistent results than the jackknife method does, though the jackknife method is still useful in Exploratory Data Analysis for assessing how each sub-sample affects the model. Frangos and Stone (1984) raised questions about the value of the jackknife.

As explained earlier, expectation, variance and probability calculated with respect to a simulation distribution are written with an asterisk * as, $E_*(\cdot)$, $Var_*(\cdot)$ and $P_*(\cdot)$, respectively, to show that they are obtained from a bootstrap analog.

The estimates of the true population size at each of the surveys and the estimate of the natural annual rate of increase in the population are obtained using algorithm 3.1. The following steps are carried out to obtain the bootstrap estimates and their confidence intervals.

Step 1

The data, which were used in this research, was time dependent, thus resampling was carried out in such a way that the dependence structure could be captured. The resamples could be generated by fitting the parameters and using the residuals in the resampling. Freedman (1981) explained why centering is necessary when resampling from the residuals. It was also noted by Efron (1979) that centering the residuals was required, that is $\hat{F}$ should have mean zero, otherwise the bootstrap may fail. In the first step residuals are formed:

$$\hat{\varepsilon}_t = y_t - \hat{\mu}_t \qquad t = 1,...,n \qquad 3.7$$

The centred residuals are then obtained by:

$$\varepsilon'_t = \frac{\hat{\varepsilon}_t - \bar{\varepsilon}}{\sqrt{1 - \frac{p}{n}}} \qquad 3.8$$

(Shao & Tu, 1995) where p=2 is the number of estimated parameters and $\bar{\varepsilon}$ is the mean of $\hat{\varepsilon}_t$ for $t = 1,...,n$.

Step 2

Take a bootstrap sample of the centred residuals randomly and with replacement from

$$\varepsilon'_1, \varepsilon'_2, \ldots, \varepsilon'_n$$

This was done by drawing uniform random integers with replacement from $U(1,n)$. We let these random integers be $U_1, U_2, ..., U_n$. The bootstrap sample of residuals is therefore denoted by:

$$\varepsilon_1^*, \varepsilon_2^*, ..., \varepsilon_n^*$$

where

$$\varepsilon_i^* = \varepsilon'_{(U_i)} \qquad i = 1, 2, ..., n$$

are the bootstrap sample of residuals, where $\varepsilon'_{(U_i)}$ denotes the U_i-th order statistic of $\varepsilon'_1, \varepsilon'_2, ..., \varepsilon'_n$.

Step 3

Form the bootstrap sample of observations by:

$$y_1^* = \hat{\mu}_1 + \hat{\varepsilon}_1^*$$

$$y_{t+1}^* = \hat{\mu}_t e^{\hat{r}s_t} - l_t \left(\frac{e^{\hat{r}s_{t1}} - 1}{\hat{r}s_t} \right) + \varepsilon_{t+1}^* \qquad for \;\; t = 1, 2, ..., n-1 \qquad 3.9$$

Step 4

Obtain the bootstrap estimates of $r, \mu_1, \mu_2 ..., \mu_n$ from the bootstrap sample of observation $y_1^*, y_2^*, ..., y_n^*$ using algorithm 3.1. The bootstrap estimates of $r, \mu_1, \mu_2 ..., \mu_n$ from the b^{th} bootstrap sample are then denoted by:

$$r_b^*, \mu_{1b}^*, \mu_{2b}^* ..., \mu_{nb}^*.$$

Step 5

Repeat the steps 2 to 4 a large number of times B. Determining the required number of replications is a complicated matter and depends on, for instance, the statistic of interest and the unknown bootstrap distribution. Davison and Hinkley (1997) reported that 1000 replications are sufficient for many applications.

To repeat steps 2 to 4 in Matlab (http://www.mathworks.com/products/matlab/) we used matrices. The centred residuals in step 1 were presented in a matrix of nxB dimension.

The column of the centred residuals was repeated B=1000 times to yield a nxB matrix of centred residuals. For each column we obtained a bootstrap sample of residuals as indicated in step 2 and produced an nxB matrix of the bootstrap samples:

$$\varepsilon^*_{ij} = \begin{bmatrix} \varepsilon^*_{11} & \varepsilon^*_{12} & \varepsilon^*_{13} & \cdots & \varepsilon^*_{1B} \\ \varepsilon^*_{21} & \varepsilon^*_{22} & \varepsilon^*_{23} & \cdots & \varepsilon^*_{2B} \\ \cdot & \cdot & \cdot & & \cdot \\ \cdot & \cdot & \cdot & & \cdot \\ \cdot & \cdot & \cdot & & \cdot \\ \varepsilon^*_{n1} & \varepsilon^*_{n2} & \varepsilon^*_{n3} & \cdots & \varepsilon^*_{nB} \end{bmatrix}_{n\text{x}B}$$

Steps 3 and 4 were then carried out on each of the B columns. The resulting matrix was an $(n+1)$ x B matrix of individual bootstrap estimates. Each column in the matrix in turn produced the average bootstrap estimate of $r, \mu_1, \mu_2 ..., \mu_n$:

$$\begin{aligned} \hat{r}^*_B &= \frac{1}{B}\sum_{b=1}^{B} r^*_b \\ \hat{\mu}^*_{1B} &= \frac{1}{B}\sum_{b=1}^{B} \mu^*_{1b} \\ &\cdot \\ &\cdot \\ &\cdot \\ \hat{\mu}^*_{nB} &= \frac{1}{B}\sum_{b=1}^{B} \mu^*_{nb} \end{aligned} \qquad 3.10$$

The estimated variances of the estimates were given by:

$$Var_B\left(\hat{r}_B^*\right)=\frac{1}{B-1}\sum_{b=1}^{B}\left(r_b^*-\hat{r}_B^*\right)^2$$

$$Var_B\left(\hat{\mu}_{1B}^*\right)=\frac{1}{B-1}\sum_{b=1}^{B}\left(\mu_{1b}^*-\hat{\mu}_{1B}^*\right)^2$$

. 3.11

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$$Var_B\left(\hat{\mu}_{nB}^*\right)=\frac{1}{B-1}\sum_{b=1}^{B}\left(\mu_{nb}^*-\hat{\mu}_{nB}^*\right)^2$$

The Matlab (http://www.mathworks.com/products/matlab/) program that was used to obtain bootstrap estimates and variances of the estimates is shown in Appendix C.

3.4 Confidence intervals

The confidence intervals for the true growth rate and true population size at each survey were derived using the percentile and standard method. The procedure described in Chapter 2 on confidence intervals was followed. The results obtained from the two methods were compared to discover which method gives the best confidence intervals for the data.

3.4.1 Standard confidence interval:

For the bootstrap estimates of true population size the confidence intervals are obtained using the formula below:

$$\left[\hat{\mu}_{iB}^*-z_{\frac{\alpha}{2}}\widehat{se}_{\hat{\mu}_{iB}^*},\hat{\mu}_{iB}^*+z_{\frac{\alpha}{2}}\widehat{se}_{\hat{\mu}_{iB}^*}\right] \qquad i=1,...,n$$

and, for the bootstrap estimate of annual rate of increase in population:

$$\left[\hat{r}_B^*-z_{\frac{\alpha}{2}}\widehat{se}_{\hat{r}_B^*},\ \hat{r}_b^*+z_{\frac{\alpha}{2}}\widehat{se}_{\hat{r}_B^*}\right]$$

Where $\hat{se}_{\mu_i^* B}$ is the estimated standard error of the bootstrap estimates of true population size while $\hat{se}_{r^* B}$ is the estimated standard error of the bootstrap estimate of the annual rate of increase.

3.4.2 Percentile confidence intervals:

Following the procedure in Chapter 2, the percentile confidence intervals are given by:

$$\left[K_{BOOT}^{-1}\left(\frac{\alpha}{2}\right), K_{BOOT}^{-1}\left(1-\frac{\alpha}{2}\right)\right]$$

where $K_{BOOT}^{-1}\left(\frac{\alpha}{2}\right)$ is obtained by arranging in ascending order the B values of r_b^* and $\hat{\mu}_{iB}^*$, $b=1,2,\ldots,B$ and considering the $B\cdot\frac{\alpha}{2}$ value of r_b^* and of $\hat{\mu}_{iB}^*$ $i=1,\ldots,n$, respectively. Similarly for $K_{BOOT}^{-1}\left(1-\frac{\alpha}{2}\right)$ we consider $B\cdot\left(1-\frac{\alpha}{2}\right)$ as described above.

The Matlab (http://www.mathworks.com/products/matlab/) program, which was used to derive the confidence intervals, is given in Appendix D.

To assess the coverage probabilities for the confidence intervals, Monte Carlo simulation, which is described below, was used.

3.5 Monte Carlo simulation

In order to assess the coverage probability of the derived confidence intervals, the following procedure was used:

Generate 1000 series from original estimated model as follows:

$$y_1 = \hat{\mu}_1 + \varepsilon_1$$

$$y_{t+1} = \hat{\mu}_t e^{\hat{r}s_t} - l_t\left(\frac{e^{\hat{r}s_t}-1}{\hat{r}s_t}\right) + \varepsilon_{t+1} \qquad t=1,\ldots,n\text{-}1 \qquad 3.12$$

where $\hat{r}$ is the estimate of natural annual rate of increase in the population obtained from fitting the model to the original survey data and $\hat{\mu}_t$ is the estimate of the true population size at survey t, also obtained from fitting the model. This was achieved by generating randomly n random numbers $\varepsilon_i \; i = 1,2,...,n$ from the normal distribution with mean zero and variance $\hat{\sigma}^2$, where $\hat{\sigma}^2$ is the variance of the estimated error terms which was obtained from fitting the model (see equation 3.5). The normal distribution is assumed because the residuals obtained from fitting the model to the Rhino data were reasonably normal.

For each of the 1000 series of data the bootstrap confidence intervals for $r, \mu_1, \mu_2, ..., \mu_n$ were calculated using the equations above. The true values of $r, \mu_1, \mu_2, ..., \mu_n$ were taken to be the estimates obtained from fitting the model to the original survey data. Using the true values coverage probabilities were estimated from respective proportions of the 1000 confidence intervals, which cover the true parameters. We also find the average length of the confidence interval of any parameter by:

$$\frac{1}{1000}\sum_{i=1}^{1000} length_i$$

where $length_i$ is the length of the confidence interval of this parameter from the i th simulation. These average confidence interval lengths were used to assess the confidence intervals. The shorter the confidence interval the more exact it is, thus shorter average lengths are preferred for the confidence intervals. The Monte Carlo simulation involves computing 1000 samples for each of the 1000 simulated samples. The Matlab (http://www.mathworks.com/products/matlab/) program for the Monte Carlo simulation studies are given in Appendix E.

3.6 Jackknife application

When applying the jackknife to the data for both the white and black rhino, one of the surveys was decreased from the sample and the model was fitted on the remaining survey estimates. This model was used to estimate the remaining true population sizes. This was

repeated over all surveys resulting in n estimates $\hat{\mu}_{t(i)}$, $i=1,\ldots,n$, of μ_t. We do not estimate μ_i when the corresponding survey estimate has been decreased from the sample.

Using the theory of the jackknife method, the standard error of the population estimate $\hat{\mu}_t$ was then estimated by (Efron 1982):

$$\hat{\sigma}_{\hat{\mu}_t} = \sqrt{\left(\frac{n-1}{n}\right)\sum_{i=1}^{n}\left(\hat{\mu}_{t(i)} - \hat{\mu}_{t(\cdot)}\right)^2}$$

where $\hat{\mu}_{t(\cdot)}$ is the average of the $\hat{\mu}_{t(i)}$, $i=1,\ldots,n$. This is a slightly conservative estimate of the standard error, since it refers to a situation where there have been $n-1$ (not n) surveys (Fatti et al. 2002). The net losses for the year removed (year t) were added to the net losses for year $t+1$.

The Matlab (http://www.mathworks.com/products/matlab/) program for the jackknife is given in Appendix F.

3. 7 Software and package

In this research the main package used for analysis was Matlab (http://www.Mathworks .com/products/matlab/). Microsoft Excel (www.office.microsoft.com/en-us/excel/ FX100487621033.aspx) was also used for some calculations, graphs and other analyses. The "R" modules BOOT and BOOTSTRAP (www.r-project.org/) and SPLUS (http://www.insightful.com/products/addons.asp) modules on bootstrapping are other packages that could be used for analysis, but were not used in this research.

Chapter 4

White Rhino Results

4.1 Calculation of net losses

Since the mortalities and relocations were recorded on a calendar year basis, but the survey always took place shortly after the middle of the year, the net losses had to be interpolated in order to correspond to the same intervals as the surveys. The following formula was used for interpolation (equation 4.1).

We define the total losses between survey t and $t+1$ (which are s_t years apart) by w_t. Let the net losses measured on a calendar year basis between surveys t and $t+1$ be denoted by l_t then the corresponding net losses interpolated to the middle of the year are given by:

$$l_t = w_t - \left[\frac{w_t}{2s_t} - \frac{w_{t+1}}{2s_{t+1}} \right] \qquad 4.1$$

These net losses for the white rhino are shown in Appendix A1.

4.2 Model fitting algorithm 3.1

Algorithm 3.1, described in Chapter 3 for fitting the model, was implemented in Matlab (http://www.mathworks.com/products/matlab/) and this provided the estimated true population sizes and error terms at each of the surveys (raw data in Appendix A1). These are shown in Table 4.1 and are displayed in Figure 4.1, together with the original survey estimates.

The estimated true population shows that the white rhino population in the park has changed over the 24 year period over which the surveys were conducted. According to

Fatti et al. (2002) the apparent steep decline between the 1973 and 1982 surveys can be partially explained by the high numbers of relocations of rhinos (and other species) to other parks because management needed to reduce stocking levels during the drought that affected the park over much of this period. After 1982 there was a steady growth in the white rhino population over most of the subsequent period up until 1994, which can be attributed to the recovery of the population after the drought. There was no specific reason for the sudden decrease in numbers between the 1994 and 1996 surveys. The survey estimate for 1996 was not associated with the largest estimated error; instead it was the 1994 figure that was furthest from the estimated true population size. The 1982 error was almost as large.

Fatti et al. (2002) consider the 1982 figure to be too low; the model gives a far more gradual decline in the numbers than suggested by the original survey estimates. The model estimates show a slight increase in numbers between the 1994 and 1996 surveys in contrast with the sudden decrease in the survey estimates. The natural annual growth rate in the population, r, was estimated to be 0.078 or 7.8% which, according to Fatti et al. (2002), falls well within the range of 6% to 8% which was considered to be realistic by the scientist at the park. Using step 3 of the algorithm, the standard deviation of the survey errors was estimated to be:

$$\hat{\sigma} = \sqrt{\frac{1}{n-2}\sum_{t=1}^{n}\varepsilon_t^2} = 276$$

Table 4.1: White rhino survey data, estimated true population sizes and estimated survey errors, 1973 to 1996

Year	Survey Estimate	Mortalities	Relocations	Net Losses	Estimated true population sizes	Estimated error
1973	2230	48	452	513	1930	300
1976	1629	128	1025	1138	1860	-231
1982	1199	106	380	424	1520	-321
1985	1530	14	24	60	1443	87
1986	1502	108	297	438	1498	5
1991	1748	101	341	430	1676	72
1994	1982	56	190	246	1634	348
1996	1364				1643	-279
$\hat{r} = 0.078$						

Figure 4.1 superimposes the graph of the estimated true population sizes on that of the survey estimates at each of the eight surveys. The graph of the estimated true population sizes obtained from the model was considered to be more realistic by the scientists than that obtained from the original survey estimates (Fatti et al. 2002).

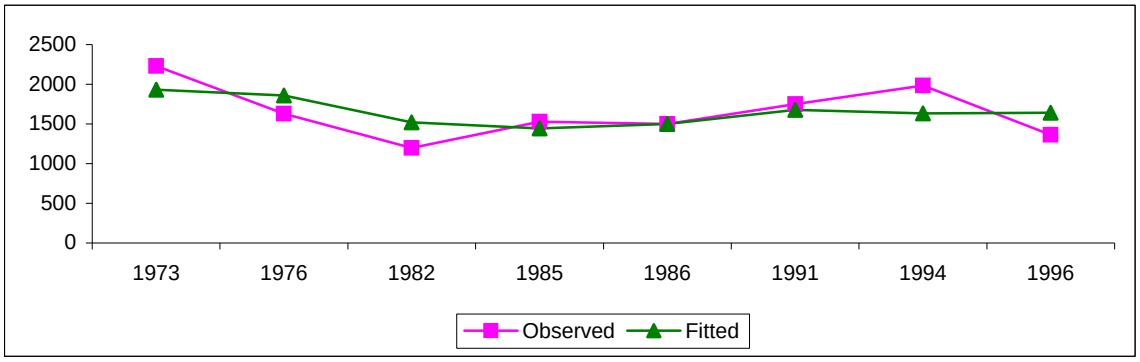


Figure 4.1: Plot of the estimated true population sizes and the survey estimates at each of the eight surveys

4.3 Bootstrapping

The bootstrap technique was implemented according to the procedure described in Chapter 3. The following sections show the estimates of the true population sizes, which were obtained from 200 and 1000 replications, respectively.

4.3.1 200 Replications

The results from 200 replications of the bootstrap technique are shown in table 4.2 below. These include the bootstrap estimates of the true population sizes at each survey and their standard errors. As before, the results show that the white rhino population has changed over the 24 year period. The survey estimates for 1982 and 1994 are associated with the largest errors (differences between the estimated population and survey estimates). The large positive error associated with the 1994 survey estimate accounts for the apparent decrease in numbers in the 1996 survey estimate. The difference between the survey estimate and bootstrap estimate for 1986 was very small. The bootstrap estimate of the natural annual growth rate in the population was 0.079 or 7.9%, which was almost the same value as that obtained on fitting the model. The 7.9% lies well within the expected 6 to 8%, which boosts confidence in the results obtained from bootstrapping. The standard error of the bootstrap estimate of the natural annual growth rate in the population was estimated to be $\widehat{se}_{\hat{r}^*_{200}} = 0.01012$, or approximately 1%.

The 1996 survey estimate showed the largest standard error. The 1973 and 1994 survey estimates also had large standard errors. The relatively small standard error for the natural annual growth rate in the population suggests that this was an accurate estimate.

Table 4.2: Bootstrap estimates of the true population sizes and the standard error of the bootstrap estimates for 200 replications

Year	Survey estimate	Bootstrap estimates of true population sizes	Standard error $se_{\hat{\mu}^*_{i,200}}$	Difference between population and survey estimates
1973	2230	1929	161	201
1976	1629	1859	142	-230
1982	1199	1518	107	-319
1985	1530	1441	96	89
1986	1502	1496	94	6
1991	1748	1679	108	69
1994	1982	1642	151	340
1996	1364	1657	194	-293
$\hat{r}^*_{200} = 0.079$ and $se_{\hat{r}^*_{200}} = 0.01012$				

Figure 4.2 gives the graph of the bootstrap estimates of the true population sizes together with the corresponding survey estimate. From 1985 there is estimated to be a steady growth rate in the white rhino population. As with the graph of the sample estimates the graph for the bootstrap estimates appears more realistic than that of the original survey estimates.

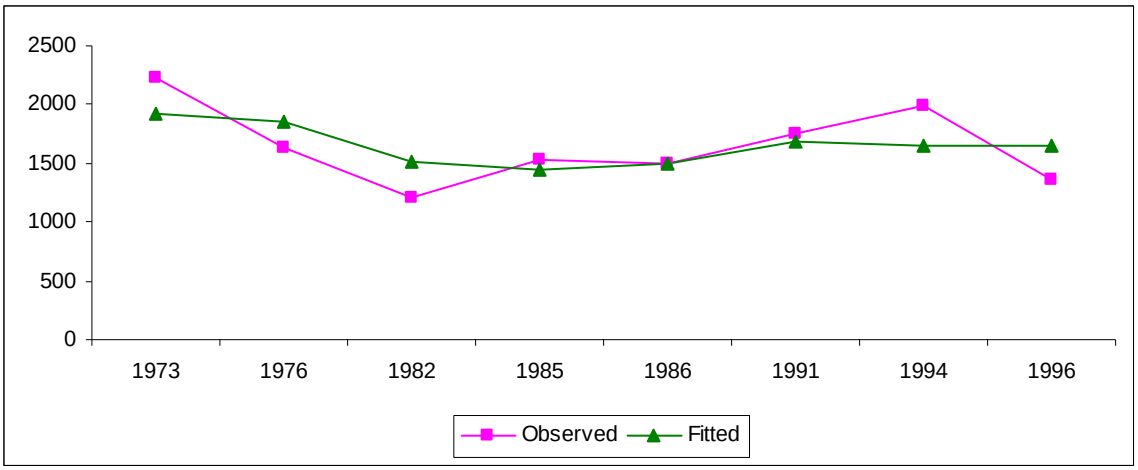


Figure 4.2: Plot of the bootstrap estimates of the true population sizes and the survey estimates for each of the eight surveys for 200 replications

a) 95% Confidence intervals for 200 replications

The 95% confidence intervals for each of the bootstrap estimates were obtained using the standard and percentile confidence intervals and are shown in Table 4.3. The confidence intervals obtained using both methods are not much different from each other. Note that for both confidence intervals the survey estimates for 1982 and 1994 do not lie within the confidence intervals obtained. The 1982 survey estimate (1199) falls below the lower limit of the standard confidence interval as well as of the percentile confidence interval. In contrast, the survey estimate for 1994 lies above the upper limit of both confidence intervals. The confidence interval results suggest that the sudden decrease in numbers between the 1994 and 1996 surveys was largely a result the 1994 survey estimate being too high. Both confidence intervals for the bootstrap estimate of the natural annual growth rate in the population include the expected rate of between 6% and 8%.

Table 4.3: Standard and percentile 95% confidence intervals obtained at 200 replications for each of the bootstrap estimates

Year	Bootstrap estimate	95% Standard confidence intervals	95% Percentile confidence intervals
	$\hat{r}^*_{200}$	[0.058 ; 0.098]	[0.060 ; 0.098]
1973	$\hat{\mu}^*_{1,200}$	[1613 ; 2245]	[1639 ; 2265]
1976	$\hat{\mu}^*_{2,200}$	[1580 ; 2138]	[1595 ; 2148
1982	$\hat{\mu}^*_{3,200}$	[1308 ; 1728]	[1313 ; 1729]
1985	$\hat{\mu}^*_{4,200}$	[1252 ; 1630]	[1256 ; 1634]
1986	$\hat{\mu}^*_{5,200}$	[1311 ; 1681]	[1316 ; 1686]
1991	$\hat{\mu}^*_{6,200}$	[1467 ; 1891]	[1460 ; 1892]
1994	$\hat{\mu}^*_{7,200}$	[1347 ; 1937]	[1345 ; 1925]
1996	$\hat{\mu}^*_{8,200}$	[1278 ; 2036]	[1287 ; 2028]

Figures 4.3 and 4.4 show the confidence intervals for the bootstrap estimates based on 200 replications. These figures illustrate the fact that the 1982 and 1994 survey estimates do not fall in the corresponding confidence interval range.

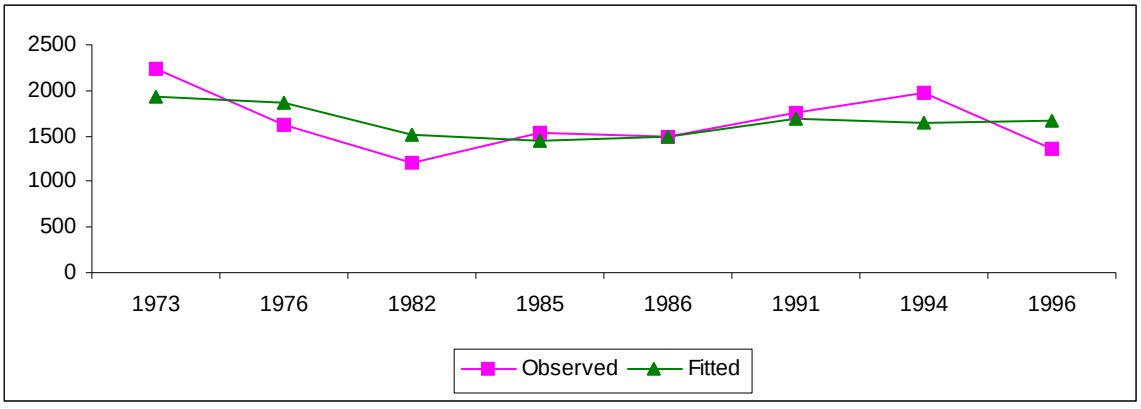


Figure 4.3: Standard confidence intervals for 200 replications

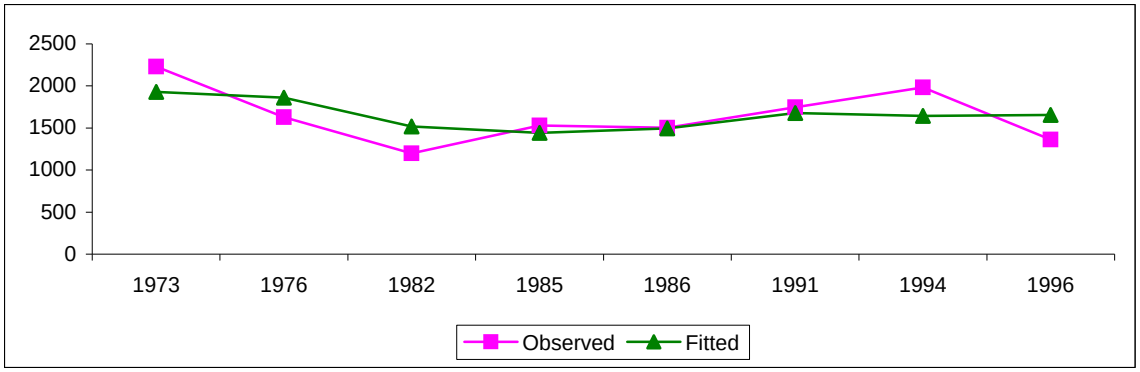


Figure 4.4: Percentile confidence intervals for 200 replications

4.3.2 1000 Replications

The bootstrap estimate of the natural annual growth rate in the population was estimated to be 0.078 or 7.8%, which lies well within the expected 6 to 8% range, and which is the same value as that obtained from fitting the model to the original sample. Increasing the number of bootstrap replications has not made much change to the estimates. The standard errors of the estimates from 200 and 1000 replications do not differ much.

Table 4.4: Bootstrap estimates of the true population sizes and the standard error of the bootstrap estimates for 1000 replications

Year	Survey estimate	Bootstrap estimates of true population sizes	Standard error $\widehat{se}_{\hat{\mu}^*_{i,1000}}$	Difference between population and survey estimates
1973	2230	1935	163	295
1976	1629	1865	144	-236
1982	1199	1522	109	-323
1985	1530	1444	98	86
1986	1502	1498	96	4
1991	1748	1679	107	69
1994	1982	1639	146	343
1996	1364	1653	188	-289
$\hat{r}^*_{1000} = 0.078$ and $\widehat{se}_{\hat{r}^*_{1000}} = 0.01038$				

Figure 4.5 superimposes the graph of the bootstrap estimates of the true population sizes on that of survey estimates obtained using 1000 replications. As with the 200 replication results a much smoother curve was obtained from the bootstrap estimates compared with the original survey estimates.

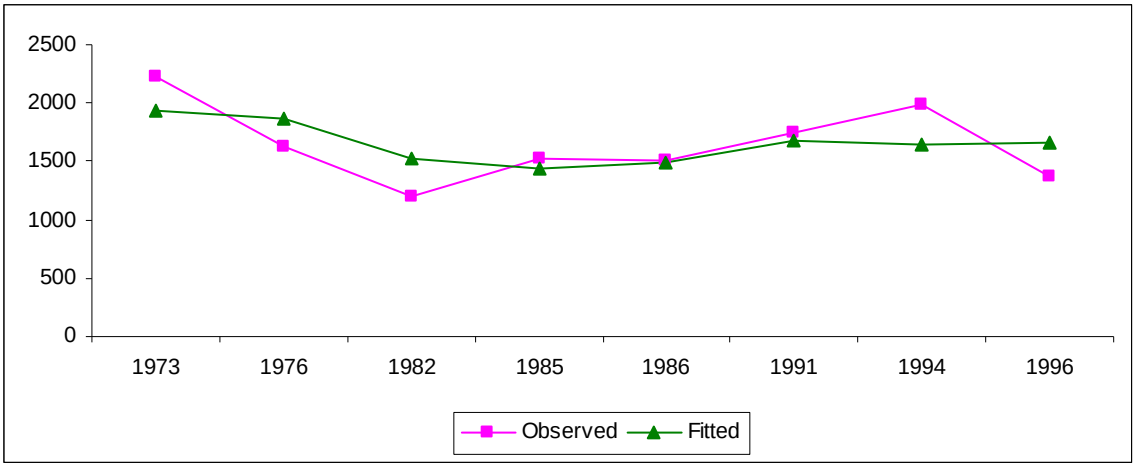


Figure 4.5: Plot of the bootstrap estimates of the true population sizes and the survey estimates for each of the eight surveys for 1000 replications

a) 95% Confidence intervals for 1000 replications

The results of the standard and percentile confidence intervals, given in Table 4.5 are again not very different nor do they differ much from those obtained from the 200 bootstrap replications. The 1982 survey estimate again fell below both confidence intervals and the 1994 survey estimate fell above its corresponding intervals. The confidence interval results again give support to the finding that the apparent decrease in numbers between the 1994 and 1996 survey estimates was largely caused by the 1994 survey error. As before, the confidence intervals for the natural annual growth rate in the population include the scientists' expected growth rate of 6% to 8%.

Table 4.5: Standard and percentile confidence intervals obtained at 1000 replications for each of the bootstrap estimates

Year	Bootstrap estimate	95% Standard confidence intervals	95% Percentile confidence intervals
	$\hat{r}^*_{1000}$	[0.059 ; 0.099]	[0.060 ; 0.098]
1973	$\hat{\mu}^*_{1,1000}$	[1616 ; 2254]	[1633 ; 2279]
1976	$\hat{\mu}^*_{2,1000}$	[1583 ; 2147]	[1591 ; 2167]
1982	$\hat{\mu}^*_{3,1000}$	[1308 ; 1736]	[1312 ; 1746]
1985	$\hat{\mu}^*_{4,1000}$	[1252 ; 1636]	[1261 ; 1639]
1986	$\hat{\mu}^*_{5,1000}$	[1310 ; 1686]	[1319 ; 1686]
1991	$\hat{\mu}^*_{6,1000}$	[1469 ; 1889]	[1472 ; 1882]
1994	$\hat{\mu}^*_{7,1000}$	[1352 ; 1926]	[1357 ; 1915]
1996	$\hat{\mu}^*_{8,1000}$	[1285 ; 2021]	[1289 ; 2013]

Figures 4.6 and 4.7 for the standard and percentile confidence intervals show a similar picture to that from 200 bootstrap replications.

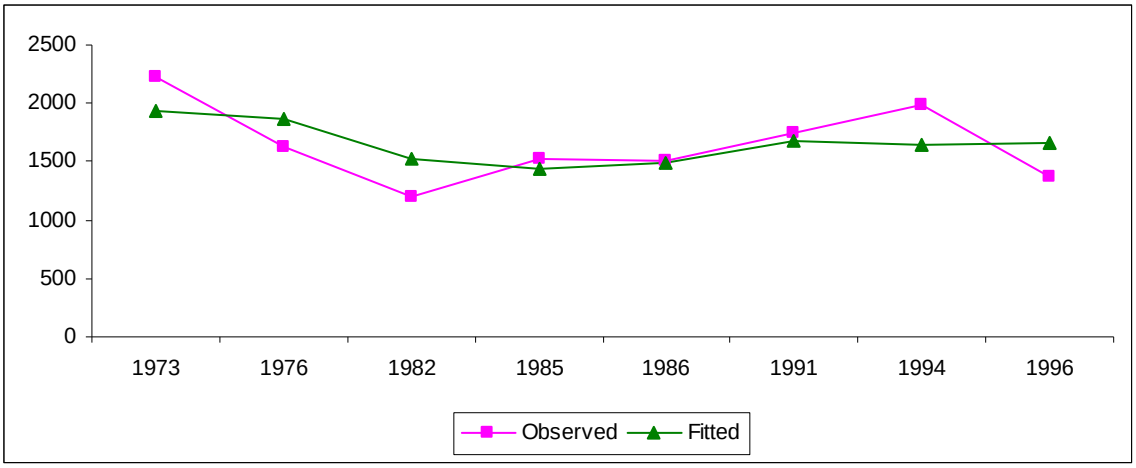


Figure4.6: Standard confidence intervals for 1000 replications

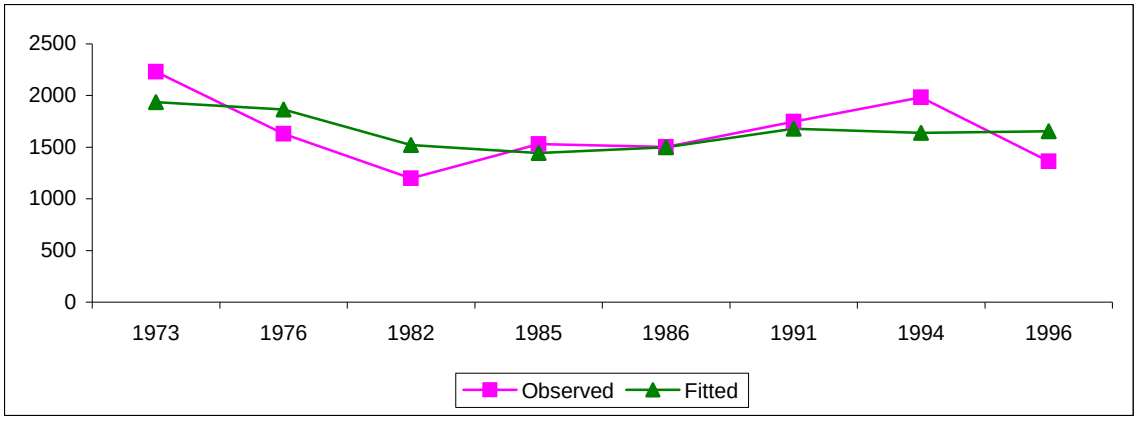


Figure 4.7: Percentile confidence intervals for 1000 replications

4.4 Comparison of bootstrap estimates and the full sample estimates of the true population sizes

a) 200 Replications vs. full sample model

Table 4.6 compares the results of fitting the model to the original survey data which used the bootstrap (200 replications). The estimates are close. The largest difference (-14) occurs at the 1996 survey. The bootstrap and full sample estimates of the natural annual growth rate are almost identical.

Table 4.6: Comparison of bootstrap estimates for 200 replications and the full sample model

Year	Survey estimate	Sample estimates	Bootstrap estimates of true population sizes (B=200)	Difference between sample estimates and bootstrap estimates
1973	2230	1930	1929	1
1976	1629	1860	1859	1
1982	1199	1520	1518	2
1985	1530	1443	1441	2
1986	1502	1498	1496	2
1991	1748	1676	1679	-3
1994	1982	1634	1642	-8
1996	1364	1643	1657	-14
$\hat{r} = 0.078$ *and* $\hat{r}^*_{200} = 0.079$				

b) 1000 Replications vs. full sample model

The estimates are again close, with largest difference (-10) and again occurring at 1996 survey. The two estimates of the natural annual growth rate are the same (see Table 4.7). There was little difference between the results of the 200 and 1000 bootstrap replications.

Table 4.7: Comparison of bootstrap estimates for 1000 replications and the full sample model

Year	Survey estimate	Sample estimates	Bootstrap estimates of true population sizes (B=1000)	Difference between sample estimates and bootstrap estimates
1973	2230	1930	1935	-5
1976	1629	1860	1865	-5
1982	1199	1520	1522	-2
1985	1530	1443	1444	-1
1986	1502	1498	1498	0
1991	1748	1676	1679	-3
1994	1982	1634	1639	-5
1996	1364	1643	1653	-10
$\hat{r} = 0.078$ *and* $\hat{r}^*_{1000} = 0.078$				

4.5 Monte Carlo simulations

Using the procedure described in Chapter 3, one thousand Monte Carlo simulations were run and the estimated coverage probabilities are shown in Table 4.8. The sample estimates were used as the true population values for these simulations, and the results are shown in Table 4.8.

4.5.1 Estimated coverage probability

a) Coverage probability of the survey estimates

The estimated coverage probabilities are very large (mostly 100%) for most of the estimates except for the 1982 and 1994 survey estimates. These estimates were previously shown to lie outside both the standard and percentile confidence intervals. This is supported by the Monte Carlo simulation study since the coverage probabilities of these two estimates are very low.

Note that, strictly speaking, the coverage probabilities refer to the true population sizes (whose values have been assumed) and not to the survey estimates. It is nevertheless interesting to compute them for the survey estimates, as it shows the large errors in the 1982 and 1994 values.

b) Coverage Probability of the sample estimates

The estimated coverage probabilities are 100% for all the sample estimates. The estimated coverage probabilities also suggest that the bootstrap confidence intervals are conservative, as the coverage probabilities should be 95% not 100%.

Table 4.8: Estimated coverage probabilities for the survey estimates and sample estimate

Year	Estimate	Coverage probability			
		Survey estimate as true population		Sample estimate as true population	
		Standard CI	Percentile CI	Standard CI	Percentile CI
	r	100%	100%	100%	100%
1973	μ_1	96%	97%	100%	100%
1976	μ_2	98%	99.5%	100%	100%
1982	μ_3	**4%**	**0.5%**	100%	100%
1985	μ_4	97%	100%	100%	100%
1986	μ_5	100%	100%	100%	100%
1991	μ_6	100%	100%	100%	100%
1994	μ_7	**10%**	**12%**	100%	100%
1996	μ_8	100%	100%	100%	100%

4.5.2 Average length of confidence interval

The average lengths of the confidence intervals were computed over the 1000 simulation runs and the results are shown in the Table 4.9 and 4.10 for the 200 and 1000 bootstrap replications, respectively.

a) Average length of the Monte Carlo confidence intervals vs. the bootstrap confidence interval length

The average lengths of the Monte Carlo confidence intervals were large compared with those of the standard and percentile confidence intervals, which had similar lengths. The intervals for the 1996 survey estimates were the longest, followed by those for 1973. In all cases the bootstrap confidence intervals were shorted than the corresponding Monte Carlo confidence intervals. There was not much difference between the Monte Carlo confidence intervals. The standard and the percentile confidence intervals were similar in all cases.

The fact that the Monte Carlo intervals are longer than the corresponding standard and percentile confidence intervals may be the reason why their coverage probabilities were high.

Table 4.9: Estimated average length of confidence interval, standard confidence interval length and the percentile confidence length for 200 bootstrap replications

Year	Estimate	Monte Carlo confidence interval		Bootstrap confidence interval length	
		Standard CI	Percentile CI	Standard CI	Percentile CI
	r	0.046	0.044	0.040	0.038
1973	μ_1	733	725	632	626
1976	μ_2	642	640	556	553
1982	μ_3	491	484	420	416
1985	μ_4	449	447	378	378
1986	μ_5	440	439	370	370
1991	μ_6	489	493	424	432
1994	μ_7	676	667	590	580
1996	μ_8	854	844	758	741

Table 4.10: Estimated average length of confidence interval, standard confidence interval length and the percentile confidence length for 1000 bootstrap replications

Year	Estimate	Monte Carlo Confidence Interval		Bootstrap confidence Interval Length	
		Standard CI	Percentile CI	Standard CI	Percentile CI
	r	0.046	0.044	0.041	0.039
1973	μ_1	733	725	638	646
1976	μ_2	642	640	564	576
1982	μ_3	491	484	428	434
1985	μ_4	449	447	384	378
1986	μ_5	440	439	376	367
1991	μ_6	489	493	420	410
1994	μ_7	676	667	574	558
1996	μ_8	854	844	736	724

4.6 Jackknife

The jackknife was also implemented, as discussed in Chapter 3, and the results obtained after removing each survey are shown in section 4.5.1. The net losses were recalculated when a survey estimate was removed, for example when the 1973 survey estimate was removed, the net loss for 1973 was removed, and that for 1976 remained the same (1138) as before. When the 1976 survey estimate was removed, the net loss between 1973 and 1982 was 513+1138=1651 and so on, until the 1996 survey was removed and the net loss between 1991 and 1994 was 430. For each removed survey the recalculated net losses are shown.

4.6.1 Results obtained on removing each time point

a) $i = 1$**: Remove 1973 survey estimate**

Table 4.11: Estimated true population after removing the 1973 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1976	1629	1138	1731	-102
1982	1199	424	1424	-225
1985	1530	60	1365	165
1986	1502	438	1426	77
1991	1748	430	1656	92
1994	1982	246	1659	323
1996	1364		1706	-342
$\hat{r} = 0.087$				

b) $i = 2$**: Remove 1976 survey estimate**

Table 4.12: Estimated true population after removing the 1976 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1973	2230	1651	2033	197
1982	1199	424	1581	-381
1985	1530	60	1492	38
1986	1502	438	1542	-40
1991	1748	430	1691	57
1994	1982	246	1622	360
1996	1364		1612	-248
$\hat{r} = 0.073$				

c) $i = 3$**: Remove 1982 survey estimate**

Table 4.13: Estimated true population after removing the 1982 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1973	2230	513	2018	212
1976	1629	1662	1955	-326
1985	1530	60	1478	52
1986	1502	438	1531	-29
1991	1748	430	1701	47
1994	1982	246	1651	331
1996	1364		1655	-291
$\hat{r} = 0.076$				

d) $i = 4$**: Remove 1985 survey estimate**

Table 4.14: Estimated true population after removing the 1985 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1973	2230	513	1913	317
1976	1629	1138	1843	-214
1982	1199	484	1501	-302
1986	1502	438	1487	15
1991	1748	430	1667	81
1994	1982	246	1626	356
1996	1364		1637	-273
$\hat{r} = 0.079$				

e) $i = 5$ **: Remove 1986 survey estimate**

Table 4.15: Estimated true population after removing the 1986 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1973	2230	513	1928	303
1976	1629	1138	1859	-230
1982	1199	424	1520	-321
1985	1530	498	1445	85
1991	1748	430	1675	74
1994	1982	246	1633	349
1996	1364		1643	-279
$\hat{r} = 0.078$				

f) $i = 6$ **: Remove 1991 survey estimate**

Table 4.16: Estimated true population after removing the 1991 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1973	2230	513	1851	380
1976	1629	1138	1804	-175
1982	1199	424	1522	-323
1985	1530	60	1482	48
1986	1502	868	1551	-48
1994	1982	246	1821	161
1996	1364		1422	-58
$\hat{r} = 0.085$				

g) $i = 7$ **: Remove 1994 survey estimate**

Table 4.17: Estimated true population after removing the 1994 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1973	2230	513	1964	267
1976	1629	1138	1880	-251
1982	1199	424	1502	-303
1985	1530	60	1402	128
1986	1502	438	1448	55
1991	1748	676	1568	180
1996	1364		1455	-91
$\hat{r} = 0.074$				

h) $i = 8$ **: Remove 1996 survey estimate**

Table 4.18: Estimated true population after removing the 1996 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1973	2230	513	1842	388
1976	1629	1138	1796	-167
1982	1199	424	1513	-314
1985	1530	60	1471	59
1986	1502	438	1540	-38
1991	1748	430	1815	-66
1994	1982		1855	127
$\hat{r} = 0.085$				

4.6.2 Jackknife standard error for the sample estimates

Table 4.19: Estimated true population estimates for each removed survey estimate

i	$\mu_{1(i)}$	$\mu_{2(i)}$	$\mu_{3(i)}$	$\mu_{4(i)}$	$\mu_{5(i)}$	$\mu_{6(i)}$	$\mu_{7(i)}$	$\mu_{8(i)}$	$r_{(i)}$
1		1731	1424	1365	1426	1656	1659	1706	0.087
2	2033		1581	1492	1542	1691	1622	1612	0.073
3	2018	1955		1478	1531	1701	1651	1655	0.076
4	1913	1843	1501		1487	1667	1626	1637	0.079
5	1928	1859	1520	1445		1675	1633	1643	0.078
6	1851	1804	1522	1482	1551		1821	1422	0.085
7	1964	1880	1502	1402	1448	1568		1455	0.074
8	1842	1796	1513	1471	1540	1815	1855		0.085
Averages	1936	1838	1509	1448	1504	1682	1695	1590	0.080

The jackknife standard errors for each of the survey estimates were obtained using the formula given earlier: $\hat{\sigma}_{\hat{\mu}_t} = \sqrt{\left(\frac{n-1}{n}\right)\sum_{i=1}^{n}\left(\hat{\mu}_{t(i)} - \hat{\mu}_{t(\cdot)}\right)^2}$.

Table 4.20 below gives the results of each survey estimate.

The 1982 survey had the smallest jackknife standard error and the 1996 survey had the largest. The jackknife standard error for the natural growth rate in population was small, approximately 1%.

The jackknife results were not much different from the model estimates. There was a large difference between the 1994 surveys (61) and the 1996 surveys (53). The 1976 surveys also differed with a notable difference of 22. The rest of the surveys did not have large differences.

Table 4.20: Average jackknife estimates and standard errors

Year	Model estimate	Average jackknife estimate	Difference between the survey estimate and average jackknife estimate	Jackknife standard error
		0.080		0.013
1973	1930	1936	-6	170
1976	1860	1838	22	161
1982	1520	1509	11	105
1985	1443	1448	-5	108
1986	1498	1504	-6	114
1991	1676	1682	-6	166
1994	1634	1695	-61	224
1996	1643	1590	53	244

4.7 Comparison of the bootstrap and jackknife

4.7.1 Comparison of the bootstrap and jackknife estimates

There was not much difference between most of the bootstrap estimates and the jackknife estimates, apart from those corresponding to the 1994 and 1996 surveys. The bootstrap estimates are much closer to the original sample estimates than are the jackknife estimates.

Table 4.21: Comparison of the bootstrap and jackknife estimates

Year	Bootstrap estimate		Average jackknife estimate	Difference between the survey estimate and average jackknife estimate	
	200 Replications	1000 Replications		200 Replication	1000 Replications
	0.079	0.078	0.080	-0.001	-0.002
1973	1929	1935	1936	-7	-1
1976	1859	1865	1838	21	27
1982	1518	1522	1509	9	13
1985	1441	1444	1448	-7	-4
1986	1496	1498	1504	-8	-6
1991	1679	1679	1682	-3	-3
1994	1642	1639	1695	-53	-56
1996	1657	1653	1590	67	63

4.7.2 Comparison of the bootstrap and jackknife standard errors

From Table 4.22 it is clear that the bootstrap performed better than the jackknife as the standard errors are less than those obtained by the jackknife. The results support what most authors, Diaconis and Efron (1983), Frangos and Stone (1984), Mooney and Duval (1993), Fan and Wang (1996) have concluded: that the bootstrap performs better than the jackknife. The bootstrap and jackknife methods both showed that the 1996 survey estimate had the largest standard error. The smallest standard error for the bootstrap method was in the 1986 survey, while with the jackknife method, the 1982 estimate had the smallest error. For the natural annual growth rate of increase the jackknife standard error was only slightly larger than for the bootstrap.

Table 4.22: Comparison of the bootstrap and jackknife standard error

Year	Bootstrap standard errors for 200 replications	Bootstrap standard errors for 1000 replications	Jackknife standard error
	0.010	0.010	0.013
1973	161	163	170
1976	142	144	161
1982	107	109	105
1985	96	98	108
1986	94	96	114
1991	108	107	166
1994	151	146	224
1996	194	188	244

Chapter 5

Black Rhino Results

5.1 Calculation of Net Losses

For the black rhino the net losses were not interpolated since the data was collected in consecutive seven year periods. The total losses were used as the net losses (raw data in Appendix A2).

5.2 Model fitting algorithm 3.1

Fitting the model with algorithm 3.1 to the seven survey estimates gives the results shown in Table 5.1 which are also displayed in Figure 5.1, together with the original survey estimates.

The results showed a steady growth over all seven years from 1990 to 1996. The survey estimate for 1993 showed the largest estimated error and is identified by the model as being too high. The 1990 survey estimate showed the next largest error.

The estimated growth rate obtained from the fitted model is 8.6% which according to Fatti et al. (2002) was slightly higher than what the scientists were expecting. As with the white rhino the expected natural annual growth rate in the population was 6% to 8%. Using step 3 of the algorithm, the standard deviation of the survey estimates was estimated to be:

$$\hat{\sigma} = \sqrt{\frac{1}{n-2}\sum_{t=1}^{n}\varepsilon_t^2} = 21$$

The estimated error for the black rhino population was much lower than that for the white rhino and this may be because the survey estimates for the White Rhino were taken over a 24 year period, whereas the black rhino survey estimates were taken over seven consecutive years. The different methods used for estimating the population abundance may also have contributed to the error.

Table 23: Black rhino survey data, estimated true population sizes and estimated survey errors, 1990 to 1996

Year	Survey estimate	Mortalities	Relocations	Total losses	Estimated true population sizes	Estimated error
1990	337	10	8	18	358	-21
1991	367	13	9	22	372	-5
1992	385	19	6	25	382	3
1993	429	16	9	25	391	38
1994	405	6	15	21	400	5
1995	409	14	6	20	414	-5
1996	416				431	-15

Figure 5.1 displays the estimated true black rhino population size superimposed on corresponding survey estimates for each of the seven years from 1990 to 1996. A much smoother curve is obtained from the model than for the survey estimates.

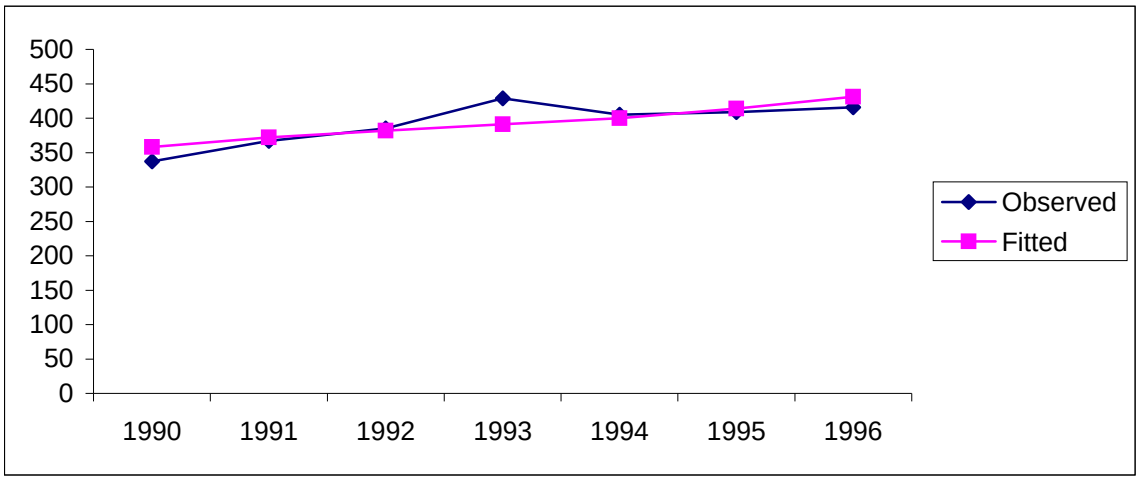


Figure 5.1: Plot of the estimated true population sizes and the survey estimates at each of the eight surveys

5.3 Bootstrapping

As with the white rhino the bootstrap technique was applied to the black rhino survey estimates and the tables below show the bootstrap estimates of true population sizes for 200 and 1000 replications, respectively.

5.3.1 200 Replications

The results from running 200 bootstrap replications confirmed the steady growth rate in the black rhino population. As was the case with the model fitted directly to the survey estimates, the survey for 1993 value had the largest error. The bootstrap estimate of the natural annual growth rate in the population was estimated to be 0.087 or 8.7%, which is almost the same as that obtained from fitting the model to the survey estimates. The standard error of the bootstrap estimate of the natural annual growth rate in the population was estimated to be $\widehat{se}_{r^*_{200}} = 0.011$, which is similar to that for the white rhino, and shows that the natural annual growth rate was small, suggesting a good estimate for the natural annual growth rate is estimated precisely.

The 1993 population estimate had the lowest standard error, despite having the largest estimated error. The standard errors for the survey estimates are small.
Note that the bootstrap population estimates are all almost identical to those obtained directly from the survey estimates.

Table 24: Bootstrap estimates of the true population sizes and the standard error of the bootstrap estimates for 200 replications

Year	Survey estimate	Bootstrap estimates of true population sizes	Standard error $\widehat{se}_{\mu^*_{i,200}}$	Difference between survey estimates
1990	337	358	13	-21
1991	367	371	11	-4
1992	385	382	9	3
1993	429	390	8	39
1994	405	399	8	6
1995	409	413	10	-4
1996	416	429	14	-13
$\hat{r} = 0.087$ and $\widehat{se}_{r^*_{200}} = 0.011$				

Figure 5.2 gives the graph of the bootstrap estimates of the true population sizes compared with that of survey estimates obtained using 200 replications. As previously, the 1993 survey estimate is shown to be too high.

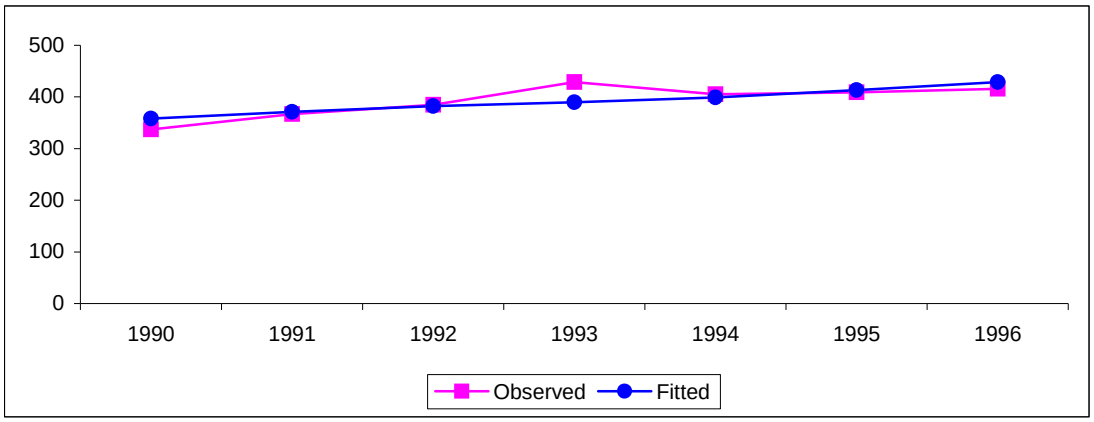


Figure 5.2: Plot of the bootstrap estimates of the true population sizes and the survey estimates for each of the seven surveys for 200 replications

a) Confidence intervals

The confidence intervals for the bootstrap estimates were obtained using the standard and percentile confidence intervals and are shown in Table 5.3. It can be seen that the confidence intervals obtained using both methods are similar. Note also that both confidence intervals do not contain the 1993 the survey estimate. This estimate (429) was considered to be too high as it was well above the upper limit of both confidence intervals. Both confidence intervals for the bootstrap estimate of the natural annual growth rate included the expected range of 6% to 8%.

Table 5.3: Standard and percentile confidence intervals obtained at 200 replications for each of the bootstrap estimates

Year	Bootstrap estimate	95 % Standard confidence intervals	95% Percentile confidence intervals
	$\hat{r}^*_{200}$	[0.064 ; 0.108]	[0.065 ; 0.103]
1990	$\hat{\mu}^*_{1,200}$	[332 ; 384]	[337 ; 388]
1991	$\hat{\mu}^*_{2,200}$	[349 ; 393]	[354 ; 397]
1992	$\hat{\mu}^*_{3,200}$	[364 ; 400]	[368 ; 402]
1993	$\hat{\mu}^*_{4,200}$	[374 ; 406]	[377 ; 408]
1994	$\hat{\mu}^*_{5,200}$	[383 ; 415]	[386 ; 419]
1995	$\hat{\mu}^*_{6,200}$	[393 ; 433]	[397 ; 440]
1996	$\hat{\mu}^*_{7,200}$	[401 ; 457]	[407 ; 466]

Figures 5.3 and 5.4 show the confidence intervals for the bootstrap estimates based on 200 replications. From the confidence intervals shown, it can be seen that the 1993 survey estimate is not included in the confidence interval range**.**

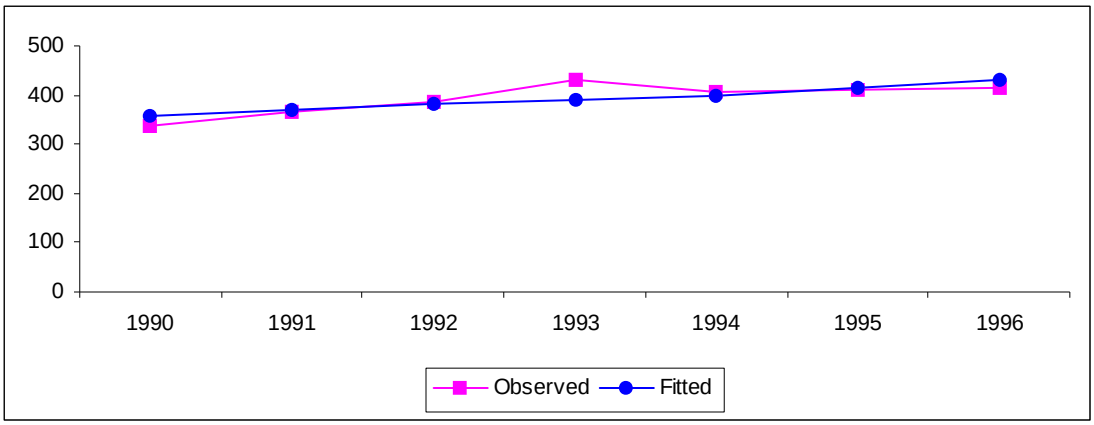


Figure 5.3: Standard confidence intervals for 200 replications

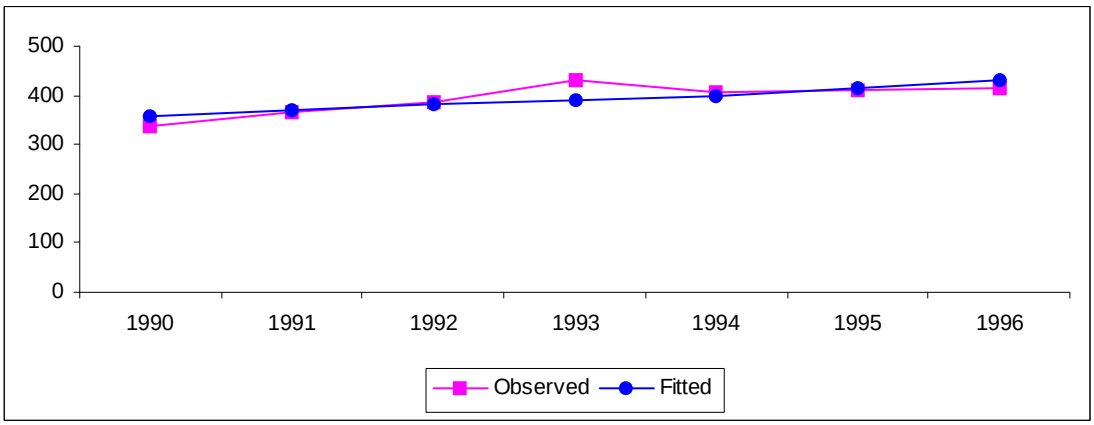


Figure 5.4: Percentile confidence intervals for 200 replications

5.3.2 1000 Replications

The bootstrap estimate of the natural annual growth rate in the population was estimated to be 0.086 or 8.6% which is the same value obtained from fitting the model directly to the survey data. The estimated standard error of the natural annual growth rate was estimated to be $\widehat{se}_{r^*_{1000}} = 0.010$, which was similar to that for the 200 bootstrap replications.

The 1993 survey estimate showed the smallest standard error although it has the largest estimated error.

Table 5.4: Bootstrap estimates of the true population sizes and the standard error of the bootstrap estimates for 1000 replications

Year	Survey estimate	Bootstrap estimates of true population sizes	Standard error $se_{\hat{\mu}^*_{i,1000}}$	Difference between survey estimates
1990	337	358	13	-21
1991	367	371	11	-4
1992	385	382	9	3
1993	429	390	7	39
1994	405	400	9	5
1995	409	414	10	-5
1996	416	431	14	-15
$\hat{r} = 0.086$ and $se_{\hat{r}^*_{200}} = 0.0102$				

Figure 5.7 superimposes the graph of the bootstrap estimates of the true population sizes on that of survey estimates obtained using 1000 replications. As before, a smoother curve was obtained from the bootstrap estimates than from the original survey estimates.

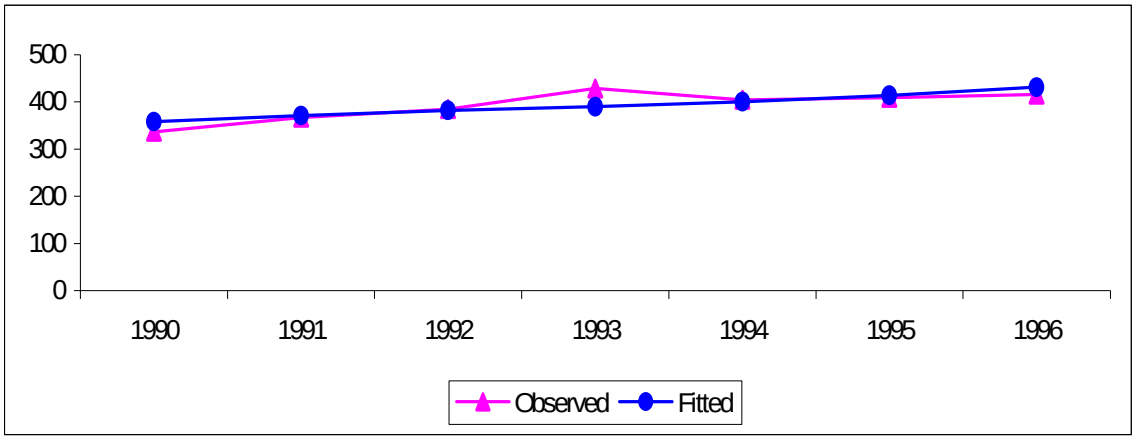


Figure 5.7: Plot of the bootstrap estimates of the true population sizes and the survey estimates for each of the eight surveys for 1000 replications

a) Confidence intervals

The results of the standard and percentile confidence intervals are again similar. The 1993 survey estimate is higher than the upper limit of both confidence intervals. Both confidence intervals for the bootstrap estimate of the natural annual growth rate include the expected growth rate by the scientist at the park of 6% to 8%.

Table 5.5: Standard and percentile confidence intervals obtained at 1000 replications for each of the bootstrap estimates

Year	Bootstrap estimate	95% Standard confidence intervals	95% Percentile confidence intervals
	$\hat{r}^*_{1000}$	[0.066 ; 0.106]	[0.068 ; 0.106]
1990	$\hat{\mu}^*_{1,1000}$	[333 ; 383]	[336 ; 385]
1991	$\hat{\mu}^*_{2,1000}$	[350 ; 392]	[353 ; 395]
1992	$\hat{\mu}^*_{3,1000}$	[365 ; 399]	[367 ; 402]
1993	$\hat{\mu}^*_{4,1000}$	[376 ; 404]	[377 ; 407]
1994	$\hat{\mu}^*_{5,1000}$	[385 ; 415]	[386 ; 418]
1995	$\hat{\mu}^*_{6,1000}$	[394 ; 434]	[397 ; 440]
1996	$\hat{\mu}^*_{7,1000}$	[403 ; 459]	[407 ; 466]

Figures 5.5 and 5.6 below for the standard and percentile confidence intervals show that the 1993 survey estimates were not included in the estimated confidence interval range, which indicates that the survey estimate may be biased.

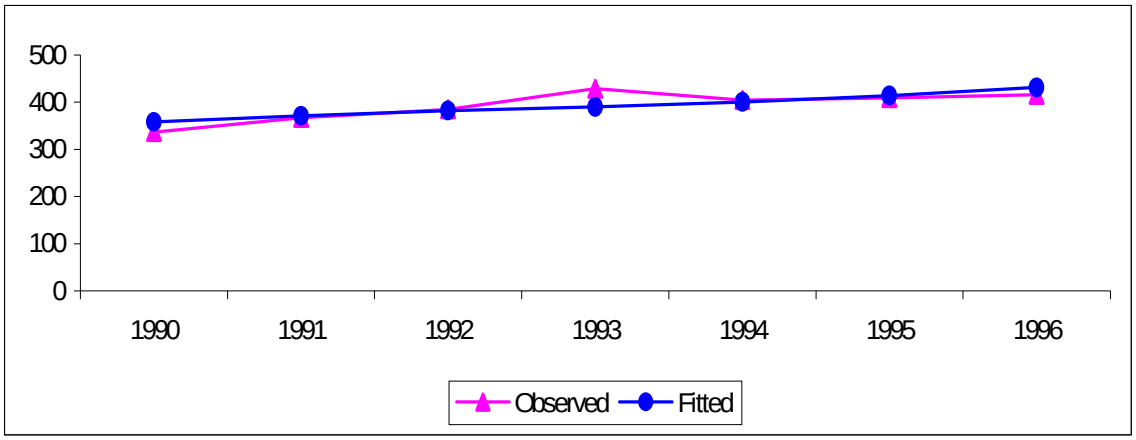


Figure 5.5: Standard confidence intervals for 1000 replications

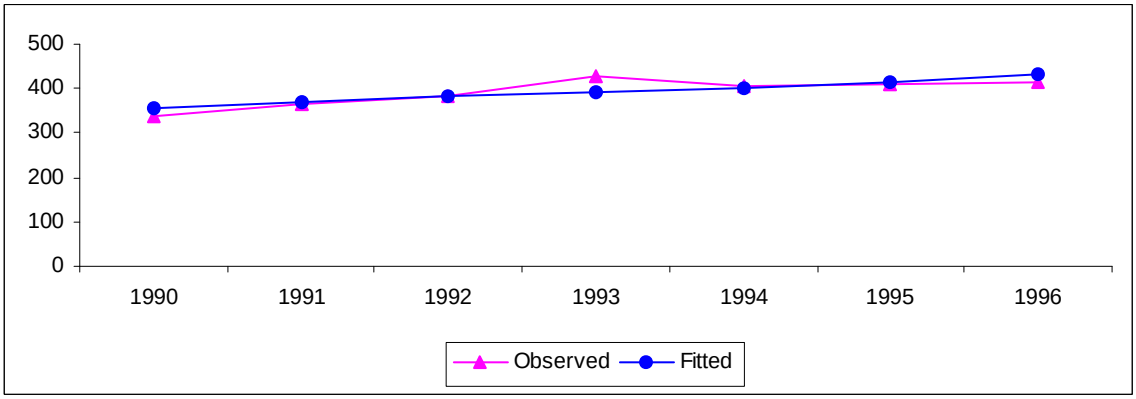


Figure 5.6: Percentile confidence intervals for 1000 replications

5.4 Comparison of bootstrap estimates and the full sample model of the true population sizes

a) 200 Bootstrap replications vs. full sample model

The results from bootstrapping are almost identical to those obtained from fitting the model directly to the survey data. The largest difference occurs for the 1996 estimates (2), which is not large.

Table 5.6: Comparison of bootstrap estimates for 200 replications and the full sample model

Year	Survey estimate	Sample estimates	Bootstrap estimates of true population sizes (B=200)	Difference between sample estimates and bootstrap estimates
1990	337	358	358	0
1991	367	372	371	1
1992	385	382	382	0
1993	429	391	390	1
1994	405	400	399	1
1995	409	414	413	1
1996	416	431	429	2
$\hat{r} = 0.086$ *and* $\hat{r}^*_{200} = 0.087$				

b) 1000 replications vs. full sample model

As with 200 bootstrap replications, the results from bootstrapping are almost identical to those obtained from fitting the model directly to the survey data.

Table 5.7: Comparison of bootstrap estimates for 1000 replications and the full sample model

Year	Survey estimate	Sample estimates	Bootstrap estimates of true population sizes (B=1000)	Difference between sample estimates and bootstrap estimates
1990	337	358	358	0
1991	367	372	371	1
1992	385	382	382	0
1993	429	391	390	1
1994	405	400	400	0
1995	409	414	414	0
1996	416	431	431	0
$\hat{r} = 0.086$ *and* $r^*_{1000} = 0.086$				

5.5 Monte Carlo Simulations

Using the procedure in Chapter 3, Monte Carlo simulations were run and the estimated coverage probabilities obtained are shown below.

5.5.1 Estimated coverage probability

The coverage probabilities were estimated using the survey estimates and considering the sample estimates to be true population values. The results are shown in Table 5.8.

a) Coverage probability using survey estimates as true population

The estimated coverage probabilities are also high as with the white rhino. For the 1993 estimate the coverage probability was small for both confidence intervals. The results support the fact that the 1993 estimate is too high.

b) Coverage probability using sample estimates as true population

The estimated coverage probabilities are 100% for all the sample estimates for both confidence intervals. The results of the Monte Carlo simulation show that the sample estimates obtained from the model are more realistic than the original survey estimates. The estimated coverage probabilities also underpin the fact that the survey estimate for 1993 was biased.

Table 5.8: Estimated coverage probability

Year	Estimate	Coverage probability			
		Survey estimate as true population		Sample estimate as true population	
		Standard CI	Percentile CI	Standard CI	Percentile CI
	r	96%	98%	100%	100%
1990	μ_1	99%	96.5%	100%	100%
1991	μ_2	97%	100%	100%	100%
1992	μ_3	100%	100%	100%	100%
1993	μ_4	**11%**	**13%**	100%	100%
1994	μ_5	100%	100%	100%	100%
1995	μ_6	98%	100%	100%	100%
1996	μ_7	100%	100%	100%	100%

5.5.2 Average length of confidence interval

Using the same formula as the white rhino table 5.15 gives the results for the average length of the confidence intervals.

a) Average length of confidence interval vs. confidence interval length

The results for both 200 and 1000 bootstrap replications (see Table 5.9 for 200 and Table 5.10 for 1000) showed that the average length for the confidence intervals is almost identical to the confidence interval length of the standard and percentile confidence intervals. The 1996 survey estimates showed the largest average length of confidence interval. The 1990 survey estimates also have large average length of the confidence intervals. The percentile confidence intervals are shorter for most of the estimates. The results for Monte Carlo confidence intervals are almost the same as the bootstrap confidence intervals.

Table 5.9: Estimated average length of confidence interval, standard confidence interval length and the percentile confidence length for 200 replications

Year	Estimate	Monte Carlo confidence interval		Bootstrap confidence interval length	
		Standard CI	Percentile CI	Standard CI	Percentile CI
	r	0.045	0.040	0.044	0.03781
1990	μ_1	53	52	52	51
1991	μ_2	46	44	44	43
1992	μ_3	37	36	36	34
1993	μ_4	38	32	42	31
1994	μ_5	35	34	32	33
1995	μ_6	42	44	40	43
1996	μ_7	61	60	56	59

Table 5.10: Estimated average length of confidence interval, standard confidence interval length and the percentile confidence length for 1000 replications

Year	Estimate	Monte Carlo confidence interval		Bootstrap confidence interval length	
		Standard CI	Percentile CI	Standard CI	Percentile CI
	r	0.045	0.040	0.040	0.038
1990	μ_1	53	52	50	49
1991	μ_2	46	44	42	42
1992	μ_3	37	36	34	35
1993	μ_4	38	32	28	30
1994	μ_5	35	34	30	32
1995	μ_6	42	44	40	43
1996	μ_7	61	60	56	59

5.6 Jackknife

Following the procedure described in Chapter three, the jackknife was implemented. As with the white rhino, the net losses were recalculated when a survey estimate was removed. When the survey estimate for 1990 was removed the net loss for 1990 was removed and that for 1991 remained the same. After removing 1991, the net loss between 1990 and 1992 was recalculated as 18+22=40. The recalculated net losses at each stage are shown in section 5.5.1.

5.6.1 Results obtained on removing each time point

a) $i=1$**: Remove 1990 survey estimate**

Table 5.11: Estimated true population after removing the 1990 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1991	367	22	383	-16
1992	385	25	391	-6
1993	429	25	397	32
1994	405	21	402	3
1995	409	20	413	-4
1996	416		425	-9
$\hat{r}=0.077$				

b) $i = 2$ **: Remove 1991 survey estimate**

Table 5.12: Estimated true population after removing the 1991 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1990	337	40	360	-23
1992	385	25	384	-15
1993	429	25	392	37
1994	405	21	401	4
1995	409	20	414	-5
1996	416		430	-4
$\hat{r} = 0.085$				

c) $i = 3$ **: Remove 1992 survey estimate**

Table 5.13: Estimated true population after removing the 1992 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1990	337	18	357	-20
1991	367	47	371	-4
1993	429	25	390	39
1994	405	21	400	5
1995	409	20	414	-5
1996	416		431	-15
$\hat{r} = 0.087$				

d) $i = 4$ **: Remove 1993 survey estimate**

Table 5.14: Estimated true population after removing the 1993 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1990	337	18	351	-4
1991	367	22	365	2
1992	385	50	376	9
1994	405	21	394	11
1995	409	20	409	0
1996	416		426	-10
$\hat{r} = 0.089$				

e) $i = 5$ **: Remove 1994 survey estimate**

Table 5.15: Estimated true population after removing the 1994 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1990	337	18	358	-21
1991	367	22	371	-4
1992	385	25	382	3
1993	429	46	390	39
1995	409	20	413	-4
1996	416		429	-13
$\hat{r} = 0.086$				

f) $i = 6$ **: Remove 1995 survey estimate**

Table 5.16: Estimated true population after removing the 1995 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1990	337	18	358	-21
1991	367	22	372	-5
1992	385	25	383	2
1993	429	25	392	37
1994	405	41	402	3
1996	416		434	-18
$\hat{r} = 0.088$				

g) $i = 7$ **: Remove 1996 survey estimate**

Table 5.17: Estimated true population after removing the 1996 survey estimate

Year	Survey estimate	Net losses	True population estimate	Estimated error
1990	337	18	353	-16
1991	367	22	369	-2
1992	385	25	383	2
1993	429	25	394	35
1994	405	21	407	-2
1995	409		426	-17
$\hat{r} = 0.095$				

5.6.2 Jackknife standard error for the sample estimates

Table 5.18: True population estimates for each

i	$\mu_{1(i)}$	$\mu_{2(i)}$	$\mu_{3(i)}$	$\mu_{4(i)}$	$\mu_{5(i)}$	$\mu_{6(i)}$	$\mu_{7(i)}$	$r_{(i)}$
1		383	391	397	402	413	425	0.077
2	360		384	392	401	414	430	0.085
3	357	371		390	400	414	430	0.087
4	351	365	376		394	409	426	0.089
5	358	371	382	390		413	429	0.086
6	358	372	383	392	402		434	0.088
7	353	369	383	394	407	426		0.095
$\mu_{t(\cdot)}$	356	371	383	393	401	415	429	$r_{(\cdot)} = 0.087$

The largest error (difference between the survey estimate and average jackknife estimate) occurs in the 1993 survey estimate. The jackknife estimate also showed that the 1993 survey estimate was too high.

Table 5.19 below gives the results of each survey estimate. Most of the survey estimates had small standard error. The 1991 survey estimate had the largest standard error. The 1993 survey estimate had the smallest standard error though it had the largest estimated error. The standard error for the natural annual growth rate in population was small.

Table 5.19: Jackknife estimates and standard errors

Year	Survey estimate	Average jackknife estimate	Difference between the survey estimate and jackknife estimate	Jackknife standard error
		0.087		0.012
1990	337	356	-19	7
1991	367	371	-4	12
1992	385	383	2	10
1993	429	393	36	6
1994	405	401	4	9
1995	409	415	-6	12
1996	416	429	-13	7

5.7 Comparison of the bootstrap and jackknife

5.7.1 Comparison of the bootstrap and jackknife estimates

The bootstrap estimates are almost identical to the jackknife estimates. The largest difference occurred in the 1993 survey (-3) for both. Unlike with the white rhino, the jackknife estimates are as close to the model estimates as the bootstrap.

Table 5.20: Comparison of the bootstrap and jackknife estimates

Year	Bootstrap estimate		Average jackknife estimate	Difference between the survey estimate and average jackknife estimate	
	200 Replications	1000 Replications		200 Replication	1000 Replications
	0.087	0.086	0.087	0	-0.001
1990	358	358	356	2	-1
1991	371	371	371	0	0
1992	382	382	383	-1	-1
1993	390	390	393	-3	-3
1994	399	400	401	-2	-1
1995	413	414	415	-2	-1
1996	429	431	429	0	2

5.7.2 Comparison of the bootstrap and jackknife standard errors

Most of the bootstrap standard errors are smaller than the jackknife standard errors. The jackknife standard errors are smaller than the bootstrap standard errors for the 1990 and 1996 surveys. For black rhino it can be concluded that the bootstrap and jackknife produced similar results. The smallest standard error for both methods was in 1993. The 1993 survey estimate showed the largest estimated error in both the bootstrap and the jackknife.

Table 5.21: Comparison of the bootstrap and jackknife standard error

Year	Bootstrap standard errors for 200 replications	Bootstrap standard errors for 1000 replications	Jackknife standard error
	0.01115	0.01017	0.012
1990	13	13	7
1991	11	11	12
1992	9	9	10
1993	8	7	6
1994	8	9	9
1995	10	10	12
1996	14	14	7

Chapter 6

Summary and Recommendations

6.1 White Rhino

The apparent sudden decline in numbers of the white rhino population between 1994 and 1996, which triggered the study by Fatti et al. (2002), can be explained by the largest observed error associated with the 1994 survey estimate. This estimate was shown to be far too high, while the 1996 survey estimate was a somewhat smaller under-estimate. Under-estimation by the 1982 survey was underpinned by the confidence interval that had a lower limit well above the survey estimate. The conclusion that the sudden decrease in numbers between the 1994 and 1996 surveys was a result of survey error, particularly in 1994, was also underpinned by the confidence interval results.

The graphs of the estimated true population sizes over time was much smoother than that of the original survey estimates, and according to Fatti et al. (2002), these were considered to be more realistic by the scientist at the park. The bootstrap standard error for the estimated natural annual growth rate was small, suggesting that this is a good estimate.

Increasing the number of bootstrap replications had little effect on the bootstrap estimates, their standard errors as well as on their confidence intervals. There was also little difference between bootstrap estimates and the original sample estimates, which boosted confidence in the bootstrap results. The Monte Carlo study suggests that the 1982 and 1994 survey estimates are biased. The jackknife estimates also supported the conclusion that the 1982 and 1994 survey estimates were biased. The jackknife standard error for the natural annual growth rate was small. The bootstrap method performed better than the jackknife although the results did not show much difference.

6.2 Black Rhino

The apparent decline in numbers between the 1993 and 1994 survey can be explained by the largest positive error being associated with the 1993 survey estimate. The fact that the 1993 survey estimate lay above the confidence interval for the true population size confirms the likelihood that this estimate was biased upwards. The graph of the estimated true population sizes is smoother than that of the original survey estimates. The standard error for the natural annual growth rate was small, again suggesting that it is a fairly accurate estimate.

As with the white rhino, there was little difference between the results of 200 and 1000 bootstrap replications. Increasing the number of bootstrap replications had little effect on the bootstrap estimates, their standard errors, as well as on their confidence intervals. The Monte Carlo study confirmed that the 1993 survey estimate was probably biased.

The results for the jackknife standard errors also support the conclusion that the 1993 survey estimate was probably biased. The jackknife standard error for the natural annual growth rate was small.

6.3 Discussion

The results of the standard confidence intervals and the percentile confidence intervals are similar. They show the same pattern in both the white and black rhino population. The use of percentile method is recommended in this research as it does not involve the normal distribution.

The variability of the distance based methods, which were used for the white rhino population, was larger than that for the black rhino, which used the mark recapture method. The variability of the distance method may be partly because of the fact that the white rhino survey estimates were obtained over a 24 year period, whereas those for black rhino were obtained over seven consecutive years.

The model for combining survey estimates over time, combined with the bootstrap technique described in this research could, also be applied to the population sizes of other species in the park such as buffalo, giraffe, kudu, wildebeest and impala.

According to Fatti et al. (2002) the use of the model to estimate population sizes has generally been accepted by the scientist at the park, though the assumptions underlying the model may in some cases not be strictly valid.

The research showed that the bootstrap method was useful in this context, worked well and gave good results. The bootstrap clearly showed that the 1994 white rhino survey was likely to be more biased than the 1996 survey. The bootstrap estimates were consistent with the confidence interval results, as well as with the Monte Carlo simulations. The standard errors also confirmed these results. Although the 1994 survey did not have the largest standard error, it was still large enough for this study to conclude that the 1994 survey was likely to be more biased than the 1996 survey.

From this research the bootstrap performance proved to be reliable than the jackknife although the results of the two methods were not different. From this study we recommend the bootstrap method over the jackknife. The jackknife procedure has the drawback that the sub replicates are of a smaller size than the original data set, which may change the statistical properties of the sample. According to Fan and Wang (1996) the bootstrap method has the advantage of retaining the actual sample size.

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A p p e n d i c e s

Appendix A: Datasets used

A1: White Rhino

Table 6.1: Data set for white rhino

Year	Survey estimate	Mortalities	Relocations	Total losses	Net losses
1973	2230	48	452	500	513
1976	1629	128	1025	1153	1138
1982	1199	106	380	486	424
1985	1530	14	24	38	60
1986	1502	108	297	405	438
1991	1748	101	341	442	430
1994	1982	56	190	246	246
1996	1364				

A2: Black Rhino

Table 6.2: Data set for black rhino

Year	Survey estimate	Mortalities	Relocations	Total losses
1990	337	10	8	18
1991	367	13	9	22
1992	385	19	6	25
1993	429	16	9	25
1994	405	6	15	21
1995	409	14	6	20
1996	416			

Appendix B: Matlab program for fitting the model

```
function f = objf(x,y,s,l) % r is the portofolio returns , need to load them.

y1=y(1);y2=y(2);y3=y(3);y4=y(4);y5=y(5);y6=y(6);y7=y(7);y8=y(8);
s1=s(1);s2=s(2);s3=s(3);s4=s(4);s5=s(5);s6=s(6);s7=s(7);
l1=l(1);l2=l(2);l3=l(3);l4=l(4);l5=l(5);l6=l(6);l7=l(7);

z2= y2 - (y1-x(1))*exp(x(2)*s1) + l1*((exp(x(2)*s1)-1)/(x(2)*s1));

z3= y3 - (y1-x(1))*exp(x(2)*(s1+s2)) + l1*((exp(x(2)*s1)-1)/(x(2)*s1))*exp(x(2)*(s2)) +
l2*((exp(x(2)*s2)-1)/(x(2)*s2));

z4= y4 - (y1-x(1))*exp(x(2)*(s1+s2+s3)) + l1*((exp(x(2)*s1)-1)/(x(2)*s1))*exp(x(2)*(s2+s3)) +
l2*((exp(x(2)*s2)-1)/(x(2)*s2))*exp(x(2)*s3) + l3*((exp(x(2)*s3)-1)/(x(2)*s3));

z5= y5 - (y1-x(1))*exp(x(2)*(s1+s2+s3+s4)) + l1*((exp(x(2)*s1)-1)/(x(2)*s1))*exp(x(2)*(s2+s3+s4))
+ l2*((exp(x(2)*s2)-1)/(x(2)*s2))*exp(x(2)*(s3+s4)) + l3*((exp(x(2)*s3)-1)/(x(2)*s3))*exp(x(2)*s4)
+ l4*((exp(x(2)*s4)-1)/(x(2)*s4));

z6= y6 - (y1-x(1))*exp(x(2)*(s1+s2+s3+s4+s5)) + l1*((exp(x(2)*s1)-
1)/(x(2)*s1))*exp(x(2)*(s2+s3+s4+s5)) + l2*((exp(x(2)*s2)-1)/(x(2)*s2))*exp(x(2)*(s3+s4+s5)) +
l3*((exp(x(2)*s3)-1)/(x(2)*s3))*exp(x(2)*(s4+s5)) + l4*((exp(x(2)*s4)-1)/(x(2)*s4))*exp(x(2)*s5) +
l5*((exp(x(2)*s5)-1)/(x(2)*s5));

z7= y7 - (y1-x(1))*exp(x(2)*(s1+s2+s3+s4+s5+s6)) + l1*((exp(x(2)*s1)-
1)/(x(2)*s1))*exp(x(2)*(s2+s3+s4+s5+s6)) + l2*((exp(x(2)*s2)-
1)/(x(2)*s2))*exp(x(2)*(s3+s4+s5+s6)) + l3*((exp(x(2)*s3)-1)/(x(2)*s3))*exp(x(2)*(s4+s5+s6)) +
l4*((exp(x(2)*s4)-1)/(x(2)*s4))*exp(x(2)*(s5+s6)) + l5*((exp(x(2)*s5)-1)/(x(2)*s5))*exp(x(2)*s6) +
l6*((exp(x(2)*s6)-1)/(x(2)*s6));

z8= y8 - (y1-x(1))*exp(x(2)*(s1+s2+s3+s4+s5+s6+s7)) + l1*((exp(x(2)*s1)-
1)/(x(2)*s1))*exp(x(2)*(s2+s3+s4+s5+s6+s7)) + l2*((exp(x(2)*s2)-
1)/(x(2)*s2))*exp(x(2)*(s3+s4+s5+s6+s7)) + l3*((exp(x(2)*s3)-
1)/(x(2)*s3))*exp(x(2)*(s4+s5+s6+s7)) + l4*((exp(x(2)*s4)-1)/(x(2)*s4))*exp(x(2)*(s5+s6+s7)) +
l5*((exp(x(2)*s5)-1)/(x(2)*s5))*exp(x(2)*(s6+s7)) + l6*((exp(x(2)*s6)-1)/(x(2)*s6))*exp(x(2)*s7) +
l7*((exp(x(2)*s7)-1)/(x(2)*s7));

f= x(1)^2 +z2^2 + z3^2 + z4^2 + z5^2 + z6^2 + z7^2 + z8^2;

%%%%%%%%%%%%%
% Minimisation Procedure
%%%%%%%%%%%%%

x0=[0,0.1];
x=fminsearch(@objfjack,x0,[],y,s,l); epsilonhat(1)=x(1); rhat=x(2);
```

Appendix C: Matlab program for bootstrap application

```
% ALGORITHM 3.1
 %1
format short g;
clear; B=100;

y=[2230  1629  1199  1530  1502  1748  1982  1364];
n=8;
s=[3  6  3  1  5  3  2];
l=[513 1138 424 60 438 430 246];

x0=[0,0.1];
x=fminsearch(@objf2,x0,[],y,s,l);

epsilonhat(1)=x(1);

  %2
for t=1:n-1
   epsilonhat(t+1)=y(t+1)-(y(t)-epsilonhat(t))*exp(x(2)*s(t))+l(t)*((exp(x(2)*s(t))-1)/(x(2)*s(t)));
end

    %3


     %4
 muhat(1)=y(1)-epsilonhat(1);
 for i=2:n
     muhat(i)=muhat(i-1)*exp(x(2)*s(i-1))-l(i-1)*((exp(x(2)*s(i-1))-1)/(x(2)*s(i-1)));
 end
 muhat;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
 %BOOTSTRAP METHOD
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%


% STEP 1
eps_hat_t=y-muhat;
eps_hat_t_boot=repmat(eps_hat_t',1,B);

% center residuals

eps_prime_t_boot=(eps_hat_t_boot-mean(eps_hat_t)*ones(8,B))/sqrt(0.75);


% STEP 2

random_boot = ceil(8*rand(8,B));
eps_star_U_boot=eps_prime_t_boot(random_boot);

% STEP 3
y_star_boot(1,1:B)=muhat(1)+eps_star_U_boot(1,:);

y_star_boot(2:8,1:B)=repmat(muhat(1:7)'.*exp(x(2)*s')-l'.*((exp(x(2)*s')-
1)./(x(2)*s')),1,B)+eps_star_U_boot(2:8,:);

% STEP 4
for i=1:B
x(i,1:2)=fminsearch(@objf2,x0,[],y_star_boot(1:8,i),s,l);
end
```

```
epstar=x(:,1); rstar=x(:,2);
Y=y_star_boot;

 mu_star(1,1:B)=Y(1,1:B)-epstar';
 for i=2:n
     mu_star(i,1:B)=mu_star(i-1,1:B).*exp(rstar'*s(i-1))-l(i-1)*((exp(rstar'*s(i-1))-1)./(rstar'*s(i-1)));
 end

 result=[r_star_B mu_star_B]

 %%%%%%%%%%%%%%%%%%%%%%%%%
  % BOOTSTRAP VARIANCE ESTIMATE
  %%%%%%%%%%%%%%%%%%%%%%%%%

 r_star_B=mean(rstar);
 mu_star_B=mean(mu_star');
 var_rstar_B=var(rstar);
 var_mustar_B=var(mu_star');
```

Appendix D: Matlab program for percentile confidence intervals

```
 Percentile Confidence Intervals
 alpha=0.05;
 rstar_sort=sort(rstar);
 Lower_95_r=rstar_sort((alpha/2)*B), Upper_95_r=rstar_sort((1-(alpha/2))*B),


mustar_sort=sort((mu_star'));
Lower_95_mu=mustar_sort((alpha/2)*B,:);
```

Upper_95_mu=mustar_sort((1-(alpha/2))*B,:);

Appendix E: Matlab program for Monte Carlo simulation

```
format short g;clear;
% DECLARING VARIABLES
y=[2230 1629 1199 1530 1502 1748 1982 1364];n=8; s=[3 6 3 1 5 3 2];l=[500 1153 486 38 405 442
246];
% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x=fminsearch(@objf2,x0,[],y,s,l); epsilonhat(1)=x(1); rhat=x(2);  % step 2 and 3
 % step 4
for t=1:n-1
   epsilonhat(t+1)=y(t+1)-(y(t)-epsilonhat(t))*exp(x(2)*s(t))+l(t)*((exp(x(2)*s(t))-1)/(x(2)*s(t)));
end
muhat(1)=y(1)-epsilonhat(1);
for i=2:n
     muhat(i)=muhat(i-1)*exp(x(2)*s(i-1))-l(i-1)*((exp(x(2)*s(i-1))-1)/(x(2)*s(i-1)));
end
% end of Algorithm 3.1
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% MONTE CARLO SIMULATION
% Generating y
sigmahat=sqrt(sum(epsilonhat.^2)/(n-2)); M=1000; % M is the number of series to be generated
epsilon_MC=sigmahat*randn(n,M);
y_MC(1,1:M)=muhat(1)+epsilon_MC(1,1:M);
y_MC(2:n,1:M)=repmat(muhat(1:n-1)'.*exp(rhat*s')-l'.*((exp(rhat*s')-
1)./(rhat*s')),1,M)+epsilon_MC(2:n,1:M);
 %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
 %Bootstrap procedure
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

B=1000; % Number of bootstrap replications
p=2;

% STEP 1
y_MC_boot=repmat(y_MC,1,B);muhat_MC_boot=repmat(muhat',1,B*M);eps_hat_t_MC_boot=y_MC_boot
-muhat_MC_boot;
eps_prime_t_MC_boot=(eps_hat_t_MC_boot-repmat(mean(eps_hat_t_MC_boot),n,1))/sqrt(1-p/n); %
center residuals


% STEP 2

random_MC_boot = ceil(8*rand(8,B*M)); % generating uniform random numbers
eps_star_U_MC_boot=eps_prime_t_MC_boot(random_MC_boot); % randomizing eps_prime_t_MC_boot

% STEP 3
y_star_MC_boot(1,1:B*M)=muhat(1)+eps_star_U_MC_boot(1,:);
y_star_MC_boot(2:n,1:B*M)=repmat(muhat(1:7)'.*exp(x(2)*s')-l'.*((exp(x(2)*s')-
1)./(x(2)*s')),1,B*M)+eps_star_U_MC_boot(2:8,:);

% STEP 4

% Minimization procedure
for i=1:B*M
x_MC_boot(i,1:2)=fminsearch(@objf2,x0,[],y_star_MC_boot(1:n,i),s,l);
end
epstar_MC_boot=x_MC_boot(:,1); rstar_MC_boot=x_MC_boot(:,2);
```

```
 mu_star_MC_boot(1,1:B*M)=y_star_MC_boot(1,1:B*M)-epstar_MC_boot';
 for i=2:n
     mu_star_MC_boot(i,1:B*M)=mu_star_MC_boot(i-1,1:B*M).*exp(rstar_MC_boot'*s(i-1))-l(i-
1)*((exp(rstar_MC_boot'*s(i-1))-1)./(rstar_MC_boot'*s(i-1)));
 end

 %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
 % Confidence Intervals
 alpha=0.05;

 % C.I. for r
 R=rstar_MC_boot';
 for i=1:B
     R1(i,:)=R(M*(i-1)+1:M*i);
 end
 R1_sort=sort(R1);
 Lower_r_MC=R1_sort((alpha/2)*B,:); Upper_r_MC=R1_sort((1-(alpha/2))*B,:);

% C.I. for mus
U=mu_star_MC_boot;
U1=U(1,:); U2=U(2,:); U3=U(3,:); U4=U(4,:); U5=U(5,:); U6=U(6,:); U7=U(7,:); U8=U(8,:);

for i=1:B
     U1_MC(i,:)=U1(M*(i-1)+1:M*i);
 end

 for i=1:B
     U2_MC(i,:)=U2(M*(i-1)+1:M*i);
 end
for i=1:B
     U3_MC(i,:)=U3(M*(i-1)+1:M*i);
 end
for i=1:B
     U4_MC(i,:)=U4(M*(i-1)+1:M*i);
 end
for i=1:B
     U5_MC(i,:)=U5(M*(i-1)+1:M*i);
 end
for i=1:B
     U6_MC(i,:)=U6(M*(i-1)+1:M*i);
 end
for i=1:B
     U7_MC(i,:)=U7(M*(i-1)+1:M*i);
 end
for i=1:B
     U8_MC(i,:)=U8(M*(i-1)+1:M*i);
 end


U1_sort=sort(U1_MC); U2_sort=sort(U2_MC);U3_sort=sort(U3_MC);U4_sort=sort(U4_MC);
U5_sort=sort(U5_MC);U6_sort=sort(U6_MC);U7_sort=sort(U7_MC);U8_sort=sort(U8_MC);
Lower_U1_MC=U1_sort((alpha/2)*B,:); Upper_U1_MC=U1_sort((1-(alpha/2))*B,:);
Lower_U2_MC=U2_sort((alpha/2)*B,:); Upper_U2_MC=U2_sort((1-(alpha/2))*B,:);
Lower_U3_MC=U3_sort((alpha/2)*B,:); Upper_U3_MC=U3_sort((1-(alpha/2))*B,:);
Lower_U4_MC=U4_sort((alpha/2)*B,:); Upper_U4_MC=U4_sort((1-(alpha/2))*B,:);
Lower_U5_MC=U5_sort((alpha/2)*B,:); Upper_U5_MC=U5_sort((1-(alpha/2))*B,:);
Lower_U6_MC=U6_sort((alpha/2)*B,:); Upper_U6_MC=U6_sort((1-(alpha/2))*B,:);
Lower_U7_MC=U7_sort((alpha/2)*B,:); Upper_U7_MC=U7_sort((1-(alpha/2))*B,:);
Lower_U8_MC=U8_sort((alpha/2)*B,:); Upper_U8_MC=U8_sort((1-(alpha/2))*B,:);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% COVERAGE PROBABILITIES

true_r=0.07;
for i=1:M
```

```
count_r(i)= ((Lower_r_MC(i) <=true_r) & (Upper_r_MC(i)>=true_r));
end


true_mu1=y(1);true_mu2=y(2);true_mu3=y(3);true_mu4=y(4);
true_mu5=y(5);true_mu6=y(6);true_mu7=y(7);true_mu8=y(8);

for i=1:M
count_mu1(i)= ((Lower_U1_MC(i) <=true_mu1) & (Upper_U1_MC(i)>=true_mu1));
end
for i=1:M
count_mu2(i)= ((Lower_U2_MC(i) <=true_mu2) & (Upper_U2_MC(i)>=true_mu2));
end
for i=1:M
count_mu3(i)= ((Lower_U3_MC(i) <=true_mu3) & (Upper_U3_MC(i)>=true_mu3));
end
for i=1:M
count_mu4(i)= ((Lower_U4_MC(i) <=true_mu4) & (Upper_U4_MC(i)>=true_mu4));
end
for i=1:M
count_mu5(i)= ((Lower_U5_MC(i) <=true_mu5) & (Upper_U5_MC(i)>=true_mu5));
end
for i=1:M
count_mu6(i)= ((Lower_U6_MC(i) <=true_mu6) & (Upper_U6_MC(i)>=true_mu6));
end
for i=1:M
count_mu7(i)= ((Lower_U7_MC(i) <=true_mu7) & (Upper_U7_MC(i)>=true_mu7));
end
for i=1:M
count_mu8(i)= ((Lower_U8_MC(i) <=true_mu8) & (Upper_U8_MC(i)>=true_mu8));
end

cp_r=100*sum(count_r)/M,
cp_mu1=100*sum(count_mu1)/M,
cp_mu2=100*sum(count_mu2)/M,
cp_mu3=100*sum(count_mu3)/M,
cp_mu4=100*sum(count_mu4)/M,
cp_mu5=100*sum(count_mu5)/M,
cp_mu6=100*sum(count_mu6)/M,
cp_mu7=100*sum(count_mu7)/M,
cp_mu8=100*sum(count_mu8)/M,

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% Average length of Confidence Intervals
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

lengthr=Upper_r_MC-Lower_r_MC;
length1=Upper_U1_MC-Lower_U1_MC;
length2=Upper_U2_MC-Lower_U2_MC;
length3=Upper_U3_MC-Lower_U3_MC;
length4=Upper_U4_MC-Lower_U4_MC;
length5=Upper_U5_MC-Lower_U5_MC;
length6=Upper_U6_MC-Lower_U6_MC;
length7=Upper_U7_MC-Lower_U7_MC;
length8=Upper_U8_MC-Lower_U8_MC;


meanr=mean(lengthr)
mean1=mean(length1)
mean2=mean(length2)
mean3=mean(length3)
mean4=mean(length4)
mean5=mean(length5)
mean6=mean(length6)
mean7=mean(length7)
mean8=mean(length8)
```

Appendix E: Matlab program for the jackknife

```
format short g;clear;

y=[2230  1629  1199  1530  1502  1748  1982  1364];

%%% I=1%%%%
% DECLARING VARIABLES
y1=[1629 1199 1530 1502 1748 1982 1364];n=7; s1=[6 3 1 5 3 2];l1=[1651 424 60 438 430 246];

% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x1=fminsearch(@objfjack,x0,[],y1,s1,l1); epsilonhat1(1)=x1(1); rhat1=x1(2);  % step 2 and 3


% step 4
for t=1:n-1
   epsilonhat1(t+1)=y1(t+1)-(y1(t)-epsilonhat1(t))*exp(x1(2)*s1(t))+l1(t)*((exp(x1(2)*s1(t))-
1)/(x1(2)*s1(t)));
end
muhat1(1)=y1(1)-epsilonhat1(1);
for i=2:n
     muhat1(i)=muhat1(i-1)*exp(x1(2)*s1(i-1))-l1(i-1)*((exp(x1(2)*s1(i-1))-1)/(x1(2)*s1(i-1)));
end
% end of Algorithm 3.1

%muhat_1=[y(1)-x1(1) muhat1]';

% sigmahat_jack=sqrt(((n-1)/n)*sum((muhat-mean(muhat)).^2));


%%%%  I=2  %%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

% DECLARING VARIABLES
y2=[2230 1199 1530 1502 1748 1982 1364];n=7; s2=[9 3 1 5 3 2];l2=[513 1562 60 438 430 246];

% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x2=fminsearch(@objfjack,x0,[],y2,s2,l2); epsilonhat2(1)=x2(1); rhat2=x2(2);  % step 2 and 3

% step 4
for t=1:n-1
   epsilonhat2(t+1)=y2(t+1)-(y2(t)-epsilonhat2(t))*exp(x2(2)*s2(t))+l2(t)*((exp(x2(2)*s2(t))-
1)/(x2(2)*s2(t)));
end
muhat2(1)=y2(1)-epsilonhat2(1);
for i=2:n
     muhat2(i)=muhat2(i-1)*exp(x2(2)*s2(i-1))-l2(i-1)*((exp(x2(2)*s2(i-1))-1)/(x2(2)*s2(i-1)));
end
% end of Algorithm 3.1

%muhat_2=[muhat2(1) y(2)-epsilonhat2(2) muhat2(2:7)]';


%%%%%   I=3   %%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% DECLARING VARIABLES
y3=[2230 1629 1530 1502 1748 1982 1364];n=7; s3=[3 9 1 5 3 2];l3=[513 1138 484 438 430 246];
% ALGORITHM 3.1
x0=[0,0.1]; % step 1
```

```
x3=fminsearch(@objfjack,x0,[],y3,s3,l3); epsilonhat3(1)=x3(1); rhat3=x3(2);  % step 2 and 3
 % step 4
for t=1:n-1
   epsilonhat3(t+1)=y3(t+1)-(y3(t)-epsilonhat3(t))*exp(x3(2)*s3(t))+l3(t)*((exp(x3(2)*s3(t))-1)/(x3(2)*s3(t)));
end
muhat3(1)=y3(1)-epsilonhat3(1);
for i=2:n
    muhat3(i)=muhat3(i-1)*exp(x3(2)*s3(i-1))-l3(i-1)*((exp(x3(2)*s3(i-1))-1)/(x3(2)*s3(i-1)));
end
% end of Algorithm 3.1

%muhat_3=[muhat3(1:2) y(3)-epsilonhat3(3) muhat3(3:7)]';


%%%%%%  I=4
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% DECLARING VARIABLES
y4=[2230 1629 1199 1502 1748 1982 1364];n=7; s4=[3 6 4 5 3 2];l4=[513 1138 424 498 430 246];
% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x4=fminsearch(@objfjack,x0,[],y4,s4,l4); epsilonhat4(1)=x4(1); rhat4=x4(2);  % step 2 and 3
 % step 4
for t=1:n-1
   epsilonhat4(t+1)=y4(t+1)-(y4(t)-epsilonhat4(t))*exp(x4(2)*s4(t))+l4(t)*((exp(x4(2)*s4(t))-1)/(x4(2)*s4(t)));
end
muhat4(1)=y4(1)-epsilonhat4(1);
for i=2:n
    muhat4(i)=muhat4(i-1)*exp(x4(2)*s4(i-1))-l4(i-1)*((exp(x4(2)*s4(i-1))-1)/(x4(2)*s4(i-1)));
end
% end of Algorithm 3.1

%muhat_4=[muhat4(1:3) y(4)-epsilonhat4(4) muhat4(4:7)]';

%%%%%%%%    I=5
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% DECLARING VARIABLES
y5=[2230 1629 1199 1530 1748 1982 1364];n=7; s5=[3 6 3 6 3 2];l5=[513 1138 424 60 868 246];
% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x5=fminsearch(@objfjack,x0,[],y5,s5,l5); epsilonhat5(1)=x5(1); rhat5=x5(2);  % step 2 and 3
% step 4
for t=1:n-1
   epsilonhat5(t+1)=y5(t+1)-(y5(t)-epsilonhat5(t))*exp(x5(2)*s5(t))+l5(t)*((exp(x5(2)*s5(t))-1)/(x5(2)*s5(t)));
end
muhat5(1)=y5(1)-epsilonhat5(1);
for i=2:n
    muhat5(i)=muhat5(i-1)*exp(x5(2)*s5(i-1))-l5(i-1)*((exp(x5(2)*s5(i-1))-1)/(x5(2)*s5(i-1)));
end
% end of Algorithm 3.1

%muhat_5=[muhat5(1:4) y(5)-epsilonhat5(5) muhat5(5:7)]';

%%%%%%%%%   I=6
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% DECLARING VARIABLES
y6=[2230 1629 1199 1530 1502 1982 1364];n=7; s6=[3 6 3 1 8 2];l6=[513 1138 424 60 438 676];
% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x6=fminsearch(@objfjack,x0,[],y6,s6,l6); epsilonhat6(1)=x6(1); rhat6=x6(2);  % step 2 and 3
% step 4
for t=1:n-1
   epsilonhat6(t+1)=y6(t+1)-(y6(t)-epsilonhat6(t))*exp(x6(2)*s6(t))+l6(t)*((exp(x6(2)*s6(t))-1)/(x6(2)*s6(t)));
```

```
end
muhat6(1)=y6(1)-epsilonhat6(1);
for i=2:n
    muhat6(i)=muhat6(i-1)*exp(x6(2)*s6(i-1))-l6(i-1)*((exp(x6(2)*s6(i-1))-1)/(x6(2)*s6(i-1)));
end
% end of Algorithm 3.1

%muhat_6=[muhat6(1:5) y(6)-epsilonhat6(6) muhat6(6:7)]';

%%%%%%%%  I=7
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% DECLARING VARIABLES
y7=[2230 1629 1199 1530 1502 1748 1364];n=7; s7=[3 6 3 1 5 5];l7=[513 1138 424 60 438 676];
% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x7=fminsearch(@objfjack,x0,[],y7,s7,l7); epsilonhat7(1)=x7(1); rhat7=x7(2);  % step 2 and 3
 % step 4
for t=1:n-1
   epsilonhat7(t+1)=y7(t+1)-(y7(t)-epsilonhat7(t))*exp(x7(2)*s7(t))+l7(t)*((exp(x7(2)*s7(t))-
1)/(x7(2)*s7(t)));
end
muhat7(1)=y7(1)-epsilonhat7(1);
for i=2:n
    muhat7(i)=muhat7(i-1)*exp(x7(2)*s7(i-1))-l7(i-1)*((exp(x7(2)*s7(i-1))-1)/(x7(2)*s7(i-1)));
end
% end of Algorithm 3.1

%muhat_7=[muhat7(1:6) y(7)-epsilonhat7(7) muhat7(7)]';


%%%%%%%  I=8
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% DECLARING VARIABLES
y8=[2230 1629 1199 1530 1502 1748 1982];n=7; s8=[3 6 3 1 5 3];l8=[513 1138 424 60 438 430];
% ALGORITHM 3.1
x0=[0,0.1]; % step 1
x8=fminsearch(@objfjack,x0,[],y8,s8,l8); epsilonhat8(1)=x8(1); rhat8=x8(2);  % step 2 and 3
% step 4
for t=1:n-1
   epsilonhat8(t+1)=y8(t+1)-(y8(t)-epsilonhat8(t))*exp(x8(2)*s8(t))+l8(t)*((exp(x8(2)*s8(t))-
1)/(x8(2)*s8(t)));
end
muhat8(1)=y8(1)-epsilonhat8(1);
muhat8(1)=y8(1)-epsilonhat8(1);
for i=2:n
    muhat8(i)=muhat8(i-1)*exp(x8(2)*s8(i-1))-l8(i-1)*((exp(x8(2)*s8(i-1))-1)/(x8(2)*s8(i-1)));
end
% end of Algorithm 3.1

%muhat_8=[muhat8(1:7) y(8)-epsilonhat8(8)]';


%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% Calculation of Jackknife Standard Error
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
n=7;
MM=[muhat_1 muhat_2 muhat_3 muhat_4 muhat_5 muhat_6 muhat_7 muhat_8];
sigmahat_jack=sqrt(((n-1)/n1)*sum((MM-mean(MM)).^2));
```