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Estimating Animal Abundance by Employing an External Experiment to Account for Detection and Count Bias with an application to Wintering Ducks in the Mississippi Alluvial Valley

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ESTIMATING ANIMAL ABUNDANCE BY EMPLOYING AN EXTERNAL EXPERIMENT TO
ACCOUNT FOR DETECTION AND COUNT BIAS WITH AN APPLICATION TO WINTERING
DUCKS IN THE MISSISSIPPI ALLUVIAL VALLEY

A Dissertation
Presented to
the Graduate School of
Clemson University

In Partial Fulfillment
of the Requirements for the Degree
Doctor of Philosophy
Mathematical Sciences

by
April L. Thomas
May 2018

Accepted by:
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Abstract

A valid concern when structuring an aerial survey of wildlife populations is the presence of visibility bias. Many studies attempt to correct for visibility bias by including additional parameters in estimators for wildlife abundance. Often these parameters are estimated through data collected during the aerial survey. Some, however, have suggested using an external visibility experiment to estimate parameters being used to adjust for visibility bias. This work considers a bias adjusted estimator, proposed by Pearse et al. (2008), in which the bias correction parameters are estimated via an external visibility experiment using decoys in place of the live animals. The bootstrap method was then used to find the standard error of this estimate. We propose a second bootstrap approach to obtain an estimate of the standard error. We find that both implementations of the bootstrap work equally well, although the computations involved may dictate the most feasible choice in a specific case. We then evaluate the performance of the estimator through the use of a simulation study of an artificial population. We find that the use of an external experiment can produce reasonable results and identify some situations where it can produce under or over estimates of the population.

Dedication

During this process I lost both my father and father in-law. This work is dedicated to the memories of my father Gary LaRose and my father-in-law Joseph Thomas. I am so thankful for your examples of what it means to be a faithful Godly person.

”Therefore we also, since we are surrounded by so great a cloud of witness,
... let us run with endurance the race that is set before us, looking unto
Jesus, the author and finisher of our faith...” (Hebrews 12:1-2)

Acknowledgments

In January 2006 my husband and I moved to Anderson South Carolina. Later that year we discussed my returning to school to get a teaching degree. He jokes with me now saying that when I talked about going back to school he didn't know that I had meant for the rest of my life.

It certainly has been a long but very rewarding journey. After receiving my Bachelors degree at Clemson University, my husband kept encouraging me to continue on in my education. I began the quest for my Masters Degree in Math Education, but Dr. Robert Taylor had other plans for me, offering me an assistantship through the mathematical sciences department. I want to give thanks to Dr. Taylor for seeing something in me I did not see in myself at that time. In 2013 I received my Masters degree in Mathematical Science.

Again through the encouragement of family I decided to continue the journey and began working on my PhD. I am so thankful for my advisers, Dr. Patrick Gerard and Dr. Brook Russell. Their support, guidance, and patience, certainly helped through this journey. Dr. Gerard, thank you for knowing just how to encourage me, especially given the circumstances of losing two dear family members. Dr. Russell, thank you for your help with the Palmetto Cluster. I want to thank Clemson University and acknowledge them for their generous allotment of computing time on the Palmetto Cluster. Thank you to my committee members, Dr. William Bridges, Dr.

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Chapter 1

Introduction

The Mississippi Alluvial Valley (MAV), located along the Mississippi river from the coast of Louisiana to Illinois, is an example of an important habitat for wintering waterfowl. The North American Waterfowl Management Plan (NAWMP) was established to address concerns that waterfowl populations were declining. Loesch et al. (2000) discuss management objectives for the region in order to maintain and improve this habitat. A necessary aspect of habitat management is to have reasonable estimates of the sizes of the populations of birds and animals it supports. In the case of waterfowl, aerial surveys are often conducted for this purpose. An aerial survey follows common, well established, sampling designs, counting the number of birds/animals in the areas selected from the region of interest for the survey sample in order to estimate the population of the entire region. Martin et al. (2005) discuss the presence of a significant number of zeros in the data sets encountered in ecological studies. They divide the source of these zeros into two categories, true zeros and false zeros. True zeros occur when there are no objects of interest present in the area being sampled. False zeros occur when the object of interest is present, but is not accounted for by the observer(s) thus creating visibility bias in the estimate. Two

sources for visibility bias that will be discussed in this work are detectability bias and count bias. Detectability bias occurs when the observer does not detect the presence of an animal or group of animals. Count bias occurs when the observer either under or over counts the group sizes of wildlife.

Several methods have been proposed in order to correct for visibility bias in aerial surveys. One method is to double sample a few of the selected survey regions by having an observer on the ground and another in the air. The ratio of ground counts to air counts is used as a visibility correction factor (Prenzlöw and Lovvorn, 1996).

Becker and Quang (2009) combine several methods in order to estimate the population of brown bears in an aerial survey in Alaska. They used an aerial line-transect survey sampling design where observers follow a line (or contour depending on the terrain) and count the number of animals or number of groups of animals they see. Since the distance from the line of travel to the group of animals impacts the probability that a group is seen, a detection function is estimated. The detection function is used to determine the probability of seeing a group of animals given the perpendicular distance between the line of travel and the animals sighted. They chose to use a Gamma density function to model detection probabilities and incorporated several covariates such as group size, canopy/shrub cover, snow cover etc. into the estimates for the parameters of the detection function. The Gamma function was chosen to model detectability since the researchers believed that the probability of seeing an animal would peak at a short distance from the line of travel and then taper off. The shape parameter of the Gamma function allowed them to accommodate this. They also used two independent observers in the study, the pilot and a passenger, to estimate the detection probabilities. This Gamma detection model was then used to adjust for visibility bias.

Steinhorst and Samuel (1989) suggest incorporating information from a sightability model that predicts the probability of detecting wildlife in order to correct for visibility bias. In their paper, they address the possibility of using an independent external experiment for estimating the detection probabilities and how to incorporate the variation from the external experiment into the estimate for total population. Pearse et al. (2008) go one step further than the procedure described by Steinhorst and Samuel (1989) to address the two previously mentioned sources of visibility bias, detectability bias and count bias. Before continuing with the discussion of correcting for visibility bias, we provide some general background information and notation for survey sampling.

1.1 Background Information For Survey Sampling

Throughout this paper, we assume that the population of interest is finite. Survey sampling methodology has been developed to incorporate the finite nature of the populations from which samples will be drawn. Since survey sampling tends to have its own notation, the most important definitions and notation will be included here to be followed by a small example adapted from Lohr (1999).

An observation unit from a survey sample is the object on which a measurement is made and the sampling unit is the object that is actually sampled. Often we have a primary sampling unit (PSU) and a secondary sampling unit (SSU). Samples are first chosen among the PSUs, and within each PSU, one can sample all or a portion of the SSUs. Associated with the i^{th} PSU, ($i = 1, \dots, I$), is a Bernoulli random variable Z_i , where $Z_i = 1$ if PSU $_i$ is chosen and 0 otherwise. Let ψ_i be the probability that PSU $_i$ is selected on the first draw, and let ϕ_i be the probability that PSU $_i$ is included in the sample. Let N be the total number of PSUs in the population, and

n be the number of PSUs that will be chosen for the sample. For a simple random sample, without replacement, $\phi_i = \frac{n}{N}$. In survey sampling, if PSUs are drawn from the population using a sampling without replacement scheme, then the draws for the PSUs are dependent. If sampling with replacement is used, then the draws for the PSUs are independent, and PSUs could be included more than once in the sample. When sampling with replacement, it may be convenient to assign the random variable Q_i to each PSU $_i$, where Q_i is number of times PSU $_i$ appears in the sample.

For example, suppose we have a population of size 300 in a region that we have divided into $N = 4$ strip transects which are sections of the habitat with equal width, but variable length. Table 1.1 gives the true number of animals in each transect. These strip transects will be the PSUs. The animals in each strip are the SSUs, and let Y_i be the number of animals in the transect. Using simple random sampling (SRS), choose $n = 1$ transects to estimate the population. For each transect, $\phi_i = \frac{1}{4} = \psi_i$ in this case since $n = 1$. An unbiased estimator for the population total T

Table 1.1: Population

Section	Length	Count = Y_i
1	100	11
2	200	20
3	300	24
4	1000	245

is $\hat{T} = \frac{N}{n} \sum_{i=1}^4 z_i Y_i$. Table 1.2 gives the estimates of the population T that result from the selection of each of the four transects. Since each of these outcomes is equally likely, $\mathbb{E}[\hat{T}] = \sum_{i=1}^4 \hat{T}_i \left(\frac{1}{4}\right) = 300$, with $\mathbb{V}ar(\hat{T}) = \sum_{i=1}^4 \left(\hat{T}_i - \mathbb{E}[\hat{T}]\right)^2 \left(\frac{1}{4}\right) = 154,488$. We can improve the variance of our estimator by allowing the probability of choosing any one PSU to be proportional to the length of its transect. In our example, defining L_i to be the length of transect i , let $\psi_i = \frac{L_i}{\sum_{i=1}^4 L_i}$ be the probability of choosing tran-

Table 1.2: SRS Estimates for the Population Total

Section in Sample	Total in Sample Y_i	Estimate of Population $\hat{T} = \frac{4}{1} Y_i$
1	22	44
2	40	80
3	48	96
4	490	980

sect i . Using the estimator $\hat{T} = \frac{1}{n} \sum_{i=1}^4 z_i \frac{Y_i}{\psi_i}$, Table 1.3 gives the resulting estimates for all possible samples. We again have $\mathbb{E}[\hat{T}] = \sum_{i=1}^4 \hat{T}_i \psi_i = 300$, but now the variance is $\text{Var}(\hat{T}) = \sum_{i=1}^4 \left(\hat{T}_i - \mathbb{E}[\hat{T}] \right)^2 (\psi_i) = 14,248$. Thus, by choosing our sample with a probability proportional to size (PPS) sampling scheme we are able to reduce the variance of our estimator. Two estimators for population totals when using a prob-

Table 1.3: PPS Estimates for the Population Total

Transect in Sample	Probability of Selection ψ_i	Estimate of Population $\hat{T} = \frac{1}{n} \frac{Y_i}{\psi_i}$
1	$\frac{1}{16}$	$\frac{1}{1} 11 \left(\frac{16}{1} \right) = 176$
2	$\frac{2}{16}$	160
3	$\frac{3}{16}$	128
4	$\frac{10}{16}$	392

ability proportional to size (PPS) sampling scheme are the Hansen-Hurwitz (HH) estimator (Hansen and Hurwitz, 1943) and the Horvitz Thompson (HT) estimator (Horvitz and Thompson, 1952).

1.1.1 HH estimator

The HH estimator uses a sampling with replacement scheme. Let ψ_i be the probability of selection for PSU_i and let Q_i be the number of times PSU_i appears in the sample. The HH estimator for the population total is

$$\hat{T}_{HH} = \frac{1}{n} \sum_{i=1}^N Q_i \frac{y_i}{\psi_i} \quad (1.1)$$

where $Q_i \sim \text{Binomial}(n, \psi_i)$. Letting \mathbf{Q} be a random vector with components Q_i , $\mathbf{Q} \sim \text{Multinomial}(n, \psi_1, \psi_2, \dots, \psi_N)$ (Lohr, 1999). The HH estimator of the population total is unbiased since

$$\begin{aligned} \mathbb{E} \left[\frac{1}{n} \sum_{i=1}^N Q_i \frac{y_i}{\psi_i} \right] &= \frac{1}{n} \sum_{i=1}^N \frac{y_i}{\psi_i} \mathbb{E}[Q_i] \\ &= \frac{1}{n} \sum_{i=1}^N \frac{y_i}{\psi_i} n \psi_i \\ &= \sum_{i=1}^N y_i \\ &= T. \end{aligned}$$

As sampling is done with replacement, the draws for the sampling units are independent; however, the Q_i are not independent since the conditions on the multinomial distribution require that $\sum_{i=1}^N \psi_i = 1$ and $\sum_{i=1}^N Q_i = n$. The variance of the estimator is

$$\text{Var}(\hat{T}_{HH}) = \frac{1}{n} \sum_{i=1}^N \psi_i \left(\frac{y_i}{\psi_i} - T \right)^2. \quad (1.2)$$

In order to estimate the variance from the sample we can use

$$\widehat{\mathbb{V}ar}(\hat{T}_{HH}) = \frac{1}{n} \sum_{i=1}^N Q_i \frac{\left(\frac{y_i}{\psi_i} - \hat{T}_{HH}\right)^2}{n-1}. \quad (1.3)$$

This variance estimator is unbiased since,

$$\begin{aligned} \mathbb{E}[\widehat{\mathbb{V}ar}(\hat{T}_{HH})] &= \mathbb{E}\left[\frac{1}{n(n-1)} \sum_{i=1}^N Q_i \left(\frac{y_i}{\psi_i} - \hat{T}_{HH}\right)^2\right] \\ &= \mathbb{E}\left[\frac{1}{n(n-1)} \sum_{i=1}^N Q_i \left(\frac{y_i}{\psi_i} - T + T - \hat{T}_{HH}\right)^2\right] \\ &= \frac{1}{n(n-1)} \mathbb{E}\left[\sum_{i=1}^N \left(Q_i \left(\frac{y_i}{\psi_i} - T\right)^2 + (\hat{T}_{HH} - T)^2 Q_i - 2(\hat{T}_{HH} - T) Q_i \left(\frac{y_i}{\psi_i} - T\right)\right)\right] \\ &= \frac{1}{n(n-1)} \left[\mathbb{E}\left[\sum_{i=1}^N \left(Q_i \left(\frac{y_i}{\psi_i} - T\right)^2\right)\right] + n(\hat{T}_{HH} - T)^2 - 2n(\hat{T}_{HH} - T)^2 \right] \\ &= \frac{1}{n(n-1)} \left[\sum_{i=1}^N n\psi_i \left(\frac{y_i}{\psi_i} - T\right)^2 \right] - \frac{1}{n-1} \mathbb{V}ar(\hat{T}_{HH}) \\ &= \frac{n}{n-1} \mathbb{V}ar(\hat{T}_{HH}) - \frac{1}{n-1} \mathbb{V}ar(\hat{T}_{HH}) \\ &= \mathbb{V}ar(\hat{T}_{HH}). \end{aligned}$$

1.1.2 HT Estimator

The HT estimator can be used for a with replacement or without replacement sampling scheme (Thompson, 2012). In the HT estimator, we use $P(Z_i = 1) = \phi_i$ where ϕ_i is the probability that PSU_{*i*} is included in the sample. Note that this is not the probability of being selected as in the HH estimator. Let ϕ_{ij} be the probability that both Z_i and Z_j are in the sample so that $\mathbb{C}ov(z_i, z_j) = \phi_{ij} - \phi_i\phi_j$. The HT

estimator for the population total is

$$\hat{T}_{HT} = \sum_{i=1}^N \frac{y_i z_i}{\phi_i}. \quad (1.4)$$

The HT estimator is also unbiased as

$$\begin{aligned} \mathbb{E} \left[\sum_{i=1}^N Z_i \frac{y_i}{\phi_i} \right] &= \sum_{i=1}^N \frac{y_i}{\pi_i} \mathbb{E}[Z_i] \\ &= \sum_{i=1}^N \frac{y_i}{\phi_i} \phi_i \\ &= \sum_{i=1}^N y_i \\ &= T. \end{aligned}$$

The variance of \hat{T}_{HT} is

$$\mathbb{V}ar(\hat{T}_{HT}) = \sum_{i=1}^N \left(\frac{1 - \phi_i}{\phi_i} \right) y_i^2 + \sum_{i=1}^N \sum_{j \neq i} \left(\frac{\phi_{ij} - \phi_i \phi_j}{\phi_i \phi_j} \right) y_i y_j. \quad (1.5)$$

There does exist an unbiased estimator for the variance,

$$\widehat{\mathbb{V}ar}(\hat{T}_{HT}) = \sum_{i=1}^n \left(\frac{1 - \phi_i}{\phi_i^2} \right) y_i^2 z_i + \sum_{i=1}^n \sum_{j \neq i} \left(\frac{\phi_{ij} - \phi_i \phi_j}{\phi_i \phi_j} \right) \frac{y_i z_i y_j z_j}{\phi_{ij}}. \quad (1.6)$$

However, this estimator can produce negative estimates and alternative methods for approximating the variance may be needed (Thompson, 2012). Another issue with the HT estimator is the difficulty in maintaining the probabilities proportional to size since the probability of selection changes with every draw (Lohr, 1999). However, in the situation where the number of sampling units N is small, the HT estimator may be preferred (Lohr, 1999).

1.2 Modifications to HH or HT estimators

Both the HH and HT estimators assume that we are able to correctly count the number of objects of interest in each sampled section. However, as has already been discussed, it is entirely plausible that the number of animals is incorrectly counted, resulting in a biased estimate. A modification that could be made to the HH and HT estimators, as was done in the Alaskan bear survey (Becker and Quang, 2009), is to include a measure of the detectability of the objects of interest. This measure could then be used to correct for detection bias. In the case where we are counting wildlife that tends to be found in groups, it is reasonable to consider the detectability of animal or bird groups when estimating the population total.

Steinhorst and Samuel (1989) developed a modification to the HT estimator in order to account for detectability. They define two random vectors \mathbf{D} and \mathbf{R} to be applied to the survey data. The components of \mathbf{D} correspond to 1 and 0 depending on whether or not PSU_i is included in the sample with $P(D_i = 1) = \phi_i$. The vector \mathbf{R} consists of indicator variables for each of the groups (SSU_{ij}) in PSU_i . If $R_{ij} = 1$, the j^{th} group in transect i is seen given transect i was chosen for the sample and $R_{ij} = 0$ otherwise. Let p_{ij} be the probability that SSU_{ij} is seen given PSU_i was chosen. Then each $R_{ij}|D_i = 1$ is a Bernoulli random variable with probability p_{ij} . Letting s_{ij} be the number of animals in SSU_{ij} , they suggest the following modified HT estimator

$$\hat{T}_{SS} = \sum_i \frac{D_i}{\phi_i} \sum_j \frac{R_{ij}s_{ij}}{p_{ij}}. \quad (1.7)$$

They find the variance of their estimator to be

$$\begin{aligned}
\mathbb{V}ar(\hat{T}_{SS}) &= \sum_i \frac{1-\phi_i}{\phi_i} \left(\sum_j s_{ij} \right)^2 \\
&+ \sum_{i \neq i'} \sum \frac{\phi_{ii'} - \phi_i \phi_{i'}}{\phi_i \phi_{i'}} \left(\sum_j s_{ij} \right) \left(\sum_j s_{i'j} \right) \\
&+ \sum_i \frac{1}{\phi_i} \sum_j \frac{1-p_{ij}}{p_{ij}} \left(\sum_j s_{ij} \right)^2,
\end{aligned} \tag{1.8}$$

which is estimated by

$$\begin{aligned}
\widehat{\mathbb{V}ar}(\hat{T}_{SS}) &= \sum_i \frac{1-\phi_i}{\phi_i} \left(\sum_j \frac{s_{ij}}{p_{ij}} \right)^2 \\
&+ \sum_{i \neq i'} \sum \frac{\phi_{ii'} - \phi_i \phi_{i'}}{\phi_i \phi_{i'}} \left(\sum_j \frac{s_{ij}}{p_{ij}} \right) \left(\sum_j \frac{s_{i'j}}{p_{i'j}} \right) \\
&+ \sum_i \frac{1}{\phi_i} \sum_j \frac{1-p_{ij}}{p_{ij}} \left(\sum_j s_{ij} \right)^2.
\end{aligned} \tag{1.9}$$

In addition to the modified HT estimator, they suggest ways to estimate p_{ij} , the probability of detection of group j in section i , and derive variance estimators that incorporate the variability from estimating each p_{ij} . However, this adjustment for detectability assumes that the group sizes are counted without error.

Pearse et al. (2008) modify the HH estimator in their work involving aerial surveys of wintering ducks in the MAV. They begin with Steinhorst and Samuel's idea for correcting for detectability bias and add another component to correct for count bias. In order to estimate the parameter p_{ij} from Equation 1.7, they chose to perform a visibility experiment following the approach of Smith et al. (1995) who proposed using duck decoys in place of observing real ducks so that the true number of duck decoys would be known. It was determined that the size of a group of ducks

and the type of cover, meaning whether the group was located in a forested habitat or an open habitat, were important covariates in predicting the probability of detecting a group of ducks during an aerial survey. Details of the experiment and how the group sizes and placement of the decoys were chosen can be found in Pearse et al. (2008). Logistic regression was used to incorporate the covariates into a model that would predict the probability of detection of a group of ducks of size s seen in habitat $h \in \{\text{Open, Forested}\}$.

Regarding the count bias, Pearse et al. (2008) felt that it was a systematic bias that could be modeled on the habitat type and the log of the group size. To estimate the proportion of ducks in a group that the observer sees, they use a multiple regression model based on data from the decoy experiment. The proportion of decoys counted, given the habitat and the log of the group size, was then used to correct for count bias. They then applied the information gathered from the visibility experiment to data collected from an aerial survey of waterfowl in the MAV in January 2004 to demonstrate their method. As the 2004 survey used stratified sampling, additional notation is needed.

Let T be the true population total, t_i be the true population total in strata i , and \hat{T}_{BC} be the bias corrected population size estimate with \hat{t}_{iBC} being the population size estimate for strata i . Also let

N_i = the number of transects in strata i , where $i = 1, \dots, I$,

n_i = the number of transects selected from strata i ,

n_{ij} = the number of groups in transect j of strata i , where $j = 1, \dots, N_i$,

s_{ijk} = the size of group k in transect j of strata i as counted by the observer, where $k = 1, \dots, n_{ij}$,

Q_{ij} = the number of times transect j of strata i is chosen,

$R_{ijk} = 1$ if group ijk is seen and 0 otherwise,

ψ_{ij} = the probability of selecting transect j of strata i ,

π_{ijk} = proportion of animals in group k that are counted,

$f_{ijk} = \frac{1}{\pi_{ijk}}$ count bias correction factor of group k in transect j of strata i , and

p_{ijk} = the probability that group k is observed given transect j of strata i is selected.

The estimator for the population total T proposed by Pearse et al. (2008) is

$$\hat{T}_{BC} = \sum_i \hat{t}_{iBC}, \quad (1.10)$$

and the estimator for the population total t_i in each strata is

$$\hat{t}_{iBC} = \frac{1}{n_i} \sum_{j=1}^{N_i} \sum_{k=1}^{n_{ij}} \frac{s_{ijk} Q_{ij}}{\psi_{ij}} \frac{R_{ijk}}{p_{ijk}} \cdot f_{ijk}. \quad (1.11)$$

There are three differences between this estimator and the one used by Steinhorst and Samuel. First, since sampling is done with replacement, the random variable Q_{ij} as described for the HH estimator is used. Second, since sampling is done with replacement, the random variable R_{ijk} is slightly different than the R_{ijk} used by Steinhorst and Samuel. In the with replacement sampling situation, $R_{ijk}|Q_{ij} \neq 0 \sim \text{Bernoulli}(p_{ijk})$ and it is assumed that each R_{ijk} is independent of another. Third is the factor f_{ijk} , which is the correction factor for the count bias. Due to the complexity of the variance calculations, as will be seen later, the nonparametric bootstrap (Efron, 1979) was used to estimate the standard error of \hat{T}_{BC} .

1.3 Background Information For The Bootstrap

Efron (1979) developed the bootstrap method in order to estimate the standard

error of a statistic when its analytical distribution is impossible or difficult to obtain. Nonparametric bootstrapping is a form of resampling. We have a sample of size n of identically and independently distributed (iid) observations from a population of interest. We treat this sample as the bootstrap population and draw samples of size n with replacement from the bootstrap population where the probability of choosing any of the observations is $\frac{1}{n}$. The function used on the original sample to form the statistic of interest is then applied to each of the bootstrap samples, creating a sampling distribution of the statistic (Efron and Tibshirani, 1993).

The bootstrap hinges on using the empirical distribution (EDF) of the sample as an estimator for the population CDF. In bootstrapping, we know \hat{F}_n , the empirical distribution of the sample, and we assume all the information about the population is contained in our sample, i.e. the sample becomes the bootstrap population (Efron and Tibshirani, 1993).

The CDF of our population is

$$F(x) = P(X \leq x). \quad (1.12)$$

The EDF using the sample data is

$$\hat{F}_n(x) = \frac{1}{n} \sum_{i=1}^n \mathbb{I}(X_i \leq x), \quad (1.13)$$

where

$$\mathbb{I}(X_i \leq x) = \begin{cases} 1, & X_i \leq x \\ 0, & \text{otherwise.} \end{cases} \quad (1.14)$$

The EDF, multiplied by the sample size, is a binomial random variable where $n\hat{F}_n(x) \sim$

Binomial($n, F(x)$). Thus, $\mathbb{E}[\hat{F}_n(x)] = F(x)$ and $\mathbb{V}ar[\hat{F}_n(x)] = \frac{F(x)[1-F(x)]}{n}$.

1.3.1 Steps to a bootstrap estimator

The following steps are a summary of the bootstrap method by Efron and Tibshirani (1993). Let $\mathcal{X} = \{x_1, x_2, x_3, \dots, x_n\}$ be the sample from some population of interest.

Let $\theta = S(\cdot)$ be the function of the parameter of interest for the population.

Now assume the sample, \mathcal{X} , is the population in the bootstrap framework, and use $\hat{\theta}$, the estimate from the sample, as a plug-in estimate of the population parameter θ .

1. Create B bootstrap samples from bootstrap population \mathcal{X} :

\mathcal{X}_1^* 1st sample of size n with replacement from \mathcal{X} ,

\mathcal{X}_2^* 2nd sample of size n with replacement from \mathcal{X} ,

\vdots

\mathcal{X}_B^* B^{th} sample of size n with replacement from \mathcal{X} .

2. Calculate the statistic of interest for each bootstrap sample, $i = 1, \dots, B$, using the function $S(\mathcal{X}_i^*)$.
3. Use all $S(\mathcal{X}_i^*)$ as a representation of the sampling distribution of $\hat{\theta}$.
4. Calculate the bootstrap estimate of the standard error where:

$$SE_{boot} = \left(\sum_{b=1}^B [S(\mathcal{X}_b^*) - S(\cdot)]^2 / (B-1) \right)^{1/2}, \text{ and} \quad (1.15)$$

$$S(\cdot) = \sum_{b=1}^B S(\mathcal{X}_b^*) / B. \quad (1.16)$$

1.4 The Modified HH estimator

Now that we have laid some ground work for survey sampling and the bootstrap method, let us consider additional details regarding the modified HH estimator proposed by Pearse et al. (2008) within the context of using an external independent experiment to calculate the bias adjustment parameters p_{ijk} and f_{ijk} . The population total T is defined to be $T = \sum_i t_i$ where t_i is the population total in each strata. Equations 1.10 and 1.11 give the estimators for the population total and strata population totals respectively. We have already seen the probability distributions for \mathbf{Q} and \mathbf{R} in Sections 1.1.1 and 1.2 respectively. Thus, we will turn our attention to the two unknown parameters in Equation 1.11, p_{ijk} and f_{ijk} , that are estimated by the external visibility experiment.

Let \mathbf{X}_{ijk} represent the vector of covariates belonging to group k from transect j of strata i that will be used to estimate p_{ijk} , the probability of detecting group ijk . The parameters p_{ijk} are modeled using

$$p_{ijk} = \frac{e^{\mathbf{X}_{ijk}\boldsymbol{\beta}}}{1 + e^{\mathbf{X}_{ijk}\boldsymbol{\beta}}}, \quad (1.17)$$

where $\boldsymbol{\beta}$ is the vector of coefficients for the predictors. The parameters f_{ijk} are weights being applied to the number of animals the observer counts to compensate for over or under counting. Let π_{ijk} be the proportion of animals counted in group k of transect j in strata i . Then,

$$f_{ijk} = \frac{1}{\pi_{ijk}}, \quad (1.18)$$

where,

$$\pi_{ijk} = \mathbf{Y}_{ijk}\boldsymbol{\gamma} + \epsilon_{ijk}. \quad (1.19)$$

Each ϵ_{ijk} has mean 0 and variance σ^2 , \mathbf{Y}_{ijk} is the vector of predictors for π_{ijk} and $\boldsymbol{\gamma}$ is the vector of coefficients for the predictors. Since the visibility experiment is conducted separately, it is assumed to be independent of the wildlife survey.

Once estimates for p_{ijk} and π_{ijk} have been obtained, the question that remains is how to estimate the standard error of the corrected point estimator. To calculate the standard error that incorporates the variance from the bias correction, we would need to know the joint distribution of the estimates of the bias correction factors $\frac{f_{ijk}}{p_{ijk}}$. Each of these correction factors are the result of predictions from the external experiment making their distribution difficult to obtain. Also, in traditional survey sampling, estimates from separate transects are considered to be independent. However, as will be seen later, after applying the correction factors in Equation 1.11, these estimates are no longer independent. Pearse et al. (2008) chose to use the bootstrap to estimate the standard error rather than finding an analytical solution.

1.5 Justifying the Use of the Bootstrap

The bootstrap, as described in Section 1.3, requires the elements of the sample to be iid, which does not incorporate the probability proportional to size sampling design used here for the wildlife survey. Thus it is reasonable to question whether or not it is an appropriate way to find the standard error for the population total.

Suppose, for ease of notation, that the population is not stratified and suppose there is a sample of n transects, each with their associated number of animals y_i and

probability of selection ψ_i . The sample of transects is drawn with replacement and suppose the animals are observed with perfect visibility. Define a set on the sample to be $\mathcal{T} := \{(y_1, \psi_1), (y_2, \psi_2), \dots, (y_n, \psi_n)\}$. Rather than include the frequency variable Q_i with each chosen transect in \mathcal{T} , if a transect is chosen multiple times for the original sample, it is included in \mathcal{T} the same number of times. The realization of the HH estimator for the population, Equation 1.1, is

$$\hat{T}_{HH} = \frac{1}{n} \sum_{i=1}^n \frac{y_i}{\psi_i}, \quad (1.20)$$

and its estimate for the variance is found by Equation 1.3. If we consider $\frac{y_i}{\psi_i}$ to be one entity, what we have is a mean of sorts – an average of several $\frac{y_i}{\psi_i}$ s, where each $\frac{y_i}{\psi_i}$ is an estimate of \hat{T} for a sample of size 1 since $\mathbb{E} \left[\frac{y_i}{\psi_i} \right] = T$.

Now, let \mathcal{T} be the bootstrap population and draw from it bootstrap samples of n pairs of (y_i^*, ψ_i^*) with replacement. The probability distribution of the bootstrap samples is displayed in Tables 1.4 and 1.5. The bootstrap HH estimate for \hat{T} is $\hat{T}_{HH}^* = \frac{1}{n} \sum_{i=1}^n \frac{y_i^*}{\psi_i^*}$ and the expected value for each $\frac{y_i^*}{\psi_i^*}$ with respect to the bootstrap distribution is $\frac{1}{n} \sum_{i=1}^n \frac{y_i}{\psi_i}$.

The expected value of the bootstrap estimate with respect to a bootstrap sample is \hat{T} and with respect to the original population it is T as shown by

Table 1.4: Distribution of pairs for bootstrap samples

$(y, \psi)^*$	$P(t, \psi)$
(y_1, ψ_1)	$\frac{1}{n}$
(y_2, ψ_2)	$\frac{1}{n}$
(y_3, ψ_3)	$\frac{1}{n}$
\vdots	\vdots
(y_n, ψ_n)	$\frac{1}{n}$

Table 1.5: Bootstrap sample distribution for sample of size n for \hat{T}

$\frac{y}{\psi}^*$	$P\left(\frac{y}{\psi}^*\right)$
$\frac{y_1}{\psi_1}$	$\frac{1}{n}$
$\frac{y_2}{\psi_2}$	$\frac{1}{n}$
$\frac{y_3}{\psi_3}$	$\frac{1}{n}$
\vdots	\vdots
$\frac{y_n}{\psi_n}$	$\frac{1}{n}$

$$\begin{aligned}
 \mathbb{E}\left[\frac{y_i^*}{\psi_i} | \mathcal{T}\right] &= \frac{1}{n} \frac{y_1}{\psi_1} + \dots + \frac{1}{n} \frac{y_n}{\psi_n} \\
 &= \hat{T}, \\
 \text{and } \mathbb{E}[\hat{T}^* | \mathcal{T}] &= \frac{1}{n} \sum_{i=1}^n \mathbb{E}\left[\frac{y_i^*}{\psi_i} | \mathcal{T}\right] \\
 &= \frac{1}{n} n \hat{T} \\
 &= \hat{T}, \\
 \text{and } \mathbb{E}\left[\mathbb{E}[\hat{T}^* | \mathcal{T}]\right] &= T.
 \end{aligned}$$

The variance of the bootstrap estimates for \hat{T} is $\frac{n-1}{n}\widehat{\mathbb{V}ar}(\hat{T}_{HH})$. To see this notice that

$$\begin{aligned}\mathbb{V}ar(\hat{T}^*|\mathcal{T}) &= \mathbb{V}ar\left(\frac{1}{n}\sum_{i=1}^n \frac{y_i^*}{\psi_i}|\mathcal{T}\right) \\ &= \frac{1}{n^2}n\mathbb{V}ar\left(\frac{y_i^*}{\psi_i}|\mathcal{T}\right) \text{ by independence} \\ &= \frac{1}{n}\mathbb{V}ar\left(\frac{y_i^*}{\psi_i}|\mathcal{T}\right).\end{aligned}$$

Also,

$$\mathbb{V}ar\left(\frac{y_i^*}{\psi_i}|\mathcal{T}\right) = \sum_{i=1}^n \frac{1}{n} \left(\frac{y_i}{\psi_i} - \hat{T}\right)^2.$$

Thus,

$$\begin{aligned}\mathbb{V}ar(\hat{T}^*|\mathcal{T}) &= \frac{1}{n^2} \sum_{i=1}^n \left(\frac{y_i}{\psi_i} - \hat{T}\right)^2 \\ &= \frac{1}{n^2} \frac{n-1}{n-1} \sum_{i=1}^n \left(\frac{y_i}{\psi_i} - \hat{T}\right)^2 \\ &= \frac{n-1}{n} \widehat{\mathbb{V}ar}(\hat{T}_{HH}).\end{aligned}$$

If we choose n large enough that the fraction $\frac{n-1}{n}$ becomes unimportant, then we have a reasonable estimate for the variance of the population total using the bootstrap method. Thus it is reasonable to apply the nonparametric bootstrap algorithm to approximate the standard error of the estimator for the population size using PPS sampling.

Chapter 2

Estimating the Variance of \hat{T}_{BC}

We will take two approaches to estimate the variance of \hat{T}_{BC} . The first is the approach used by Pearse et al. (2008) where bootstrap samples are taken from both the survey data and the visibility experiment. This is also the one-stage bootstrap algorithm as described by Ogden and Tarpey (2006). The second approach is to only take bootstrap samples from the visibility experiment, form an estimate of the covariance matrix of the correction factors, and then apply the results to a direct variance calculation for \hat{T}_{BC} . The first approach requires more computing time as we must take a bootstrap sample from two data sets and the end result could include extra variation. The second approach requires an expression for the variance of \hat{T}_{BC} , which reduces the computing time as only one data set is used in the bootstrap algorithm. It is hoped that a more accurate estimate of the variance for \hat{T}_{BC} will be found in the second approach since the bootstrap is only used on the visibility experiment data.

2.1 Bootstrap Both the Survey Data and Visibility Experiment

When using bootstrapping to find the variance of a statistic, we need to mimic the original sampling procedure. In the aerial survey, samples were taken from several strata. Thus in the bootstrap world we will need to select bootstrap samples for each strata during each iteration of the algorithm. Additionally, we need to be able to capture all of the interactions between the sample data and the visibility experiment. The purpose of the visibility experiment is to use decoys in place of live animals to be able to estimate the parameters in the models for visibility bias. However, the model parameter estimates from the visibility experiment are not directly used to correct for bias in the survey data. It is the predictions from those models based on the group sizes and habitats observed in the survey samples that are used.

The following algorithm is used for each iteration of the bootstrap. Let $\mathcal{X}_i := \{(y_{i1}, \psi_{i1}), (y_{i2}, \psi_{i2}), \dots, (y_{in_i}, \psi_{in_i})\}$, $i = 1 \dots 5$, be the set of transects chosen from strata i of the aerial study. Let \mathcal{Y} be the set of observations from the visibility experiment.

1. Draw bootstrap sample \mathcal{X}_i^* from \mathcal{X}_i , $i = 1, \dots, 5$, and \mathcal{Y}^* from \mathcal{Y} . For each transect chosen to be in the bootstrap sample, there are several animal groups $k = 1, \dots, n_{ij}$ associated with it. Thus selecting a particular transect implies we have chosen all of its groups with their respective group sizes and habitat types.
2. Use \mathcal{Y}^* to predict p_{ijk} and f_{ijk} for each combination of group size and habitat type belonging to \mathcal{X}_i^* , $i = 1 \dots 5$. Note that the group sizes used to calculate values for \hat{p}_{ijk} are adjusted first by \hat{f}_{ijk} . It seems reasonable to follow this order since the group detection probabilities are based on the true group sizes. Pearse et al. (2008) used this and other combinations when applying the correction

factors. The order of applying \hat{f}_{ijk} first to correct for count bias and then applying \hat{p}_{ijk} to correct for detection bias is maintained throughout this work.

3. Use Equations 1.10 and 1.11 and results of step 2 to calculate the bootstrap estimate \hat{T}_{BC}^* .
4. Repeat steps 1 to 3 B times.

Finally, use the bootstrap results for all iterations to estimate the standard error of \hat{T}_{BC} .

2.2 Bootstrap the Visibility Experiment

In the second implementation of the bootstrap method, we calculate an estimate of the covariance matrix for the estimates of $\frac{f_{ijk}}{p_{ijk}}$. This matrix provides plug-in estimates to be used in the expression for the variance of \hat{T}_{BC} for a direct variance calculation. Since the values for the expression $\frac{f_{ijk}}{p_{ijk}}$ that come from the visibility experiment are always seen together, let $a_{ijk} = \frac{f_{ijk}}{p_{ijk}}$. Let \mathbf{A} be a column vector where each component is a_{ijk} . Let $\hat{\mathbf{A}}$ be an estimator of \mathbf{A} with mean $\boldsymbol{\mu}_{\hat{\mathbf{A}}}$ and covariance matrix $\boldsymbol{\Sigma}_{\hat{\mathbf{A}}}$. Let \mathbf{Q} and \mathbf{R} be random column vectors where each component is respectively Q_{ij} and R_{ijk} as described previously.

The expected value of \hat{T}_{BC} is

$$\mathbb{E}[\hat{T}_{BC}] = \mathbb{E}\left[\sum_i \hat{t}_{iBC}\right], \quad (2.1)$$

where

$$\begin{aligned}
\mathbb{E}[\hat{t}_{iBC}] &= \mathbb{E}_{\mathbf{Q}} \mathbb{E}_{\mathbf{R}|\mathbf{Q}} \mathbb{E}_{\hat{\mathbf{A}}|\mathbf{QR}} \left[\sum_j \sum_k \frac{Q_{ij}}{n_i \psi_{ij}} \cdot s_{ijk} \cdot R_{ijk} \cdot \hat{a}_{ijk} \right], \\
&= \sum_j \sum_k s_{ijk} \cdot \mu_{\hat{a}_{ijk}} \cdot p_{ijk}.
\end{aligned} \tag{2.2}$$

If we have an unbiased estimator for $\mu_{\hat{a}_{ijk}}$, then

$$\begin{aligned}
\mathbb{E}[\hat{t}_{iBC}] &= \sum_j \sum_k s_{ijk} \cdot \frac{f_{ijk}}{p_{ijk}} \cdot p_{ijk}, \\
&= \sum_j \sum_k f_{ijk} \cdot s_{ijk}.
\end{aligned} \tag{2.3}$$

When calculating the variance, we need to keep in mind that each strata uses information from the same visibility experiment. In stratified sampling, the samples from each strata are taken independently of all other samples from different strata and hence we can simply add up the variances from each strata (Lohr, 1999). Yet, as pointed out by Fieberg and Giudice (2008), once we use the same adjustment factors in each of the strata, we lose independence and cannot simply add the variance estimates from each strata. Thus the expression for the variance of \hat{T}_{BC} is

$$\text{Var}(\hat{T}_{BC}) = \sum_i \text{Var}(\hat{t}_{iBC}) + \sum_{i \neq i'} \text{Cov}(\hat{t}_{iBC}, \hat{t}_{i'BC}) \tag{2.4}$$

where

$$\begin{aligned}
\mathbb{V}ar(\hat{t}_{iBC}) &= \mathbb{V}ar_{\mathbf{Q}}(\mathbb{E}_{\mathbf{R}\hat{\mathbf{A}}|\mathbf{Q}}(\hat{t}_{iBC})) + \mathbb{E}_{\mathbf{Q}}(\mathbb{V}ar_{\mathbf{R}\hat{\mathbf{A}}|\mathbf{Q}}(\hat{t}_{iBC})) \\
&= \mathbb{V}ar_{\mathbf{Q}}(\mathbb{E}_{\mathbf{R}|\mathbf{Q}}\mathbb{E}_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC})) \\
&\quad + \mathbb{E}_{\mathbf{Q}} \left[\mathbb{V}ar_{\mathbf{R}|\mathbf{Q}}\mathbb{E}_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC}) \right] \\
&\quad + \mathbb{E}_{\mathbf{Q}} \left[\mathbb{E}_{\mathbf{R}|\mathbf{Q}}(\mathbb{V}ar_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC})) \right] \\
&= \sum_j \frac{1}{n_i \psi_{ij}} (1 - \psi_{ij}) \left(\sum_k s_{ijk} \cdot \mu_{\hat{a}_{ijk}} \cdot p_{ijk} \right)^2 \\
&\quad - \sum_{j \neq j'} \frac{\sum_k s_{ijk} \mu_{\hat{a}_{ijk}} p_{ijk} \sum_k s_{ij'k} \mu_{\hat{a}_{ij'k}} p_{ij'k}}{n_i} \\
&\quad + \sum_j \frac{\sum_k s_{ijk}^2 \mu_{\hat{a}_{ijk}}^2 p_{ijk} (1 - p_{ijk})}{n_i \psi_{ij}} (1 + (n_i - 1) \psi_{ij}) \\
&\quad + \sum_{j \neq j'} \sum_{k \neq k'} s_{ijk} s_{ij'k'} p_{ijk} p_{ij'k'} \mathbb{C}ov(\hat{a}_{ijk}, \hat{a}_{ij'k'}) \frac{(n_i - 1)}{n_i} \\
&\quad + \sum_{j=1}^{n_i} \left(\frac{1 - \psi_{ij}}{n_i \psi_{ij}} + 1 \right) \left[\sum_{k=1}^{n_{ij}} s_{ijk}^2 \mathbb{V}ar(\hat{a}_{ijk}) p_{ijk} \right] \\
&\quad + \sum_j \left(\frac{1 - \psi_{ij}}{n_i \psi_{ij}} + 1 \right) \left[\sum_{k \neq k'} s_{ijk} s_{ij'k'} \mathbb{C}ov(\hat{a}_{ijk}, \hat{a}_{ij'k'}) p_{ijk} p_{ij'k'} \right],
\end{aligned}$$

and

$$\begin{aligned}
\mathbb{C}ov(\hat{t}_{iBC}, \hat{t}_{i'BC}) &= \mathbb{E}[\hat{t}_{iBC} \cdot \hat{t}_{i'BC}] - \mathbb{E}[\hat{t}_{iBC}] \cdot \mathbb{E}[\hat{t}_{i'BC}] \\
&= \sum_{j=1}^{N_i} \sum_{k=1}^{n_{ij}} \sum_{y=1}^{N_{i'}} \sum_{z=1}^{n_{i'y}} s_{ijk} p_{ijk} s_{i'yz} p_{i'yz} \mathbb{C}ov(\hat{a}_{ijk}, \hat{a}_{i'yz}).
\end{aligned}$$

More information on the derivation of the variance of \hat{T}_{BC} can be found in Appendix

A. To estimate the variance from our data we propose using

$$\widehat{\mathbb{V}ar}(\hat{T}_{BC}) = \sum_i \widehat{\mathbb{V}ar}(\hat{t}_{iBC}) + \sum_{i \neq i'} \widehat{\mathbb{C}ov}(\hat{t}_{iBC}, \hat{t}_{i'BC}), \quad (2.5)$$

with

$$\begin{aligned} \widehat{\mathbb{V}ar}(\hat{t}_{iBC}) &= \sum_{j=1}^{n_i} \frac{(1 - \psi_{ij})Q_{ij}}{(n_i\psi_{ij})^2} \left[\sum_{k=1}^{n_{ij}} s_{ijk}^2 R_{ijk} \hat{\mu}_{\hat{a}_{ijk}}^2 \hat{p}_{ijk} \right] \\ &+ \sum_{j=1}^{n_i} \frac{(1 - \psi_{ij})Q_{ij}}{(n_i\psi_{ij})^2} \left[\sum_{k \neq k'} s_{ijk} s_{ijk'} R_{ijk} R_{ijk'} \hat{\mu}_{\hat{a}_{ijk}} \hat{\mu}_{\hat{a}_{ijk'}} \right] \\ &- \frac{1}{n_i^2(n_i - 1)} \sum_{j \neq j'} \frac{Q_{ij}Q_{ij'}}{\psi_{ij}\psi_{ij'}} \left(\sum_{k, k'} s_{ijk} s_{ij'k'} R_{ijk} R_{ij'k'} \hat{\mu}_{\hat{a}_{ijk}} \hat{\mu}_{\hat{a}_{ij'k'}} \right) \\ &+ \sum_{j=1}^{n_i} \frac{Q_{ij}(1 + (n_i - 1)\psi_{ij})}{n_i^2\psi_{ij}^2} \sum_k s_{ijk}^2 R_{ijk} \hat{\mu}_{\hat{a}_{ijk}}^2 (1 - \hat{p}_{ijk}) \\ &+ \sum_{j \neq j'} \sum_{k \neq k'} \frac{Q_{ij}Q_{ij'}}{n_i^2\psi_{ij}\psi_{ij'}} s_{ijk} s_{ij'k'} R_{ijk} R_{ij'k'} \widehat{\mathbb{C}ov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}) \\ &+ \sum_j \left(\frac{1 - \psi_{ij}}{n_i\psi_{ij}} + 1 \right) \frac{Q_{ij}}{n_i\psi_{ij}} \sum_k s_{ijk}^2 R_{ijk} \widehat{\mathbb{V}ar}(\hat{a}_{ijk}) \\ &+ \sum_j \left(\frac{1 - \psi_{ij}}{n_i\psi_{ij}} + 1 \right) \frac{Q_{ij}}{n_i\psi_{ij}} \sum_{k \neq k'} s_{ijk} s_{ijk'} R_{ijk} R_{ijk'} \widehat{\mathbb{C}ov}(\hat{a}_{ijk}, \hat{a}_{ijk'}), \end{aligned}$$

and

$$\widehat{\mathbb{C}ov}(\hat{t}_{iBC}, \hat{t}_{i'BC}) = \sum_{j=1}^{N_i} \sum_{k=1}^{n_{ij}} \sum_{y=1}^{N_{i'}} \sum_{z=1}^{n_{i'y}} \frac{Q_{ij}Q_{i'y}}{n_i n_{i'} \psi_{ij} \psi_{i'y}} s_{ijk} R_{ijk} s_{i'yz} R_{i'yz} \mathbb{C}ov(\hat{a}_{ijk}, \hat{a}_{i'yz}).$$

2.3 Results of the Two Bootstrap Implementations

Before considering the two bootstrap approaches to the standard error, we summarize results from the decoy experiment. Pearse et al. (2008) found, after evaluating the parameter estimates from the logistic model, that group sizes only mattered for the detection probabilities in open habitats. The estimates for β_0 and β_{size} for Equation 1.17 for open habitats were 0.084 and 0.129 respectively. In the forested habitats they felt that the probability of detection $p_{ijk} = p$ for all group sizes, and estimated p by simply using the proportion of groups from forested habitats that were detected. The detection probability for groups in forested habitats was 0.707. They also felt that the linear model in Equation 1.19 was unnecessary, that $\pi_{ijk} = \pi$ and used the proportion of decoys counted in the groups to estimate π . Their estimate for $f = \frac{1}{\pi}$ was 1.28. Using the data from the 2004 aerial survey, without making any corrections for visibility bias, they found the point estimate for the stratified sampling design was $\hat{T}_{uncorrected} = 264,622$ ducks with standard error of 22,656. Applying the corrections for visibility bias, the corrected point estimate was $\hat{T}_{BC} = 363,278$.

Using the method from Section 2.1 we calculate the estimate of the standard error of \hat{T}_{BC} to be 42,076 ducks. A problem encountered when using the bootstrap was, sometimes the detection probabilities found in the logistic regression were too small, making the estimates for the duck population inside of the bootstrap framework unstable. Thus, the detection probabilities for open habitats in the bootstrap algorithm was set to a minimum of $\frac{1}{40}$, where 40 was the largest number of transects chosen in the aerial study. This is similar to what was done by Pearse et al. (2008). There were a few times when the logistic regression procedure within the bootstrap algorithm did not converge and $\frac{1}{40}$ was used in these situations as well.

In order to reduce the occurrences when the bootstrap sample chosen for the

logistic regression did not converge, the procedure for bootstrapping the visibility experiment was slightly altered. Pearse et al. (2008) had used a balanced bootstrap for the visibility data where the same quartiles and habitats were used in each bootstrap sample as was used for the original decoy placement. The quartiles of group sizes for the decoys were 1 – 8 decoys, 9 – 20 decoys, 21 – 40 decoys and 41 – 100 decoys. Each of these group size categories were represented in the forested and open habitats. Thus when taking a bootstrap sample, the number of group sizes in each category and habitat were maintained.

To evaluate the performance of the balanced bootstrap, 100 repetitions of 1,000 bootstrap samples are performed under both the non-balanced and balanced bootstrap procedures. The average number of non-convergences in the balanced bootstrap was 6.8 and for the non-balanced, 9.9. The minimum number of occurrences of non-convergence for both methods was 2. The maximum for the balanced bootstrap was 11 and the maximum for non-balanced was 21. By following the balanced bootstrap approach, not only were the number of occurrences of non-convergence reduced, but the standard error of \hat{T}_{BC} was reduced to 37,455 ducks. Since the balanced bootstrap method for the visibility experiment is more stable, it is used for the remainder of the study.

Another concern to be addressed is the number of bootstrap resamples to use. The original work of Pearse et al. (2008) uses 1,000 bootstrap re-samples. To build a 95% confidence interval it is suggested that 999 bootstrap resamples be used (Davidson and Hinkley, 1997). To get an idea of how many bootstrap samples should be taken in order for the estimate of the standard error to stabilize in this situation, a sequence of bootstrap procedures is run on bootstrap samples of size 100, 200, ..., 10,000. This sequence is run for both methods of calculating the standard error. Figure 2.1 plots the standard error of \hat{T}_{BC} when using the bootstrap method on both the survey

and the visibility experiment as described in Section 2.1. Figure 2.2 shows the plot of the standard error of \hat{T}_{BC} when using the bootstrap method only with the visibility experiment as described in Section 2.2.

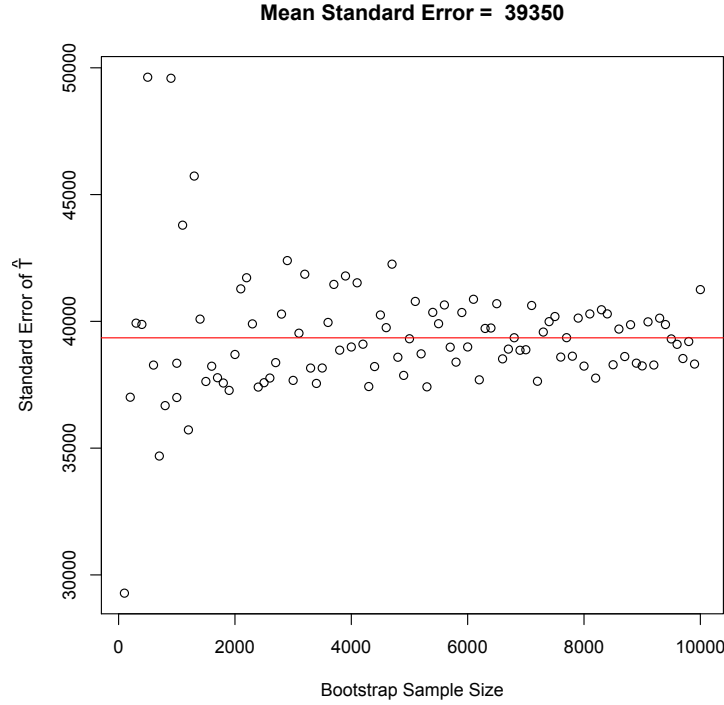


Figure 2.1: Standard Errors: Bootstrap Both Survey and Visibility Experiment

As can be seen from Figure 2.1, the method where we use the bootstrap on both the survey data and the visibility experiment, the standard error calculation stabilizes after 2,000 bootstrap samples and the variability in the estimate of the standard error diminishes. The standard deviation for all estimates of the standard error was 2,383, but falls to 1,250 for bootstrap sample sizes of 2,000 to 10,000. When we only use the bootstrap on the data from the visibility experiment, from Figure 2.2 we can see that the standard error calculation is more stable across all sample sizes. However, as the bootstrap sample size increases, the variability of the estimates of the standard error does not decrease as much as when the bootstrap is

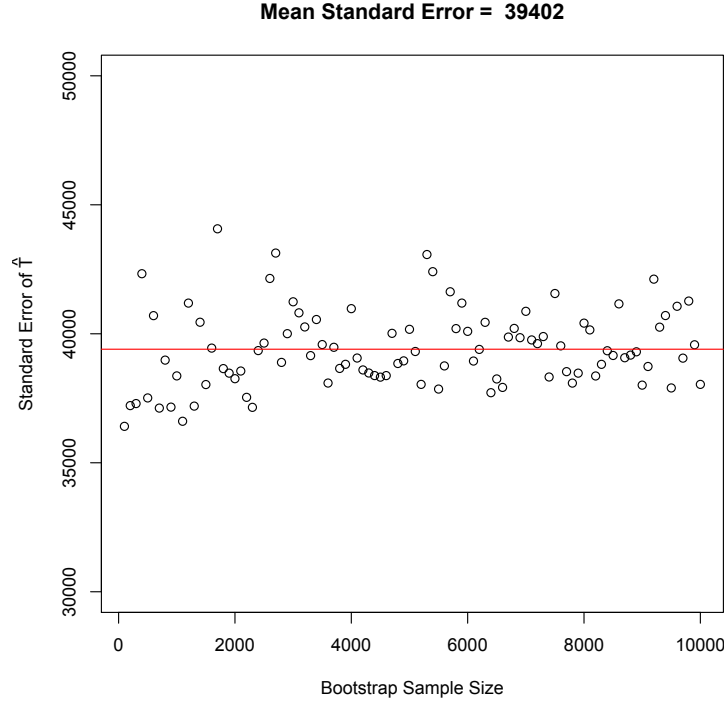


Figure 2.2: Standard Errors: Direct Variance Calculation

applied to both the survey and the visibility experiment.

Another sequence of bootstrap samples with sizes ranging from 10,000 to 50,000 is run for the visibility experiment only. After nearly 30,000 bootstrap samples, we see in Figure 2.3 that the standard error estimate stabilizes at about 39,600 ducks. The standard deviation of all the standard errors for sample sizes 100 to 50,000 was about 900. To determine if the covariance matrix itself was stable, the infinity norm was computed for each covariance matrix at each sample size. The infinity norm of a square matrix is the maximum absolute row sum, $\|\hat{\mathbf{A}}\| = \max_j \sum_{j=1}^n |\hat{a}_{ij}|$. As can be seen from Figure 2.4, as the bootstrap sample size got larger, the infinity norm began to stabilize around 20,000 bootstrap samples, just prior to where the standard error calculation stabilized for the direct variance calculation.

The time to run 2,000 bootstrap samples when we bootstrap both the visibil-

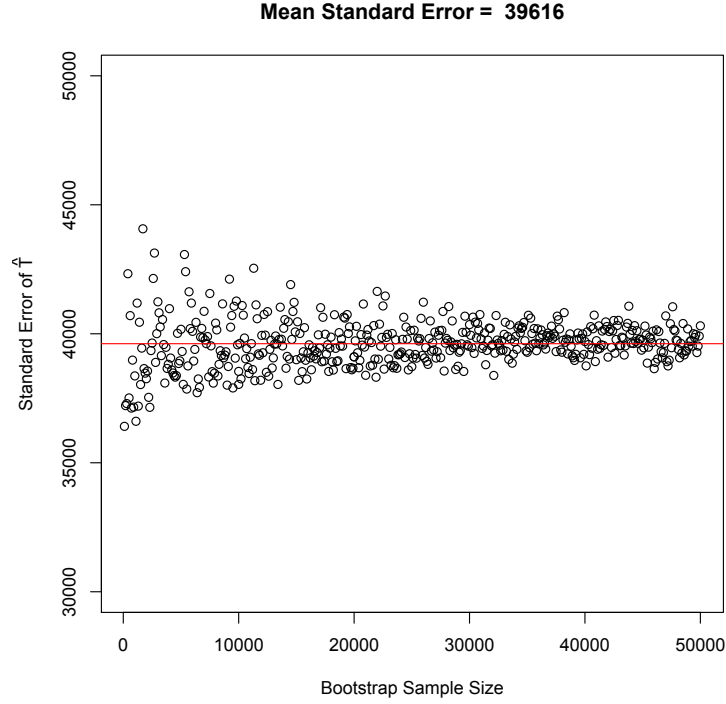


Figure 2.3: Standard Errors: Direct Variance Calculation

ity experiment and the survey data is about 21 minutes 15 seconds on a MacBook Pro using a 2.26 GHz Intel Core 2 Duo processor and 8 GB 1067 MHz DDR3 ram. The time to run 2,000 bootstrap samples of the visibility experiment is only about 10 seconds on the same machine. The estimate of the standard error, bootstrapping 2,000 samples of both the survey and experiment was 42,178 ducks and for bootstrapping 2,000 samples of the visibility experiment only it was 43,033 ducks. If we increase the number of bootstrap samples to 30,000 and only bootstrap the visibility experiment, the standard error was 38,974 ducks. The time to complete 30,000 bootstrap resamples of the visibility experiment was about 3 minutes.

Bootstrapping only the visibility experiment has the advantage in the amount of processing time required even though it requires taking a large number of bootstrap samples for the covariance matrix to stabilize. However solving for the variance

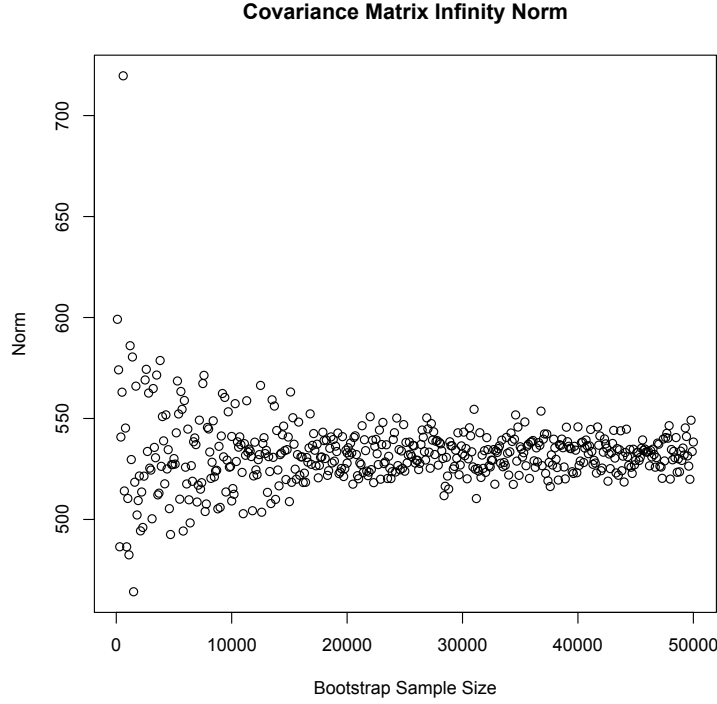


Figure 2.4: Infinity Norm

expression in Equation 2.4 was difficult the and it was challenging to program the calculations needed when using the plug-in estimates. While bootstrapping both the visibility experiment and the original survey takes significantly more computing time, it has the advantage of simplicity. There was a concern that it may not capture all of the dependencies between the bias adjustment factors. In order to attempt to capture all sources of variation, in each iteration of the overall bootstrap procedure, all of the bias correction factors for one bootstrap survey sample are created at the same time from one bootstrap sample of the visibility experiment. If we compare Figure 2.1 to Figure 2.2, both bootstrap approaches stabilize to similar values at 39,350 and 39,402. It appears that the bootstrap algorithm developed by Pearse et al. (2008) is able to incorporate the dependencies in the data into the estimate of the standard error.

Chapter 3

Simulation Study

To better evaluate the estimator \hat{T}_{BC} and the bootstrap method's ability to estimate its standard error when parameters needed for the estimate are themselves estimated by an external independent experiment, a simulation study is used. To conduct the simulation study we need an artificial population of animals, an external experiment for the decoys, and a simulated flyover for the aerial survey of the artificial population and the decoys. By using an artificial population we know the truth about the population and can compare the results of the simulation to the known population parameters. Another advantage of using simulations with artificial populations is that we are able to experiment to determine methods that will most likely produce good results without the expense of actually trying the methods on a live population (Nuno et al., 2013).

The simulation study was designed to address four main questions.

1. Does the bootstrap method capture the dependencies introduced by the bias correction from the decoy experiment?
2. How sensitive is this procedure to misspecification? It is certainly reasonable to

question whether or not an observer detects and counts decoys in an external experiment differently than live ducks as in the actual survey. In addition to the differences between detecting decoys and live animals, other conditions may vary between the two surveys such as time of day, time of year, etc.

3. How do some of the methods for forming confidence intervals from bootstrap samples compare when combining information from two sources?
4. How sensitive is the use of the bootstrap method to the sample size when combining data from two sources?

3.1 Creating the Artificial Population

To create the artificial population, we begin with the information available from Pearse et al. (2008) about the 2004 aerial survey. The study area was divided into 5 strata, labeled H, NE, NW, SE, and SW. There are a total of 2,976 transects of equal width but varying length. For the artificial population, the number of strata and transects per strata are kept the same as in the original survey. The total length of the transects in each strata from the 2004 study was known, but only the individual lengths of the surveyed transects were given. Using the total length of the transects within each strata and the minimum and maximum transect lengths in the survey sample, 2,976 transects of varying lengths are created so that the total transect length per strata of the artificial study area is close to the total transect length from the original study area.

Each transect is then assigned a number of duck groups between 1 and 9. Groups are randomly assigned a habitat based on the percentage of open and forested habitats in the 2004 survey. Lastly, groups are assigned a number of ducks by ran-

domly selecting from the pool of group sizes in the original survey which ranged in size from 0 to 600. The frequency of the group sizes was incorporated so that the artificial population would be similar to results from the actual aerial survey. The details of the artificial population are as follows. The true total number of ducks is 430,146. The mean and standard deviation of the number of ducks per transect in each strata is given in Table 3.1.

Table 3.1: Mean and standard deviation per transect

	H	NE	NW	SE	SW
Mean	130.3	148.7	149.3	147.2	138.7
Standard Deviation	97.6	119.0	117	124	113

3.2 Simulating the Visibility Experiment

Since the visibility experiment with the decoys designed by Pearse et al. (2008) was already a sample from an artificial population, another population for the decoy experiment is not recreated. The details of how the decoys are assigned to transects and groups, as already mentioned, is described in their paper and uses some of the same methodology as a previous, albeit more complex, decoy study reported by Smith et al. (1995).

3.3 Simulating the Aerial Survey

There are many variables that could be considered in simulating an aerial survey such as aircraft type, aircraft speed, weather conditions etc. In their simulation of an aerial survey of impalas, Nuno et al. (2013) listed 12 variables that could be manipulated in their virtual environment. Rather than using a virtual study area,

Smith et al. (1995) actually performed several real aerial surveys of decoys in which various covariates, such as transect width, flight speed, type of aircraft etc. were altered. Pearse et al. (2008) chose to study only two covariates that they felt most affected visibility bias based on the work by Smith et al. (1995): the group size of the ducks and the type of habitat. The simulation study therefore only adjusts parameters for these two covariates.

The multiple regression model for the proportion of birds counted, π_{ijk} , in the simulation study is

$$\pi_{ijk} = \gamma_0 + \gamma_{habitat}Y_{h_{ijk}} + \gamma_{\log(size)}Y_{ls_{ijk}} + \epsilon_{ijk}, \quad (3.1)$$

where $Y_{h_{ijk}}$ is 0 if group ijk is in a forested habitat and 1 if it is in an open habitat, $Y_{ls_{ijk}}$ is the log of the group size and ϵ_{ijk} has mean 0 and variance σ^2 . For the probability of seeing a group of animals, p_{ijk} , the simulation study uses a logistic regression model based on habitat type and group size. The logistic model is

$$p_{ijk} = \frac{e^{\beta_0 + \beta_{habitat}X_{h_{ijk}} + \beta_{size}X_{s_{ijk}}}}{1 + e^{\beta_0 + \beta_{habitat}X_{h_{ijk}} + \beta_{size}X_{s_{ijk}}}}, \quad (3.2)$$

where $X_{h_{ijk}}$ is 0 if group ijk is in a forested habitat and 1 if it is in an open habitat and $X_{s_{ijk}}$ is the group size.

For the simulation of the aerial survey of the artificial population, a sample is chosen using stratified sampling and probability proportional to size sampling. For most of the simulations, there were 125 transects chosen as this was the sample size used by Pearse et al. (2008). The number of transects to be sampled from each strata is chosen using optimum allocation (Thompson, 2012). The number of transects selected are 11 from strata H, 34 from strata NE, 32 from strata NW, 21 from strata

SE, and 27 from strata SW. The theoretical standard error of the HH estimator for \hat{T} for a stratified sample of 125 transects, from Equation 1.2 is 37,114.0 ducks.

To determine whether or not a group of ducks from the sample is seen in the simulated flyover, a Bernoulli random variable is generated using the probabilities calculated from the logistic model in Equation 3.2. To obtain the number of ducks counted in each group that is spotted, we first find the proportion of the group counted using Equation 3.1. We then reduce (or increase) the true number of ducks in the group according to the calculated proportion. Next, the sample is modified to include only the adjusted group counts for the groups that are classified as seen and their habitats as though we had no knowledge of the true sample values. Finally, for the simulation of the decoy experiment, Equation 3.1 is used to determine the proportion of the group that is counted and Equation 3.2 is used to determine whether or not a group of decoys is seen. The information recorded for the visibility experiment is the true decoy group size, the adjusted group size, the group habitat, and whether or not the group is seen.

3.4 Results of Simulation Study

3.4.1 Evaluating \hat{T}_{BC} and the Bootstrap Estimates of Standard Error

The first questions to address with the simulation study are whether or not the external experiment is able to adjust for visibility bias and whether or not the bootstrap is able to produce a reasonable estimate of the standard error of \hat{T}_{BC} . To answer these questions, a comparison of three population estimators is used. The first estimator is an unmodified HH estimator \hat{T}_{PS} . Since the true number of animals of

interest in the artificial population is known, any unmodified sample taken represents perfect sightability. This estimate both makes sure that the sampling algorithm is working correctly and works as a point of comparison for the bias corrected estimate. The sample consists of a total of 125 transects from the 5 strata as described above.

Next, a simulated aerial survey of the sample is performed in order to introduce visibility bias following the method in Section 3.3. Four different simulations are used and the parameters for the multiple and logistic regression models are given in given Table 3.2. After completing the simulated aerial survey the second population estimate, \hat{T}_{IS} , is calculated. This is an unmodified HH estimate of the population with imperfect sightability. This second estimate demonstrates the impact of detectibility and count bias on the usual HH estimate and its standard error.

Table 3.2: Parameters for Simulations 1-4

		Simulation 1	Simulation 2
π_{ijk}	γ_0	0.800	0.500
	$\gamma_{habitat}$	0.090	0.090
	$\gamma_{\log(\text{size})}$	-0.003	-0.003
	ϵ	$\sim N(0, 0.01)$	$\sim N(0, 0.1)$
p_{ijk}	β_0	-0.040	-0.100
	$\beta_{habitat}$	0.040	0.040
	β_{size}	0.100	0.080
		Simulation 3	Simulation 4
π_{ijk}	γ_0	0.500	0.500
	$\gamma_{habitat}$	0.090	0.090
	$\gamma_{\log(\text{size})}$	-0.003	-0.003
	ϵ	$\sim \text{Uniform}(-0.1, 0.1)$	$\sim \text{Beta}(\alpha = 2, \beta = 8) - .2$
p_{ijk}	β_0	-0.100	-0.100
	$\beta_{habitat}$	0.040	0.040
	β_{size}	0.080	0.080

An aerial survey of the decoys is simulated using using the method from Section 3.3 and the same sets of parameters from Table 3.2. Once we have the visibility experiment results, we estimate the parameters for the logistic and linear regression

models that will be used to account for visibility bias as though we had no knowledge of the actual parameters given in Table 3.2. Finally, the bias adjustment factors f_{ijk} and p_{ijk} for the groups seen in the simulated aerial survey are estimated using the estimated models from the simulated decoy experiment. Once we have the bias adjustment factors we calculate the third population estimate \hat{T}_{BC} from Equations 1.10 and 1.11. The bootstrap is then applied using the two methods described in Section 2 to calculate an estimate of the standard error of \hat{T}_{BC} .

In order to make fair comparisons between these three estimators and between the two bootstrap standard error calculations, 1,024 stratified samples of 125 transects are selected via PPS from the artificial population for each of the four simulations. For each sample from the artificial population, a decoy experiment is simulated. To calculate the standard errors, bootstrap resamples are taken for each of the 1,024 samples and both bootstrap methods of calculating the standard error are implemented. These larger simulations are run on the Clemson Palmetto Cluster using 1 node and 8 cores and the Parallel package in R. It takes about 5 hours of computing time using the Palmetto Cluster to calculate the standard errors for the 1,024 samples when 1,000 bootstrap resamples were used and about 20 hours when 6,000 bootstrap resamples were used. Thus, 1,000 bootstrap resamples were used in simulations 1 through 4. The estimates of the population totals for Simulations 1 through 4 are listed in Table 3.3. The summary statistics for the standard error estimates calculated by the bootstrap methods are listed in Table 3.4.

Simulation 1

If all of the ducks present in the surveyed transects are correctly counted, the average estimate of the population total is 430,685 ducks with a standard error of 36,027. These estimates are very close to their true values of 430,146 and 37,114

respectively. When visibility bias is present, both the estimate of the population total and its standard error are quite a bit smaller at 357,323 and 31,362 respectively.

The average bias adjusted population estimate was 432,618 ducks with a standard error of 37,574 ducks. The bias adjustment procedure did bring the estimate back up to within one standard deviation from the true population total of 430,146 ducks. We expect the bias adjusted standard error to be higher than the standard error for a perfect survey as it includes the variation from the external decoy experiment. The average standard errors calculated by the two bootstrap methods are 38,491 and 39,041.

Table 3.3: Mean and Standard Deviation of 1024 Estimates for Artificial Duck Population Total

	Simulation 1	Simulation 2	Simulation 3	Simulation 4
\hat{T}_{PS}	429,437	430,781	430,878	431,069
$se_{\hat{T}_{PS}}$	36,027	36,070	37,410	37,780
\hat{T}_{IS}	357,323	229,955	230,488	230,431
$se_{\hat{T}_{IS}}$	31,362	20,613	21,199	21,923
\hat{T}_{BC}	432,618	432,238	431,963	432,777
$se_{\hat{T}_{BC}}$	37,574	42,016	40,635	43,875

The distribution of the bias adjusted standard errors is right skewed, as seen in Figure 3.1, regardless of which bootstrap procedure was used. The standard error calculation that uses plug-in estimates from the decoy visibility experiment has slightly less variability than when the bootstrap is applied to both the survey of the ducks and the decoy experiment. A surprising result is the approximately Normal shape of the histograms, as seen in Figure 3.2, for all three estimates for the population total. Since it appears a Normal distribution might fit the bias adjusted estimates, a 95% Normal approximation confidence interval was calculated for each of the 1,024 estimates of \hat{T}_{BC} using the standard error calculated by the two bootstrap methods.

Table 3.4: Bootstrap Calculation of $se_{\hat{T}_{BC}}$

		Simulation 1	Simulation 2
Bootstrap Both Ducks and Decoys	Mean	38,491	42,104
	St. Dev.	8,978	13,240
	Median	37,020	39,773
	IQR	10,101	11,251
Bootstrap Decoys only	Mean	39,041	42,614
	St. Dev.	8,766	12,225
	Median	37,470	40,362
	IQR	9,988	11,277
		Simulation 3	Simulation 4
Bootstrap Both Ducks and Decoys	Mean	40,911	44,322
	St. Dev.	10,982	19,967
	Median	38,791	41,289
	IQR	11,218	12,264
Bootstrap Decoys only	Mean	41,434	44,647
	St. Dev.	10,889	18,937
	Median	39,260	41,680
	IQR	11,302	12,341

The coverage of the confidence intervals when we bootstrap both data sets is 93.8% and for bootstrapping only the visibility experiment it is 94.1%

Simulation 2

The initial attempt to adjust for bias in the estimate of the population total for the artificial survey in Simulation 1 used a very small standard deviation for the errors, ϵ_{ijk} . Simulation 2 includes a larger standard deviation for ϵ_{ijk} . The average estimate of \hat{T}_{PS} in this second simulation is 430,781 ducks with a standard error of 36,070. The average value of \hat{T}_{IS} is 229,955 with a standard error of 20,613 both of which are again much smaller than \hat{T}_{PS} once visibility bias is introduced. The average of the 1,024 estimates of \hat{T}_{BC} is 432,238 ducks. The averages of the standard error calculations for \hat{T}_{BC} from the two bootstrap procedures are 42,104 and 42,614 ducks.

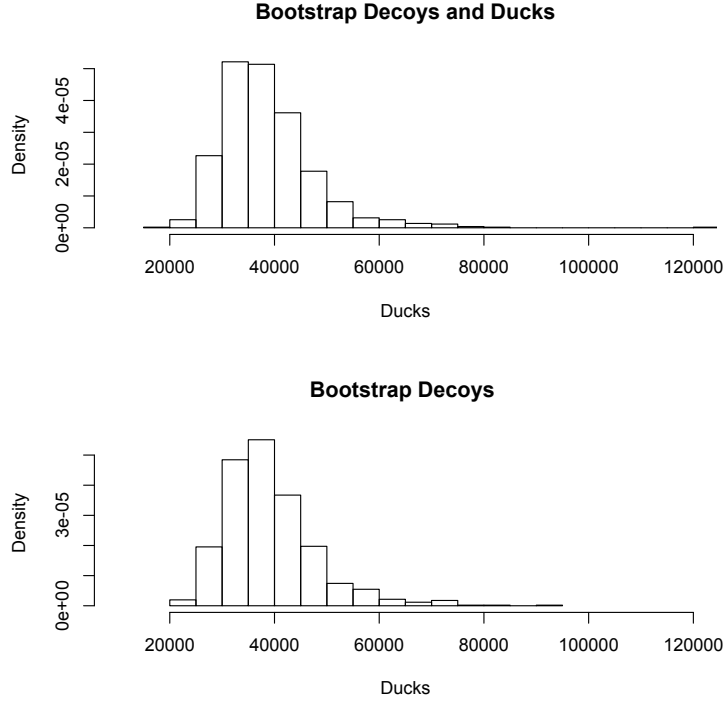


Figure 3.1: Estimates for $se_{\hat{T}_{\text{bias adjusted}}}$ Simulation 1

In Simulation 2, the bias correction procedure again tends to restore the number of ducks actually present. The presence of the additional variation in the count bias is reflected, as expected, in a larger standard error for \hat{T}_{BC} as compared to Simulation 1.

Figure 3.3 shows the histograms of the three population estimators which appear slightly right skewed. The graph for \hat{T}_{BC} has a similar shape to the graph for \hat{T}_{PS} , but with a bit more variability. Using a 95% Normal based approximation confidence interval, the coverage, under both methods for calculating the standard error was 94.4% and 94.7% respectively.

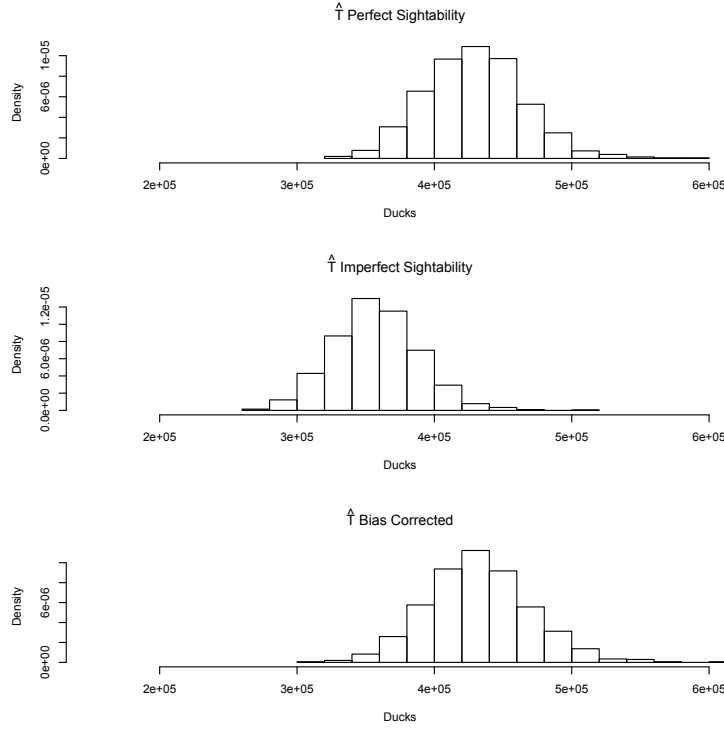


Figure 3.2: Estimates for \hat{T} Simulation 1

Simulation 3

In Simulations 1 and 2, the model for the proportion of ducks counted included an error structure that was Normally distributed and the histograms of the bias adjusted estimates \hat{T}_{BC} maintain the approximately normal distribution shape present in the perfect visibility estimates, albeit with more variability. Simulation 3 uses a uniform error structure. The average estimate of the population total for \hat{T}_{PS} is 430,878 ducks with a standard deviation of 37,410. The average estimate for \hat{T}_{IS} is 230,488 ducks with a standard deviation of 21,199. The bias correction procedure produces an average estimate of 431,963 ducks with a standard deviation of 40,635. The bootstrap procedures returned average standard errors of 40,911 and 41,434 which are again reasonable based on the standard deviation of the 1,024 estimates of

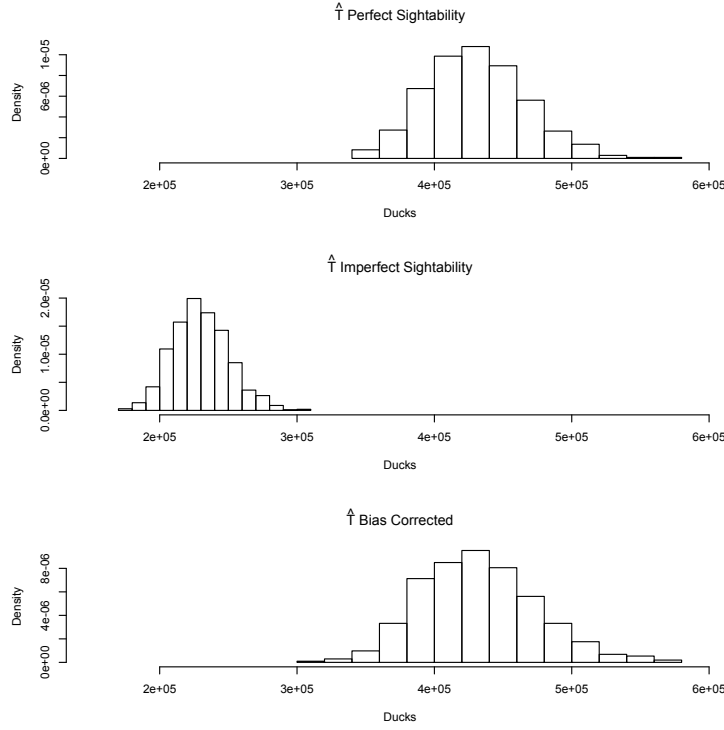


Figure 3.3: Estimates for \hat{T} Simulation 2

\hat{T}_{BC} .

Figure 3.4 provides the histograms of the three population estimators for simulation 3 which are slightly right skewed as the graph of \hat{T}_{BC} is picking up the shape of \hat{T}_{PS} . Using a 95% Normal based approximation confidence interval, the coverage, under both methods for calculating the standard error was 94.9% and 95.3%.

Simulation 4

Simulations 1 through 3 use symmetric error structures. Simulation 4 uses right skewed errors from a Beta distribution with parameters $\alpha = 2$ and $\beta = 8$. So that the mean of the errors is still 0, the mean of the Beta distribution, 0.2, was subtracted from each value generated from the Beta distribution.

The average estimate for the population total for \hat{T}_{PS} is 431,069 ducks with

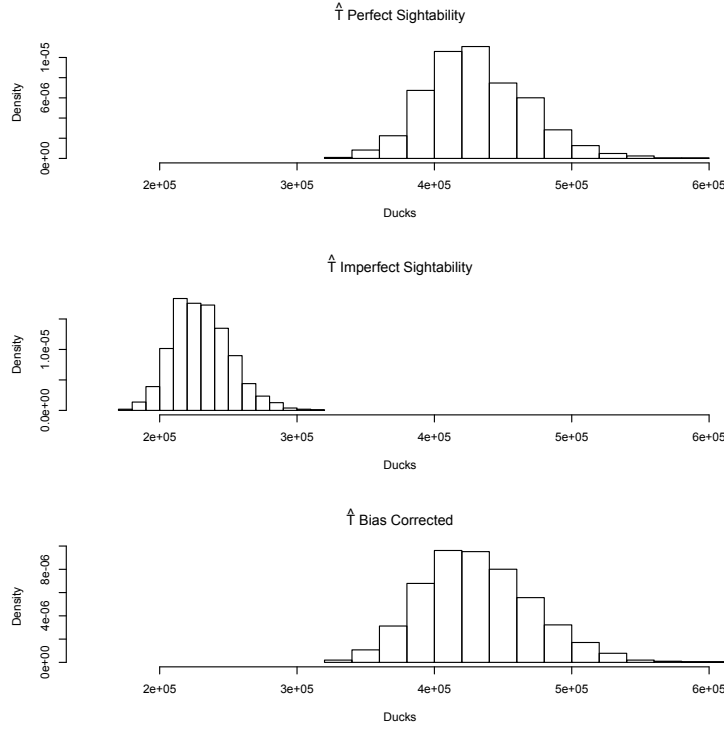


Figure 3.4: Estimates for \hat{T} Simulation 3

a standard deviation of 37,780. The average estimate for \hat{T}_{IS} is 230,431 ducks with a standard deviation of 21,923. The bias correction procedure produces an average estimate of 432,777 ducks with a standard deviation of 43,875. The bootstrap procedures returned average standard errors of 44,322 and 44,647.

Figure 3.5 presents the histogram for the perfect sightability, imperfect sightability, and bias corrected estimates, which all have an approximate Normal shape. The coverage of the Normal based approximation confidence intervals was 94.1% and 94.3%.

3.4.2 Sensitivity to Misspecification

Section 3.4.1 assumes that the visibility bias models for the observer are the same for both the live animals and the decoys. It is reasonable to question whether or

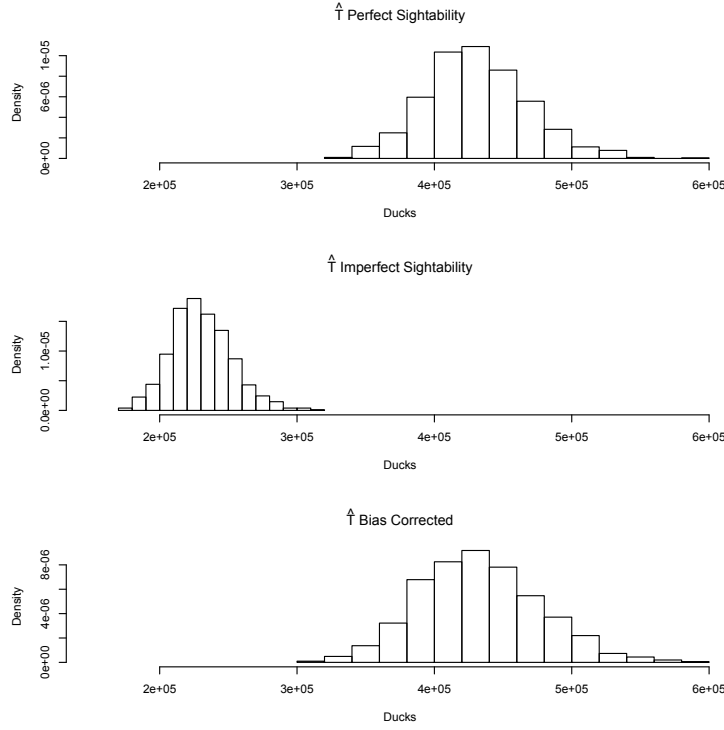


Figure 3.5: Estimates for \hat{T} Simulation 4

not this is an appropriate assumption. Two more simulations are run to attempt to demonstrate how sensitive the model can be to misspecification. In Simulation 5, the probability of detection for the decoys and the proportion of decoys in a group that are counted are systematically altered. In Simulation 6, the random error structures between the live animals and the decoys are different.

Simulation 5

One sample of 125 transects is selected from the artificial population as in Section 3.3. The parameters for the count bias model and the detectability model for the aerial survey of the sample are given in Table 3.5. To obtain the parameters of the models for visibility bias for the decoy experiment, the coefficients of the aerial survey models are multiplied by a constant c where c varies from 0.8 to 1.2 in increments

of 0.01. For example, the parameters for π_{ijk} from Table 3.5 for the aerial survey of the artificial population are $[0.75, 0.2, -0.03]^T$. The parameters for π_{ijk} for the decoy experiment then are $c[0.75, 0.2, -0.03]^T$. Figure 3.6 shows the true multiple regression model for the proportion of ducks counted per habitat and group size and the proportion of decoys counted per habitat and group size for $c = 0.8$. To calculate the standard error in Simulation 5, the bootstrap method was applied to the visibility experiment only in order to get plug-in estimates for the direct variance calculation in Formula 2.4.

When the decoy visibility bias models match the visibility bias models of the sample from the artificial population, i.e. when $c = 1$, the bias corrected estimate of the population total from this sample is 402,836.87 ducks with a standard error of 34,639.02. Figure 3.7 plots the population total estimates \hat{T}_{BC} against c when c is applied to the model for π_{ijk} . In this situation as c increases by .01, \hat{T}_{BC} decreases on average by 3,475 ducks. Figure 3.8 plots \hat{T}_{BC} against c when c is applied to the model for p_{ijk} . Here, most of the estimates for the population total are underestimates as c varies from 0.8 to 1.2. The average value of \hat{T}_{BC} across the different values of c is 393,811. Figures 3.9 and 3.10 plot the standard errors of \hat{T}_{BC} verses c when c is applied to the model for π_{ijk} and p_{ijk} respectively. In both situations, the standard error is generally underestimated. As seen in Figure 3.9 the standard error estimates show a slight downward trend when c is applied to the model for π_{ijk} .

Simulation 6

In this Simulation, the parameters for the visibility bias models were the same for both the live animals and the decoys and are given in Table 3.6. The errors, however, have different underlying distributions. For the decoy simulation, the random error added into the multiple regression model is Normally distributed with mean 0

Table 3.5: Parameters Simulation 5

Parameters	
π_{ijk}	$\gamma_0 = 0.75$ $\gamma_{habitat} = 0.2$ $\gamma_{\log(\text{size})} = -0.03$ $\epsilon \sim N(0, .1)$
p_{ijk}	$\beta_0 = -0.6$ $\beta_{habitat} = 0.5$ $\beta_{size} = 0.1$

and standard deviation of 0.1 while in the live animal survey simulation the errors, $\epsilon + 0.2$, follow the Beta distribution with parameters 2 and 8.

There are 1,024 samples taken using the mismatched error structures with \hat{T}_{BC} and \hat{T}_{PS} calculated for each sample. In order to make a comparison, there are also 1,024 samples taken using Normally distributed errors in both the live animal survey and the decoy survey simulations. For the mismatched errors, the average estimate of \hat{T}_{BC} is 424,946 ducks with an average standard error of 39,793. The average estimate of \hat{T}_{PS} from this group of samples is 430,036 ducks, a difference of 5,090. Keeping the error structure the same, the average estimate of \hat{T}_{BC} is 429,870 ducks with an average standard error of 41,101. The average estimate of \hat{T}_{PS} from these samples is 430,488, a difference of only 618. Simulation 6 shows that having different error structures can have an impact on the bias corrected estimates.

Table 3.6: Parameters Simulation 6

Parameters	
π_{ijk}	$\gamma_0 = 0.8$ $\gamma_{habitat} = 0.09$ $\gamma_{\log(\text{size})} = -0.003$
p_{ijk}	$\beta_0 = -0.6$ $\beta_{habitat} = 0.5$ $\beta_{size} = 0.1$

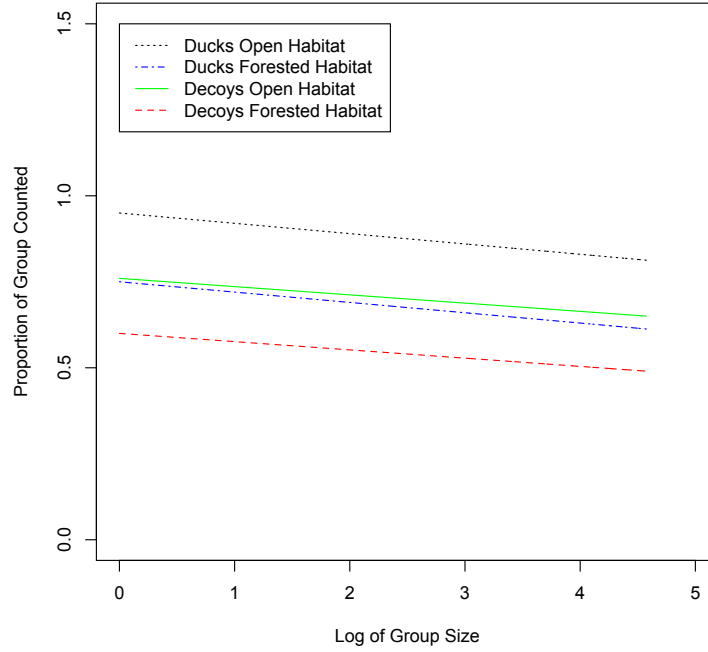


Figure 3.6: Multiple Regression Model, $c = 0.8$

3.4.3 Confidence Intervals

Several methods have been developed to calculate confidence intervals when using the bootstrap method to estimate the standard error, but we will only consider three methods. The first, and probably the simplest and most familiar method is to calculate Normal based approximation confidence intervals as was done in Simulations 1 through 4 using the formula

$$\hat{T}_{BC} \pm z_{\frac{\alpha}{2}} se_{\hat{T}_{BC}}. \quad (3.3)$$

The second is a percentile interval. To form this interval we find the $\frac{\alpha}{2}$ and $1 - \frac{\alpha}{2}$ percentiles of the bootstrap estimates and use those values as the lower and upper bounds respectively of the confidence interval. The third confidence interval is a

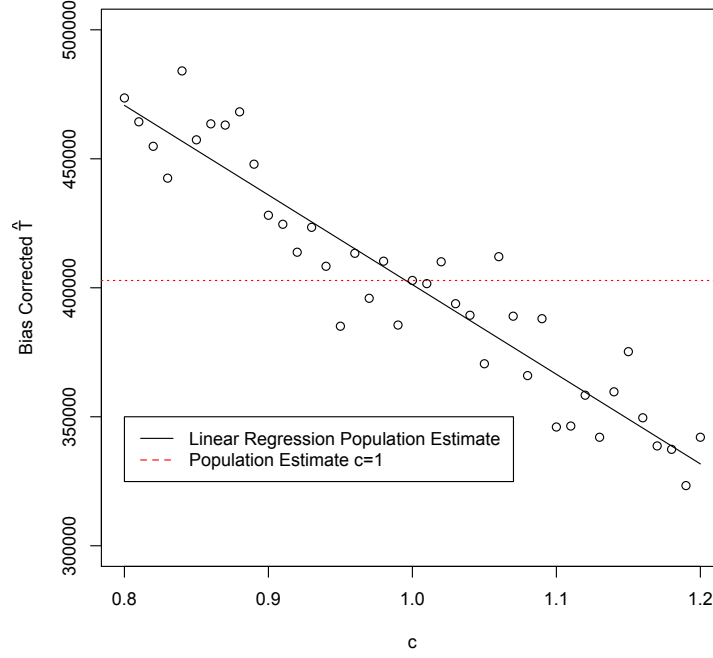


Figure 3.7: \hat{T}_{BC} vs c with c applied to π_{ijk}

pivotal interval. To form a pivot for any parameter T we subtract T from its estimate \hat{T} to form a new random variable K (Wasserman, 2006). We also need to know the CDF of K so that we can find its $\frac{\alpha}{2}$ and $1 - \frac{\alpha}{2}$ percentiles. Since the CDF of K is unknown, we can use the bootstrap to find estimates for the percentiles. The resulting formulae for the lower and upper bounds (LB and UB) for the pivotal confidence interval of the population total are

$$LB = 2\hat{T} - \hat{T}_{1-\frac{\alpha}{2}}^*, \text{ and} \quad (3.4)$$

$$UB = 2\hat{T} - \hat{T}_{\frac{\alpha}{2}}^*, \quad (3.5)$$

where $\hat{T}_{\frac{\alpha}{2}}^*$ and $\hat{T}_{1-\frac{\alpha}{2}}^*$ are the $\frac{\alpha}{2}$ and $1 - \frac{\alpha}{2}$ percentiles of the bootstrap estimates.

The percentile interval and the pivotal interval both require that we form

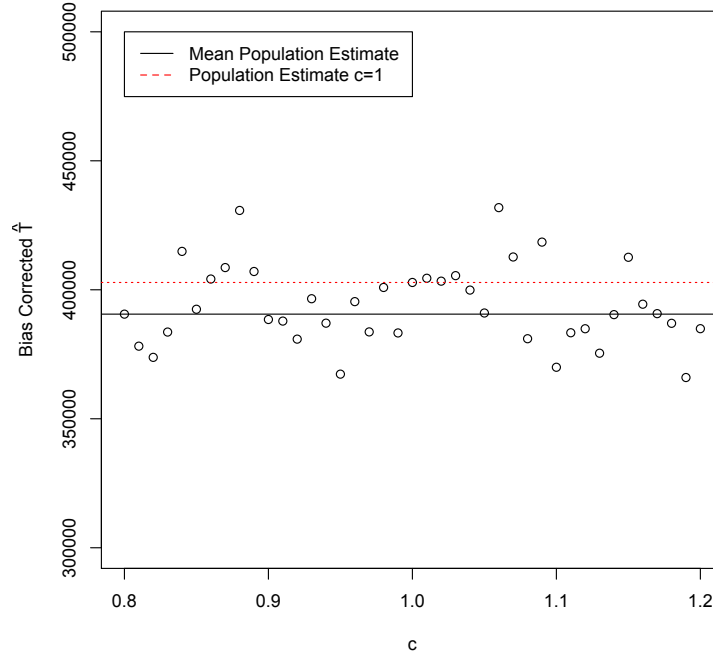


Figure 3.8: \hat{T}_{BC} vs c with c applied to p_{ijk}

bootstrap estimates of \hat{T} . Thus, only the the bootstrap method of Section 2.1 is used where both the duck survey and the decoy survey are resampled. For each confidence interval, 3,000 bootstrap samples are taken. There are 1,024 95% confidence intervals created using each of the methods discussed above and using the parameters from Simulation 5 in Table 3.5. By forming multiple confidence intervals, we can evaluate their coverage. Two error structures in the model for count bias are used,

$$\epsilon_1 \sim \text{Normal}(\mu = 0, \sigma = .1),$$

and letting $\epsilon'_2 = \epsilon_2 + .2$

$$\epsilon'_2 \sim \text{Beta}(\alpha = 2, \beta = 8).$$

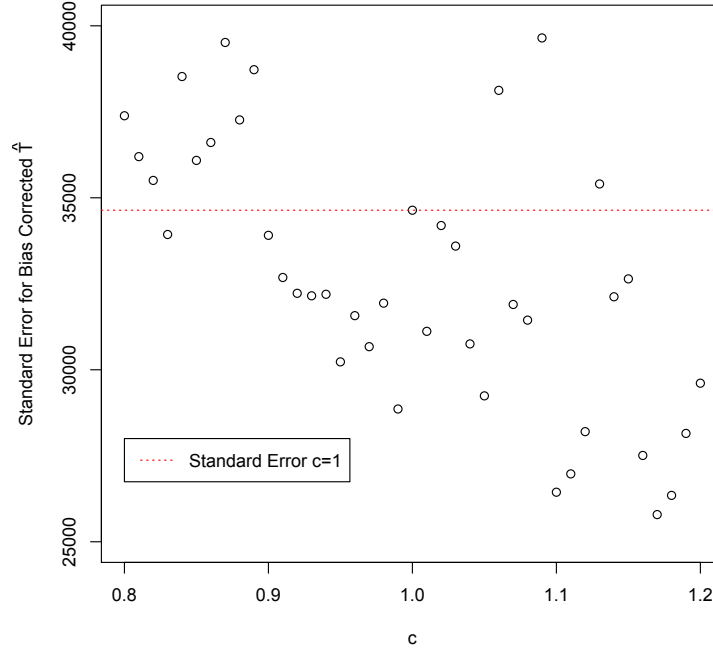


Figure 3.9: Standard error of \hat{T}_{BC} vs. c with c applied to π_{ijk}

Using the skewed errors from the Beta distribution, the coverage for the Normal approximation, percentile and pivotal intervals are 93.3%, 93.3% and 92.0% respectively. The average width of the pivotal and percentile confidence intervals is 157,437. The average width of the Normal approximation confidence interval is longer at 158,680. Using the Normally distributed errors, the coverage for the Normal approximation, percentile and pivotal intervals are 92.9%, 93.1% and 91.7% respectively. The average width of the pivotal and percentile confidence intervals is 153,067. The average width of the Normal approximation confidence interval is 154,907. In this particular simulation, the percentile confidence interval performs the best.

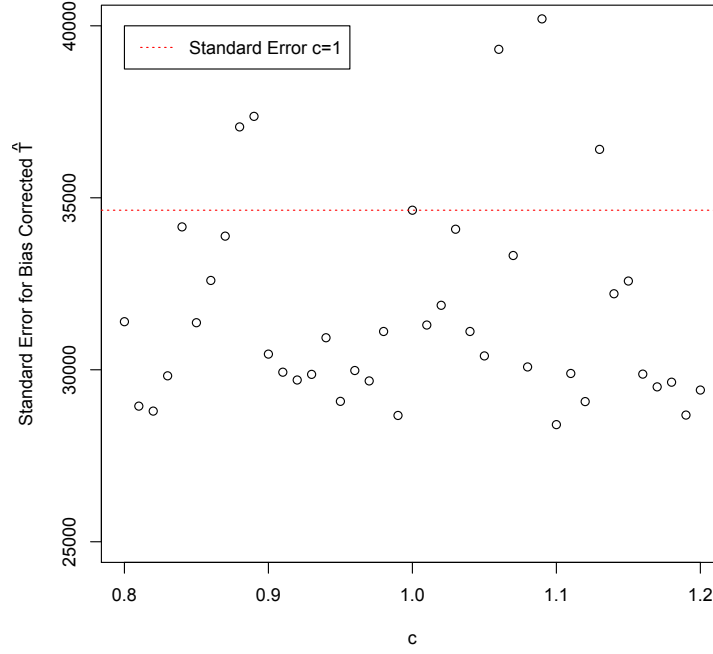


Figure 3.10: Standard error of \hat{T}_{BC} vs. c with c applied to p_{ijk}

3.4.4 Changing the Sample Size of the Live Animal Simulation

The standard error of an estimate is greatly impacted by the sample size and the smaller the sample, the larger the standard error. We would like to know how the sample size affects the standard error estimates when we combine the information from the visibility experiment. The parameters and the error structure used are the same as in Simulation 4. The decoy experiment is not changed but the sample sizes per strata for the live animal survey are 2, 4, 8, 16, 25, 30, 40 and 50. At each sample size, 1,024 estimates for \hat{T}_{BC} and its standard error are calculated. The standard errors are estimated by both of the bootstrap implementations.

Table 3.7 reports the average of estimates for \hat{T}_{BC} , the theoretical standard

Table 3.7: Effect of Sample Size per Strata on Standard Error Estimate

Sample Size Per Strata	Average \hat{T}_{BC}	Theoretical se	St. Dev \hat{T}_{BC}	Bootstrap Both Avg. \hat{se}	Bootstrap Visibility Avg. \hat{se}
2	429,699	140,169	154,416	86,733	119,107
4	431,395	99,114	104,171	81,319	92,394
8	431,279	70,084	77,113	67,072	70,677
16	431,340	49,557	55,370	53,356	54,386
25	433,096	39,646	47,679	46,214	46,622
30	432,331	36,191	41,347	43,406	43,743
40	432,482	31,343	39,509	39,669	39,743
50	432,398	28,034	35,118	36,294	36,404

error from Equation 1.2 if we had perfect visibility, the standard deviation of the 1,024 estimates and the average standard error estimates calculated by the bootstrap methods. As we can see from the table, the averages of the bias corrected population estimates at each sample size are all very reasonable. We would expect that the standard error estimates are larger for the smaller sample sizes. However, the bootstrap methods are unable to properly estimate the standard error at the smaller sample sizes. Once the sample size reaches 16 transects per strata, the bootstrap methods are able to estimate the standard errors quite well. This result serves as a reminder that the bootstrap procedure cannot correct a poorly designed study.

Chapter 4

Discussion

4.1 Conclusions

We embarked on this journey to evaluate a bias corrected estimator for a population total, \hat{T}_{BC} proposed by Pearse et al. (2008) and ways in which to estimate its standard error. The goal of the estimator was to compensate for two types of visibility bias present in aerial surveys of wildlife, detection bias and count bias. However, the estimator itself contained parameters that were estimated by an external experiment making its standard error calculation difficult. Pearse et al. (2008) chose to use the bootstrap method on both the data from an animal survey and the data from the external experiment to calculate an estimate of the standard error. In this work we find the analytical expression for the variance of \hat{T}_{BC} , and propose an estimator for $\text{Var}(\hat{T}_{BC})$ in Equation 2.5. This estimator of the variance also requires estimates for the variance and covariance of the bias correction factors f_{ijk} and p_{ijk} which are obtained through a bootstrap algorithm on only the data from the decoy experiment.

The two approaches to find the standard error of \hat{T}_{BC} are compared and applied

to the same 2004 aerial survey of wintering ducks in the MAV as was used by Pearse et al. (2008). We find that using the approach where bootstrap samples are taken from both the survey data and the decoy experiment, the standard error stabilizes near 39,400 ducks after 2,000 bootstrap resamples. If we only bootstrap from the decoy experiment and use a direct variance calculation, the standard error stabilizes near 39,600 ducks after 30,000 bootstrap resamples. Thus the approach of Pearse et al. (2008) is able to incorporate the dependencies in the data into the estimate of the standard error and works equally well as compared to the more analytical approach in this situation. A concern when choosing which bootstrap method to use is how the resulting information will be used. For example, if pivotal or percentile confidence intervals need to be computed, then we should bootstrap from both the survey data and the visibility experiment. We did find in our simulation study that the bias adjusted population estimates were approximately Normally distributed. We could therefore use a Normal based approximation confidence interval that only required bootstrapping from the visibility experiment to estimate the standard error. However, we cannot assume, going into the study that we will end up with a common probability distribution for the estimator.

Having established that the two bootstrap algorithms produce similar results in estimating the standard error, we turn to the question of whether or not the approach of using an external experiment has the potential to correct for detection bias and count bias for wildlife populations similar to the ducks in the MAV. To address this concern we create an artificial population of ducks and simulate an aerial survey of this artificial population and of the decoy experiment. From Simulations 1 through 4 we see that if the observer detects and counts groups of decoys in the same manner as live animals, then the bias correction procedure works quite well.

Pearse et al. (2008) mention in their discussion of the decoy experiment, that

they felt they could work with decoy groups of up to size 100, even though a few larger groups of ducks had been sighted. It is generally not advised to use regression models on values outside of the scope of the data used to create them. This simulation assumes that the proportion of animals counted follows the same model for groups larger than 100. Hence it does not address the existence of potential problems if the proportion of animals counted is indeed different at larger group sizes. This points to the value of a simulation study mentioned by Nuno et al. (2013) in that a researcher can experiment with parameters inside a virtual study area before going through the expense of an actual study. The simulation study could be altered to include a different model for larger group sizes in the live animals to determine the impact of capping the sizes of groups of decoys below the group sizes observed in live animals.

The misspecification part of the simulation study in Section 3.4.2 was developed because of concerns that live ducks behave differently than decoys. For example, they could react to the presence of the aircraft while decoys would not. Also, it may be easier for an observer to spot live animals from their movements than decoys which are fairly still. There are numerous ways in which the parameters included in the simulation could have been manipulated. This simulation study is certainly not an exhaustive study of the different combinations of parameters that could be important in an aerial survey and the impact of the external experiment. Nonetheless, we have demonstrated that misspecification can be a problem. It appears that we need to be reasonably sure that the visibility experiment and the decoys used will actually be an adequate substitute for live animals. Again, we see the value of a simulation study in determining whether or not a proposed external experiment can produce results that are within the tolerance limits of a researcher.

Another way in which the simulation study can be a valuable tool is in determining an appropriate sample size. In forming confidence intervals, if we know what

margin of error we will accept, know the approximate underlying probability distribution, and have a guess for the standard error, we can solve for the needed sample size. However by adding in the bias correction factors and the need for the bootstrap procedure, we would have a difficult time reaching a solution. In our particular simulation study, we had a large number of PSUs from which to choose. We see that once we reach a sample size of 16 transects per strata, the bootstrap procedure is able to calculate a reasonable estimate for the standard error. The choice for the number of transects per strata depends heavily on the specific situation and the costs involved in performing an aerial survey. By using a simulation we can determine an acceptable lower bound on the sample sizes needed for consistent results from the standard error estimate calculations.

4.2 Future Work

4.2.1 Improved Bootstrap Algorithms

Creating some of the other bootstrap confidence intervals that were not calculated in this work involve additional computations within the bootstrap algorithm. Of particular interest is the studentized pivotal confidence interval. The difference with the studentized interval versus the pivot interval from Section 3.4.3 is that at each iteration of the bootstrap, an estimate of the variance is needed to form the pivot using the formula $z_b^* = \frac{\hat{T}_b^* - \hat{T}}{se_{\hat{T}_b^*}}$ where b is the b^{th} bootstrap iteration (Wasserman, 2006). The $\frac{\alpha}{2}$ and $1 - \frac{\alpha}{2}$ percentiles are found among the values for z_b^* . The confidence

interval is found using

$$LB = \hat{T} - z_{1-\frac{\alpha}{2}}^* \hat{se}_{\hat{T}} \text{ and} \quad (4.1)$$

$$UB = \hat{T} - z_{\frac{\alpha}{2}}^* \hat{se}_{\hat{T}}. \quad (4.2)$$

To find the variance estimate at each iteration, we could perform an inner bootstrap algorithm. One way this is done is, at the current bootstrap sample, take a bootstrap sample from it for each iteration. Since it takes a long time to bootstrap from both the survey and the decoy experiment, it would make sense to only perform the inner bootstrap algorithm on the visibility experiment and gather the necessary plug-in estimates for the variance equation. Given the number of additional computations that would be required by an inner bootstrap, a faster more clever algorithm and a more efficient way to locate and apply the variance estimates from the covariance matrix is needed.

Also, in the case of applying the bootstrap method to regression type models, another approach is to resample the residuals or deviances of the regression procedures rather than resample the entire data set. Using this method of resampling might reduce the instances of non-convergence in the logistic regression calculations within the bootstrap procedure.

4.2.2 Multiple Observer Methods

In this work, it is assumed that we have one observer. In many studies, multiple observers are used to attempt to correct for visibility bias and count bias. For example, Walsh et al. (2009) uses an estimator proposed by DasGupta and Rubin (2005) for group size based on the maximum group counts from several independent observers in their work estimating elk populations. With multiple observers, we could

perhaps include a random observer effect in the models for the probability of detecting a group, or for the proportion of the groups counted in the external experiment.

Appendices

Appendix A Derivation of Variance for \hat{T}_{BC}

We provide details of the derivation of the expression for the variance of \hat{T}_{BC} given in Equation 2.4 in this Appendix. The two main components of the variance are

$$\mathbb{V}ar(\hat{T}_{BC}) = \sum_i \mathbb{V}ar(\hat{t}_{iBC}) + \sum_{i \neq i'} \mathbb{C}ov(\hat{t}_{iBC}, \hat{t}_{i'BC}).$$

It is unusual to include a covariance term in stratified sampling. But as noted in Section 2.2, the presence of the estimated bias correction factors causes dependencies between the population estimates in each strata. For the first main component we have

$$\begin{aligned} \mathbb{V}ar(\hat{t}_{iBC}) &= \mathbb{V}ar_{\mathbf{Q}}(\mathbb{E}_{\mathbf{R}\hat{\mathbf{A}}|\mathbf{Q}}(\hat{t}_{iBC})) + \mathbb{E}_{\mathbf{Q}}(\mathbb{V}ar_{\mathbf{R}\hat{\mathbf{A}}|\mathbf{Q}}(\hat{t}_{iBC})), \\ &= \mathbb{V}ar_{\mathbf{Q}}(\mathbb{E}_{\mathbf{R}|\mathbf{Q}}\mathbb{E}_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC})) \\ &\quad + \mathbb{E}_{\mathbf{Q}} \left[\mathbb{V}ar_{\mathbf{R}|\mathbf{Q}}\mathbb{E}_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC}) \right] \\ &\quad + \mathbb{E}_{\mathbf{Q}} \left[\mathbb{E}_{\mathbf{R}|\mathbf{Q}}(\mathbb{V}ar_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC})) \right]. \end{aligned}$$

We derive each of these three pieces of $\mathbb{V}ar(\hat{t}_{iBC})$ separately. First,

$$\mathbb{V}ar_{\mathbf{Q}}(\mathbb{E}_{\mathbf{R}|\mathbf{Q}}\mathbb{E}_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC})) = \mathbb{V}ar_{\mathbf{Q}} \sum_j \frac{1}{n_i} \frac{Q_{ij}}{\psi_{ij}} \left(\sum_{k=1}^{n_{ij}} s_{ijk} \cdot \mu_{\hat{a}_{ijk}} \cdot p_{ijk} \right).$$

Let $d_{ij} = \frac{\sum_k s_{ijk} \mu_{\hat{a}_{ijk}} p_{ijk}}{n_i \psi_{ij}}$. Then

$$\begin{aligned}
\mathbb{C}ov \left(\sum_j d_{ij} Q_{ij}, \sum_j d_{ij} Q_{ij} \right) &= \sum_j d_{ij}^2 \mathbb{V}ar(Q_{ij}) + 2 \left(\sum_{j \neq j'} d_{ij} d_{ij'} \mathbb{C}ov(Q_{ij}, Q_{ij'}) \right), \\
&= \sum_j \frac{1}{n_i \psi_{ij}} (1 - \psi_{ij}) \left(\sum_k s_{ijk} \cdot \mu_{\hat{a}_{ijk}} \cdot p_{ijk} \right)^2 \\
&\quad - \sum_{j \neq j'} d_{ij} d_{ij'} n_i \psi_{ij} \psi_{ij'}, \\
&= \sum_j \frac{1}{n_i \psi_{ij}} (1 - \psi_{ij}) \left(\sum_k s_{ijk} \cdot \mu_{\hat{a}_{ijk}} \cdot p_{ijk} \right)^2 \\
&\quad - \sum_{j \neq j'} \frac{\sum_k s_{ijk} \mu_{\hat{a}_{ijk}} p_{ijk}}{n_i \psi_{ij}} \frac{\sum_k s_{ij'k} \mu_{\hat{a}_{ij'k}} p_{ij'k}}{n_i \psi_{ij'}} n_i \psi_{ij} \psi_{ij'}, \\
&= \sum_j \frac{1}{n_i \psi_{ij}} (1 - \psi_{ij}) \left(\sum_k s_{ijk} \cdot \mu_{\hat{a}_{ijk}} \cdot p_{ijk} \right)^2 \\
&\quad - \sum_{j \neq j'} \frac{\sum_k s_{ijk} \mu_{\hat{a}_{ijk}} p_{ijk}}{n_i} \frac{\sum_k s_{ij'k} \mu_{\hat{a}_{ij'k}} p_{ij'k}}{n_i}.
\end{aligned}$$

Second, let $c_{ijk} = s_{ijk} \cdot \mu_{\hat{a}_{ijk}}$ and $\mathbf{c}_{ij} = [s_{ijk} \cdot \mu_{\hat{a}_{ijk}}]$. Then

$$\begin{aligned}
\mathbb{E}_{\mathbf{Q}} \left[\text{Var}_{\mathbf{R}|\mathbf{Q}} \mathbb{E}_{\hat{\mathbf{A}}|\mathbf{R}\mathbf{Q}}(\hat{t}_{iBC}) \right] &= \mathbb{E}_{\mathbf{Q}} \text{Var}_{\mathbf{R}|\mathbf{Q}} \left(\sum_j \sum_k \frac{Q_{ij}}{n_i \psi_{ij}} \cdot c_{ijk} \cdot R_{ijk} \right), \\
&= \mathbb{E}_{\mathbf{Q}} \text{Var}_{\mathbf{R}|\mathbf{Q}} \left(\sum_j \frac{Q_{ij}}{n_i \psi_{ij}} \cdot \mathbf{c}_{ij}^T \cdot \mathbf{R}_{ij} \right), \\
&\quad \text{and since } R_{ijk} \text{'s are independent,} \\
&= \mathbb{E}_{\mathbf{Q}} \left[\sum_j \left(\frac{Q_{ij}}{n_i \psi_{ij}} \right)^2 \text{Var}_{\mathbf{R}|\mathbf{Q}} (\mathbf{c}_{ij}^T \cdot \mathbf{R}_{ij}) \right], \\
&= \mathbb{E}_{\mathbf{Q}} \left[\sum_j \left(\frac{Q_{ij}}{n_i \psi_{ij}} \right)^2 \mathbf{c}_{ij}^T \cdot \Sigma_{\mathbf{R}_{ij}} \cdot \mathbf{c}_{ij} \right], \\
&= \sum_j \frac{\mathbf{c}_{ij}^T \cdot \Sigma_{\mathbf{R}_{ij}} \cdot \mathbf{c}_{ij}}{n_i^2 \psi_{ij}^2} \mathbb{E}_{\mathbf{Q}}[Q_{ij}^2], \\
&= \sum_j \frac{\mathbf{c}_{ij}^T \Sigma_{\mathbf{R}_{ij}} \mathbf{c}_{ij}}{n_i^2 \psi_{ij}^2} [n_i \psi_{ij} (1 - \psi_{ij}) + n_i^2 \psi_{ij}^2], \\
&= \sum_j \frac{\mathbf{c}_{ij}^T \Sigma_{\mathbf{R}_{ij}} \mathbf{c}_{ij}}{n_i \psi_{ij}} (1 + (n_i - 1) \psi_{ij}), \\
&= \sum_j \frac{\sum_k s_{ijk}^2 \mu_{\hat{a}_{ijk}}^2 p_{ijk} (1 - p_{ijk})}{n_i \psi_{ij}} (1 + (n_i - 1) \psi_{ij}).
\end{aligned}$$

Third,

$$\begin{aligned}
& \mathbb{E}_{\mathbf{Q}} \left[\mathbb{E}_{\mathbf{R}|\mathbf{Q}} (\text{Var}_{\hat{\mathbf{A}}|\mathbf{RQ}}(\hat{t}_{iBC})) \right] \\
&= \mathbb{E}_{\mathbf{Q}} \mathbb{E}_{\mathbf{R}|\mathbf{Q}} \text{Var}_{\hat{\mathbf{A}}|\mathbf{RQ}} \left(\sum_j \sum_k \frac{Q_{ij} s_{ijk} R_{ijk}}{n_i \psi_{ij}} \cdot a_{ijk} \right), \\
&= \mathbb{E}_{\mathbf{Q}} \mathbb{E}_{\mathbf{R}|\mathbf{Q}} \sum_j \sum_{j'} \sum_k \sum_{k'} \frac{Q_{ij} s_{ijk} R_{ijk}}{n_i \psi_{ij}} \cdot \frac{Q_{ij'} s_{ij'k'} R_{ij'k'}}{n_i \psi_{ij'}} \cdot \text{Cov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}), \\
&= \mathbb{E}_{\mathbf{Q}} \frac{1}{n_i^2} \sum_j \sum_{j'} \sum_k \sum_{k'} \frac{Q_{ij} s_{ijk} Q_{ij'} s_{ij'k'}}{\psi_{ij} \psi_{ij'}} \text{Cov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}) \cdot \mathbb{E}[R_{ijk} R_{ij'k'}], \\
&= \mathbb{E}_{\mathbf{Q}} \frac{1}{n_i^2} \sum_j \sum_{j'} \sum_k \sum_{k'} \frac{Q_{ij} s_{ijk} Q_{ij'} s_{ij'k'}}{\psi_{ij} \psi_{ij'}} \text{Cov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}) \cdot (\text{Cov}(R_{ijk} R_{ij'k'}) + \mathbb{E}[R_{ijk}] \mathbb{E}[R_{ij'k'}]), \\
&= \mathbb{E}_{\mathbf{Q}} \frac{1}{n_i^2} \left[\sum_{j \neq j'} \sum_{k \neq k'} \frac{Q_{ij} Q_{ij'}}{\psi_{ij} \psi_{ij'}} s_{ijk} s_{ij'k'} \text{Cov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}) p_{ijk} p_{ij'k'} \right] \\
&\quad + \mathbb{E}_{\mathbf{Q}} \frac{1}{n_i^2} \left[\sum_j \frac{Q_{ij}^2}{\psi_{ij}^2} \left[\sum_k s_{ijk}^2 \text{Var}(\hat{a}_{ijk}) p_{ijk} - \sum_{k \neq k'} s_{ijk} s_{ij'k'} \text{Cov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}) p_{ijk} p_{ij'k'} \right] \right] \\
&\quad + \mathbb{E}_{\mathbf{Q}} \frac{1}{n_i^2} \left[\sum_j \sum_k \left(\frac{Q_{ij} s_{ijk}}{\psi_{ij}} \right)^2 \text{Var}(\hat{a}_{ijk}) (\text{Var}(R_{ijk}) + \mathbb{E}^2[R_{ijk}]) \right], \\
&= \sum_{j \neq j'} \sum_{k \neq k'} s_{ijk} s_{ij'k'} p_{ijk} p_{ij'k'} \text{Cov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}) \frac{(n_i - 1)}{n_i} \\
&\quad + \sum_{j=1}^{n_i} \left(\frac{1 - \psi_{ij}}{n_i \psi_{ij}} + 1 \right) \left[\sum_{k=1}^{n_{ij}} s_{ijk}^2 \text{Var}(\hat{a}_{ijk}) p_{ijk} \right] \\
&\quad + \sum_j \left(\frac{1 - \psi_{ij}}{n_i \psi_{ij}} + 1 \right) \left[\sum_{k \neq k'} s_{ijk} s_{ij'k'} \text{Cov}(\hat{a}_{ijk}, \hat{a}_{ij'k'}) p_{ijk} p_{ij'k'} \right].
\end{aligned}$$

For the covariance we have $\text{Cov}(\hat{t}_{iBC}, \hat{t}_{i'BC}) = \mathbb{E}[\hat{t}_{iBC} \cdot \hat{t}_{i'BC}] - \mathbb{E}[\hat{t}_{iBC}] \cdot \mathbb{E}[\hat{t}_{i'BC}]$, where

$$\begin{aligned}
\mathbb{E}[\hat{t}_{iBC}] \cdot \mathbb{E}[\hat{t}_{i'BC}] &= \left(\sum_{j=1}^{N_i} \sum_{k=1}^{n_{ij}} s_{ijk} \mu_{\hat{a}_{ijk}} p_{ijk} \right) \cdot \left(\sum_{y=1}^{N_{i'}} \sum_{z=1}^{n_{i'y}} s_{i'yz} \mu_{\hat{a}_{i'yz}} p_{i'yz} \right), \text{ and} \\
\mathbb{E}[\hat{t}_{iBC} \cdot \hat{t}_{i'BC}] &= \mathbb{E}_{\mathbf{Q}} \mathbb{E}_{\mathbf{R}|\mathbf{Q}} \mathbb{E}_{\hat{\mathbf{a}}|\mathbf{QR}} \left[\left(\sum_j \sum_k \frac{Q_{ij}}{n_i \psi_{ij}} s_{ijk} R_{ijk} \hat{a}_{ijk} \right) \cdot \left(\sum_y \sum_z \frac{Q_{i'y}}{n_{i'} \psi_{i'y}} s_{i'yz} R_{i'yz} \hat{a}_{i'yz} \right) \right], \\
&= \frac{1}{n_i n_{i'}} \mathbb{E}_{\mathbf{Q}} \mathbb{E}_{\mathbf{R}|\mathbf{Q}} \mathbb{E}_{\hat{\mathbf{a}}|\mathbf{QR}} \left[\sum_j \frac{Q_{ij}}{\psi_{ij}} \sum_k s_{ijk} R_{ijk} \left(\sum_y \frac{Q_{i'y}}{\psi_{i'y}} \sum_z s_{i'yz} R_{i'yz} \hat{a}_{ijk} \hat{a}_{i'yz} \right) \right], \\
&= \frac{1}{n_i n_{i'}} \mathbb{E}_{\mathbf{Q}} \mathbb{E}_{\mathbf{R}|\mathbf{Q}} \left[\sum_j \frac{Q_{ij}}{\psi_{ij}} \sum_k s_{ijk} R_{ijk} \left(\sum_y \frac{Q_{i'y}}{\psi_{i'y}} \sum_z s_{i'yz} R_{i'yz} \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] \right) \right], \\
&= \frac{1}{n_i n_{i'}} \mathbb{E}_{\mathbf{Q}} \left[\sum_j \frac{Q_{ij}}{\psi_{ij}} \sum_k s_{ijk} \left(\sum_y \frac{Q_{i'y}}{\psi_{i'y}} \sum_z s_{i'yz} \mathbb{E}[R_{ijk} R_{i'yz}] \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] \right) \right], \\
&= \frac{1}{n_i n_{i'}} \mathbb{E}_{\mathbf{Q}} \left[\sum_j \frac{Q_{ij}}{\psi_{ij}} \sum_k s_{ijk} \left(\sum_y \frac{Q_{i'y}}{\psi_{i'y}} \sum_z s_{i'yz} p_{ijk} p_{i'yz} \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] \right) \right], \\
&= \frac{1}{n_i n_{i'}} \left[\sum_j \sum_k s_{ijk} \left(\sum_y \mathbb{E} \left[\frac{Q_{ij}}{\psi_{ij}} \frac{Q_{i'y}}{\psi_{i'y}} \right] \sum_z s_{i'yz} p_{ijk} p_{i'yz} \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] \right) \right], \\
&= \frac{1}{n_i n_{i'}} \left[\sum_j \sum_k s_{ijk} \left(\sum_y \left[\frac{n_i \psi_{ij}}{\psi_{ij}} \frac{n_{i'} \psi_{i'yz}}{\psi_{i'y}} \right] \sum_z s_{i'yz} p_{ijk} p_{i'yz} \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] \right) \right], \\
&= \sum_j \sum_k s_{ijk} \left(\sum_y \sum_z s_{i'yz} p_{ijk} p_{i'yz} \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] \right).
\end{aligned}$$

Finally, putting the pieces of the covariance together we obtain

$$\begin{aligned}
\mathbb{C}ov(\hat{t}_{iBC}, \hat{t}_{i'BC}) &= \sum_j \sum_k s_{ijk} \left(\sum_y \sum_z s_{i'yz} p_{ijk} p_{i'yz} \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] \right) \\
&\quad - \left(\sum_{j=1}^{N_i} \sum_{k=1}^{n_{ij}} s_{ijk} \mu_{\hat{a}_{ijk}} p_{ijk} \right) \cdot \left(\sum_{y=1}^{N_{i'}} \sum_{z=1}^{n_{i'y}} s_{i'yz} \mu_{\hat{a}_{i'yz}} p_{i'yz} \right) \\
&= \sum_j \sum_k s_{ijk} p_{ijk} \left(\sum_y \sum_z s_{i'yz} p_{i'yz} \mathbb{E}[\hat{a}_{ijk} \hat{a}_{i'yz}] - \mu_{\hat{a}_{ijk}} s_{i'yz} \mu_{\hat{a}_{i'yz}} p_{i'yz} \right), \\
&= \sum_{j=1}^{N_i} \sum_{k=1}^{n_{ij}} \sum_{y=1}^{N_{i'}} \sum_{z=1}^{n_{i'y}} s_{ijk} p_{ijk} s_{i'yz} p_{i'yz} \mathbb{C}ov(\hat{a}_{ijk}, \hat{a}_{i'yz}).
\end{aligned}$$

Appendix B R-Code

In this Appendix, we provide some of the R-code that is used for the simulation study. The program consists of

- Loading and pre-processing the .csv files containing the information for the entire artificial population and for the visibility experiment,
- Defining the necessary functions which includes the bootstrap function `boot.duck4`,
- Defining the main function `mc.fun` that selects a sample from the artificial population, and performs the simulated aerial surveys.

```
#####  
## Simulation with Artificial Population  #  
#####  
  
#####  
## Initialize Global Variables and      #  
## Global data sets                    #  
#####  
  
# load files with artificial population  
# information and decoy information  
# The csv files used here are:  
# art.pop for the artificial population  
# art.tran for basic population information of  
#   Transect ID  
#   Strata ID
```

```

#   Length of transect
#   Number of groups in the transect
# vis for the decoy visibility experiment

library(survey)
library(parallel)

# Count Bias: multiple regression coefficients
# Intercept, Habitat Type, Log of Group Size
B<-c(.8,.09,-.003)

# Visibility Bias: coefficients for linear
# portion of logistic regression model
# Intercept, Habitat Type, Group Size
BL<-c(-.04,.04,.1)

#Subset information into the 5 strata
# H  NE  NW  SE  SW

tot.tran=sum(art.tran$Length) #Total transect length
art.tran.H=subset(art.tran,art.tran[,2]=="H")
art.tran.NE=subset(art.tran,art.tran[,2]=="NE")
art.tran.NW=subset(art.tran,art.tran[,2]=="NW")
art.tran.SE=subset(art.tran,art.tran[,2]=="SE")
art.tran.SW=subset(art.tran,art.tran[,2]=="SW")
tot.tran.H=sum(art.tran.H$Length)
tot.tran.NE=sum(art.tran.NE$Length)

```

```

tot.tran.NW=sum(art.tran.NW$Length)
tot.tran.SE=sum(art.tran.SE$Length)
tot.tran.SW=sum(art.tran.SW$Length)
tru.pop.size=sum(art.pop$ducks)
strata=unique(art.pop$Strata)
num.tran=c(294,802,726,474,680) #Number of transects per strata
art.tran1<-seq(1,294,by=1);art.tran2<-seq(1,802,by=1)
art.tran3<-seq(1,726,by=1);art.tran4<-seq(1,474,by=1)
art.tran5<-seq(1,680,by=1)
art.pop1<-art.pop[art.pop[,2]==strata[1],]
art.pop2<-art.pop[art.pop[,2]==strata[2],]
art.pop3<-art.pop[art.pop[,2]==strata[3],]
art.pop4<-art.pop[art.pop[,2]==strata[4],]
art.pop5<-art.pop[art.pop[,2]==strata[5],]
#sample sizes for each strata
n1<-11;n2<-34;n3<-32;n4<-21;n5<-27
n<-c(n1,n2,n3,n4,n5)

#Set up Decoy experiment data
#in a manner that will be used
#in this program

decoy<-vis[,1:3]
obs<-as.numeric(vis[,1])
decoy[,1]=obs
decoy[,2]=as.numeric(vis[,2])

```

```

decoy[,2]=decoy[,2]-1
N.pop<-length(decoy[,1])

```

```

#####
## Define functions                                #
#####

```

```

#####
## COUNTER                                          #
#####

```

```

counter<-function(tr){
aa1<-sort(unique(tr))
aa2<-rep(0,length(aa1))
for (i in 1:length(aa1)){
aa2[i]<-sum(tr==aa1[i])
}
return(aa2)
}

```

```

#####
## BOOTSTRAP FUNCTION                              #
## Performs both Bootstrap methods                #
#####

```

```

boot.duck4<-function(index,M,data.vis,g,ng,X.fo.l,

```



```

tran1,tran2,tran3,tran4,tran5){

gs<-g
n.gs<-ng
data.vis.o<-subset(data.vis,data.vis[,2]==1)
data.vis.f<-subset(data.vis,data.vis[,2]==0)
no1=10;no2=10;no3=10;no4=10;nf1=11;nf2=10;nf3=10;nf4=10

data.vis.o1<-subset(data.vis.o,data.vis.o[,3]<9)
data.vis.o2<-subset(data.vis.o,data.vis.o[,3]<21&data.vis.o[,3]>8)
data.vis.o3<-subset(data.vis.o,data.vis.o[,3]<41&data.vis.o[,3]>20)
data.vis.o4<-subset(data.vis.o,data.vis.o[,3]>40)

data.vis.f1<-subset(data.vis.f,data.vis.f[,3]<9)
data.vis.f2<-subset(data.vis.f,data.vis.f[,3]<21&data.vis.f[,3]>8)
data.vis.f3<-subset(data.vis.f,data.vis.f[,3]<41&data.vis.f[,3]>20)
data.vis.f4<-subset(data.vis.f,data.vis.f[,3]>40)

data1<-M[M[,2]==strata[1],]
data2<-M[M[,2]==strata[2],]
data3<-M[M[,2]==strata[3],]
data4<-M[M[,2]==strata[4],]
data5<-M[M[,2]==strata[5],]

btran1<-sort(sample(tran1,n1,replace=TRUE))
btran2<-sort(sample(tran2,n2,replace=TRUE))
btran3<-sort(sample(tran3,n3,replace=TRUE))

```

```

btran4<-sort(sample(tran4,n4,replace=TRUE))
btran5<-sort(sample(tran5,n5,replace=TRUE))

b.data1<-NULL
for(i in 1:n1){
b.data1<-rbind(b.data1,data1[data1$Transect==btran1[i],])
}

b.data2<-NULL
for(i in 1:n2){
b.data2<-rbind(b.data2,data2[data2$Transect==btran2[i],])
}

b.data3<-NULL
for(i in 1:n3){
b.data3<-rbind(b.data3,data3[data3$Transect==btran3[i],])
}

b.data4<-NULL
for(i in 1:n4){
b.data4<-rbind(b.data4,data4[data4$Transect==btran4[i],])
}

b.data5<-NULL
for(i in 1:n5){
b.data5<-rbind(b.data5,data5[data5$Transect==btran5[i],])
}

```

```
}
```

```
b.data<-rbind(b.data1,b.data2,b.data3,b.data4,b.data5)
```

```
##### Get visibility sample
```

```
##### Balanced bootstrap
```

```
subscripts=sample((1:no1),no1,replace=TRUE)
```

```
data.vis.ro1=data.vis.o1[subscripts,]
```

```
subscripts=sample((1:no2),no2,replace=TRUE)
```

```
data.vis.ro2=data.vis.o2[subscripts,]
```

```
subscripts=sample((1:no3),no3,replace=TRUE)
```

```
data.vis.ro3=data.vis.o3[subscripts,]
```

```
subscripts=sample((1:no4),no4,replace=TRUE)
```

```
data.vis.ro4=data.vis.o4[subscripts,]
```

```
subscripts=sample((1:nf1),nf1,replace=TRUE)
```

```
data.vis.rf1=data.vis.f1[subscripts,]
```

```
subscripts=sample((1:nf2),nf2,replace=TRUE)
```

```
data.vis.rf2=data.vis.f2[subscripts,]
```

```
subscripts=sample((1:nf3),nf3,replace=TRUE)
```

```

data.vis.rf3=data.vis.f3[subscripts,]

subscripts=sample((1:nf4),nf4,replace=TRUE)
data.vis.rf4=data.vis.f4[subscripts,]

datastar=rbind(data.vis.ro1,data.vis.ro2,data.vis.ro3,data.vis.ro4,
               data.vis.rf1,data.vis.rf2,data.vis.rf3,data.vis.rf4)

###use bootstrap visibility experiment for linear and logistic models
Data.seen<-subset(datastar, datastar[,6]==1)
prop.ct<-lm(Data.seen[,5]~Data.seen[,2]+Data.seen[,7])
y=datastar[,6];size=datastar[,3];hab=datastar[,2]
prob.seen.glm<-glm(y~hab+size,family=binomial(logit))

###find bootstrap corrected point estimate
b.duck2<-b.data
b.a<-cbind(rep(1,length(b.data[,1])),b.duck2$habitat,log(b.duck2$ducks))

b.ct.bias<-1/(b.a%*%prop.ct$coeff)

b.DUCKS.adj.ct<-b.ct.bias*b.duck2$ducks

b.b<-cbind(rep(1,length(b.data[,1])),b.duck2$habitat,b.DUCKS.adj.ct)
b.eta.adj<-b.b%*%prob.seen.glm$coef
b.vis.bias=1/(1+exp(-b.eta.adj))
for (i in 1:length(b.vis.bias)){

```

```

if (b.vis.bias[i]<(1/40)) b.vis.bias[i]=1/40
}

b.DUCKS.adj.ct.vis<-b.DUCKS.adj.ct/b.vis.bias

b.duck.corrected<-b.DUCKS.adj.ct.vis*b.duck2$n.w
b.tot.corrected=sum(b.duck.corrected)
b.tot.corrected

### find set of correction factors for original group sizes
ctbias<-X.fo.l%*%prop.ct$coeff
ctbias[1]=1;ctbias[n.gs+1]=1
gs.adj2=gs/ctbias
X.f<-cbind(rep(1,n.gs),rep(0,n.gs))
X.o<-cbind(rep(1,n.gs),rep(1,n.gs))
X.fo.1<-rbind(X.f,X.o)
X.fo<-cbind(X.fo.1,gs.adj2)
eta.visbias<-X.fo%*%prob.seen.glm$coef
visbias<-1/(1+exp(-eta.visbias))
for (i in 1:length(visbias)){
  if (visbias[i]<(1/40)) visbias[i]=1/40
}

cor.factors<-1/(ctbias*visbias)
max(cor.factors)
return(c(b.tot.corrected,cor.factors))

```

```
}
```

```
#####
```

```
#####
```

```
## Find variance in strata i      #
```

```
## Using Equation 2.5            #
```

```
#####
```

```
var.strata.i<-function(V,ni,cov.mat){
```

```
n=rep(ni,length(V[,1]))
```

```
var.test1<-cbind(V$Transect,V$habitat,V$ducks,n,V$ni.psi,
```

```
                V$p_hat,V$mu.a_hat_mean,V$n.w,V$cov.mat.pos)
```

```
####get a list of the transects#####
```

```
tran1.test<-unique(var.test1[,1])
```

```
tran1.len<-ni
```

```
###count the number of groups in a transect###
```

```
### first column is the transect, second is the number of groups
```

```
cot=rep(0,ni)
```

```
for (i in 1:ni){ cot[i]=sum(V$Transect==tran1.test[i])}
```

```
####matrix of sample size and psi i's
```

```
eee<-matrix(cbind(var.test1[,1],var.test1[,4],var.test1[,5]),ncol=3)
```

```
eef<-(lapply(1:tran1.len,function(x){eeg<-
```

```
subset(eee,eee[,1]==tran1.test[x]))}))
```

```

ee1<-sapply(eef,"[,1,2);ee2<-sapply(eef,"[,1,3)
# the sapply function takes a list, and grabs the first element
# of the indicated column in the list to get the transect information
tran.info<-cbind(ee1,ee2)

##### first and second summation of variance estimate #####

var.comp.1=sum(((1-(var.test1[,5]/var.test1[,4]))/(var.test1[,5]^2))*
               var.test1[,3]^2*var.test1[,7]^2*var.test1[,6])

dd<-var.test1[,3]*var.test1[,7]
ee<-matrix(cbind(var.test1[,1],dd),ncol=2)
ff<-unlist(lapply(1:tran1.len,function(x)
               {gg<-subset(ee,ee[,1]==tran1.test[x]);
                kk<-matrix(gg,ncol=2);
                hh<-matrix(cbind(rep(kk[,2],(length(kk[,2])))),
                           nrow=length(kk[,2]),ncol=length(kk[,2])));
                ii<-sum(hh%*%kk[,2]-(kk[,2]*kk[,2]))}))
qij2.terms<-(1-ee2/ee1)/(ee2^2)
var.comp.2=t(qij2.terms)%*%ff

##### third summation of variance estimate ###
aaa<-unique(var.test1[,1])
ccc<-unlist(lapply(1:length(aaa),
                  function(x){bbb<-subset(var.test1,var.test1[,1]==aaa[x]);
                  sum(apply(matrix(bbb[,c(3,7,8)],ncol=3),1,prod))}))

```

```

ddd<-matrix(cbind(rep(ccc,(length(ccc))))),nrow=length(ccc),ncol=length(ccc))
eee<-ddd%*%ccc-(ccc*ccc)
var.comp.3=sum(-1/(tran.info[,1]-1)*eee)

##### fourth summation of variance estimate #####
fff<-unlist(lapply(1:length(aaa),function(x)
{
  ggg<-subset(var.test1,var.test1[,1]==aaa[x]);
  hhh<-matrix(ggg,ncol=9);
  sum(hhh[,3]^2*hhh[,7]^2*(1-hhh[,6]))}))

qij4.terms<-(1+(tran.info[,1]-1)*(tran.info[,2]/tran.info[,1]))
/(tran.info[,2]^2)
var.comp.4<-t(qij4.terms)%*%fff

##### fifth summation of variance estimate #####
b=0;pos=1;p=1
for (i in 1:(tran1.len-1)){
  t=var.test1[pos,1]
  while (var.test1[pos,1]==t){
    for (j in (p+cot[i]):length(var.test1[,1])){
      cov.el=cov.mat[var.test1[pos,9],var.test1[j,9]]
      c=cov.el*var.test1[pos,3]*var.test1[j,3]/(var.test1[pos,5]*var.test1[j,5])
      b=b+c
    }
    pos=pos+1
  }
}

```



```

    p=p+cot[i]
  }
var.comp.5=2*b

##### sixth summation of variance estimate #####
diag.el<-diag(cov.mat)
qij6.terms<-((1-tran.info[,2]/tran.info[,1])/(tran.info[,2]^2))
            +(1/(tran.info[,2]))
mmm<-unlist(lapply(1:length(aaa),function(x)
              {ggg<-subset(var.test1,var.test1[,1]==aaa[x]);
                hhh<-matrix(ggg,ncol=9);s1<-hhh[,9];
                sum(hhh[,3]^2*diag.el[s1]))}))
var.comp.6=t(qij6.terms)%*%mmm

##### seventh summation of variance estimate #####
qij7.terms<-2*qij6.terms
pos=1;p=1;
y=rep(0,tran1.len)
for (i in 1:tran1.len){
  ending=pos+cot[i]-1
  e<-0
  for (j in pos:(ending-1)) {
    for (k in (j+1):ending){
      if (cot[i]>1){
        s1<-var.test1[j,9];s2<-var.test1[k,9]
        cov.el=cov.mat[s1,s2]
      }
    }
  }
  y[i]=e
  pos=pos+cot[i]
}

```

```

        e=var.test1[j,3]*var.test1[k,3]*cov.el
y[i]=y[i]+e
}
else {
e=0
y[i]=y[i]+e
}
}
pos=pos+1
}
p=p+cot[i]
pos=p
}
var.comp.7=t(qij7.terms)%*%y

sum.var.comps=var.comp.1+var.comp.2+var.comp.3+
                var.comp.4+var.comp.5+var.comp.6+var.comp.7
}

#####
## Get covariance between two strata      #
## from Equation 2.5                      #
#####
cov.fun<-function(st1,st2,tran1,tran2,n1,n2,count1,count2,cov.mat){
aaaa<-lapply(1:n1,function(x){subset(st1,st1$Transect==tran1[x])})
bbbb<-lapply(1:n2,function(x){subset(st2,st2$Transect==tran2[x])})

```

```

cov.sum=0
for(j in 1:n1){
  cccc<-matrix(unlist(aaaa[j]),nrow=count1[j],ncol=10)
  for(y in 1:n2){
    dddd<-matrix(unlist(bbbb[y]),nrow=count2[y],ncol=10)
    a=0
    for(k in 1:count1[j]){
      for(z in 1:count2[y]){
        s1=cccc[k,10];s2=dddd[z,10]
        a=a+cccc[k,5]*dddd[z,5]*cccc[k,6]*dddd[z,6]*cov.mat[s1,s2]
      }
    }
    cov.sum=cov.sum+a
  }
}
cov.sum=2*cov.sum
}

```

```

#####
## function to get perfect sightability    #
## estimates from survey package          #
#####

```

```

t.hat.per<-function(data.sim){

data.sim.H<-subset(data.sim,data.sim$Strata=="H")

```

```

tranH<-sort(unique(data.sim.H$Transect))
freqH<-counter(data.sim.H$Transect)
H.tran.info=cbind(tranH,freqH)

data.sim.NE<-subset(data.sim,data.sim$Strata=="NE")
tranNE=sort(unique(data.sim.NE$Transect))
freqNE<-counter(data.sim.NE$Transect)
NE.tran.info=cbind(tranNE,freqNE)

data.sim.NW<-subset(data.sim,data.sim$Strata=="NW")
tranNW=sort(unique(data.sim.NW$Transect))
freqNW<-counter(data.sim.NW$Transect)
NW.tran.info=cbind(tranNW,freqNW)

data.sim.SE<-subset(data.sim,data.sim$Strata=="SE")
tranSE=sort(unique(data.sim.SE$Transect))
freqSE<-counter(data.sim.SE$Transect)
SE.tran.info=cbind(tranSE,freqSE)

data.sim.SW<-subset(data.sim,data.sim$Strata=="SW")
tranSW=sort(unique(data.sim.SW$Transect))
freqSW<-counter(data.sim.SW$Transect)
SW.tran.info=cbind(tranSW,freqSW)

## sum up number of ducks in each transect
hhh<-unlist(lapply(1:length(tranH),function(x){

```

```

aaa<-subset(data.sim.H,data.sim.H$Transect==tranH[x]);
sum(aaa$ducks)
}))

```

```

nene<-unlist(lapply(1:length(tranNE),function(x){
aaa<-subset(data.sim.NE,data.sim.NE$Transect==tranNE[x]);
sum(aaa$ducks)
}))

```

```

nwnw<-unlist(lapply(1:length(tranNW),function(x){
aaa<-subset(data.sim.NW,data.sim.NW$Transect==tranNW[x]);
sum(aaa$ducks)
}))

```

```

sese<-unlist(lapply(1:length(tranSE),function(x){
aaa<-subset(data.sim.SE,data.sim.SE$Transect==tranSE[x]);
sum(aaa$ducks)
}))

```

```

swsw<-unlist(lapply(1:length(tranSW),function(x){
aaa<-subset(data.sim.SW,data.sim.SW$Transect==tranSW[x]);
sum(aaa$ducks)
}))

```

```

numducks=c(hhh,nene,nwnw,sese,swsw)
data.unco<-NULL

```

```

for (i in 1:n1){
pos=which(data.sim.H$Transect==H.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim.H[pos[1],])
}

for (i in 1:n2){
pos=which(data.sim.NE$Transect==NE.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim.NE[pos[1],])
}

for (i in 1:n3){
pos=which(data.sim.NW$Transect==NW.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim.NW[pos[1],])
}

for (i in 1:n4){
pos=which(data.sim.SE$Transect==SE.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim.SE[pos[1],])
}

for (i in 1:n5){
pos=which(data.sim.SW$Transect==SW.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim.SW[pos[1],])
}

```

```

data.unco$ducks=numducks

wts=data.unco$w

sd.perfect=svydesign(id=~1,strata=~Strata,fpc=NULL,
                    data=data.unco,weights=wts)

t_hat.perfect<-svytotal(~ducks,sd.perfect)
return(t_hat.perfect)
}

#####
## function to get uncorrected estimates  #
## for imperfect sightability            #
## from survey package                   #
#####

t.hat.imper<-function(data.sim1){
data.sim1.H<-subset(data.sim1,data.sim1$Strata=="H")
tranH=sort(unique(data.sim1.H$Transect))
freqH<-counter(data.sim1.H$Transect)
H.tran.info=cbind(tranH,freqH)

data.sim1.NE<-subset(data.sim1,data.sim1$Strata=="NE")
tranNE=sort(unique(data.sim1.NE$Transect))
freqNE<-counter(data.sim1.NE$Transect)
NE.tran.info=cbind(tranNE,freqNE)

```

```

data.sim1.NW<-subset(data.sim1,data.sim1$Strata=="NW")
tranNW=sort(unique(data.sim1.NW$Transect))
freqNW<-counter(data.sim1.NW$Transect)
NW.tran.info=cbind(tranNW,freqNW)

data.sim1.SE<-subset(data.sim1,data.sim1$Strata=="SE")
tranSE=sort(unique(data.sim1.SE$Transect))
freqSE<-counter(data.sim1.SE$Transect)
SE.tran.info=cbind(tranSE,freqSE)

data.sim1.SW<-subset(data.sim1,data.sim1$Strata=="SW")
tranSW=sort(unique(data.sim1.SW$Transect))
freqSW<-counter(data.sim1.SW$Transect)
SW.tran.info=cbind(tranSW,freqSW)

## sum up number of ducks in each transect
hhh<-unlist(lapply(1:length(tranH),function(x){
aaa<-subset(data.sim1.H,data.sim1.H$Transect==tranH[x]);
sum(aaa$ducks)
}))

nene<-unlist(lapply(1:length(tranNE),function(x){
aaa<-subset(data.sim1.NE,data.sim1.NE$Transect==tranNE[x]);
sum(aaa$ducks)

```



```
)))
```

```
nwnw<-unlist(lapply(1:length(tranNW),function(x){  
  aaa<-subset(data.sim1.NW,data.sim1.NW$Transect==tranNW[x]);  
  sum(aaa$ducks)  
}))
```

```
sese<-unlist(lapply(1:length(tranSE),function(x){  
  aaa<-subset(data.sim1.SE,data.sim1.SE$Transect==tranSE[x]);  
  sum(aaa$ducks)  
}))
```

```
swws<-unlist(lapply(1:length(tranSW),function(x){  
  aaa<-subset(data.sim1.SW,data.sim1.SW$Transect==tranSW[x]);  
  sum(aaa$ducks)  
}))
```

```
numducks=c(hhh,nene,nwnw,sese,swws)
```

```
data.unco<-NULL
```

```
for (i in 1:n1){  
  pos=which(data.sim1.H==H.tran.info[i,1])  
  data.unco<-rbind(data.unco,data.sim1.H[pos[1],])  
}
```

```

for (i in 1:n2){
pos=which(data.sim1.NE==NE.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim1.NE[pos[1],])
}

```

```

for (i in 1:n3){
pos=which(data.sim1.NW==NW.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim1.NW[pos[1],])
}

```

```

for (i in 1:n4){
pos=which(data.sim1.SE==SE.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim1.SE[pos[1],])
}

```

```

for (i in 1:n5){
pos=which(data.sim1.SW==SW.tran.info[i,1])
data.unco<-rbind(data.unco,data.sim1.SW[pos[1],])
}

```

```

data.unco$ducks=numducks

```

```

##t_hat1=sum(data.unco$ducks*data.unco$n.w)

```

```

wts=data.unco$n.w

```

```

sd.imperfect=svydesign(id=~1,strata=~Strata,fpc=NULL,
                      data=data.unco,weights=wts)

t_hat.imperfect<-svytotal(~ducks,sd.imperfect)
return(t_hat.imperfect)
}

#####
## FUNCTION TO DO ALL STEPS OF SIMULATION #
#####

mc.fun<-function(ind){

#1. draw sample
stran1<-sort(sample(art.tran1,n1,replace=TRUE))
stran2<-sort(sample(art.tran2,n2,replace=TRUE))
stran3<-sort(sample(art.tran3,n3,replace=TRUE))
stran4<-sort(sample(art.tran4,n4,replace=TRUE))
stran5<-sort(sample(art.tran5,n5,replace=TRUE))

s.art.pop1<-NULL
for (i in 1:n1){
s.art.pop1<-rbind(s.art.pop1,art.pop1[art.pop1[,1]==stran1[i],])
}

w1=tot.tran.H/(s.art.pop1$Length*n1)

```

```

a11=unique(s.art.pop1$Transect)
a12=counter(s.art.pop1$Transect)
a1=cbind(a11,a12)
for (i in 1:length(a1[,1])) {
  bb=which(s.art.pop1$Transect==a1[i,1])
  if (a1[i,2]!=s.art.pop1$NumGroups[bb[1]]) {
    dup=a1[i,2]/s.art.pop1$NumGroups[bb[1]]
    renum=bb[1]+s.art.pop1$NumGroups[bb[1]]
    for(j in 1:(dup-1)){
      s.art.pop1$Transect[renum:(renum+
s.art.pop1$NumGroups[bb[1]]-1)]=s.art.pop1$Transect
[renum:(renum+s.art.pop1$NumGroups[bb[1]]-1)]+(1000*j)
renum=renum+s.art.pop1$NumGroups[bb[1]]
    }
  }
}

s.art.pop2<-NULL
for (i in 1:n2){
  s.art.pop2<-rbind(s.art.pop2,art.pop2[art.pop2[,1]==stran2[i],])
}

w2=tot.tran.NE/(s.art.pop2$Length*n2)
a21=unique(s.art.pop2$Transect)
a22=counter(s.art.pop2$Transect)
a2=cbind(a21,a22)
for (i in 1:length(a2[,1])) {

```

```

bb=which(s.art.pop2$Transect==a2[i,1])
if (a2[i,2]!=s.art.pop2$NumGroups[bb[1]]) {
  dup=a2[i,2]/s.art.pop2$NumGroups[bb[1]]
  renum=bb[1]+s.art.pop2$NumGroups[bb[1]]
  for(j in 1:(dup-1)){
    s.art.pop2$Transect[renum:(renum
+s.art.pop2$NumGroups[bb[1]]-1)]=s.art.pop2$Transect
[renum:(renum+s.art.pop2$NumGroups[bb[1]]-1)]+(1000*j)
    renum=renum+s.art.pop2$NumGroups[bb[1]]
  }
}
}

s.art.pop3<-NULL
for (i in 1:n3){
  s.art.pop3<-rbind(s.art.pop3,art.pop3[art.pop3[,1]==stran3[i],])
}

w3=tot.tran.NW/(s.art.pop3$Length*n3)
a31=unique(s.art.pop3$Transect)
a32=counter(s.art.pop3$Transect)
a3=cbind(a31,a32)
for (i in 1:length(a3[,1])) {
  bb=which(s.art.pop3$Transect==a3[i,1])
  if (a3[i,2]!=s.art.pop3$NumGroups[bb[1]]) {
    dup=a3[i,2]/s.art.pop3$NumGroups[bb[1]]
    renum=bb[1]+s.art.pop3$NumGroups[bb[1]]

```

```

for(j in 1:(dup-1)){
s.art.pop3$Transect[renum:(renum+
s.art.pop3$NumGroups[bb[1]]-1)]=s.art.pop3$Transect
[renum:(renum+s.art.pop3$NumGroups[bb[1]]-1)]+(1000*j)
renum=renum+s.art.pop3$NumGroups[bb[1]]
}
}
}

s.art.pop4<-NULL
for (i in 1:n4){
s.art.pop4<-rbind(s.art.pop4,art.pop4[art.pop4[,1]==stran4[i],])
}

w4=tot.tran.SE/(s.art.pop4$Length*n4)
a41=unique(s.art.pop4$Transect)
a42=counter(s.art.pop4$Transect)
a4=cbind(a41,a42)
for (i in 1:length(a4[,1])) {
bb=which(s.art.pop4$Transect==a4[i,1])
if (a4[i,2]!=s.art.pop4$NumGroups[bb[1]]) {
dup=a4[i,2]/s.art.pop4$NumGroups[bb[1]]
renum=bb[1]+s.art.pop4$NumGroups[bb[1]]
for(j in 1:(dup-1)){
s.art.pop4$Transect[renum:(renum+
s.art.pop4$NumGroups[bb[1]]-1)]=s.art.pop4$Transect
[renum:(renum+s.art.pop4$NumGroups[bb[1]]-1)]+(1000*j)

```

```

renum=renum+s.art.pop4$NumGroups[bb[1]]
}
}
}

s.art.pop5<-NULL
for (i in 1:n5){
s.art.pop5<-rbind(s.art.pop5,art.pop5[art.pop5[,1]==stran5[i],])
}

w5=tot.tran.SW/(s.art.pop5$Length*n5)
a51=unique(s.art.pop5$Transect)
a52=counter(s.art.pop5$Transect)
a5=cbind(a51,a52)
for (i in 1:length(a5[,1])) {
bb=which(s.art.pop5$Transect==a5[i,1])
if (a5[i,2]!=s.art.pop5$NumGroups[bb[1]]) {
dup=a5[i,2]/s.art.pop5$NumGroups[bb[1]]
renum=bb[1]+s.art.pop5$NumGroups[bb[1]]
for(j in 1:(dup-1)){
s.art.pop5$Transect[renum:(renum+
s.art.pop5$NumGroups[bb[1]]-1)]=s.art.pop5$Transect
[renum:(renum+s.art.pop5$NumGroups[bb[1]]-1)]+(1000*j)
renum=renum+s.art.pop5$NumGroups[bb[1]]
}
}
}

```

```
w=c(w1,w2,w3,w4,w5)
```

```
s.art.pop<-rbind(s.art.pop1,s.art.pop2,s.art.pop3,s.art.pop4,s.art.pop5)
```

```
s.art.pop<-cbind(s.art.pop,w)
```

```
#2. calculate perfect sightability t-hat
```

```
t.hat.1<-t.hat.per(s.art.pop)
```

```
#3. perform flyover of ducks
```

```
len=length(s.art.pop$ducks)
```

```
noise=rnorm(len,mean=0,sd=.01)
```

```
c1=rep(1,len)
```

```
c3=log(s.art.pop$ducks)
```

```
Y=cbind(c1,s.art.pop$habitat,c3)
```

```
YL=cbind(c1,s.art.pop$habitat,s.art.pop$ducks)
```

```
prop.ctd=Y%*%B+noise
```

```
# this corrects when the group size is 0 you count all of it
```

```
for (i in 1:len){
```

```
if (prop.ctd[i]>1) prop.ctd[i]=1
```

```
}
```

```
eta.seen=YL%*%BL
```

```
prob.seen=1/(1+exp(-eta.seen))
```



```

seen.sim<-unlist(lapply(1:len,function(x){rbinom(1,1,prob.seen[x])}))
count.sim<-round(s.art.pop$ducks*prop.ctd,digits=0)

s.fly=cbind(s.art.pop,seen.sim,count.sim)
d.fly=subset(s.fly,s.fly$seen.sim==1)

s.fly.H=subset(s.fly,s.fly$Strata=="H")
s.fly.NE=subset(s.fly,s.fly$Strata=="NE")
s.fly.NW=subset(s.fly,s.fly$Strata=="NW")
s.fly.SE=subset(s.fly,s.fly$Strata=="SE")
s.fly.SW=subset(s.fly,s.fly$Strata=="SW")

d.fly.H=subset(d.fly,d.fly$Strata=="H")
d.fly.NE=subset(d.fly,d.fly$Strata=="NE")
d.fly.NW=subset(d.fly,d.fly$Strata=="NW")
d.fly.SE=subset(d.fly,d.fly$Strata=="SE")
d.fly.SW=subset(d.fly,d.fly$Strata=="SW")

## Make sure if a transect was selected
## But no groups were seen that
## It is still included with a count of zero
s.c.H=unique(s.fly.H$Transect)
d.c.H=unique(d.fly.H$Transect)
match.H=intersect(s.c.H,d.c.H)
all.H=union(s.c.H,d.c.H)

```

```
non.matched.H<-all.H[!all.H %in% match.H]
```

```
s.c.NE=unique(s.fly.NE$Transect)
```

```
d.c.NE=unique(d.fly.NE$Transect)
```

```
match.NE=intersect(s.c.NE,d.c.NE);
```

```
all.NE=union(s.c.NE,d.c.NE)
```

```
non.matched.NE<-all.NE[!all.NE %in% match.NE]
```

```
s.c.NW=unique(s.fly.NW$Transect)
```

```
d.c.NW=unique(d.fly.NW$Transect)
```

```
match.NW=intersect(s.c.NW,d.c.NW);
```

```
all.NW=union(s.c.NW,d.c.NW)
```

```
non.matched.NW<-all.NW[!all.NW %in% match.NW]
```

```
s.c.SE=unique(s.fly.SE$Transect)
```

```
d.c.SE=unique(d.fly.SE$Transect)
```

```
match.SE=intersect(s.c.SE,d.c.SE);
```

```
all.SE=union(s.c.SE,d.c.SE)
```

```
non.matched.SE<-all.SE[!all.SE %in% match.SE]
```

```
s.c.SW=unique(s.fly.SW$Transect)
```

```
d.c.SW=unique(d.fly.SW$Transect)
```

```
match.SW=intersect(s.c.SW,d.c.SW);
```

```
all.SW=union(s.c.SW,d.c.SW)
```

```
non.matched.SW<-all.SW[!all.SW %in% match.SW]
```

```

    if(length(non.matched.H>=1)){
for (i in 1:length(non.matched.H)){
k=which(s.fly.H$Transect==non.matched.H[i])
d.fly.H=rbind(d.fly.H,s.fly.H[(k[1]),])
newrow=length(d.fly.H$Transect)
d.fly.H$count.sim[newrow]=0
}
}

    if(length(non.matched.NE>=1)){
for (i in 1:length(non.matched.NE)){
k=which(s.fly.NE$Transect==non.matched.NE[i])
d.fly.NE=rbind(d.fly.NE,s.fly.NE[(k[1]),])
newrow=length(d.fly.NE$Transect)
d.fly.NE$count.sim[newrow]=0
}
}

    if(length(non.matched.NW>=1)){
for (i in 1:length(non.matched.NW)){
k=which(s.fly.NW$Transect==non.matched.NW[i])
d.fly.NW=rbind(d.fly.NW,s.fly.NW[(k[1]),])
newrow=length(d.fly.NW$Transect)
d.fly.NW$count.sim[newrow]=0
}
}

```

```

if(length(non.matched.SE>=1)){
  for (i in 1:length(non.matched.SE)){
    k=which(s.fly.SE$Transect==non.matched.SE[i])
    d.fly.SE=rbind(d.fly.SE,s.fly.SE[(k[1]),])
    newrow=length(d.fly.SE$Transect)
    d.fly.SE$count.sim[newrow]=0
  }
}

if(length(non.matched.SW>=1)){
  for (i in 1:length(non.matched.SW)){
    k=which(s.fly.SW$Transect==non.matched.SW[i])
    d.fly.SW=rbind(d.fly.SW,s.fly.SW[(k[1]),])
    newrow=length(d.fly.SW$Transect)
    d.fly.SW$count.sim[newrow]=0
  }
}

d.fly.adj=rbind(d.fly.H,d.fly.NE,d.fly.NW,d.fly.SE,d.fly.SW)
### Create new flyover dataframe ###
data.simulate=data.frame(d.fly.adj$Transect,d.fly.adj$Strata,
  d.fly.adj$Length,d.fly.adj$habitat,d.fly.adj$count.sim,d.fly.adj$w,
  stringsAsFactors=FALSE)
colnames(data.simulate)<-c("Transect","Strata",

```

```
"Length","habitat","ducks","n.w")
```

```
#4. perform flyover of decoys
```

```
data.vis.1<-vis
```

```
X<-matrix(cbind(rep(1,N.pop),decoy[,2],vis[,7]),nrow=N.pop,ncol=3)
```

```
pi.ijk<-X%*%B
```

```
noise<-rnorm(N.pop,mean=0,sd=.01)
```

```
pi.ijk.n<-pi.ijk+noise
```

```
X.logistic<-matrix(cbind(rep(1,N.pop),decoy[,2],decoy[,3]),  
                    nrow=N.pop,ncol=3)
```

```
eta<-X.logistic%*%BL
```

```
p.ijk=1/((exp(-eta))+1)
```

```
seen.sim<-unlist(lapply(1:N.pop,function(x){rbinom(1,1,p.ijk[x])}))
```

```
count.sim<-round(decoy[,3]*pi.ijk.n,digits=0)
```

```
prop.sim<-count.sim/decoy[,3]
```

```
decoy.sim<-cbind(decoy,count.sim,prop.sim,seen.sim,vis[,7])
```

```
colnames(decoy.sim)<-c("obs","habitat","size",  
                      "count.sim","prop.sim","seen.sim","lsize")
```

```
data.vis<-decoy.sim
```

```
#5. calculated uncorrected t-hat
```

```
t.hat.2<-t.hat.imper(data.simulate)
```

```
#6. bootstrap both sides t-hat
```

```

data<-data.simulate

data1<-data[data[,2]==strata[1],]
data2<-data[data[,2]==strata[2],]
data3<-data[data[,2]==strata[3],]
data4<-data[data[,2]==strata[4],]
data5<-data[data[,2]==strata[5],]

tran1<-sort(unique(data1[,1]))
tran2<-sort(unique(data2[,1]))
tran3<-sort(unique(data3[,1]))
tran4<-sort(unique(data4[,1]))
tran5<-sort(unique(data5[,1]))

count1=counter(data1$Transect)
count2=counter(data2$Transect)
count3=counter(data3$Transect)
count4=counter(data4$Transect)
count5=counter(data5$Transect)

group.size=factor(data$ducks)
gs=as.numeric(levels(group.size))
n.gs=length(gs)

cov.mat.pos=rep(0,length(data$habitat))
for (i in 1:length(cov.mat.pos)){

```

```

cov.mat.pos[i]=which(gs==data$ducks[i])
if (data$habitat[i]==1) cov.mat.pos[i]=cov.mat.pos[i]+n.gs
}

ni.psi<-1/data$n.w

X.f<-cbind(rep(1,n.gs),rep(0,n.gs),gs)
X.o<-cbind(rep(1,n.gs),rep(1,n.gs),gs)
X.logistic<-rbind(X.f,X.o)
X.f.l<-cbind(rep(1,n.gs),rep(0,n.gs),log(gs))
X.o.l<-cbind(rep(1,n.gs),rep(1,n.gs),log(gs))
X.linear<-rbind(X.f.l,X.o.l)

#####
## Visibility Data Point Estimates      #
#####

Data.seen<-subset(data.vis, data.vis[,6]==1)
prop.ct<-lm(Data.seen$prop.sim~Data.seen$habitat+Data.seen$size)
y=data.vis$seen.sim;size=data.vis$size;hab=data.vis$habitat
prob.seen.glm<-glm(y~hab+size,family=binomial(logit))

#####
## original point estimate from data    #
#####

duck2<-data

```

```

a<-cbind(rep(1,length(data[,1])),data$habitat,log(duck2$ducks))

ct.bias<-1/(a%*%prop.ct$coeff)
for (i in 1:length(ct.bias)){
  if (ct.bias[i]==0) ct.bias[i]=1
}
#cbind(ct.bias,duck2$ducks)

DUCKS.adj.ct<-ct.bias*duck2$ducks
#cbind(duck2$ducks,DUCKS.adj.ct)

b<-cbind(rep(1,length(data[,1])),data$habitat,DUCKS.adj.ct)
eta.adj<-b%*%prob.seen.glm$coef
vis.bias=exp(eta.adj)/(1+exp(eta.adj));p_hat=vis.bias;
#cbind(duck2$ducks,vis.bias)

DUCKS.adj.ct.vis<-DUCKS.adj.ct/vis.bias

duck.corrected<-DUCKS.adj.ct.vis*duck2$n.w
t_hat.adj=sum(duck.corrected)

ssize=1000
samptstar<-(sapply(1:ssize,boot.duck4,M=data,
                  data.vis=decoy.sim,X.fo.l=X.linear,n=n.gs,g=gs,
                  tran1=tran1,tran2=tran2,tran3=tran3,tran4=tran4,tran5=tran5))
t.boot=samptstar[1,]

```



```

m.boot=mean(t.boot)

sd.boot=sd(t.boot)


#7. Use correction factors for
#   Bootstrap Visibilty Experiment Only
#   Method

vis.exp.samps=t(samptstar[2:length(samptstar[,1]),])
cov.mat<-var(vis.exp.samps)
mean.b=colMeans(vis.exp.samps)
mu.a_hat_mean<-rep(mean.b[1],length(duck2$habitat))
for (i in 1:length(duck2$habitat)){
  pos=cov.mat.pos[i]
  mu.a_hat_mean[i]=mean.b[pos]
}

var_comp<-cbind(duck2,ni.psi,p_hat,mu.a_hat_mean,cov.mat.pos)


data.1<-subset(var_comp,var_comp$Strata=="H")
var.test<-data.1
var.strata.1<-var.strata.i(var.test,n1,cov.mat)


data.2<-subset(var_comp,var_comp$Strata=="NE")
var.test<-data.2
var.strata.2<-var.strata.i(var.test,n2,cov.mat)


data.3<-subset(var_comp,var_comp$Strata=="NW")
var.test<-data.3

```

```

var.strata.3<-var.strata.i(var.test,n3,cov.mat)

data.4<-subset(var_comp,var_comp$Strata=="SE")
var.test<-data.4
var.strata.4<-var.strata.i(var.test,n4,cov.mat)

data.5<-subset(var_comp,var_comp$Strata=="SW")
var.test<-data.5
var.strata.5<-var.strata.i(var.test,n5,cov.mat)

var.strata<-var.strata.1+var.strata.2+var.strata.3+
            var.strata.4+var.strata.5

co12<-cov.fun(data.1,data.2,tran1,tran2,n1,n2,count1,count2,cov.mat)
co13<-cov.fun(data.1,data.3,tran1,tran3,n1,n3,count1,count3,cov.mat)
co14<-cov.fun(data.1,data.4,tran1,tran4,n1,n4,count1,count4,cov.mat)
co15<-cov.fun(data.1,data.5,tran1,tran5,n1,n5,count1,count5,cov.mat)

co23<-cov.fun(data.2,data.3,tran2,tran3,n2,n3,count2,count3,cov.mat)
co24<-cov.fun(data.2,data.4,tran2,tran4,n2,n4,count2,count4,cov.mat)
co25<-cov.fun(data.2,data.5,tran2,tran5,n2,n5,count2,count5,cov.mat)

co34<-cov.fun(data.3,data.4,tran3,tran4,n3,n4,count3,count4,cov.mat)
co35<-cov.fun(data.3,data.5,tran3,tran5,n3,n5,count3,count5,cov.mat)

co45<-cov.fun(data.4,data.5,tran4,tran5,n4,n5,count4,count5,cov.mat)

```

```

cov.terms=co12+co13+co14+co15+co23+co24+co25+co34+co35+co45

var.dir.calc<-cov.terms+var.strata
sd.dir.calc<-sqrt(var.dir.calc)
sd.boot
sd.boot-sd.dir.calc
t.hat.3<-c(t_hat.adj,sd.boot)
t.hat.4<-c(t_hat.adj,sd.dir.calc)

#8.  return vector of t-hats and st. err
return(c(t.hat.1,SE(t.hat.1),t.hat.2,SE(t.hat.2),t.hat.3,t.hat.4))
}

#####

## Output

#####

REP=1024

out<-mclapply(1:REP, mc.fun,mccores=8)
mat<-matrix(unlist(out),ncol=8,byrow=TRUE)

#save results of mat to file

```

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