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A Spatiotemporal Bayesian Model for Population Analysis

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by

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A Spatiotemporal Bayesian Model for Population Analysis by Mohamed Jaber

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Abstract

Title:

A Spatiotemporal Bayesian Model for Population Analysis

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Spatiotemporal population analysis based on incomplete, redundant, and unidentified observations is critically important, yet it is a very challenging problem. Different approaches have been proposed and several methods have been implemented to address this problem. Capture-recapture methods have been widely used and have become the standard sampling and analytical framework for ecological statistics with applications to population analysis. Despite the fact that capture-recapture methods have been commonly used, these methods do not consider the spatial structure of the population. Moreover, conventional capture-recapture methods do not use any explicit spatial information with regard to the spatial nature of the sampling and spatial distribution of individual encounters. Recently a spatial capture-recapture method has been introduced by Royle and Chandler to link observed encounter histories of individuals to spatial population ecology and study the population using new technologies such as remote cameras and acoustic sampling. The first objective of this study was investigating feral hog population in the Kennedy Space Center (KSC) which is part of Merritt Island National Wildlife Refuge in Titusville, about 60 miles east of city of Orlando in Brevard and Volusia Counties in Florida. Due to the size of KSC and the limited resources, two study sites within KSC were chosen for investigation, monitoring, and data collection. These sites were: 1. Happy Creek (HC); and 2. Tel-4. We estimated the hog population using the spatial capture model introduced by Royle and Chandler. The estimated hog population for HC was between 55 and 108 hogs. The estimated hog population for Tel-4 was between 61 and 114 hogs. To estimate the hog population in KSC, we combined the results obtained from two study sites within KSC. We calculated and assigned specific weights to the estimated hog populations in HC and Tel-4 based on their percentage areas in comparison with the entire area of KSC. As a result, the calculated weights were 0.73 and 0.27 for HC and Tel-4 respectively. The estimated hog population N using the proposed weighted averaging was between $3,058$ to $5,862$ hogs. Although the spatial capture method is promising, the estimated population size is not robust and suffers from spatial complexity. Therefore, the second objective of this research was to perform a comprehensive study of the parameters of the spatial capture model and their impacts on the estimated population size. The third goal was focused on identification of parameters with significant impact on the estimated population size and to develop informative priors for the identified parameters. The fourth objective was to improve the spatial capture model by integrating camera spatial locations and regularizing spatiotemporal parameters for the estimation of the population size.

Table of Contents

List of Figures

List of Tables

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Dedication

This thesis work is dedicated to my wife, Aomaima, who has been a constant source of support and encouragement to pursue my doctoral degree and life. I am genuinely thankful for having you in my life. This work is also dedicated to my parents, Mubarka and Shaban, who have always loved me unconditionally and whose good examples have taught me to work hard for the things that I aspire to achieve. To my children Asil and Areen who have been affected in every way possible by this quest. To my beloved brothers and sisters, to all my family who are the symbol of love and giving, to my friends who encourage and support me. Thank You All! My love for you all, can never be quantified. Allah Bless You

Chapter 1

Introduction

Population analysis based on spatial sampling is an emerging field of research due to its broad range of applications. Some important applications are to preserve the population of endangered species and control the population of invasive species which are not native to the host ecosystem. The first step to control the population is estimating the population size. Several methods have been developed to estimate the abundance of animals [1–3].

A popular approach to estimate the abundance of animals is by counting the individuals or their signs. In this way, the estimated number of individuals per unit of the area can be obtained. This estimate is proportionate to the whole population and can be used to estimate the population size using the population area.

Capture-recapture methods have been widely used and have become the standard sampling and analytical framework for ecological statistics with applications to population analysis. In this framework, a series of samples are taken from the animal population under study. The first time that an animal is captured, it is tagged and released. The second sample will likely contain some tagged animals and some without a tag. All animals in the second sample are recorded and released after tagging those without a tag. At the end of survey, each animal has a unique capture history. For instance, a history of five samples ”10010” for a specific animal means that it has been caught in the first and fourth sampling occasions. The intuition behind the capture-mark-recapture technique is that if we mark a significant number of individuals in a population and release them, the fraction that we recapture in the second sample can be used to extrapolate the size of the entire population. Three pieces of information are needed to estimate the population size using this approach. The number of individuals that are marked in the first sampling occasion M, the number of individuals that were caught in the second sampling occasion, and the number of individuals that were captured in the first sample and recaptured in the second sample R [3].

These methods depend on physical capture of individuals. It means, we need to capture the individuals physically to collect the encounter history. Nowadays, due to the technological advances, the ability to obtain the encounter history data has improved. Some new capture methods do not require physical capture and handling of animals. The encounter history can be collected using detection devices such as camera traps, acoustic recordings, and DNA samples.

Cameras are usually placed near the animal trails or food sources. After animals are photographed, they must be identified either manually or by machine learning methods. Other problems with camera trappings are capturing multiple camera encounters of the same animal in a short time period. Unidentifiable camera encounters can occur especially at night.

Despite the fact that capture-recapture methods have been commonly used, these methods do not consider the spatial structure of the population in the sampling and analysis. Moreover, conventional capture-recapture methods do not use any explicit spatial information with regard to the spatial nature of the sampling and spatial distribution of individual encounters. Recently a spatial capture-recapture method has been introduced by Royle and Chandler [4] to link observed encounter histories of individuals to spatial population ecology and study the population using new technologies such as remote cameras and acoustic sampling. While this method is promising, the estimated population size is not robust and suffers from spatial complexity problems. An open ended problem is to address the shortcomings of this method and make the model robust with regard to spatial sampling and spatiotemporal population analysis. Therefore, the first objective of this research is to perform a comprehensive study of the model parameters and their impacts on the estimated population size. The second goal will then focus on identification of parameters with significant impact on the estimated population size and to develop informative priors for the identified parameters. The third objective is to introduce a hybrid spatiotemporal capture-recapture/capture-removal method and enhance the estimation of the population size by incorporating the collected data using capture-removal method.

1.1 A Review of Hog Population

Invasive species are defined as any kind of living organism (animals, plants, bacteria, insects, fish, fungus, or even an organism's seeds or eggs) that are not indigenous or native to an ecosystem [5]. These species usually cause massive harm to wildlife in many ways when introduced to a new area [6]. Moreover, invasive species are rapidly growing, spreading aggressively with potential, adapting, they conquer. As a result, they can compete with native wildlife for resources and disrupting the entire ecosystem [7]. Invasive species jeopardize local economies, threatening human health, infrastructure, and devastating entire ecosystems. For these reasons, they cost the global economy over a trillion dollars each year [8], and almost $\$120$ billion in US [9].

The spread of invasive species into new habitats is associated with human activity, often unintentionally. However, some invasive species are introduced intentionally to their new environment as a form of pest control. For example, cane toads were brought to Australia in the early 20^{th} century to control destructive beetles in Queensland's sugarcane crops [10]. Moreover, invasive species can be introduced as a food source or even as home decoration [8, 11]. Invasive species may also escape to the wild accidentally through natural factors such as a storm, climate shift, or human intervention [12].

1.2 Feral Hogs (*Sus scrofa*) Population

The species of interest here in this work is *Sus scrofa* which includes wild boars, feral, and domesticated hogs. The differences between wild boars and hogs is that wild boars do not have any domesticated ancestry, while feral hogs are descendants of domesticated hogs that now live outside of captivity and have become undomesticated. Domestic pigs generally have thinner and bristlier coats than wild boars. Wild boars have noticeable hair running along their backs (especially bristles), and have longer tails, legs, snouts, and larger heads. After only a few generations of domestic pigs being in the wild (hybrids hogs), distinguishing physical characteristics of domestic and wild ones is very difficult [13, 14]. The average lifespan of feral hogs is about four to six years. However, they may live up to eight years [13].

Feral hogs exhibit sexual dimorphism, with the male hogs being about $(5-10)\%$ larger and about $(25-30)\%$ heavier than females. Male hogs can weigh as much as 250 lbs, while female hogs may weigh up to 180 lbs. Their social structure is female-dominated. Adult males tend to live in seclusion, but may form small groups as developing adults. Feral hogs will reproduce $(1-2)$ times per year depending on their habitat [15]. However, the time between litters is not consistent, as behavioral, biological, and environmental factors have a substantial influence [16].

Hogs are omnivores, but mostly consume plant matter [17]. They tend to eat energy-rich plant food including acorns, pine seeds, cereal grains, and other crops. There are seasonal, interannual, and regional differences in their diets. *Sus scrofa* are opportunistic omnivores whose diet is largely determined by the relative availability of different food types during the season, year, or region [18, 19].

Wild boars can be found in a wide variety of habitats across the world. Generally, they prefer tropical climates but can survive elsewhere. Hogs prefer to stay in the shade with dense vegetation during the day [20]. Their priorities for habitat are food availability, shelter, and hunter presence. The types of habitats preferred by hogs include palm-oak-wax myrtle, citrus groves, grass swales, and grass ponds [21, 22]. We study the population of feral hogs in Kennedy Space Center refuge [23] which is part of Merritt Island Wildlife Refuge. Feral hogs in Merritt Island Wildlife Refuge tend to eat plant matter with high carbohydrate content rather than high protein or high lipids [24]. Feral hogs in Merritt Island Wildlife Refuge prefer shaded habitats during warmer months.

1.2.1 History of Feral Hogs in the US

Wild pigs were first brought to the United States in the 1500s as a source of food by Spanish Explorer, Hernando De Soto [25]. He brought the first ”thirteen sows” to Tampa Bay, Florida, in 1539. In three years' time, the population of pigs had grown to 700 – a very conservative estimate. This estimate excludes pigs that are eaten by his troops, given to or stolen by Indians and those that escaped and became wild-living pigs. Due to the ability of hogs to occupy a relatively wide range of habitats, pigs spread rapidly through the southeastern United States establishing the first feral hog population in North America [12, 26].

In the early 1900s, Eurasian or Russian wild boars were introduced to the United States in a game preserve in Hooper Bald, Graham County, North Carolina. The third type of hogs was introduced interbreeding occurred between those two types of feral hogs . From the 1950s on, wild pig populations started on a strong growth curve that has never stopped. These feral hogs have found in 47 states with established populations in at least 38 states.

In Florida early 1981, feral hogs were reported in 66 of 67 counties, and eight years later reported the occurrence of pigs in every county in Florida [27].

Hogs were introduced into Merritt Island in the 16^{th} century during Spanish control of Florida. When NASA bought Merritt Island in the early 1960s, the farmers who had owned the land were ordered to remove all hogs from the propriety. However, not all hogs were

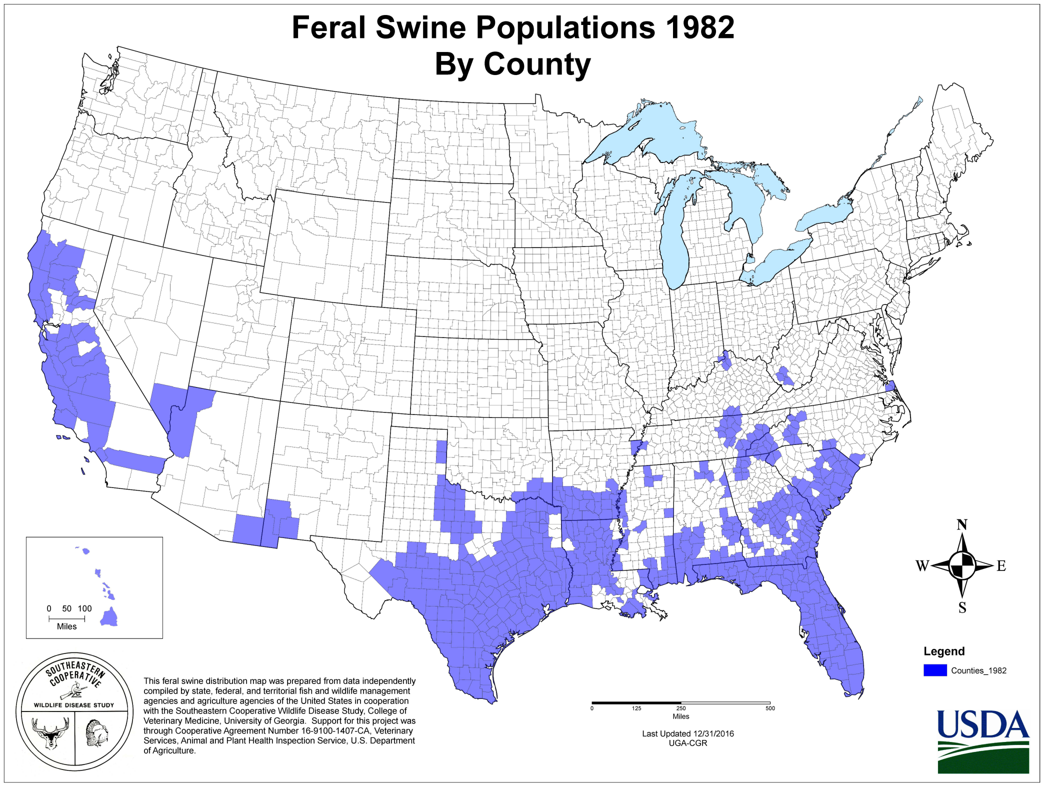


Figure 1.1: Feral Swine Populations 1982 by County

captured; thus implies that the feral hogs that inhabit Merritt Island originated from these hogs [28].

The feral hogs are an invasive species, as *Sus scrofa* are not indigenous to North America. Hogs originate from across Europe and Asia. The hogs brought to Florida were thought to be initially captured in Asia, and then brought to the Caribbean. From there, the hogs were brought to Florida in multiple landings. In 2013, the United States is home to an estimated 6.3 million feral hogs (*Sus scrofa*) about two-third of them range in the southeastern United States (Florida and Texas) [29, 30].

Comparing Figures 1.1 and 1.2, shows the magnitude of the alarming increase in the size of the hogs population in the United States of America [31].

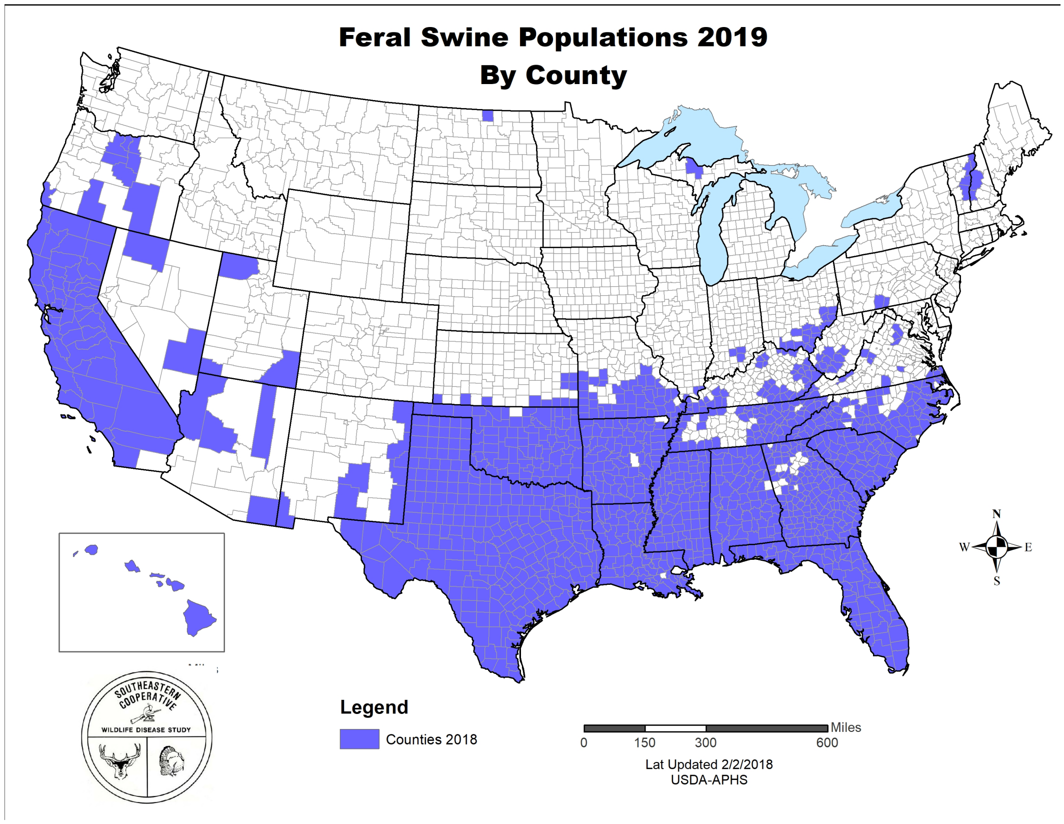


Figure 1.2: Feral Swine Populations 2019 by County

1.2.2 Food Habits of Feral Hogs

The damage feral hogs cause is wide-ranging and far-reaching. With populations expanding everywhere in the United States, this invasive animal negatively impacts everything from cultivation and the environment to human health and public safety.

Feral hogs can destroy ecosystems by over-foraging, rooting the ground until it becomes destabilized, and eliminating native species through consumption. As well as with their feeding, rooting, trampling, and wallowing behaviors. Alongside that, feral hogs cause massive damage to agriculture, consuming crops and causing property damage. Specifically, feral hogs have caused at least $2.5 million in damage to agriculture and infrastructure. The federal government spends about $30.5 million annually to counteract these damages made by hogs (U.S. Department of Agriculture).

Studies indicate that feral hogs can carry a large number of parasites and pathogens (at least 30 diseases, and approximately 40 types of parasites) that can affect people, pets, livestock, and wildlife by transmitting disease. However, diseases caused by feral hogs do not pose a major threat to humans. These diseases can be a concern for cattle. The transmission occurs through direct contact with feral hogs that use the same pastures or feedlots with cattle. Brucellosis (Brucella species bacteria) is just one example of these diseases. Some diseases such as tuberculosis that may be exposed from indirect contact with feral hogs if they can access feed and water sources utilized by cattle. Besides, some of these diseases can be transmitted with direct or indirect contact with feral hogs such as Leptospirosis.

Feral hogs were chosen as the study species because of the damage they cause to Kennedy Space Center. They cause a lot of rooting and wallowing damage alongside roads and native plant destruction. However, one of the major issues with feral hogs at Kennedy Space Center is the car accidents they cause. Hogs can cause serious damage in car accidents to the driver and the car. There was over $26,000 in-car damage that was caused by accidents with hogs from 2011 to 2012. There is at least 1 confirmed fatal accident on Kennedy Space Center that was caused by a hog.

1.3 Study Area

This study was conducted in the Titusville, Florida to investigate feral hog population in the Kennedy Space Center (KSC).

Data was collected in two study sites shown in Figure 1.3. This investigation took place within the boundaries of the Kennedy Space Center along with the east-central coast of Florida [32], specifically on the Merritt Island National Wildlife Refuge (MINWR), about 60 miles east of the city of Orlando in Brevard and Volusia Counties. Because of the limited number of cameras, two sites, Happy Creek and Tel-4 in KSC were selected for study. The Happy Creek study site is a scrub landscape centrally located within KSC. It is

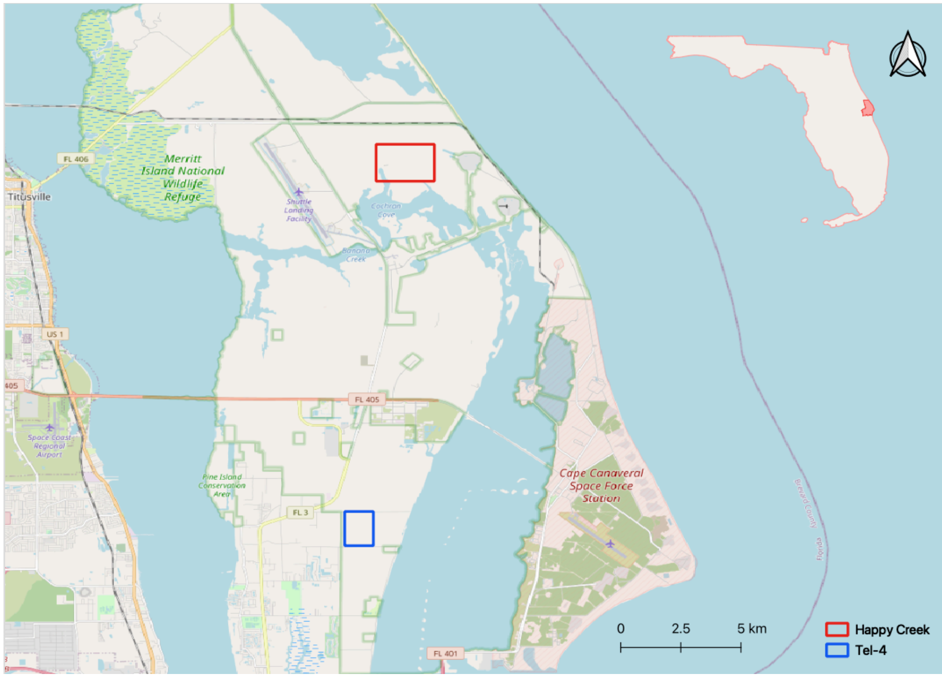


Figure 1.3: Kennedy Space Center (KSC), and the two main study sites at Happy Creek (Red) and Tel-4 (Blue)

a 536-ha study site dominated by well-drained soils and scrub oaks. Unlike the Tel-4 study site, Happy Creek has very little pine overstory, and forests occur in the form of hardwood hammocks on mesic sites. Swale marshes at Happy Creek also are interspersed but are deeper and larger than the marshes found at Tel-4.

The Tel-4 study site is 14 km south of Happy Creek [33]. It is a 295-ha located near the southern boundary of KSC [32]. Mesic shrubs dominate Poorly-drained upland sites (e.g., *Lyonia spp.*, *Serenoa repens*, *llex sp.*), while scrub oaks (*Quercus spp.*) dominated on well-drained upland sites.

Merritt Island National Wildlife is in a humid subtropical zone with short, mild winters and hot, humid summers. The average range (1985 - 2015) of winter temperature (in January) is 50 F at dawn and 71 during the afternoon. However, in the summer (in August), the average temperature from 71 to 90. Besides, the averages (May to October) 49 inches of rain a year. The mean dawn relative humidity (RH) is between 88 and 95 percent through-

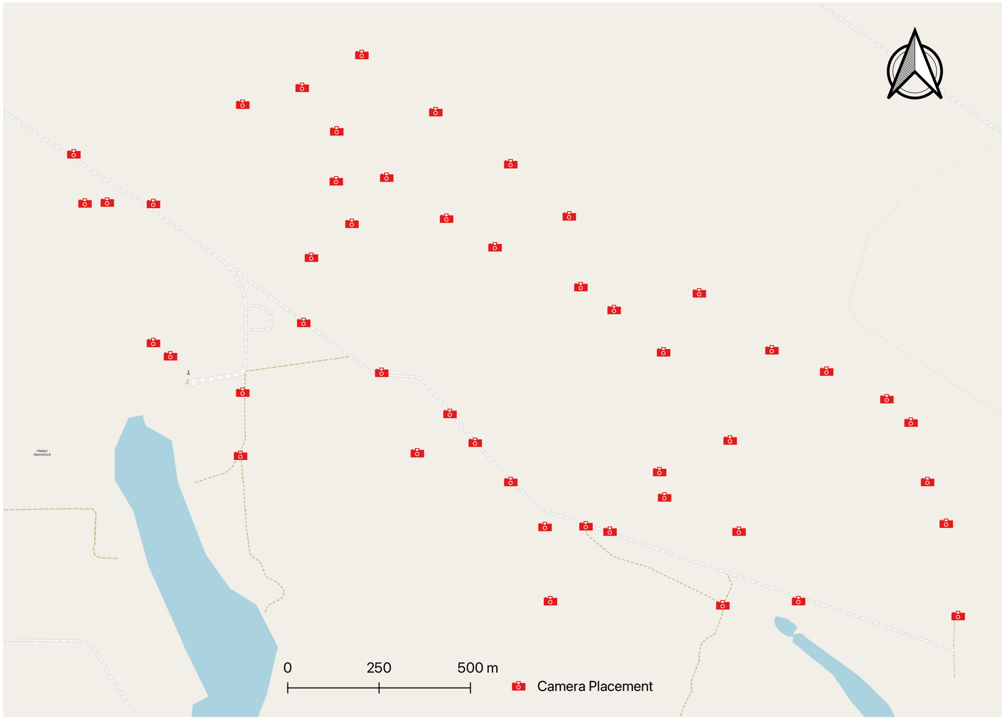


Figure 1.4: Camera Placement in Happy Creek, KSC, Florida

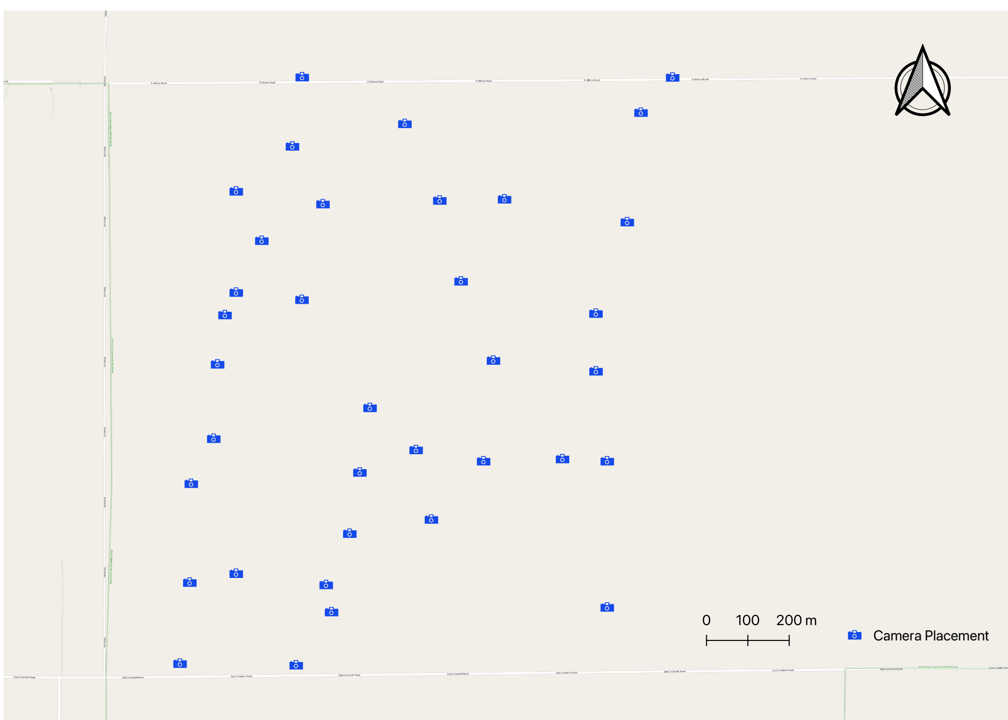


Figure 1.5: Camera Placement in Tel-4, KSC, Florida

out the year, while readings in the mid-afternoon are between 55 and 67 percent [34].

Chapter 2

An Overview of Bayesian Statistics and Markov Chain Monte Carlo

There are two different approaches for statistical data analysis: the classical or Frequentist approach and the Bayesian approach [35]. In the Frequentist approach, it is assumed that for a given population, the probability distribution $f(X, \theta)$ is applicable for an unknown parameter or parameter set θ. The aim is to estimate the parameter using a point estimator or find a confidence interval for the unknown parameter. Also, a specific hypothesis about this parameter can be tested using a random sample from the population [36].

In many cases, extra information about the parameter θ is available either from previous studies or from researcher prior experience. Using this information can help to estimate the unknown parameter. This approach is called Bayesian approach introduced by Thomas Bayes (1701 - 1761) [37]. The fundamental difference from the classical approach is that the parameter θ might take different values, then it will be a random variable instead of fixed value [38]. As a result, θ has a probability distribution $\pi_0(\theta)$. This distribution is before the data is observed and is called a prior distribution of the parameter θ. However, the distribution for θ after the data count is called posterior distribution $\pi(\theta \mid X)$ and it can be written as:

$$\pi\left(\theta \mid X\right)=\frac{\pi_{0}\left(\theta\right) f\left(X \mid \theta\right)}{f\left(X\right)} \tag{2.1}$$

where $f(X)$ is prior predictive distribution [39] that is a normalizing function to guarantee that the posterior distribution is a valid probability distribution. If θ is a continuous value: $f\left(X\right)=\int \pi_{0}\left(\theta\right) f\left(X \mid \theta\right) d\theta$). Exceptionally, θ can be discrete. In such cases, the integral will be replaced by sum. Note that this constant $f\left(X\right)$ does not depend on θ and then does not provide any additional information about the posterior distribution. As a result, this value is not necessary to be calculated to evaluate the properties of the posterior distribution. Thus, we can rewrite 2.1 as:

$$\pi\left(\theta \mid X\right) \propto \pi_{0}\left(\theta\right) f\left(X \mid \theta\right) \tag{2.2}$$

where $\pi\left(\theta \mid X\right)$ provides information from the data. If this function is considered as a function of θ, it can be rewritten as $L\left(\theta; X\right)$ where $L\left(\theta; X\right) \propto \pi\left(\theta \mid X\right)$. It is called the likelihood function and thus;

$$\pi\left(\theta \mid X\right) \propto \pi_{0}\left(\theta\right) L\left(\theta; X\right) \tag{2.3}$$

In Bayesian statistics, the goal is to find the posterior distribution by combining the information from the data and the prior distribution [40].

As we mentioned earlier, the unknown parameter θ is assumed to be a constant value in Frequentist framework. Thus, we can get the point estimate for true parameter θ and use this statistic to calculate the confidence interval to express the uncertainty around the estimated value. On the other hand, Bayesian inference is based on the posterior distribution of θ. We can use mean or median of the posterior distribution, which provides a measure of the center of the posterior distribution. This point estimate will be used for constructing a confidence interval or a credible interval (in Bayesian framework) [39] of the posterior distribution.

The main difference between Bayesian credible interval and the Frequentist confidence interval is that in Frequentist, the parameter is fixed (but unknown) and the lower bound and upper bounds of the confidence interval are random variables. In contrast, Bayesian credible interval treats the estimated parameter as a random variable while the information from the prior distribution is used to quantify our belief about this value. As a result, the bounds of the interval are treated as fixed values. Thus, we can say $\int_a^b \pi\left(\theta \mid X\right) = 1 - \alpha$ which means the true parameter is in the interval (a, b) with probability $1 - \alpha$. Finally, the most common method for obtaining a credible interval is the highest posterior density (HPD) interval. There are other methods such as the equal-tail interval.

2.1 Bayesian Statistics: Advantages and Disadvantages

We should point out that, Bayesian and Frequentist statistics have some similarities, and each of them has some advantages and risks. By increasing the sample size, the results obtained by Bayesian and Frequentist inferences get closer, which means the posterior mean and the MLE are approximately equal [39]. Thus, the question is which method is preferred based on the information that we have. However, there are some advantages in using Bayesian statistics over Frequentist statistics. First, it is easy to interpret. For example, we can say the probability that the true parameter θ falls in credible interval $[a, b]$ is 95%, which is not the case in classical Frequentist approach. Second, in Frequentist statistics, when new observations become available, we have to recalculate all statistics again to get the new estimate for the parameter of interest. In contrast, the outcome of Bayesian inference is the posterior distribution and can be used as prior distribution when new samples become available [41]. Third, Bayesian statistics offers a direct method to estimate any function of parameters. Forth, it obeys the likelihood principle, which is not the case in classical statistics. In Bayesian, if two experiments have the same likelihood, then all inferences around θ must be the same. Since all information about the parameter in the data is already included in the likelihood function. Another important advantage of Bayesian statistics is that, if we have a vector of parameters $\Theta = (\theta_1, \theta_2, \cdots, \theta_p)$, posterior distribution of any parameter or any subgroup of parameters can be obtained using marginalization, that is, the posterior distribution of a nuisance parameter of interest can be obtained by $\pi(\theta_1 \mid X) = \int \pi(\Theta \mid X)\, d\theta_2, \ldots, d\theta_p$. If marginalization is not possible, Markov chain Monte Carlo (MCMC) algorithm and *empirical Bayes* technique can be used to estimate the posterior distribution of nuisance parameter. Finally, there are some risks that may cause misleading results or may increase the computational costs. Since there is no guaranteed way to choose the prior distribution, Bayesian inference requires a way to integrate our beliefs into prior distribution. As a result, we can say that choosing the prior distribution is an essential task in the Bayesian approach. It can be a primary advantage or a major disadvantage over classical frequentis statistics.

2.2 Prior Distribution

It is imperative to have a way of making statistical inference to reflect beliefs (or prior information). Bayes theorem, allows updating our beliefs based on new information, which means our belief can be changed based on new observations. This is the core idea of a prior distribution, the information about a parameter before we observe any evidence. It will allow us to change our belief using Bayesian statistics. Mathematically, we take prior belief and update it using the observations to obtain the posterior distribution of the parameter. The question now is: how can we choose the prior distribution?

The choice of the prior distribution is considered the heart of the Bayesian inference. It is not an easy task to choose the correct prior to obtain a reasonable estimate of the parameter. Also, different priors may produce different posteriors. A conjugate prior is often a relevant choice. The prior distribution of parameter θ is conjugate prior for the likelihood

Table 2.1: The Probability Distributions Associated with its Conjugate Priors

The Distribution of X	The Parameter	The Conjugate Prior Distribution
Binomial	Prob. of success	Beta
Poisson	Mean	Gamma
Exponential	The inverse of mean	Gamma
Normal	Mean (known variance)	Normal
Normal	Variance (known mean)	Inverse Gamma

function if the prior and posterior distributions belong to the same family. Conjugate prior can be formed by removing the factors that do not depend on the parameter θ in likelihood function and replace the expressions which depend on data with parameters. The sample size must be also replaced. In this way, we will find a kernel for the conjugate prior. A normalizing constant is required to obtain a valid prior distribution. For example, for a Poisson distribution, the likelihood function is:

$$L(X;\theta) = \prod_{i=1}^{n} \frac{\theta^{x} e^{-\theta}}{x!} \propto \theta^{\sum_i x_i} e^{-n\theta} \tag{2.4}$$

By replacing $\sum_i x_i$ which depends on data and the sample size n with parameters λ_1 and λ_2 respectively, we obtain the conjugate prior;

$$\pi(\theta) \propto \theta^{\lambda_1} e^{-\lambda_2 \theta} \tag{2.5}$$

which is proportional to Gamma distribution with parameters $\lambda_1 + 1$ and λ_2. As a result, we can say that the conjugate prior of Poisson distribution is Gamma distribution.

If we choose prior distribution as a conjugate to likelihood, the posterior will have the same form as the prior distribution. The main advantage of using the conjugate prior is its low computational cost. However, choosing a conjugate prior requires that the parameter of interest follows the selected distribution. Otherwise, it may produce a misleading posterior distribution. In other words, if we do not have enough information about the parameter of interest, we should choose a prior distribution that minimally depends on the posterior distribution. That is, the inference is not affected by the prior information and is mainly influenced by the observed data. This kind of prior distribution is called objective or non-informative prior. The prior $\pi_0(\theta)$ is called a non-informative prior if it has a minimal impact on the posterior distribution of θ. Uniform distribution is a typical non-informative prior introduced by Laplace [42]. Notice that, if the parameter range is: $[-\infty, \infty]$, the prior is called improper prior. A non-informative prior is said to be improper if its integral $(\int \pi_0(\theta) d\theta)$ is not equal to one and in turn it is not a valid (proposer) distribution. Hence, rather we can use the Jeffreys prior:

$$\pi_0(\theta) \propto \sqrt{|I(\theta)|} \tag{2.6}$$

where $I(\theta)$ is the Fisher information for θ.

An informative prior dominates the likelihood, and thus it has a noticeable impact on the posterior distribution. Notice that, for a given sample size, the more informative the prior, the more significant will be its influence on the posterior distribution. While for a given prior distribution, the larger the sample size, the more significant will be the influence of likelihood on the posterior distribution. In practice, a precise estimate of posterior distribution can be obtained using smaller sample sizes if we use more informative priors. To achieve a similar precision using a weak or non-informative prior, a larger sample size is required.

2.3 Markov Chain Monte Carlo (MCMC)

The concept of Monte Carlo was introduced by the Polish-American mathematician, Stanislaw Ulam. Nowadays, Monte Carlo simulation is considered as one of the most potent statistical tools in many fields of research in engineering and science. Monte Carlo refers to the methods used to generate random numbers. In Monte Carlo method, we generate sets of random numbers from different distributions. For example, we generate a random sample from a Normal distribution with mean μ and variance σ^2, called proposal distribution. Proposal distribution will be used to accept/reject samples. Using the random samples generated from the proposal distribution, we can estimate the distribution of θ.

2.3.1 Markov Chain

Markov chain is a stochastic process to generate a sequence of states such that a new state is generated based on the previous state, and in turn it depends on the previous state in the sequence. For instance, the value of θ in time t is drawn from a Normal proposal distribution where the mean (center) of the Normal distribution is set to the value of θ in time $t-1$:

$$\begin{aligned} \theta_0 = 0.500, \quad \theta_t \sim N(\theta_{t-1}, \sigma) \\ \theta_1 \sim N(0.500, \sigma), \theta_1 = 0.599 \\ \theta_2 \sim N(0.599, \sigma), \theta_2 = 0.579 \\ \theta_3 \sim N(0.579, \sigma), \theta_3 = 0.583 \end{aligned} \tag{2.7}$$

If we generate a large sample using MCMC, a trace plot of θ demonstrates a random walk. Note that the resulting probability density function of θ does not resemble the proposal distribution.

2.4 Metropolis-Hasting Algorithm

Metropolis-Hastings (M-H) algorithm was introduced by N. Metropolis, A. Rosenbluth, M. Rosenbluth, A. Teller, and E. Teller (1953) and generalized by Hastings (1970). M-H algorithm is used to decide which proposed values of θ must be accepted or rejected. It begins by generating a sample from prior distribution of θ. The posterior probability of θ will then be estimated using the previous value of θ. Notice that, the functional form of the posterior distribution is not required, since the posterior distribution is the product of prior distribution and the likelihood function. Calculate the ratio of the posterior probability of the candidate value of the parameter of interest θ to the posterior probability of the previous value of θ:

$$r(\theta_t, \theta_{t-1}) = \frac{\text{posterior probability of } \theta_t}{\text{posterior probability of } \theta_{t-1}}$$

$$= \frac{prior(\theta_t)}{prior(\theta_{t-1})} \frac{Likelihood(\theta_t)}{Likelihood(\theta_{t-1})} \tag{2.8}$$

If this ratio is greater than one, the new value of θ will be accepted. If the ratio is less than one, it will be considered as acceptance probability, α, which is the probability of moving from the current value θ_{t-1} to the proposed value θ_t:

$$\alpha(\theta_t, \theta_{t-1}) = min[r(\theta_t, \theta_{t-1}), 1] \tag{2.9}$$

Next, draw a value u from a uniform distribution and compare it with α. If $u > \alpha$, accept the new value of θ, otherwise reject it and return to the previous step.

Algorithm 1: Metropolis-Hastings algorithm

Initialize $\theta^{(0)} \sim q(\theta)$

for iteration t=1,2,...**do**

Propose: $\theta^{cand} \sim q(\theta^{(t)}|\theta^{(t-1)})$

Acceptance Probability:

$\alpha(\theta^{cand}|\theta^{(t-1)}) = min\{1, \frac{q(\theta^{(t-1)}|\theta^{cand})\pi(\theta^{cand})}{q(\theta^{cand}|\theta^{t-1})\pi(\theta^{t-1})}\}$

$u \sim Uniform(u; 0, 1)$

if u $< \alpha$ **then**

Accept the proposal: $\theta^t \leftarrow \theta^{cand}$

else

Reject the proposal: $\theta^t \leftarrow \theta^{t-1}$

end if

end for

2.5 Gibbs Sampler

Gibbs sampling is special case of Metropolis-Hastings where the proposed values will always be accepted since the acceptance probability is equal to one. Gibbs sampler repeatedly samples from the posterior distribution of each variable given all other variables [43] using MCMC. In this way, the Markov chain is constructed by sampling from the conditional distribution for each parameter θ_i in turn, while treating all other parameters as observed. One cycle of the Gibbs sampler is done when iterating over all parameters is completed. For example, suppose that we have two variables $[\theta_1, \theta_2]$, where sampling from the joint density function $P(\theta_1, \theta_2)$ is not possible, but rather sampling from the conditional distributions $P(\theta_1|\theta_2)$ and $P(\theta_2|\theta_1)$ are fairly simple. To generate a sequence of random values,

$$\left(\theta_1^{(0)}, \theta_2^{(0)}\right), \left(\theta_1^{(1)}, \theta_2^{(1)}\right), \left(\theta_1^{(2)}, \theta_2^{(2)}\right), ..., \left(\theta_1^{(M)}, \theta_2^{(M)}\right) \tag{2.10}$$

we first set initial value $\theta_2^{(0)}$ and then iteratively obtain the rest by generating values using 2.10:

$$\begin{aligned}\theta_1^{(j)} &\sim P\left(\theta_1|\theta_2^{(j)}\right)\\ \theta_2^{(j+1)} &\sim P\left(\theta_2|\theta_1^{(j)}\right)\end{aligned} \tag{2.11}$$

Algorithm 2: Gibbs Sampling Algorithm

Initialize $\theta^{(0)} \sim q(\theta)$

for iteration i=1, 2, ..., **do**

$\theta_1^{(i)} \sim P\left(\theta_1|\theta_2^{(i-1)}, \theta_3^{(i-1)}, ..., \theta_M^{(i-1)}\right)$

$\theta_2^{(i)} \sim P\left(\theta_2|\theta_1^{(i)}, \theta_3^{(i-1)}, ..., \theta_M^{(i-1)}\right)$

.

.

.

$\theta_M^{(i)} \sim P\left(\theta_M|\theta_1^{(i)}, \theta_2^{(i)}, ..., \theta_{M-1}^{(i-1)}\right)$

end for

2.6 MCMC Convergence Diagnostic

In Bayesian inference, the stationary state of the Markov chain is considered the posterior distribution:

$$\lim_{n\to\infty} X_n = \pi(\theta|X) \tag{2.12}$$

Hence, we should make sure that Markov chain has converged to its stationary distribution. This is essential due to the fact that the target distribution will not be well explained using samples drawn from a Markov chain that has not converged to its stationary state. In a similar way, we should check out the convergence of all parameters in the model to avoid obtaining misleading results [44]. Although, it is difficult to prove the convergence, we can check (while cannot prove) whether or not the chain has converged [45]. There are different diagnostic methods to check whether the chain has converged to its stationary distribution. These methods are divided into two groups, pre-convergence, and post-convergence [46].

In this section, we will discuss these two approaches to check whether the MCMC has converged to its stationary distribution, and whether we have obtained large enough sample size from this distribution to accurately estimate the posterior distribution and/or any quantity of interest such as mean and median of the posterior distribution.

2.6.1 History of Trace Plot

Trace plot is a visual analysis of the Markov chain. It is a useful tool in assessing convergence and can be used to check MCMC sampler performance. Figure 2.1 displays typical trace plots where the number of iterations of MCMC is on the x-axis and the parameter value drawn at each iteration is on the y-axis. Generally, we plot a separate trace plot for each parameter. The top row in Figure 2.1 displays a well mixed trace plot. A well mixed chain indicates that the chain has converged. A well mixed chain looks like white noise. Note that if we run more than one chain initialized by different initial conditions, then each chain will be shown in a different color. If the Markov chain converges, different chains demonstrate similar well mixed results.

The second row in Figure 2.1 shows a trace plot with a bad initial value. However, it is transitioned to a well mixed chain after a few hundred iterations. The starting value can be influential when we first start the chain. To avoid the substantial impact of the starting value on the analysis, the starting part of chain so called Burn-in or warm-up period will be discarded [47]. Often 10 to 20 percent of the samples (from the starting point) are discarded as Burn-in samples. However, some researchers consider all samples as valid samples from the posterior distribution and do not discard any sample. Some others discard up to 50 percent of samples if it allows a faster convergence. The third row in Figure 2.1 shows a trace plot with high auto-correlation. We should point out that, in MCMC, if the proposed sample which is drawn from the proposal distribution is rejected, $x_{t+1} = x_t$. It means the

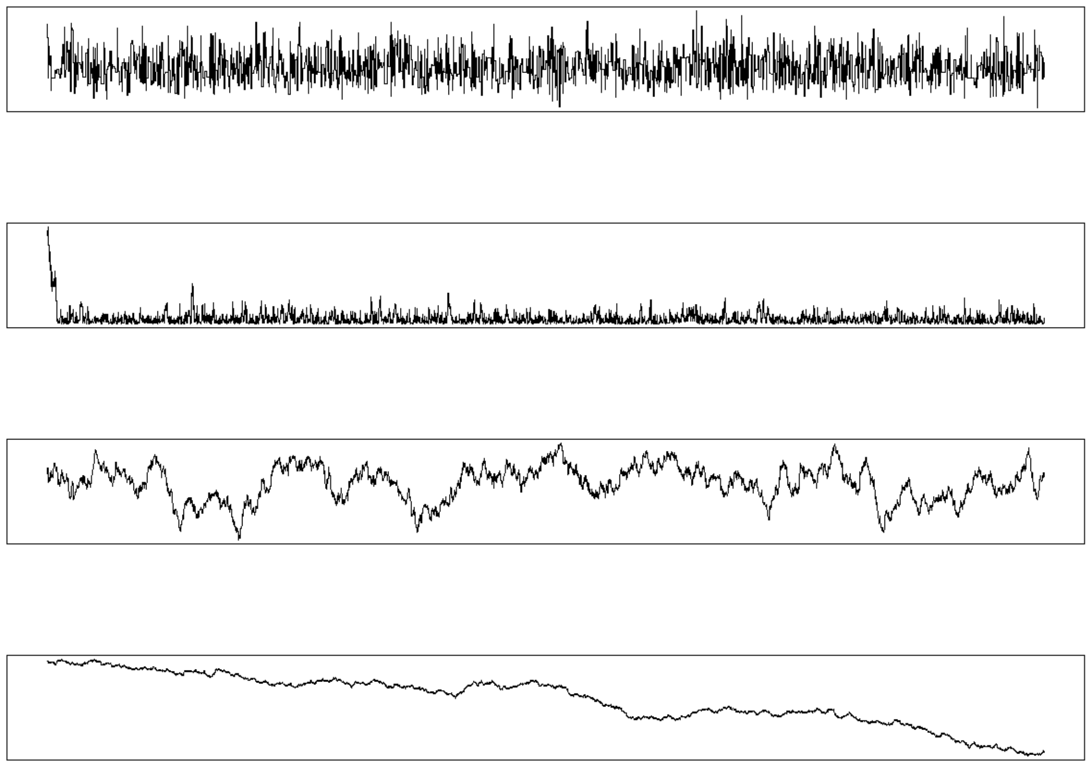


Figure 2.1: Typical Trace Plots: Good Mixing (first row), Burn-In (second row), Thinning (third row), Non-convergence (fourth row)

higher the rejection rate, the higher the auto-correlation of the chain. Thinning method is a potential solution for a highly correlated chain and can improve statistical. Finally, the fourth row in Figure 2.1 shows a trace plot with an obvious trend which is not converging. This chain does not seem to converge to its stationary distribution. It can be due to either an error in the MCMC algorithm or insufficient number of iteration [48]. As a result, we cannot estimate a reliable posterior distribution of the parameter using this chain [49].

2.6.2 Auto-correlation Plot

Auto-correlation plot is a commonly used tool for checking randomness/independence of the samples produced by the Markov chain. Auto-correlation plot can help to analyze available information in the Markov chain, whether the chain is well mixed, and how independent the samples are. In MCMC, by design, generated samples from one iteration to the next will be somewhat correlated. In a well mixed chain, the correlation is small and the auto-correlation should drop relatively quickly. Samples will be highly correlated if the chain is not well mixed. If the correlation decays slowly, it means a large number of iterations is required to reach the stationary distribution of the Markov chain. The auto-correlation can take a value between -1 and +1, and quantifies the correlation between the current value of the chain and its past values (lags). Lag k auto-correlation represents the auto-correlation between the current sample and k^{th} preceding sample.

2.6.3 Effective Sample Size

The effective sample size (ESS) is another way to study the convergence of the chain. The effective sample size of a parameter is the estimated number of independent observations our sample is equivalent to. In other words, how many independent samples are generated from the stationary distribution. As we have mentioned, the samples generated by MCMC are somewhat correlated. It means, less information is provided by highly correlated or poor mixing chains. Using a thinning technique, ESS can get closer to the sample size n. Small ESS indicates a poor estimate of the posterior distribution. ESS is computed by:

$$ESS = \frac{n}{1 + 2\sum_{k=1}^{\infty} \rho_k} \tag{2.13}$$

where n is the total sample size and ρ_k is the lag k auto-correlation of the parameter [50].

2.6.4 Gelman-Rubin Diagnostic

This test is one of the most popular tests for diagnosing whether the MCMC has converged to the target distribution. In this test, we run multiple chains with different initial values [51] to diagnose whether the chains have forgotten their initial values which would essentially mean that they have converged to the same stationary distribution [52]. This diagnostic test compares the within chain variance to the between chain variance [53]. When between chain variability is substantially lower than the within chain variability, it is a sign for convergence to the stationary distribution. The PSRF (potential scale reduction factor) computed by $\hat{R}$ is close to 1 [5]:

$$\hat{R} = \sqrt{\frac{n-1}{n} + \frac{m+1}{mn}\frac{B}{W}} \tag{2.14}$$

where m is the number of chains (generated with different starting values), B is the between-chain variance in n iterations, and W is the within-chain variance [53]. This test assumes that the marginal target distribution is normally distributed [54] and it might be helpful to use an appropriate transformation of the parameter of interest such as log and logit. The correction factor $\frac{d}{d-2}$ or $\frac{d+3}{d+1}$ must be used:

$$\hat{R}_c = \frac{d+3}{d+1}\hat{R} \tag{2.15}$$

where d is the estimated degree of freedom (using method of moments) based on an approximation of the posterior distribution.

2.6.5 Heidelberg-Welch (H-W) Diagnostic

This is another tool to determine whether the MCMC chain has been running long enough and it has converged to its stationary distribution. The convergence test is based on the Cramer-von-Mises statistics to test the hypothesis whether or not the sampled value comes from a stationary distribution. This diagnostic can be summarized as follows. Consider the entire chain from time zero (iteration 1) to current time (current completed iteration). If the test fails, discard the first 10% of the samples and check if the remaining 90% has converged. If not, repeat the procedure with 20% and continue until it gets down to 50% of the chain samples. If the second half of chain (last 50% samples) has not converged to a stationary distribution, the entire test fails. However, when the chain passes the test, we know how many iterations must be kept.

In the next step, we can move to the half-width test which calculates a 95% confidence interval for the mean, using the remaining part that has passed the H-W test. To do this, the marginal error which is the half of the confidence interval of the mean will be compared with the estimated mean. The ratio of the marginal error of the mean and the estimated mean is calculated. If this ratio is less than ϵ (by default ϵ = 0.1), the half-width test is passed. Otherwise, the chain should be extended to estimate the mean within the desired level of accuracy. It is recommended to increase the chain's length by a factor of $I > 1.5$ to have a reasonably large proportion of new data.

2.6.6 Raftery Diagnostic

Running the MCMC chain for long enough is a crucial step to reach convergence as fast as possible. Raftery diagnostic is a run length control diagnostic to find the approximate number of iterations required to estimate a specific quantile Q within an accuracy of $+/-r$ with probability P. An estimate of the dependence factor I, which is a measure of dependency of the samples in the chain, can be obtained by this test. The value of I should be less than 5. Values of I larger than 5 indicate a strong auto-correlation, which could be due to a poor choice of starting value or high posterior correlation of the MCMC algorithm. One solution to reduce I is to run the chain longer to get more samples. To achieve a certain level of accuracy, a specific percentage of samples (Burn-in samples) can be removed from the beginning of the chain.

Chapter 3

Spatial Models for Population Estimation Using Physical Traps or Camera Encounters

In this chapter three models for estimation of the population size are discussed. In short term studies, it can be fairly assumed that the population of interest is a closed-population.

3.1 Capture Mark Recapture Model

In this model, probability of detection is assumed constant which implies that every individual in the population has a constant and equal probability to be captured in each trapping occasion. Similarly, capture and marking do not change the chance of an individual to be captured in future occasions. Furthermore, the occasions do not have any impact on the probability of capture. There are two unknown parameters in this model, the population size N and the probability of detection. The probability of capturing an individual with specific capture history h is:

$$P[X_h] = \frac{N!}{[\prod_h X_h!](N-M)!} . p^{n.} (1-p)^{KN-n.} \quad (3.1)$$

where $n. = \sum_{k=1}^{K} n_k$ is the total number of captures in the experiment (during all occasions), n_k is the number of animals captured in the k^{th} occasion, $k = 1, 2, ..., K$, $M = \sum_{k=1}^{K} u_k$ is the number of distinct individuals captured during the experiment (K is fixed for a given experiment), u_k is the number of new (unmarked) animals captured in the k^{th} occasion, X_h is the number of animals with a specific capture history h. For example $X_{h=\{10100\}}$ is the number of individuals captured on trapping occasions 1 and 3, and the set of all possible capture histories is defined by $\{X_h\}$.

3.2 Data Augmentation Model

This model is an extension to the capture mark recapture model that was explained in the previous section. However, in place of physical traps, individual animals are monitored virtually using camera encounters. Moreover, animals that make camera encounters are not marked. Similar to the previous model, assume a single closed population of N individuals that has been monitored in K occasions. In turn, in contrast with the previous model, rather than having a trap capture history, each individual in this model has a camera encounter history as a sequence of 0's and 1's. For example $y = (1, 0, 1, 0, 0)$, shows encounters for an individual that is observed at the first and the third occasion in total of $K = 5$ occasions. The encounter of individual $i = 1, 2, ..., N$ in occasion $k = 1, 2, ..., K$ is defined by y_{ik}. It follows a Bernoulli distribution: $y_{ik} \sim$ Bernoulli(p), where p is probability of detection (success). The probability of detection p is assumed to be constant for all individuals $i = 1, 2, ..., N$, and in all occasions $k = 1, 2, ..., K$ [55]. The unknown parameters are population size N and the probability of detection p.

In this model, two camera encounter histories are constructed. The full capture history of all N animals is represented by an $N \times K$ matrix including those individuals that were not observed (zero capture history). Practically, because N is unknown, we cannot observe the full capture history. Another matrix then is constructed to only represent the history of observed individuals. This matrix has K columns (number of occasions) and R rows $(R \leq N)$, one row for each observed distinct individual. Assuming $y_{ik} \sim Binomial(K, p)$, i.e., y_{ik}'s are independent and identically distributed Bernoulli random variables:

$$y_i = \sum_{k=1}^{K} y_{ik}$$

Since N is unknown, we are only able to construct the history of observed individuals. Therefore, a technical challenge is that the dimension of observed history may change at every iteration. To address this challenge, data augmentation can be effectively used by adding an arbitrary number of zeros (NZ) L to the encounter data. In turn in place of estimation of abundance N (using an abundance model), occupancy probability ψ (using occupancy model) will be estimated [56]. In this model, the augmented history will be represented by an $M \times K$ matrix, where M is an integer number and $M >> N$. A small M may introduce a condensed posterior distribution of $\hat{N}$ and results in $\hat{N} = M$, while a very large M, will drastically increase the computational cost. Now, each individual i in the hypothetical population of size $M = N + L$, where L is the number of added zeros, will be represented by a binary indicator $w = (z_1, z_2, ..., z_M)$. Each z_i takes a value of 1 if the individual belongs to the actual population of size N (real individual), and takes 0 otherwise:

$$y_i|z_i = \begin{cases} 1 & \sim \; Binomial(K, p) \\ 0 & \sim \delta\,(0) \end{cases}$$

where $z_i \sim$ Bernoulli(ψ), and $\psi \sim Uniform(0, 1)$ is the occupancy probability, i.e., the probability that an individual is an actual member of the true population of size N [57]. After estimating ψ using the occupancy model, the population size N will be estimated using:

$$E[N] = M \times \psi \tag{3.2}$$

where E is the expected value.

3.3 Hierarchical Spatial Capture Recapture

The spatial capture model [4] is an extension of the simplified model discussed in the previous section. All assumptions for the simplified model must be satisfied in this model. However, the assumption that the individual in a population is uniquely identified is not a requirement. In addition, this model allows for individuals to be captured at multiple cameras.

In this model, the sample of individuals are associated with a location parameter, which means each animal has a specific home range. The home range associated with each animal is unknown. It means, the population size N is equal to the number of unknown activity centers [58]. Camera encounters are considered as a virtual trap to detect individuals in the study area. Using distance sampling, the distance between the trap location and center of activity is calculated. It is assumed that an individual i has a fixed center of activity defined with the coordinates $s_i = (s_x, s_y)$ where $i = 1, 2, ..., N$, and N centers of activities are randomly distributed over the area of study S. A bivariate uniform prior is used to model unknown s_i:

$$s_i \sim Uniform(S) \tag{3.3}$$

There are J camera locations, each is defined by the coordinate $x_j, j = 1, 2, ..., J$. Notice that an individual can be detected at multiple cameras, and/or at multiple times by the same camera during a sampling occasion. A Poisson distribution is used to model a camera encounter history y_{ijk} for individual i, at camera j, in occasion k:

$$y_{ijk} \sim Poisson(\lambda_{ij}) \tag{3.4}$$

where λ_{ij} is the encounter rate, i.e. the expected number of capture or detection of an individual i at camera j, which is a function of the Euclidean distance between activity center s_i and the camera location $d_{ij} = ||s_i - x_j||$:

$$\lambda_{ij} = \lambda_0 g_{ij} \tag{3.5}$$

where λ_0 is the baseline encounter rate and g_{ij} is a function of the distance which monotonically decreases and is modeled using a half Gaussian function:

$$g_{ij} = exp\left(-d_{ij}^2/\sigma^2\right) \tag{3.6}$$

where σ is a scale parameter estimated from data. If an individual can be captured once during a sampling occasion, the encounter history takes binary values, that is y_{ijk} takes a value of 1 if the individual i is captured, or 0 otherwise. However, if an individual can be captured more than once during a sampling occasion, y_{ijk} will be the number of times that the individual i has been detected at camera j on occasion k. Therefore, a $(J \times K)$ encounter history matrix is considered for each individual. Obviously, the capture histories y_{ijk} cannot be directly observed for unmarked individuals. To estimate unknown population size, Chandler and Royle (2013) have implemented a data augmentation method. The number of camera encounters at camera j in occasion k is modeled by:

$$n_{jk} = \sum_{i=1}^{N} y_{ijk} \tag{3.7}$$

The full conditional latent encounter data is defined by a multinomial distribution:

$$\{y_{1jk}, y_{2jk}, ..., y_{Njk}\} \sim Multinomial(n_{jk}, \{\pi_{1j}, \pi_{2j}, ..., \pi_{Nj}\}) \tag{3.8}$$

where $\pi_{ij} = \lambda_{ij}/\sum_i \lambda_{ij}$. The camera encounter counts are modeled using a Poisson distribution:

$$n_{jk} \sim Poisson(\Lambda_j) \tag{3.9}$$

where

$$\Lambda_j = \lambda_0 \sum_{i=1}^{N} g_{ij} \tag{3.10}$$

The number of camera encounters at camera j can be obtained by:

$$n_{j.} = \sum_{k=1}^{K} n_{jk} \tag{3.11}$$

Because Λ_j and K are independent:

$$n_j. \sim Poisson(K\Lambda_j) \tag{3.12}$$

In the data augmentation method by Royle, Dorazio and Link (2007), and Royle and Dorazio (2007), they augmented the camera encounter histories with a set off all-zeros camera encounter histories. In turn, a hypothetical population size of M individuals in the study area is considered. Augmented parameter M is an integer number and is recommended to be much greater than unknown N to avoid the truncation of the posterior distribution of N. Notice that, a very large value of M will increase the computational time. They considered uninformative prior distributions for the parameters. Prior distributions of λ_0, σ, and ψ are considered Uniform(0,1), where ψ is the probability that an individual in the occupancy model of size M is a member of the original model of size N. A binomial prior distribution, $N \sim Binomial(M, \psi)$ is assumed for N where $\psi \sim Uniform(0, 1)$. Assuming a discrete uniform distribution for detection of individuals in the hypothetical population of size M, $M - n$ individuals are associated with all-zeros encounter histories. In turn indicator variables $z_1, z_2, ..., z_M$ are introduced such that:

$$z_i = \begin{cases} 1 & \text{if the individual i is a member of the population (i=1,2,...,N)} \\ 0 & \text{if the individual i is a fixed zero (i=N+1,...,M)} \end{cases}$$

where $z_i \sim Bernoulli(\psi), i = 1, 2, ..., M$. Hence, the encounter data for each individual in the augmented population can be modeled by:

$$\begin{aligned} (y_{ijk}|z_i = 1) &\sim Poisson(\lambda_{ij} z_i) \\ (y_{ijk}|z_i = 0) &\sim I(y_{ijk} = 0) \end{aligned} \tag{3.13}$$

and in turn, the population size can be obtained by $N = \sum_{i=1}^{M} z_i$.

Assuming mutual independence of the prior distributions, the joint prior distribution is:

$$[\psi, \lambda_0, \sigma] \propto [\psi][\lambda_0][\sigma] \tag{3.14}$$

and in turn the joint posterior distribution of the parameters is:

$$[y, z, s, \psi, \lambda_0, \sigma, |n, X] \propto \left\{ \prod_{i=1}^{M} \left\{ \prod_{j=1}^{J} \prod_{k=1}^{K} [n_{jk}|y_{ijk}][y_{ijk}|z_i, s_i, \sigma, \lambda_0] \right\} [z_i|\psi][s_i] \right\} [\psi][\lambda_0][\sigma]$$

Notice that the distribution of λ_0 and σ are uninformative priors in the original model. Chandler and Royle (2013) developed spatial Metropolis-within-Gibbs MCMC algorithms for estimating the model parameters.

Chapter 4

Proposed Regularized Integrated Spatial Model

In this chapter we discuss our proposed model for population analysis. The estimated posterior distribution by spatial capture model is sensitive to its parameters including probability of detection, added number of zeros by data augmentation, number of occasions, and radius of home range. To investigate the sensitivity of the model to each parameter, other parameters were considered to be fixed.

Several simulations were carried out in order to study the model sensitivity to different parameters such as the camera encounter rate, radius of the home range, and home range centers in estimation of the population size N.

4.1 Sensitivity of the Model to the Added Number of Zeros in Data Augmentation

In this section, we use the simulation to demonstrate the sensitivity of the spatial model to the data augmentation parameter L (added number of zeros). It will be followed by the study of sensitivity of the model to L using a real data set.

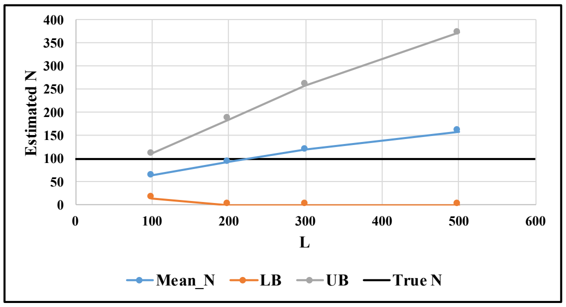
Data augmentation model is implemented to estimate unknown population size N, home range σ, λ_0 and density (individual home range centers). In this way a large value as an upper bound for population size $M = N + L$ (total number of hypothetical individuals) is selected. In this way, estimated N can assume values between zero and M. We performed several simulations to test the sensitivity of the model to the selected value of M for true value of $N = 100$.

The results are summarized in Table 4.1. We can observe that the estimated N has assumed a broad range of values between 63 and 164. The sensitivity of the model to the added number of zeros L is more noticeable for low probability of detection. The sensitivity decreases as we increase the probability of detection. The estimated N is fairly consistent for probability of detection of 0.25 or higher. As it is depicted in Figure 4.1, regardless of the number of added zeros L, a fair estimate of N is obtained for probability of detection of 0.25 or higher. However, based on the estimated values of standard error and the length of confidence interval in Table 4.1, to achieve an absolute estimation error of 10% or less, the probability of detection should reach to 0.5 or better.

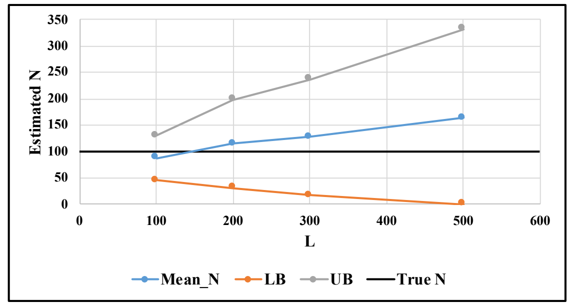
The convergence of posterior distributions of N and P are shown in Figure 4.2 for $P = 0.05$ and Figure 4.3 for $P = 0.05$. We can clearly see in these density plots that Markov chains for the probability of detection of 0.3 (and $L = 100$) converge to almost the same posterior distribution. As it can be observed in Figure 4.3, all chains are well mixed and the running mean for the first 1500 iterations are almost the same. Moreover, the auto-correlation of the chains for $P = 0.3$ drops considerably faster than that of $P = 0.05$.

Table 4.1: Estimated Mean of N for Different Number of Zeros L Added to the Model and Probability of Detection P

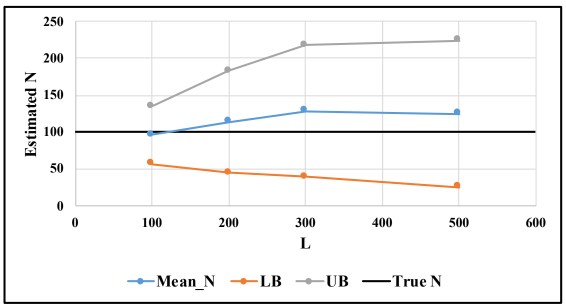
P	L	$\hat{N}$	Sd_N	Median	LB$_{Adj}$	UB	d
0.05	100	63.117	23.836	60.803	15.444	110.790	95.346
	200	92.557	46.258	84.495	0.041	185.073	185.032
	300	118.736	70.290	103.380	0	259.316	281.160
	500	158.755	106.403	131.850	0	372.135	425.546
0.10	100	87.561	20.936	87.455	45.690	129.433	83.743
	200	114.996	41.742	109.135	31.513	198.480	166.967
	300	127.075	55.131	116.400	16.814	237.337	220.523
	500	163.893	84.067	143.835	0	332.027	336.269
0.15	100	96.244	19.387	95.480	57.470	135.018	77.548
	200	113.999	34.327	107.975	45.344	182.653	137.309
	300	128.747	44.564	120.235	39.619	217.875	178.255
	500	124.806	49.577	112.955	25.653	223.960	198.307
0.20	100	102.536	18.035	101.115	66.466	138.606	72.140
	200	112.681	27.015	107.935	58.651	166.711	108.060
	300	116.144	31.775	109.760	52.594	179.694	127.100
	500	116.129	32.978	109.225	50.173	182.086	131.913
0.25	100	103.320	15.866	101.765	71.589	135.052	63.463
	200	110.304	20.596	106.990	69.112	151.497	82.385
	300	107.958	20.690	104.440	66.577	149.339	82.762
	500	105.027	19.699	101.745	65.629	144.425	78.796
0.30	100	104.417	13.511	102.810	77.395	131.440	54.045
	200	104.887	14.861	102.745	75.166	134.609	59.442
	300	106.259	15.258	104.060	75.743	136.774	61.031
	500	104.208	14.765	102.020	74.678	133.738	59.061
0.35	100	103.611	11.107	102.180	81.397	125.824	44.427
	200	102.305	11.132	100.870	80.041	124.569	44.528
	300	105.014	11.624	103.510	81.766	128.262	46.496
	500	102.525	10.918	101.090	80.690	124.361	43.671
0.40	100	103.678	8.853	102.595	85.972	121.384	35.411
	200	101.986	8.678	101.005	84.631	119.342	34.712
	300	102.677	8.713	101.635	85.252	120.103	34.851
	500	103.194	8.787	102.170	85.619	120.768	35.149
0.45	100	101.257	6.517	100.540	88.223	114.291	26.067
	200	101.053	6.741	100.320	87.571	114.536	26.965
	300	101.617	6.788	100.840	88.042	115.192	27.151
	500	101.955	6.891	101.180	88.172	115.737	27.564
0.50	100	100.616	5.247	100.020	90.121	111.110	20.988
	200	101.476	5.334	100.855	90.807	112.144	21.336
	300	102.179	5.586	101.560	91.007	113.351	22.344
	500	102.098	5.439	101.570	91.221	112.976	21.755
0.75	100	99.980	1.426	99.727	97.128	102.831	5.703
	200	99.868	1.412	99.640	97.021	102.631	5.610
	300	100.144	1.396	99.920	97.353	102.936	5.584
	500	100.173	1.459	99.880	97.248	103.093	5.846



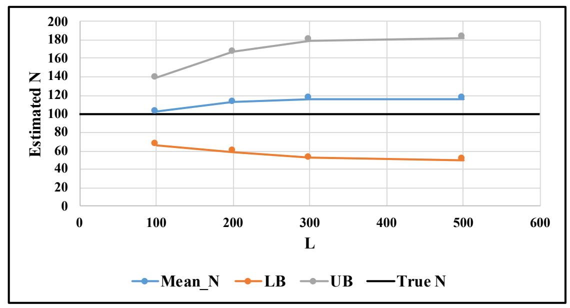
(a) $P = 0.05$



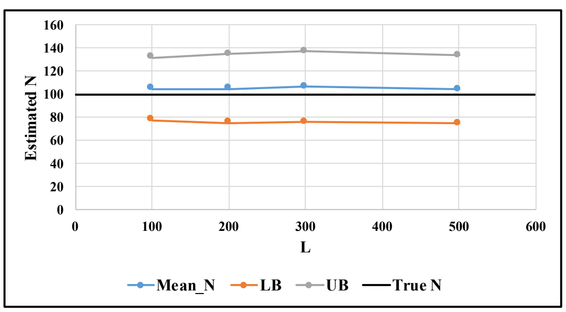
(b) $P = 0.10$



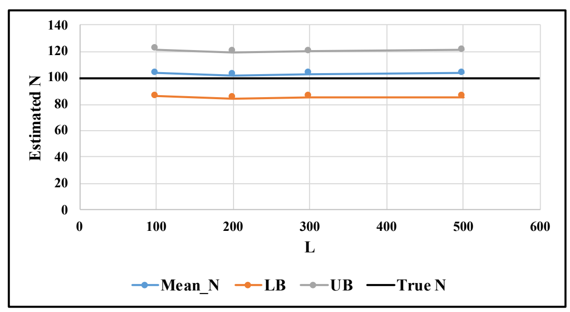
(c) $P = 0.15$



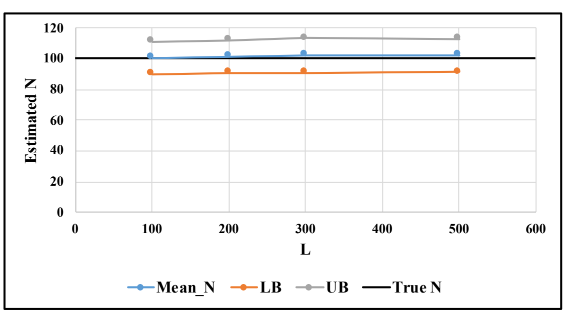
(d) $P = 0.20$



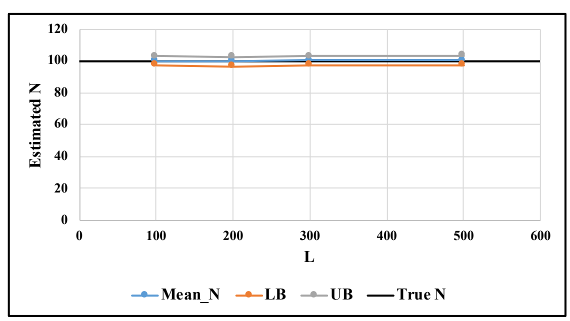
(e) $P = 0.30$



(f) $P = 0.40$



(g) $P = 0.50$



(h) $P = 0.75$

Figure 4.1: Estimated Value of N for Different Values of Probability of Detection P and Different Values of L (Number of Added Zeros). True N (black), Estimated N (blue), and Upper and Lower Confidence Interval Limit (gray and orange respectively)

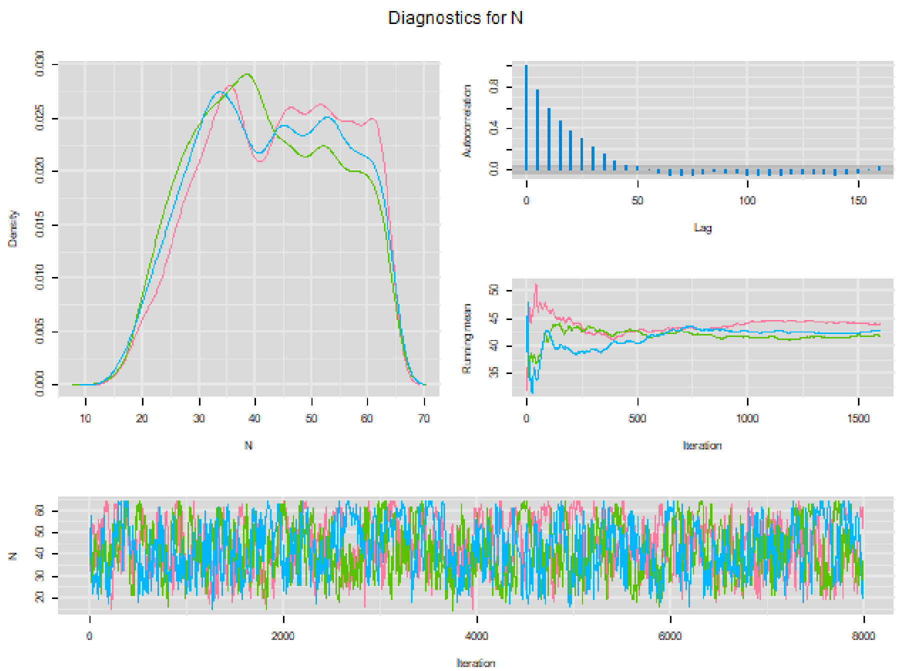


Figure 4.2: Diagnostic Plots for N with $P = 0.05$ and $L = 100$. Density (top left), Autocorrelation (top right), Ruining mean (middle right), and Trace (bottom)

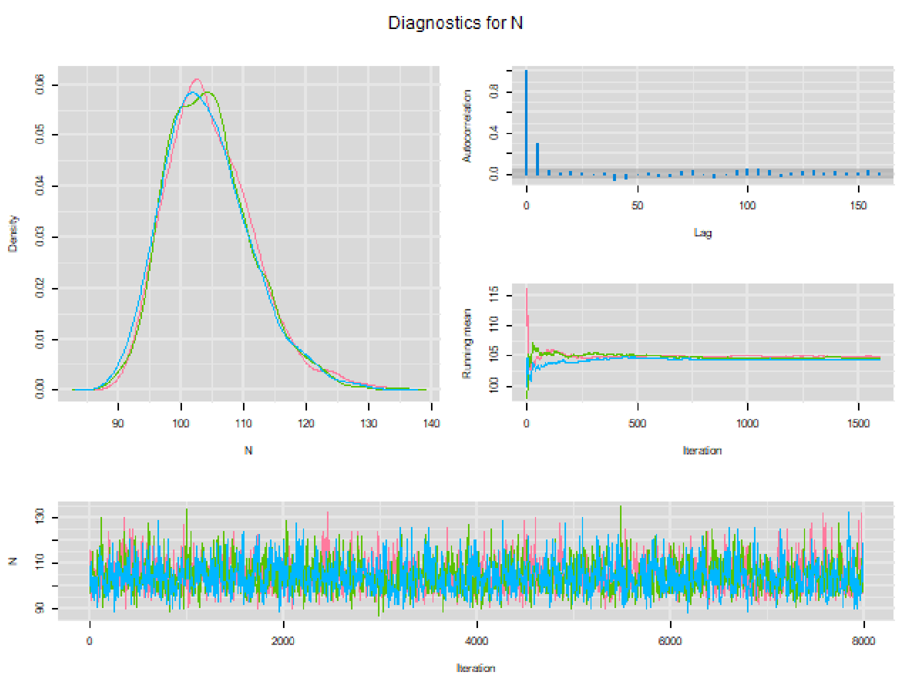
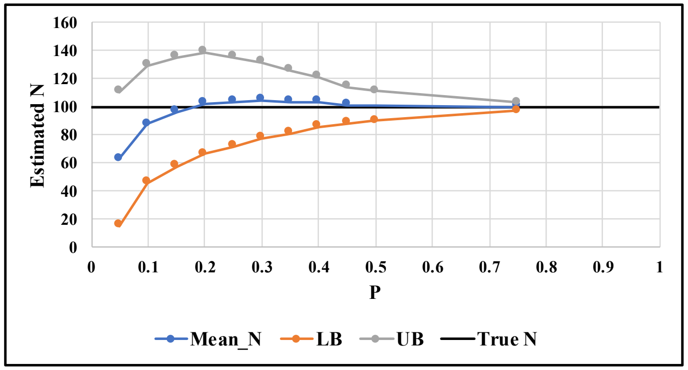


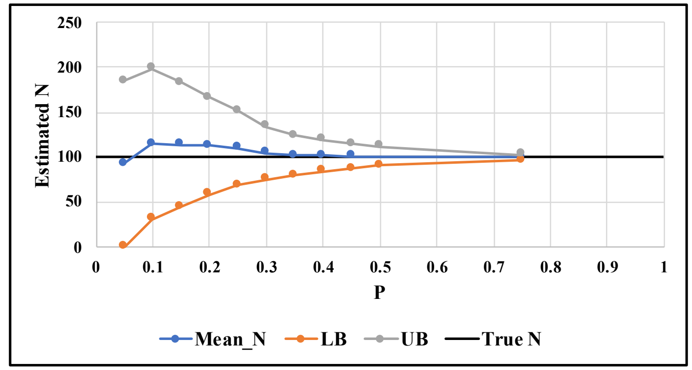
Figure 4.3: Diagnostic Plots for N with $P = 0.30$ and $L = 100$. Density (top left), Autocorrelation (top right), Ruining mean (middle right), and Trace (bottom)

4.2 Sensitivity of the Model to the Probability of Detection

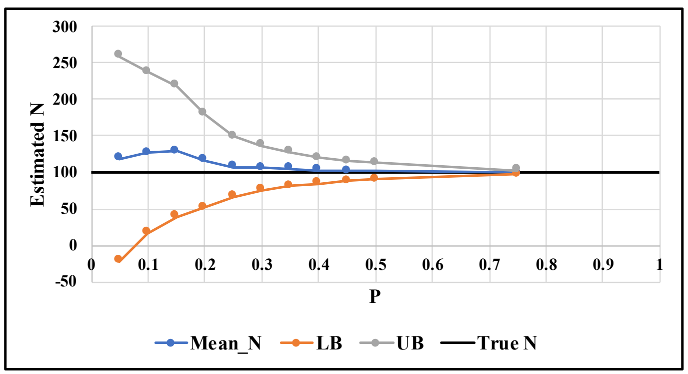
In this section, we study the sensitivity of the model to the probability of detection. To do this, we sample unknown probability of detection using a non-informative prior distribution and assume cameras are randomly located with regard to home range centers. In this way, P_{ij} can be set based on the distance of the camera location and the spatial location of individual animal. Results in previous simulations show that with a large enough number of zeros L added to the model, we can get a reasonable estimate for N. Again from the simulation results in a Table 4.1 and Figure 4.4 we would like to study the variation of estimated value of N with regard to different levels of probability of detection. As we can see, the estimated value of N is improved as we increase the probability of detection.



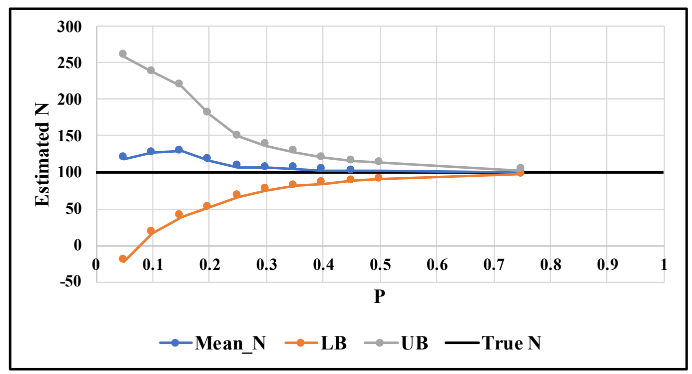
(a) $L = 100$



(b) $L = 200$



(c) $L = 300$



(d) $L = 400$

Figure 4.4: Estimated Value of N for Different Values of Probability of Detection P and L. True N (black), Estimated N (blue), Upper and Lower Confidence Interval Limit (gray and orange respectively)

From diagnostic Figures 4.5, and 4.6, display that from the trace plots, we have perfect mixing chains in the case of $P = 0.30$ and $L = 100$ comparing with worst-case scenario $P = 0.05$ and $L = 100$. Also, the autocorrelation drops faster in the case of $P = 0.30$ and $L = 100$. Additionally, from the first 1500 iterations, we see that all three chains convergence to the same mean in an early number of iteration. That means, the starting values do not impact on the estimated mean. Overall, we can get convergence even with low levels of probability of detection with large enough L add to the model.

From simulation results in Table 4.2 and Figure 4.7, shows that the estimated value of the probability of detection associated with different L added to the model. We can observe that the estimated value of the probability of detection is a great estimate regardless to the L added to the model when the true value of P is quite large (bigger than 0.20). Overall, the estimated value of the probability of detection has less sensitivity to the L added to the model than estimated N. Still we can get a reasonable estimate of P even when the true value of P as low as 0.05 with (100%) of L add to the model.

4.3 Sensitivity of the Model to the Number of Occasions

For all previous simulations, we conclude that we have to maintain a reasonable level of probability of detection to have reliable estimate of the population size. The problem is that the probability of detection itself is unknown, due to that we do not know how animals occur in front of the camera trap and detect them. Also, it is not easy to estimate the probability unless we can take many samples. Therefore, we will do one more simulation to see the impact of the number of samples (occasions) on the population size and probability of detection.

From simulation results in Table 4.3 and Figure 4.8, we observe that at a low number of occasions K, the probability of detection has an impact on the mean of the estimated value of the population size N. As we increase K, the estimated value N is not affected by the

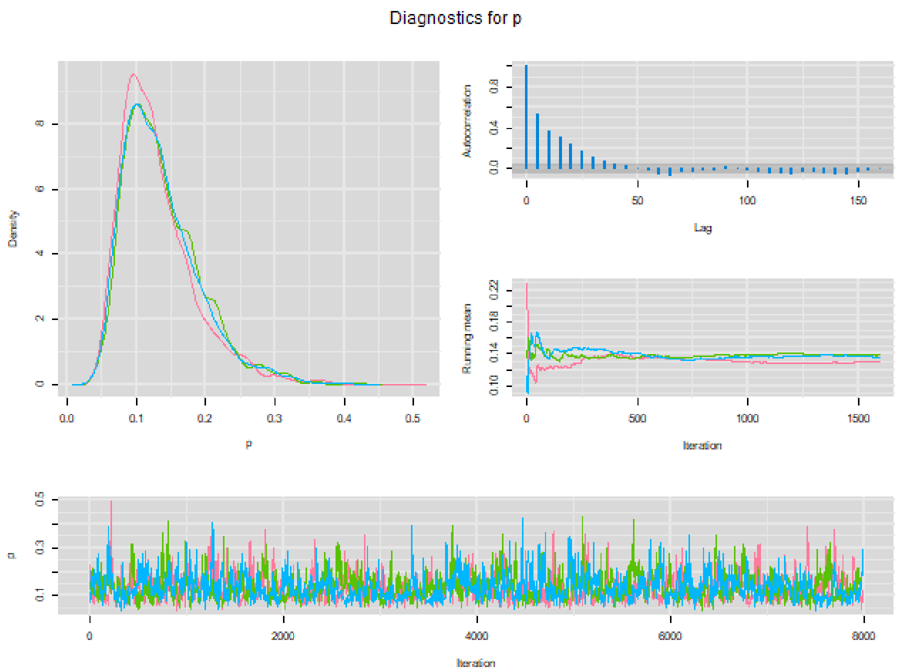


Figure 4.5: Diagnostics for Estimated P with $P = 0.05$ and $L = 100$. Density (top left), Autocorrelation (top right), Ruining mean (middle right), and Trace (bottom)

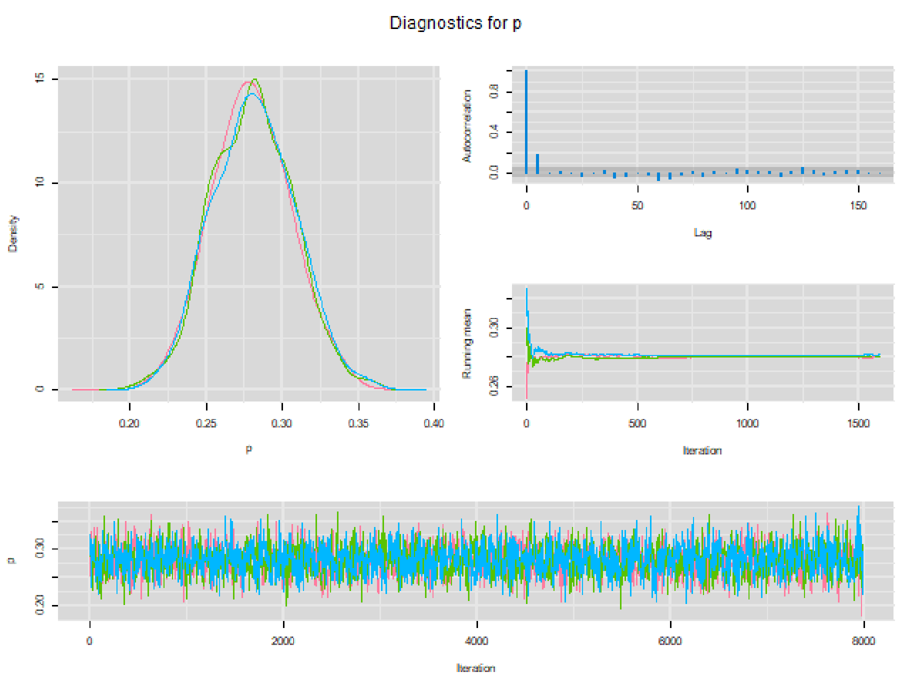
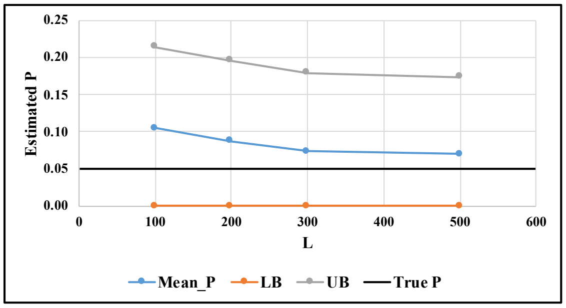


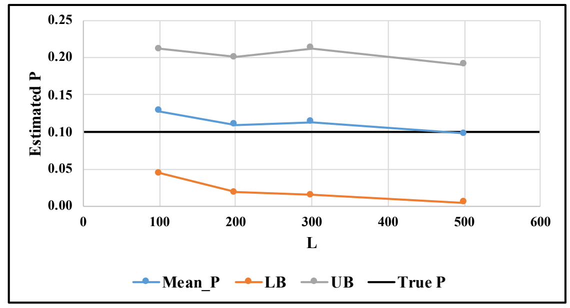
Figure 4.6: Diagnostics for Estimated P with $P = 0.30$ and $L = 100$. Density (top left), Autocorrelation (top right), Ruining mean (middle right), and Trace (bottom)

Table 4.2: Estimated Mean of P for Different Values of L and for Different Levels of Probability of Detection

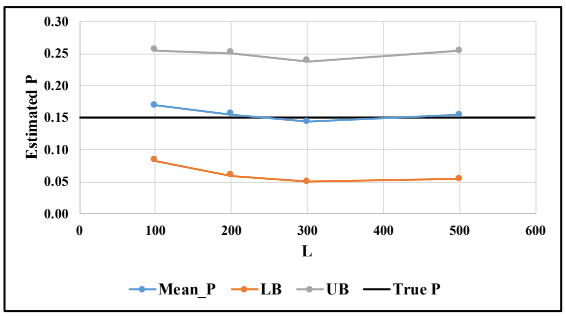
P	L	$\hat{P}$	sd_P	Median	LB_{Adj}	UB	d
0.05	100	0.105	0.054	0.092	0.000	0.214	0.217
	200	0.088	0.054	0.074	0.000	0.196	0.216
	300	0.074	0.053	0.059	0.000	0.179	0.211
	500	0.070	0.052	0.056	0.000	0.173	0.206
0.10	100	0.128	0.042	0.121	0.045	0.212	0.167
	200	0.109	0.046	0.101	0.018	0.201	0.182
	300	0.113	0.049	0.105	0.015	0.212	0.197
	500	0.098	0.046	0.089	0.005	0.191	0.186
0.15	100	0.169	0.043	0.164	0.083	0.255	0.172
	200	0.156	0.048	0.151	0.060	0.251	0.191
	300	0.144	0.047	0.139	0.050	0.238	0.189
	500	0.154	0.050	0.149	0.054	0.254	0.201
0.20	100	0.211	0.044	0.207	0.123	0.300	0.177
	200	0.198	0.048	0.195	0.103	0.293	0.190
	300	0.192	0.048	0.190	0.096	0.289	0.193
	500	0.198	0.049	0.196	0.101	0.296	0.195
0.25	100	0.253	0.045	0.251	0.163	0.343	0.180
	200	0.243	0.046	0.241	0.151	0.336	0.185
	300	0.250	0.047	0.248	0.156	0.344	0.189
	500	0.251	0.048	0.250	0.156	0.346	0.190
0.30	100	0.299	0.044	0.297	0.210	0.388	0.178
	200	0.296	0.045	0.295	0.205	0.387	0.182
	300	0.295	0.045	0.294	0.204	0.385	0.181
	500	0.297	0.046	0.296	0.205	0.388	0.183
0.35	100	0.345	0.043	0.345	0.258	0.432	0.174
	200	0.349	0.044	0.348	0.261	0.437	0.175
	300	0.342	0.044	0.342	0.255	0.430	0.175
	500	0.351	0.044	0.351	0.263	0.439	0.175
0.40	100	0.393	0.042	0.393	0.310	0.476	0.167
	200	0.396	0.042	0.396	0.312	0.480	0.168
	300	0.398	0.042	0.398	0.314	0.481	0.167
	500	0.395	0.042	0.394	0.311	0.478	0.167
0.45	100	0.454	0.040	0.455	0.375	0.533	0.158
	200	0.449	0.040	0.449	0.368	0.529	0.160
	300	0.447	0.040	0.447	0.367	0.527	0.160
	500	0.444	0.040	0.445	0.364	0.525	0.160
0.50	100	0.502	0.038	0.502	0.426	0.577	0.151
	200	0.501	0.038	0.501	0.425	0.577	0.152
	300	0.489	0.038	0.490	0.413	0.566	0.153
	500	0.496	0.038	0.496	0.420	0.571	0.152
0.75	100	0.748	0.027	0.749	0.694	0.802	0.108
	200	0.750	0.027	0.751	0.696	0.804	0.107
	300	0.752	0.027	0.753	0.698	0.806	0.107
	500	0.744	0.027	0.745	0.690	0.799	0.109



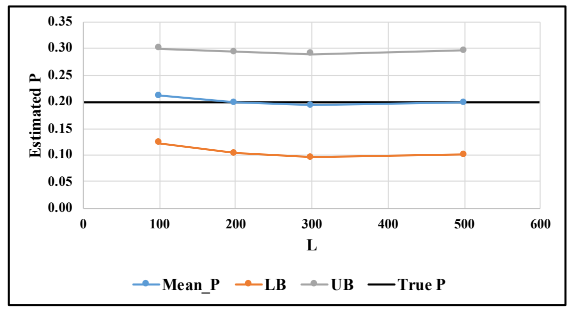
(a) $P = 0.05$



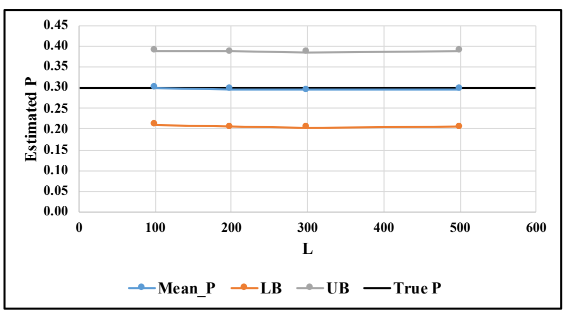
(b) $P = 0.10$



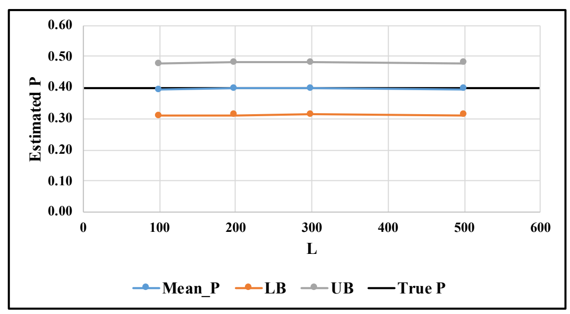
(c) $P = 0.15$



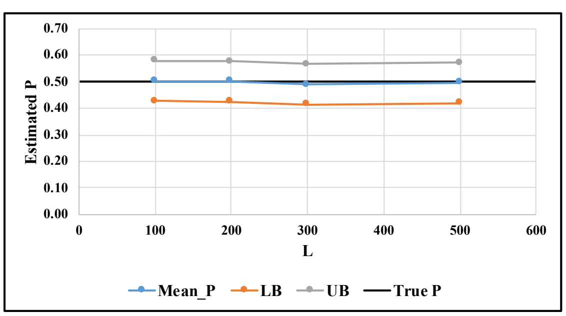
(d) $P = 0.20$



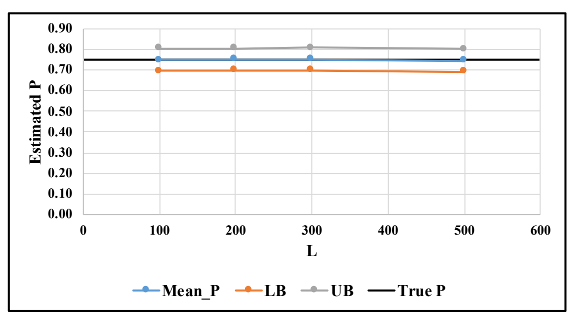
(e) $P = 0.30$



(f) $P = 0.40$



(g) $P = 0.50$



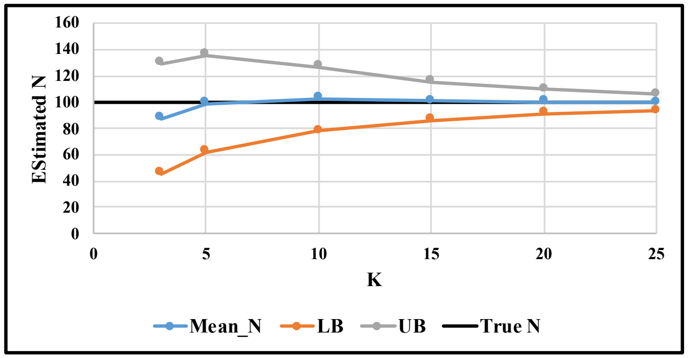
(h) $P = 0.75$

Figure 4.7: Estimated Value of P for Different Values of Probability of Detection P and L. True P (black), Estimated P (blue), Upper and Lower Confidence Interval Limit (gray and orange respectively)

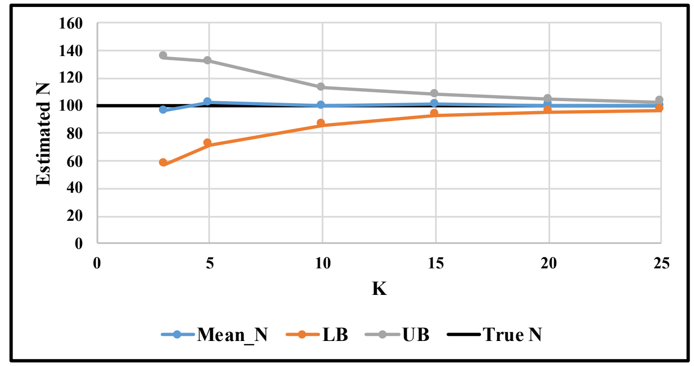
Table 4.3: Estimated Mean of N for Different Number of Occasions and for Different Levels of Probability of Detection

K	P	$\hat{N}$	Sd_N	Median	LB	UB	d	# of_det
3	0.10	87.561	20.936	87.455	45.690	129.433	83.743	27.450
	0.15	96.057	19.428	95.360	57.202	134.912	77.710	38.300
	0.20	100.310	17.810	98.970	64.691	135.929	71.239	38.300
	0.25	104.373	16.066	102.750	72.241	136.506	64.265	57.100
5	0.10	98.903	18.249	98.260	62.405	135.401	72.996	40.280
	0.15	101.974	15.193	100.400	71.587	132.361	60.774	56.120
	0.20	103.402	12.086	101.960	79.230	127.575	48.345	56.120
	0.25	101.285	8.659	100.370	83.967	118.602	34.634	75.980
10	0.10	102.521	12.239	101.120	78.043	126.998	48.955	65.100
	0.15	99.711	6.770	99.020	86.171	113.251	27.080	79.460
	0.20	99.748	4.266	99.310	91.217	108.279	17.062	79.460
	0.25	99.779	2.802	99.435	94.174	105.383	11.209	93.740
15	0.10	100.763	7.213	100.085	86.337	115.190	28.853	78.690
	0.15	100.843	3.748	100.420	93.347	108.339	14.992	91.500
	0.20	99.963	2.074	99.740	95.816	104.110	8.294	91.500
	0.25	100.490	1.271	100.200	97.948	103.032	5.084	99.000
20	0.10	100.432	4.572	99.990	91.288	109.576	18.288	87.710
	0.15	100.238	2.206	99.970	95.826	104.650	8.824	95.520
	0.20	99.931	1.124	99.760	97.682	102.180	4.497	95.520
	0.25	100.026	0.559	99.714	98.909	101.143	2.234	99.714
25	0.10	99.595	3.179	99.200	93.237	105.954	12.717	91.280
	0.15	99.942	1.404	99.680	97.134	102.749	5.615	98.140
	0.20	99.975	0.637	99.590	98.702	101.249	2.547	99.520
	0.25	99.983	0.286	99.900	99.411	100.555	1.144	99.900

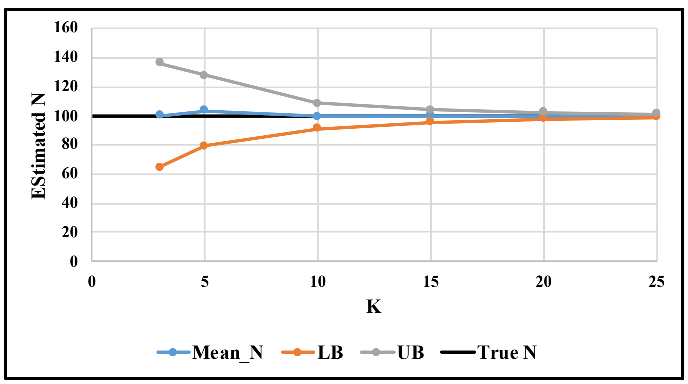
probability of detection. For instance, the estimated value of N associated with $K = 5$ and $P = 0.10$ is around 99 knowing that the true value is 100. As a result, we can conclude, if the probability of detection is small or we do not have enough information about the abundance of animals, increasing the number of occasions can lead to have a good estimate of the population size.



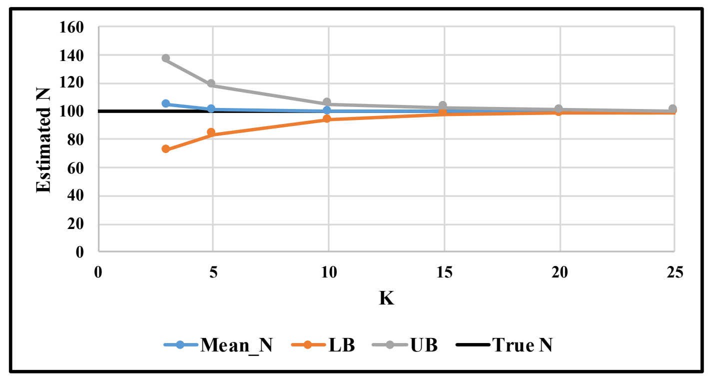
(a) $P = 0.10$



(b) $P = 0.15$



(c) $P = 0.20$



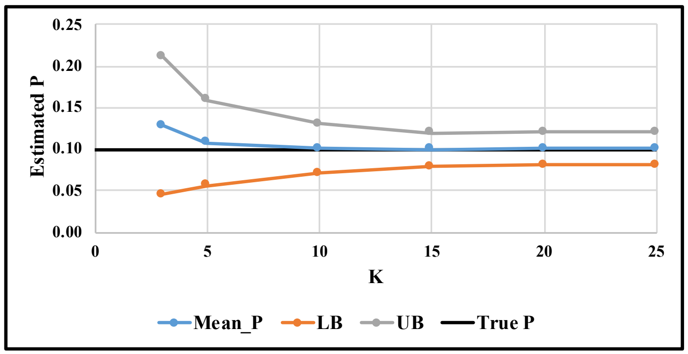
(d) $P = 0.25$

Figure 4.8: Estimated Value of N for Different Values of Probability of Detection P and Different Number of Occasions K. True N (black), Estimated N (blue), Upper and Lower Confidence Interval Limit (gray and orange respectively)

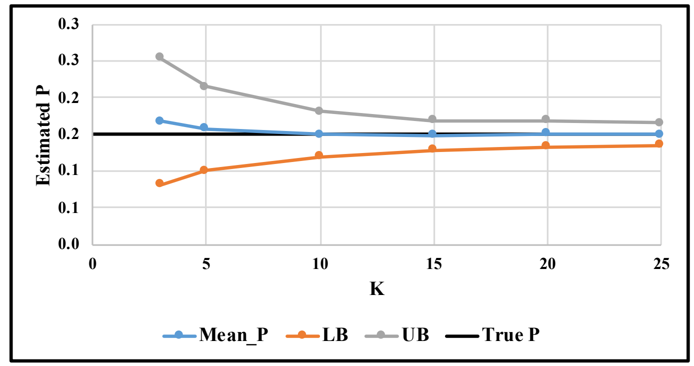
Simulation results in Table 4.4 and Figure 4.9 shows that the estimated value of the probability of detection is less sensitive to the number of occasions where increasing the number of occasions is not affecting the estimated value of the probability of detection.

Table 4.4: Estimated P for Different Number of Occasions and for Different Levels of Probability of Defections

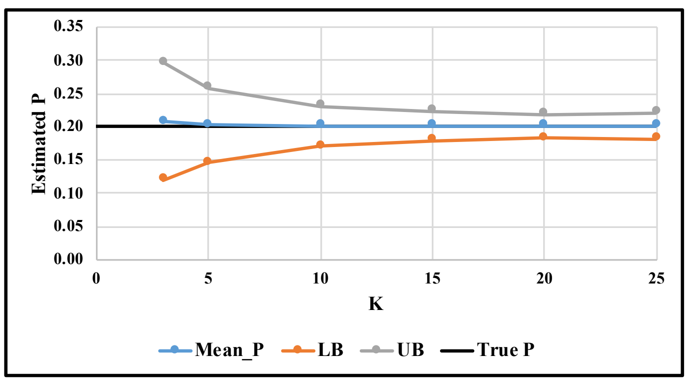
K	P	$\hat{P}$	Sd_P	Median	LB	UB	d
3	0.10	0.128	0.042	0.121	0.045	0.212	0.167
	0.15	0.168	0.043	0.163	0.082	0.254	0.172
	0.20	0.208	0.044	0.204	0.119	0.296	0.177
	0.25	0.250	0.045	0.248	0.161	0.339	0.178
5	0.10	0.108	0.026	0.105	0.056	0.160	0.103
	0.15	0.158	0.029	0.156	0.101	0.215	0.114
	0.20	0.202	0.028	0.201	0.146	0.259	0.113
	0.25	0.251	0.030	0.250	0.191	0.311	0.120
10	0.10	0.101	0.015	0.100	0.071	0.131	0.060
	0.15	0.150	0.015	0.150	0.120	0.181	0.062
	0.20	0.201	0.015	0.201	0.171	0.231	0.061
	0.25	0.251	0.019	0.251	0.214	0.289	0.075
15	0.10	0.099	0.010	0.099	0.079	0.119	0.040
	0.15	0.149	0.010	0.149	0.129	0.169	0.040
	0.20	0.202	0.011	0.202	0.180	0.224	0.044
	0.25	0.247	0.010	0.247	0.227	0.267	0.040
20	0.10	0.101	0.010	0.101	0.081	0.121	0.040
	0.15	0.151	0.009	0.151	0.133	0.169	0.037
	0.20	0.201	0.009	0.201	0.183	0.219	0.036
	0.25	0.254	0.010	0.254	0.234	0.274	0.040
25	0.10	0.101	0.010	0.101	0.081	0.121	0.040
	0.15	0.150	0.007	0.150	0.135	0.165	0.030
	0.20	0.201	0.010	0.201	0.181	0.221	0.040
	0.25	0.249	0.010	0.249	0.229	0.269	0.040



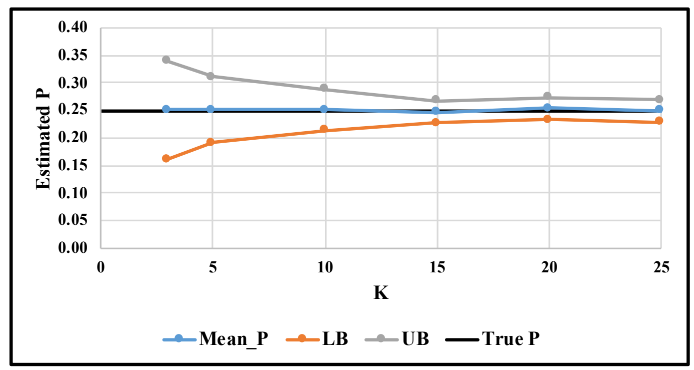
(a) $P = 0.10$



(b) $P = 0.15$



(c) $P = 0.20$



(d) $P = 0.25$

Figure 4.9: Estimated Value of P for Different Levels of Probability of Detection P and Different Number of Occasions K. True P (black), Estimated P (blue), Upper and Lower Confidence Interval Limit (gray and orange respectively)

4.4 Sensitivity of the Model to ψ

In this section, we study the sensitivity of the original spatial model to parameter ψ in estimating the population size. Simulation experiments were designed in order to study the impact of ψ on estimation of the population size.

First, we used an uninformative prior to sample the parameter ψ with no constraint, i.e., accepting all sampled values in the range of $[0, 1]$. Next, we performed a set of simulations using different constraints for the sampled parameter ψ.

To obtain an accurate estimate of N, ψ must be equal to $\frac{N}{M}$. However, in real applications, population size N is unknown and it is not practical to set $\psi = \frac{N}{M}$. Rather ψ can be estimated by $\hat{\psi} = \frac{\hat{N}}{M}$ in each iteration of MCMC, where we assume that the parameter $\hat{\psi}$ has a beta distribution with parameters $[1 + \sum w]$ and $[1 + M - \sum w]$. As it was discussed before, the value of M must be chosen to be an integer number much greater than N $(M >> N)$.

Table 4.5: Summary of the Estimated Mean of σ, λ_0, ψ, and Population Size N for Different ranges of ψ and $M \in \{100, 200\}$

M	ψ	$\hat{\sigma}$	$\hat{\lambda}_0$	$\hat{\psi}$	$\hat{N}$	ESS$_N$	ESS$_\psi$	Lag10$_N$	Lag10$_\psi$
100	0.00_1.00	0.437	0.589	0.313	30.887	1113.233	1297.546	0.668	0.625
	0.00_0.50	0.451	0.606	0.274	27.107	1850.818	2180.853	0.482	0.412
	0.10_0.40	0.465	0.585	0.253	25.255	2679.348	3232.658	0.403	0.324
	0.05_0.35	0.479	0.584	0.231	23.326	2505.535	3144.948	0.395	0.309
	0.10_0.35	0.471	0.589	0.237	23.862	2738.365	3681.929	0.352	0.26
200	0.00_1.00	0.416	0.596	0.199	39.231	250.556	263.285	0.909	0.894
	0.00_0.50	0.443	0.579	0.158	30.979	1066.802	1140.428	0.674	0.623
	0.10_0.40	0.415	0.579	0.174	33.433	2340.808	2727.217	0.496	0.431
	0.05_0.35	0.443	0.579	0.153	29.922	2082.790	2203.174	0.547	0.486
	0.10_0.35	0.411	0.592	0.173	33.34	3017.466	3701.673	0.446	0.375

Table 4.5 shows results from a single simulation repeated five times (choosing the same random samples) and each time we set a constraint on the parameter ψ except the first one with no constraint.The estimated values of σ, λ_0, ψ, and N were calculated, and the effective sample size (ESS) and $lag10$ for N and ψ. Comparing the estimated values of the population size N before the constraint was set on the parameter ψ and after. In all

cases, the estimated values of N are better with the constraints on ψ. Also, we notice that as we decrease the range of the parameter ψ using N/M as a center of the interval, the effective sample size will increase. However, we can not get this range extremely narrow due to the simulation cost; the rejection rate will be high, and ψ's true value is unknown. Finally, since we do not know precisely how large the value of M in the real data, we will stick with two constraints for the parameter ψ. From 0 to 0.5 and from 0.10 to 0.40 and compare the results from 50 simulations where we can not generalize the results from just a single simulation.

Table 4.6: Summary of 50 Runs of the Estimated Mean of σ, λ_0, ψ, and Population size N for Different ranges of ψ and $M \in \{100, 200\}$

M	ψ	$\hat{\sigma}$	$\hat{\lambda}_0$	$\hat{\psi}$	$\hat{N}$	ESS$_N$	ESS$_\psi$	Lag10$_N$	Lag10$_\psi$
100	0.00_1.00	0.560	0.497	0.323	31.943	1674.270	1862.417	0.635	0.593
	0.00_0.50	0.563	0.546	0.273	27.173	3661.706	4368.037	0.393	0.334
	0.10_0.40	0.516	0.557	0.261	26.251	5986.954	7677.659	0.270	0.205
200	0.00_1.00	0.546	0.527	0.170	33.321	1490.301	1778.776	0.670	0.620
	0.00_0.50	0.527	0.564	0.158	31.026	2647.456	3152.341	0.528	0.473
	0.10_0.40	0.496	0.545	0.165	31.168	3879.974	4606.632	0.412	0.355

Table 4.6 shows the estimated values of σ, λ_0, ψ with its ESS and $Lag10$ and N with its ESS and $Lag10$. For $M = 100$, the estimated value of the population size N in the case of no constraint on the parameter ψ is around 32, with ESS equal to 1862.4. After the parameter ψ range is reduced to 0.00 to 0.50 and reject all samples with $\psi > 0.50$, the estimated value of N is around 27 with 4368 ESS. Moreover, reducing ψ range from 0.10 to 0.40 will improve the estimated value to 26, and the ESS will be 7677.6.

Comparing Figures 4.10, 4.11, and 4.12, parameter sigma and λ_0 are comparable, and in all cases, we set that the densities of the parameter converged to the posterior distribution. In the case with the constraint on parameter ψ, we have a better mixing of the chains, making the estimated in is more accurate.

For $M = 200$, the average of the estimated population size N with no constraint on the parameter ψ is around 33 with 1778.8 ESS. For other two constraints on the parameter ψ, we notice that the estimated population size N in both cases is around 31. However, the

ESS value is higher with the reduced range of ψ (0.10 to 0.40), for more details see tables. In addition, comparing the results for $M = 100$ with $M = 200$, we can see that in the case of $M = 100$ the ψ value from 0.10 to 0.40 has the highest $ESS = 7677.6$ and then it has the best estimate of N ($\hat{N} = 26$). Notice that $ESS = 7677$ means the $90,000$ MCMC sample (iterations) is equivalent to 7677 independent sample [where MCMC sample is highly correlated]. Generally, in the cases that we get the values of ESS are very close, we can use the constraint for ψ; 0 to 0.50.

If ψ is not regularized, estimated σ is between 0.3 and 2.03 with an average of 0.56. After regularizing ψ by constraining its range to [0,0.50], the estimated value of σ is between 0.4 and 1.7. After regularizing ψ and constraining its range to [0.1,0.40], the estimated σ is between 0.39 and 0.8 with an average of 0.52 that has the lowest absolute error. The estimated λ_0 for the aforementioned range of ψ are 0.497, 0.546, and 0.557, respectively.

The estimated population size ranges from 8 to 61 with an average of 32 for no restriction on ψ, from 6 to 37 with an average of 27 for ψ belongs to [0,0.50], and from 16 to 37 with an average of 26 for for ψ belongs to [0.1,0.40]. We can see the estimated value of the population size is more accurate, and the range of estimated values is narrower after regularizing ψ (see Tables A.1 to A.3).

Moreover, for no restrictions on ψ, the standard error for the estimated population size ranges from 5.8 to 24.7, with a 14.37 average. Additionally, the standard error is between 5.8 and 13, with an average of 8.56 for $\psi \leq 0.5$. Furthermore, by reducing ψ constraint from 0.10 to 0.40, the standard error ranges from 5 to 9 with an average of 6.8 (see Tables 4.7 to 4.9).

Table 4.7: Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population size N with no Constraint on ψ and $M = 100$

Sim #	Mean	Median	Mode	sd	Credible interval (HDI)	
					LB	UB
1	46.594	43	27.976	23.309	13	88
2	38.620	33	23.031	21.047	11	71
3	35.607	30	9.056	24.702	4	72
4	39.617	37	33.996	15.136	19	62
5	47.420	43	32.977	20.393	20	81
6	15.129	14	10.999	8.916	1	24
7	36.459	34	35.981	14.743	16	58
8	43.232	39	29.028	18.875	18	73
9	61.516	61	55.981	20.859	35	100
10	37.617	34	25.024	18.753	11	67
11	35.184	35	5.019	18.703	4	57
12	14.074	12	10.063	7.066	6	24
13	38.323	35	35.981	15.142	17	59
14	32.097	28	18.951	15.439	13	52
15	29.161	27	29.017	12.394	13	48
16	28.835	25	16.986	15.326	11	48
17	37.492	35	33.027	15.816	15	62
18	38.681	35	36.021	15.956	17	64
19	27.289	25	23.037	11.143	13	42
20	23.206	21	19.042	8.960	12	35
21	37.039	36	35.020	17.176	10	60
22	17.509	17	16.000	5.812	10	26
23	25.269	23	20.004	12.264	7	42
24	25.343	23	21.967	10.221	13	38
25	20.912	19	20.000	9.204	9	32
26	34.684	28	13.015	23.311	6	72
27	31.442	29	27.019	11.634	17	48
28	39.457	34	23.005	19.003	15	69
29	25.126	23	21.015	11.612	11	42
30	44.033	40	28.971	17.065	21	70
31	27.587	26	24.001	10.766	14	42
32	17.123	16	15.012	6.959	8	27
33	31.891	29	29.008	15.093	11	53
34	25.522	24	23.054	10.933	10	39
35	26.965	23	16.043	15.035	9	48
36	26.291	23	14.953	13.708	11	43
37	7.616	3	2.029	9.711	2	18
38	30.783	29	27.039	11.893	14	48
39	22.957	22	19.976	6.827	14	33
40	53.207	49	37.968	19.757	25	86
41	16.335	13	9.067	10.820	5	28
42	24.173	23	20.991	8.568	13	37
43	18.290	17	15.018	7.091	9	28
44	40.149	38	33.996	14.749	19	63
45	48.687	44	34.989	19.959	21	81
46	23.265	20	13.962	13.316	7	41
47	48.052	44	31.981	18.581	22	78
48	38.741	36	34.974	16.320	15	66
49	23.422	21	20.038	11.791	8	40
50	39.106	36	25.014	16.789	15	63
Mean	31.943	29.080	23.726	14.373	12.800	52.960
Min	7.616	3	2.029	5.812	1	18
Max	61.516	61	55.981	24.702	35	100

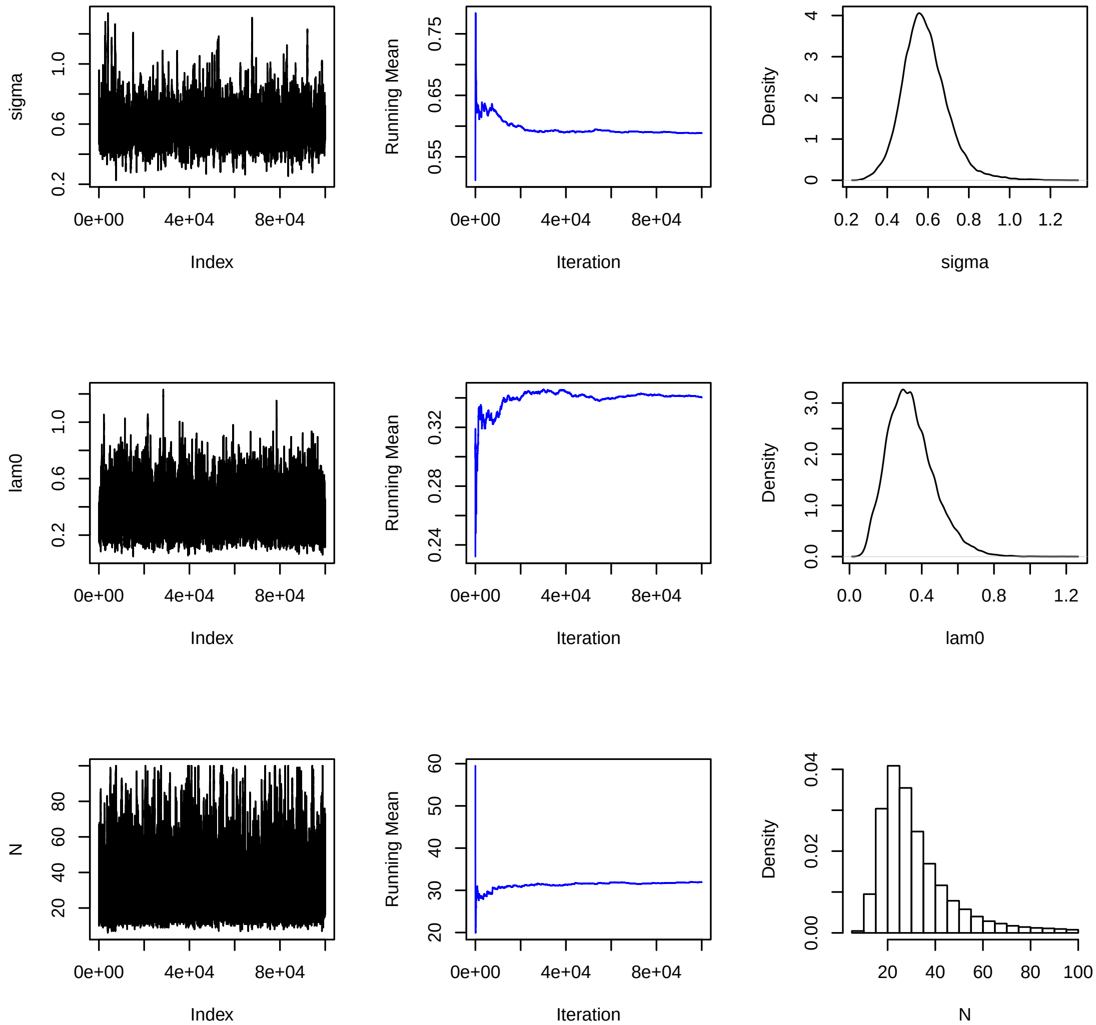


Figure 4.10: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with no Constraint on ψ and $M = 100$

Table 4.8: Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population size N with $\psi \in [0, 0.50]$ and $M = 100$

Sim #	Mean	Median	Mode	sd	Credible interval (HDI)	
					LB	UB
1	15.961	12	6.998	10.393	5	39
2	23.497	22	21.986	8.739	9	42
3	29.486	29	25.002	9.475	14	49
4	34.753	34	30.000	7.706	22	51
5	23.674	23	20.000	8.015	10	40
6	35.129	35	35.994	9.041	19	53
7	35.331	35	37.006	8.049	21	51
8	6.311	4	2.017	6.885	2	21
9	27.271	26	16.987	9.996	12	47
10	18.626	18	17.005	5.776	9	30
11	36.326	37	35.976	10.393	17	58
12	24.611	23	15.978	10.383	9	46
13	16.466	15	13.031	7.603	6	33
14	25.798	24	18.974	8.218	13	43
15	25.463	24	24.012	7.954	13	43
16	13.702	12	12.012	6.527	6	27
17	28.947	28	24.985	9.549	14	49
18	32.953	33	27.992	9.080	17	50
19	31.333	31	24.974	8.498	17	49
20	23.745	23	20.017	8.286	10	41
21	21.302	20	21.019	6.915	11	36
22	22.409	21	18.945	6.570	12	36
23	26.768	26	24.992	7.747	14	43
24	37.145	37	39.012	7.979	24	54
25	19.587	18	19.019	6.849	9	34
26	27.441	26	23.032	8.931	14	47
27	21.185	20	20.008	7.019	10	36
28	30.886	30	24.001	9.462	15	50
29	29.765	29	27.004	9.796	14	50
30	29.288	28	25.970	10.190	13	50
31	31.077	32	34.979	12.982	4	52
32	37.623	38	37.065	8.808	22	55
33	31.815	31	25.009	9.248	16	50
34	29.531	29	27.000	8.451	16	47
35	29.670	29	26.987	9.259	15	49
36	24.040	23	21.989	6.962	13	39
37	36.223	36	30.977	7.976	23	53
38	37.492	38	38.996	8.750	21	53
39	29.247	29	24.001	10.909	9	51
40	29.912	29	25.990	9.251	15	49
41	24.976	23	17.975	8.736	12	44
42	23.978	23	19.010	7.000	13	39
43	36.558	37	29.985	8.872	21	54
44	32.551	33	35.977	11.703	11	54
45	22.691	22	19.945	6.920	12	38
46	33.604	33	27.988	8.166	20	50
47	17.826	17	16.985	6.443	8	31
48	25.594	24	23.997	9.033	12	45
49	21.052	19	17.041	8.066	9	38
50	28.013	27	26.981	8.282	15	46
Mean	27.173	26.300	24.057	8.557	13.360	44.700
Min	6.311	4	2.017	5.776	2	21
Max	37.623	38	39.012	12.982	24	58

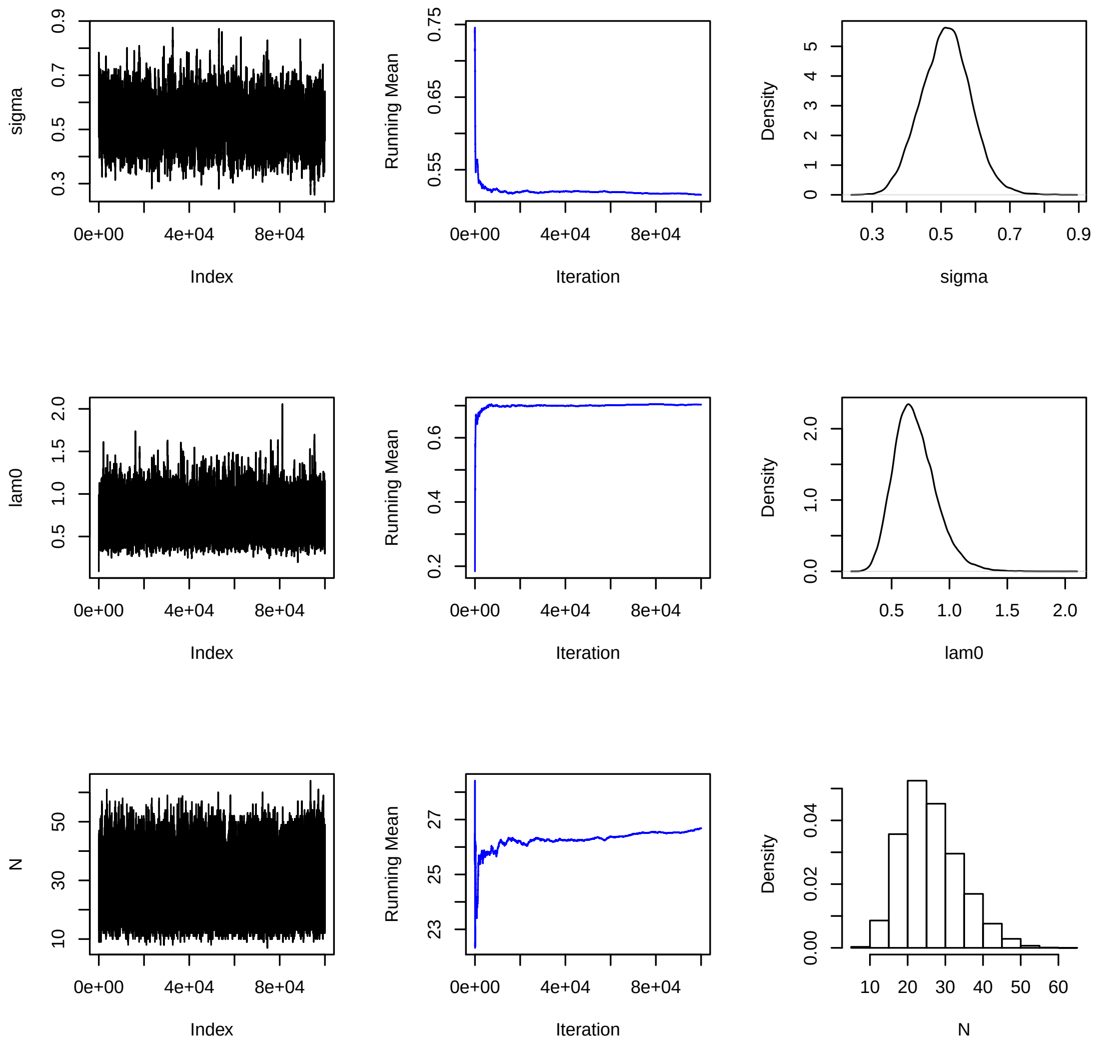


Figure 4.11: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with $\psi \in [0, 0.50]$ and $M = 100$

Table 4.9: Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population size N with $\psi \in [0.10, 0.40]$ and $M = 100$

Sim #	Mean	Median	Mode	sd	Credible interval (HDI)	
					LB	UB
1	29.159	29	25.974	6.129	19	42
2	24.919	24	20.994	7.921	12	41
3	23.655	23	24.001	6.364	13	36
4	26.832	26	23.020	6.139	17	40
5	27.923	28	24.997	7.189	15	41
6	19.963	19	19.988	6.253	10	33
7	29.888	30	32.003	6.218	19	42
8	26.117	25	22.997	6.785	15	40
9	21.702	20	20.992	8.176	9	38
10	34.317	35	34.997	6.468	22	47
11	25.729	25	20.966	8.166	12	41
12	31.279	31	32.998	7.173	18	45
13	27.167	27	27.031	6.842	15	40
14	23.889	23	21.992	8.986	10	42
15	22.732	22	21.017	6.376	12	35
16	32.604	33	33.006	6.415	21	45
17	23.994	23	19.013	7.103	13	39
18	26.383	26	22.017	8.399	12	42
19	27.906	28	21.991	7.035	16	42
20	18.636	18	15.990	6.042	10	32
21	32.836	33	34.010	6.491	21	46
22	22.798	22	21.991	8.295	10	39
23	36.800	37	37.012	5.579	26	47
24	16.097	15	16.022	5.186	8	26
25	27.947	28	29.030	7.540	15	43
26	26.937	27	22.984	6.391	16	40
27	26.021	26	30.005	8.024	12	40
28	28.736	29	26.991	7.382	16	44
29	34.275	35	34.014	6.545	22	47
30	27.847	28	23.971	6.539	17	41
31	21.297	20	20.005	6.999	10	35
32	24.071	24	20.998	6.867	13	39
33	26.627	26	21.993	7.589	14	42
34	28.644	28	23.983	6.748	17	42
35	22.743	22	22.000	6.414	12	35
36	30.205	30	31.026	7.378	17	44
37	34.228	35	33.970	6.582	22	47
38	27.206	27	24.014	7.076	15	41
39	17.133	16	16.013	4.918	10	28
40	29.206	29	31.001	7.501	16	44
41	22.291	21	19.019	6.736	11	35
42	34.094	34	36.035	6.639	22	47
43	25.009	24	23.004	6.191	15	38
44	31.366	31	32.006	6.439	20	44
45	26.443	26	24.000	6.836	14	39
46	21.593	21	18.012	6.843	11	36
47	28.088	28	22.995	7.208	16	43
48	18.725	18	17.028	6.017	10	32
49	18.541	17	17.014	6.827	9	34
50	19.956	19	16.013	5.942	11	33
Mean	26.251	25.820	24.643	6.838	14.760	39.880
Min	16.097	15	15.990	4.918	8	26
Max	36.800	37	37.012	8.986	26	47

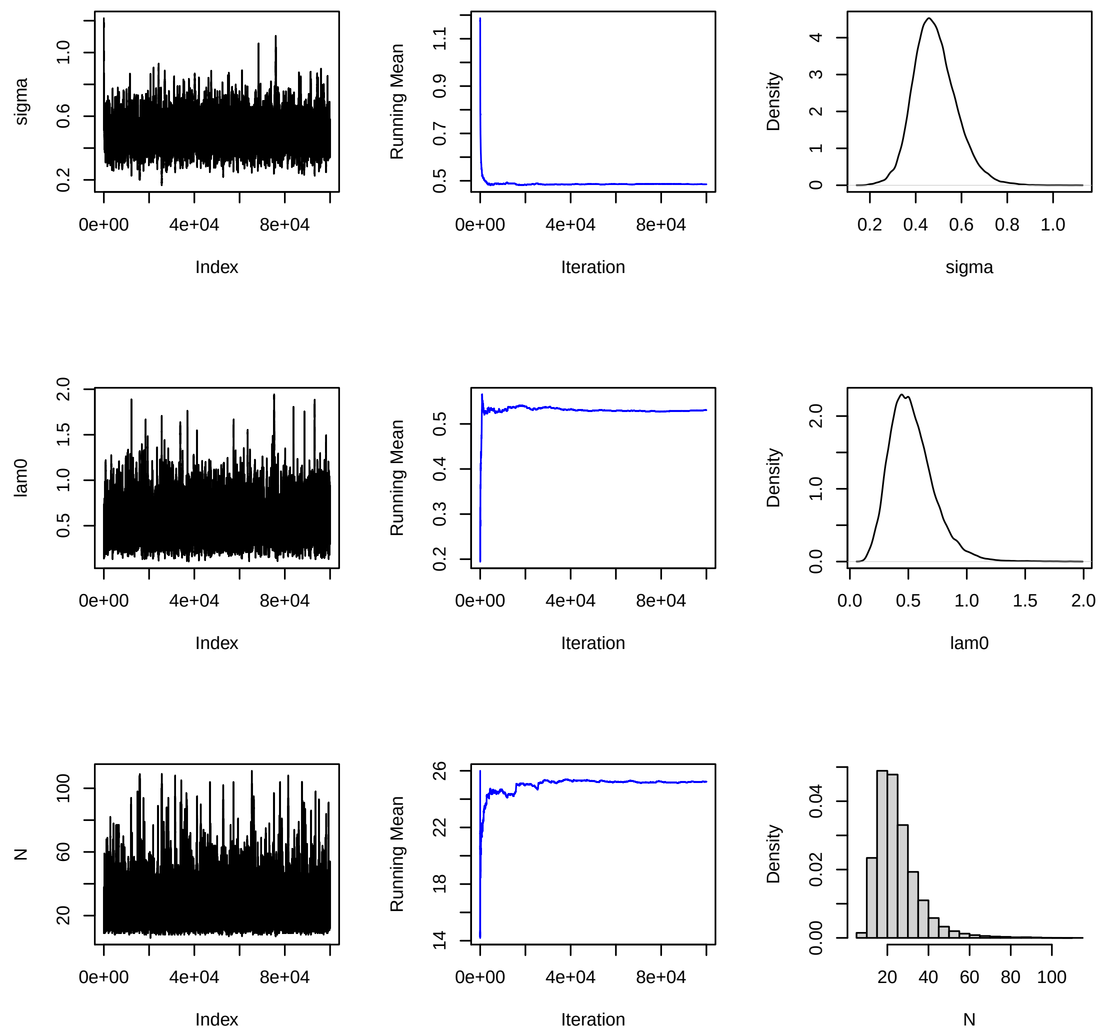


Figure 4.12: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with $\psi \in [0.10, 0.40]$ and $M = 100$

For $M = 200$, the estimated value of σ and λ_0 are comparable for all cases; 0.546, 0.527, and 0.496 for σ and 0.527, 0.564, and 0.545 for λ_0). However, the range of the estimated parameter is tighter as the range of ψ is reduced (see results in Tables A.4 to A.6).

The estimated population size ranges from 6 to 107 with an average of 33 with no constraint on ψ. By reducing the range of ψ to less than or equal to 0.50, the range of estimated N is from 11 to 61 with an average of 31. For ψ between 0.10 and 0.40, the estimated N ranges from 19 to 47 with an average of 31.

Comparing Figures 4.13, 4.14, and 4.15, in all cases, we observe that the densities of the parameter converged to the posterior distribution. Moreover, with a constraint on parameter ψ, we have a better mixing of the chains, making the estimated in is more accurate. The histogram tail of the estimated N is shorter with the constraint 0.10 to 0.40.

Finally, the average standard error for the estimated population size N is 18.5, and it ranges from 3 to 51.9 for no restrictions on ψ. Additionally, the standard error ranges from 3.9 to 24.4, with an average of 13 for $\psi \leq 0.5$, and for ψ between 0.10 and 0.40, the standard error ranges from 5.1 to 16.4 with an average of 10.6 as shown in Tables 4.10 to 4.12.

Table 4.10: Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population size N with no Constraint on ψ and $M = 200$

Sim #	Mean	Median	Mode	sd	Credible interval (HDI)	
					LB	UB
1	32.062	27	27.009	22.406	5	71
2	33.923	31	24.950	13.286	15	60
3	6.269	4	3.034	6.990	1	19
4	11.800	9	5.040	8.593	3	28
5	35.968	34	26.995	13.632	15	61
6	29.156	26	20.004	17.579	10	56
7	31.532	27	23.972	18.759	10	62
8	28.962	26	26.968	13.433	11	55
9	26.670	24	18.938	13.569	11	49
10	6.628	6	4.995	3.031	3	12
11	20.689	19	13.882	10.020	9	38
12	6.769	6	4.074	4.184	3	14
13	30.677	28	21.935	14.582	12	57
14	12.648	12	12.013	4.739	6	23
15	45.056	38	36.061	26.709	14	98
16	31.795	28	19.985	15.480	13	62
17	12.354	11	9.033	6.713	3	25
18	20.768	18	14.885	13.254	6	44
19	17.976	16	13.806	10.688	7	32
20	44.185	41	33.978	17.207	18	77
21	24.546	21	17.000	17.306	4	52
22	27.044	24	20.928	13.330	12	48
23	22.761	20	17.894	13.606	8	45
24	18.978	18	13.975	7.031	9	33
25	21.125	19	16.923	10.803	8	40
26	49.104	24	17.913	50.010	8	170
27	33.149	29	23.972	18.317	12	64
28	56.048	47	43.104	30.523	20	128
29	21.875	18	15.928	15.746	4	46
30	66.648	45	29.105	48.71	17	178
31	56.766	44	32.915	37.253	12	146
32	33.674	31	27.970	12.611	17	58
33	28.945	27	25.878	12.228	13	48
34	24.424	23	19.038	8.194	11	40
35	32.501	29	24.013	15.524	11	63
36	26.326	23	20.966	13.249	10	51
37	28.025	25	18.012	15.200	7	57
38	30.152	28	23.972	10.287	15	51
39	29.509	28	6.984	18.344	5	64
40	33.082	28	23.972	20.543	11	68
41	32.765	30	27.936	13.845	14	61
42	106.598	102	83.090	46.672	33	195
43	35.537	25	19.986	31.500	8	112
44	17.486	16	14.020	7.191	8	26
45	102.871	99	44.047	51.849	29	185
46	34.88	29	25.982	23.048	14	54
47	47.434	38	34.096	32.679	13	81
48	38.49	35	31.999	16.431	19	60
49	51.749	41	35.045	34.361	18	88
50	47.666	43	43.008	21.111	22	72
Mean	33.321	28.800	23.225	18.447	11.340	66.540
Min	6.269	4	3.034	3.031	1	12
Max	106.598	102	83.090	51.849	33	195

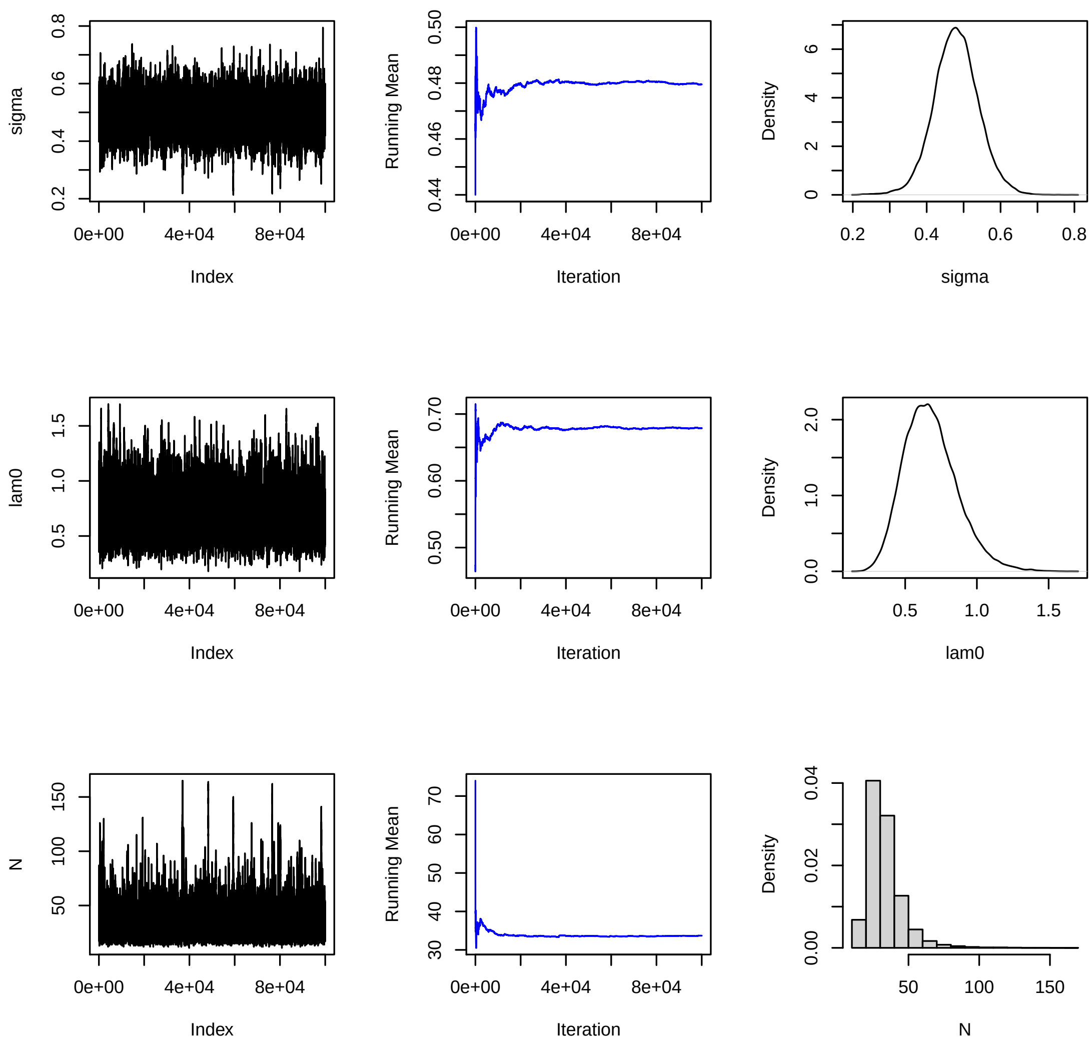


Figure 4.13: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with no Constraint on ψ and $M = 200$

Table 4.11: Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population size N with $\psi \in [0, 0.50]$ and $M = 200$

Sim #	Mean	Median	Mode	Sd_N	Credible interval (HDI)	
					LB	UB
1	43.012	36	29.051	22.796	13	91
2	23.433	22	20.965	8.634	10	41
3	22.297	21	16.006	8.236	10	38
4	33.096	30	29.025	15.802	10	68
5	36.655	33	33.033	16.016	12	70
6	49.402	49	46.956	23.764	9	94
7	16.325	15	14.043	8.477	4	33
8	21.625	21	16.997	7.138	10	35
9	19.885	18	20.010	8.052	8	36
10	31.491	29	29.014	13.542	13	61
11	45.702	43	42.999	15.407	21	80
12	43.621	41	41.989	15.083	21	77
13	41.679	38	26.983	18.740	14	83
14	25.083	23	20.022	9.341	11	43
15	28.388	26	24.008	10.483	13	50
16	35.338	34	31.006	10.346	19	56
17	18.235	17	19.000	5.459	10	29
18	23.003	22	20.046	9.187	6	40
19	28.767	27	27.029	10.598	13	49
20	48.774	45	30.017	20.503	19	94
21	41.805	39	39.984	15.353	18	76
22	26.085	24	20.981	10.424	12	47
23	47.601	44	41.039	22.343	11	95
24	15.414	12	12.989	11.843	3	37
25	35.971	33	34.963	15.877	12	70
26	37.320	35	33.036	13.117	17	64
27	18.529	17	14.999	8.062	8	35
28	11.234	9	4.993	6.856	3	25
29	15.867	12	9.036	13.358	2	43
30	30.112	28	26.994	10.979	15	52
31	32.660	27	19.048	20.130	8	79
32	30.691	28	27.966	11.335	15	55
33	36.815	34	32.043	14.265	16	68
34	16.915	16	15.994	5.528	8	28
35	40.058	35	24.929	18.792	14	82
36	27.430	26	24.068	8.286	15	44
37	36.404	34	35.996	14.970	13	67
38	26.706	25	19.960	8.865	13	45
39	31.562	30	28.987	11.024	14	53
40	21.900	19	16.025	10.801	7	41
41	32.010	29	32.025	15.732	5	64
42	16.359	14	12.017	7.842	6	31
43	20.778	20	20.984	6.031	11	33
44	41.873	37	30.058	24.402	5	90
45	11.678	11	10.038	3.924	6	20
46	19.856	17	17.016	9.701	8	40
47	55.258	53	44.038	23.504	17	99
48	60.856	59	49.033	19.839	29	99
49	35.424	33	30.038	13.965	14	64
50	40.311	37	38.042	15.722	17	74
Mean	31.026	28.540	26.110	13.009	11.760	57.760
Min	11.234	9	4.993	3.924	2	20
Max	60.856	59	49.033	24.402	29	99

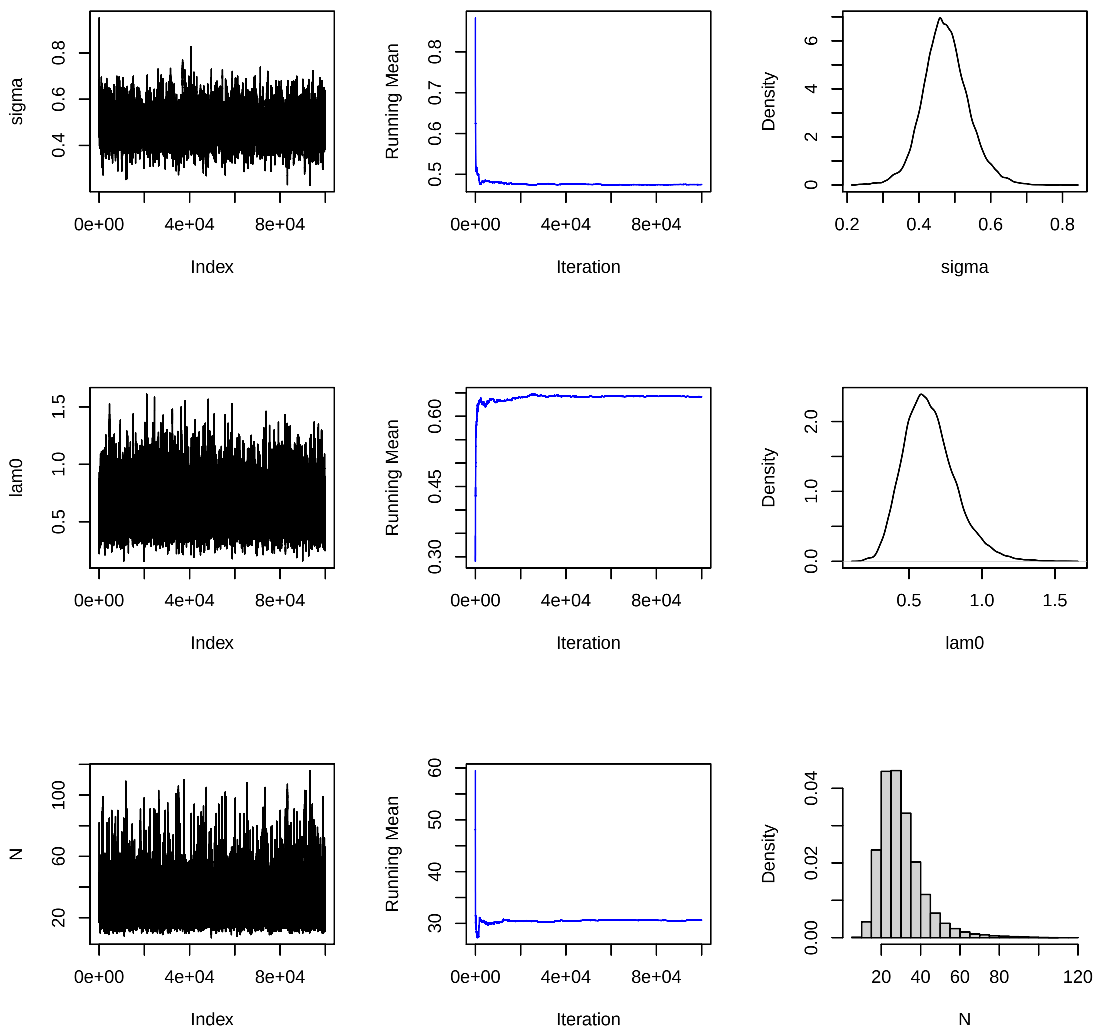


Figure 4.14: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with $\psi \in [0, 0.50]$ and $M = 200$

Table 4.12: Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population size N with $\psi \in [0.10, 0.40]$ and $M = 200$

Sim #	Mean	Median	Mode	sd	Credible interval (HDI)	
					LB	UB
1	28.156	27	21.998	8.197	18	40
2	30.306	29	24.998	8.041	20	43
3	37.205	35	34.992	13.139	18	67
4	38.657	35	26.978	14.592	19	62
5	37.701	36	31.982	11.805	22	57
6	46.980	45	39.978	16.426	22	72
7	30.231	27	27.008	12.560	14	59
8	28.780	27	24.000	8.989	17	41
9	32.771	28	21.944	14.393	16	55
10	27.730	26	24.009	7.681	17	38
11	43.179	41	38.021	13.886	24	67
12	23.441	23	19.974	5.776	16	32
13	34.571	32	32.010	12.290	18	53
14	28.246	26	23.032	10.673	14	43
15	24.357	23	21.006	7.760	13	40
16	33.154	31	31.014	10.434	19	48
17	34.739	33	32.007	9.511	22	49
18	30.829	29	24.995	8.948	19	44
19	30.639	29	28.001	9.987	18	45
20	34.644	32	34.011	12.044	19	53
21	28.206	26	24.032	10.737	14	42
22	24.396	23	21.022	6.269	15	38
23	34.882	32	24.938	12.953	18	54
24	30.776	29	27.032	9.600	18	43
25	32.172	29	32.009	12.096	16	49
26	25.856	24	20.959	9.234	14	36
27	30.770	28	26.002	11.652	16	48
28	29.274	27	25.041	10.842	14	52
29	28.747	27	26.001	8.936	15	47
30	42.586	40	40.014	15.603	19	75
31	18.854	18	15.950	5.869	10	31
32	32.762	30	28.050	12.051	16	60
33	32.969	29	27.032	14.08	13	65
34	29.423	27	23.985	10.888	15	53
35	35.327	33	31.033	12.057	18	62
36	26.611	25	22.015	9.469	12	46
37	28.045	26	22.995	8.815	15	46
38	38.125	35	23.954	14.295	17	69
39	26.929	25	22.992	8.514	15	45
40	26.072	24	21.006	10.342	12	48
41	26.291	24	20.018	9.267	13	46
42	25.418	24	23.994	7.477	13	40
43	20.214	19	17.973	5.576	12	32
44	32.189	29	26.042	12.816	15	62
45	36.304	34	31.035	11.386	19	62
46	24.373	23	21.994	6.401	15	38
47	29.801	27	25.018	11.155	15	55
48	39.826	37	25.968	15.070	17	71
49	43.891	42	39.986	14.394	21	73
50	21.015	20	19.951	5.139	13	31
Mean	31.168	29.000	26.400	10.602	16.400	50.540
Min	18.854	18	15.950	5.139	10	31
Max	46.980	45	40.014	16.426	24	75

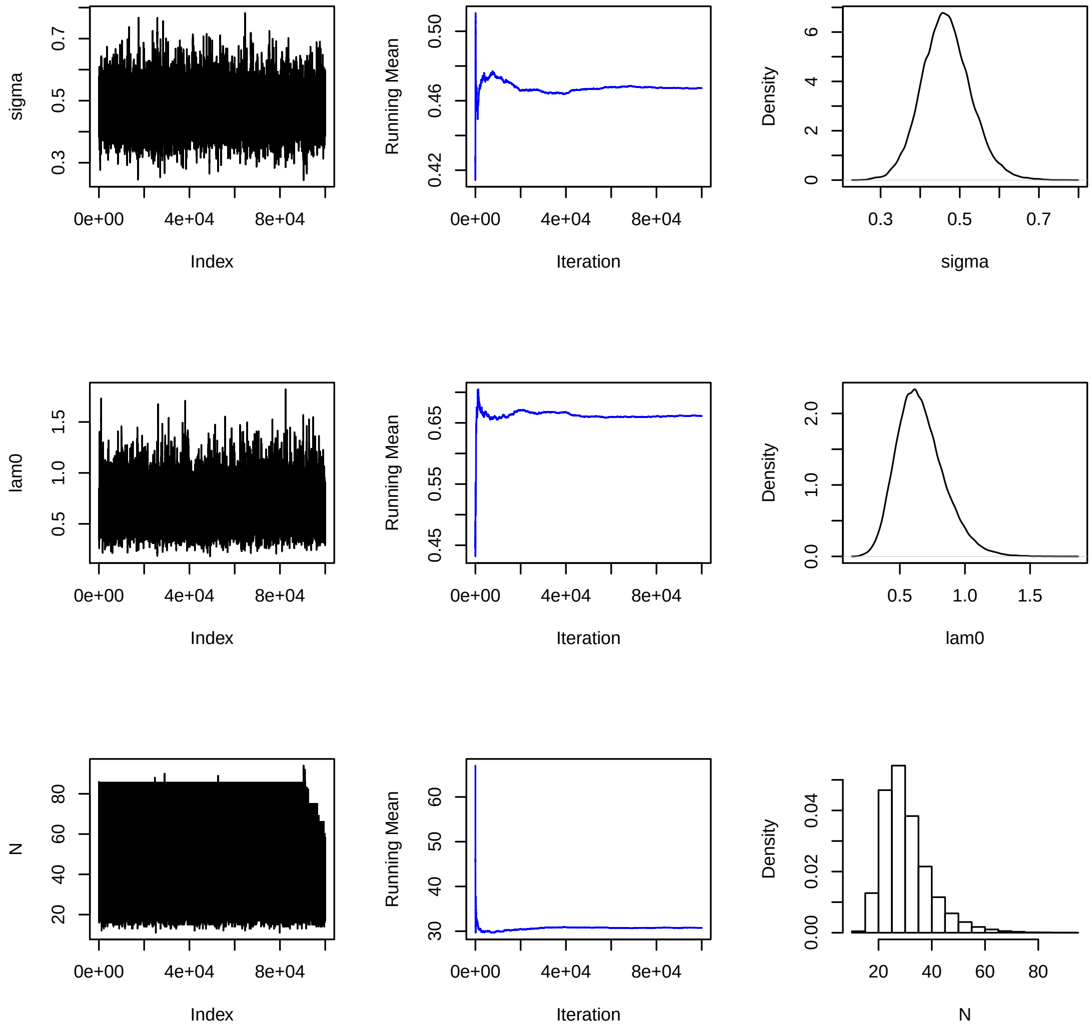


Figure 4.15: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with $\psi \in [0.10, 0.40]$ and $M = 200$

In conclusion, by reducing the range of the parameter ψ, ESS increases, lag_{10} and standard error decrease. As a result, we obtain a more accurate estimated N.

4.5 Regularized Integrated Model using Spatial Camera Coordinates and Informative Prior Distributions

This model is an extension of the spatial capture model [4]. Some assumptions of the spatial model must also be satisfied in this model. However, there are some assumptions, constraints, and prior distributions that are specifically considered in the proposed model. Similar to the spatial model, the individuals in the population are not uniquely identified the individuals might be captured at multiple cameras.

Each individual in the hypothetical population with size M will be assigned a spatial location (x, y) based on the home range radius. It means M activity centers are considered in the study area. Camera encounters provide the number of detected individuals, not necessarily identified individuals. In contrast with the spatial model, we divide M individuals to two groups: 1. Detected group of size n, total number of camera encounters; and 2. Undetected group of size $b = M - n$. Assume each individual d from group 1 with a fixed center of activity defined with the coordinate point $s_d = [s_x, s_y]_d$ where $d = 1, 2, ..., n$, and each individual i from group 2 with a fixed center of activity defined with the coordinate point $s_i = [s_x, s_y]_i$. We assume that each individual in detected group (size n) has a center of activity randomly sampled from a Normal distribution:

$$s_d \sim Normal(\mu = C_d = [C_x, C_y]_d, \sigma) \tag{4.1}$$

where $[C_x, C_y]_d$ is the spatial camera coordinates and σ is the home range radius. We also assume that each individual in group 2 (size b) has a center of activity randomly sampled from a uniform distribution:

$$s_i \sim Uniform(S) \tag{4.2}$$

where S is the two-dimensional study area, i.e., a Uniform prior is considered over both dimensional. The J camera locations are defined by the coordinate $C_j = [C_x, C_y]_j, j =$

$1, 2, ..., J$. We assume y_{djk} as the unknown encounter at camera j on occasion k for individual d in group 1 with a Poisson distribution:

$$y_{djk} \sim Poisson(\lambda_{dj}) \tag{4.3}$$

where λ_{dj} is the encounter rate, i.e. the expected number of camera encounters of individual d at camera j and is defined by:

$$\lambda_{dj} = \lambda_0 g_{dj} \tag{4.4}$$

and λ_0 is the baseline encounter rate, and g_{dj} is a monotonically decreasing function of the distance defined by a half Normal distribution:

$$g_{dj} = exp\left(-D_{dj}^2/\sigma^2\right) \tag{4.5}$$

and D_{dj} is the Euclidean distance between activity center and the camera location:

$$D_{dj} = ||s_d - C_j|| \tag{4.6}$$

where σ is the scale parameter equal to the home range radius. Similarly, y_{ijk} as the unknown encounter at camera j on occasion k for individual i in group 2 has a Poisson distribution:

$$y_{ijk} \sim Poisson(\lambda_{ij}) \tag{4.7}$$

where λ_{ij} is the encounter rate, i.e. the expected number of camera encounters of individual i at camera j and is defined by:

$$\lambda_{ij} = \lambda_0 g_{ij}, \tag{4.8}$$

and λ_0 is the baseline encounter rate, and g_{ij} is a monotonically decreasing function of the distance defined by a half Normal distribution:

$$g_{ij} = exp\left(-D_{ij}^2/\sigma^2\right), \tag{4.9}$$

and D_{ij} is the Euclidean distance between activity center and the camera location:

$$D_{ij} = ||s_i - x_j|| \tag{4.10}$$

where σ is the scale parameter equal to the home range radius. If an individual can be detected at most once during a sampling occasion y_{djk} takes a binary value. It means, y_{djk} takes a value of 1 if the individual d has made a camera encounter or 0 otherwise. If more than one camera encounter per camera per occasion is possible, then y_{djk} is the number of times that an individual d has been detected at camera j on occasion k and y_{djk} represents the encounter or capture history. Therefore, we will have a $(J \times K)$ encounter history matrix for each individual.

The camera encounter histories y_{djk} and y_{ijk} cannot be directly observed for unmarked individuals. The number of camera encounters at camera j in occasion k, n_{jk}, can be written as:

$$n_{jk} = \sum_{d=1}^{N} y_{djk} + \sum_{i=1}^{N} y_{ijk} \tag{4.11}$$

and the number of camera encounters at camera j over all K occasion $n_{j.}$ can be written as:

$$n_{j.} = \sum_{k=1}^{K} n_{jk} \tag{4.12}$$

The full conditional latent encounter has a multinomial distribution and using the data augmentation we can write:

$$\{y_{1jk}, y_{2jk}, ..., y_{Njk}\} \sim Multinomial(n_{jk}, \{\pi_{1j}, \pi_{2j}, ..., \pi_{Nj}\}) \tag{4.13}$$

where $\pi_{lj} = \lambda_{lj}/\sum_l \lambda_{lj}$, $l \in \{i, d\}$. The number of camera encounters at camera j in occasion k, n_{jk} has a Poisson distribution:

$$n_{jk} \sim Poisson(\Lambda_j) \tag{4.14}$$

where

$$\Lambda_j = \lambda_0 \sum_{l=1}^{N} g_{lj} \tag{4.15}$$

Because Λ_j is independent of k we can aggregate the camera counts:

$$n_{j}. \sim Poisson(K\Lambda_j) \tag{4.16}$$

In contrast with the spatial model, in place of using improper uniform distribution for σ and ψ, we define informative priors for them. Using the proposed regression model earlier in this chapter for estimation of hog home range, we define prior distribution of σ by:

$$\sigma \sim Normal(\mu = \hat{\sigma}_{reg}, \sigma_h) \tag{4.17}$$

where σ is the home range radius, $\hat{\sigma}_{reg}$ is estimated home range radius using multiple regression, and σ_h is standard error of estimated home range radius. Next, we define an informative prior for ψ. We remind that, ψ is the probability that an individual in the occupancy model of size M is a member of the original model of size N:

$$N \sim Binomial(M, \psi) \tag{4.18}$$

Therefore:

$$\psi = \frac{E[N]}{M} \tag{4.19}$$

where $E[N]$ is expected value of N. However N is unknown and in turn we use its estimate:

$$\hat{\psi} = \frac{\hat{N}}{M} \tag{4.20}$$

In turn, we use the estimate of ψ to define an informative distribution for ψ:

$$\psi \sim Normal(\mu = \hat{\psi}, \sigma_{\psi}) \tag{4.21}$$

where $\sigma_{\psi} = \frac{n}{M}$, and n is the number of camera encounters. In the hypothetical population of M individuals, $b = M - n$ of them are associated with all-zeros encounter histories:

$$z_i = \begin{cases} 1 & \text{if the individual i is a member of the population (i=1,2,...,N)} \\ 0 & \text{if the individual i is a fixed zero (i=N+1,...,M)} \end{cases}$$

where $z_i \sim Bern(\psi); i = 1, 2, ..., M$. Hence, the encounter data for each individual in the augmented population can be modeled by:

$$\begin{aligned} (y_{ijk}|z_i = 1) &\sim Poisson(\lambda_{ij}) \\ (y_{ijk}|z_i = 0) &\sim I(y_{ijk} = 0) \end{aligned} \tag{4.22}$$

and hence, the population size is:

$$N = \sum_{i=1}^{M} z_i \tag{4.23}$$

In turn we have:

$$\hat{N} = \sum_{i=1}^{M} \hat{z}_i \tag{4.24}$$

Finally, the joint posterior distribution can be written by:

$$[y, z, s_d, s_i, \lambda_0, \psi | n, [C_d, C_j], \sigma_{reg}, M, S] \propto$$

$$\left\{\prod_{d=1}^{n}\left\{\prod_{j=1}^{J}\prod_{k=1}^{K}[n_{jk}|y_{djk}][y_{djk}|z_d, s_d, \sigma, \lambda_0]\right\}[z_d|\psi][s_d]\right\}[\psi][\lambda_0][\sigma_{reg}]$$

$$+\left\{\prod_{i=1}^{b=M-n}\left\{\prod_{j=1}^{J}\prod_{k=1}^{K}[n_{jk}|y_{ijk}][y_{ijk}|z_i, s_i, \sigma, \lambda_0]\right\}[z_i|\psi][s_i]\right\}[\psi][\lambda_0][\sigma_{reg}] \tag{4.25}$$

where prior distributions are assumed to be independent and hence:

$$[\psi, \lambda_0, \sigma_{reg}] \propto [\psi][\lambda_0][\sigma_{reg}] \tag{4.26}$$

Chapter 5

A Real Application of the Model for Population Estimation

This investigation took place within the boundaries of the Kennedy Space Center (KSC) along with the east-central coast of Florida, specifically on the Merritt Island National Wildlife Refuge (MINWR). In this study, we apply the spatial model and the proposed model to estimate the hog population in KSC. Data for this research was collected in two study sites in KSC.

5.1 Population Estimation: Happy Creek

Population size, encounter rate, density, home range, and home range centers of Happy Creek were estimated separately for each batch. The estimated parameters for different values of M are depicted in Table 5.1. The estimated population size N ranges from 39 to 64 hogs for $M = 150$ and from 89 to 125 for $M = 300$ that represents a considerable difference. Interquartile range of estimated N for different batches of data for HC is shown in Table 5.2. Overall, the interquartile range for all batches for HC is 89 with minimum 25th percentile of 9 and maximum 75th percentile of 98.

The estimated N using different time batches were merged by averaging the size to determine the final estimate of HC, which is 55 using $M = 150$ and 108 for $M = 300$.

Table 5.1: Estimated Population Size for HC Using Different Batches of Data

Batch	M = 150				M = 300			
	$\hat{N}$	Sd	λ_0	σ	$\hat{N}$	Sd	λ_0	σ
1	54.16	42.42	1.30	3.44	106.07	86.00	2.04	0.25
2	38.42	41.19	0.06	3.59	88.92	85.21	0.06	2.86
3	52.55	40.71	0.38	0.64	99.46	85.02	0.34	0.54
4	63.87	41.66	0.30	0.54	120.9	84.22	0.26	0.53
5	63.66	41.10	0.32	1.98	124.64	84.09	0.36	0.36

5.2 Population Estimation: Tel-4

In a similar way, population size, encounter rate, density, home range, and home range centers of Tel-4 were estimated separately for each batch. The estimated parameters for the different values of M are depicted in Table 5.3. The estimated N varies considerably from 54 to 76 for $M = 150$ and from 89 to 125 for $M = 300$. The interquartile range of the estimated N for different batches of data for Tel-4 is shown in Table 5.4. Overall, the interquartile range for all batches of Tel-4 is 98 with a minimum 25^{th} percentile of 13 and a maximum 75^{th} percentile of 111.

The estimated N using different batches were averaged to determine the final estimate of Tel-4, which is 62 using $M = 150$ and 115 for $M = 300$.

Table 5.2: Interquartile Range for the Estimated N for HC Using Different Batches of Data

Batch	P_{25}	P_{50}	P_{75}
1	16	46	91
2	9	38	88
3	23	46	85
4	32	60	98
5	23	45	84

Table 5.3: Estimated Population Size for Tel-4 Using Different Batches of Data

Batch	M=150				M=300			
	$\hat{N}$	Sd	λ_0	σ	$\hat{N}$	Sd	λ_0	σ
1	53.45	44.03	2.81	0.37	106.2	87.53	1.99	0.16
2	63.87	42.93	0.99	0.24	114.63	86.96	0.56	0.28
3	52.46	43.49	3.77	0.17	97.88	86.8	0.95	0.15
4	75.52	40.65	0.35	0.27	138.16	82.58	0.32	0.19

Table 5.4: Interquartile Range for the Estimated N of Tel-4 Using Different Batches of Data

Batch	P_{25}	P_{50}	P_{75}
1	13	42	88
2	26	53	93
3	19	53	97
4	46	77	111

5.3 Estimated Population of KSC

The estimated population using different batches of HC and Tel-4 are shown in Figures 5.1 and 5.2. To estimate the population size of KSC, we used the estimated N of HC and Tel-4. First, we assumed KSC has a homogenous habitat as HC, and as a result, we proportionally calculated the N based on the study areas of KSC and HC. With regard to different values of M, the estimated N for HC is 55 and 108 (Table 5.5). The area of HC is 1765 ac or 7.1 sq km, and the area of KSC is $63,000$ ac or 254.8 sq km, which is 35.7 times larger than HC. Hence, the estimated N of KSC using the estimated population of HC is $1,947$ for $M = 150$ and $3,856$ for $M = 300$.

By contrast, the area of Tel-4 is 638.3 ac or 2.58 sq km, which means that KSC is 98.8 times larger than Tel-4. As a result, the estimated N of KSC assuming it has a homogenous habitat as Tel-4, which is $6,060$ for $M = 150$ and $11,285$ for $M = 300$.

Next, we designed a weighted averaging procedure with regard to the area of each study site:

$$\hat{N}_{KSC} = \omega_{HC} \times \hat{N}_{HC} + \omega_{Tel-4} \times \hat{N}_{Tel-4} \tag{5.1}$$

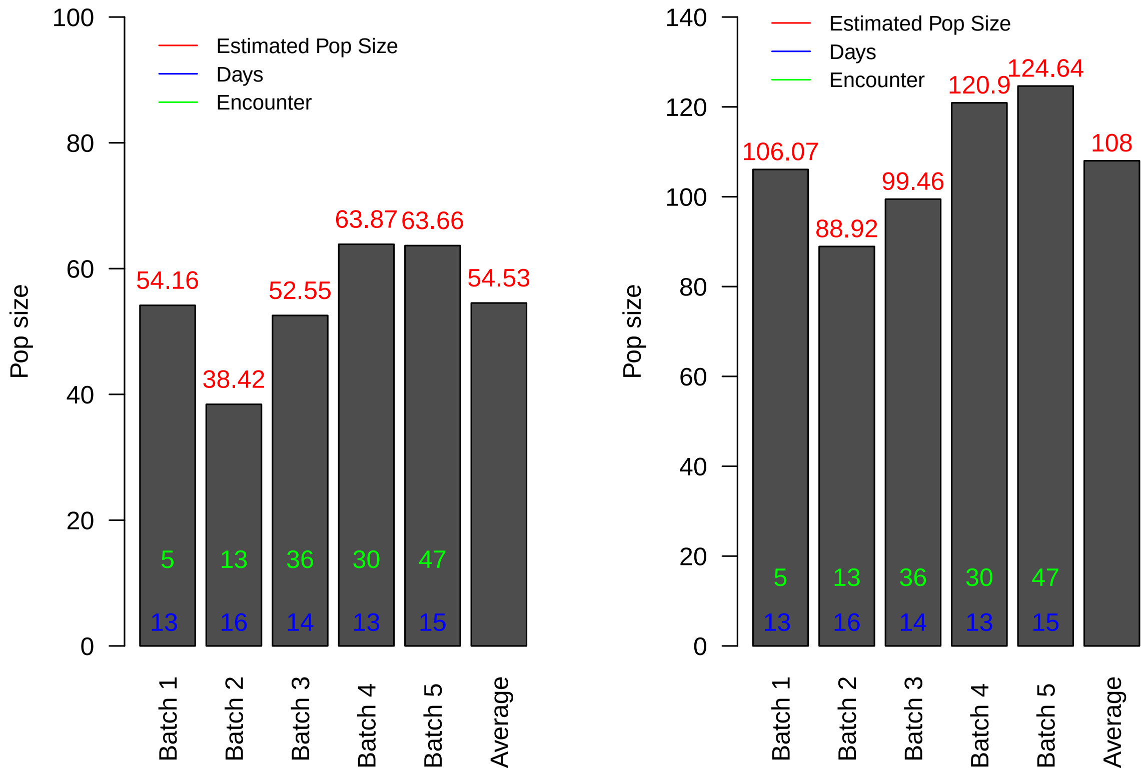
Table 5.5: Estimated Population Size of KSC Using the Estimates of HC and Tel-4

	Area			Population Size		Weighted Average	
Study Area	AC	Sq-KM	KSC Ratio	M = 150	M= 300	M = 150	M= 300
HC	1765	7.14	35.7	54.53	108		
Tel-4	638.3	2.58	98.8	61.33	114.22		
KSC (HC)	63000	254.8	1	1946.7	3855.6		
KSC (Tel4)	63000	254.8	1	6059.4	11,285		
KSC (HC & Tel4)	63000	254.8	1			3057.2	5861.5

Therefore, since HC (7.1 sq km) is about 2.76 times of Tel-4 (2.58 sq km), the assigned weights of HC and Tel-4 are 0.73 and 0.27, respectively. The estimated N using the proposed weighted averaging is $3,058$ for $M = 150$ and $5,862$ for $M = 300$ (Table 5.5). These estimates suggest a hog density of 0.048 per acre for $M = 150$ and 0.094 per acre for $M = 300$.

5.4 Sensitivity of the Estimated Population Size to M

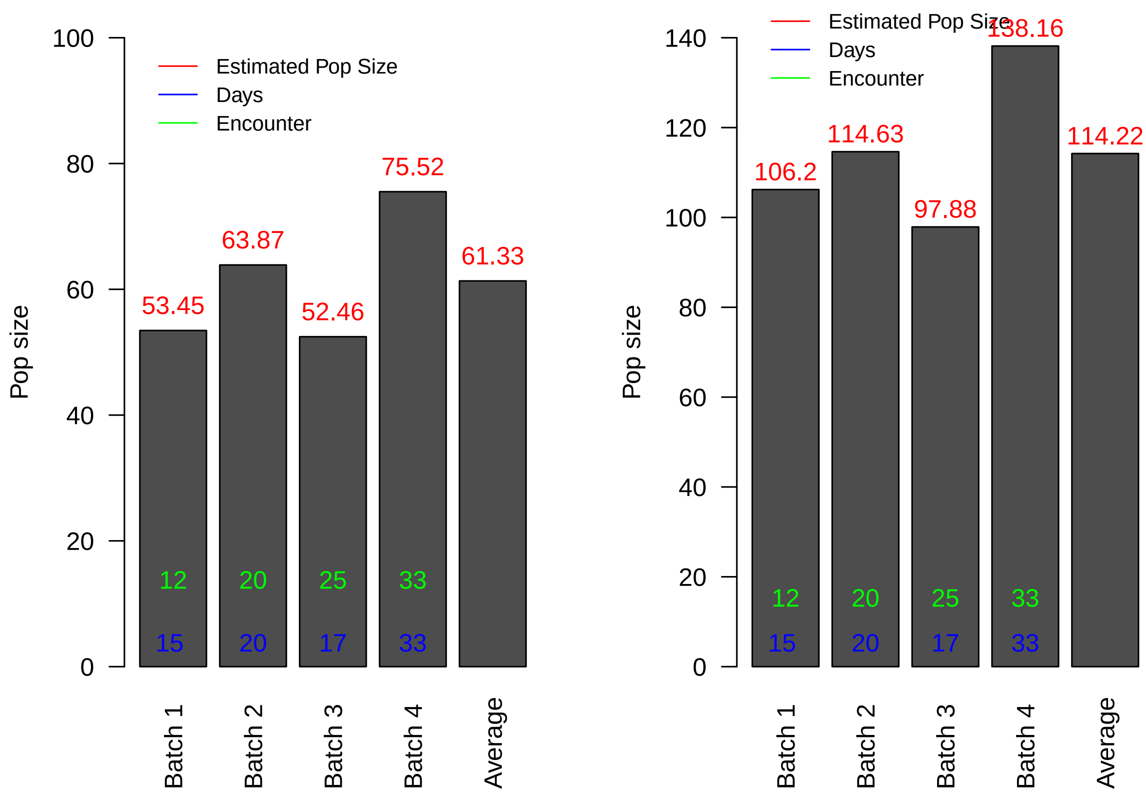
An estimated value of N for happy creek for batch three with 30 camera encounters over two-week period is shown in Table 5.6. As shown in Table 5.6, the estimated population size $\hat{N}$ is highly sensitive to value of M and sensitivity increases by increasing the value of M. This sensitivity could be potentially related to convergence problems of the model for large values of M. However, to gain some insight into the complexity and dimensionality of the problem, assume M is 300, which means that there are 300 centers of activity, each of which have two coordinates (x and y), with a total of 600 coordinate parameters. In addition, to these potential activity centers, we are also trying to estimate 300 z's (i.e., whether or not a hypothetical individual belongs to the actual population), along with home range, encounter rate, and population size. This will introduce an approximately $1,000$ dimensional search space to solve for all parameters, and as a result the model may not converge to the global solution. Therefore, to address the variation in the estimated N and the sensitivity of the estimates to M, we studied the convergence of the model. Figure 5.3 shows



(a) Using M=150 (b) Using M=300

Figure 5.1: Estimated Population Size Based on Each Batch for HC

the convergence plots for estimated parameters. At first glance it appears that the model has converged for all parameters. However, upon further investigation, and examining the estimated posterior densities of the parameters (Figure 5.4), it appears that the model has not converged, since the posterior density of $\hat{N}$ has a heavy upper tail. We concluded that due to the complexity of the problem with regard to the number of unknowns including population size, home range centers, density, home range radius, and encounter rate, the model may not converge. Even if it does converge, it may converge to a local solution, because of the complexities of the different combinations of these values and because of the nature of Gibbs sampling and the MCMC algorithm.



(a) Using M=150

(b) Using M=300

Figure 5.2: Estimated Population Size Based on Each Batch of Tel-4

Table 5.6: Study the Sensitivity of the Estimated Posterior Population Mean to M Using Batch 3 Data Collected for HC

M	$\hat{N}$	Median	Mode	$\hat{\sigma}$	$\hat{\lambda}_0$
50	24.06	23.00	8.00	0.946	0.287
100	49.09	47.00	23.00	0.504	0.297
150	63.15	56.00	5.00	0.643	0.304
200	88.67	81.00	6.00	0.445	0.278
250	108.40	100.00	14.00	0.429	0.282
300	121.12	106.00	5.00	0.545	0.243

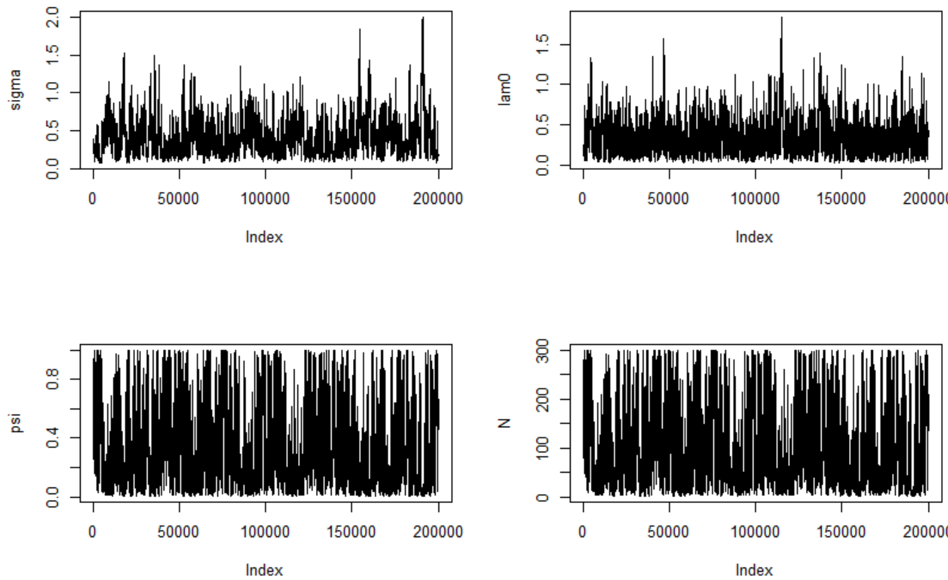


Figure 5.3: Convergence Plots for Estimated σ (top left), λ_0 (top right), ψ (bottom left) and N (bottom right)

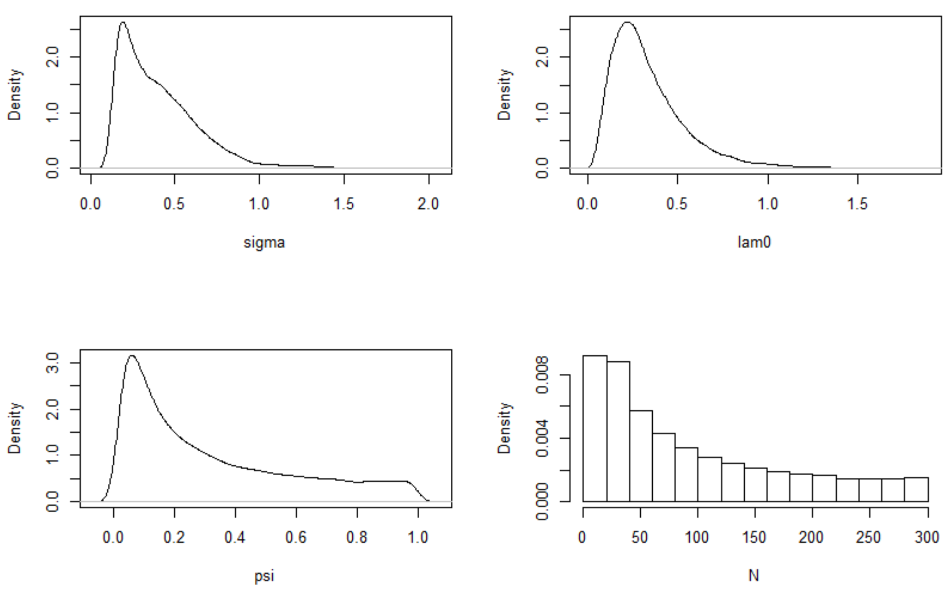


Figure 5.4: Estimated Posterior Densities for σ (top left), λ_0 (top right), ψ (bottom left) and N (bottom right)

5.5 A Regression Model to Estimate Home Range

We used previous studies to estimate the home ranges of the hogs. To this end, 32 reported studies [59] regarding the home range of hogs were used. We designed a multivariate regression mode:

$$Y = B_0 + B_1 X_1 + B_{X2} + B_3 X_3, \tag{5.2}$$

where Y is the home range (HR), X_1 is the average annual precipitation (Rain), X_2 is the average annual land temperature (Tmp), and X_3 is the elevation (Elv). The estimated coefficients are

$$HR = -7.96 - 0.005 * Rain + 0.92 * Tmp + 0.011 * Elv. \tag{5.3}$$

This model was used to predict home range of hogs at KSC, where recorded average monthly temperatures in 2017 were $16, 16, 20, 22, 25, 27, 28, 28, 27, 24, 19,$ and 16 °C for January to December, respectively. The average annual temperature was then calculated as 22.3 °C in 2017. Average annual rainfall in 2017 was 58.5 in., equal to $1,486.4$ mm and KSC's elevation was considered similar to Cape Canaveral's elevation of 3.048 m. Latitude was not significant and was removed from the proposed multivariate model. The estimated home range in the present study, 4.84 sq km, is very close to the median home range of 4.85 sq km of the reported studies. The home range is positively correlated with the temperature and elevation but has a negative correlation with precipitation. Poffenberger's (1979) previous estimate of the home range at KSC is 130 ac or 1.3 sq km.Using both estimates, we ascertain a range of 640 to 1200 m for the home range radius.

As discussed earlier, the estimate of N is somewhat sensitive to the selected value of M. When using different M values, the model converges due to the nature of Gibbs sampling in the MCMC method. When multiple parameters are estimated at the same time, the model may converge toward a different set of estimated values. While the estimate of N for $M = 300$ is greater than that of 150, the estimated σ for $M = 300$ is less than that of $M = 150$. The smaller σ indicates lower correlations in camera encounters while larger σ suggests higher correlations in camera encounters. This means that using the same encounter data, the model will converge toward a different estimated vector for different values of M. By comparing the estimated σ using two different values of M, we selected the estimate of N that is obtained using $M = 150$, because the calculated home range using estimated σ is closer to the proposed range for the hog's home range in KSC. The estimated population was calculated by extrapolation using the weighted average of the estimated population for HC and Tel-4. The estimated population for selected M was $3,058$. The weighted interquartile range is 91.5 with the 25^{th} percentile of 10 hogs and the 75^{th} percentile of 101.5 hogs for estimated N for HC and Tel-4. The extrapolated interquartile range for KSC was calculated using these two sites, and was 3953 with the 25^{th} percentile of 432 hogs and 75^{th} percentile of 4385 hogs.

We should point out that a more accurate estimate of hog population size in KSC can be obtained by installing more cameras to cover more sections of the KSC area. However, due to the limited resources, we monitored two study sites, i.e. HC and Tel-4. As a result, the estimated population size for KSC was calculated as an extrapolation using a weighted averaging of estimated population for these two study sites. Therefore, this may not accurately represent the whole population of KSC.

5.6 Informative Prior Distribution for Estimating the Population

The numerical optimization techniques aim to find the optimum values of the objective function [60]. However, with high dimensional space, finding the globally optimal solution is not an easy task and may be unreachable. In our problem, we could conclude that the separate trials are not converged to the same posterior distribution, but we can argue that we can reach the optimal solution even the problem is highly dimensional.

Moreover, since we do not have enough information for prior distributions, a new set of random sampling of each parameter generated. As a result, we have separate spaces in each trial. For Tel-4 site Batch 1, for example, we wanted to see if the 50 trials came from the same distribution set. In Figure 5.5, we can see that the samples are not in the bell shape and that the distribution is multimodal. In the quantile-quantile (QQ) plot, we can visualize that the points do not match along a straight line, which shows that the quantiles do not match, leading us to reason that the sampling distribution of 50 trials most likely does not come from identical distributions. As a result, we conclude that the chain has converged to a different posterior distribution in each trial.

The only informative prior distribution is for σ with a shape parameter of 10 and a scale parameter of 55, which are the equivalent values of the home range's estimated values using the regression model. The results in the next two sections summarizes a four-month study on feral hog population analysis and management at the Kennedy Space Center (KSC). In this study, we monitored hogs in two study sites using two 12-camera systems for 16 weeks in two-week periods in the summer of 2018. The collected images were preprocessed to remove nonanimal images and the number of animals counted and recorded along with pole identification numbers, dates, times, and genders (if possible).

A camera grid map with the camera distances, coordinates, and number of camera encounters were produced for each two-week monitoring period. At the beginning of a new two-week period, new poles were installed in each study site, and cameras were moved from previous poles to the new positions. After four time periods and after substantial coverage in each study area, we chose new camera locations by randomizing the existing installed poles.

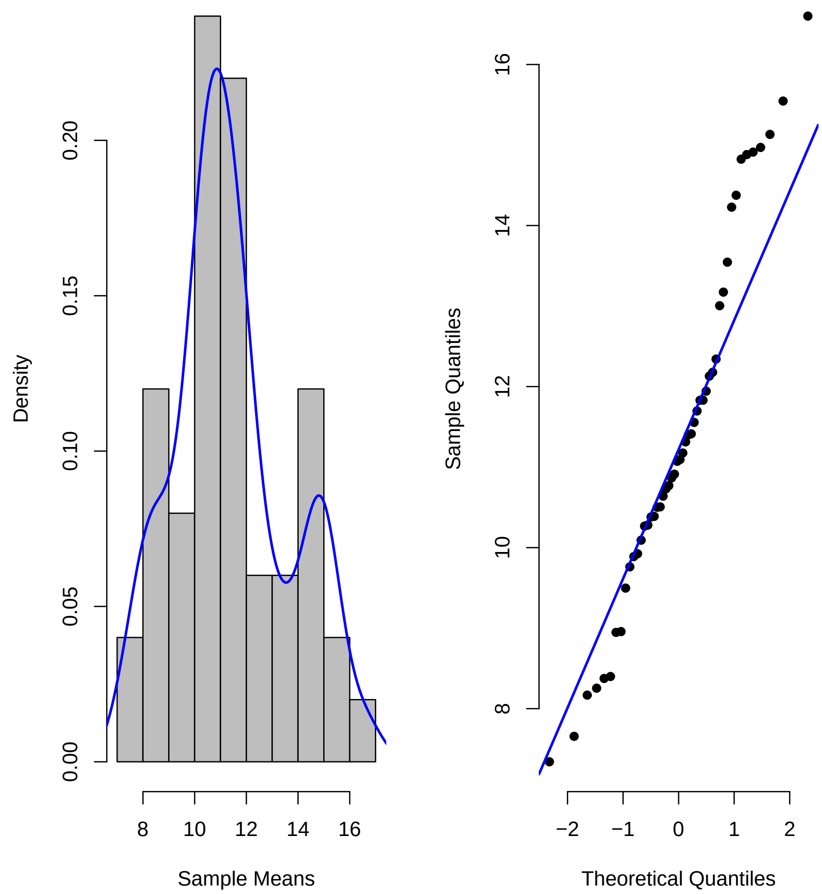


Figure 5.5: Histogram (left) and QQ Plot (right) of 50 Runs using Batch 1 Collected for Tel-4

5.6.1 Estimated Population in Happy Creek (HC)

The population size, encounter rate, density, home range, and home range centers of Happy Creek were estimated separately for each batch. The estimated parameters for the value of $M = 100$.

As we can see in Table 5.7, the estimated population size N ranges from 10 to 20 hogs using the first sampling batch (Batch1). The average estimated population is approximately 15 hogs. The standard error of the estimates is between 18 to 24. The range of the highest Bayesian credible interval from 1 to 43 is quite wide. However, the estimated median ranges from 3 to 9. The estimated value for σ is more stable since we used gamma distribution as a prior distribution. The estimated mean and median for sigma are 485 and 471, respectively. Moreover, the estimated mean and median ranges are comparable, from 436 to 532 for the mean and 424 to 515 for the median (see Table A.7 and Figure 5.6).

The correlation of estimated σ and N are not small enough. However, by looking at the histogram and the running mean of the estimated values, we conclude that they reached their converged values as we can see in Figure 5.7, A.1, and A.2.

Table 5.7: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Happy Creek Using Batch 1

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	15.247	5	21.743	1	45
2	14.445	6	20.378	1	40
3	13.278	5	19.612	1	37
4	15.05	5	21.381	1	44
5	16.839	6	22.223	1	49
6	16.83	6	22.63	1	50
7	10.465	3	17.782	1	27
8	15.598	5	22.524	1	47
9	13.769	6	19.188	1	37
10	17.791	7	22.538	1	50
11	18.522	8	23.423	1	53
12	19.743	9	24.079	1	56
13	14.985	5	21.338	1	44
14	13.533	4	20.639	1	40
15	12.71	4	19.73	1	36
16	12.951	4	20.741	1	38
17	18.468	8	23.474	1	53
18	13.774	4	21.028	1	41
19	13.917	5	20.988	1	41
20	16.858	6	23.437	1	51
21	12.41	4	19.168	1	35
22	16.621	6	22.796	1	50
23	18.131	7	23.507	1	53
24	15.126	5	21.076	1	44
25	17.132	6	23.182	1	51
26	11.974	4	18.985	1	33
27	13.474	4	20.103	1	39
28	18.128	7	23.555	1	54
29	13.817	5	20.155	1	39
30	12.493	4	19.458	1	35
31	12.139	4	19.183	1	34
32	17.035	6	23.451	1	51
33	13.807	5	20.183	1	39
34	14.437	5	20.808	1	41
35	10.432	3	17.928	1	28
36	15.957	6	21.781	1	46
37	16.277	6	21.751	1	47
38	16.052	6	22.178	1	47
39	14.562	5	20.637	1	42
40	12.771	4	20.147	1	36
41	15.31	5	22.072	1	45
42	11.957	4	18.928	1	34
43	16.192	6	22.09	1	48
44	16.947	6	22.746	1	49
45	18.538	7	23.756	1	54
46	13.943	5	20.434	1	39
47	15.374	5	22.063	1	46
48	15.241	5	22.337	1	46
49	12.463	4	19.933	1	36
50	10.885	3	18.691	1	29
Mean	14.888	5.26	21.239	1	42.98
Min	10.432	3	17.782	1	27
Max	19.743	9	24.079	1	56

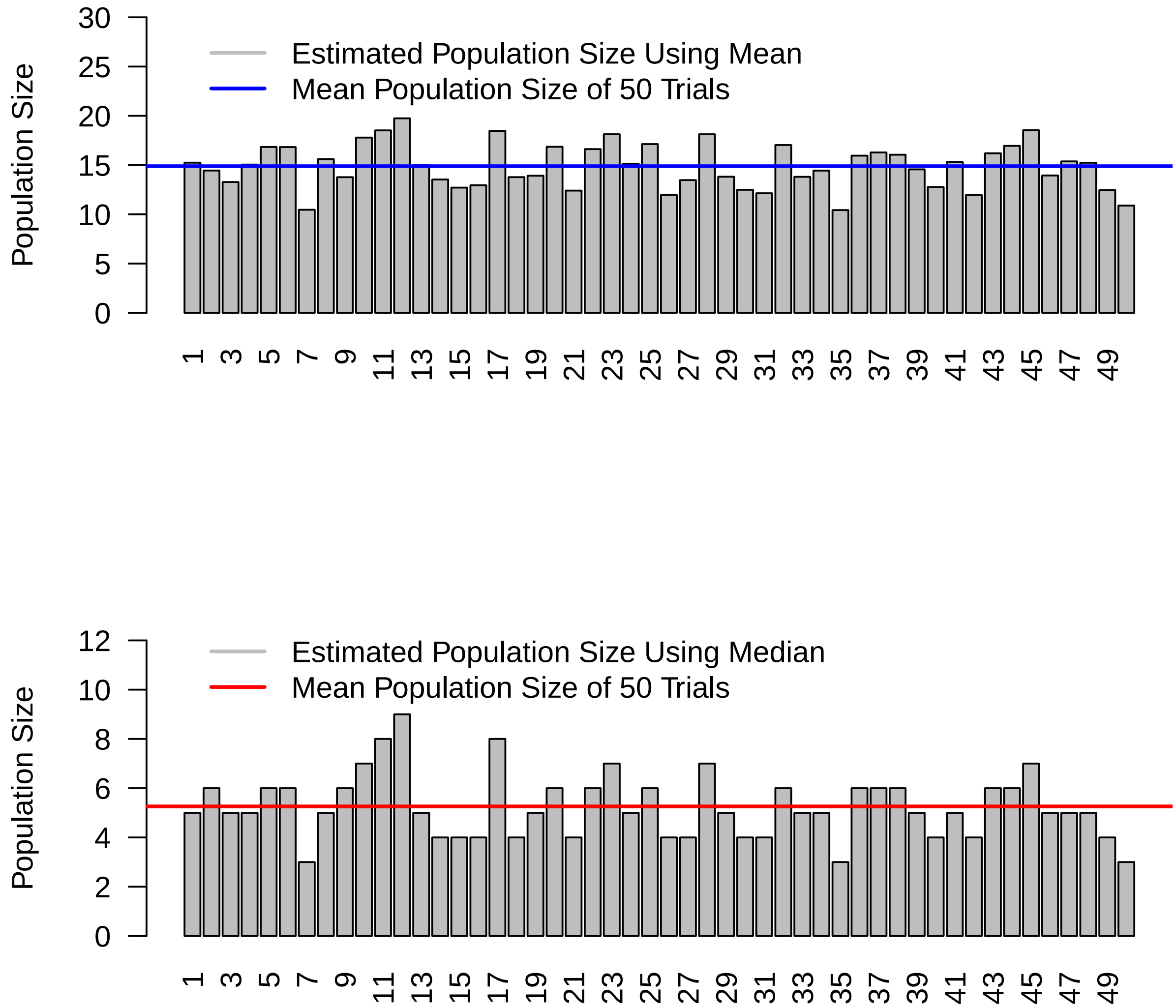


Figure 5.6: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 1 from HC

For Batch 2, the average estimated N is about 19 hogs and ranges from 11 to 26 hogs. Clearly, the density function of the population size twists on the right with an average of the median about 10 hogs. The standard error of the estimate N ranges from 16 to 26. The Bayesian credible interval is from 1 to 48 as illustrate in Table 5.8 and Figure 5.8.

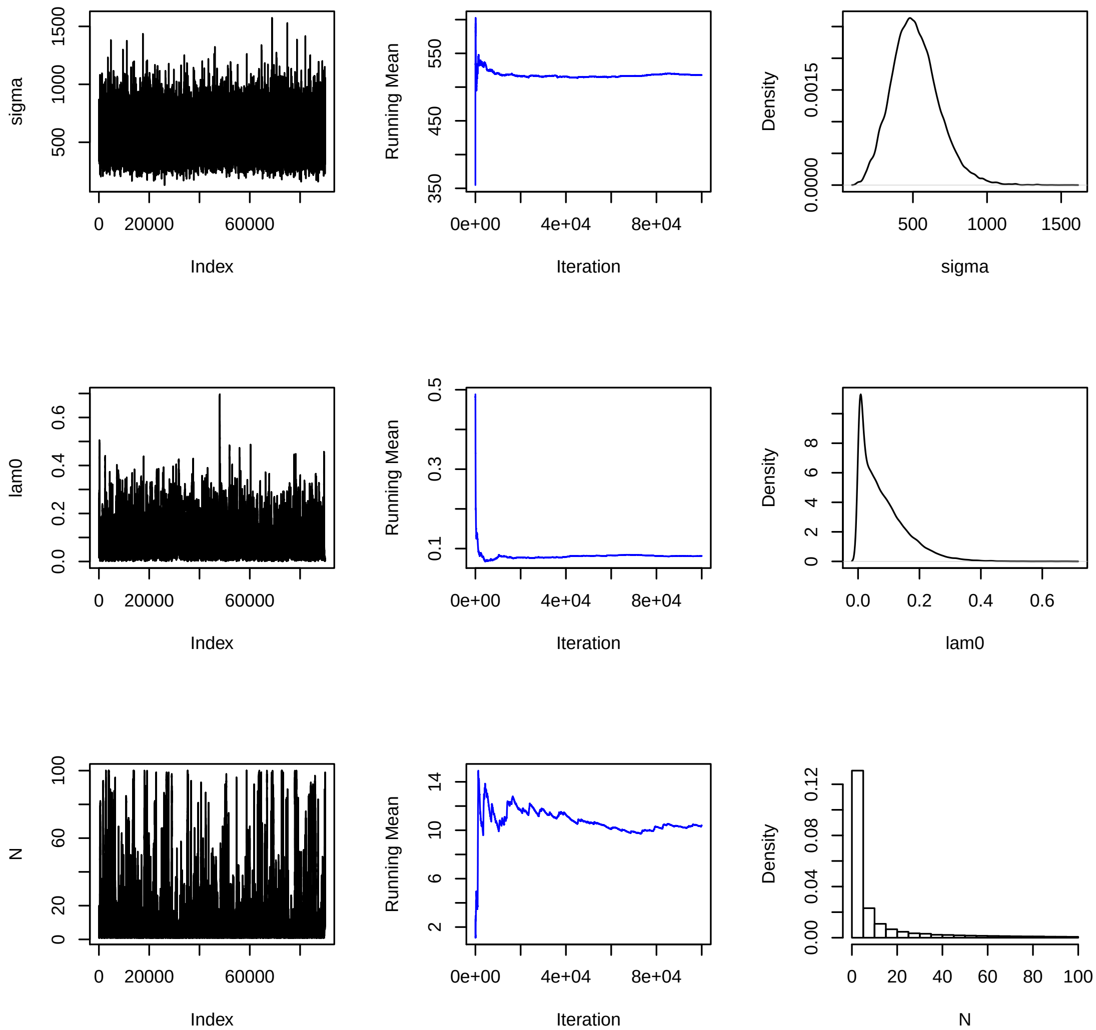


Figure 5.7: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 1

The running mean of the estimated values of the population size N converges to its posterior distribution as it is demonstrated in Figures 5.9, A.3, and A.4 for three different trials. The average mean and median of σ are comparable with the values of 522 and 504, respectively as shown in Table A.8. The credible interval for the mean of σ ranges from 257 to 768.

Table 5.8: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Happy Creek Using Batch 2

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	18.647	9	21.883	1	49
2	21.672	11	24.521	1	59
3	21.065	11	23.608	1	56
4	11.631	5	16.364	1	28
5	21.547	11	24.181	1	59
6	18.314	9	21.726	1	48
7	21.019	11	23.39	1	56
8	14.37	6	19.495	1	39
9	23.829	13	25.188	1	63
10	22.952	12	25.528	1	63
11	21.226	11	23.571	1	56
12	19.555	10	22.448	1	52
13	18.611	9	22.741	1	51
14	19.711	10	22.269	1	51
15	17.483	9	20.416	1	44
16	12.469	6	16.652	1	30
17	17.335	8	21.462	1	47
18	18.557	10	21.503	1	48
19	18.848	10	21.549	1	49
20	24.941	16	24.487	1	62
21	13.15	5	19.122	1	34
22	17.927	9	21.02	1	47
23	13.441	6	18.195	1	33
24	17.21	8	22.135	1	47
25	15.817	8	19.75	1	40
26	26.053	17	24.866	1	64
27	15.089	7	19.595	1	40
28	23.381	13	24.062	1	60
29	17.341	9	20.899	1	45
30	22.25	13	23.931	1	58
31	17.554	8	21.74	1	47
32	15.11	7	19.039	1	38
33	11.212	5	15.536	1	26
34	11.488	6	15.948	1	26
35	20.028	10	22.749	1	53
36	25.748	15	25.669	1	66
37	20.357	11	22.452	1	53
38	18.87	9	22.297	1	50
39	25.634	15	26.318	1	68
40	23.358	13	24.812	1	61
41	13.133	7	16.301	1	31
42	14.336	7	18.273	1	36
43	15.926	8	19.645	1	41
44	19.56	10	22.837	1	53
45	20.488	11	22.313	1	53
46	14.756	8	17.879	1	36
47	14.778	6	20.28	1	39
48	19.39	10	22.113	1	51
49	22.474	12	24.035	1	59
50	21.074	11	23.263	1	55
Mean	18.614	9.62	21.601	1	48.4
Min	11.212	5	15.536	1	26
Max	26.053	17	26.318	1	68

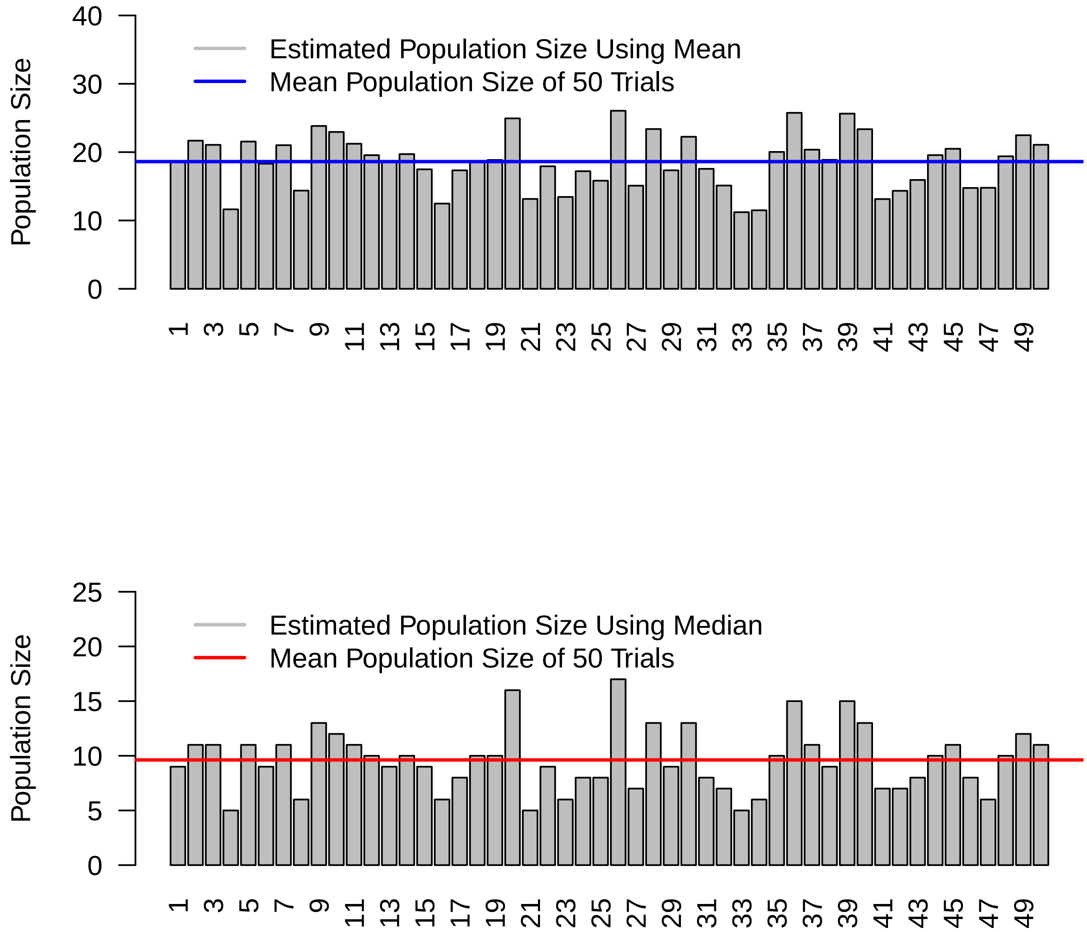


Figure 5.8: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 2 from HC

Figure 5.10 shows the estimated N for Batch 3, using the mean of 50 trials and the fluctuations of the estimated N in each trial, comparing the average N, which is about 10 hogs, a number that is still acceptable considering all prior informative distributions we had. The range of estimated N is from 4 to 22. For the median, the average is around 7 hogs, ranging from 3 to 17 hogs. Comparing the average mean with the average median, the density function of the posterior distribution twists to the right. The average of the

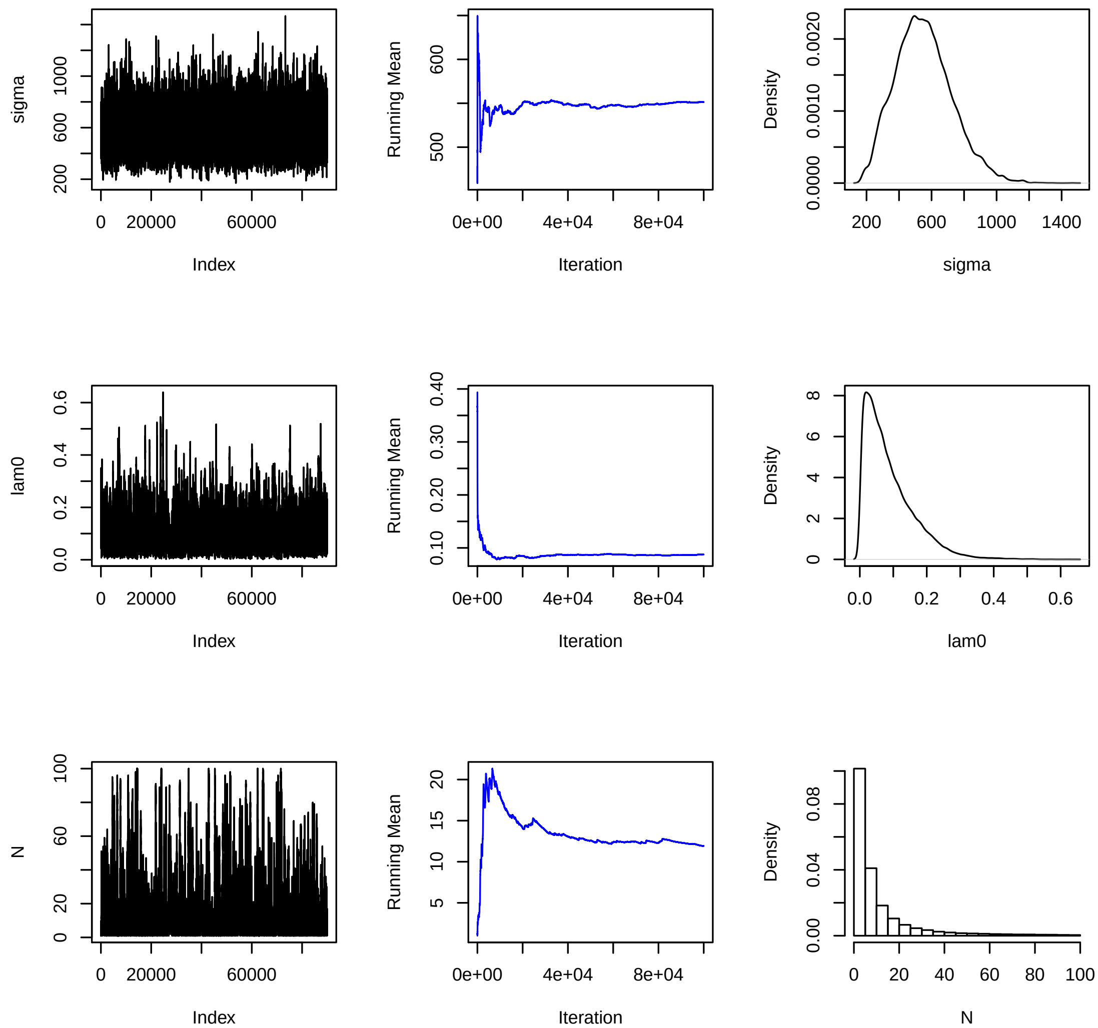


Figure 5.9: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 2

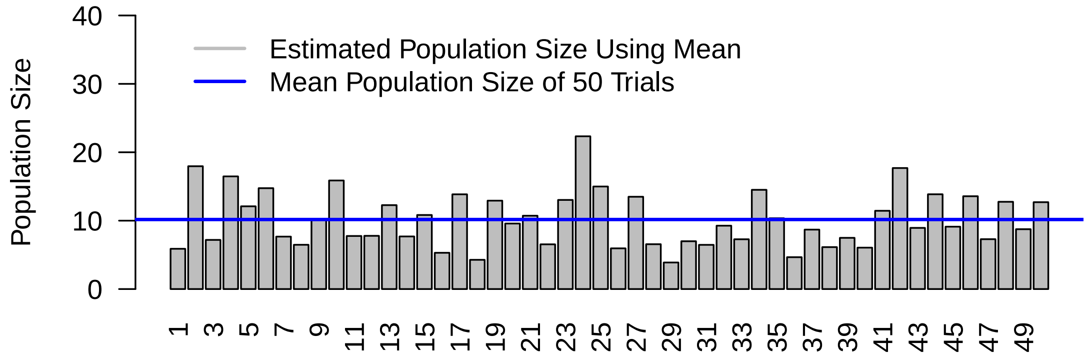
highest Bayesian credible interval ranges from 1 to 20 as we can observe in Table 5.9.

In Table A.9, the average mean and median of σ are comparable at 432 and 405, respectively. Additionally, the estimated σ ranged from 229 to 610 for the mean and from 256 to 597 for the median.

In Figures 5.11, A.5 and A.6, the running mean still gradually converges to its posterior distribution. For a strong convergence, running more simulations are needed.

Table 5.9: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Happy Creek Using Batch 3

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	5.887	4	4.890	1	12
2	17.958	14	14.589	2	37
3	7.187	5	7.303	1	14
4	16.474	11	16.158	1	36
5	12.098	9	11.765	1	24
6	14.749	12	11.774	1	28
7	7.668	6	6.381	1	15
8	6.471	4	6.793	1	14
9	10.159	7	10.505	1	22
10	15.874	12	14.100	1	33
11	7.759	6	7.514	1	16
12	7.781	7	5.789	1	15
13	12.27	9	11.242	1	23
14	7.691	7	5.214	1	14
15	10.828	8	10.914	1	23
16	5.300	4	5.110	1	11
17	13.851	9	15.138	1	31
18	4.275	3	4.429	1	8
19	12.925	9	12.365	1	26
20	9.577	7	9.702	1	18
21	10.718	9	7.857	1	20
22	6.538	5	7.520	1	13
23	13.029	8	14.394	1	29
24	22.337	17	17.609	1	44
25	14.994	11	13.893	1	30
26	5.950	4	6.753	1	12
27	13.495	10	13.185	1	29
28	6.557	5	5.578	1	13
29	3.882	3	3.853	1	8
30	6.991	5	6.384	1	14
31	6.464	3	6.545	1	15
32	9.265	7	8.204	1	17
33	7.280	6	6.035	1	14
34	14.507	12	11.11	1	27
35	10.351	8	10.122	1	20
36	4.657	3	4.731	1	9
37	8.692	5	9.790	1	19
38	6.130	5	4.983	1	11
39	7.485	5	8.048	1	15
40	6.053	4	5.856	1	13
41	11.441	8	10.904	1	24
42	17.693	14	14.498	1	34
43	8.943	7	7.330	1	18
44	13.86	10	13.207	1	28
45	9.121	7	8.473	1	17
46	13.572	10	12.072	1	30
47	7.293	5	7.023	1	15
48	12.759	9	12.613	1	25
49	8.753	7	8.173	1	17
50	12.7	9	11.843	1	25
Mean	10.166	7.48	9.405	1.02	20.5
Min	3.882	3	3.853	1	8
Max	22.337	17	17.609	2	44



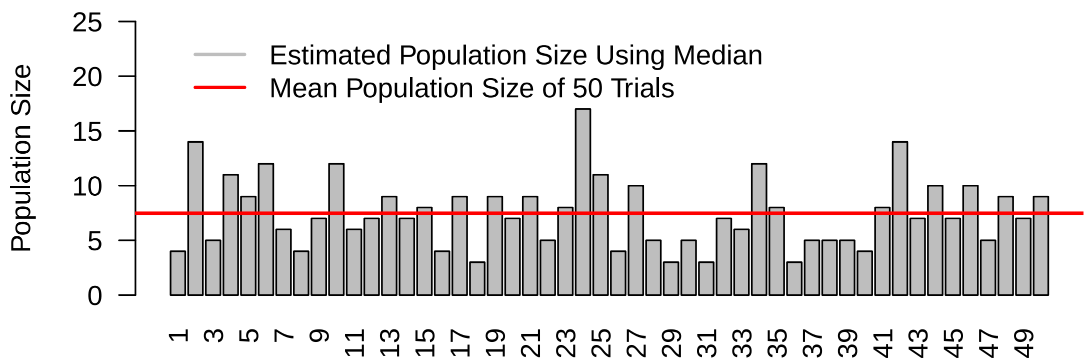


Figure 5.10: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 3 from HC

For Batch 4, the estimated value of the population size N range from 17 to 41 hogs with an average of 17 hogs. The density of population size twists to the right with a median average of 10 hogs, and the median ranges from 11 to 36 hogs. Moreover, the credible interval is between 1 and 64 as we can see in Table 5.10 and Figure 5.12. In Table A.10, the average estimated mean and median for σ are 474 and 450, respectively. The average standard error of σ is about 168, and its credible interval ranges from 218 to 715.

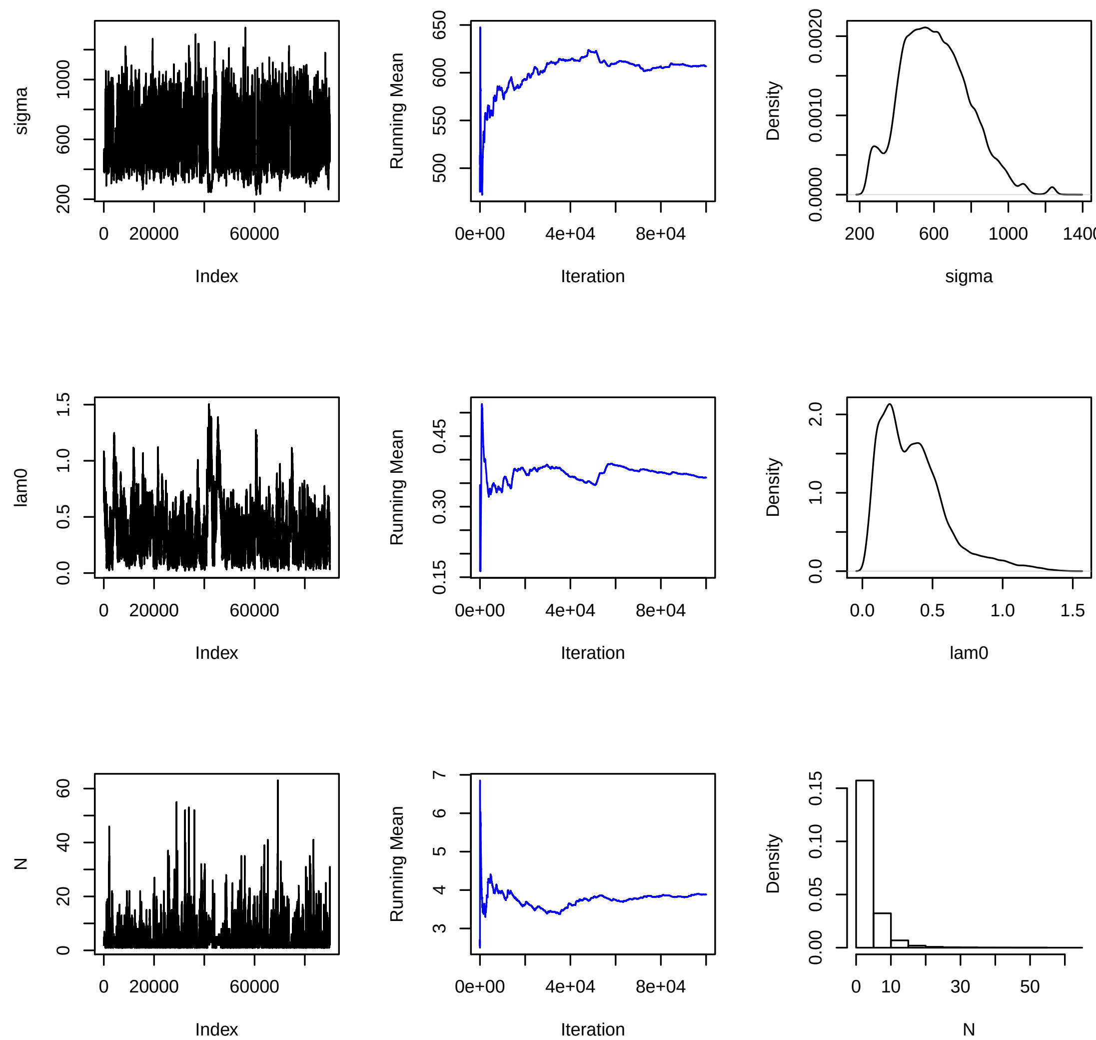
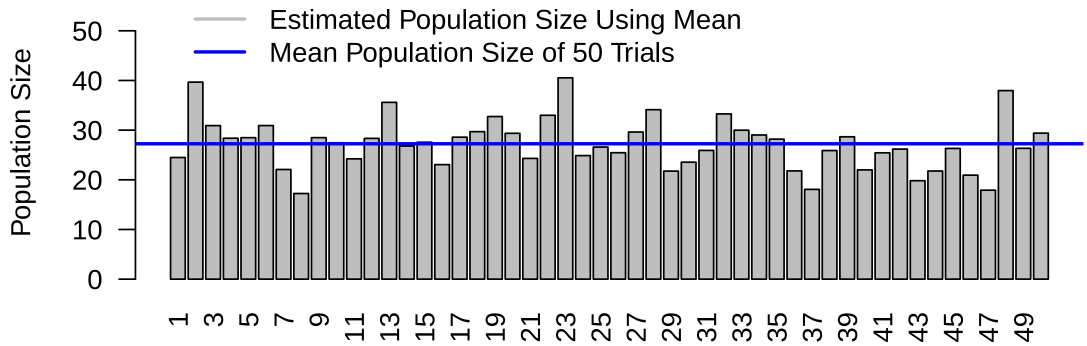


Figure 5.11: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 3

The histogram and the running mean of the estimated values reached their converged posterior distributions as demonstrates in Figures 5.13, A.7, and A.8.

Table 5.10: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Happy Creek Using Batch 4

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	24.484	17	22.053	1	56
2	39.661	34	27.013	3	81
3	30.911	21	27.252	1	74
4	28.370	20	23.966	2	65
5	28.481	19	25.630	1	69
6	30.918	21	26.839	1	73
7	22.076	14	22.053	1	54
8	17.236	11	18.676	1	39
9	28.488	20	24.624	2	68
10	27.448	19	24.776	1	65
11	24.219	14	24.078	1	61
12	28.337	20	23.916	2	65
13	35.590	28	26.668	2	78
14	26.799	17	24.551	1	64
15	27.565	19	23.387	2	63
16	23.053	14	22.496	1	56
17	28.583	21	24.295	1	65
18	29.695	21	25.525	2	70
19	32.738	25	25.516	2	72
20	29.357	21	25.188	1	68
21	24.308	14	24.236	1	62
22	32.988	24	26.721	1	75
23	40.529	35	27.200	4	84
24	24.874	15	24.195	1	61
25	26.595	18	24.260	1	64
26	25.450	16	24.264	1	63
27	29.620	20	26.311	1	70
28	34.118	26	26.326	1	74
29	21.748	13	21.783	1	53
30	23.547	14	23.629	1	59
31	25.918	17	23.655	2	63
32	33.263	25	26.412	1	74
33	29.987	22	25.735	1	69
34	29.025	19	25.993	1	69
35	28.182	19	25.563	1	68
36	21.788	13	22.329	1	54
37	18.070	10	20.355	1	45
38	25.888	17	23.562	1	61
39	28.660	19	26.003	1	69
40	21.992	12	22.751	1	56
41	25.434	17	22.727	1	58
42	26.182	17	23.925	1	63
43	19.821	12	20.329	1	46
44	21.765	14	21.375	1	51
45	26.317	18	23.449	2	63
46	20.937	12	22.555	1	54
47	17.909	11	19.013	1	41
48	37.962	32	27.103	2	79
49	26.341	17	24.735	1	64
50	29.395	20	25.272	2	70
Mean	27.252	18.68	24.205	1.32	63.76
Min	17.236	10	18.676	1	39
Max	40.529	35	27.252	4	84



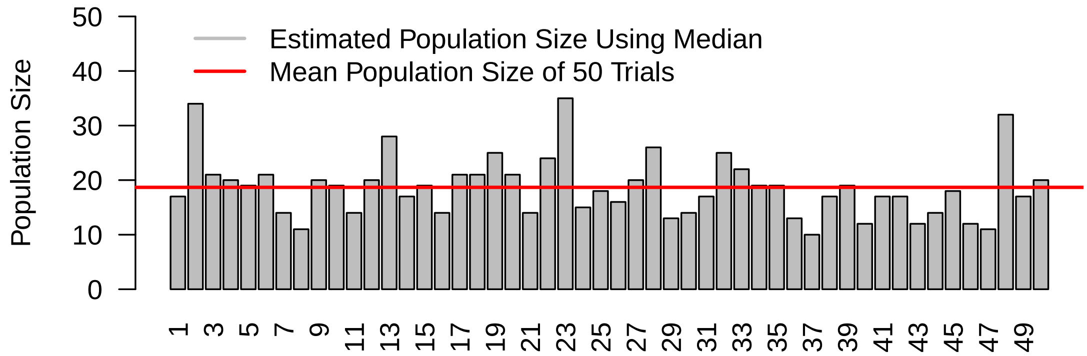


Figure 5.12: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 4 from HC

For Batch 5, from simulation summary results in Table 5.11 and Figure 5.14, we conclude that the average mean and median of the estimated population size are 16 and 12 hogs respectively, with a standard error of about 14. The estimated mean ranges from 12 to 31 and 7 to 25 for the estimated median. Moreover, the highest density credible interval is between 2 and 31. For σ, the average of the mean and median is 350 and 316 with a standard error of 317. The credible interval for σ ranges from 172 to 520 as we can see in

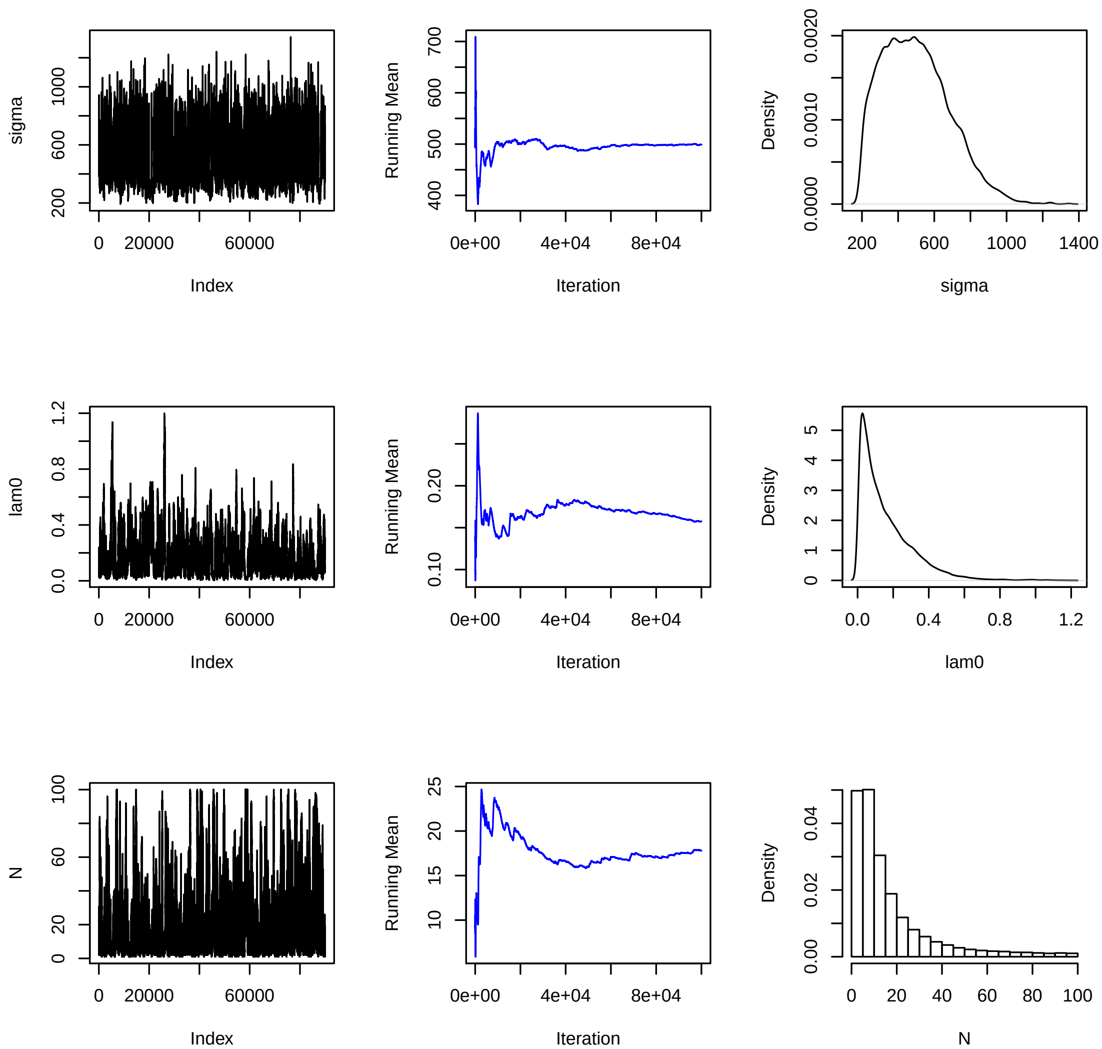


Figure 5.13: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 4

Table A.11. The running mean of the estimated values of the population size N converges gradually to their posterior distributions as we can see in Figures 5.15, A.9, and A.10

Table 5.11: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Happy Creek Using Batch 5

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	16.066	12	12.769	4	31
2	12.015	10	7.609	4	22
3	22.254	15	20.246	2	49
4	31.421	25	21.376	4	63
5	13.623	10	10.930	3	25
6	11.826	9	9.597	3	21
7	12.293	10	10.26	3	21
8	19.176	13	17.008	3	40
9	12.293	10	8.689	4	23
10	14.715	11	14.600	1	23
11	12.376	8	14.252	2	22
12	13.899	7	17.882	1	31
13	15.301	11	15.263	1	26
14	14.412	12	10.106	4	26
15	17.253	13	14.742	3	32
16	18.082	14	14.454	3	33
17	14.602	10	15.406	2	28
18	15.417	12	12.089	3	27
19	12.577	9	12.686	2	23
20	19.761	13	18.714	2	43
21	16.776	11	16.744	2	32
22	17.746	12	17.392	2	36
23	19.450	13	18.539	3	43
24	14.054	9	15.107	2	25
25	14.717	13	8.711	4	27
26	27.465	23	19.517	3	53
27	25.152	20	17.520	4	49
28	18.800	15	12.478	4	35
29	14.522	11	12.187	3	26
30	14.162	10	14.467	2	22
31	15.429	13	9.095	5	28
32	18.671	14	15.956	3	36
33	15.771	13	10.088	4	28
34	11.818	8	12.816	1	20
35	17.324	13	14.662	3	32
36	15.292	11	14.080	3	30
37	16.842	12	13.495	4	34
38	16.326	11	15.743	3	32
39	12.669	10	10.549	3	22
40	18.750	15	12.598	5	36
41	15.253	11	13.136	3	30
42	16.473	12	14.175	3	31
43	12.595	9	11.928	3	23
44	17.667	14	13.640	4	33
45	14.668	11	12.642	3	28
46	20.594	12	21.027	1	49
47	12.163	10	10.951	3	20
48	18.467	14	16.180	2	35
49	12.216	10	8.255	4	21
50	16.584	12	14.715	3	33
Mean	16.356	12.12	13.941	2.92	31.16
Min	11.818	7	7.609	1	20
Max	31.421	25	21.376	5	63

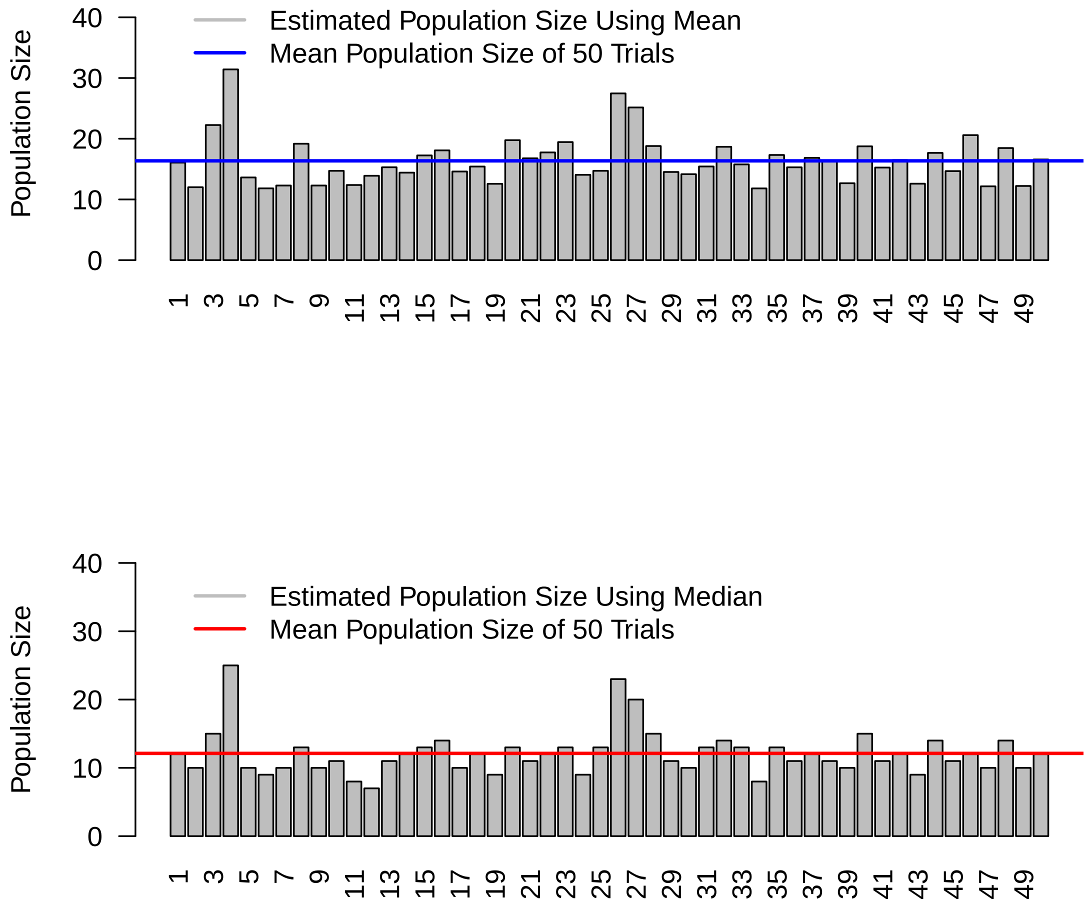


Figure 5.14: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 5 from HC

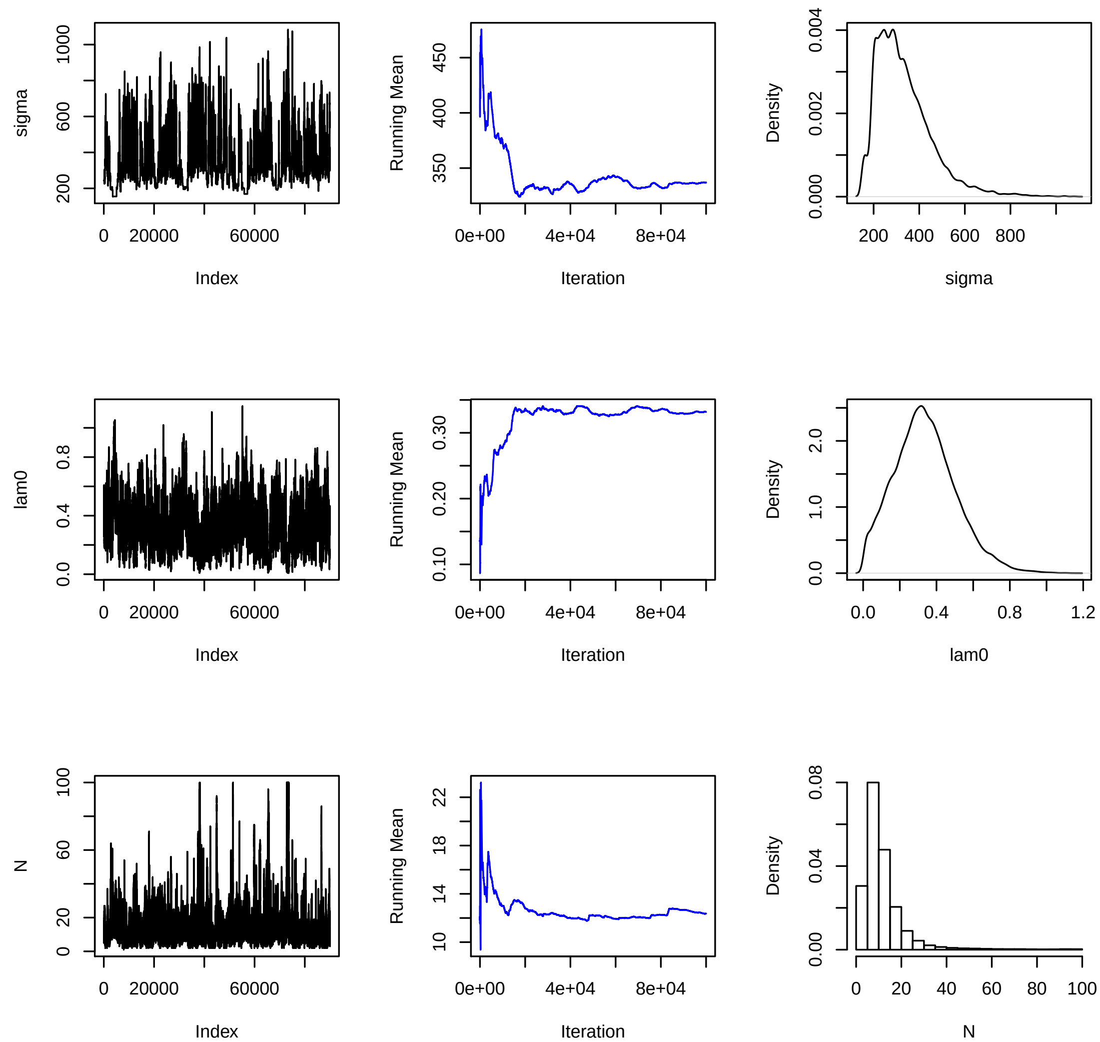


Figure 5.15: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 5

5.6.2 Estimated Population in Tel-4

In a similar way, population size, density, home range, and home range centers were estimated separately for Tel-4 for each batch. The estimated parameters for $M = 100$. For Batch 1, the average estimated population size N varies from 7 to 17 hogs with a mean of 11 hogs. The standard error is 17.7, and the highest density credible interval ranges from

1 to 29. Clearly, the density function of the posterior distribution twists to the right with a median of 4 hogs and a range of 3 to 7 hogs (Table 5.12 and Figure 5.16). Moreover, the running mean of the estimated values of the N converges to the posterior distributions (Figures 5.17, A.11, and A.12).

The summary of results to estimate σ depicted in Table A.12 shows that the average estimated mean and median are comparable with values of 420 for the mean and 398 for the median. The standard error is about 161, and the credible interval is from 171 to 643.

For Batch 2, the estimated population size N ranges from 27 to 34 hogs with an average of about 30 hogs. The standard error of the estimates N is between 25.4 and 27.8. Moreover, the highest Bayesian credible interval ranges from 1.6 to 74.6. The estimated median ranges from 16 to 24 with an average of about 20 hogs (Table 5.13 and Figure 5.18). The running mean of the estimated parameters converges to the posterior distributions (Figures 5.19, A.13, and A.14). The estimated mean and median of σ are 404 and 382, respectively, and they range from 387 to 424 for the mean and from 361 to 404 for the median (Table A.13).

Using the collected data from Batch 3, the estimated N ranges from 10 to 12 hogs with an average of 11 hogs. The median average is about 6 hogs, ranging from 5 to 7 hogs. Comparing the average mean with the average median, the density function of the posterior distribution twists to the right. The average of the highest Bayesian credible interval ranges from 1 to 40 (Table 5.14 and Figure 5.20). Moreover, the running mean of the estimated parameters converges to the posterior distributions (Figures 5.21, A.15, and A.16). The mean and median of σ are comparable with an average of 340 and 332, respectively. Additionally, the estimated σ ranges from 332 to 347 for the mean and from 326 to 339 for the median (Table A.14).

For Batch 4, the average estimated population size N is about 9 hogs and ranges from 5 to 25 hogs and the Bayesian credible interval is from 2 to 18 (Table 5.15 and Figure 5.22). The density function of the population size twists to the right with an average of the median about 6 hogs (Figures 5.23, A.17, and A.18). The standard error of the estimate N ranges from 3.9 to 22.5 with an average of 10.1. The average mean and median of σ are comparable with the values of 338 and 310, respectively (Table A.15). The credible interval for the estimated N ranges from 160 to 527.

Table 5.12: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Tel-4 Using Batch 1

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	7.340	3	13.519	1	13
2	10.388	4	16.242	1	25
3	10.501	4	17.431	1	26
4	13.545	4	20.214	1	39
5	11.175	3	18.758	1	31
6	9.761	3	17.097	1	23
7	13.004	5	19.894	1	36
8	10.866	4	17.060	1	28
9	8.375	3	14.394	1	18
10	10.639	4	16.985	1	26
11	8.399	3	15.377	1	18
12	10.912	4	18.293	1	28
13	14.881	6	20.635	1	43
14	10.730	4	17.203	1	27
15	12.341	5	17.645	1	32
16	11.697	5	18.054	1	29
17	16.601	7	21.945	1	46
18	9.889	4	15.223	1	23
19	11.830	4	19.052	1	32
20	12.130	5	18.254	1	31
21	10.280	4	16.098	1	24
22	13.173	5	19.547	1	35
23	15.132	6	20.721	1	43
24	9.497	3	16.500	1	22
25	8.947	3	15.837	1	20
26	8.168	3	14.553	1	17
27	11.413	4	18.204	1	28
28	11.313	4	18.387	1	31
29	15.546	5	22.679	1	48
30	11.094	4	18.083	1	29
31	11.831	5	16.814	1	30
32	11.401	4	17.708	1	29
33	10.267	3	17.383	1	27
34	11.072	4	17.963	1	29
35	11.943	4	18.797	1	33
36	12.177	5	17.907	1	30
37	8.957	4	14.271	1	18
38	8.254	3	14.563	1	18
39	7.656	3	13.640	1	17
40	10.381	4	16.389	1	26
41	10.092	4	16.050	1	25
42	14.228	5	20.800	1	40
43	10.506	4	16.376	1	25
44	9.924	3	17.268	1	24
45	14.912	5	20.705	1	42
46	11.555	4	18.091	1	30
47	14.970	6	20.889	1	42
48	10.770	4	17.621	1	26
49	14.824	5	21.409	1	44
50	14.376	5	20.772	1	41
Mean	11.393	4.18	17.786	1	29.34
Min	7.34	3	13.519	1	13
Max	16.601	7	22.679	1	48

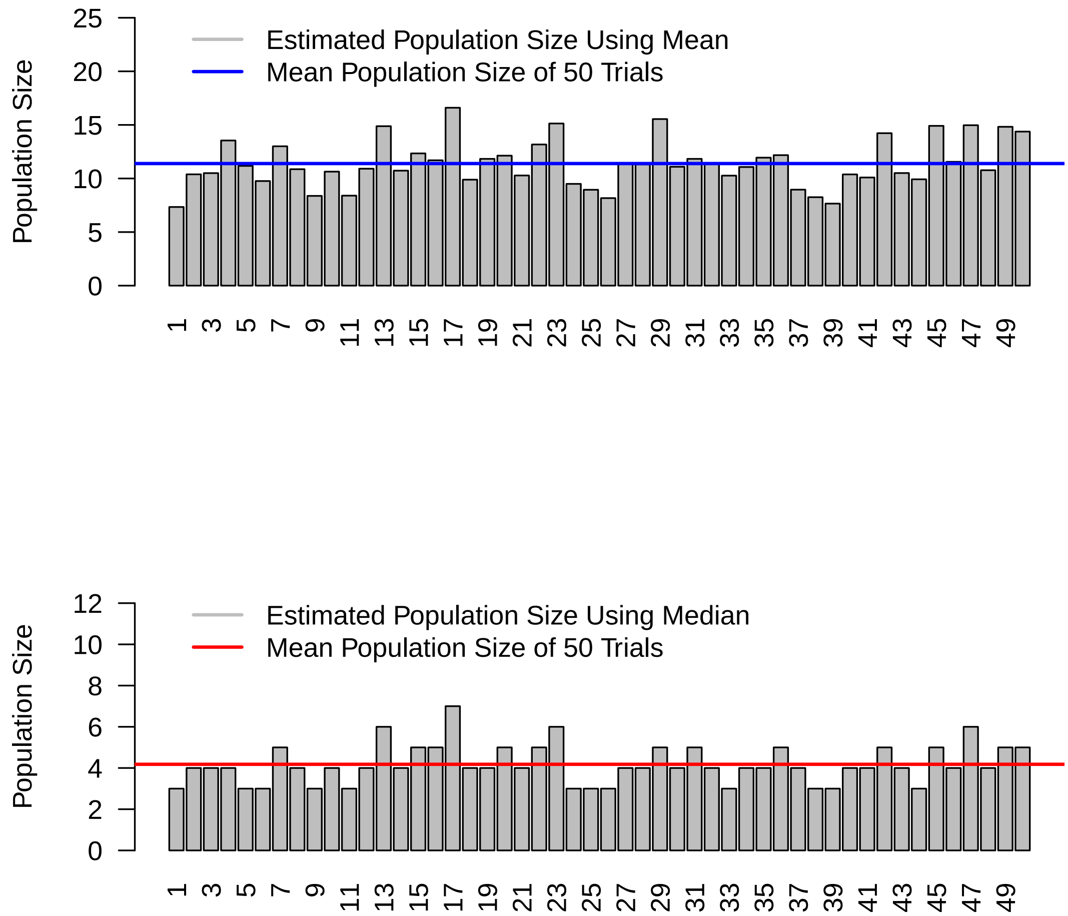


Figure 5.16: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 1 from Tel-4

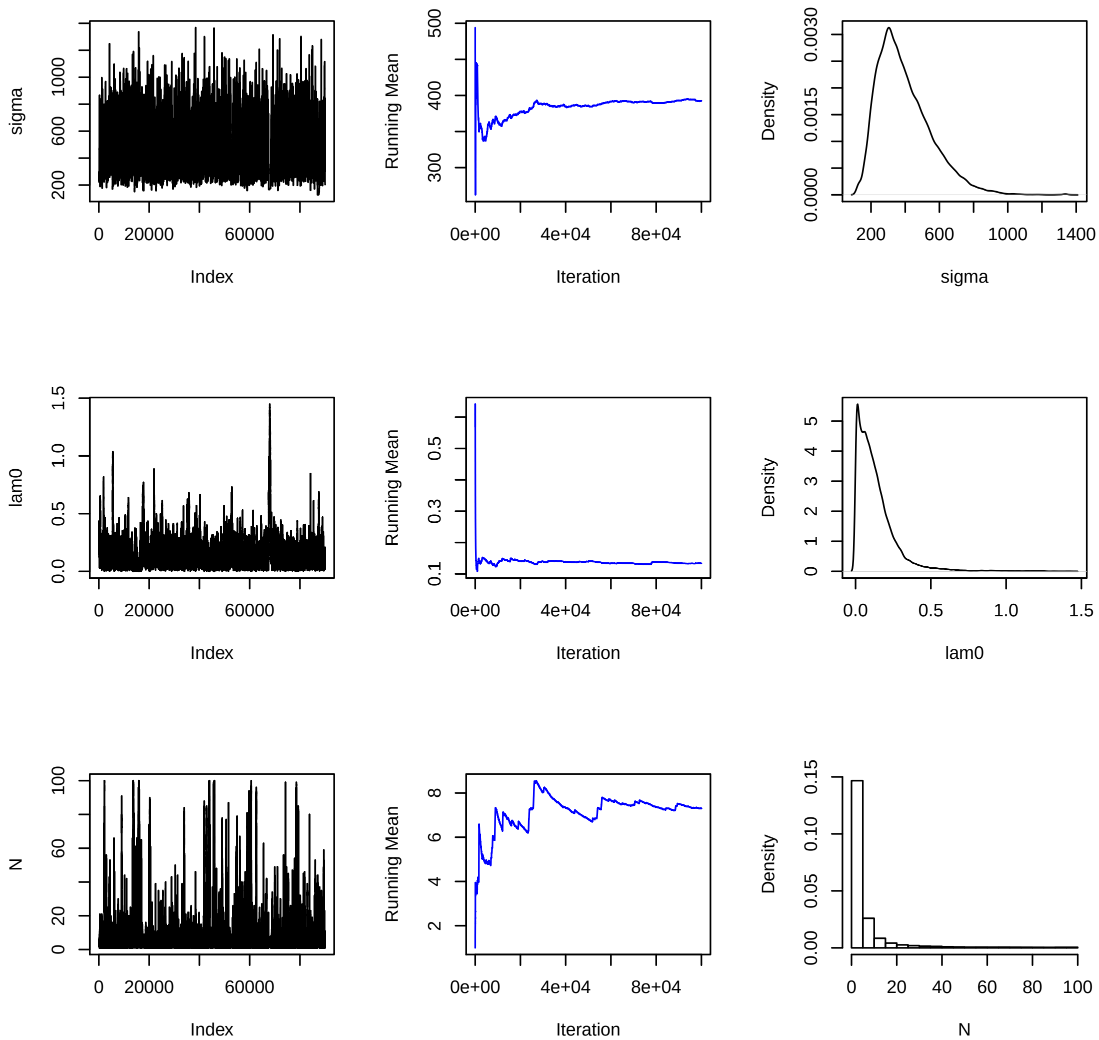


Figure 5.17: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 1

Table 5.13: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Tel-4 Using Batch 2

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	29.834	19	26.598	1	73
2	32.676	23	27.353	2	77
3	29.043	19	26.608	1	73
4	29.783	19	26.630	2	74
5	32.853	23	27.491	2	78
6	30.060	20	26.786	2	75
7	28.347	18	26.347	1	72
8	31.124	21	27.056	2	76
9	32.509	23	27.180	2	77
10	30.551	20	26.759	2	75
11	28.494	18	26.687	1	73
12	27.932	17	26.131	1	71
13	30.838	21	26.745	2	75
14	27.259	17	26.061	1	70
15	30.903	20	27.097	2	76
16	27.485	17	26.035	1	70
17	30.369	20	26.987	1	75
18	32.544	22	27.369	2	77
19	30.761	20	26.809	2	76
20	32.699	22	27.492	1	77
21	30.418	20	27.104	2	76
22	31.317	21	27.203	2	77
23	28.379	18	26.266	1	72
24	29.559	19	26.781	2	75
25	30.535	20	26.897	2	76
26	28.759	18	26.446	1	73
27	30.231	20	26.748	2	75
28	27.509	17	26.363	1	71
29	30.968	20	27.207	2	77
30	31.372	21	27.026	2	76
31	30.005	20	26.626	2	75
32	30.011	19	26.898	2	75
33	27.594	17	25.907	1	70
34	29.810	19	26.584	2	75
35	31.169	21	27.280	2	77
36	31.795	21	27.398	2	77
37	32.513	22	27.360	2	78
38	26.540	16	25.399	1	68
39	34.191	24	27.762	2	79
40	28.879	18	26.527	1	73
41	29.397	19	26.799	1	74
42	30.843	21	26.847	2	76
43	29.628	19	26.535	1	73
44	32.092	22	27.244	2	77
45	28.824	18	26.422	1	73
46	31.010	20	27.30	2	77
47	29.953	19	27.104	2	76
48	29.974	19	26.908	2	75
49	29.383	18	26.843	2	75
50	27.907	17	26.126	1	71
Mean	30.133	19.640	26.803	1.620	74.640
Min	26.540	16.000	25.399	1.000	68.000
Max	34.191	24.000	27.762	2.000	79.000

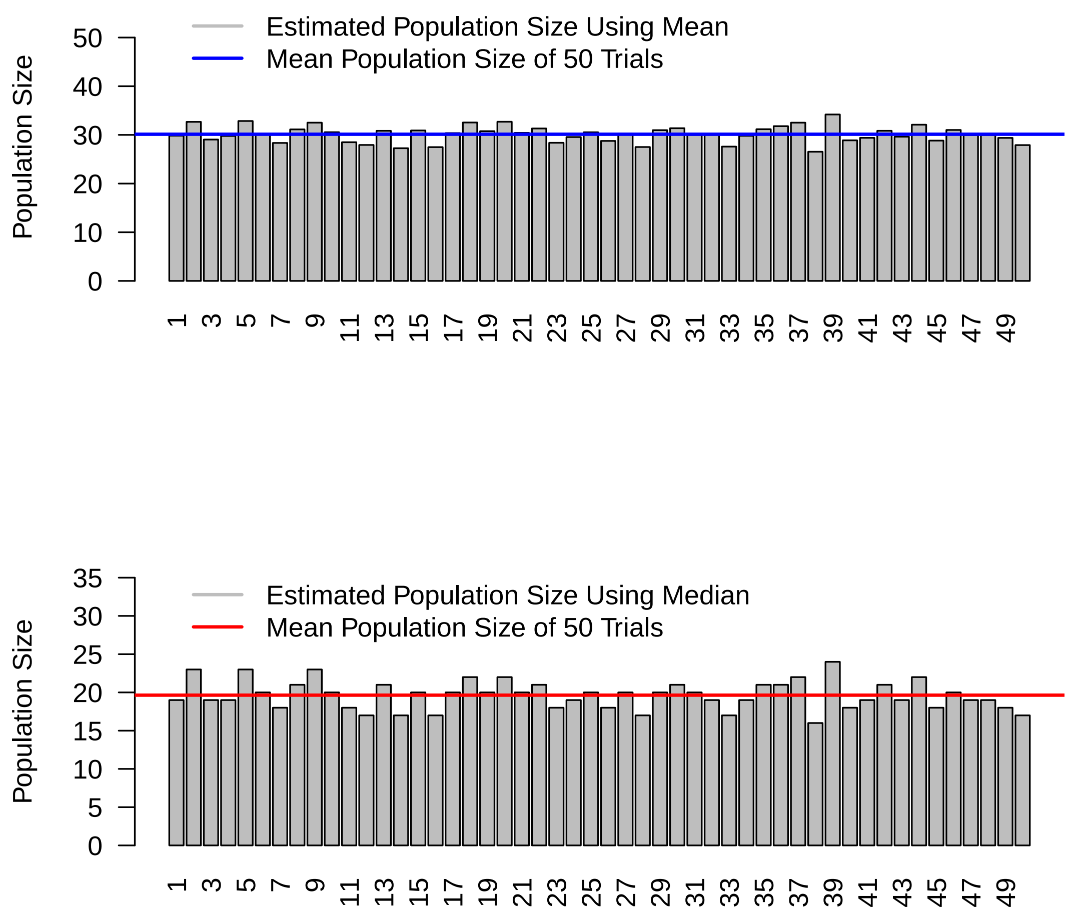


Figure 5.18: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 2 from Tel-4

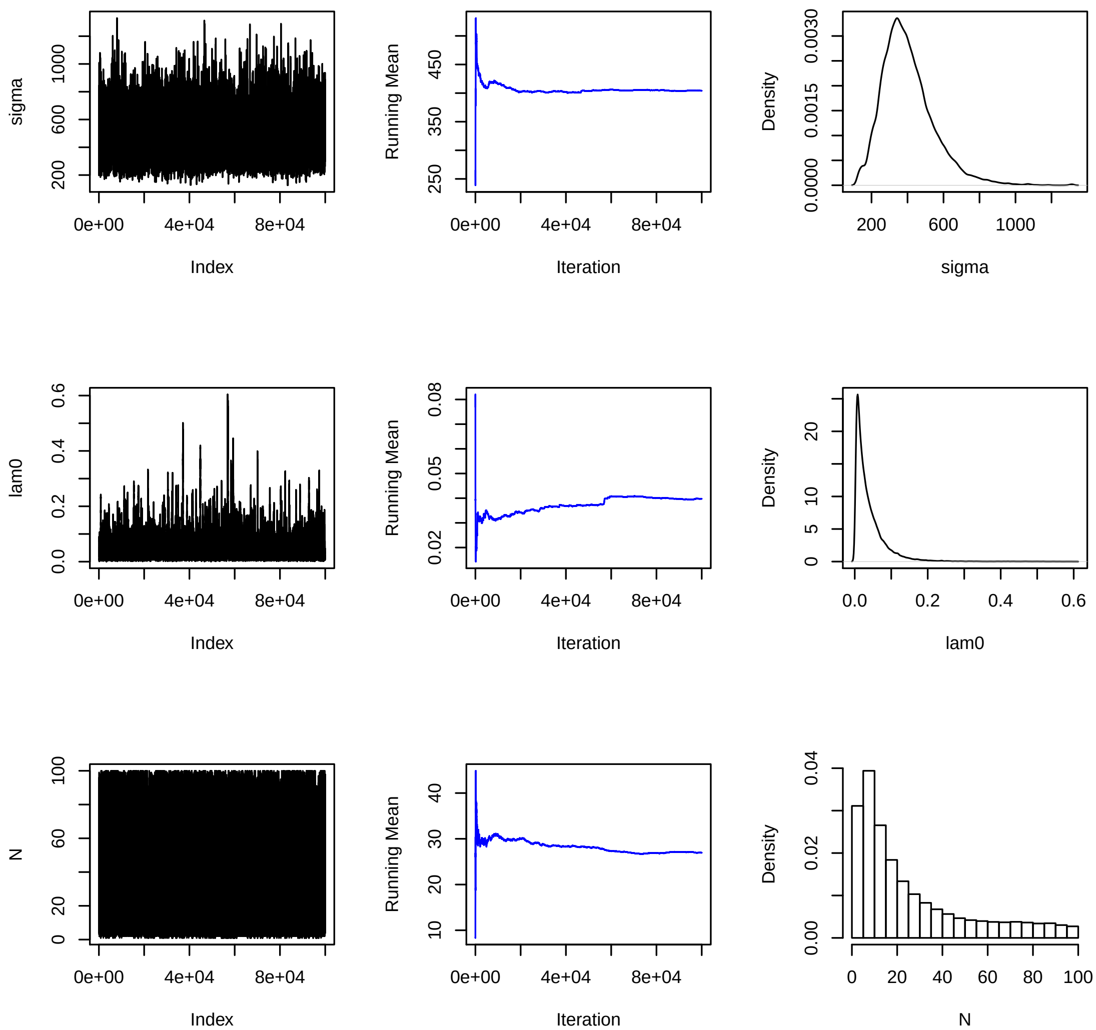


Figure 5.19: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 2

Table 5.14: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Tel-4 Using Batch 3

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	10.741	6	15.555	1	43
2	10.256	6	13.974	1	36
3	11.354	6	15.668	1	44
4	10.436	6	14.551	1	39
5	11.175	6	15.261	1	42
6	12.066	7	16.137	1	47
7	10.525	6	14.414	1	37
8	11.826	6	16.729	1	49
9	11.267	6	15.419	1	43
10	10.896	6	14.803	1	40
11	11.147	6	15.051	1	41
12	10.047	5	14.606	1	38
13	9.928	6	13.328	1	33
14	11.329	6	15.421	1	43
15	11.449	6	15.692	1	44
16	10.626	6	14.515	1	38
17	10.961	6	15.708	1	43
18	10.812	6	14.780	1	39
19	10.941	6	14.847	1	40
20	11.140	6	14.840	1	40
21	10.499	6	14.120	1	36
22	10.102	6	13.607	1	35
23	11.104	6	15.390	1	43
24	11.017	6	15.203	1	41
25	10.191	6	13.912	1	36
26	11.417	6	15.331	1	42
27	11.431	6	15.449	1	43
28	11.197	6	14.755	1	41
29	11.588	6	15.774	1	45
30	11.483	6	15.733	1	45
31	11.248	6	15.071	1	41
32	11.618	6	15.721	1	44
33	10.905	6	14.501	1	39
34	10.572	6	14.291	1	37
35	10.969	6	14.839	1	40
36	11.404	6	15.764	1	44
37	11.024	6	14.751	1	40
38	11.099	6	14.809	1	40
39	11.746	7	15.306	1	43
40	10.778	6	14.873	1	40
41	10.215	6	13.743	1	34
42	11.449	6	15.703	1	44
43	10.997	6	14.734	1	39
44	9.8670	6	13.481	1	34
45	11.041	6	14.823	1	40
46	10.758	6	14.256	1	38
47	10.672	6	14.586	1	38
48	10.403	6	14.056	1	37
49	11.336	6	15.921	1	45
50	10.532	6	14.751	1	39
Mean	10.952	6.020	14.931	1.000	40.440
Min	9.867	5	13.328	1	33
Max	12.066	7	16.729	1	49

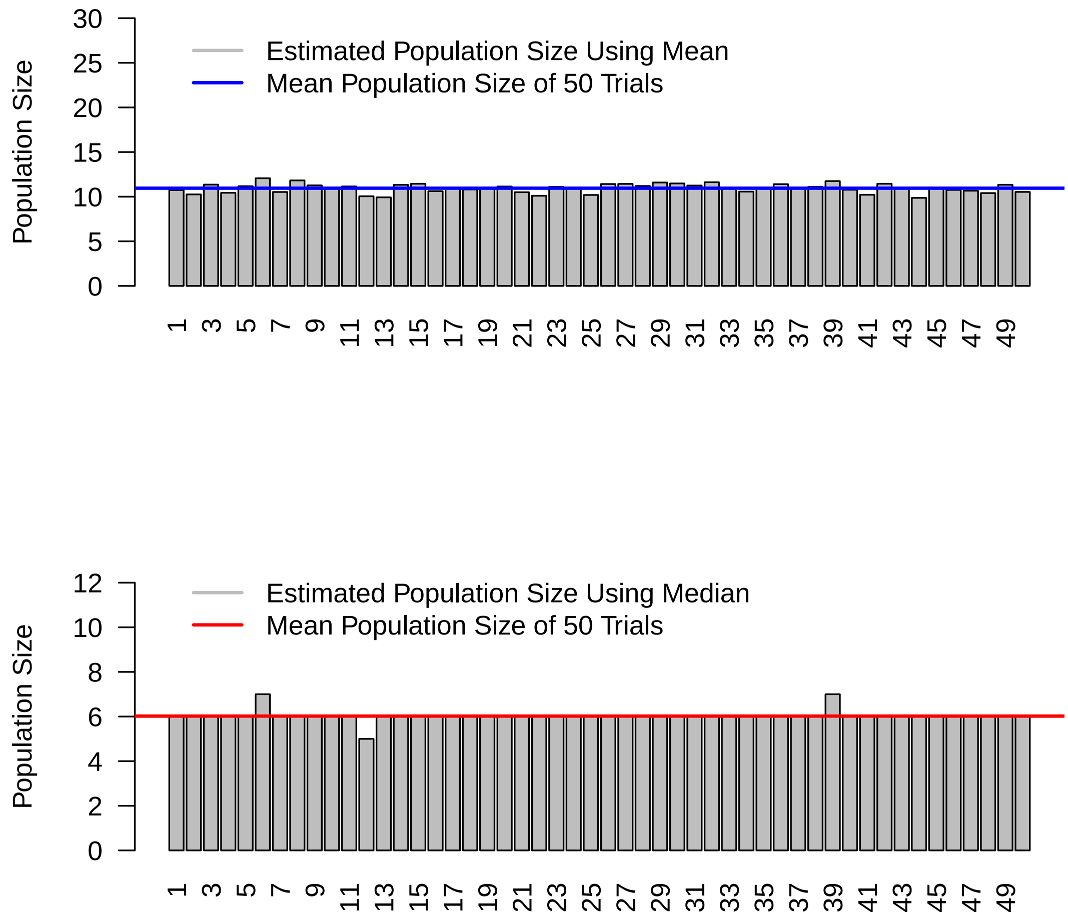


Figure 5.20: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 3 from Tel-4

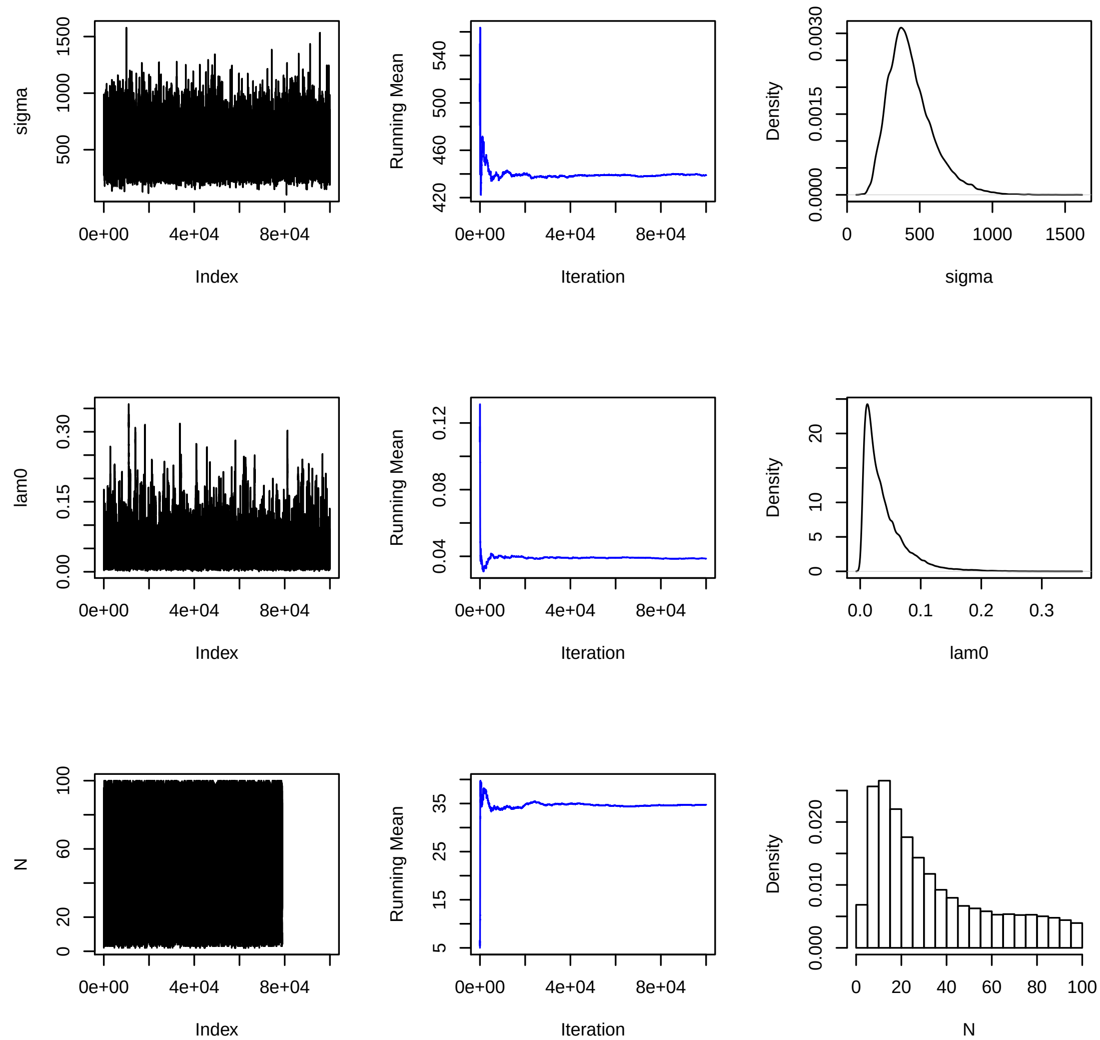


Figure 5.21: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 3

Table 5.15: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N for Tel-4 Using Batch 4

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	9.399	6	10.108	2	19
2	11.447	7	13.94	2	25
3	14.339	10	13.559	2	29
4	8.499	5	12.217	2	15
5	8.734	6	10.151	2	17
6	9.288	7	9.802	2	17
7	12.028	9	11.611	2	23
8	7.257	5	6.989	2	14
9	12.621	11	8.783	2	23
10	18.273	14	15.452	2	38
11	25.022	17	22.492	2	58
12	8.044	6	7.444	2	15
13	9.858	6	11.41	2	20
14	6.853	4	9.139	2	12
15	11.284	8	11.342	2	23
16	8.479	5	10.806	2	17
17	9.152	6	10.478	2	17
18	7.134	5	7.854	2	13
19	7.199	5	8.098	2	13
20	6.344	5	6.723	2	12
21	5.778	4	5.19	2	11
22	6.752	4	8.234	2	13
23	5.533	4	4.739	2	11
24	7.956	5	8.713	2	15
25	9.959	7	9.934	2	18
26	9.155	6	9.352	2	19
27	5.192	3	5.601	2	9
28	10.534	7	12.017	2	20
29	9.4	7	10.494	2	17
30	7.857	4	10.597	2	16
31	5.466	4	5.053	2	10
32	8.705	6	8.453	2	16
33	10.055	5	14.207	2	21
34	12.765	9	12.695	2	27
35	5.599	5	3.911	2	10
36	13.377	10	11.178	2	27
37	8.559	5	12.477	2	15
38	12.419	7	14.966	2	26
39	7.328	4	9.707	2	15
40	5.603	4	4.319	2	11
41	6.837	5	6.495	2	13
42	9.221	6	11.514	2	15
43	7.85	5	9.371	2	14
44	10.374	7	12.144	2	20
45	7.47	5	9.691	2	14
46	10.928	7	11.803	2	21
47	7.292	6	6.975	2	12
48	8.285	6	9.078	2	15
49	11.694	6	14.854	2	25
50	8.539	6	11.541	2	14
Mean	9.355	6.32	10.074	2	18.2
Min	5.192	3	3.911	2	9
Max	25.022	17	22.492	2	58

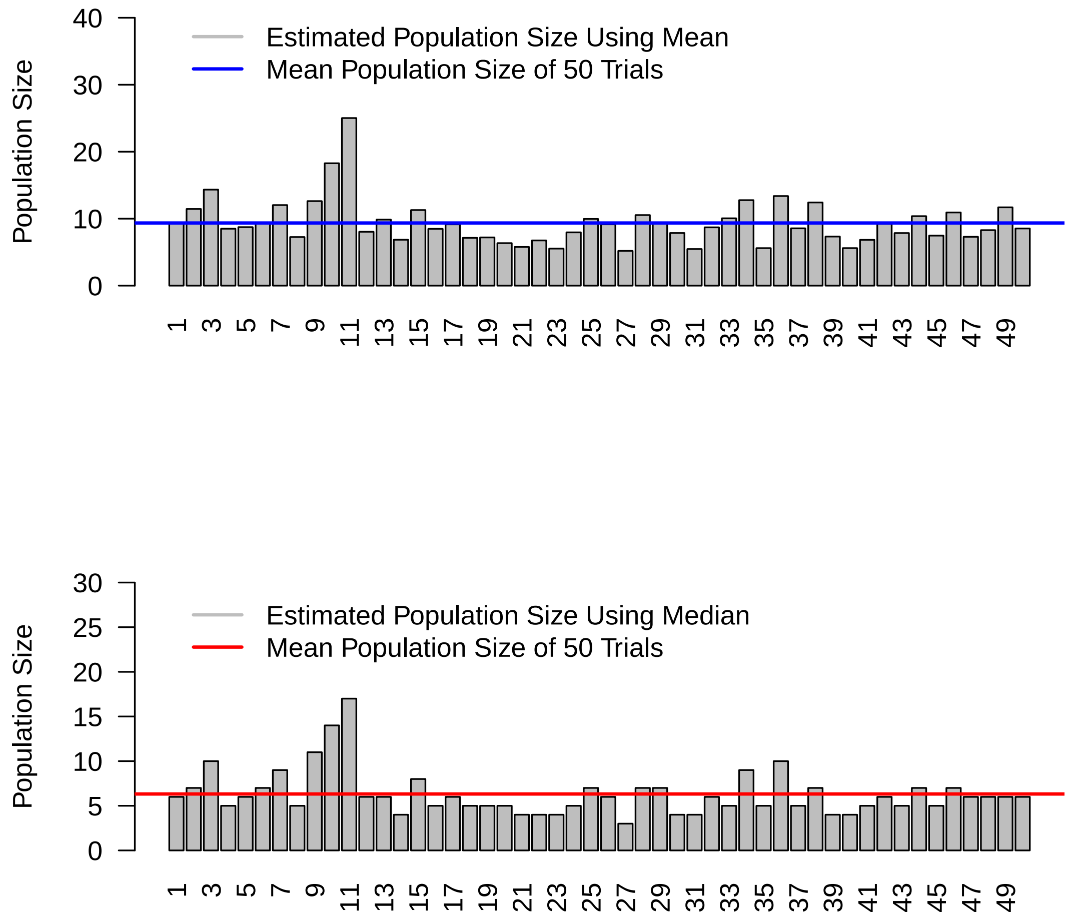


Figure 5.22: The Estimated Population Size by Mean (top) and Median (bottom) using the Average of 50 Runs of Batch 4 from Tel-4

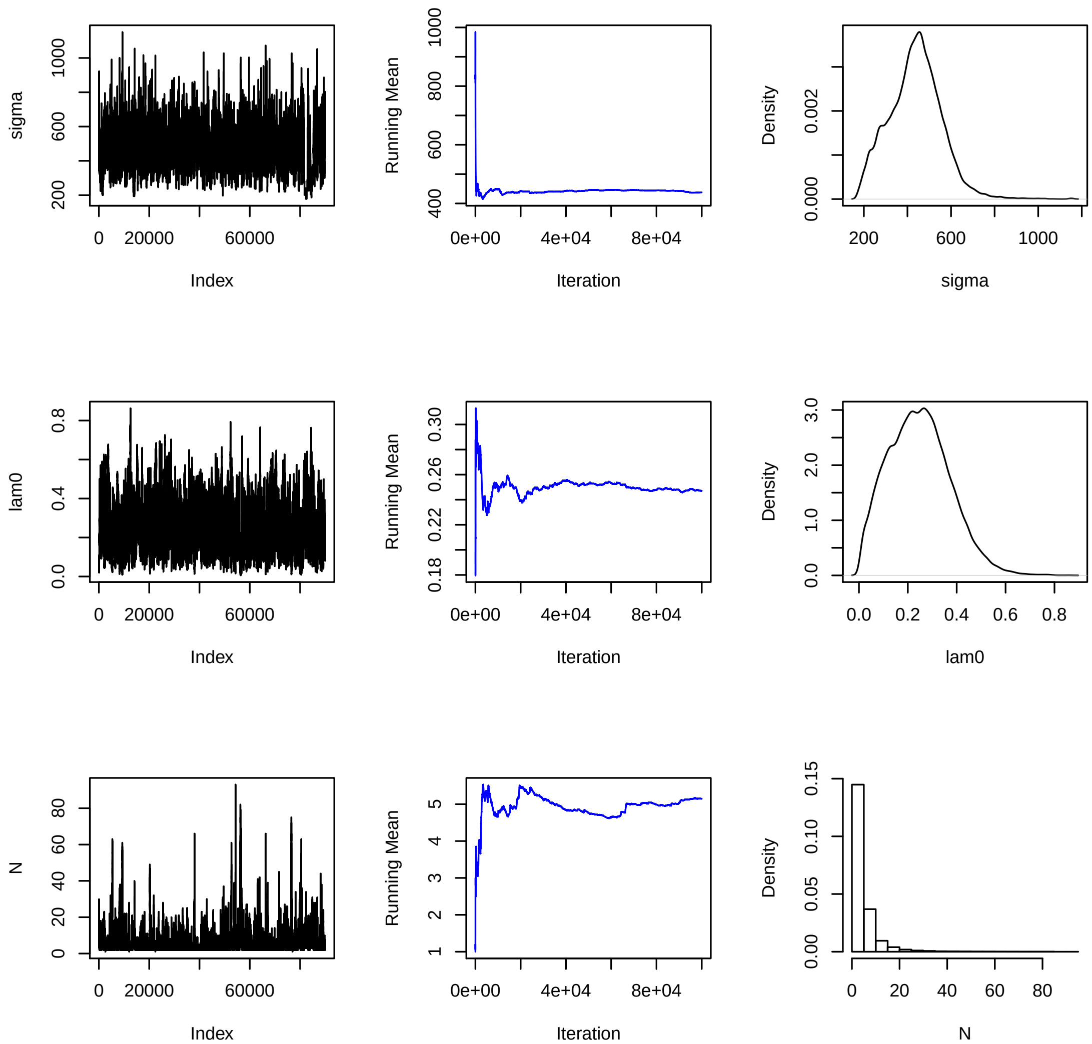


Figure 5.23: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 4

5.7 Estimating Hog Population using Regularized ψ

Results in Table 5.16 show the simulations for Happy Creek (HC) using Batch 4 of the collected data. The highest effective sample size ESS for N and ψ are 842.2 and 902.9, respectively, associated with the constraint $\psi \leq 0.50$ and $M = 100$.

The results in Tables 5.17 and 5.18 reveal the range of the N with no constraint on

Table 5.16: Summary of the Estimated Mean of σ, λ_0, ψ, and N with a Constraint on ψ (0 to 0.5) and $M = 200$

	ψ	$\hat{\sigma}$	$\hat{\lambda}_0$	$\hat{\psi}$	$\hat{N}$	ESS_N	ESS_ψ	$Lag10_N$	$Lag10_\psi$
M=100	0.00_1.00	473.783	0.120	0.277	27.252	451.415	472.341	0.871	0.860
	0.00_0.50	459.706	0.148	0.182	17.739	842.211	902.896	0.741	0.708
M=200	0.00_1.00	461.215	0.110	0.217	42.797	251.548	258.152	0.926	0.921
	0.00_0.50	459.776	0.126	0.139	27.206	491.443	508.260	0.839	0.825

parameter ψ is 17 to 41 hogs with an average of 17. The estimated N ranges between 14 and 22 hogs with an average of 18 under the constraint on the ψ between 0.00 and 0.50. Furthermore, the standard error ranges between 18.7 to 27.2 with an average of 24.2 under no constraint on the ψ. When $\psi \leq 0.5$, then the average standard error ranges from 11.2 to 13.6, reduced to 12.7, a much smaller number than the standard error obtained with no constraint on the ψ.

For $M = 200$, the estimated N with no constraint on parameter ψ ranges between 27 and 58 hogs with an average of about 43. After setting the constraint on the psi, the estimated N ranges from 21 to 35 hogs with an average of 27. The standard error ranges from 34.8 to 53.8 with an average of 46 with no constraint on parameter ψ. For $\psi \leq 0.5$, the average standard error ranges from 20.5 to 26.6 with an average of 24.3. With a constraint, the smaller standard error ranges from 6.1 to 19 in comparison with the estimated values for no constraint on the ψ (Tables 5.19 and 5.20).

Comparing Figures 5.24 to 5.27, parameter sigma and $lambda_0$ are comparable, and in all cases, we see that the densities of the parameter converged to the posterior distribution. In the case with the constraint on parameter ψ, we have a better mixing of the chains, making the estimated in is more accurate.

With 0 to 0.50 constraint on the parameter ψ and $M = 100$, which has the highest $ESS = 842.211$, we have good mixing of chains of the unknown parameters. The densities are twists to the right. Moreover, the histogram tail of the estimated N is shorter than all cases.

Table 5.17: Happy Creek, Batch 4, Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population Size N with no Constraint on the ψ and $M = 100$

Sim Number	Estimated *N*	Median	sd	Credible interval (HDI)	
				LB	UB
1	24.484	17	22.053	1	56
2	39.661	34	27.013	3	81
3	30.911	21	27.252	1	74
4	28.370	20	23.966	2	65
5	28.481	19	25.630	1	69
6	30.918	21	26.839	1	73
7	22.076	14	22.053	1	54
8	17.236	11	18.676	1	39
9	28.488	20	24.624	2	68
10	27.448	19	24.776	1	65
11	24.219	14	24.078	1	61
12	28.337	20	23.916	2	65
13	35.590	28	26.668	2	78
14	26.799	17	24.551	1	64
15	27.565	19	23.387	2	63
16	23.053	14	22.496	1	56
17	28.583	21	24.295	1	65
18	29.695	21	25.525	2	70
19	32.738	25	25.516	2	72
20	29.357	21	25.188	1	68
21	24.308	14	24.236	1	62
22	32.988	24	26.721	1	75
23	40.529	35	27.200	4	84
24	24.874	15	24.195	1	61
25	26.595	18	24.260	1	64
26	25.450	16	24.264	1	63
27	29.620	20	26.311	1	70
28	34.118	26	26.326	1	74
29	21.748	13	21.783	1	53
30	23.547	14	23.629	1	59
31	25.918	17	23.655	2	63
32	33.263	25	26.412	1	74
33	29.987	22	25.735	1	69
34	29.025	19	25.993	1	69
35	28.182	19	25.563	1	68
36	21.788	13	22.329	1	54
37	18.070	10	20.355	1	45
38	25.888	17	23.562	1	61
39	28.660	19	26.003	1	69
40	21.992	12	22.751	1	56
41	25.434	17	22.727	1	58
42	26.182	17	23.925	1	63
43	19.821	12	20.329	1	46
44	21.765	14	21.375	1	51
45	26.317	18	23.449	2	63
46	20.937	12	22.555	1	54
47	17.909	11	19.013	1	41
48	37.962	32	27.103	2	79
49	26.341	17	24.735	1	64
50	29.395	20	25.272	2	70
Mean	27.252	18.68	24.205	1.32	63.76
Min	17.236	10	18.676	1	39
Max	40.529	35	27.252	4	84

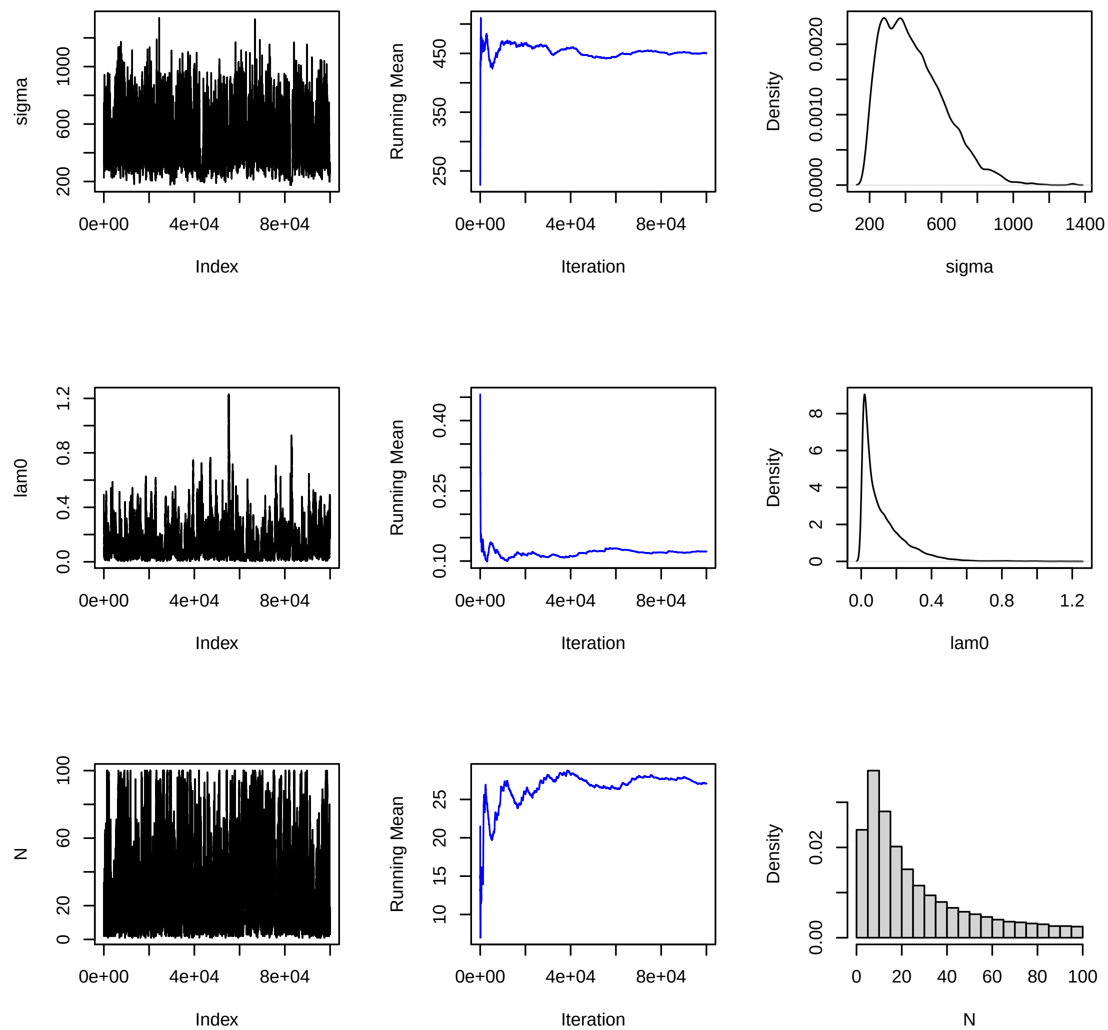


Figure 5.24: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with no Constraint on the ψ and $M = 100$ for Happy Creek, Batch 4

Table 5.18: Happy Creek, Batch 4, Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population Size N with $\psi \in [0, 0.50]$ and $M = 100$

Sim #	Mean	Median	sd	Credible interval (HDI)	
				LB	UB
1	18.187	15	12.732	2	45
2	16.214	12	12.472	1	42
3	18.159	15	12.736	2	44
4	16.469	13	11.914	1	41
5	19.020	16	13.328	1	45
6	16.513	12	12.911	1	43
7	17.825	14	13.120	1	44
8	16.566	13	12.260	2	43
9	17.856	14	13.361	1	44
10	22.343	20	13.477	3	48
11	19.716	17	12.619	2	45
12	15.699	13	11.489	1	40
13	20.327	18	13.502	2	46
14	16.702	13	12.423	1	42
15	16.606	13	12.627	1	43
16	16.503	12	12.735	1	43
17	15.053	11	12.642	1	42
18	21.455	19	13.29	2	46
19	15.647	12	12.411	1	42
20	15.209	12	11.462	1	40
21	21.322	19	13.125	3	47
22	13.864	10	11.156	1	38
23	15.968	12	12.442	1	42
24	20.514	18	13.172	2	46
25	15.129	11	12.615	1	42
26	21.308	19	13.111	3	47
27	21.220	19	12.890	2	45
28	17.079	13	12.821	1	43
29	16.619	13	12.886	1	43
30	15.628	12	12.665	1	42
31	16.786	13	12.577	2	44
32	18.541	15	13.170	2	45
33	18.845	16	13.161	1	44
34	17.787	14	13.273	1	44
35	16.202	13	12.342	1	42
36	18.339	15	12.655	2	44
37	17.142	13	12.886	1	43
38	17.428	14	12.887	2	44
39	18.133	15	13.094	1	44
40	17.655	14	12.591	2	44
41	18.483	16	12.291	2	43
42	17.097	14	12.280	1	42
43	16.546	13	12.563	1	43
44	17.031	13	12.666	1	43
45	18.195	15	12.756	2	44
46	20.351	18	12.907	2	45
47	18.457	15	13.103	2	45
48	20.334	17	13.549	2	47
49	16.558	13	12.136	1	41
50	16.305	13	12.177	1	42
Mean	17.739	14.38	12.709	1.48	43.52
Min	13.864	10	11.156	1	38
Max	22.343	20	13.549	3	48

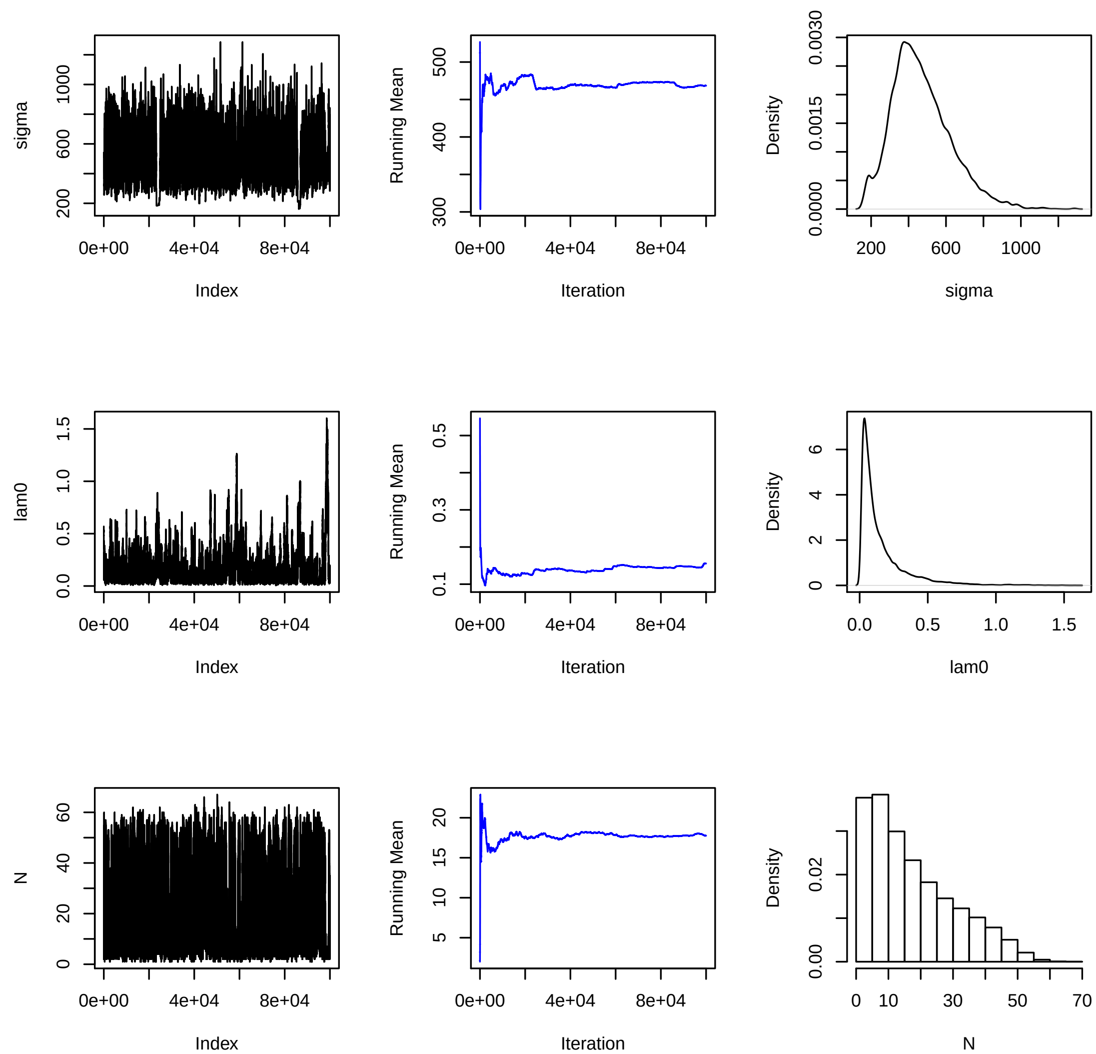


Figure 5.25: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with $\psi \in [0, 0.50]$ and $M = 100$ for Happy Creek, Batch 4

Table 5.19: Happy Creek, Batch 4, Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population Size N with no Constraint on the ψ and $M = 200$

Sim #	Mean	Median	sd	Credible interval (HDI)	
				LB	UB
1	44.281	23	47.868	1	158
2	41.266	23	44.932	1	148
3	40.701	22	46.255	1	153
4	57.476	40	51.584	1	167
5	35.218	18	41.774	1	133
6	53.462	32	52.538	1	169
7	48.087	29	47.572	1	157
8	32.923	16	40.488	1	132
9	41.830	20	47.350	1	150
10	47.513	26	50.882	1	166
11	34.244	18	39.543	1	128
12	34.797	14	46.164	1	152
13	44.958	25	47.975	1	157
14	26.555	13	34.831	1	108
15	43.255	23	47.501	1	157
16	42.764	23	46.334	1	152
17	30.819	15	37.915	1	120
18	33.053	17	38.984	1	124
19	51.725	31	50.990	1	163
20	37.179	18	44.436	1	144
21	44.846	21	51.656	1	166
22	48.986	29	49.402	1	160
23	33.839	17	40.184	1	130
24	47.368	25	50.587	1	165
25	36.842	21	40.032	1	133
26	46.203	26	50.007	1	167
27	41.092	23	44.173	1	145
28	52.396	32	50.981	1	165
29	45.932	26	48.259	1	160
30	46.324	29	45.912	1	151
31	44.944	22	50.726	1	162
32	37.963	21	41.236	1	137
33	46.456	25	49.310	1	159
34	55.794	34	53.792	1	171
35	43.774	26	45.097	1	149
36	43.015	25	45.458	1	146
37	57.198	38	52.735	1	171
38	40.024	19	46.612	1	150
39	55.812	36	51.391	1	166
40	35.497	20	39.131	1	127
41	42.303	24	45.005	1	145
42	48.266	30	47.181	2	157
43	32.617	17	38.570	1	121
44	54.578	37	50.261	2	168
45	38.321	21	43.334	1	142
46	38.13	20	43.132	1	142
47	46.526	24	50.706	1	166
48	39.645	22	43.965	1	142
49	33.179	15	42.942	1	140
50	39.876	22	43.831	1	145
Mean	42.797	23.86	46.031	1.04	149.72
Min	26.555	13	34.831	1	108
Max	57.476	40	53.792	2	171

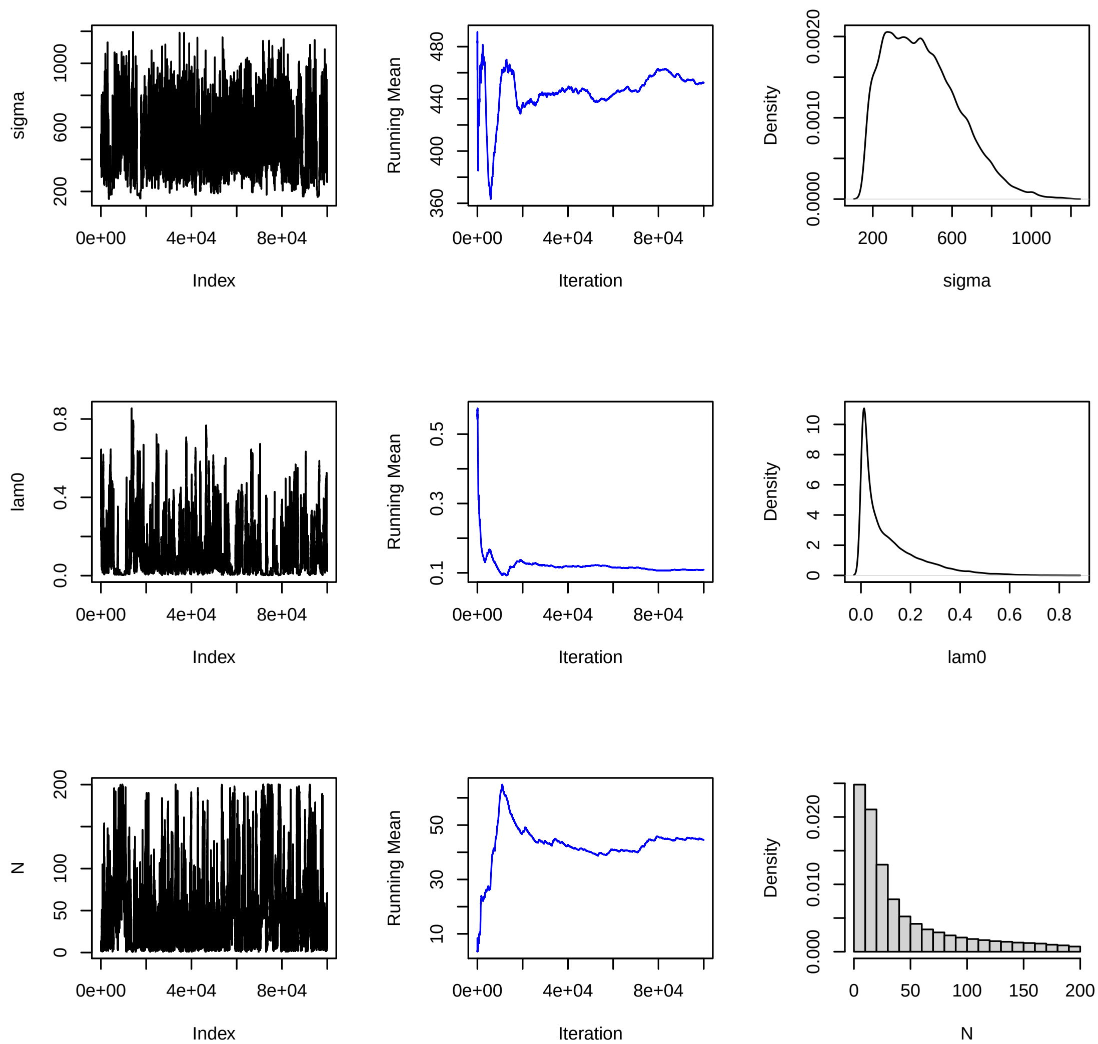


Figure 5.26: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with no Constraint on the ψ and $M = 200$ for Happy Creek, Batch 4

Table 5.20: Happy Creek, Batch 4, Summary of 50 Runs to Estimate Mean, Median, Mode, Standard Error, and Credible Interval of Population Size N with $\psi \in [0, 0.50]$ and $M = 200$

Sim #	Mean	Median	sd	Credible interval (HDI)	
				LB	UB
1	30.893	22	25.526	2	85
2	22.083	13	22.130	1	72
3	30.012	22	25.149	1	83
4	26.992	17	25.460	1	83
5	27.050	17	24.907	1	82
6	31.127	22	26.329	1	86
7	24.667	15	24.722	1	81
8	28.685	19	25.585	1	84
9	22.912	14	22.175	1	74
10	27.123	18	24.951	1	83
11	31.937	24	25.767	1	85
12	22.797	15	22.498	1	75
13	28.807	22	23.360	1	79
14	28.721	21	24.695	1	81
15	31.335	23	26.023	1	85
16	24.917	16	23.983	1	79
17	30.237	22	25.067	1	83
18	31.004	23	24.794	1	83
19	26.500	18	23.757	1	80
20	25.847	17	23.698	1	79
21	25.561	15	25.254	1	83
22	26.248	17	24.066	1	80
23	28.936	19	25.916	1	85
24	29.666	20	26.509	1	85
25	32.339	24	26.198	1	86
26	27.319	19	23.936	1	80
27	26.231	17	24.028	2	81
28	23.738	15	22.982	1	76
29	24.175	14	24.069	1	79
30	20.746	13	20.512	1	68
31	25.029	17	21.906	1	74
32	28.182	20	24.521	1	82
33	25.188	16	23.954	1	79
34	29.594	22	24.643	1	82
35	26.881	18	24.319	1	80
36	24.284	16	22.632	1	76
37	28.730	20	25.309	1	83
38	26.981	18	24.548	1	81
39	23.952	15	23.015	1	77
40	28.684	20	24.442	1	82
41	25.902	17	23.755	1	79
42	28.479	20	24.918	1	82
43	24.393	16	22.709	1	76
44	30.076	22	25.398	2	85
45	21.163	13	20.994	1	70
46	27.604	18	25.294	1	83
47	25.847	17	24.102	1	80
48	30.641	22	26.038	1	85
49	34.929	27	26.637	2	89
50	25.131	16	23.691	1	80
Mean	27.206	18.46	24.337	1.08	80.6
Min	20.746	13	20.512	1	68
Max	34.929	27	26.637	2	89

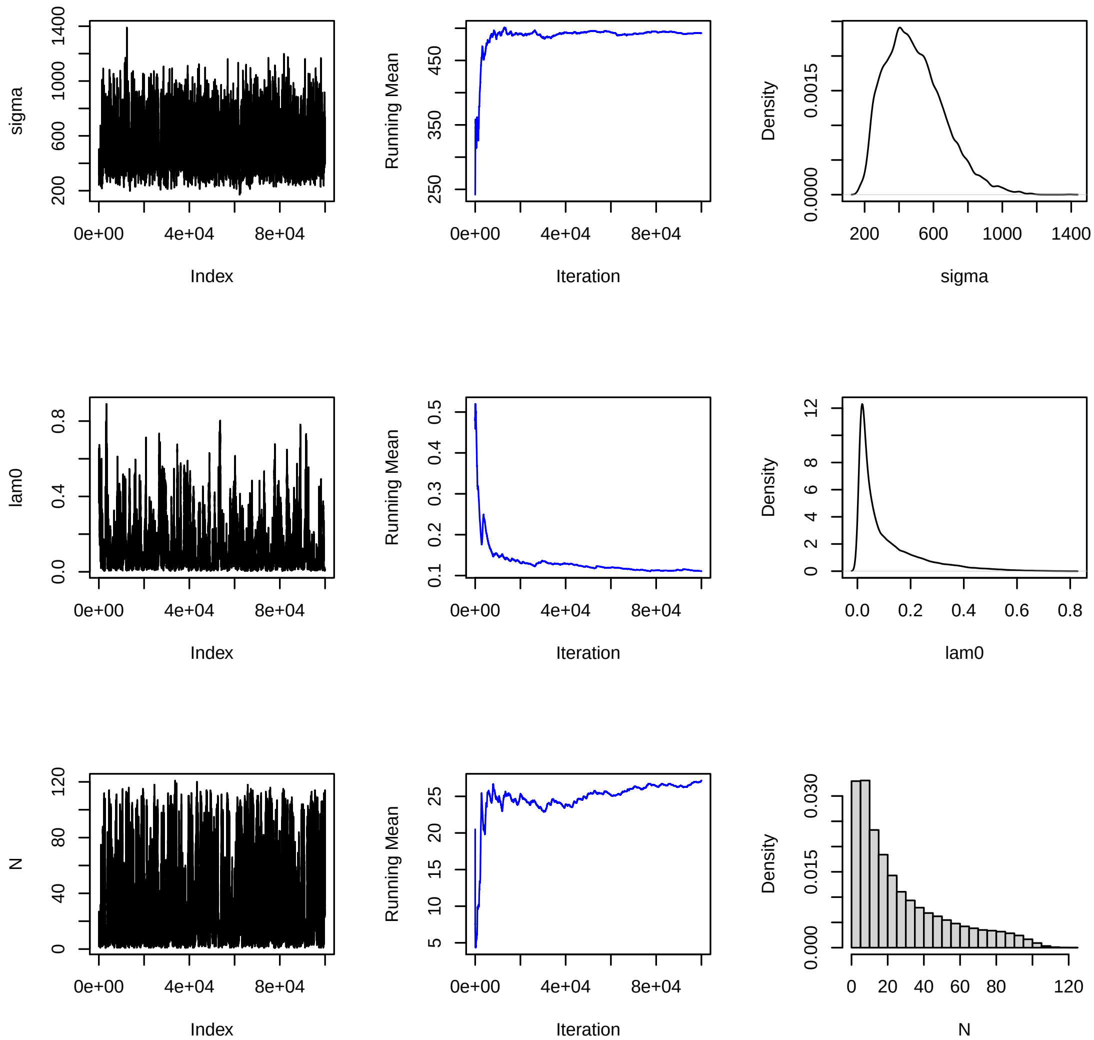


Figure 5.27: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) with $\psi \in [0, 0.50]$ and $M = 200$ for Happy Creek, Batch 4

Chapter 6

Discussion, Contributions, and Conclusions

In this work, a real population analysis problem was investigated. Population analysis based on virtual spatial sampling using camera encounters is an emerging field of research and is finding a broad range of applications. Important applications include preservation of the population of endangered species and controlling the population of invasive species, which might not be native to the host ecosystem. The main task in population analysis, whether for preservation of endangered animals or control of invasive ones is to estimate the population size.

Conventional capture-mark-recapture methods have been widely employed by sampling the population using physical traps, marking the captured individuals and release them, re-sampling the population, counting the marked ones, and marking the unmarked captures and then continue this procedure for a prefixed number of sampling occasions. The intuition behind this method is that some marked and some unmarked animals will be captured in the consecutive sampling. At the end of survey, each marked animal will have a capturing history. For instance, a history of six samples ”100110” for a specific animal means that it has been caught in the first, fourth, and fifth sampling occasions. The fraction of the captured animals that are recaptured will be used to extrapolate the size of the entire population.

One of the shortcomings of the capture-mark-recapture methods is required resources to perform physical capturing and marking of the animals. In contrast with the capture-mark-recapture methods, the recent virtual spatial sampling methods rely on camera encounters to collect the encounter history data. In these methods, cameras are placed near the animal habitats to monitor them. Although, virtual trapping methods eliminate the need for physical capture and marking, they have their own challenges. Virtual marking of the animals demands for identification of animals in the phonographs. Because, animal identification methods have not been well developed yet, often these methods are reduced to virtually capture-recapture of unmarked animals. As a result, an Non-deterministic polynomial acceptable problems hard count problem is inherited. It means we need to deal with multiple camera encounters of the same animal possibly at the same camera location, multiple camera locations, one sampling occasion, or multiple sampling occasions.

The contributions of this work to population analysis using virtual traps are summarized below.

- Comprehensive study of the current state of the art spatial capture model. We investigated the sensitivity of the spatial capture method to the independent variables and unknown parameters including:
  - Data Augmentation Parameter M
  - Probability of Detection P
  - Number of Occasions K
  - Base encounter rate λ_0
  - Probability that an individual in the augmented population of size M is a member of the actual population (of size N) ψ

- Extending and improving the spatial capture model by:
  - Introducing an informative prior distribution for ψ using adaptive estimation of ψ based on estimated population size $\hat{N}$
  - Introducing an informative prior distribution for home range radius σ based on a multiple regression model of climate and geographical factors
  - Using convergence criteria including effective sample size (ESS) and auto-correlation lag of posterior distribution, as a secondary acceptance measure in Gibbs Sampler
  - Introducing two groups including detected and missed based on camera encounters in the augmented population
  - Improving the Bayesian model using spatial camera coordinates in conjunction with detected and missed groups
- Addressing and solving a real application of KSC hog population analysis as follow:
  - Designing and optimizing a camera grid for two different study sites based on available resources
  - Randomizing pole locations near hog habitats and installing camera poles for sampling using motion activated photography for a period of about two weeks. Repeat this task several times to collect multiple samples
  - Preprocessing of collected image sequences to clean up and remove non hog images
  - Processing and counting the number of hogs at each camera location in each occasion in each study site to generate camera encounter histories of unmarked individuals
  - Use the proposed spatial model to estimate hog population in KSC

We should point out that activity center of each member of hypothetical population has two unknown coordinates (x, y). As a result, the search space is highly dimensional and grows with a factor of $2M$ where M is data augmentation parameter. In the original spatial capture model, they sample the spatial activity center locations from M uninformative bivariate priors. The proposed model has extended the original spatial capture model by introducing n informative bivariate priors for sampling spatial activity center locations. To this end, we could improve the original model. However, we still need $M-n$ uninformative priors to sample spatial locations of undetected members of hypothetical population. For further improving this model, it is crucial to perform digital marking of virtually captured individuals through camera encounters. This demands for advanced identification techniques to recognize each virtually captured individual and assign a unique ID to them. A potential future extension of the proposed model is using deep learning methods to develop advanced feature identification algorithms for the species of interest.

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Appendix

A.1 Estimated Parameters for $M = 100$

Table A.1: Summary of 50 Runs to Estimate σ, λ_0, ψ, and Population size N with no Constraint on ψ and $M = 100$

Sim #	$\hat{\sigma}$	$\hat{\lambda_0}$	$\hat{\psi}$	$\hat{N}$
1	0.622	0.262	0.466	46.594
2	0.452	0.348	0.389	38.620
3	0.826	0.179	0.359	35.607
4	0.414	0.515	0.398	39.617
5	0.401	0.552	0.475	47.420
6	0.888	0.378	0.158	15.129
7	0.540	0.470	0.367	36.459
8	0.365	0.509	0.434	43.232
9	0.301	0.508	0.613	61.516
10	0.568	0.330	0.379	37.617
11	0.531	0.544	0.355	35.184
12	0.663	0.588	0.148	14.074
13	0.485	0.463	0.385	38.323
14	0.586	0.342	0.324	32.097
15	0.570	0.497	0.296	29.161
16	0.574	0.369	0.293	28.835
17	0.590	0.360	0.377	37.492
18	0.500	0.505	0.389	38.681
19	0.471	0.723	0.277	27.289
20	0.460	0.568	0.237	23.206
21	0.635	0.410	0.373	37.039
22	0.592	0.833	0.181	17.509
23	0.588	0.443	0.257	25.269
24	0.564	0.505	0.258	25.343
25	0.538	0.499	0.215	20.912
26	0.747	0.191	0.350	34.684
27	0.455	0.690	0.318	31.442
28	0.415	0.385	0.397	39.457
29	0.574	0.418	0.256	25.126
30	0.370	0.522	0.441	44.033
31	0.484	0.531	0.280	27.587
32	0.497	0.660	0.178	17.123
33	0.446	0.552	0.323	31.891
34	0.465	0.884	0.260	25.522
35	0.657	0.414	0.274	26.965
36	0.484	0.517	0.268	26.291
37	2.026	0.283	0.084	7.616
38	0.440	0.631	0.312	30.783
39	0.440	0.805	0.235	22.957
40	0.364	0.616	0.531	53.207
41	0.727	0.362	0.170	16.335
42	0.476	0.612	0.247	24.173
43	0.507	0.739	0.189	18.290
44	0.580	0.483	0.404	40.149
45	0.320	0.661	0.487	48.687
46	0.699	0.321	0.238	23.265
47	0.437	0.522	0.481	48.052
48	0.507	0.513	0.390	38.741
49	0.594	0.474	0.240	23.422
50	0.561	0.360	0.394	39.106
Mean	0.560	0.497	0.323	31.943
Min	0.301	0.179	0.084	7.616
Max	2.026	0.884	0.613	61.516

Table A.2: Summary of 50 Runs to Estimate σ, λ_0, ψ, and Population size N with $\psi \in [0, 0.50]$ and $M = 100$

Sim #	$\hat{\sigma}$	$\hat{\lambda_0}$	$\hat{\psi}$	$\hat{N}$
1	0.824	0.344	0.166	15.961
2	0.535	0.559	0.239	23.497
3	0.548	0.390	0.296	29.486
4	0.450	0.807	0.346	34.753
5	0.534	0.744	0.241	23.674
6	0.545	0.420	0.347	35.129
7	0.475	0.518	0.350	35.331
8	1.720	0.242	0.072	6.311
9	0.460	0.591	0.274	27.271
10	0.492	0.853	0.192	18.626
11	0.570	0.379	0.357	36.326
12	0.648	0.413	0.249	24.611
13	0.560	0.386	0.171	16.466
14	0.538	0.734	0.261	25.798
15	0.480	0.704	0.258	25.463
16	0.396	0.959	0.144	13.702
17	0.611	0.363	0.291	28.947
18	0.408	0.599	0.328	32.953
19	0.529	0.481	0.314	31.333
20	0.606	0.447	0.242	23.745
21	0.524	0.566	0.218	21.302
22	0.481	0.827	0.229	22.409
23	0.515	0.704	0.271	26.768
24	0.391	0.791	0.366	37.145
25	0.533	0.593	0.202	19.587
26	0.569	0.374	0.277	27.441
27	0.507	0.646	0.217	21.185
28	0.513	0.454	0.309	30.886
29	0.595	0.336	0.298	29.765
30	0.409	0.535	0.293	29.288
31	1.284	0.154	0.308	31.077
32	0.543	0.342	0.369	37.623
33	0.585	0.355	0.318	31.815
34	0.503	0.663	0.297	29.531
35	0.534	0.538	0.298	29.670
36	0.445	0.780	0.245	24.040
37	0.474	0.580	0.358	36.223
38	0.520	0.397	0.368	37.492
39	0.694	0.276	0.293	29.247
40	0.490	0.605	0.300	29.912
41	0.407	0.907	0.254	24.976
42	0.436	0.764	0.244	23.978
43	0.447	0.628	0.360	36.558
44	0.688	0.208	0.322	32.551
45	0.515	0.633	0.232	22.691
46	0.472	0.629	0.335	33.604
47	0.543	0.644	0.184	17.826
48	0.487	0.420	0.259	25.594
49	0.584	0.498	0.216	21.052
50	0.541	0.538	0.283	28.013
Mean	0.563	0.546	0.273	27.173
Min	0.391	0.154	0.072	6.311
Max	1.720	0.959	0.369	37.623

Table A.3: Summary of 50 Runs to Estimate σ, λ_0, ψ, and Population size N with $\psi \in [0.10, 0.40]$ and $M = 100$

Sim #	$\hat{\sigma}$	$\hat{\lambda_0}$	$\hat{\psi}$	$\hat{N}$
1	0.464	0.639	0.288	29.159
2	0.627	0.284	0.250	24.919
3	0.432	0.715	0.240	23.655
4	0.405	0.799	0.268	26.832
5	0.480	0.601	0.276	27.923
6	0.581	0.476	0.207	19.963
7	0.456	0.685	0.294	29.888
8	0.462	0.579	0.261	26.117
9	0.530	0.321	0.222	21.702
10	0.453	0.628	0.325	34.317
11	0.752	0.250	0.257	25.729
12	0.600	0.394	0.303	31.279
13	0.515	0.453	0.270	27.167
14	0.795	0.319	0.241	23.889
15	0.408	0.770	0.232	22.732
16	0.487	0.543	0.314	32.604
17	0.605	0.452	0.243	23.994
18	0.516	0.464	0.262	26.383
19	0.448	0.694	0.276	27.906
20	0.485	0.587	0.195	18.636
21	0.460	0.611	0.315	32.836
22	0.586	0.452	0.232	22.798
23	0.470	0.502	0.342	36.800
24	0.657	0.626	0.173	16.097
25	0.404	0.458	0.276	27.947
26	0.496	0.622	0.269	26.937
27	0.564	0.707	0.259	26.021
28	0.510	0.660	0.283	28.736
29	0.528	0.376	0.324	34.275
30	0.418	0.755	0.276	27.847
31	0.487	0.467	0.218	21.297
32	0.517	0.527	0.244	24.071
33	0.547	0.436	0.265	26.627
34	0.483	0.678	0.283	28.644
35	0.485	0.908	0.232	22.743
36	0.631	0.311	0.294	30.205
37	0.386	0.503	0.324	34.228
38	0.470	0.551	0.270	27.206
39	0.547	0.963	0.182	17.133
40	0.534	0.447	0.286	29.206
41	0.509	0.424	0.227	22.291
42	0.538	0.445	0.323	34.094
43	0.464	0.693	0.252	25.009
44	0.536	0.503	0.305	31.366
45	0.444	0.598	0.264	26.443
46	0.580	0.460	0.222	21.593
47	0.507	0.507	0.278	28.088
48	0.441	0.855	0.196	18.725
49	0.545	0.564	0.195	18.541
50	0.564	0.579	0.207	19.956
Mean	0.516	0.557	0.261	26.251
Min	0.386	0.250	0.173	16.097
Max	0.795	0.963	0.342	36.8

A.2 Estimated Parameters for $M = 200$

Table A.4: Summary of 50 Runs to Estimate σ, λ_0, ψ, and Population size N with no Constraint on ψ and $M = 200$

Sim #	$\hat{\sigma}$	$\hat{\lambda_0}$	$\hat{\psi}$	$\hat{N}$
1	0.672	0.316	0.164	32.062
2	0.500	0.448	0.173	33.923
3	1.493	0.278	0.036	6.269
4	1.189	0.280	0.063	11.800
5	0.544	0.454	0.183	35.968
6	0.502	0.516	0.149	29.156
7	0.464	0.537	0.161	31.532
8	0.437	0.651	0.148	28.962
9	0.534	0.504	0.137	26.670
10	0.732	0.592	0.038	6.628
11	0.491	0.602	0.107	20.689
12	0.646	0.828	0.038	6.769
13	0.505	0.499	0.157	30.677
14	0.568	0.791	0.068	12.648
15	0.462	0.420	0.228	45.056
16	0.719	0.318	0.162	31.795
17	0.629	0.565	0.066	12.354
18	0.649	0.305	0.108	20.768
19	0.491	0.623	0.094	17.976
20	0.457	0.541	0.224	44.185
21	0.641	0.318	0.127	24.546
22	0.364	1.146	0.139	27.044
23	0.501	0.371	0.117	22.761
24	0.488	0.766	0.099	18.978
25	0.593	0.503	0.109	21.125
26	0.302	0.886	0.248	49.104
27	0.520	0.355	0.169	33.149
28	0.370	0.592	0.282	56.048
29	0.549	0.351	0.113	21.875
30	0.299	0.718	0.335	66.648
31	0.434	0.471	0.286	56.766
32	0.48	0.678	0.172	33.674
33	0.499	0.557	0.148	28.945
34	0.524	0.598	0.126	24.424
35	0.647	0.326	0.166	32.501
36	0.523	0.381	0.135	26.326
37	0.684	0.319	0.144	28.025
38	0.502	0.592	0.154	30.152
39	0.751	0.372	0.151	29.509
40	0.455	0.536	0.169	33.082
41	0.519	0.430	0.167	32.765
42	0.326	0.579	0.533	106.598
43	0.438	0.568	0.181	35.537
44	0.725	0.514	0.092	17.486
45	0.293	0.541	0.514	102.871
46	0.405	0.752	0.178	34.880
47	0.479	0.436	0.240	47.434
48	0.459	0.506	0.196	38.490
49	0.378	0.652	0.261	51.749
50	0.454	0.462	0.241	47.666
Mean	0.546	0.527	0.169	33.321
Min	0.293	0.278	0.036	6.269
Max	1.493	1.146	0.533	106.598

Table A.5: Summary of 50 Runs to Estimate σ, λ_0, ψ, and Population size N with $\psi \in [0, 0.50]$ and $M = 200$

Sim #	$\hat{\sigma}$	$\hat{\lambda_0}$	$\hat{\psi}$	$\hat{N}$
1	0.514	0.333	0.217	43.012
2	0.546	0.573	0.121	23.433
3	0.518	0.606	0.115	22.297
4	0.719	0.305	0.169	33.096
5	0.576	0.351	0.186	36.655
6	0.639	0.226	0.248	49.402
7	0.778	0.388	0.086	16.325
8	0.525	0.725	0.112	21.625
9	0.650	0.500	0.104	19.885
10	0.562	0.400	0.161	31.491
11	0.378	0.862	0.231	45.702
12	0.451	0.583	0.221	43.621
13	0.594	0.294	0.211	41.679
14	0.531	0.540	0.129	25.083
15	0.645	0.383	0.146	28.388
16	0.465	0.759	0.180	35.338
17	0.479	0.932	0.095	18.235
18	0.541	0.612	0.119	23.003
19	0.469	0.793	0.147	28.767
20	0.344	0.533	0.245	48.774
21	0.438	0.650	0.212	41.805
22	0.397	0.748	0.134	26.085
23	0.555	0.278	0.240	47.601
24	0.589	0.343	0.081	15.414
25	0.411	0.674	0.183	35.971
26	0.360	0.821	0.189	37.320
27	0.571	0.714	0.097	18.529
28	0.758	0.337	0.061	11.234
29	1.099	0.232	0.084	15.867
30	0.414	0.734	0.154	30.112
31	0.455	0.343	0.166	32.660
32	0.475	0.642	0.157	30.691
33	0.482	0.459	0.187	36.815
34	0.474	0.790	0.089	16.915
35	0.378	0.503	0.203	40.058
36	0.446	0.835	0.141	27.430
37	0.453	0.716	0.185	36.404
38	0.442	0.837	0.137	26.706
39	0.476	0.532	0.161	31.562
40	0.521	0.671	0.113	21.900
41	0.662	0.329	0.163	32.010
42	0.727	0.521	0.086	16.359
43	0.466	0.882	0.108	20.778
44	0.613	0.311	0.211	41.873
45	0.491	1.227	0.063	11.678
46	0.634	0.430	0.103	19.856
47	0.401	0.340	0.276	55.258
48	0.321	0.665	0.304	60.856
49	0.454	0.520	0.180	35.424
50	0.473	0.427	0.204	40.311
Mean	0.527	0.564	0.158	31.026
Min	0.321	0.226	0.061	11.234
Max	1.099	1.227	0.304	60.856

Table A.6: Summary of 50 Runs to Estimate σ, λ_0, ψ, and Population size N with $\psi \in [0.10, 0.40]$ and $M = 200$

Sim #	$\hat{\sigma}$	$\hat{\lambda_0}$	$\hat{\psi}$	$\hat{N}$
1	0.436	0.776	0.150	28.156
2	0.489	0.606	0.158	30.306
3	0.510	0.417	0.191	37.205
4	0.443	0.406	0.198	38.657
5	0.534	0.451	0.193	37.701
6	0.634	0.235	0.236	46.980
7	0.513	0.324	0.161	30.231
8	0.430	0.664	0.153	28.780
9	0.383	0.910	0.172	32.771
10	0.472	0.580	0.148	27.730
11	0.531	0.372	0.219	43.179
12	0.397	1.236	0.132	23.441
13	0.621	0.255	0.179	34.571
14	0.506	0.569	0.153	28.246
15	0.555	0.521	0.136	24.357
16	0.469	0.563	0.172	33.154
17	0.472	0.674	0.178	34.739
18	0.467	0.662	0.161	30.829
19	0.404	0.613	0.161	30.639
20	0.486	0.537	0.179	34.644
21	0.580	0.485	0.152	28.206
22	0.461	0.859	0.135	24.396
23	0.435	0.483	0.180	34.882
24	0.433	0.610	0.161	30.776
25	0.501	0.372	0.169	32.172
26	0.424	0.787	0.142	25.856
27	0.598	0.322	0.163	30.770
28	0.628	0.300	0.156	29.274
29	0.526	0.460	0.153	28.747
30	0.430	0.412	0.216	42.586
31	0.534	0.546	0.121	18.854
32	0.440	0.424	0.171	32.762
33	0.411	0.507	0.173	32.969
34	0.367	0.865	0.156	29.423
35	0.481	0.459	0.182	35.327
36	0.602	0.394	0.146	26.611
37	0.390	0.808	0.150	28.045
38	0.543	0.300	0.196	38.125
39	0.536	0.624	0.146	26.929
40	0.481	0.405	0.144	26.072
41	0.530	0.410	0.144	26.291
42	0.640	0.479	0.140	25.418
43	0.438	0.703	0.123	20.214
44	0.754	0.215	0.169	32.189
45	0.505	0.500	0.187	36.304
46	0.432	0.743	0.135	24.373
47	0.515	0.410	0.158	29.801
48	0.596	0.232	0.203	39.826
49	0.430	0.504	0.222	43.891
50	0.394	1.271	0.124	21.015
Mean	0.496	0.545	0.165	31.168
Min	0.367	0.215	0.121	18.854
Max	0.754	1.271	0.236	46.98

A.3 Estimated Parameters for KSC-HC

Table A.7: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Happy Creek Using Batch 1

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	481.377	465.845	159.531	207.233	692.991
2	467.96	456.646	159.008	214.95	720.624
3	498.778	483.435	157.023	255.599	741.304
4	490.336	475.791	156.654	240.117	725.721
5	479.962	468.672	157.073	234.225	717.903
6	482.39	466.913	153.779	250.216	724.68
7	524.96	509.671	156.419	279.222	764.028
8	484.991	469.937	155.823	213.564	694.574
9	446.185	448.2	190.215	95.152	672.55
10	450.115	445.947	174.526	190.034	750.515
11	467.558	453.714	157.283	210.048	698.404
12	455.003	440.277	160.253	198.431	696.771
13	481.562	470.232	164.496	217.231	724.678
14	490.843	478.042	166.349	226.391	743.59
15	500.999	484.392	155.905	249.982	726.928
16	507.397	494.554	159.381	254.536	749.111
17	469.728	451.703	150.841	236.416	688.643
18	503.245	489.103	157.081	248.712	735.412
19	504.055	492.257	159.968	242.381	737.933
20	473.845	459.096	159.708	219.92	704.183
21	491.886	474.744	154.783	239.027	717.685
22	472.736	458.061	157.792	217.529	707.259
23	471.691	462.04	167.737	152.374	683.513
24	477.03	463.277	161.492	218.696	717.367
25	489.284	475.522	160.105	231.246	731.859
26	507.946	490.374	151.95	272.161	735.006
27	477.214	467.415	162.131	198.889	705.071
28	474.014	459.358	163.072	220.441	724.982
29	474.425	463.129	165.715	228.807	750.828
30	483.955	465.385	157.582	241.333	721.254
31	502.883	489.065	155.886	264.57	749.054
32	475.005	463.922	167.246	188.516	703.802
33	489.64	476.399	159.728	243.749	735.11
34	491.927	478.18	159.407	251.471	751.013
35	517.549	505.576	159.846	260.609	755.011
36	435.611	423.865	172.883	159.946	660.772
37	462.969	452.573	167.476	191.245	718.042
38	472.159	456.812	158.472	222.765	718.203
39	463.927	450.822	170.49	177.047	705.809
40	514.986	502.109	153.333	266.631	739.998
41	503.612	487.897	153.26	264.547	734.248
42	513.564	498.598	156.339	271.211	752.939
43	462.449	448.298	159.836	188.581	687.342
44	471.989	457.727	159.685	211.599	705.711
45	466.991	447.782	147.284	237.881	683.277
46	478.805	463.031	151.792	244.046	717.883
47	490.956	475.914	155.02	244.761	719.646
48	496.766	481.156	157.549	239.345	723.243
49	511.822	498.719	158.003	248.218	741.101
50	532.057	514.88	156.191	284.826	760.843
Mean	484.743	471.141	159.868	227.329	721.368
Min	435.611	423.865	147.284	95.152	660.772
Max	532.057	514.88	190.215	284.826	764.028

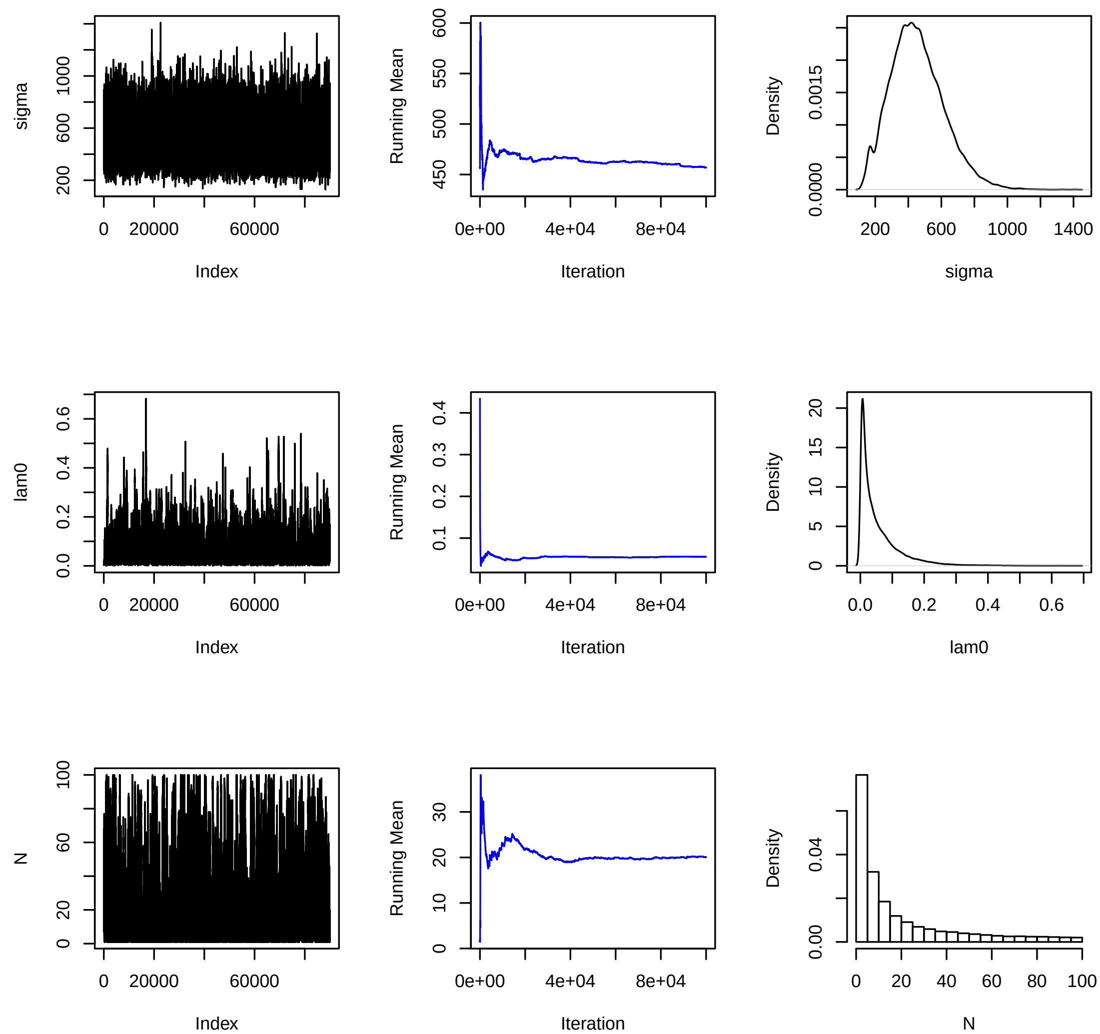


Figure A.1: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 1

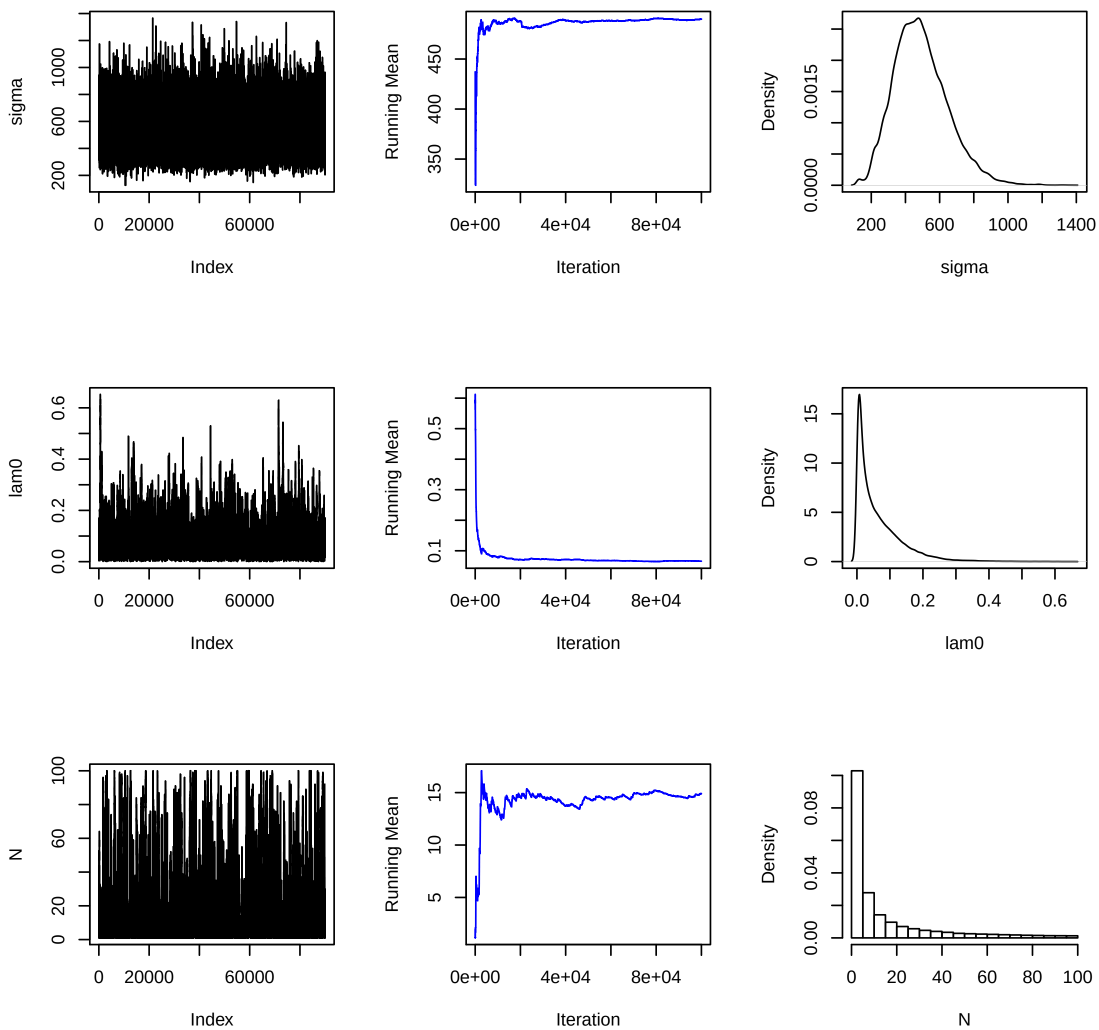


Figure A.2: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 1

Table A.8: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Happy Creek Using Batch 2

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	520.352	502.889	157.937	268.12	756.787
2	511.906	490.748	177.174	237.843	769.903
3	510.359	490.78	155.002	278.39	749.712
4	562.599	551.209	168.538	305.363	835.105
5	509.226	492.641	168.223	248.396	762.050
6	519.158	499.609	160.163	268.254	759.461
7	479.972	464.959	176.550	188.498	734.813
8	549.412	533.802	163.228	285.804	785.790
9	504.527	486.085	160.955	247.363	747.182
10	539.511	521.718	162.505	289.736	787.172
11	523.339	507.786	169.133	249.317	771.144
12	530.800	516.821	167.536	259.411	778.145
13	540.128	520.628	167.063	286.272	798.010
14	508.145	488.230	167.631	244.545	756.650
15	515.001	493.401	165.437	261.249	764.897
16	544.524	530.078	167.078	278.635	795.529
17	544.364	524.535	157.469	298.353	777.371
18	518.887	499.193	171.830	249.715	775.054
19	510.172	493.911	162.483	256.531	753.383
20	488.314	467.358	166.344	225.068	720.203
21	567.899	548.075	164.358	308.534	805.505
22	527.116	510.360	155.008	283.639	755.553
23	548.390	534.513	158.251	284.645	777.634
24	564.702	548.150	166.242	304.351	814.566
25	529.470	515.389	162.884	267.151	767.479
26	477.951	458.709	168.563	213.421	719.919
27	542.559	531.077	175.095	236.206	781.660
28	486.045	468.988	167.739	230.599	740.597
29	536.139	518.047	167.231	274.871	788.225
30	480.939	461.824	173.21	225.843	748.156
31	531.377	519.330	169.366	246.926	777.906
32	540.454	519.217	173.222	265.862	795.023
33	551.904	540.614	173.494	264.033	804.868
34	538.638	518.867	168.945	269.562	782.516
35	526.480	509.322	162.031	272.759	770.070
36	456.234	434.846	180.517	165.762	691.685
37	492.409	474.014	169.939	219.811	736.817
38	527.531	513.401	166.419	257.224	770.883
39	492.444	473.687	165.533	209.685	714.364
40	494.035	476.535	173.631	216.881	743.588
41	519.381	510.319	168.761	216.174	756.560
42	540.807	526.903	160.542	292.826	792.552
43	528.574	513.024	163.778	262.285	764.079
44	535.316	518.414	177.579	248.065	796.303
45	511.123	494.150	158.408	267.901	760.044
46	521.885	501.827	173.110	255.74	791.755
47	540.578	522.153	164.988	287.777	798.109
48	524.253	506.286	159.175	266.553	753.973
49	492.167	468.338	167.280	225.481	735.855
50	526.299	508.864	162.117	273.564	767.879
Mean	521.676	504.433	166.594	256.819	767.649
Min	456.234	434.846	155.002	165.762	691.685
Max	567.899	551.209	180.517	308.534	835.105

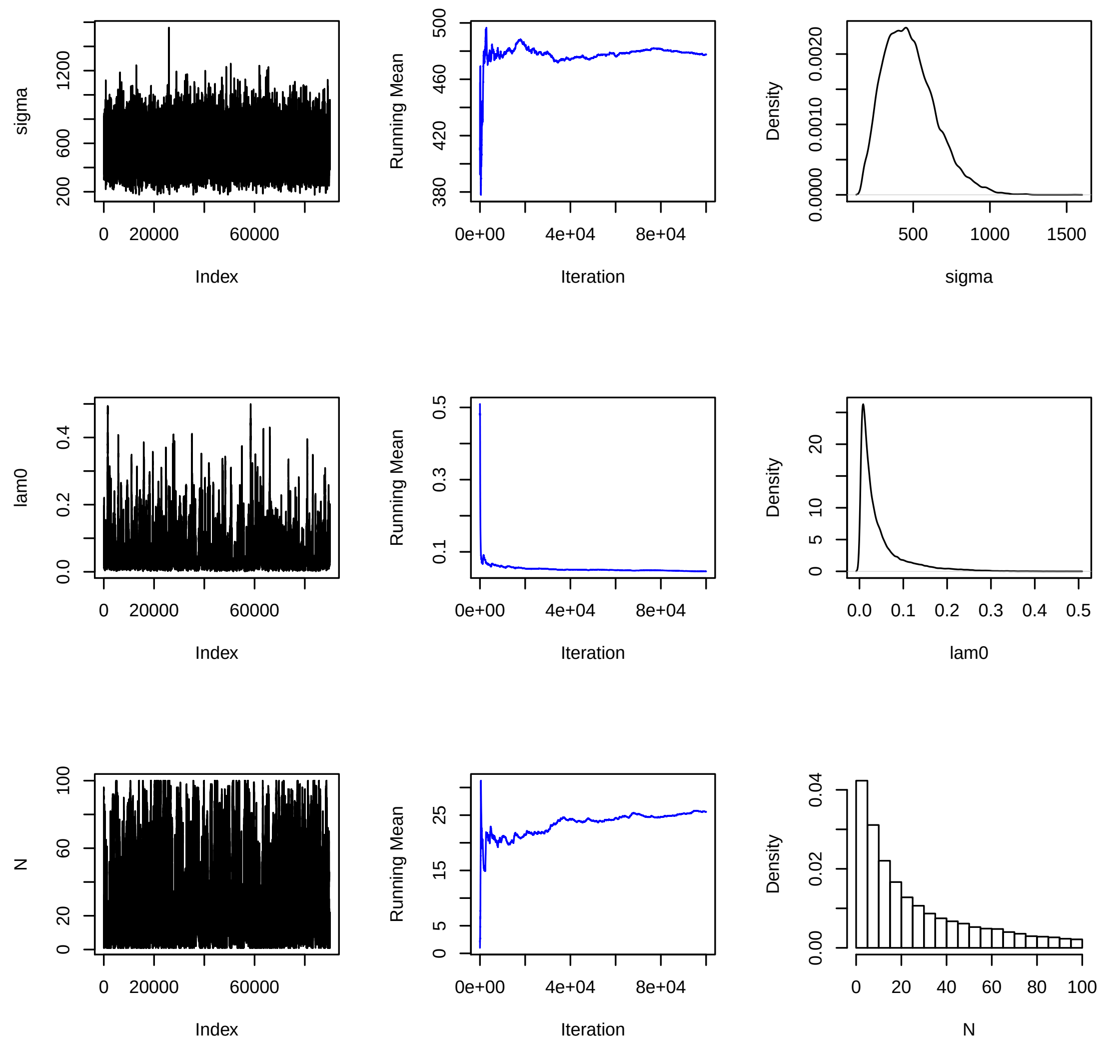


Figure A.3: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 2

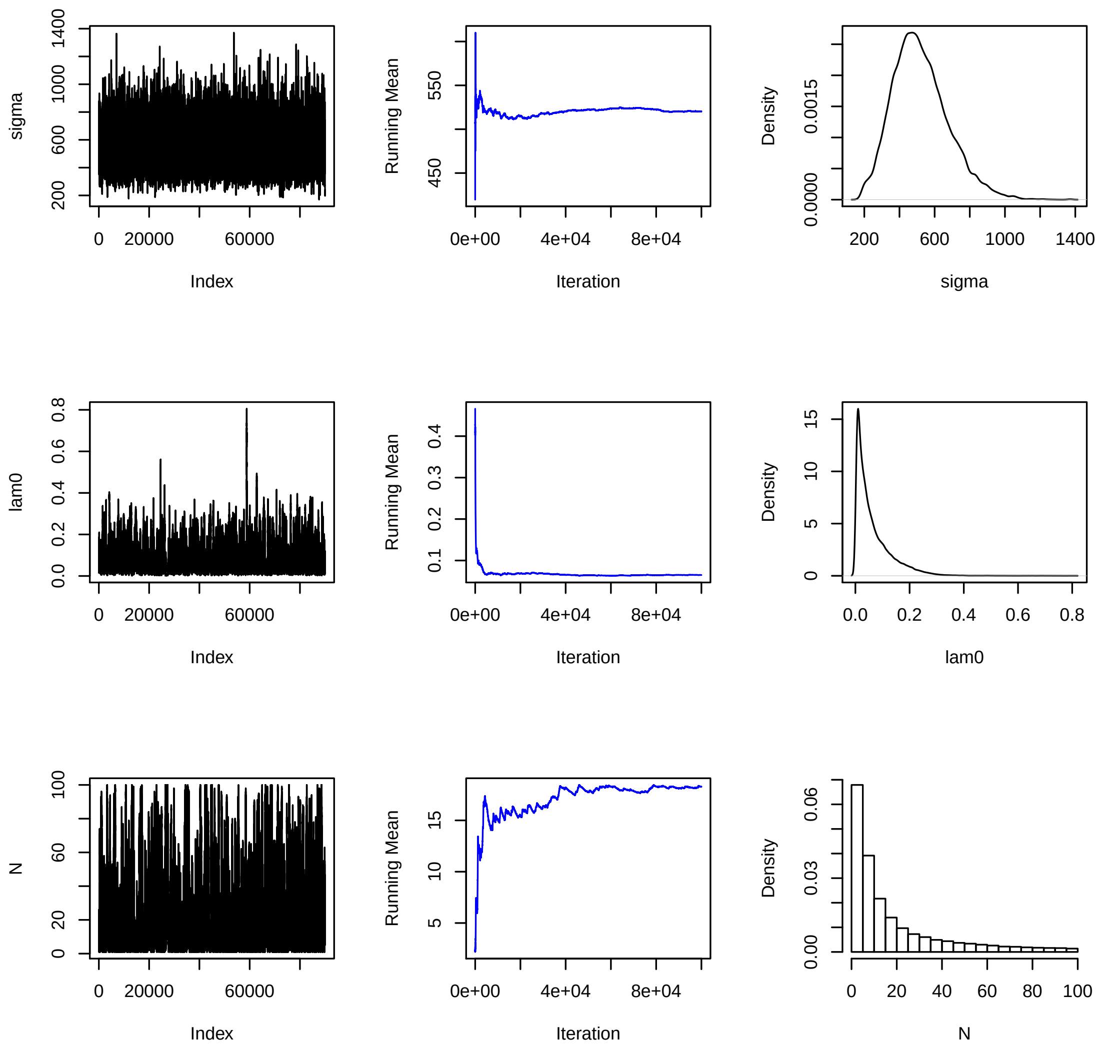


Figure A.4: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 2

Table A.9: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Happy Creek Using Batch 3

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	488.626	468.090	156.003	263.467	761.218
2	356.476	324.783	146.018	156.385	544.775
3	471.020	443.263	168.380	214.287	725.176
4	354.908	312.179	155.325	157.334	550.017
5	409.777	383.258	156.639	171.911	614.117
6	342.790	290.969	154.006	159.726	550.689
7	441.901	413.004	153.514	202.109	649.521
8	499.805	504.400	189.304	149.522	734.849
9	474.783	466.330	165.055	153.149	675.686
10	387.431	363.929	168.837	136.214	602.529
11	440.711	432.385	138.976	204.432	604.974
12	369.557	312.943	185.248	154.485	630.956
13	392.844	370.164	153.109	170.262	587.482
14	406.711	364.558	151.450	202.425	600.779
15	411.015	395.082	168.513	153.645	627.961
16	524.418	505.717	142.046	305.370	748.644
17	407.102	390.186	154.159	165.318	609.504
18	509.965	482.606	134.961	327.800	745.136
19	397.183	366.512	153.044	176.604	602.583
20	436.777	418.084	170.211	167.139	671.662
21	363.432	319.880	138.476	193.857	565.133
22	530.928	529.206	199.850	193.087	809.351
23	480.071	454.710	162.717	211.601	717.489
24	288.894	256.000	116.739	151.471	416.013
25	397.122	366.764	176.550	166.091	638.735
26	518.459	505.171	166.567	202.518	750.405
27	385.411	356.755	169.450	138.415	593.017
28	474.998	455.406	155.635	222.878	678.028
29	609.823	597.120	179.882	328.288	902.328
30	454.849	434.179	157.917	223.276	671.042
31	438.617	453.042	175.102	161.149	636.044
32	417.122	372.697	168.694	193.714	656.589
33	432.632	400.920	186.663	175.779	684.368
34	346.686	310.152	125.901	184.705	508.925
35	433.261	413.480	149.362	209.613	632.028
36	503.020	480.395	149.039	263.676	732.917
37	496.931	484.931	150.237	281.568	758.575
38	441.847	402.036	168.525	219.427	686.081
39	467.895	446.308	162.446	218.053	701.720
40	481.487	466.443	153.019	235.195	712.134
41	433.984	416.863	169.787	174.111	666.014
42	335.328	293.073	139.776	158.507	517.898
43	412.223	387.431	160.541	185.588	614.836
44	403.782	375.916	174.901	163.141	645.765
45	429.361	397.433	156.371	204.881	643.225
46	366.993	303.972	209.239	136.342	668.194
47	484.643	471.562	154.846	219.114	698.768
48	410.149	390.965	160.575	170.162	628.721
49	421.237	390.487	160.168	194.13	638.108
50	394.504	349.955	164.768	174.121	620.012
Mean	431.589	405.834	160.571	194.921	652.614
Min	288.894	256.000	116.739	136.214	416.013
Max	609.823	597.12	209.239	328.288	902.328

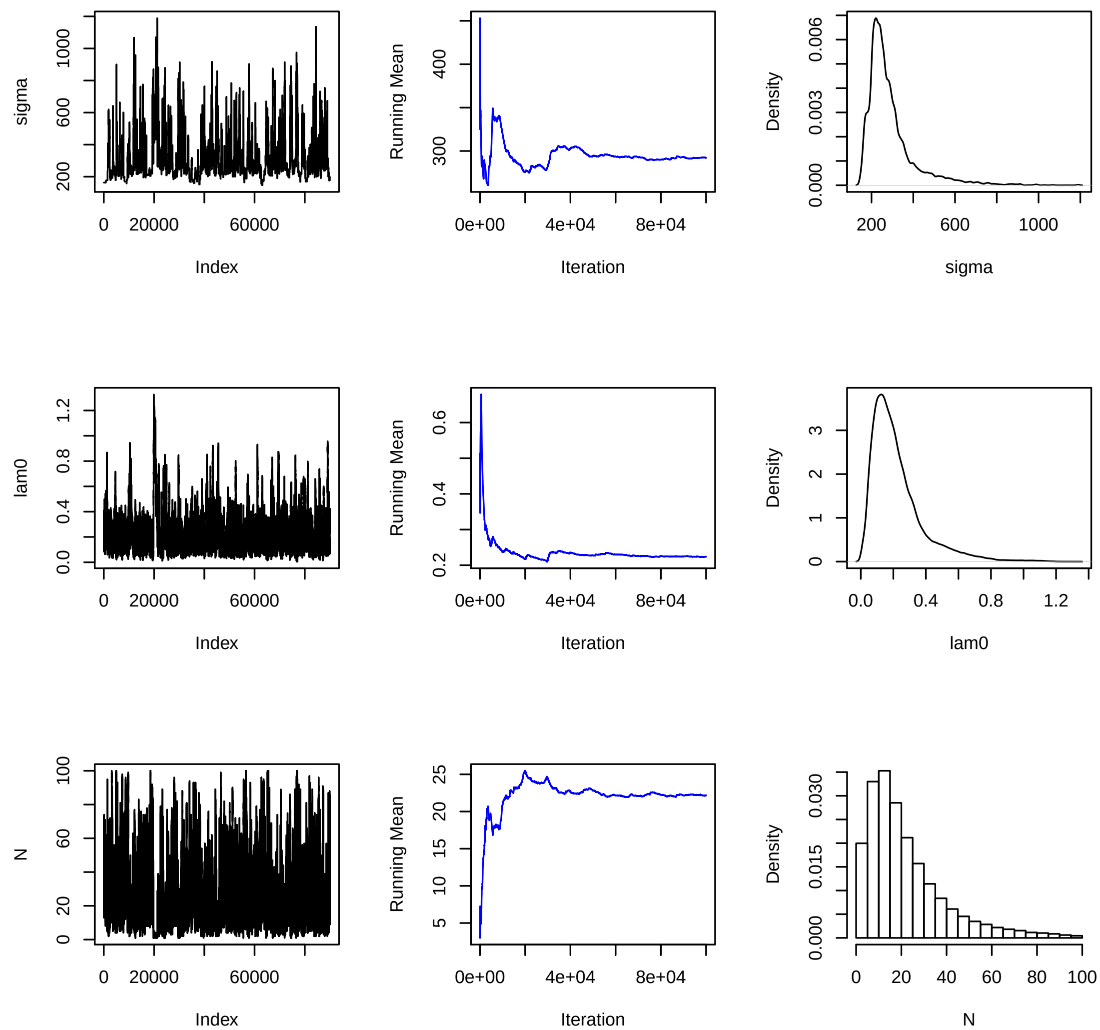


Figure A.5: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 3

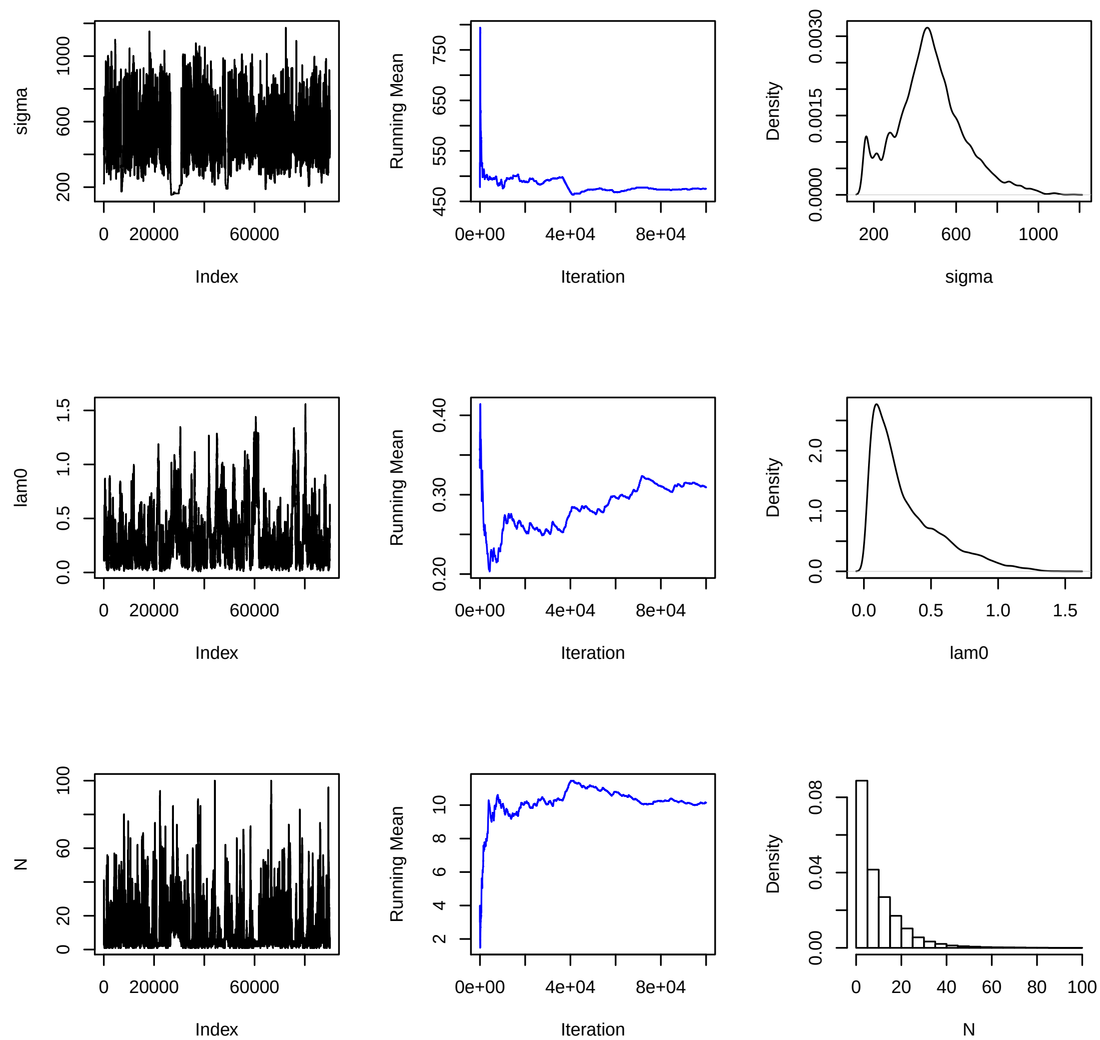


Figure A.6: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 3

Table A.10: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Happy Creek Using Batch 4

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	439.332	409.374	191.278	126.684	693.625
2	360.644	328.890	140.204	152.396	542.669
3	548.876	529.362	163.613	298.609	795.552
4	401.785	374.941	173.413	130.964	630.816
5	460.672	435.096	164.002	214.422	692.028
6	563.224	553.881	164.905	289.887	818.920
7	483.042	457.713	168.823	231.522	745.337
8	498.396	482.327	183.215	199.248	742.104
9	431.696	407.286	161.457	161.774	640.591
10	454.718	435.620	177.119	160.453	681.609
11	482.373	455.288	164.389	224.86	703.222
12	396.306	357.004	161.998	173.451	619.524
13	480.938	457.259	166.175	236.202	740.091
14	515.750	499.100	167.024	250.321	762.304
15	405.614	375.672	158.708	187.434	650.083
16	512.340	503.969	185.061	216.275	765.886
17	392.705	358.716	173.263	140.927	622.913
18	493.011	473.522	147.835	269.609	716.982
19	417.286	385.774	159.899	196.183	654.978
20	440.309	419.586	161.891	171.102	649.219
21	498.318	475.713	161.575	254.73	740.851
22	443.019	412.569	155.382	221.492	671.774
23	347.478	318.639	145.351	153.174	533.533
24	494.094	467.888	165.851	254.23	755.856
25	476.756	454.452	162.539	238.114	726.543
26	506.635	489.521	170.500	256.01	778.952
27	543.779	522.565	156.061	311.247	783.618
28	423.542	392.781	161.782	186.417	640.740
29	503.853	487.563	177.573	222.127	771.147
30	486.530	464.133	180.459	208.456	755.073
31	451.763	422.878	180.128	178.18	691.244
32	486.436	461.425	160.372	230.069	710.277
33	555.875	541.768	156.719	302.485	785.947
34	534.420	521.957	166.282	261.681	779.247
35	480.466	454.988	165.260	226.005	721.179
36	503.971	485.287	187.048	220.600	790.942
37	537.111	526.529	198.072	215.454	807.406
38	458.976	438.546	163.485	206.19	686.550
39	521.051	501.576	160.712	274.288	762.597
40	516.143	502.139	177.697	234.584	792.749
41	459.644	430.282	165.523	202.224	685.835
42	455.014	428.868	171.294	204.788	712.219
43	459.614	427.227	174.942	222.69	729.137
44	462.385	428.960	189.899	187.086	732.312
45	440.979	403.189	172.714	197.173	685.874
46	513.433	497.369	169.245	260.359	769.252
47	512.021	494.351	184.386	218.679	772.031
48	382.037	349.030	170.111	150.929	604.940
49	574.939	557.495	155.467	325.615	801.285
50	479.866	459.196	151.188	255.841	715.082
Mean	473.783	450.385	167.838	218.265	715.253
Min	347.478	318.639	140.204	126.684	533.533
Max	574.939	557.495	198.072	325.615	818.920

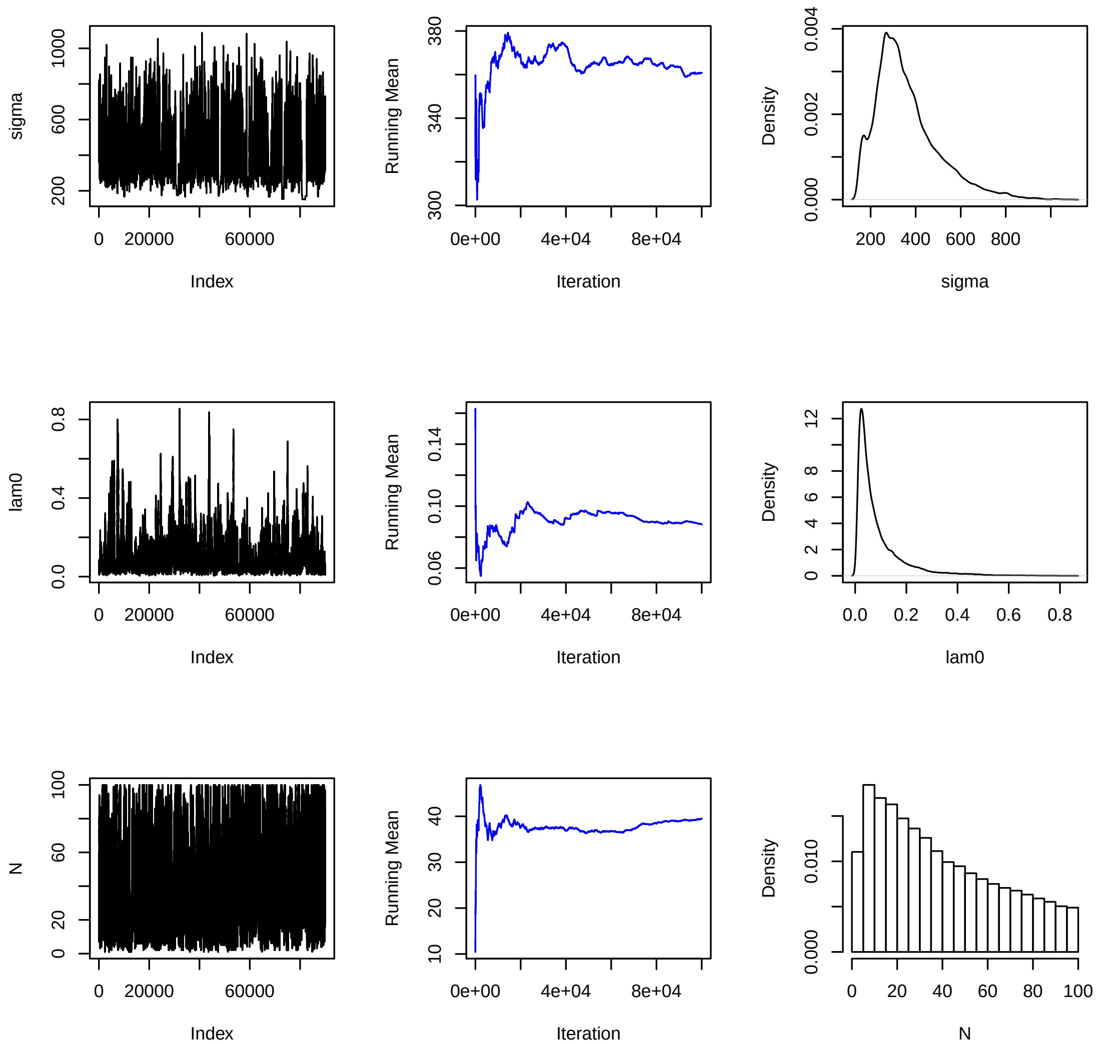


Figure A.7: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 4

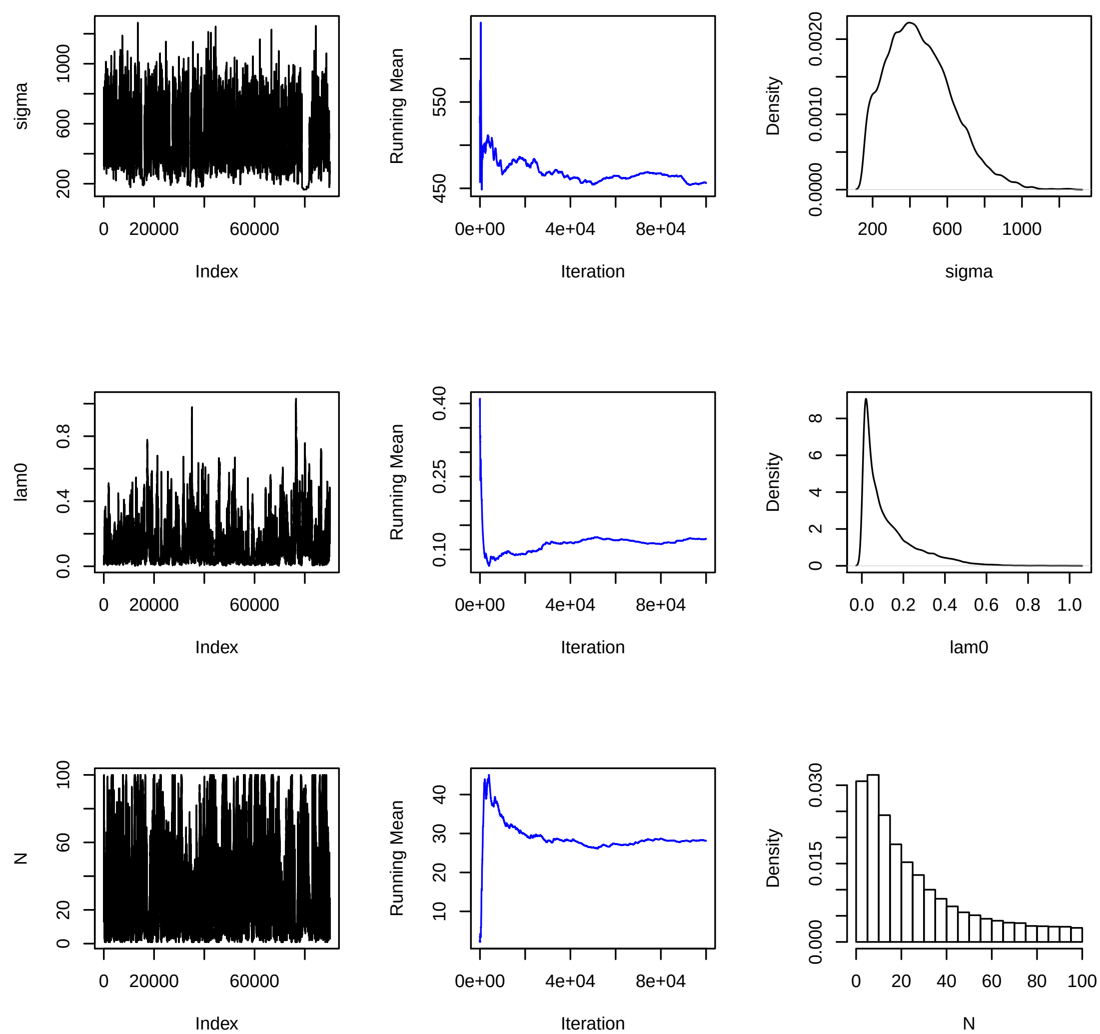


Figure A.8: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 4

Table A.11: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Happy Creek Using Batch 5

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	290.486	269.393	101.238	144.699	396.815
2	321.918	298.484	106.798	194.132	441.923
3	368.628	335.514	139.11	199.44	551.599
4	229.078	209.327	87.985	127.1	334.628
5	331.675	300.156	135.285	160.524	478.103
6	345.335	313.145	123.067	181.086	489.916
7	332.920	307.587	121.952	155.076	477.458
8	376.705	341.300	138.535	177.249	546.918
9	350.159	327.205	125.948	177.231	479.862
10	374.182	306.922	187.535	170.483	640.862
11	476.531	430.218	199.772	177.135	749.371
12	518.343	450.861	215.184	231.014	818.000
13	380.638	317.440	183.375	170.159	634.912
14	303.706	277.185	114.678	163.797	429.926
15	322.343	288.147	125.722	177.343	439.257
16	331.339	296.395	126.435	170.749	488.603
17	402.502	341.341	188.236	169.743	641.422
18	295.962	261.920	139.153	142.275	441.393
19	389.816	351.574	146.675	199.682	564.592
20	420.740	387.062	168.730	184.947	652.465
21	440.165	389.798	188.777	180.97	700.529
22	375.499	350.834	134.532	180.065	544.714
23	368.886	344.045	125.509	174.474	521.497
24	409.442	373.952	158.822	178.952	617.789
25	321.504	296.888	128.559	163.715	472.585
26	287.918	262.069	140.700	121.047	440.123
27	267.429	238.263	111.310	138.257	402.157
28	277.423	266.930	91.980	129.423	386.738
29	334.100	317.225	96.835	187.299	440.200
30	395.432	317.883	205.653	170.725	697.182
31	269.207	259.426	69.046	165.946	352.167
32	344.701	305.281	137.814	172.943	511.892
33	271.550	246.645	95.658	161.332	374.103
34	447.778	400.342	189.656	193.304	708.186
35	322.881	303.720	92.045	195.907	448.256
36	329.354	304.726	115.576	191.123	466.744
37	287.443	275.654	86.066	170.953	374.223
38	365.886	330.654	146.575	157.029	546.863
39	391.940	356.644	143.897	194.455	564.365
40	267.655	250.971	87.229	150.192	369.031
41	407.332	383.530	167.856	147.729	617.378
42	327.534	300.887	118.105	175.117	453.305
43	390.024	345.859	155.739	191.016	579.878
44	318.939	282.233	128.351	162.396	463.131
45	326.437	304.959	103.904	182.383	450.523
46	412.726	367.423	168.869	190.933	638.412
47	367.949	306.361	178.508	176.623	614.350
48	377.459	325.085	183.784	161.761	626.626
49	318.224	299.070	87.402	206.655	426.355
50	327.510	292.858	130.140	163.980	472.026
Mean	350.267	316.228	136.886	172.211	519.587
Min	229.078	209.327	69.046	121.047	334.628
Max	518.343	450.861	215.184	231.014	818.000

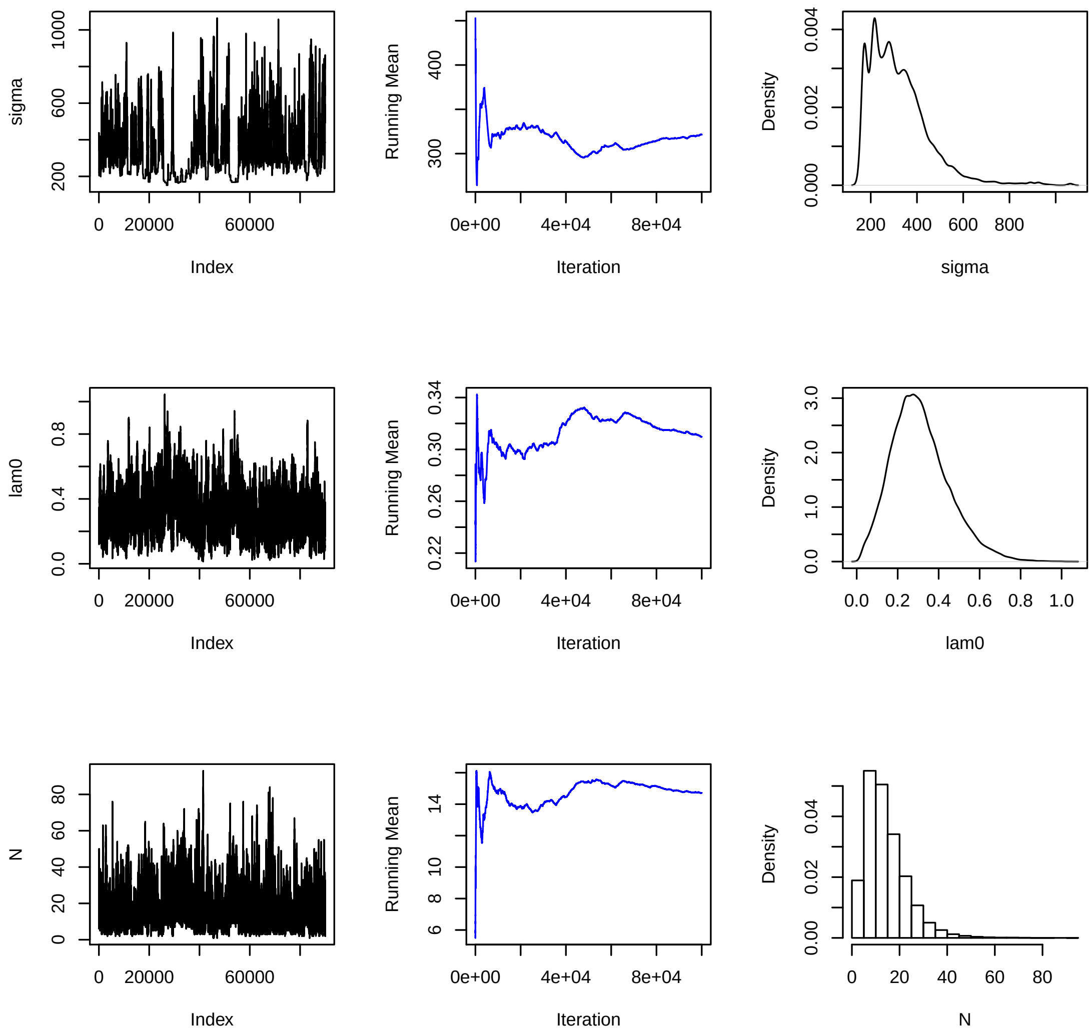


Figure A.9: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 5

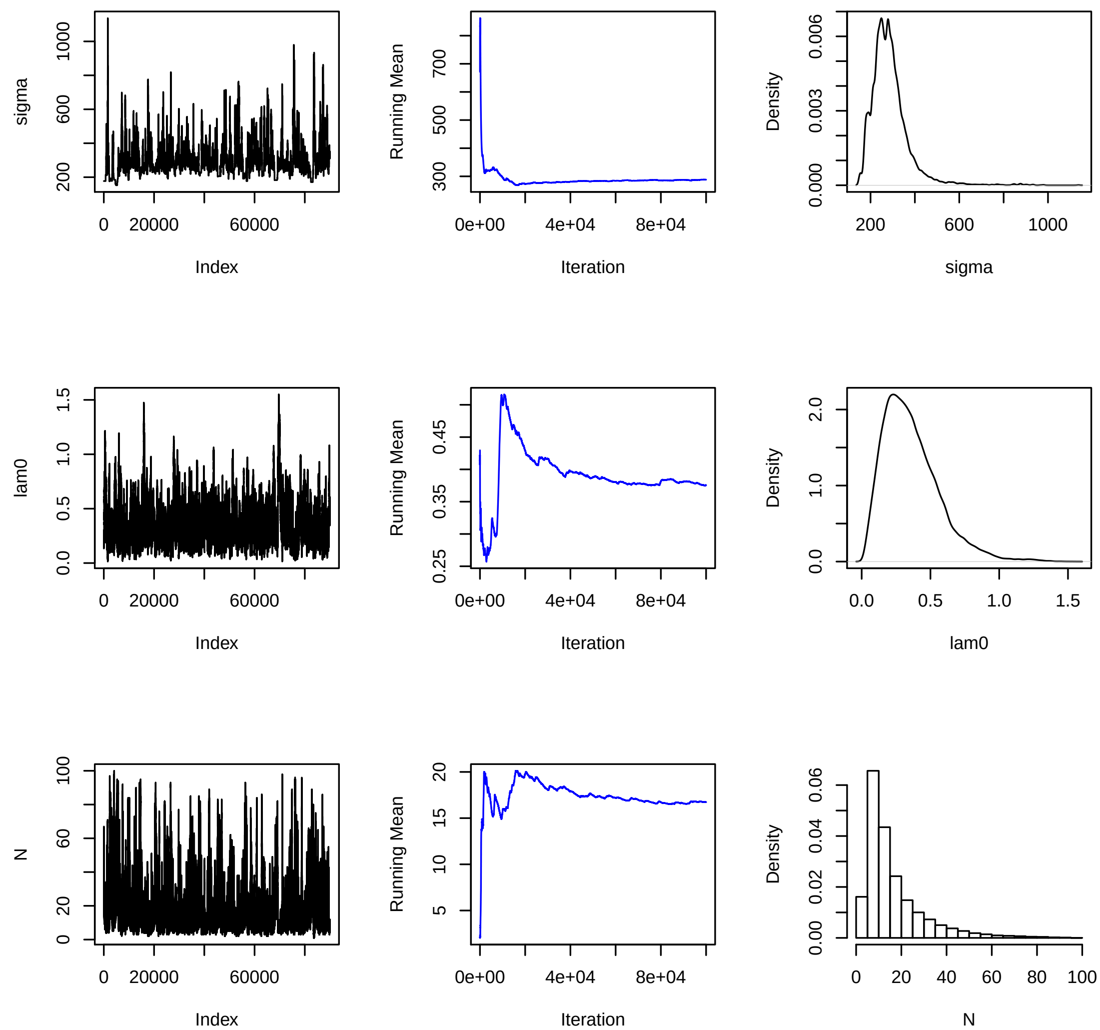


Figure A.10: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Happy Creek Using Batch 5

A.4 Estimated Parameters for Tel-4 in KSC

Table A.12: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Tel-4 Using Batch 1

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	395.635	364.385	157.081	158.786	607.869
2	411.890	389.303	155.833	176.939	639.123
3	432.038	409.551	163.279	185.179	661.107
4	455.023	434.258	156.795	206.552	672.612
5	438.103	420.612	169.103	149.005	652.639
6	401.861	368.313	163.548	184.497	648.461
7	399.702	373.319	162.325	139.126	619.861
8	431.342	417.217	174.651	134.444	651.961
9	436.985	417.808	162.958	175.317	656.926
10	415.773	389.672	161.314	168.6	629.429
11	452.174	434.288	157.789	212.934	682.909
12	441.512	422.628	164.015	165.307	665.262
13	407.115	384.253	155.665	164.161	616.503
14	380.113	348.516	152.098	160.519	596.659
15	374.850	350.542	150.860	149.259	571.817
16	402.317	377.516	149.950	183.248	622.816
17	428.505	405.636	155.964	200.153	665.356
18	408.151	383.665	154.670	172.208	624.856
19	455.753	437.833	162.934	187.19	667.302
20	381.980	355.416	149.456	164.061	599.805
21	383.255	356.821	165.538	131.74	604.830
22	413.400	391.368	163.616	163.105	649.457
23	425.643	407.210	167.259	141.975	638.827
24	418.224	393.201	161.853	153.062	628.023
25	435.718	415.311	165.035	173.021	668.153
26	422.006	400.775	164.755	167.987	645.74
27	405.848	382.096	161.950	153.998	625.076
28	472.730	453.410	157.875	225.622	700.454
29	423.305	402.431	166.024	175.762	672.317
30	438.866	420.213	157.940	169.096	647.758
31	360.692	331.772	157.091	150.161	612.125
32	443.339	430.117	172.449	172.15	690.739
33	415.025	388.146	163.997	165.124	643.718
34	428.277	405.233	157.518	177.267	639.440
35	464.279	447.907	157.225	215.786	688.501
36	373.102	345.051	152.553	163.076	592.510
37	390.540	376.302	186.822	106.728	624.462
38	444.669	428.614	173.440	166.548	681.263
39	442.059	421.113	162.512	193.186	662.014
40	426.483	403.635	158.255	194.118	643.981
41	441.745	435.526	173.257	158.598	693.080
42	412.611	385.496	156.533	173.427	632.469
43	361.160	327.094	142.347	169.112	561.657
44	462.356	445.789	165.811	200.468	704.318
45	434.471	416.328	162.482	175.335	665.467
46	399.435	369.424	159.638	193.397	656.19
47	428.984	409.666	150.915	186.030	634.760
48	380.859	354.824	155.490	131.979	579.141
49	458.391	440.181	153.739	197.713	661.063
50	426.788	406.622	159.909	183.187	647.797
Mean	419.702	397.528	160.682	171.325	642.972
Min	360.692	327.094	142.347	106.728	561.657
Max	472.73	453.410	186.822	225.622	704.318

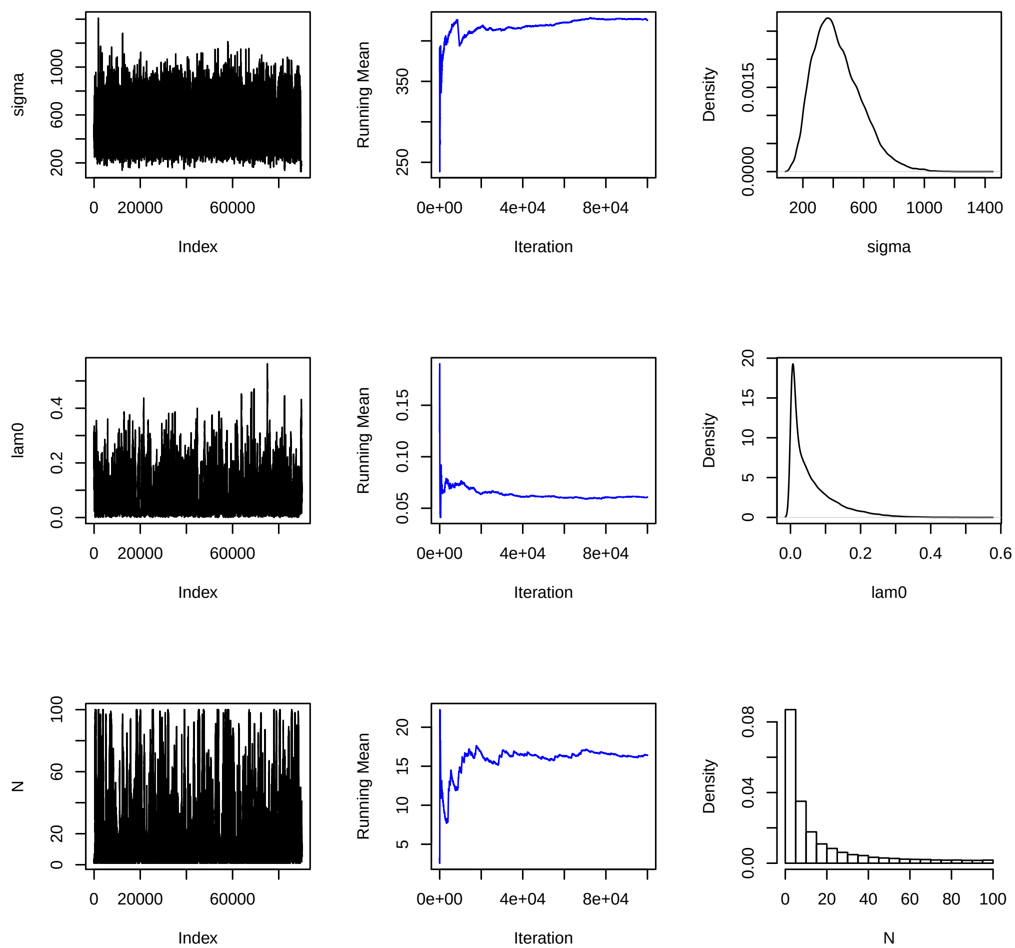


Figure A.11: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 1

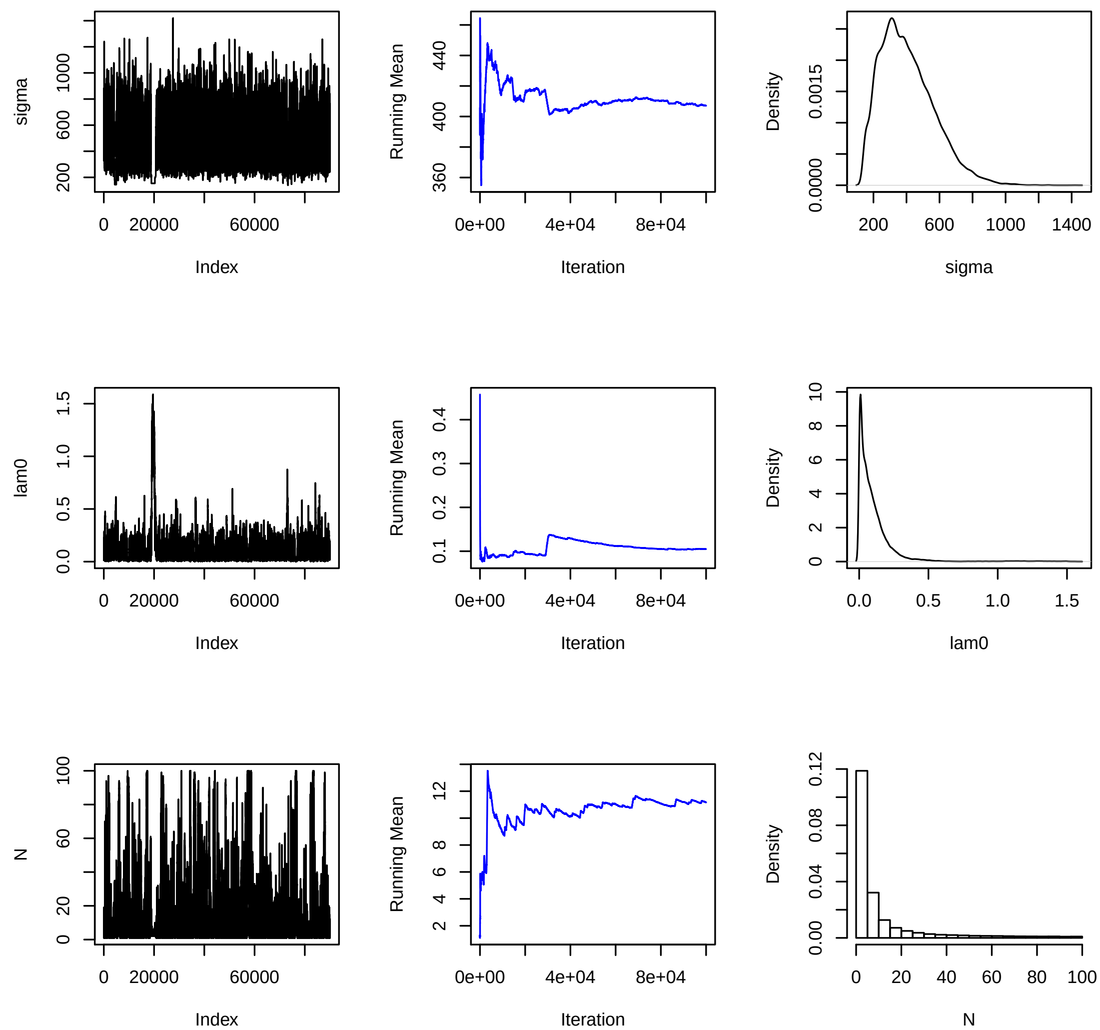


Figure A.12: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 1

Table A.13: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Tel-4 Using Batch 2

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	404.258	382.444	141.217	189.342	598.843
2	399.173	377.599	139.189	178.751	590.333
3	406.848	385.983	146.715	185.026	613.061
4	394.743	373.494	138.577	188.153	589.453
5	395.614	374.953	136.619	182.549	578.599
6	407.790	386.325	136.957	190.581	601.616
7	400.525	375.906	144.944	182.181	599.434
8	386.994	360.841	146.603	174.558	596.153
9	393.926	374.124	140.428	184.037	595.753
10	401.383	379.721	139.950	198.931	606.783
11	419.359	395.899	146.095	206.403	631.043
12	405.636	382.201	144.445	186.555	602.085
13	395.614	371.792	143.332	188.382	604.434
14	416.359	393.997	143.830	200.835	617.676
15	408.189	386.840	142.345	189.281	611.025
16	405.718	383.216	146.999	184.649	612.706
17	401.569	378.265	143.459	184.482	604.713
18	396.382	376.272	141.104	174.564	589.697
19	394.554	376.310	141.344	170.577	589.371
20	406.625	386.703	138.906	205.479	617.920
21	400.312	377.561	140.371	180.803	600.800
22	412.275	387.789	145.282	202.255	628.359
23	406.886	387.700	139.211	197.651	613.866
24	405.127	385.464	138.316	194.453	597.813
25	403.784	381.745	138.606	190.512	598.519
26	402.962	380.418	139.920	208.016	616.100
27	397.365	376.405	138.509	193.573	597.642
28	424.285	403.790	144.767	199.587	631.347
29	406.216	384.023	139.477	196.220	611.568
30	404.700	383.223	139.645	194.584	603.666
31	402.453	378.611	141.334	186.120	601.755
32	413.461	391.391	139.821	205.226	618.333
33	415.692	394.837	141.585	195.650	619.850
34	409.602	388.152	139.250	201.224	615.550
35	396.895	373.427	140.609	182.673	595.232
36	401.167	378.288	144.169	196.100	614.157
37	397.505	375.815	137.595	189.713	592.287
38	402.771	380.625	144.351	183.166	605.646
39	391.666	369.837	141.494	183.705	600.525
40	416.829	396.318	141.522	198.489	616.930
41	406.212	383.891	142.335	195.339	611.124
42	397.720	378.979	142.182	165.831	593.862
43	405.881	386.371	144.030	200.466	639.733
44	396.054	375.851	137.734	183.062	597.899
45	411.425	389.412	143.950	200.684	628.190
46	404.924	383.490	139.376	183.289	596.082
47	405.369	382.003	144.667	188.402	616.021
48	406.790	381.780	146.049	196.685	627.065
49	396.671	372.780	137.819	181.355	586.016
50	408.019	384.036	146.154	202.143	631.976
Mean	403.846	381.938	141.664	190.446	607.172
Min	386.994	360.841	136.619	165.831	578.599
Max	424.285	403.790	146.999	208.016	639.733

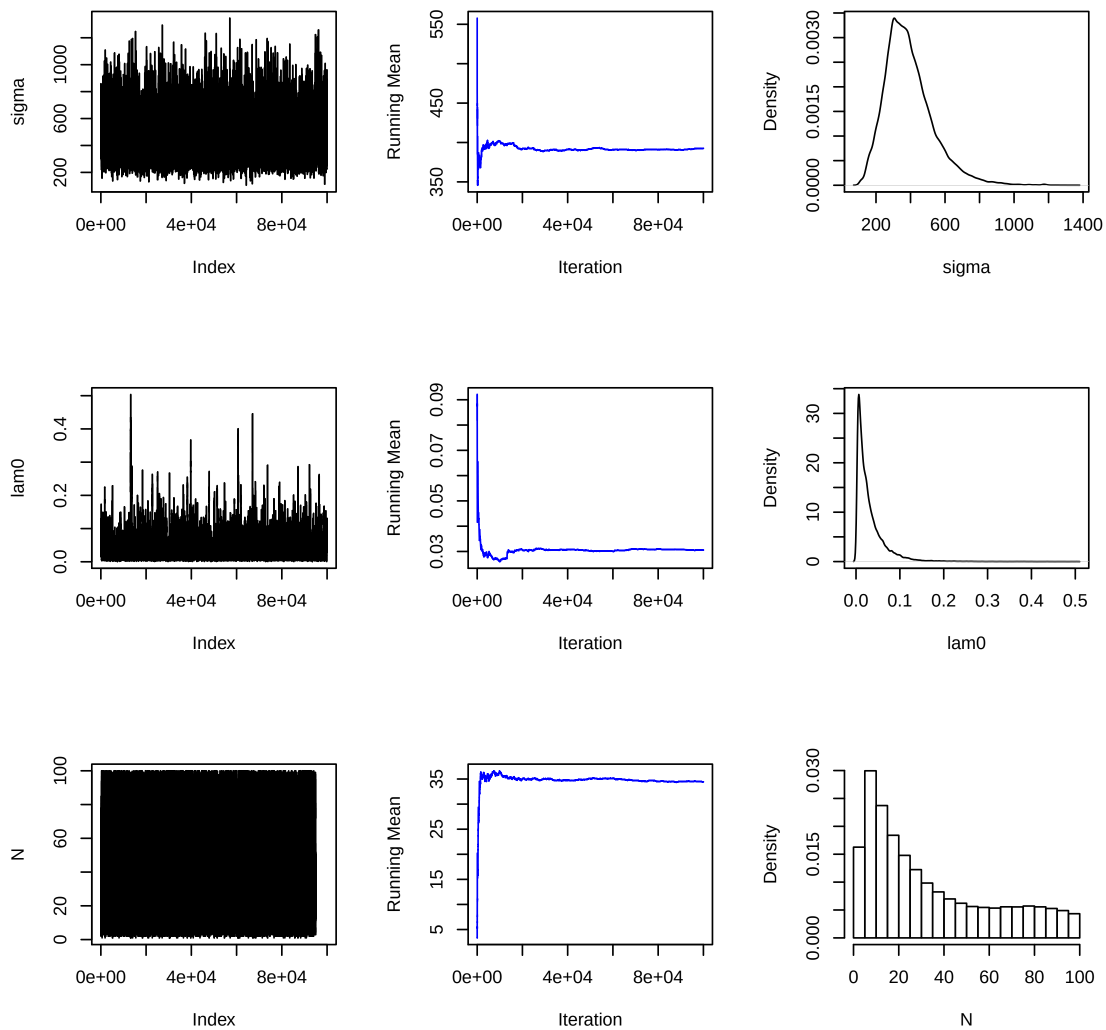


Figure A.13: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 2

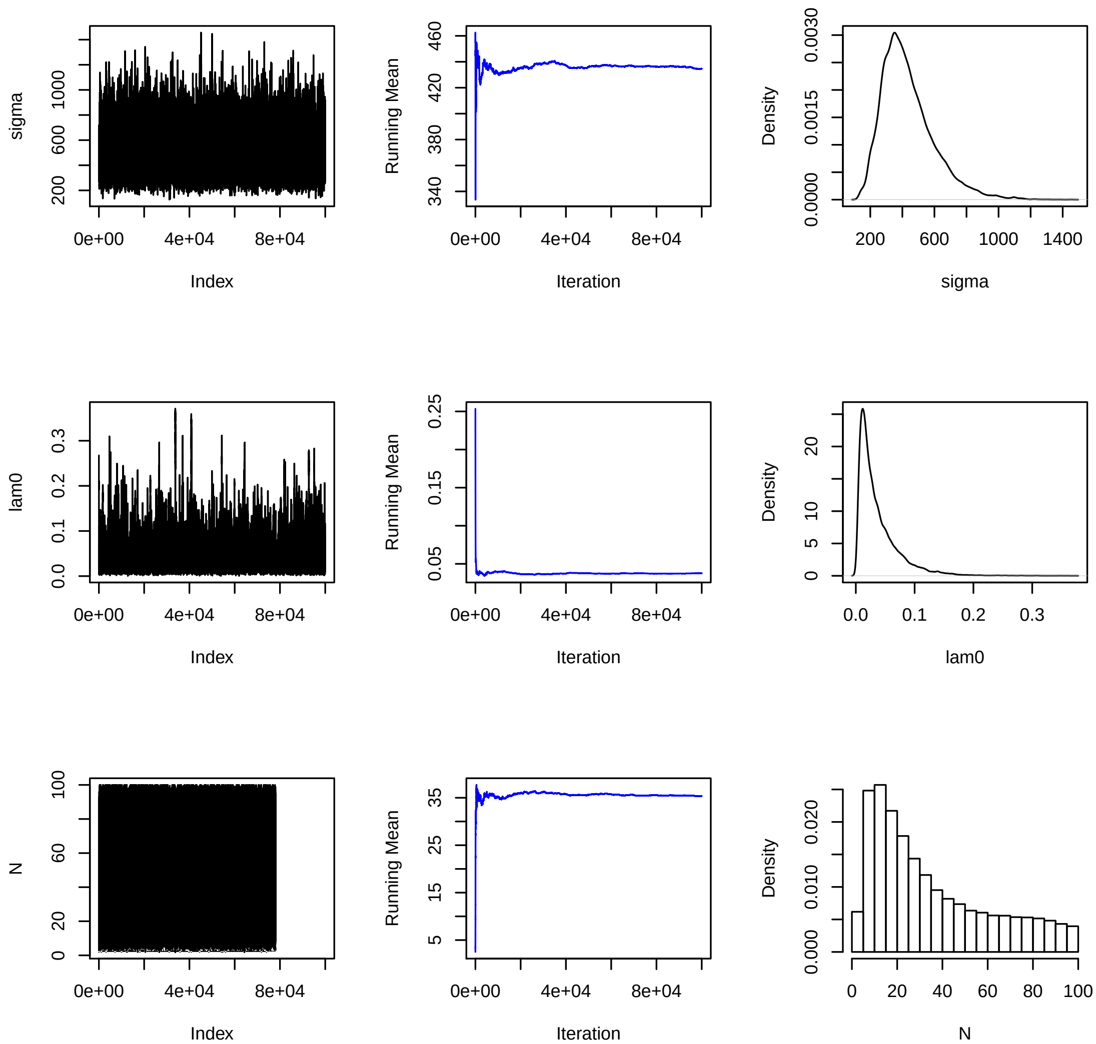


Figure A.14: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 2

Table A.14: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Tel-4 Using Batch 3

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	343.998	336.579	93.48	178.327	524.638
2	342.515	335.792	92.655	163.703	500.575
3	337.875	330.717	96.912	177.443	540.463
4	338.774	332.801	93.212	171.829	505.661
5	338.249	330.272	94.867	157.214	497.56
6	335.708	327.146	102.471	143.84	522.988
7	335.319	326.908	93.788	169.31	510.094
8	344.405	337.02	96.429	169.204	507.169
9	346.139	337.549	95.406	180.282	515.983
10	337.592	330.918	95.74	173.679	519.318
11	341.252	331.6	96.037	157.294	506.755
12	343.751	336.803	94.257	164.89	510.428
13	339.192	335.063	96.005	162.696	529.124
14	341.081	333.601	100.368	172.011	518.186
15	341.09	332.101	94.152	175.999	510.937
16	341.84	335.429	91.658	177.859	501.54
17	346.675	339.018	93.936	177.582	519.087
18	340.225	330.888	95.991	164.587	519.592
19	343.081	334.074	94.986	175.704	519.618
20	340.668	330.1	96.595	167.32	510.94
21	337.074	329.035	93.108	158.743	498.095
22	340.914	334.389	91.463	172.742	506.072
23	341.271	333.636	95.105	162.634	512.543
24	342.437	335.593	95.072	158.035	508.003
25	342.688	336.974	95.022	166.446	504.176
26	342.237	334.478	98.132	166.552	537.885
27	339.251	329.633	95.94	154.729	504.107
28	341.368	331.763	97.257	170.314	517.58
29	346.849	338.752	97.738	178.212	536.348
30	339.694	331.869	96.331	157.779	505.227
31	338.614	328.43	100.156	165.632	520.054
32	336.761	330.228	99.236	155.701	521.731
33	332.477	326.574	98.87	135.255	493.717
34	338.257	330.977	94.49	149.135	497.812
35	342.18	334.582	92.789	170.889	512.44
36	343.386	334.029	96.244	172.83	507.502
37	341.304	333.466	96.186	167.398	507.545
38	337.145	325.642	96.629	174.001	519.457
39	336.846	327.961	97.555	169.065	524.605
40	338.909	331.444	92.024	186.525	520.898
41	337.837	329.757	95.719	158.667	500.538
42	336.422	331.124	99.408	160.554	527.919
43	337.459	329.662	96.229	168.145	516.277
44	342.827	336.749	91.337	181.956	515.288
45	340.08	332.486	94.505	163.737	525.504
46	342.793	336.004	96.221	179.343	519.741
47	337.489	330.144	96.097	161.797	498.466
48	335.386	332.242	92.645	134.702	486.468
49	345.279	338.326	97.332	160.452	514.972
50	345.552	338.522	92.516	184.532	512.1
Mean	340.404	332.777	95.606	166.546	513.275
Min	332.477	325.642	91.337	134.702	486.468
Max	346.849	339.018	102.471	186.525	540.463

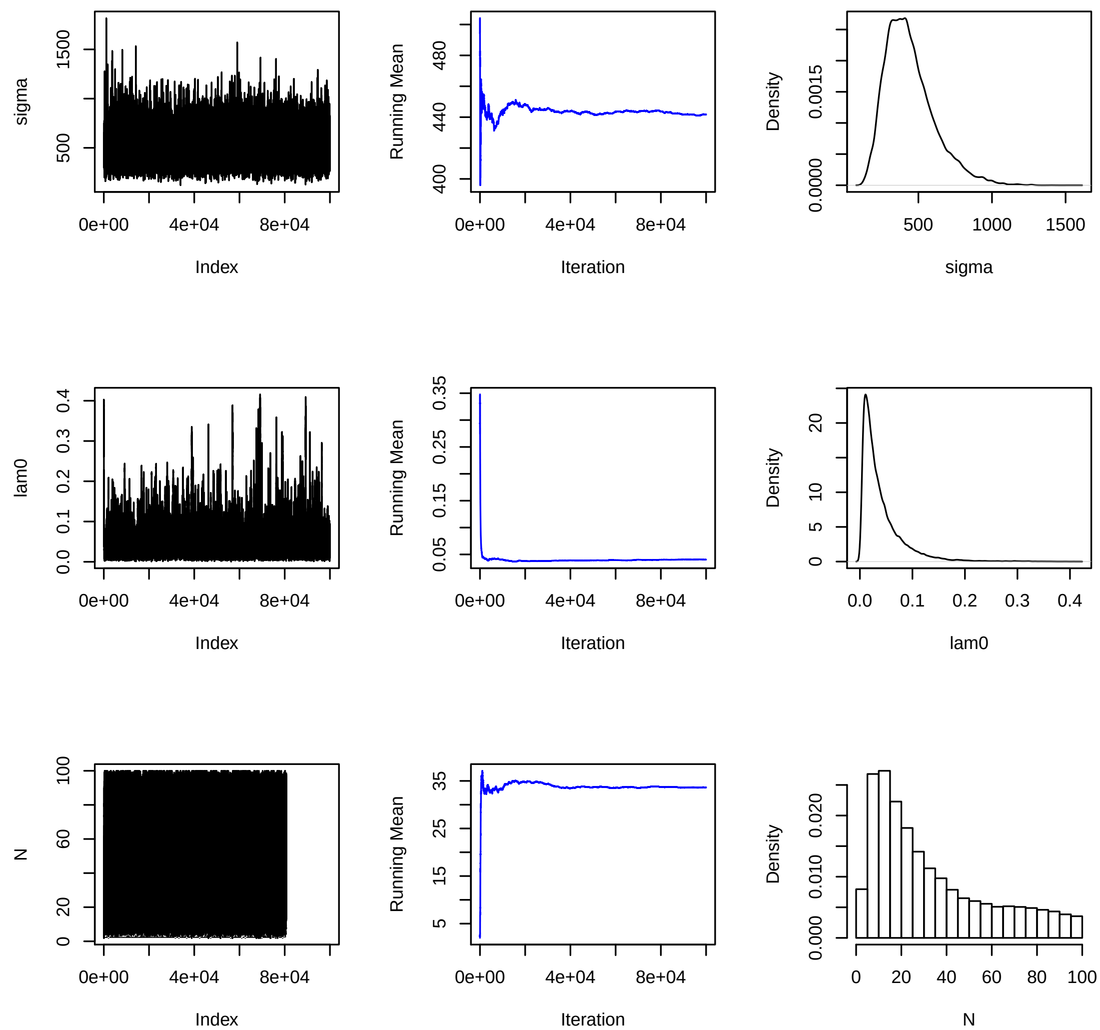


Figure A.15: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 3

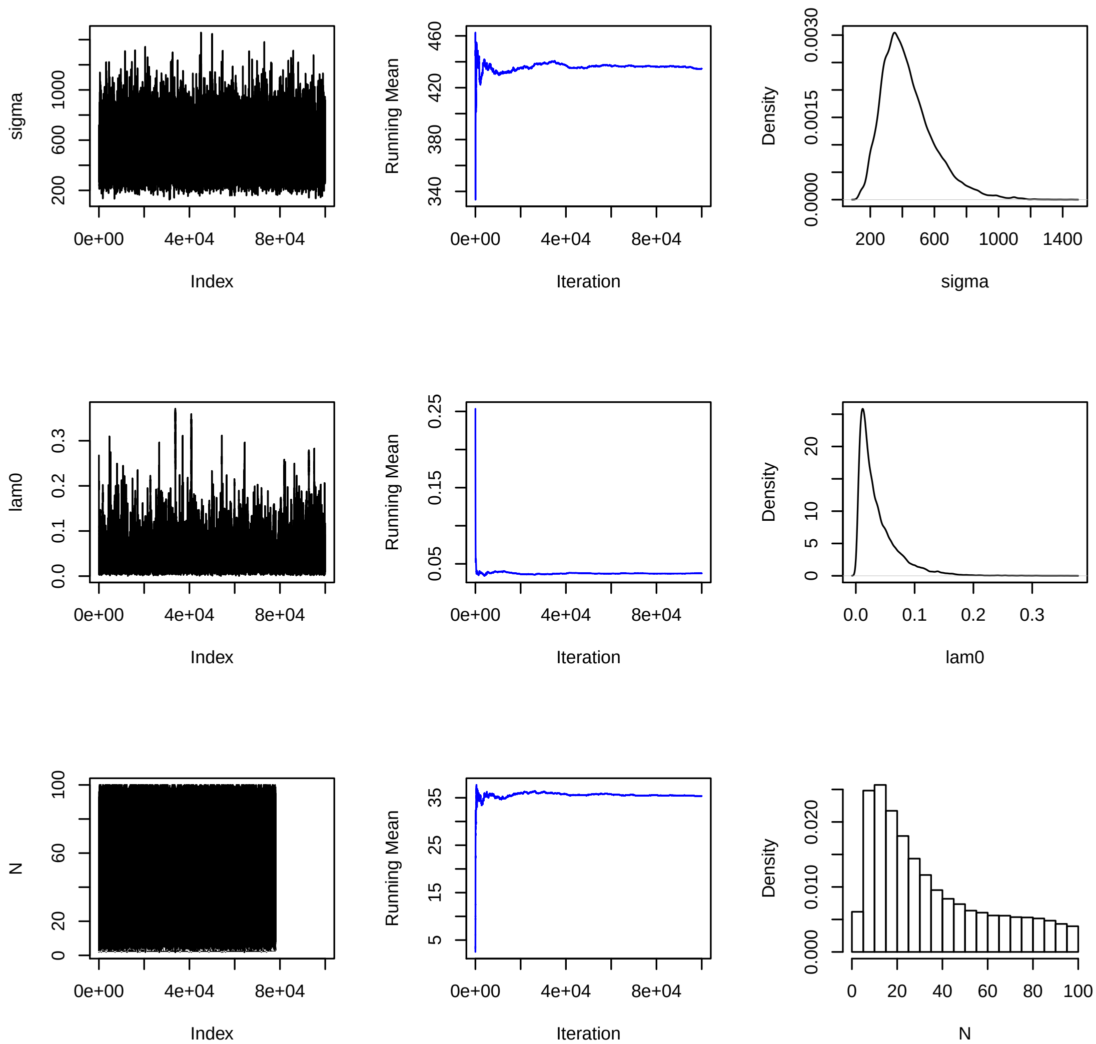


Figure A.16: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 3

Table A.15: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of σ for Tel-4 Using Batch 4

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	338.088	306.098	153.247	142.096	539.871
2	368.692	345.644	127.97	161.017	540.105
3	258.827	209.569	124.953	136.291	447.999
4	395.583	389.675	123.502	203.48	542.264
5	344.713	327.818	152.881	129.517	535.301
6	338.684	308.221	133.01	158.947	515.607
7	275.073	226.666	122.306	143.819	466.86
8	339.082	301.313	134.948	160.219	528.439
9	249.164	190.746	131.171	125.554	459.104
10	215.477	143.915	144.212	110.237	442.611
11	210.315	164.435	116.359	110.595	389.332
12	328.204	284.964	135.446	175.145	551.809
13	340.461	304.789	120.331	189.2	511.649
14	385.459	383.899	142.886	191.381	583.891
15	286.319	237.913	132.942	143.539	503.417
16	384.047	390.854	132.516	168.478	554.907
17	320.115	272.81	150.848	124.859	528.995
18	379.491	363.953	127.481	188.734	553.121
19	328.822	271.15	143.574	145.642	529.423
20	387.773	385.993	139.641	185.232	573.553
21	398.337	408.512	134.485	178.433	572.772
22	417.44	418.376	120.832	219.695	580.932
23	367.262	382.048	147.079	151.803	542.209
24	338.007	314.344	133.253	151.221	504.813
25	299.686	238.924	135.588	163.739	513.076
26	338.118	316.878	150.772	145.844	545.148
27	436.772	439.081	119.306	219.437	589.795
28	334.534	308.604	134.756	149.119	518.029
29	287.475	230.174	140.415	134.714	490.514
30	390.267	399.38	137.622	149.491	548.49
31	374.72	390.835	139.042	165.348	548.936
32	311.096	253.586	138.718	160.391	513.636
33	394.264	399.504	129.728	189.292	582.287
34	319.309	293.298	164.305	125.361	540.145
35	359.531	304.934	171.639	147.308	571.079
36	234.147	166.368	140.417	111.204	449.272
37	384.856	373.667	136.097	177.206	548.29
38	329.127	290.232	126.713	167.114	515.435
39	413.774	416.996	129.617	209.425	602.526
40	348.991	326.997	139.294	147.746	528.64
41	305.224	261.085	137.297	139.79	495.414
42	315.819	249.479	157.574	149.991	528.813
43	397.323	392.913	134.866	188.278	569.292
44	332.964	293.046	133.042	161.734	515.431
45	394.741	395.331	134.355	180.616	560.338
46	302.025	254.458	136.612	144.573	499.848
47	319.126	274.013	126.391	170.772	497.23
48	306.153	271.901	126.213	147.206	484.724
49	352.498	321.213	130.728	175.939	536.573
50	339.481	289.327	145.323	170.391	539.745
Mean	338.349	309.719	136.446	159.743	526.633
Min	210.315	143.915	116.359	110.237	389.332
Max	436.772	439.081	171.639	219.695	602.526

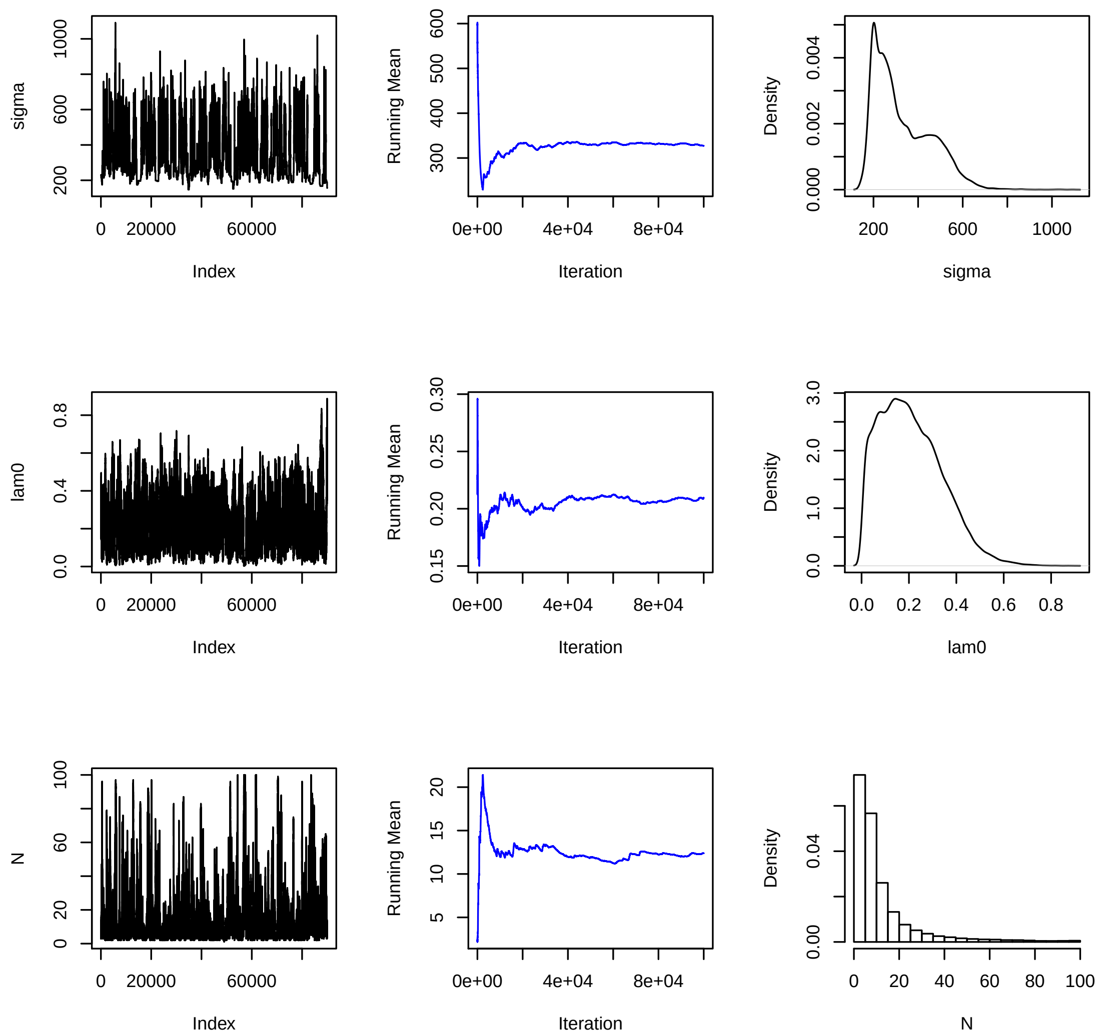


Figure A.17: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 4

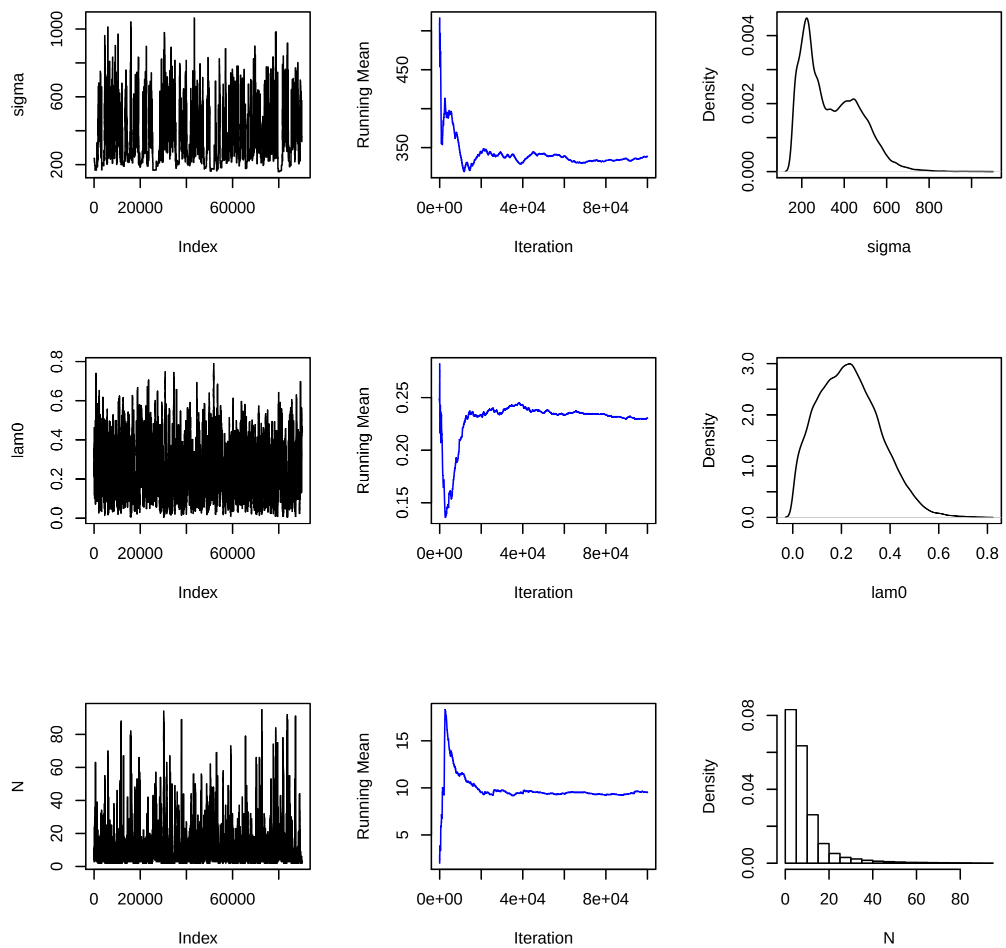


Figure A.18: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) for Tel-4 Using Batch 4

Table A.16: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N by Original Spatial Model for Tel-4 Using Batch 2

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	3.731	2	5.095	1	8
2	1.827	1	2.019	1	4
3	2.229	1	2.802	1	4
4	2.834	1	3.754	1	6
5	2.477	1	3.079	1	5
6	1.856	1	1.748	1	4
7	1.948	1	2.503	1	4
8	3.049	1	3.629	1	7
9	2.944	2	3.971	1	6
10	2.935	1	3.593	1	6
11	1.732	1	1.857	1	3
12	2.092	1	3.099	1	4
13	1.811	1	1.876	1	4
14	1.742	1	1.722	1	3
15	2.686	1	5.421	1	5
16	2.6	1	3.622	1	6
17	1.697	1	1.558	1	3
18	3.695	1	5.955	1	9
19	1.413	1	1.218	1	2
20	2.026	1	2.235	1	4
21	4.864	2	8.989	1	11
22	2.665	1	3.219	1	6
23	2.325	1	3.306	1	5
24	2.229	1	3.781	1	4
25	4.173	2	5.649	1	9
26	1.92	1	1.869	1	4
27	2.605	1	4.045	1	5
28	2.417	1	2.939	1	5
29	4.733	2	6.592	1	10
30	2.026	1	2.431	1	4
31	2.168	1	2.352	1	4
32	2.289	1	2.715	1	5
33	4.19	1	8.424	1	9
34	1.289	1	0.875	1	2
35	2.778	1	3.479	1	6
36	1.9	1	2.216	1	4
37	2.918	1	5.122	1	6
38	2.64	1	2.867	1	6
39	3.319	1	5.258	1	7
40	2.251	1	2.444	1	5
41	2.096	1	2.59	1	4
42	2.494	1	3.376	1	5
43	2.562	1	3.793	1	6
44	2.699	1	3.941	1	6
45	1.603	1	1.658	1	3
46	2.541	1	3.737	1	5
47	6.642	3	9.715	1	15
48	3.703	1	5.01	1	10
49	1.892	1	3.034	1	3
50	2.014	1	2.352	1	4
Mean	2.625	1.14	3.571	1	5.5
Min	1.289	1	0.875	1	2
Max	6.642	3	9.715	1	15

Table A.17: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of of σ by Original Spatial Model for Tel-4 Using Batch 2

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	468.502	480.668	124.816	252.005	650.082
2	518.366	524.286	107.833	344.545	698.074
3	511.731	527.921	127.339	305.94	703.81
4	489.592	504.178	132.011	262.251	689.49
5	495.836	503.82	120.749	289.975	686.608
6	498.436	507.002	110.625	311.124	671.207
7	517.851	519.442	109.937	345.521	704.835
8	466.987	480.923	133.004	224.488	644.061
9	464.206	469.403	123.123	256.252	651.319
10	478.286	484.555	121.688	272.89	659.325
11	528.681	535.24	104.757	364.831	700.627
12	527.805	533.742	107.508	349.027	704.338
13	527.64	532.119	110.032	353.255	716.777
14	528.695	535.908	113.903	359.737	714.337
15	511.184	518.533	112.999	316.543	685.087
16	511.164	520.825	128.05	274.8	693.461
17	528.09	530.576	98.558	366.355	683.601
18	477.615	502.047	149.847	211.005	700.152
19	549.415	552.383	103.541	391.827	723.107
20	514.846	520.132	103.31	339.472	675.575
21	450.843	462.946	153.213	190.423	677.933
22	490.673	510.998	139.274	257.178	699.032
23	498.21	509.221	114.145	301.648	672.19
24	496.312	506.979	118.716	289.493	677.201
25	449.317	468.759	147.978	165.27	622.668
26	536.086	545.881	120.805	327.694	720.958
27	499.689	510.468	123.814	293.239	690.993
28	509.612	522.582	125.248	289.446	693.067
29	442.152	447.47	133.777	216.168	626.193
30	535.577	542.605	111.53	335.146	699.22
31	515.535	520.455	104.915	328.094	669.433
32	481.09	495.47	125.13	253.266	665.362
33	485.21	500.783	137.558	249.316	695.599
34	535.847	535.582	88.309	409.074	691.517
35	491.138	505.907	127.473	264.001	673.485
36	517.179	524.044	106.014	330.192	678.965
37	483.133	501.83	132.148	255.84	686.021
38	485.813	491.79	113.997	291.187	653.139
39	484.649	494.328	118.906	278.233	657.722
40	511.258	526.283	121.63	305.623	697.187
41	501.175	506.25	114.513	314.521	680.908
42	509.59	518.854	128.235	293.321	704.81
43	512.684	526.87	120.151	304.505	699.683
44	519.843	528.596	119.263	311.955	700.449
45	525.818	529.727	101.468	377.453	698.767
46	506.417	520.574	117.398	304.252	684.244
47	416.622	418.801	145.172	185.256	620.621
48	447.275	502.569	179.853	127.411	625.432
49	557.453	564.995	110.623	376.993	734.938
50	517.297	532.177	116.572	308.977	689.534
Mean	500.569	511.150	121.229	294.540	682.863
Min	416.622	418.801	88.309	127.411	620.621
Max	557.453	564.995	179.853	409.074	734.938

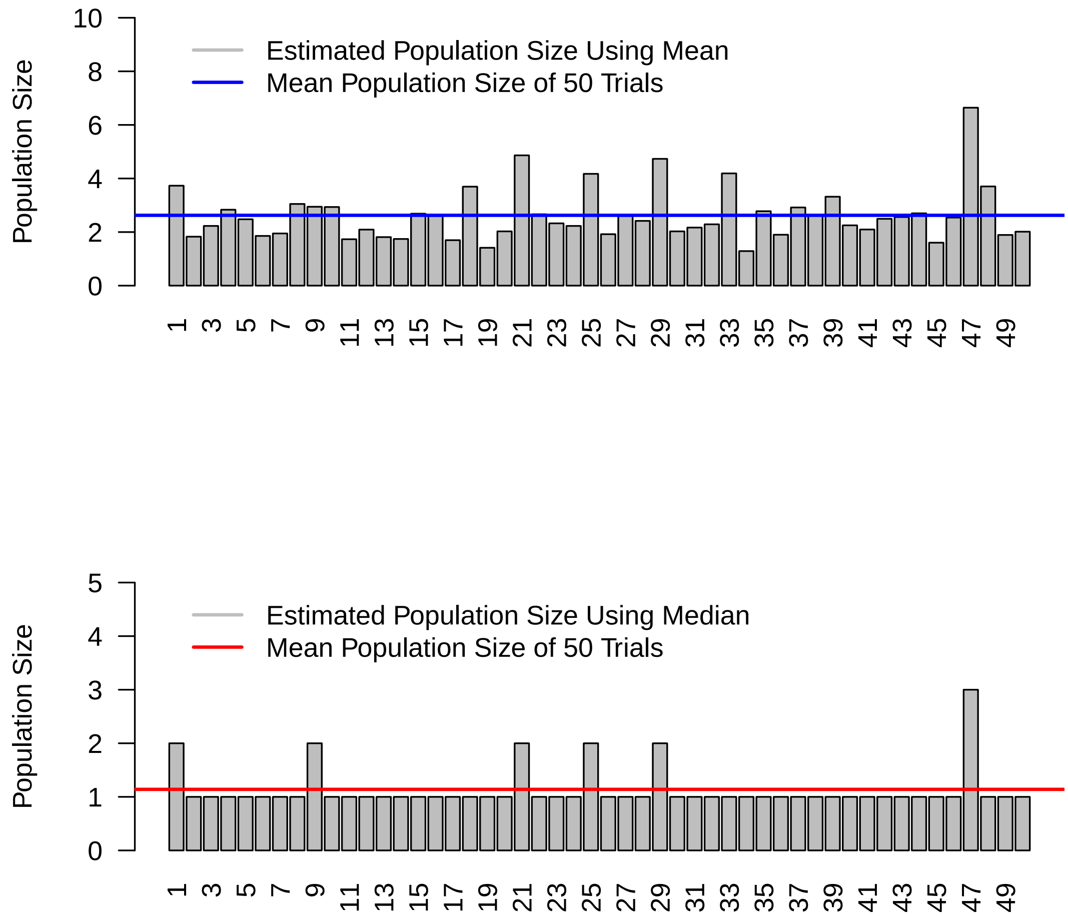


Figure A.19: The Estimated Population Size of Tel-4 Using Mean and Median, and Their Averages Over 50 Runs Using Batch 2 by Original Spatial Model

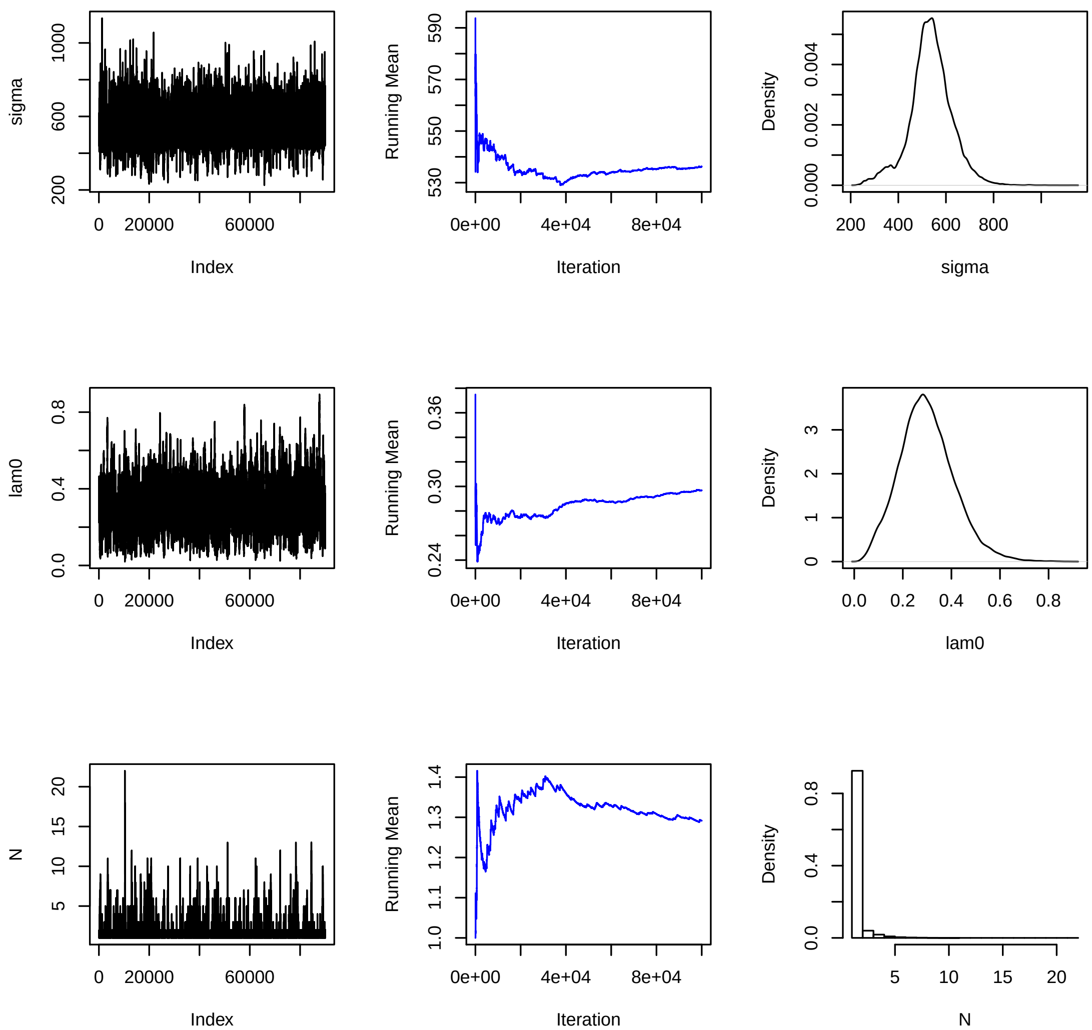


Figure A.20: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) by Original Spatial Model for Tel-4 Using Batch 2 for M=100

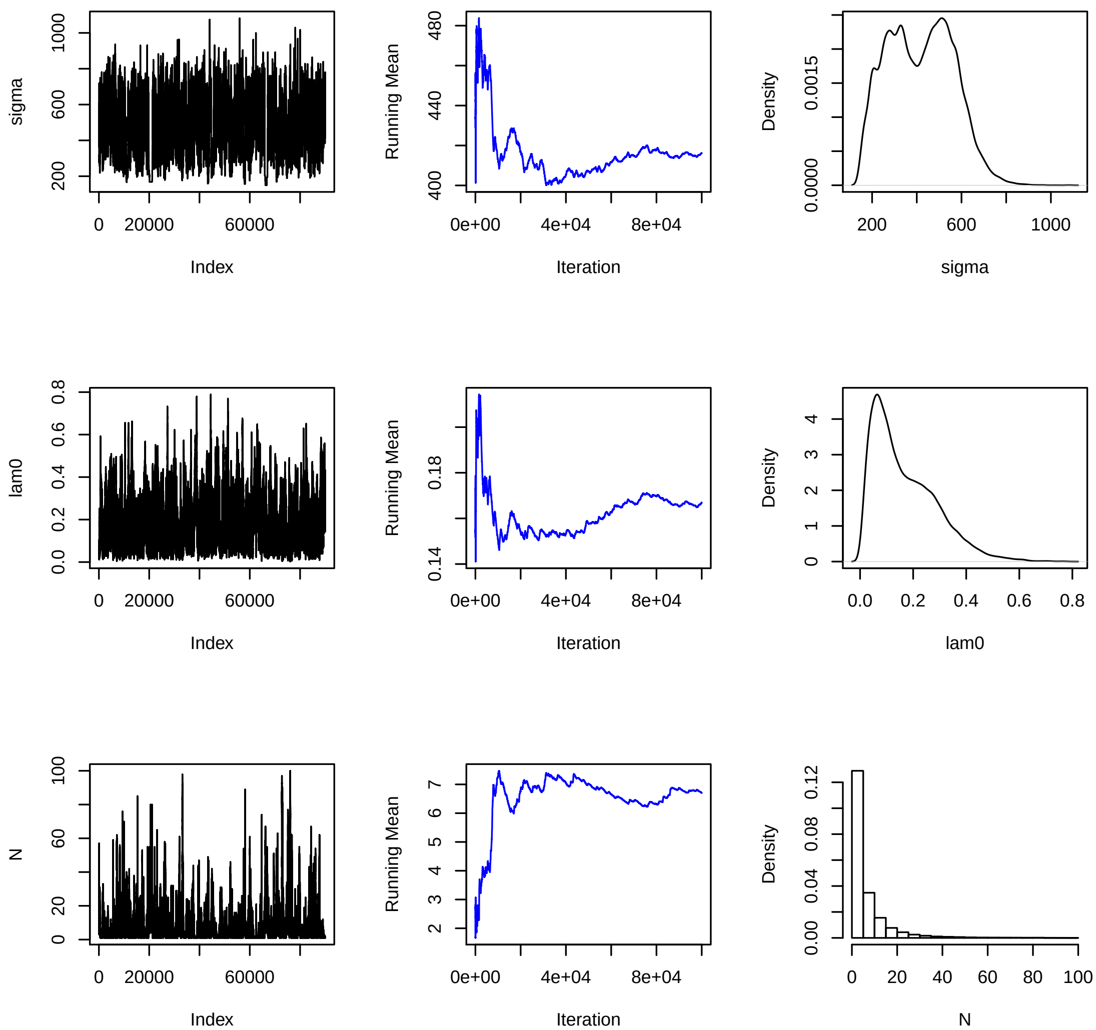


Figure A.21: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) by Original Spatial Model for Tel-4 Using Batch 2 for M=100

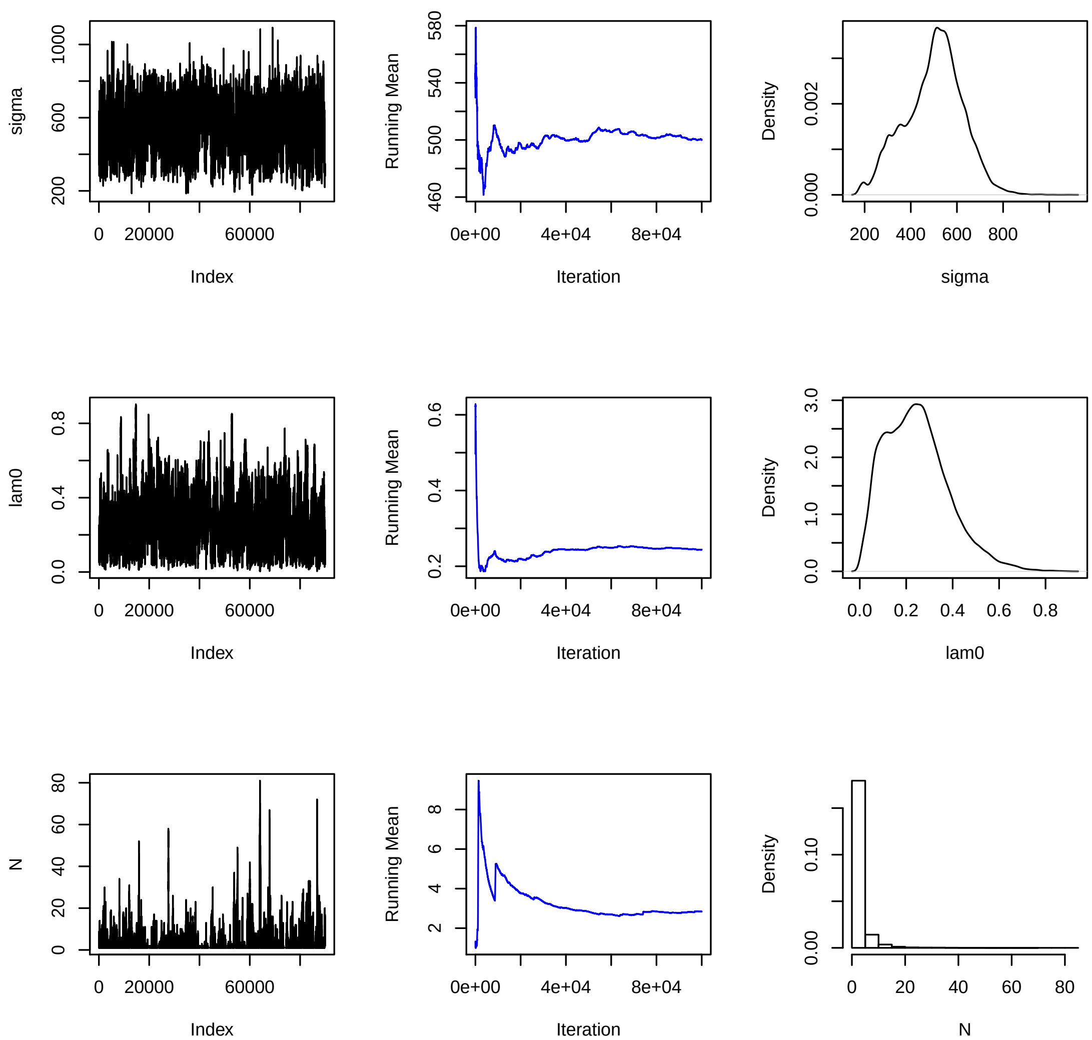


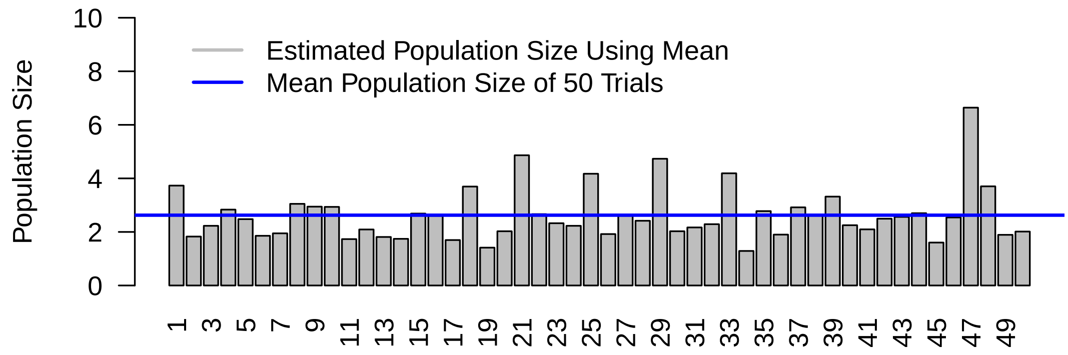
Figure A.22: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) by Original Spatial Model for Tel-4 Using Batch 2 for M=100

Table A.18: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of Population Size N by Original Spatial Model for Tel-4 Using Batch 3

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	1.588	1	1.194	1	3
2	1.548	1	1.349	1	3
3	1.696	1	1.271	1	3
4	1.938	1	1.595	1	4
5	1.473	1	1.193	1	2
6	2.134	1	2.048	1	4
7	1.814	1	1.618	1	4
8	2.054	1	1.528	1	4
9	2.306	2	1.934	1	5
10	1.625	1	1.129	1	3
11	1.657	1	1.375	1	3
12	3.868	1	4.652	1	10
13	1.235	1	0.844	1	2
14	1.538	1	1.101	1	3
15	3.063	3	1.916	1	5
16	1.53	1	1.174	1	3
17	1.61	1	1.21	1	3
18	1.423	1	1.008	1	2
19	1.569	1	1.608	1	3
20	1.622	1	1.171	1	3
21	1.818	1	1.599	1	3
22	1.567	1	1.334	1	3
23	1.747	1	1.288	1	3
24	1.978	1	1.504	1	4
25	2.33	2	1.952	1	5
26	2.388	1	2.672	1	5
27	1.906	1	1.648	1	4
28	1.667	1	1.44	1	3
29	2.042	1	1.686	1	4
30	2.26	2	1.852	1	4
31	2.49	1	2.761	1	6
32	1.634	1	1.505	1	3
33	1.503	1	1.131	1	2
34	1.431	1	0.996	1	2
35	1.379	1	0.973	1	2
36	2.133	1	1.816	1	4
37	1.654	1	1.411	1	3
38	2.663	2	2.679	1	6
39	1.502	1	0.988	1	2
40	2.369	1	2.344	1	5
41	1.728	1	1.438	1	3
42	1.379	1	0.96	1	2
43	1.912	1	1.286	1	3
44	1.779	1	1.278	1	3
45	1.56	1	1.141	1	3
46	2.645	2	3.157	1	5
47	1.848	1	1.501	1	4
48	1.847	1	1.35	1	3
49	1.869	1	1.758	1	4
50	1.675	1	1.575	1	3
Mean	1.880	1.14	1.599	1	3.56
Min	1.235	1	0.844	1	2
Max	3.868	3	4.652	1	10

Table A.19: Summary of 50 Runs to Estimate Mean, Median, Standard Error, and Credible Interval of of σ by Original Spatial Model for Tel-4 Using Batch 3

Sim #	Mean	Median	sd	Credible Interval (HDI)	
				LB	UB
1	362.709	363.582	67.501	257.914	478.642
2	403.746	418.226	79.764	268.158	531.494
3	399.767	404.216	79.047	267.76	521.98
4	359.069	363.778	80.779	228	476.684
5	374.111	376.158	67.056	267.048	479.082
6	374.042	373.41	84.073	228.657	501.103
7	371.029	375.227	76.555	243.538	497.018
8	349.453	336.988	81.331	233.025	481.195
9	371.271	380.602	84.66	217.383	486.423
10	387.509	393.265	81.497	260.773	512.872
11	396.327	402.823	76.023	269.454	516.069
12	338.403	395.402	152.702	96.451	492.598
13	422.84	430.935	71.898	302.423	532.32
14	399.013	400.007	66.104	295.231	507.416
15	309.629	287.797	98.043	169.909	463.772
16	398.508	395.568	57.793	309.014	487.8
17	383.703	397.957	87.025	233.913	519.5
18	400.619	401.306	67.482	303.947	516.137
19	402.994	413.44	81.037	282.708	532.03
20	404.927	409.24	68.987	297.429	522.425
21	398.899	403.981	76.078	278.283	527.216
22	391.477	399.487	72.722	269.696	499.433
23	385.73	393.322	79.853	246.672	502.843
24	355.495	361.21	75.351	223.888	458.317
25	373.313	376.697	86.793	202.472	491.575
26	378.815	394.74	96.498	205.781	514.874
27	386.952	392.49	69.382	272.189	496.247
28	394.944	397.276	73.091	267.553	501.38
29	356.19	356.036	82.798	219.269	479.79
30	354.671	356.277	79.26	222.231	475.292
31	356.817	369.581	88.156	193.414	480.008
32	372.849	372.563	69.656	265.726	495.291
33	399.762	402.62	65.855	299.806	509.954
34	399.877	401.942	63.125	304.303	499.887
35	417.808	424.435	74.853	301.832	535.035
36	374.7	373.168	75.605	254.408	493.194
37	391.189	403.462	90.249	245.41	519.315
38	337.001	348.538	84.097	172.842	438.474
39	389.582	389.274	69.246	286.601	500.441
40	358.095	364.367	84.547	202.045	478.614
41	380.201	391.676	85.109	241.625	511.644
42	412.974	419.095	71.47	307.406	520.785
43	368.846	379.62	84.469	225.929	497.515
44	373.378	377.086	74.849	244.59	483.525
45	378.929	386.036	81.208	243.803	497.666
46	353.824	347.438	90.443	221.953	505.401
47	390.882	400.553	79.691	246.751	505.15
48	372.358	361.86	79.273	260.006	505.391
49	390.566	404.458	89.761	209.718	507.524
50	385.586	392.552	77.739	259.121	510.237
Mean	379.828	385.235	79.612	248.561	499.972
Min	309.629	287.797	57.793	96.451	438.474
Max	422.84	430.935	152.702	309.014	535.035



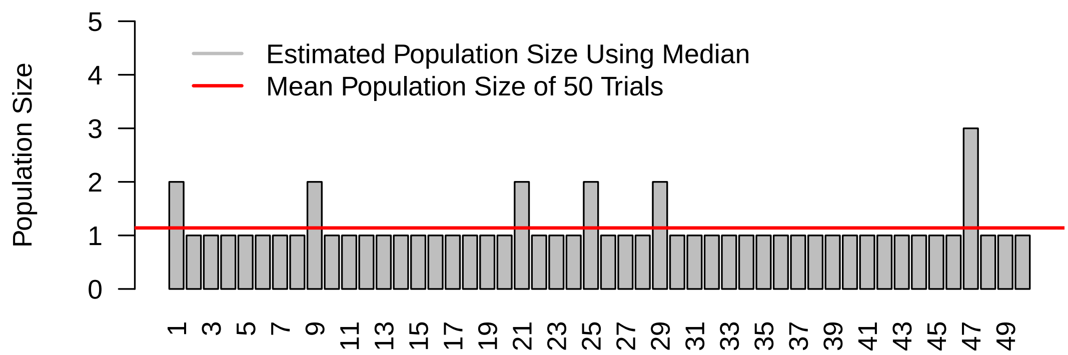


Figure A.23: The estimated population size for Tel-4 using Batch 2 obtained by Mean and Median, and their averages over 50 runs by Original Spatial Model

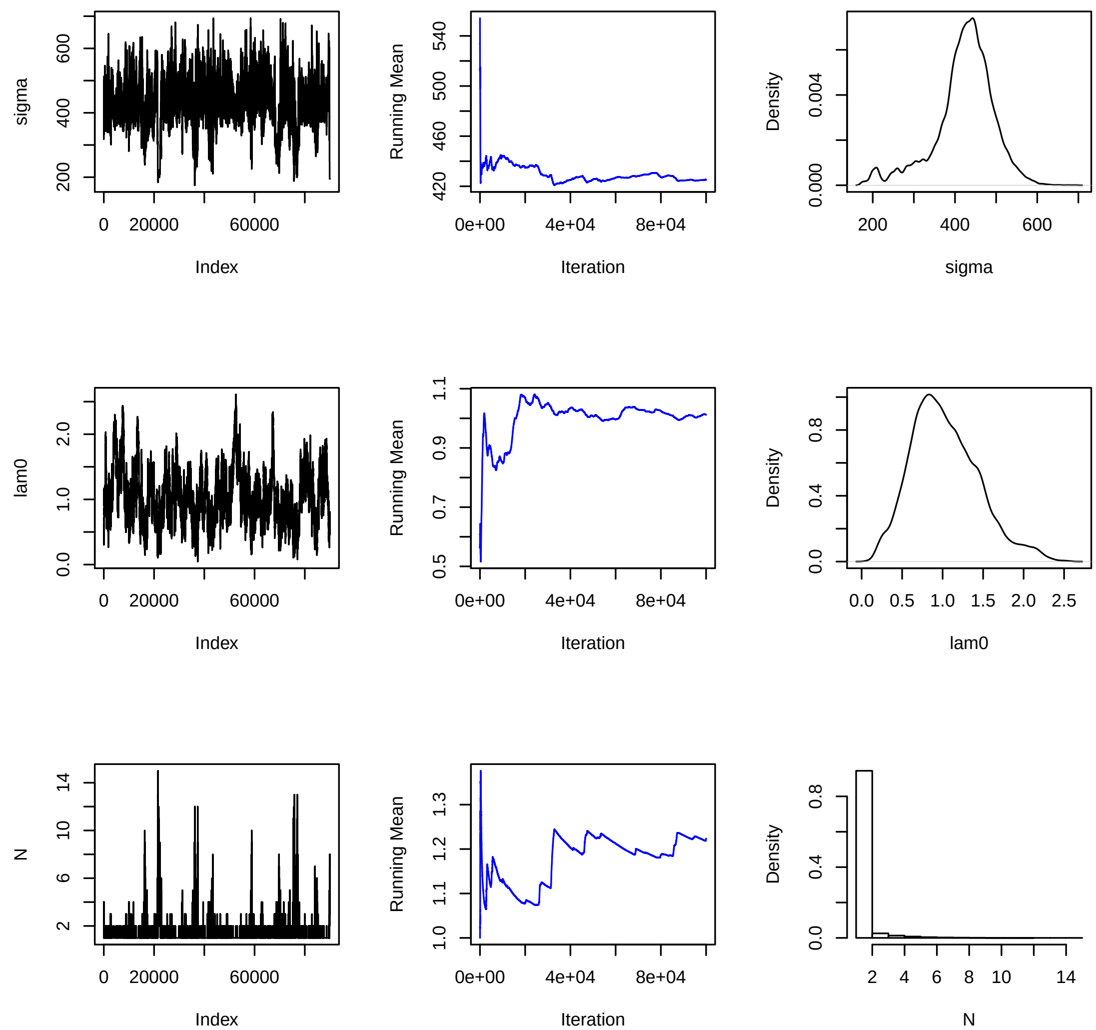


Figure A.24: Random Trial 1: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) by Original Spatial Model for Tel-4 Using Batch 3 for M=100

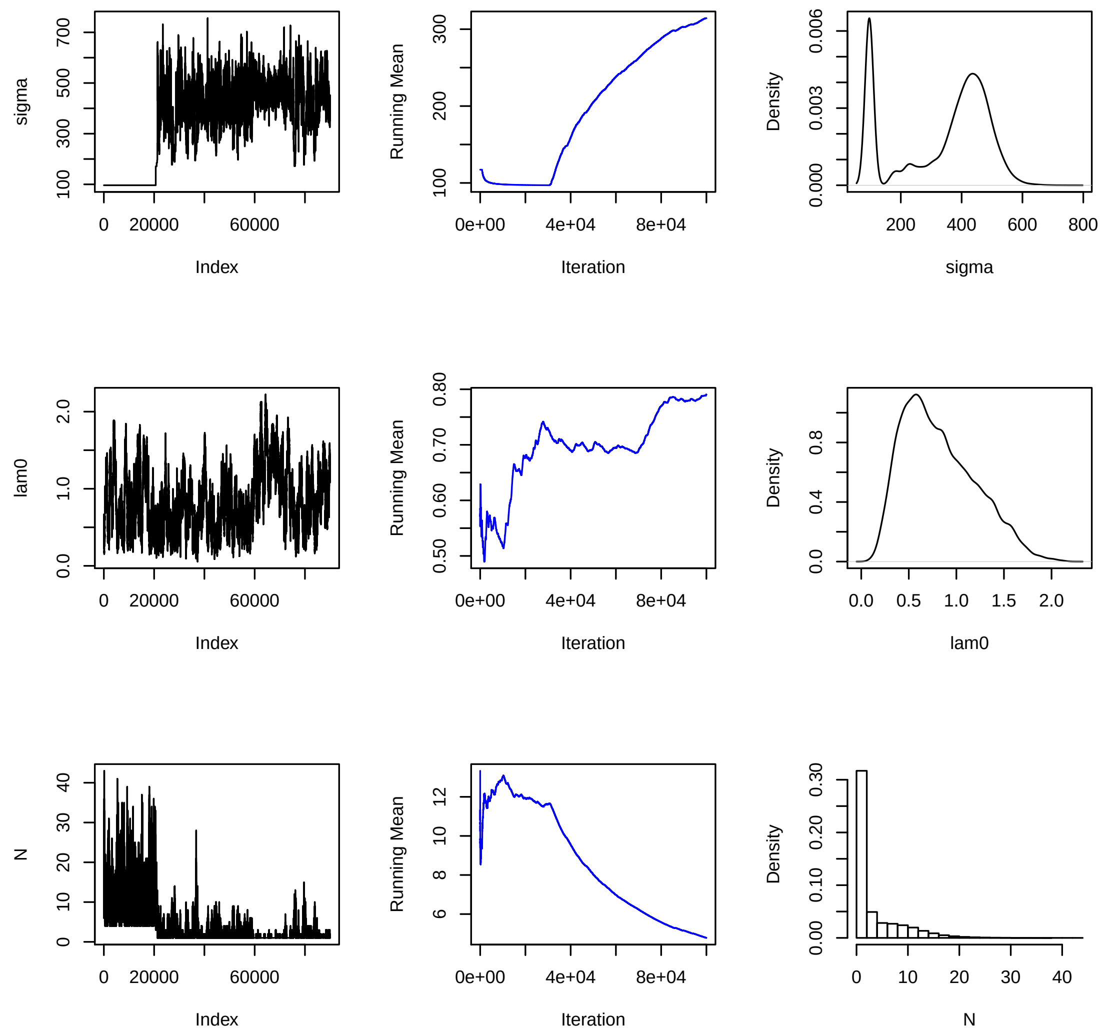


Figure A.25: Random Trial 2: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) by Original Spatial Model for Tel-4 Using Batch 3 for M=100

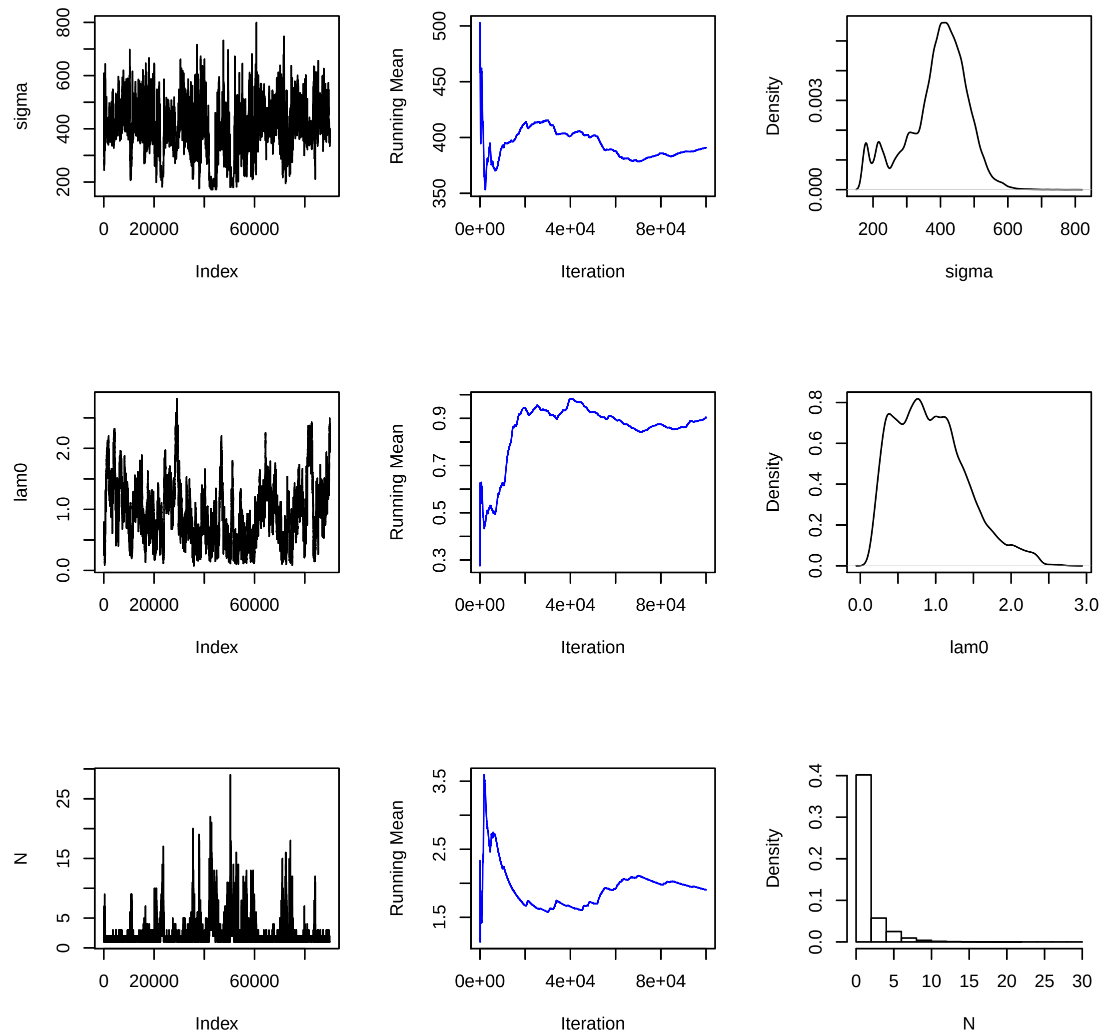


Figure A.26: Random Trial 3: Convergence plots (first column), Running Mean (second column), and Estimated Posterior Densities (third column) for σ (first row), λ_0 (second row) and N (third row) by Original Spatial Model for Tel-4 Using Batch 3 for M=100

A.5 Examples of Images Collected During This Research Using Motion Activated Cameras Installed in The Study Sites

Figure A.27: Photo 1: A closeup picture from a hog

Figure A.28: Photo 2: A hog picture taken in its habitat with dominant green background

Figure A.29: Photo 3: A partial hog picture in the background