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Closed Population Models

4

p0005 In this chapter we introduce ordinary *non-spatial* capture-recapture (CR) models for estimating population size in closed populations. A closed population is one whose size, N , does not change during the study. Two forms of closure are often discussed: demographic closure, meaning that no births or deaths occur, and geographic closure, which states that no individuals move onto or off of the sampled area during the study. Although few populations are actually closed except during very short time intervals, closed population CR models serve as the basis for the development of the rest of the models presented in this book, including the models for open populations discussed in Chapter 16.

p0010 We begin with the most basic capture-recapture model, colloquially referred to as “model M_0 ” (Otis et al., 1978), in which encounter probability is strictly constant in all respects (across individuals, and replicates). This allows us to highlight the basic structure of closed population models as binomial GLMs. We then consider some important extensions of ordinary closed population models that accommodate various types of “individual effects”—either in the form of explicit, observed covariates (sex, age, body mass) or unstructured “heterogeneity” in the form of an individual random effect, which represent unobserved or unmeasured covariates. A special type of individual covariate models is distance sampling, which could be thought of as the most primitive spatial capture-recapture model. All of these different types of closed population models are closely related to binomial (or logistic) regression-type models. In fact, when N is known, they are precisely logistic regression models.

p0015 We emphasize Bayesian analysis of capture-recapture models and we accomplish this using a method related to classical “data augmentation” from the statistics literature (e.g., Tanner and Wong, 1987). This is a general concept in statistics but, in the context of capture-recapture models where N is unknown, it has a consistent implementation across classes of capture-recapture models and one that is really convenient from the standpoint of doing MCMC (Royle et al., 2007; Royle and Dorazio, 2012). We use data augmentation throughout this book and thus emphasize its conceptual and technical origins and demonstrate applications to closed population models. We refer the reader to Kéry and Schaub (2012, chapter 6) for an accessible and complementary development of Bayesian analysis of ordinary, i.e., non-spatial closed population models.

4.1 The simplest closed population model: model M_0

s0005

To start looking at the simplest capture-recapture model, let's suppose there exists a population of N individuals which we subject to repeated sampling, say over K "occasions," such as trap nights, where individuals are captured, marked, released, and subsequently recaptured. We suppose that individual encounter histories are obtained, and these are of the form of a sequence of 0's and 1's indicating capture ($y = 1$) or not ($y = 0$) during any sampling occasion. As an example, suppose $K = 5$ sampling occasions, then an individual captured during occasions 2 and 3 but not otherwise would have an encounter history of the form $\mathbf{y} = (0, 1, 1, 0, 0)$. Thus, the observation \mathbf{y}_i for each individual ($i = 1, 2, \dots, N$) is a vector having elements denoted by y_{ik} for $k = 1, 2, \dots, K$. Usually this is organized as a row of a matrix with elements y_{ik} , see Table 4.1. Except where noted explicitly, we suppose that observations are independent within individuals and among individuals. Formally, this allows us to say that y_{ik} are independent and identically distributed ("iid") Bernoulli random variables and we may write $y_{ik} \sim \text{Bernoulli}(p)$. Consequently, for this very simple model in which p is constant (i.e., there are no individual or temporal covariates that affect p) the original binary detection variables can be aggregated into the total number of encounters for each individual $y_i = \sum_k y_{ik}$, and the observation model changes from a Bernoulli distribution to a binomial distribution based on a sample of size K . That is

p0020

$$y_i = \sum_k y_{ik} \sim \text{Binomial}(p, K)$$

for every individual in the population $i = 1, 2, \dots, N$, where N is the number of individuals in the population (i.e., population size).

Table 4.1 A toy capture-recapture data set with $n = 6$ observed individuals and $K = 5$ sample occasions. Under a model with constant encounter probability, the binary detection history data can be summarized in the detection frequency (the total number of detections, y_i), which is shown in the rightmost column.

sp050

| Indiv i | Sample occasion | | | | | y_i |
|-----------|-----------------|---|---|---|---|-------|
| | 1 | 2 | 3 | 4 | 5 | |
| 1 | 1 | 0 | 0 | 1 | 0 | 2 |
| 2 | 0 | 1 | 0 | 0 | 1 | 2 |
| 3 | 1 | 0 | 0 | 1 | 0 | 2 |
| 4 | 1 | 0 | 1 | 0 | 1 | 3 |
| 5 | 0 | 1 | 0 | 0 | 0 | 1 |
| $n = 6$ | 1 | 0 | 0 | 0 | 0 | 1 |

¹We use the common "dot notation" to denote having summed over one or more indices of a variable. $y_i = \sum_j y_{ij}$, $y_{..} = \sum_i \sum_j y_{ij}$, etc. np005

p0025 We emphasize the central importance of the basic Bernoulli encounter model—an individual is either encountered in a sample, or not—which forms the cornerstone of almost all of classical capture-recapture models, including many spatial capture-recapture models discussed in this book.

p0030 Evidently, the basic capture-recapture model is a simplistic version of a logistic-regression model with only an intercept term ($\text{logit}(p) = \text{constant}$). To say that all capture-recapture models are just logistic regressions is a slight oversimplification. In fact, we are proceeding here as if we knew N . In practice we don't, of course, and estimating N is actually the central objective. But, by proceeding as if N were known, we can specify a simple model ~~and then deal with the fact that N is unknown~~ using standard methods that you are already familiar with (i.e., GLMs - see Chapter 3).

p0035 Assuming individuals in the population are encountered independently, the joint probability distribution of the observations is the product of N binomials

$$\Pr(y_1, \dots, y_N | p) = \prod_{i=1}^N \text{Binomial}(y_i | K, p). \quad (4.1.1)$$

We emphasize that this expression is conditional on N , in which case we get to observe the $y_i = 0$ observations and the resulting data are just *iid* binomial counts. Because this is a binomial regression model of the variety described in Chapter 3, fitting this model using a **BUGS** engine poses no difficulty.

p0040 Equation (4.1.1) can be simplified even further if we reformat the observations as encounter frequencies. Specifically, let n_k denote the number of individuals captured exactly k times after K survey occasions, $n_k = \sum_{i=1}^N I(y_i = k)$ where $I()$ is the indicator function evaluating to 1 if its argument is true and 0 otherwise. For sake of illustration, we converted the data from Table 4.1 to this format (Table 4.2). What is important to note is that if we know N , then we know n_0 , i.e., the number of individuals not captured. In this case, an alternative and equivalent expression to Eq. (4.1.1) is

$$\Pr(y_1, \dots, y_N | p) = \prod_{k=0}^K \pi_k^{n_k} \quad (4.1.2)$$

where $\pi_k = \Pr(y = k)$ under the binomial model with parameter p and sample size K . The essential problem in capture-recapture, however, is that N is *not* known because the number of uncaptured individuals (n_0) is unknown. Consequently, the observed capture frequencies n_k are no longer independent because n_0 is a function of the other

sp055 **Table 4.2** Data from Table 4.1 formatted as capture frequencies. Since N is unknown, the number of individuals not captured (n_0) is also unknown.

| | k | | | | | |
|--|---------|---|---|---|---|---|
| | 0 | 1 | 2 | 3 | 4 | 5 |
| Number of individuals captured k times (n_k) | $N - 6$ | 2 | 3 | 1 | 0 | 0 |

frequencies, $n_0 = N - \sum_{k=1}^K n_k$. Hence, their joint distribution is multinomial (e.g., see Illian et al. (2008, p. 61)):

$$n_0, n_1, \dots, n_K \sim \text{Multinomial}(N, \pi_0, \pi_1, \dots, \pi_K) \quad (4.1.3)$$

We gave a general overview of the multinomial distribution in Section 2.2. The multinomial distribution is the standard model for discrete responses that can fall into a fixed number ($K + 1$ in this case) of possible categories. In the context of capture-recapture, the multinomial posits a population of N individuals with $K + 1$ possible outcomes defined by the possible encounter frequencies: encountered $y = 1, 2, \dots, K$ times or not encountered at all. These possible outcomes occur with probabilities π_k , which we refer to as “cell probabilities” or in the specific context of capture-recapture, encounter history probabilities.

To fit the model in which N is *unknown*, we can regard n_0 as a parameter and maximize the multinomial likelihood directly. Direct likelihood analysis of the multinomial model is straightforward, but that is not always sufficiently useful in practice because we seldom are concerned with models for the aggregated encounter history frequencies, which entail that capture probabilities are the same for all individuals. In many instances, including for spatial capture-recapture (SCR) models, we require a formulation of the model that can accommodate individual-level covariates to account for differences in detection among individuals, which we address subsequently in this chapter, and in Chapter 7.

4.1.1 The core capture-recapture assumptions

This basic capture-recapture model—model M_0 —comes with a host of specific biological and statistical assumptions. In addition to the basic assumption of population closure, Otis et al. (1978) list the following:

1. animals do not lose their marks during the experiment,
2. all marks are correctly noted and recorded at each trapping occasion, and
3. each animal has a constant and equal probability of capture on each trapping occasion.

The remainder of their classic work is dedicated to relaxing assumption 3. While assumptions 1 and 2 are undoubtedly necessary for inference from basic CR methods to be valid, and while they are also assumed by most of the models we present in the following chapters, we refrain from repeatedly making such statements. Our opinion is that all model assumptions are apparent when a model is clearly specified, and it is both redundant and impossible to list all the things not allowed by the model. For example, closed population models also assume that other sources of error do not occur, but it is not necessary to enumerate each possibility. Rather, it is necessary to make clear statements such as

$$y_i \stackrel{iid}{\sim} \text{Bernoulli}(p) \quad \text{for } i = 1, \dots, N.$$

This simple model description carries a tremendous amount of information, and it leaves very little left to say with respect to assumptions. Although we will not always show the *iid* symbol, it will be assumed unless otherwise noted, and this assumption is critical for valid inference. It implies that the encounter of one individual does not affect the encounter of another individual, and encounter does not affect future encounter. Under this assumption, it is easy to write down the likelihood of the parameters and obtain parameter estimates; however, whether or not it is true depends upon biological and sampling issues. If this assumption is deemed false, the model can be discarded in favor of a more realistic alternative. However, once we have settled on our model, statistical inference proceeds by assuming the model is truth—not an approximation to truth—but actual truth.

p0060 In spite of the fact that we assume that all models are truth, but we acknowledge that all models are wrong due to their assumptions, assumptions should not be viewed as a necessary evil. In fact, one way to view assumptions is as embodiments of our ecological hypotheses. If we make these assumptions too complex or too specific, then we will never be able to study general phenomena that hold true across space and time. Furthermore, in practice, we will rarely have enough data to estimate the parameters of highly complex models.

s0015 4.1.2 Conditional likelihood

p0065 We saw that the closed population model is a simple logistic regression model if N is known and, when N is unknown, the model is multinomial with index or sample size parameter N . This multinomial model, being conditional on N , is sometimes referred to as the “joint likelihood” the “full likelihood,” or the “unconditional likelihood” (~~sometimes “model” in place of “likelihood”~~) (Sanathanan, 1972; Borchers et al., 2002). This formulation differs from the so-called “conditional likelihood” approach in which the likelihood of the observed encounter histories is devised conditional on the event that an individual is captured at least once. To construct this likelihood, we have to recognize that individuals appear or not in the sample based on the value of the random variable y_i , that is, if and only if $y_i > 0$. The observation model is therefore based on $\Pr(y_i > 0)$. For the simple case of model M_0 , the resulting conditional distribution is a “zero truncated” binomial distribution which accounts for the fact that we cannot observe the value $y = 0$ in the data set. Both the conditional and unconditional models are legitimate modes of analysis in all capture-recapture types of studies. They provide equally valid descriptions of the data and, for many practical purposes provide equivalent inferences, at least in large sample sizes (Sanathanan, 1972).

p0070 In this book we emphasize Bayesian analysis of capture-recapture models using data augmentation (described in Section 4.2 below), which produces yet a third distinct formulation of capture-recapture models based on the *zero-inflated* binomial distribution that we describe in the next section. Thus, there are three distinct formulations of the model—or modes of analysis—for analyzing all capture-recapture models based on the (1) binomial model for the joint or unconditional specification; (2) zero-truncated binomial that arises “conditional on n ”; and (3) the zero-inflated

Table 4.3 Modes of analysis of capture-recapture models. Closed population models can be analyzed using the joint or “full likelihood” which contains N as an explicit parameter, the conditional likelihood which does not involve N , or by data augmentation which replaces N with ψ . Each approach yields a distinct likelihood.

sp060

| Mode of analysis | Parameters in model | Statistical model |
|------------------------|---------------------|----------------------------|
| Joint likelihood | p, N | multinomial with index N |
| Conditional likelihood | p | zero-truncated binomial |
| Data augmentation | p, ψ | zero-inflated binomial |

binomial that arises under data augmentation. Each formulation has distinct model parameters (shown in Table 4.3 for model M_0).

4.2 Data augmentation

s0020

We consider a method of analyzing closed population models using parameter-expanded data augmentation (PX-DA), which we abbreviate to “data augmentation” or DA, which is useful for Bayesian analysis and, in particular, analysis of models using the various **BUGS** engines and other Bayesian model fitting software. Data augmentation is a general statistical concept that is widely used in statistics in many different settings. The classical reference is [Tanner and Wong \(1987\)](#), but see also [Liu and Wu \(1999\)](#). Data augmentation can be adapted to provide a very generic framework for Bayesian analysis of capture-recapture models with unknown N . This idea was introduced for closed populations by [Royle et al. \(2007\)](#), and has subsequently been applied to a number of different contexts including individual covariate models ([Royle, 2009b](#)), open population models ([Royle and Dorazio, 2008, 2012](#); [Gardner et al., 2010a](#)), spatial capture-recapture models ([Royle and Young, 2008](#); [Royle et al., 2009a](#); [Gardner et al., 2009](#)), and many others. [Kéry and Schaub \(2012, Chapters 6 and 10\)](#) provide a good introduction to data augmentation in the context of closed and open population models.

p0075

Conceptually, the technique of data augmentation represents a reparameterization of the “complete data” model—i.e., that conditional on N . The reparameterization is achieved by embedding this data set into a larger data set having $M > N$ “rows” (individuals) and re-expressing the model conditional on M instead of N . The great thing about data augmentation is that we do not need to know N for this reparameterization. Although this has a whiff of arbitrariness or even outright ad hocery to it, in the choice of M , it is always possible, in practice, to choose M pretty easily for a given problem and context and results will be insensitive to choice of M .² Then, under data augmentation, analysis is focused on the “augmented data set.” That is, we

p0080

²Unless the data set is sufficiently small that parameters are weakly identified.

np010

analyze the bigger data set—the one having M rows—with an appropriate model that accounts for the augmentation. This is achieved by a Bernoulli sampling process that determines whether an individual in M is also a member of N . Inference is focused ~~directly~~ on estimating the proportion $\psi = E[N]/M$, ~~instead of directly on N~~ , where ψ is the “data augmentation parameter.”

s0025 **4.2.1 DA links occupancy models and closed population models**

p0085 There is a close correspondence between so-called “occupancy” models and closed population models (see Royle and Dorazio, 2008, Section 5.6). In occupancy models (MacKenzie et al., 2002; Tyre et al., 2003) the sampling situation is that M sites, or patches, are sampled multiple times to assess whether a species occurs at the sites. This yields encounter data such as that illustrated in the left panel of Table 4.4. The important problem is that a species may occur at a site, but go undetected, yielding an all-zero encounter history for the site, which in the case of occupancy studies, are *observed*.

sp065 **Table 4.4** Hypothetical occupancy data set (left), capture-recapture data in standard form (center), and capture-recapture data augmented with all-zero capture histories (right).

| Occupancy data | | | | Capture-recapture | | | | Augmented C-R | | | |
|----------------|-------|-------|-------|-------------------|-------|-------|-------|---------------|-------|-------|-------|
| site | k = 1 | k = 2 | k = 3 | ind | k = 1 | k = 2 | k = 3 | ind | k = 1 | k = 2 | k = 3 |
| 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 2 | 1 | 0 | 1 | 2 | 1 | 0 | 1 | 2 | 1 | 0 | 1 |
| 3 | 0 | 1 | 0 | 3 | 0 | 1 | 0 | 3 | 1 | 0 | 1 |
| 4 | 1 | 0 | 1 | 4 | 1 | 0 | 1 | 4 | 1 | 0 | 1 |
| 5 | 0 | 1 | 1 | 5 | 0 | 1 | 1 | 5 | 1 | 0 | 1 |
| . | 0 | 1 | 1 | . | 0 | 1 | 1 | . | 0 | 1 | 1 |
| . | 1 | 1 | 1 | . | 1 | 1 | 1 | . | 0 | 1 | 1 |
| . | 1 | 1 | 1 | . | 1 | 1 | 1 | . | 1 | 1 | 1 |
| . | 1 | 1 | 1 | . | 1 | 1 | 1 | . | 1 | 1 | 1 |
| n | 1 | 1 | 1 | n | 1 | 1 | 1 | n | 1 | 1 | 1 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| . | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| M | 0 | 0 | 0 | . | | | | . | 0 | 0 | 0 |
| | | | | | | | | . | . | . | . |
| | | | | | | | | . | . | . | . |
| | | | | | | | | . | . | . | . |
| | | | | | | | | M | 0 | 0 | 0 |

However, some of the zero vectors will typically correspond to sites where the species in fact *does* occur. Thus, while the zeros are observed, there are too many of them and, in a sense, the inference problem is to partition the zeros into “structural” (fixed) and “sampling” (or stochastic) zeros, where the former are associated with unoccupied sites and the latter with occupied sites where the species went undetected. More formally, inference is focused on the parameter ψ , the probability that a site is occupied.

In contrast to occupancy studies, in classical closed population studies, we observe a data set as in the middle panel of Table 4.4 where *no* zeros are observed. The inference problem is, essentially, to estimate how many sampling zeros there are—or should be—in a “complete” data set. This objective (how many sampling zeros?) is precisely the same for both types of problems if an upper limit M is specified for the closed population model. The only distinction being that, in occupancy models, M is set by design (i.e., the number of sites in the sample), whereas a natural choice of M for capture-recapture models may not be obvious. However, the choice of M induces a uniform prior for N on the integers $[0, M]$ (Royle et al., 2007). Then, one can analyze capture-recapture models by adding $M - n$ all-zero encounter histories to the data set and regarding the augmented data set, essentially, as a site-occupancy data set, where the occupancy or data augmentation parameter (ψ) takes the place of the abundance parameter (N). p0090

Thus, the heuristic motivation of data augmentation is to fix the size of the data set by adding *too many* all-zero encounter histories to create the data set shown in the right panel of Table 4.4, and then analyze the augmented data set using an occupancy-type model which includes both “unoccupied sites” (in capture-recapture, augmented individuals that are not members of the real population that was sampled) as well as “occupied sites” (in capture-recapture, individuals that are members of the population but that were undetected by sampling) ~~at which detections did not occur~~. We call these $M - n$ all-zero histories “potential individuals” because they exist to be recruited (in a non-biological sense) into the population, for example during an analysis by MCMC. p0095

To analyze the augmented data set, we recognize that it is a zero-inflated version of the known- N data set. That is, some of the augmented all-zero rows are sampling zeros (corresponding to actual individuals that were missed) and some are “structural” zeros, which do not correspond to individuals in the population. For a basic closed population model, the resulting likelihood under data augmentation—that is, for the data set of size M —is a simple zero-inflated binomial likelihood. The zero-inflated binomial model can be described “hierarchically,” by introducing a set of binary latent variables, z_1, z_2, \dots, z_M , to indicate whether each individual i is ($z_i = 1$) or is not ($z_i = 0$) a member of the population of N individuals exposed to sampling. We assume that $z_i \sim \text{Bernoulli}(\psi)$ where ψ is the probability that an individual in the data set of size M is a member of the sampled population—in the sense that $1 - \psi$ is the probability of a “structural zero” in the augmented data set. The zero-inflated binomial model which arises under data augmentation can be formally expressed by the following set of assumptions (we include typical priors for a Bayesian analysis): p0100

$$y_i | z_i = 1 \sim \text{Binomial}(K, p)$$

$$\begin{aligned} y_i | z_i = 0 &\sim I(y = 0) \\ z_i &\stackrel{iid}{\sim} \text{Bernoulli}(\psi) \\ \psi &\sim \text{Uniform}(0, 1) \\ p &\sim \text{Uniform}(0, 1) \end{aligned}$$

for $i = 1, \dots, M$, where $I(y = 0)$ is a point mass at $y = 0$. It is sometimes convenient to express the conditional-on- z observation model concisely in just one step:

$$y_i | z_i \sim \text{Binomial}(K, z_i p)$$

and we understand this to mean, if $z_i = 0$, then y_i is necessarily 0 because its success probability is $z_i p = 0$.

p0105 Note that, under data augmentation, N is no longer an explicit parameter of this model. In its place, we estimate ψ and functions of the latent variables z . In particular, under the assumptions of the zero-inflated model, $z_i \stackrel{iid}{\sim} \text{Bernoulli}(\psi)$; therefore, N is a function of these latent variables:

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

Further, we note that the latent z_i parameters *can be* removed from the model by integration, in which case the joint probability of the data is

$$\Pr(y_1, \dots, y_M | p, \psi) = \prod_{i=1}^M (\psi * \text{Binomial}(y_i | K, p) + I(y_i = 0)(1 - \psi)) \quad (4.2.1)$$

Interpreted as a likelihood, we can directly maximize this expression to obtain the MLEs of the structural parameters ψ and p or those of other more complex models (e.g., see Royle, 2006). We could estimate these parameters and then use them to obtain an estimator of N using the so-called “Best unbiased predictor” (see Royle and Dorazio, 2012). Normally, however, we will analyze the model in its “conditional-on- z ” form using methods of MCMC either in the BUGS engines or using our own MCMC algorithms (see Chapter 17).

s0030 4.2.2 Model M_0 in BUGS

p0110 It is helpful to understand data augmentation by seeing what its effect is on implementing model M_0 . For this model, in which we can aggregate the encounter data to individual-specific encounter frequencies, the augmented data are given by the vector of frequencies $(y_1, \dots, y_n, 0, 0, \dots, 0)$ where the augmented values of $y = 0$ represent the encounter frequency for potential individuals y_{n+1}, \dots, y_M . The zero-inflated model of the augmented data combines the model of the latent variables, $z_i \sim \text{Bernoulli}(\psi)$. The BUGS model description of the closed population model M_0 is shown in Panel 4.1. The last line of the model specification provides the expression

```
model{
  p ~ dunif(0,1)
  psi ~ dunif(0,1)

  # nind = number of individuals captured at least once
  # nz = number of uncaptured individuals added for DA
  for(i in 1:(nind+nz)){
    z[i] ~ dbern(psi)
    mu[i] <- z[i]*p
    y[i] ~ dbin(mu[i],K)
  }

  N<-sum(z[1:(nind+nz)])
}
```

PANEL 4.1

Model M_0 under data augmentation. Here y , K , $nind$, and nz are provided as data. The population size, N , is computed as a function of the data augmentation variables z .

for computing N from the data augmentation variables z_i . Note that, to improve readability of code snippets (especially of large ones), we will sometimes deviate from our standard notation a bit. In this case we use $nind$ for n (the number of encountered individuals), and $M = nind + nz$ is the total size of the augmented data set. In other cases we might also use $nocc$ in place of K and $ntraps$ in place of J . We find that word definitions make code easier to understand, especially without having to read surrounding text.

Specification of a more general model in terms of the individual encounter observations y_{ik} is not much more difficult than for the individual encounter frequencies. We define the observation model by a double loop and change the indexing of quantities accordingly, i.e.,

```
for(i in 1: (nind+nz)){
  z[i] ~ dbern(psi)
  for(k in 1:K){
    mu[i,k] <- z[i]*p
    y[i,k] ~ dbin(mu[i,k],1)
  }
}
```

In this manner, it is straightforward to incorporate covariates on p for both individuals and sampling occasions (see discussion of this below and Chapter 7) as well as to devise other extensions of the model, including models for open populations (see Chapter 16).

s0035 4.2.3 Formal development of data augmentation (DA)

p0125 Use of parameter-expanded data augmentation (PX-DA), or DA for short, for solving inference problems with unknown N can be justified as originating from the choice of a uniform prior on N . The Uniform(0, M) prior for N is innocuous in the sense that the posterior associated with this prior is equal to the likelihood for sufficiently large M . One way of inducing the Uniform(0, M) prior on N is by assuming the following hierarchical prior:

$$\begin{aligned} N &\sim \text{Binomial}(M, \psi) \\ \psi &\sim \text{Uniform}(0, 1). \end{aligned} \quad (4.2.2)$$

The model assumptions, specifically the multinomial model (Eq. (4.1.3)) and Eq. (4.2.2), may be combined to yield a reparameterization of the conventional model that is appropriate for the augmented data set of known size M :

$$(n_1, n_2, \dots, n_K) \sim \text{Multinomial}(M, \psi\pi_1, \psi\pi_2, \dots, \psi\pi_K) \quad (4.2.3)$$

This expression arises by removing N from Eq. (4.1.3) by integrating over the binomial prior distribution for N . Thus, the models we analyze under data augmentation arise formally by removing the parameter N from the ordinary closed population model, which is conditional on N , by integrating over a binomial prior distribution for N .

p0130 Note that the $M - n$ unobserved individuals in the augmented data set have probability $\psi\pi(0) + (1 - \psi)$, indicating that these unobserved individuals are a mixture of individuals that are sampling zeros ($\psi\pi_0$), and belong to the population of size N , and others that are “structural zeros” (occurring in the augmented data set with probability $1 - \psi$). In Eq. (4.2.3), N has been eliminated as a formal parameter of the model by marginalization (integration) and replaced with the new parameter ψ , the data augmentation parameter. However, the full likelihood containing both N and ψ can also be analyzed (see Royle et al., 2007).

s0040 4.2.4 Remarks on data augmentation

p0135 Data augmentation may seem like a strange and mysterious black-box, and likely it is unfamiliar to most people, even to many of those with substantial experience with capture-recapture models. However, it really is just a formal reparameterization of capture-recapture models in which N is marginalized out of the ordinary (conditional-on- N) model (by summation over a binomial prior). As a result, we could refer to the resulting model as the “binomial-integrated likelihood” to reflect that an estimator could be obtained from the ordinary likelihood, integrated over a binomial prior. Other such “integrated likelihood” models are sensible. For example, we could place a Poisson prior on N with mean Λ and marginalize N over the Poisson prior. This produces a likelihood in which Λ replaces N , instead of ψ replacing N . We note that this type of marginalization (over a Poisson prior) is done by the **R** package `secr` for analysis of spatial capture-recapture models (see Section 6.5.3).

We emphasize the motivation for data augmentation being that it produces a data set of fixed size, so that the parameter dimension in any capture-recapture model is also fixed. As a result, MCMC is a relatively simple proposition using standard Gibbs sampling. And, in particular, capture-recapture models become trivial to implement in BUGS. Consider the simplest context—analyzing model M_0 ~~using the occupancy-type model~~. In this case, DA converts model M_0 to a basic occupancy model, and the parameters p and ψ have known full conditional distributions (in fact, beta distributions) that can be sampled from directly. Furthermore, the data augmentation variables, i.e., the collection of z 's, can be sampled from Bernoulli full conditionals. MCMC is not much more difficult for complicated models—sometimes the hyperparameters need to be sampled using a Metropolis-Hastings step (e.g., Chapter 17), but nothing more sophisticated than that is required. p0140

Potential sensitivity of parameter estimates to M (especially of N) might be cause for some concern. The guiding principle is that it should be chosen large enough so that the posterior for N is not truncated, but it should not be too large due to the increased computational burden. It seems likely that the properties of the Markov chains should be affected by M and so some optimal choice of M might exist (Gopalaswamy, 2012). Formal analysis of this is needed. p0145

There are other approaches to analyzing models with unknown N , using reversible jump MCMC (RJMCMC) or other so-called “trans-dimensional” (TD) algorithms (King and Brooks, 2001; Durban and Elston, 2005; King et al., 2008; Schofield and Barker, 2008; Wright et al., 2009). What distinguishes DA from RJMCMC and related TD methods is that DA is used to create a distinctly new model that is unconditional on N and we (usually) analyze the unconditional model. The various TD/RJMCMC approaches seek to analyze the conditional-on- N model in which the dimension of the parameter space is a function of N , and will therefore typically vary at each iteration of the MCMC algorithm. TD/RJMCMC approaches might appear to have the advantage that one can model N explicitly or consider alternative priors for N . However, despite that N is removed as an explicit parameter in DA, it is possible to develop hierarchical models that involve structure on N (Converse and Royle, 2012; Royle et al., 2012c; Royle and Converse, in review) which we consider in Chapter 14. Furthermore, data augmentation is often easier to implement than RJMCMC, and the details of the DA implementation are the same for all capture-recapture problems. p0150

4.2.5 Example: Black bear study on Fort Drum

To illustrate the analysis of model M_0 using data augmentation, we use a data set collected at Fort Drum Military Installation in upstate New York by P.D. Curtis and M.T. Wegan of Cornell University and their colleagues at the Fort Drum Military Installation. These data have been analyzed in various forms by Wegan (2008); Gardner et al. (2009) and Gardner et al. (2010b). The specific data used here are encounter histories on 47 individuals obtained from an array of 38 baited “hair snares” (Figure 4.1) during June and July 2006. Barbed wire traps were baited and checked for hair samples each week for 8 weeks, thus we distinguished $K = 8$ weekly sample intervals. s0045 p0155

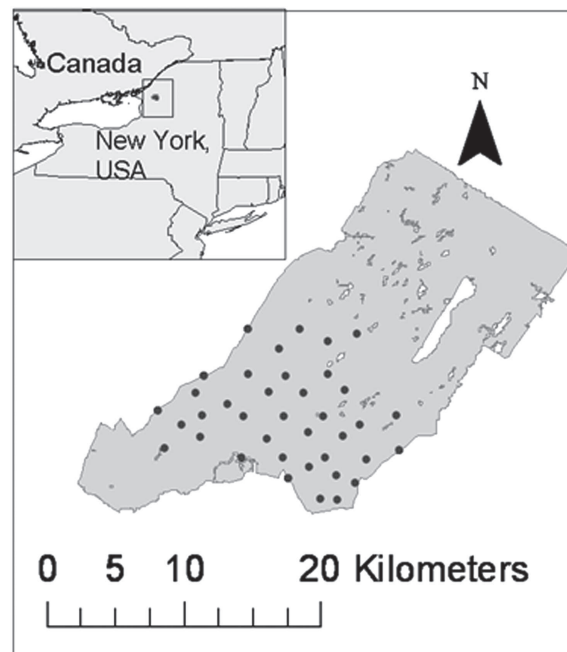


FIGURE 4.1

Fort Drum Black bear study area and the 38 baited hair snare locations operated for 8 weeks during June and July, 2006.

The data are provided in the **R** package `scrbook`, can be loaded by typing `data(beardata)` at the **R** prompt, and the analysis can be set up and run as follows (see `?beardata` for the commands to do the analysis). Here, the data were augmented with 128 all-zero encounter histories, resulting in a total sample size of $M = 175$.

```
o0055 > library(scrbook)
o0060 > data(beardata)           # load the bear data and extract components
o0065 > trapmat <- beardata$trapmat
o0070 > nind <- dim(beardata$bearArray)[1]
o0075 > K <- dim(beardata$bearArray)[3]
o0080 > ntraps <- dim(beardata$bearArray)[2]
o0085 > M <- 175
o0090 > nz <- M-nind
o0095 > Yaug <- array(0, dim = c(M,ntraps,K))

o0100 > Yaug[1:nind,,] <- beardata$bearArray
o0105 > y <- apply(Yaug,c(1,3),sum) # summarize by ind x rep
o0110 > y[y > 1] <- 1              # toss out multiple encounters per occasion
o0115                                # b/c traditional CR models ignore space
```

p0160 The raw data object, `beardata$bearArray`, is a three-dimensional array $nind \times ntraps \times K$ of individual encounter events (i.e., $y_{ijk} = 1$ if individual i was

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encountered in trap j during occasion k , and 0 otherwise). For fitting model M_0 (or M_h , see below), it is sufficient to reduce the data to individual encounter frequencies which we have re-labeled “ y ” above. The BUGS model file along with commands to fit the model are as follows:

```
> set.seed(2013) # to obtain the same results each time o0120
> library(R2WinBUGS) # load R2WinBUGS, set-up: o0125
> data0 <- list(y = y, M = M, K = K) # data ... o0130
> params0 <- c('psi','p','N') # parameters ... o0135
> zst <- c(rep(1,nind),rbinom(M-nind, 1, .5)) # inits ..... o0140
> inits <- function(){ list(z = zst, psi = runif(1), p = runif(1)) } o0145

> cat(" o0150
model{ o0155

psi ~ dunif(0, 1) o0160
p ~ dunif(0,1) o0165

for (i in 1:M){ o0170
  z[i] ~ dbern(psi) o0175
  for(k in 1:K){ o0180
    tmp[i,k] <- p*z[i] o0185
    y[i,k] ~ dbin(tmp[i,k],1) o0190
  } o0195
} o0200
N<-sum(z[1:M]) o0205
} o0210
",file="modelM0.txt") o0215

## Run the model: o0220
> fit0 <- bugs(data0, inits, params0, model.file="modelM0.txt",n.chains = 3, o0225
n.iter = 2000, n.burnin = 1000, n.thin = 1,debug = TRUE,working.directory = getwd()) o0230
```

This produces the following posterior summary statistics: p0165

```
> print(fit0,digits = 2) o0235
Inference for Bugs model at "modelM0.txt", fit using WinBUGS, o0240
3 chains, each with 2000 iterations(first 1000 discarded) o0245
n.sims = 3000 iterations saved o0250
```

| | mean | sd | 2.5% | 25% | 50% | 75% | 97.75% | Rhat | n.eff |
|----------|--------|-------|--------|--------|--------|--------|--------|------|-------|
| psi | 0.29 | 0.04 | 0.22 | 0.26 | 0.29 | 0.31 | 0.36 | 1 | 3000 |
| p | 0.30 | 0.03 | 0.25 | 0.28 | 0.30 | 0.32 | 0.35 | 1 | 3000 |
| N | 49.94 | 1.99 | 47.00 | 48.00 | 50.00 | 51.00 | 54.00 | 1 | 3000 |
| deviance | 489.05 | 11.28 | 471.00 | 480.45 | 488.80 | 495.40 | 513.70 | 1 | 3000 |

[... some output deleted ...]

WinBUGS did well in choosing an MCMC algorithm for this model—we have p0170
 $\hat{R} = 1$ for each parameter, and an effective sample size of 3000, equal to the total
number of posterior samples.³ We see that the posterior mean of N under this model is
49.94 and a 95% posterior interval is 48, 54. We revisit these data later in the context
of more complex models.

³This is even a little suspicious.... np015

p0175 In order to obtain an estimate of density, D , we need an area to associate with the estimate of N , and in Chapter 1 we already went through a number of commonly used procedures to conjure up such an area, including buffering the trap array by the home range radius, often estimated by the mean maximum distance moved (MMDM) (Parmenter et al., 2003), 1/2 MMDM (Dice, 1938) or directly from telemetry data (Wallace et al., 2003). Typically, the trap array is defined by the convex hull around the trap locations, and this is what we applied a buffer to. We computed the buffer by using a telemetry-based estimate of the mean female home range radius (2.19 km) (Bales et al., 2005) instead of using an estimate based on our relatively ~~more~~ sparse recapture data. For the Fort Drum study, the convex hull has an area of 157.135 km², and the buffered convex hull has an area of 277.011 km². To create this we used functions contained in the **R** package `rgeos` and created a utility function `bcharea` which is in our **R** package `scrbook`. The commands are as follows:

```
o0255 > library(rgeos)
o0260 > bcharea <- function(buff,traplocs){
o0265   p1 <- Polygon(rbind(traplocs,traplocs[1,]))
o0270   p2 <- Polygons(list(p1 = p1),ID = 1)
o0275   p3 <- SpatialPolygons(list(p2 = p2))
o0280   plch <- gConvexHull(p3)
o0285   bp1 <- (gBuffer(plch, width = buff))
o0290   plot(bp1, col='gray')
o0295   plot(plch, border='black', lwd = 2, add = TRUE)
o0300   gArea(bp1)
o0305 }
o0310 > bcharea(2.19,traplocs = trapmat)
```

The resulting buffered convex hull is shown in Figure 4.2.

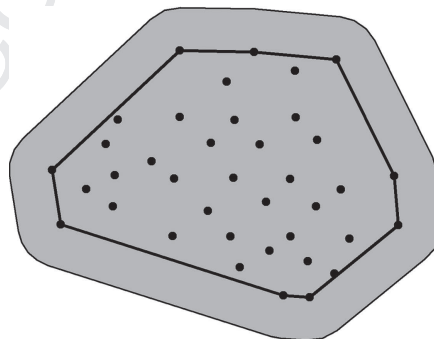


FIGURE 4.2

Convex hull of the bear hair snare array at Fort Drum, NY, buffered by mean female home range radius (2.19 km).

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To conjure up a density estimate under model M_0 , we compute the appropriate posterior summary of the ratio of N and the prescribed area (277.011 km²):

```
> summary(fit0$sims.list$N/277.011)
      Min.   1st Qu.   Median     Mean   3rd Qu.    Max.
0.1697   0.1733   0.1805   0.1803   0.1841   0.2130

> quantile (fit0$sims.list$N/277.011,c (0.025,0.975))
      2.5%      97.5%
0.1696684  0.1949381
```

which yields a density estimate of about 0.18 ind/km², and a 95% Bayesian confidence interval of (0.170, 0.195). Our estimate of density should be reliable if we have faith in our stated value of the “sampled area.” Clearly though this is largely subjective, and not something we can formally evaluate (or estimate) from the data based on model M_0 .

4.3 Temporally varying and behavioral effects

The purpose of this chapter is mainly to emphasize the central importance of the binomial model in capture-recapture and so we have considered models for individual encounter frequencies—the number of times individuals are captured out of K occasions. Sometimes we can’t aggregate the encounter data for each individual, such as when encounter probability varies over time among samples. Time-varying responses that are relevant in many capture-recapture studies are “effort” such as amount of search time, number of observers, or trap nights, or encounter probability varying over time, as a function of date or season (Kéry et al., 2010) due to species behavior. A common situation in many animal studies is that in which there exists a “behavioral response” to trapping (even if the animal is not physically trapped).

Behavioral response is an important concept in animal studies because individuals might learn to come to baited traps or avoid traps due to trauma related to being encountered. There are a number of ways to parameterize a behavioral response to encounter. The distinction between persistent and ephemeral was made by Yang and Chao (2005) who considered a general behavioral response model of the form:

$$\text{logit}(p_{ik}) = \alpha_0 + \alpha_1 y_{i,k-1} + \alpha_2 x_{ik}$$

where x_{ik} is a covariate indicator variable of previous capture (i.e., $x_{ik} = 1$ if captured in any previous period). Therefore, encounter probability changes depending on whether an individual was captured in the immediate previous period (a Markovian or ephemeral behavioral response; (Yang and Chao, 2005)), described by the term $\alpha_1 y_{i,k-1}$ or in any previous period (persistent behavioral response), described by the term $\alpha_2 x_{ik}$. Because spatial capture-recapture models allow us to include trap-specific

covariates, we can describe a third type of behavioral response—a local behavioral response that is trap-specific (Royle et al., 2011b). In this local behavioral response, the encounter probability is modified for an individual trap depending on previous capture in that trap. Models with temporal effects are easy to describe and analyze in the BUGS language and we provide a number of examples in Chapter 7 and elsewhere.

4.4 Models with individual heterogeneity

s0055

p0195

Models in which encounter probability varies by individual have a long history in capture-recapture and, indeed, this so-called “model M_h ” is one of the elemental capture-recapture models in (Otis et al., 1978). Conceptually, we imagine that the individual-specific encounter probability parameters, p_i , are random variables distributed according to some probability distribution, $[\theta]$. We denote this basic model assumption as $p_i \sim [\theta]$. This type of model is similar in concept to extending a GLM to a GLMM but in the capture-recapture context N is unknown. The basic class of models is often referred to as “model M_h ” (“h” for heterogeneity), but really this is a broad class of models, each being distinguished by the specific distribution assumed for p_i . There are many different varieties of model M_h including parametric and various non-parametric approaches (Burnham and Overton, 1978; Norris and Pollock, 1996; Pledger, 2004). One important practical matter is that estimates of N can be extremely sensitive to the choice of heterogeneity model (Fienberg et al., 1999; Dorazio and Royle, 2003; Link, 2003). Indeed, Link (2003) showed that in some cases it’s possible to find models that yield precisely the same expected data, yet produce wildly different estimates of N . In that sense, N for most practical purposes is not identifiable across classes of different heterogeneity models, and this should be understood before fitting any such model. One solution to this problem is to seek to model explicit factors that contribute to heterogeneity, e.g., using individual covariate models (See 4.5 below). Indeed, spatial capture-recapture models do just that, by modeling heterogeneity due to the spatial organization of individuals in relation to traps or other encounter mechanism. For additional background and applications of model M_h see Royle and Dorazio (2008, Chapter 6) and Kéry and Schaub (2012, Chapter 6).

p0200

We will work with a specific type of model M_h here, which is a natural extension of the basic binomial observation model of model M_0 so that

$$\text{logit}(p_i) = \mu + \eta_i$$

where μ is a fixed parameter (the mean) to be estimated, and η_i is an individual random effect assumed to be normally distributed:

$$\eta_i \sim \text{Normal}(0, \sigma_p^2)$$

We could as well combine these two steps and write $\text{logit}(p_i) \sim \text{Normal}(\mu, \sigma_p^2)$. This “logit-normal mixture” was analyzed by Coull and Agresti (1999) and elsewhere. It

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is a natural extension of the basic model with constant p , as a **mixed** GLMM, and similar models occur throughout statistics. It is also natural to consider a beta **prior** distribution for p_i (Dorazio and Royle, 2003) and so-called “finite-mixture” models are also popular (Norris and Pollock, 1996; Pledger, 2004). In the latter, individuals are assumed to belong to a finite number of latent classes, each of which has its own capture probability.

Model M_h has important historical relevance to spatial capture-recapture situations (Karanth, 1995) because investigators recognized that the juxtaposition of individuals with the array of trap locations should yield heterogeneity in encounter probability, and thus it became common to use some version of model M_h in spatial trapping arrays to estimate N . While this doesn't resolve the problem of not knowing the effective sample area, it does yield an estimator that accommodates the heterogeneity in p induced by the spatial aspect of capture-recapture studies. To see how this juxtaposition induces heterogeneity, we have to understand the relevance of movement in capture-recapture models. Imagine a quadrat that can be uniformly searched by a crew of biologists for some species of reptile (see Royle and Young, 2008). Figure 4.3 shows a sample quadrat searched repeatedly over a period of time. Further, suppose that the species exhibits some sense of spatial fidelity in the form of a home range or territory, and individuals move about their home range (home range centroids are given by the solid dots) in some kind of random fashion. Heuristically, we imagine that each individual in the vicinity of the study area is liable to experience variable exposure to encounter due to the overlap of its home range with the sampled area—essentially the long-run proportion of times the individual is within the sample plot boundaries, say ϕ . We might model the exposure or *availability* of an individual to capture by supposing

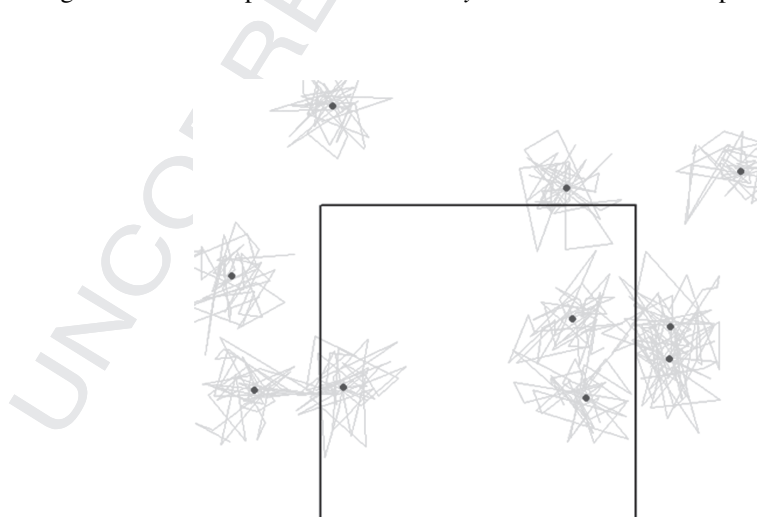


FIGURE 4.3

A quadrat searched for lizards over some period of time (simulated data). The locations of encounter for each of 10 lizards are connected by lines—the dots are activity centers.

that $a_i = 1$ if individual i is available to be captured (i.e., within the survey plot) during any sample, and 0 otherwise. Then, $\Pr(a_i = 1) = \phi$. In the context of spatial studies, it is natural that ϕ should depend on *where* an individual lives, i.e., it should be individual-specific ϕ_i (Chandler et al., 2011). This system describes, precisely, that of “random temporary emigration” (Kendall et al., 1997) where ϕ_i is the individual-specific probability of being “available” for capture.

p0210 Conceptually, SCR models aim to deal with this problem of variable exposure to sampling due to movement in the proximity of the trapping array explicitly and formally with auxiliary spatial information. If individuals are detected with probability p_0 , conditional on $a_i = 1$, then the marginal probability of detecting individual i is

$$p_i = p_0 \phi_i$$

so we see clearly that individual heterogeneity in encounter probability is induced as a result of the juxtaposition of individuals (i.e., their home ranges) with the sample apparatus and the movement of individuals about their home range.

s0060 4.4.1 Analysis of model M_h

p0215 If N is known, it is worth taking note of the essential simplicity of model M_h as a binomial GLMM. This is a type of model that is widely applied throughout statistics using standard methods of inference based either on integrated likelihood (Laird and Ware, 1982; Berger et al., 1999), which we discuss in Chapter 6, or standard Bayesian methods. However, because N is not known, inference is somewhat more challenging. We address that here using Bayesian analysis based on data augmentation. Although we use data augmentation in the context of Bayesian methods here, we note that heterogeneity models formulated under DA are easily analyzed by conventional likelihood methods as zero-inflated binomial mixtures (Royle, 2006) and more traditional analysis of model M_h based on integrated likelihood, without using data augmentation, has been considered by Coull and Agresti (1999), Dorazio and Royle (2003), and others.

p0220 As with model M_0 , we have the Bernoulli model for the zero-inflation variables: $z_i \sim \text{Bernoulli}(\psi)$ and the model of the observations expressed conditional on these latent variables z_i . For $z_i = 1$, we have a binomial model with individual-specific p_i :

$$y_i | z_i = 1 \sim \text{Binomial}(K, p_i)$$

and otherwise $y_i | z_i = 0 \sim I(y = 0)$, i.e., a point mass at $y = 0$. Further, we prescribe a distribution for p_i . Here we assume

$$\text{logit}(p_i) \sim \text{Normal}(\mu, \sigma^2)$$

For prior distributions we assume $p_0 = \text{logit}^{-1}(\mu) \sim \text{Uniform}(0, 1)$ and, for the standard deviation $\sigma \sim \text{Uniform}(0, B)$ for some large B . Another common default prior is to assume $\tau = 1/\sigma^2 \sim \text{Gamma}(.1, .1)$, although we usually choose $\sigma \sim \text{Uniform}(0, B)$.

4.4.2 Analysis of the Fort Drum data with model M_h

s0065

Here we provide an analysis of the Fort Drum bear survey data using the logit-normal heterogeneity model, and we used data augmentation to produce a data set of $M = 700$ individuals. We have so far mostly used **WinBUGS** but we are now transitioning to the use of **JAGS** run from within **R** using the **useful** packages **R2jags** or **rjags**. The function **jags** from the **R2jags** package runs essentially like the **bugs** function which we demonstrate here for setting up and running model M_h for the Fort Drum bear data:

p0225

```
[... get data as before ...]
> set.seed(2013)
> cat("
model{
  p0 ~ dunif(0,1)          # prior distributions
  mup <- log(p0/(1-p0))
  sigmap ~ dunif(0,10)
  taup <- 1/(sigmap*sigmap)
  psi ~ dunif(0,1)

  for(i in 1:(nind + nz)){
    z[i] ~ dbern(psi)      # zero inflation variables
    lp[i] ~ dnorm(mup,taup) # individual effect
    logit(p[i]) <- lp[i]
    mu[i] <- z[i]*p[i]
    y[i] ~ dbin(mu[i],K)   # observation model
  }

  N<-sum(z[1:(nind + nz)])

  },file="ModelMh.txt")

> datal <- list(y = y, nz = nz, nind = nind, K = K)
> params1 <- c('p0','sigmap','psi','N')
> inits <- function(){ list(z = as.numeric(y>=1), psi=.6, p0 = runif(1),
  sigmap = runif(1,.7,1.2),lp = rnorm(M,-2)) }
> library(R2jags)
> wabout <- jags(datal, inits, params1, model.file = "modelMh.txt", n.chains = 3,
  n.iter = 1010000, n.burnin = 10000, working.directory = getwd())
```

o0325

o0330

o0335

o0340

o0345

o0350

o0355

o0360

o0365

o0370

o0375

o0380

o0385

o0390

o0395

o0400

o0405

o0410

o0415

o0420

o0425

o0430

o0435

o0440

o0445

o0450

We provide an **R** function **modelMhBUGS** in the package **scrbook** which will fit the model using either **JAGS** or **WinBUGS** as specified by the user. In addition, for fun, we construct our own MCMC algorithm using a Metropolis-within-Gibbs algorithm for model M_h in Chapter 17, where we also develop MCMC algorithms for spatial capture-recapture models. Using **modelMhBUGS**, we ran 3 chains of 1 million iterations (mixing is poor for this model and this data set), which produced the posterior distribution for N shown in Figure 4.4. Posterior summaries of parameters are given in Table 4.5.

p0230

We used $M = 700$ for this analysis and we note that while the posterior mass of N is concentrated away from this upper bound (Figure 4.4), the posterior has an extremely long right tail, with some MCMC draws at the upper boundary $N = 700$,

p0235

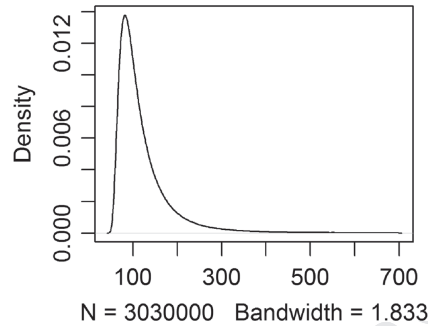


FIGURE 4.4 Posterior of N for Fort Drum bear study data under the logit-normal version of model M_h .

sp070

| Table 4.5 Posterior summaries from model M_h fitted to the Fort Drum black bear data. Results were obtained using WinBUGS running 3 chains, each with 1010000 iterations, discarding the first 10000 for a total of three <i>million</i> posterior samples. | | | | | | | |
|--|---------|--------|--------|---------|---------|-------|-------|
| Parameter | Mean | SD | 2.5% | 50% | 97.5% | Rhat | n.eff |
| ρ_0 | 0.072 | 0.056 | 0.002 | 0.060 | 0.203 | 1.008 | 540 |
| σ_p | 2.096 | 0.557 | 1.215 | 2.025 | 3.373 | 1.003 | 820 |
| ψ | 0.176 | 0.101 | 0.084 | 0.147 | 0.458 | 1.006 | 650 |
| N | 122.695 | 69.897 | 62.000 | 102.000 | 319.000 | 1.006 | 630 |

suggesting that an even higher value of M may be called for. To characterize the posterior distribution of density we produce the relevant summaries of the posterior distribution of $D = N/277.11$ (recall the buffered area of the convex hull is 277.11 km²):

```
o0455 > summary(wbout$sims.list$N/277.11)

      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
0.1696   0.2959   0.3681   0.4428   0.4944   2.5260

o0460 > quantile(wbout$sims.list$N/277.11,c(0.025,0.50,0.975))

      2.5%      50%      97.5%
0.2237379 0.3680849 1.1511674
```

Therefore, the point estimate, characterized by the posterior median, is around 0.37 bears per square km and a 95% Bayesian credible interval is (0.224, 1.151).

4.4.3 Comparison with MLE

s0070

The posterior of N is highly skewed; therefore, we see that the posterior mean ($N = 122.7$) is considerably higher than the posterior median ($N = 102$). Further, it may be surprising that these posterior summaries do not compare well with the MLE. We used the **R** code contained in Panel 6.1 from Royle and Dorazio (2008) to obtain the MLE of $\log(n_0)$, the logarithm of the number of uncaptured individuals, is $\log(n_0) = 3.86$ and therefore $\hat{N} = \exp(3.86) + 47 = 94.47$, which is larger than the mode shown in Figure 4.4. To see this, we compute the posterior mode, by finding the posterior value of N with the highest mass. Because N is discrete, we can use the `table()` function in **R** and find the most frequent value.⁴ If we want to smooth out some of the Monte Carlo errors a bit, we can use a smoother of some sort applied to the tabled posterior frequencies of N . Here we use a smoothing spline (**R** function `smooth.spline`) with the degree of smoothing chosen by cross-validation (the `cv = TRUE` argument):

```
> N <- table(jout$BUGSoutput$sims.list$N)
> xg <- as.numeric(names(N))

> sp <- smooth.spline (xg,N,cv = TRUE)

> sp

Call:
smooth.spline (x = xg, y = N, cv = TRUE)

Smoothing Parameter spar = 0.09339815 lambda = 8.201724e-09 (17 iterations)
Equivalent Degrees of Freedom (Df): 121.1825
Penalized Criterion: 2544481
PRESS: 5903.4
```

We obtain the mode of the smoothed frequencies as follows:

```
sp$x[sp$y==max(sp$y)]
[1] 82
```

We don't dwell too much on the difference between the MLE and features of the posterior, but we do note here that the posterior distribution for the parameters of this model, for the Fort Drum data set, is very sensitive to the prior distributions. In the present case, the use of a Uniform(0, 1) prior for $p_0 = \text{logit}^{-1}(\mu)$ is somewhat informative—in particular, it is not at all “flat” on the scale of μ , and this affects the posterior. We generally always recommend use of a Uniform(0, 1) prior for $\text{logit}^{-1}(\mu)$ in such models. That said, we were surprised at this result, and we experimented with other prior configurations including putting a flat prior on μ directly. This kind of small sample instability has been widely noted in model M_h (Fienberg et al., 1999; Dorazio and Royle, 2003), as has extreme sensitivity to the specific form of model M_h (Link, 2003). In summary, while the mode is well defined, the data set is relatively sparse and hence inferences are poor and sensitive to model choice.

⁴For a continuous random variable we can use the `functiondensity()` to smooth the posterior samples and obtain the mode.

s0075 4.5 Individual covariate models: toward spatial capture-recapture

p0255 A standard situation in capture-recapture models is when a covariate which is thought to influence encounter probability is measured for each individual. These are often called “individual covariate models” but, in keeping with the classical nomenclature on closed population models, [Kéry and Schaub \(2012\)](#) referred to this class of models as “model M_x ” (the x here being an explicit covariate). As with other closed population models, we begin with the basic binomial observation model:

$$y_i \sim \text{Binomial}(K, p_i).$$

To model the covariate, we use a logit model for encounter probability of the form:

$$\text{logit}(p_i) = \alpha_0 + \alpha_1 x_i \quad (4.5.1)$$

where x_i is the covariate value for individual i and the parameters $\alpha = (\alpha_0, \alpha_1)$ are the regression coefficients. Classical examples of covariates influencing detection probability are type of animal (juvenile/adult or male/female), a continuous covariate such as body mass, or a discrete covariate such as group or cluster size. For example, in models of aerial survey data, it is natural to model the detection probability of a group as a function of the observation-level individual covariate, “group size” ([Royle, 2008](#); [Langtimm et al., 2011](#)).

p0260 Model M_x is similar in structure to model M_h , except that the individual effects are *observed* for the n individuals that appear in the sample. These models are important here because spatial capture-recapture models can be described precisely as a form of model M_x , where the covariate describes *where* the individual is located in relation to the trapping array. Specifically, SCR models *are* individual covariate models, but where the individual covariate is only observed imperfectly (or partially observed) for each captured individual. Unlike model M_h , in SCR models (and model M_x) we do have some direct information about the latent variable, which comes from the spatial locations/distribution of individual recaptures.

p0265 Traditionally, estimation of N in model M_x is achieved using methods based on ideas of unequal probability sampling (i.e., Horvitz-Thompson estimation⁵; [Huggins \(1989\)](#), [Alho \(1990\)](#), and [Borchers et al. \(2002\)](#)). An estimator of N is

$$\hat{N} = \sum_{i=1}^n \frac{1}{\tilde{p}_i}$$

where \tilde{p}_i is the probability that individual i appeared in the sample. This quantity is $\tilde{p}_i = \Pr(y_i > 0)$ and, in closed population capture-recapture models, it can be computed as:

$$\Pr(y_i > 0) = 1 - (1 - p_i)^K$$

where p_i is a function of parameters α_0 and α_1 according to Eq. (4.5.1). In practice, parameters are estimated from the conditional likelihood of the observed encounter

np025 ⁵For a quick summary of the idea see: http://en.wikipedia.org/wiki/Horvitz-Thompson_estimator.

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histories which is, for observation y_i ,

$$\mathcal{L}_c(\boldsymbol{\alpha}|y_i) = \frac{\text{Binomial}(y_i|\boldsymbol{\alpha})}{\tilde{p}_i}. \quad (4.5.2)$$

This derives from a straightforward application of the law of total probability. Conceptually, we partition $\Pr(y)$ according to $\Pr(y) = \Pr(y|y > 0) \Pr(y > 0) + \Pr(y|y = 0) \Pr(y = 0)$. For any positive value of y the second term is necessarily 0, and so we rearrange to obtain $\Pr(y|y > 0) = \Pr(y) / \Pr(y > 0)$ which, in the specific case where $\Pr(y)$ is the binomial probability mass function (pmf), produces Eq. (4.5.2).

Here we take a formal model-based approach to Bayesian analysis of such models based on the joint likelihood using data augmentation (Royle, 2009b). Classical likelihood analysis of the so-called “full likelihood” is covered by Borchers et al. (2002). For Bayesian analysis of model M_x , because the individual covariate is unobserved for the $n_0 = N - n$ uncaptured individuals, we require a model to describe variation in x among individuals, essentially allowing the sample to be extrapolated to the population. For example, if we have a continuous trait measured on each individual, then we might assume that x has a normal distribution:

$$x_i \sim \text{Normal}(\mu, \sigma^2)$$

Data augmentation can be applied directly to this class of models. In particular, reformulation of the model under DA yields a basic zero-inflated binomial model of the following form, for each $i = 1, 2, \dots, M$:

$$\begin{aligned} z_i &\sim \text{Bernoulli}(\psi) \\ y_i|z_i=1 &\sim \text{Binomial}(K, p_i(x_i)) \\ y_i|z_i=0 &\sim I(y=0) \\ x_i &\sim \text{Normal}(\mu, \sigma^2) \end{aligned}$$

~~Fully spatial capture-recapture models use this formulation with a latent covariate that is directly related to the individual detection probability (see next section).~~ As with the previous models, implementation is trivial in the **BUGS** language. The **BUGS** specification is very similar to that for model M_h , but we require the distribution of the covariate to be specified, along with priors for the parameters of that distribution.

4.5.1 Example: location of capture as a covariate

Here we consider a special type of model M_x that is especially relevant to spatial capture-recapture. Intuitively, some measure of distance from home range center to traps for an individual should be a reasonable covariate to explain heterogeneity in encounter probability, i.e., individuals with more exposure to traps should have higher encounter probabilities and vice versa. So we can imagine *estimating* such a quantity, say average distance from home range center to “the trap array”, and then using it as an individual covariate in capture-recapture models. A version of this idea

was put forth by [Boulanger and McLellan \(2001\)](#) (see also [Ivan, 2012](#)), but using the Huggins-Alho estimator and with covariate “distance from home range center to edge” of the trapping array, where the home range center is estimated by the average capture location. This is intuitively appealing because we can imagine, in some kind of an ideal situation where we have a dense grid of traps over some geographic region, that the average location of capture would be a decent estimate (heuristically) of an individual’s home range center. We provide an example of this type of approach using a fully model-based analysis of the version of model M_x described above, analyzed by data augmentation. We take a slightly different approach than that adopted by [Boulanger and McLellan \(2001\)](#). By analyzing the full likelihood and placing a prior distribution on the individual covariate, we will resolve the problem of having an ill-defined sample area. After you read later chapters of this book, it will be apparent that SCR models represent a formalization of this heuristic procedure.

p0280 For our purposes here, we define the scalar individual covariate x_i to be the distance from the average encounter location of individual i , say \mathbf{s}_i , to the centroid of the trap array, \mathbf{x}_0 : $x_i = \|\mathbf{s}_i - \mathbf{x}_0\|$. Note that $\|\mathbf{u}\|$ is standard notation for Euclidean norm or magnitude of the vector \mathbf{u} , and we use it throughout the book. In practice, people have used distance from edge of the trap array but that is less easy to quantify, as “edge” itself is not precisely defined. Conceptually, individuals in the middle of the array should have a higher probability of encounter and, as x_i increases, p_i should therefore decrease. We note that we have defined \mathbf{s}_i in terms of a sample quantity—the observed mean encounter location—which, while ad hoc, is consistent with the use of individual covariate models in the literature. For an expansive, dense trapping grid we might expect the sample mean encounter location to be a good estimate of home range center but, clearly this is biased for individuals that live around the edge (or off) the trapping array.

p0285 A key point is that \mathbf{s}_i is missing for each individual that is not encountered and so x_i is also missing. Therefore, it is a latent variable, and we need to specify a probability distribution for it. As a measurement of distance we know it must be positive-valued, and it seems sensible that an individual located extremely far from the array of traps would not be captured. Therefore, let’s assume that x_i is uniformly distributed from 0 to some large number, say B , beyond which it would be difficult to imagine an individual being captured by the trap array:

$$x_i \sim \text{Uniform}(0, B)$$

where B is a specified constant, which we may choose to be arbitrarily large. For example, B should be at least a home range diameter past the furthest trap from the centroid of the array.

s0085 4.5.2 Fort Drum bear study

p0290 We have to do a little bit of data processing to fit this individual covariate model to the Fort Drum data. We need to compute the individual covariate \mathbf{x}_i (distance from the centroid of the trapping array) using the **R** function `spiderplot` provided in

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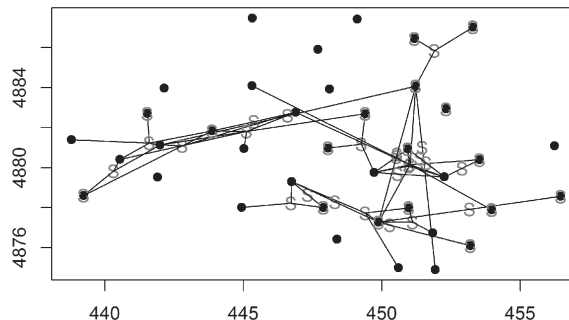


FIGURE 4.5

Spider plot of the Fort Drum study data. The black dots represent the 47 trap locations with the “S” symbols being the average capture location of each bear, i.e., its estimated home range center. All traps in which a bear was captured are connected to its estimated home range center with a line.

scrbook. This function also produces the keen plot shown in Figure 4.5 which we call a “spider plot.” The **R** commands for obtaining the individual covariate “distance from trap centroid” (the variable `xcent` returned by `spiderplot`) and making the spider plot are as follows:

```
> library(scrbook)                                o0525
> data(beardata)                                   o0530
> toad <- spiderplot(beardata$bearArray,beardata$trapmat) o0535
> xcent <- toad$xcent                               o0540
```

For the analysis of these data using the individual covariate “distance from centroid” we used $x_i \sim \text{Uniform}(0, B)$ with $B = 11.5 \text{ km}^2$, which is about the distance from the array center to the furthest trap. Once we choose a value for B , the direct implication is that the population size parameter, N , applies to the area within 11.5 units of the trap centroid. Therefore, the model associates a precise area within which the population of N individuals resides. We will see shortly that N does, in fact, scale with our choice of B to reflect the changing area over which the N individuals of the model reside. The **BUGS** model specification and **R** commands to package the data and fit the model are as follows:

```
cat("
model{
  p0 ~ dunif(0,1)                                # prior distributions o0545
  alpha0 <- log(p0/(1-p0))                         o0550
  psi ~ dunif(0,1)                                 o0555
  beta ~ dnorm(0,.01)                              o0560
                                                    o0565
                                                    o0570
```

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```

o0575 for(i in 1:(nind + nz)){
o0580   xcent[i] ~ dunif(0,B)
o0585   z[i] ~ dbern(psi)           # DA variables
o0590   lp[i] <- alpha0 + beta*xcent[i] # individual effect
o0595   logit(p[i]) <- lp[i]
o0600   mu[i] <- z[i]*p[i]
o0605   y[i] ~ dbin(mu[i],K)       # observation model
o0610 }

o0615 N <- sum(z[1:(nind + nz)])
o0620 }
o0625 ",file="modelMcov.txt")

o0630 data2 <- list(y = y,nz = nz, nind = nind, K = K, xcent = xcent,B = 11.5)
o0635 params2 <- c('p0','psi','N','beta')
o0640 inits <- function() {list(z = zst, psi = psi, p0 = runif(1), beta = rnorm(1)) }
o0645 fit2 <- bugs(data2, inits, params2, model.file="modelMcov.txt",
o0650                  n.chains = 3, n.iter = 11000, n.burnin = 1000, n.thin = 1)

```

p0300 This produces the posterior summary statistics in Table 4.6. 

p0305 We note that the estimated N is much lower than obtained by model M_h but there is a good explanation for this which we discuss in the next section. That issue notwithstanding, it is worth pondering how this model could be an improvement (conceptually or technically) over some other model/estimator including M_0 and M_h considered previously. Well, for one, we have accounted formally for heterogeneity due to spatial location of individuals relative to exposure to the trap array, characterized by the centroid of the array. Moreover, we have done so using a model that is based on an explicit mechanism, as opposed to a phenomenological one such as model M_h . In addition, and importantly, using our new model, *the estimated N applies to an explicit area which is defined by our prescribed value of B* . That is, this area is a fixed component of the model and the parameter N therefore has explicit spatial context, as the number of individuals with home range centers less than B from the centroid of the trap array. As such, the implied “effective area” of the trap array for a given B is a precisely defined quantity—it is that of a circle with radius B .

sp075

Table 4.6 Posterior summaries from the individual covariate model (model M_x) with covariate “distance from the centroid of the trap array,” fitted to the Fort Drum black bear data. Results were obtained using **WinBUGS** running 3 chains, each with 11,000 iterations, discarding the first 1,000 for a total of 30,000 posterior samples.

| Parameter | Mean | SD | 2.5% | 50% | 97.5% | Rhat | n.eff |
|-----------|-------|------|-------|-------|-------|------|-------|
| p_0 | 0.54 | 0.07 | 0.40 | 0.54 | 0.67 | 1 | 1100 |
| ψ | 0.34 | 0.05 | 0.25 | 0.34 | 0.44 | 1 | 3500 |
| N | 58.92 | 5.49 | 50.00 | 58.00 | 71.00 | 1 | 1900 |
| β | -0.25 | 0.06 | -0.36 | -0.25 | -0.12 | 1 | 780 |

4.5.3 Extension of the model

s0090

The model developed in the previous section is not a very good model for one important reason: imposing a uniform prior distribution on x implies that density is *not constant* over space. In particular, this model implies that density *decreases* as we move away from the centroid of the trap array. That is, $x_i \sim \text{Uniform}(0, B)$ implies constant N in each distance band from the centroid but obviously the *area* of each distance band is increasing. This is one reason we have a lower estimate of density than that obtained previously from model M_h (Section 4.4.2) and also why, if we were to increase B , we would see density continue to decrease.

p0310

Fortunately, we are not restricted to use of this specific distribution for the individual covariate. Clearly, it is a bad choice and, therefore, we should think about whether we can choose a better distribution for B —one that doesn't imply a decreasing density as distance from the centroid increases. Conceptually, what we want to do is impose a prior on distance from the centroid, x , such that abundance should be proportional to the amount of area in each successive distance band as you move farther away from the centroid, so that density is *constant*. In fact, theory exists which tells us we should choose $[x] = 2x/B^2$. This can be derived by noting that $F(x) = \Pr(X < x) = (\pi x^2)/(\pi B^2)$. Then, $f(x) = dF/dx = 2x/B^2$. This is a sort of triangular distribution in density induced because the incremental area in each additional distance band increases linearly with radius (i.e., distance from centroid). This can be verified empirically as follows:

p0315

```
> u <- runif (10000,-1,1)
> v <- runif (10000,-1,1)
> d <- sqrt (u*u + v*v)
> hist (d[d < 1])
> hist (d[d < 1],100)
> hist (d[d < 1],100,probability = TRUE)
> abline (0,2)
```

o0655

o0660

o0665

o0670

o0675

o0680

o0685

It would be useful if we could describe this distribution directly in **BUGS** but there is not a built-in way to do so. However, we can implement a discrete version of the pdf.⁶ To do this, we break B into L distance classes of width δ , with probabilities proportional to $2x$. In particular, if we denote the cut-points by $g_1 = 0, g_2, \dots, g_{L+1} = B$ and the interval midpoints are $m_i = g_{i+1} - \delta$. Then the interval probabilities are, approximately,⁷ $p_i = \delta(2m_i/B^2)$, which we can compute once and then pass them to **BUGS** as data. The **R** commands for doing all of this (noting that we have already loaded and processed the Fort Drum bear data) are given in the following **R/BUGS** script:

p0320

```
> a <- .2
> xcent <- xcent%%delta + 1 # Put x in bins
```

o0690

o0695

⁶We might also be able to use what is referred to in **WinBUGS** jargon as the “zeros trick” (see *Advanced BUGS tricks* in the manual) although we haven't pursued this approach.

np030

⁷This is just length \times width, the area of small rectangles approximating the integral.

np035

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```

o0700 > midpts <- seq (delta,Dmax,delta)
o0705 > xprobs <- delta*(2*midpts/(B*B))
o0710 > xprobs <- xprobs/sum (xprobs)

o0715 > cat ("
o0720 model{
o0725 p0 ~ dunif (0,1) # Prior distributions
o0730 alpha0 <- log (p0/(1-p0))
o0735 psi ~ dunif (0,1)
o0740 beta ~ dnorm (0,.01)

o0745 for (i in 1: (nind+nz)){
o0750 xbin[i] ~ dcat (xprobs[])
o0755 z[i] ~ dbern (psi) # DA variables
o0760 lp[i] <- alpha0 + beta*xbin[i]*delta # Individual covariate model
o0765 logit (p[i]) <- lp[i]
o0770 mu[i] <- z[i]*p[i]
o0775 y[i] ~ dbin (mu[i],K) # Observation model
o0780 }

o0785 N <- sum (z[1: (nind+nz)]) # N is derived
o0790 }
o0795 ",file="modelMcov.txt")

```

p0325 In the model description, the variable x (observed distance from centroid of the trap array) has been rounded or binned (placed into a distance bin) so that the discrete version of the pdf of x can be used, as described previously. The new variable labeled $xbin$ is then the *integer category* in units of δ from 0. Thus, to convert back to distance in the expression for $lp[i]$, $xbin[i]$ has to be multiplied by δ . To fit the model, keeping in mind that the data objects required below have been defined in previous analyses of this chapter, we do this:

```

o0800 > data2 <- list (y = y, nz = nz, nind = nind, K = K, xbin = xbin, xprobs = xprobs,
o0805 delta = delta)
o0810 > params2 <- c('p0','psi','N','beta')
o0815 > inits <- function() { list (z = z, psi = psi, p0 = runif (1),beta = rnorm(1) ) }
o0820 > fit <- bugs (data2, inits, params2, model.file="modelMcov.txt",
o0825 working.directory=getwd (), debug = FALSE, n.chains = 3,
o0830 n.iter = 11000, n.burnin = 1000, n.thin = 2)

```

p0330 By specification of B , this model induces a clear definition of area in which the population of N individuals resides. The parameter N of the model is the population size that applies to the particular value of B and, as such, we will see that N scales with our choice of B . This might be disconcerting to some—we can get whatever value of N we want by changing B ! However, it is intuitively reasonable that, as we increase the area under consideration, there should be more individuals in it. Fortunately, we find empirically, that while N is highly sensitive to the prescribed value of B , density appears invariant to B as long as B is sufficiently large. We fit the model for a set of values of B from $B = 12$ (restricting values of x to be in close proximity to the trap array) on upto 20. The results are given in Table 4.7.

p0335 We see that the posterior mean and SD of density (individuals per square km) appear insensitive to choice of B once we reach about $B = 17$ or so. The estimated

Table 4.7 Analysis of Fort Drum bear hair snare data using the individual covariate model, for different values of B , the upper limit of the uniform distribution of ‘distance from centroid of the trap array’. ~~“Density” is the posterior mean of density.~~

sp080

| B | Density (post. mean) | Posterior SD |
|-----|----------------------|--------------|
| 12 | 0.230 | 0.038 |
| 15 | 0.244 | 0.041 |
| 17 | 0.249 | 0.044 |
| 18 | 0.249 | 0.043 |
| 19 | 0.250 | 0.043 |
| 20 | 0.250 | 0.044 |

density of 0.25 per km² is actually quite a bit lower than we reported using model M_h for which no relevant “area” quantity is explicit in the model (and so we had to make it up). Using MLEs of N in conjunction with buffer strips (see Table 1.1) our estimates were in the range of 0.32–0.43 ~~and see Section 4.4 above.~~ On the other hand, our estimate of $\hat{D} = 0.25$ here (based on the posterior mean) is higher than that reported from model M_0 using the buffered area ($\hat{D} = 0.18$). There is no basis really for comparing or contrasting these various estimates. In particular, application of models M_0 and M_h are distinctly *not* spatially explicit models—the area within which the population resides is not defined under either model. There is therefore no reason at all to think that the estimates produced under either closed population model, based on a buffered “trap area,” are justifiable by any theory. In fact, we would get exactly the same estimate of N no matter what we declare the area to be. On the other hand, the individual covariate model uses an explicit model for “distance from centroid” ~~that~~ is a reasonable and standard null model—it posits, in the absence of direct information, that individual home range centers are randomly distributed in space and that probability of detection depends on the distance between home range center and the centroid of the trap array. Under this definition of the system, we see that density is invariant to the choice of area, which seems like a desirable feature.

4.5.4 Invariance of density to B

s0095

Under model M_x , and under models that we consider in later chapters, a general property of the estimators is that while N increases with the prescribed area of the model (defined by B in this model), we expect that density estimators should be invariant to this area. In the model used above, we note that $\text{Area}(B) = \pi B^2$ and $\mathbb{E}(N(B)) = \lambda \text{Area}(B)$ and thus $\mathbb{E}(\text{Density}(B)) = \lambda$, i.e., constant. This should be interpreted as the *prior* density. Absent data, ~~then~~ realizations under the model, will have density λ , regardless of what B is prescribed to be. As we verified empirically above, posterior summaries of density are also invariant to B as long as the prescribed area is sufficiently large.

p0340

s0100 4.5.5 Toward fully spatial capture-recapture models

p0345 While the use of an individual covariate model resolves two important problems inherent in almost all capture-recapture studies (induced heterogeneity and absence of a precise relationship between N and area), is not ideal for all purposes because it does not make full use of the spatial information in the data set, i.e., the trap locations and the locations of each individual encounter, so that we cannot use this model to model trap-specific effects (e.g., trap effort or type). Moreover, we applied this model for “data” being the average observed encounter location, and equated that summary to the home range center s_i . Intuitively, taking the average encounter location as an estimate of home range center makes sense, but more so when the trapping grid is dense and expansive relative to typical home range sizes, which might not be reasonable in practice. Moreover, this approach also ignored the variable precision with which each s_i is estimated. Finally, it ignores that estimates of s_i around the “edge” (however we define that) are biased because the observations are truncated—we can only observe locations interior to the array.

p0350 However, there is hope to extend this model in order to resolve these remaining deficiencies. In the next chapter we provide a further extension of this individual covariate model that definitively resolves the *ad hoc* nature of the approach we took here. In that chapter we build a model in which s_i are regarded as latent variables and the observation locations (i.e., trap-specific encounters) are linked to those latent variables with an explicit model. We note that the model fitted previously could be adapted easily to deal with s_i as a latent variable, simply by adding a prior distribution for s_i . This is actually easier, and less *ad hoc* in a number of respects, and you should try it out.

s0105 4.6 Distance sampling: a primitive SCR model

p0355 Distance sampling is a class of methods for estimating animal density from measurements of distance from an observer to individual animals (or groups). The basic assumption is that detection probability is a function of distance. Distance sampling is one of the most popular methods for estimating animal abundance (Burnham et al., 1980; Buckland et al., 2001; Buckland, 2004) because, unlike ordinary closed population models, distance sampling provides explicit estimates of *density*. In terms of methodological context, the distance sampling model is a special case of a closed population model with an individual covariate. The covariate in this case, x , is the distance between an individual’s location say \mathbf{u} and the observation location or transect. In fact, distance sampling is precisely an individual-covariate model, except that observations are made at only $K = 1$ sampling occasion. Distance sampling eliminates the need to explicitly identify individuals (except they need to be *distinguished* from other individuals) repeatedly and so distance sampling can be applied to unmarked populations. This first and most basic spatial capture-recapture model has been used routinely for decades and, formally, it is a spatially explicit model in the sense that it describes, explicitly, the spatial organization of individual locations (although this

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is not always stated explicitly) and, as a result, somewhat general models of how individuals are distributed in space can be specified (Hedley et al., 1999; Royle et al., 2004; Johnson, 2010; Niemi and Fernández, 2010; Sillett et al., 2012).

As with other models we've encountered in this chapter, the distance sampling model, under data augmentation, includes a set of M zero-inflation variables z_i and a binomial observation model expressed conditional on z_i (binomial for $z_i = 1$, and fixed zeros for $z_i = 0$). In distance sampling we pay for having only a single sample occasion (i.e., $K = 1$) by requiring constraints on the model of detection probability, normally imposed as the assumption that detection probability is 1.0 when distance equals 0. A standard model for detection probability is the “half-normal” model:

$$p_i = \exp(-\alpha_1 x_i^2)$$

for $\alpha_1 > 0$, where x_i denotes the distance at which the i th individual is detected relative to some reference location where perfect detectability ($p = 1$) is assumed. This encounter probability model is more often written with $\alpha_1 = 1/2\sigma^2$. If $K > 1$ then an intercept in this model, say α_0 , is identifiable and such models are usually called “capture-recapture distance sampling” (Alpizar-Jara and Pollock, 1996; Borchers et al., 1998).

As with previous examples, we require a distribution for the individual covariate x_i . The customary choice is

$$x_i \sim \text{Uniform}(0, B)$$

wherein $B > 0$ is a known constant, being the upper limit of data recording by the observer (i.e., the point count radius, or transect half-width). Specification of this distance sampling model in the **BUGS** language is shown in Panel 4.2, taken from Royle and Dorazio (2008).

```
alpha1 ~ dunif(0,10)          # Prior distributions
psi ~ dunif(0,1)

for(i in 1:(nind+nz)){
  z[i] ~ dbern(psi)           # DA variables
  x[i] ~ dunif(0,B)           # B=strip width
  p[i] <- exp(logp[i])        # Detection function
  logp[i] <- - alpha1*(x[i]*x[i])
  mu[i] <- z[i]*p[i]
  y[i] ~ dbern(mu[i])         # Observation model
}

N <- sum(z[1:(nind+nz)])      # N is a derived parameter
D <- N/striparea              # D = N/total area of transects
```

PANEL 4.2

Distance sampling model in **BUGS** for a line transect situation, using a half-normal detection function.

p0370 As with the individual covariate model in the previous section, the distance sampling model can be equivalently specified by putting a prior distribution on individual *location* instead of distance between individual and observation point (or transect). Thus we can write the general distance sampling model as

$$p_i = h(\|\mathbf{u}_i - \mathbf{x}_0\|, \alpha_1)$$

along with

$$\mathbf{u}_i \sim \text{Uniform}(\mathcal{S})$$

where \mathbf{x}_0 is a fixed point (or line) and \mathbf{u}_i is the individual's location, which is observed for the sample of n individuals. In practice, it is easier to record distance instead of location. Basic math can be used to argue that if individuals have a uniform distribution in space, then the distribution of Euclidean distance is also uniform. In particular, if a transect of length L is used and x is distance to the transect, then $F(x) = \Pr(X \leq x) = \frac{x}{L}$ and $f(x) = dF/dx = (1/L)$. For measurements of radial distance, we provided the analogous argument in the previous section.

p0375 The preceding paragraph makes it clear that distance sampling is a special case of spatial capture-recapture models, such as those derived from model M_x of the previous section, where the encounter probability is related directly to *distance*, which is a reduced information summary of *location*, \mathbf{u} . Some intermediate forms of SCR/DS models can be described (Royle et al., 2011a). In the context of our general characterization of SCR models (Chapter 2.6), we suggested that every SCR model can be described, conceptually, by a hierarchical model of the form:

$$[y|\mathbf{u}][\mathbf{u}|\mathbf{s}][\mathbf{s}].$$

Distance sampling ignores the part of the model pertaining to \mathbf{s} , and deals only with the model components for the observed data \mathbf{u} .⁸ Thus, we are left with a hierarchical model of the form

$$[y|\mathbf{u}][\mathbf{u}].$$

In contrast, as we will see in the next chapters, many SCR models (Chapter 5) ignore \mathbf{u} and condition on \mathbf{s} , which is not observed:

$$[y|\mathbf{s}][\mathbf{s}]$$

Since $[\mathbf{u}]$ and $[\mathbf{s}]$ are both assumed to be uniformly distributed, these are equivalent models! The main differences have to do with interpretation of model components and whether or not the latent variables are observable (in distance sampling they are).

p0380 So why bother with SCR models when distance sampling yields density estimates and accounts for spatial heterogeneity in detection? For one, imagine trying to collect distance sampling data on species such as jaguars or tigers! Clearly, distance sampling requires that one can collect large quantities of distance data, which is not always possible. For tigers, it is much easier, efficient, and safer to employ camera traps or track

np040 ⁸Equivalently, we could also say that $[\mathbf{u}]$ in the distance sampling model is $[\mathbf{u}] = \int [\mathbf{u}|\mathbf{s}][\mathbf{s}]d\mathbf{s}$.

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plates and then apply SCR models. Furthermore, as we will see in Chapter 15, SCR models can make use of distance data, allowing us to study distribution, movement, and density. Thus, SCR models are more general and versatile than distance sampling models (which clearly are a special case), and can accommodate data from virtually all animal survey designs.

4.6.1 Example: Sonoran desert tortoise study

s0110

We illustrate the application of distance sampling models using data on the Sonoran desert tortoise (*Gopherus agassizii*), shown in Figure 4.6, collected along transects in southern Arizona (see Zylstra et al. (2010) for details). The data are from 120 square transects having four 250-m sides, although we ignore this detail in our analysis here and regard them as 1 km transects, and we pooled the detection data from all 120 transects. The histogram of encounter distances from the 65 encountered individuals is shown in Figure 4.7.

p0385

Commands for reading in and organizing the data for analysis using **WinBUGS** are given in the help file ?tortoise provided with the **scrbook** package. To compute density, the total sampled area of the transects `striparea` is input as data, and computed as: 120 (transects) multiplied by the length (1000 m) and half-width ($B = 40$ m), then multiplied by 2, and divided by 10000 to convert to units of individuals per ha. We also provide commands for analyzing the data with unmarked (Fiske and Chandler, 2011) using hierarchical distance sampling models (Royle et al., 2004).

p0390

Posterior summaries for the tortoise data are given in Table 4.8. Estimated density (posterior mean) is 0.54 individuals per ha and the estimated scale parameter of the distance function (posterior mean) is $\sigma = 9.12$ m. The \hat{R} -hat statistics of around 1.02

p0395



FIGURE 4.6

Desert tortoise in its native habitat (Photo credit: Erin Zylstra, Univ. of Arizona).

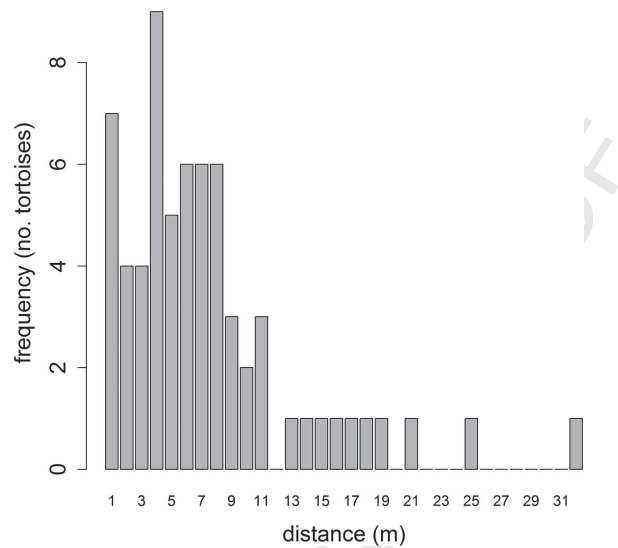


FIGURE 4.7 Distance histogram of $n = 65$ Sonoran desert tortoise detections from a total of 120 km of survey transect.

sp085

| Table 4.8 Posterior summaries from the tortoise distance sampling data. Results were obtained using WinBUGS running 3 chains, each with 3000 iterations and the first 1000 discarded, thinning by 2. | | | | | | | |
|--|--------|-------|--------|--------|--------|------|-------|
| Parameter | Mean | SD | 2.5% | 50% | 97.5% | Rhat | n.eff |
| α_1 | 0.01 | 0.00 | 0.00 | 0.01 | 0.01 | 1.02 | 130 |
| σ | 9.12 | 0.77 | 7.77 | 9.07 | 10.77 | 1.02 | 130 |
| N | 516.67 | 54.71 | 415.00 | 516.00 | 632.00 | 1.02 | 100 |
| D | 0.54 | 0.06 | 0.43 | 0.54 | 0.66 | 1.02 | 100 |
| ψ | 0.61 | 0.07 | 0.49 | 0.61 | 0.75 | 1.02 | 96 |

~~suggest that slightly longer MCMC simulations might be called for.~~ The posterior mass of the data augmentation parameter ψ is located away from the upper bound $\psi = 1$ and so the degree of data augmentation appears sufficient.

s0115

4.7 Summary and outlook

p0400

Traditional closed population capture-recapture models are closely related to binomial generalized linear models. Indeed, the only real distinction is that in capture-recapture

models, the population size parameter N (~~corresponding also to the size of a hypothetical “complete” data set~~) is unknown. This requires special consideration in the analysis of capture-recapture models. The classical approach to inference recognizes that the observations don’t have a standard binomial distribution but, rather, a truncated binomial (from which the so-called *conditional likelihood* derives) since we only have encounter frequency data on observed individuals. If instead we analyze the models using data augmentation, which arises under a $\text{Uniform}(0, M)$ prior for N , the observations can be modeled using a zero-inflated binomial distribution. ~~When we deal with the unknown- N problem using data augmentation then we are left with zero-inflated GLMs and GLMMs instead of ordinary GLMs or GLMMs.~~ The analysis of such zero-inflated models is practically convenient, especially using the **BUGS** variants.

Spatial capture-recapture models ~~that we will consider~~ in the rest of the chapters p0405 of this book are closely related to individual covariate models (model M_x). ~~Naturally,~~ spatial capture-recapture models arise by defining individual covariates based on observed locations of individuals—we can think of using some function of mean encounter location as an individual covariate. We did this in a novel way, by using distance to the centroid of the trapping array as a covariate. We analyzed the *full likelihood* using data augmentation, and placed a prior distribution on the individual covariate which was derived from an assumption that individual locations are, a priori, uniformly distributed in space. This assumption provides for invariance of the density estimator to the choice of ~~population size~~ area (induced by maximum distance from the centroid of the trap array). The model addressed some important problems in the use of closed population models: it allows for heterogeneity in encounter probability due to the spatial juxtaposition of individuals with the array of traps, and it also provides a direct estimate of density because area is a feature of the model (via the prior on the individual covariate). The model is still not completely general, however, because it does not make full use of the spatial encounter histories, which provide direct information about the locations and density of individuals.

A specific individual covariate model that is in widespread use is classical distance p0410 sampling. The model underlying distance sampling is precisely a special kind of SCR model—but one without replicate samples. Understanding distance sampling and individual covariate models more broadly provides a solid basis for understanding and analyzing spatial capture-recapture models. In fact if, instead of placing an explicit model on *distance* in the classical distance sampling model, we were to place the prior distribution on *location*, s , of each individual, then the form of the distance sampling model more closely resembles the SCR model we introduce in the next chapter.

Non Print Items

sp005

Abstract: In this chapter we introduce traditional (non-spatial) closed-population capture-recapture models for estimating abundance, emphasizing analysis in a Bayesian framework. If population size (N) is known, these models resemble simple logistic regressions, where the observations (0 = not captured or 1 = captured on each occasion) are Bernoulli trials with detection probability p . Usually, though, we are interested in estimating N , and we can do so using data augmentation, which involves adding a large number of all-zero encounter histories to the n observed encounter histories, and estimating how many of these hypothetical individuals are part of the population but were never observed. This reformulation of the capture-recapture model facilitates Bayesian analysis and the inclusion of individual covariates, and thus we use data augmentation frequently throughout the rest of the book. To demonstrate data augmentation, we present examples and BUGS code for non-spatial capture-recapture models incorporating different sources of variation in p . The drawback of non-spatial estimates of abundance is that they are not linked to a specific area and so ad hoc approaches are necessary to define an area in order to estimate density. We present some common approaches to do so and discuss their shortcomings. We show that individual covariate models, where the covariate is some description of an animal's location in space, such as average capture location, are a step towards fully spatial capture-recapture models. The last section of this chapter highlights the parallels of distance sampling and spatial capture-recapture. Providing background on capture-recapture in general, the chapter facilitates understanding of spatial capture-recapture models, which are fully introduced in the following chapter.

Keywords: Behavioral response, Data augmentation, Density estimation, Detection probability, Distance sampling, Effective area sampled, Heterogeneity model, Individual covariate model, MMDM, Model Mh, Non-spatial capture-recapture