

₁ **Chapter 1**

₂ **Introduction**

Chapter 2

Introduction to Bayesian Analysis of GL(M)Ms Using R/WinBUGS

A major theme of this book is that spatial capture-recapture models are, for the most part, just generalized linear models (GLMs) wherein the covariate, distance between trap and home range center, is partially or fully unobserved – and therefore regarded as a random effect. Such models are usually referred to as Generalized Linear Mixed Models (GLMMs) and, therefore, SCR models can be thought of as a specialized type of GLMM. Naturally then, we should consider analysis of these slightly simpler models in order to gain some experience and, hopefully, develop a better understanding of spatial capture-recapture models.

In this chapter, we consider classes of GLM models - Poisson and binomial (i.e., logistic regression) GLMs - that will prove to be enormously useful in the analysis of capture-recapture models of all kinds. Many readers are probably familiar with these models because they represent probably the most generally useful models in all of Ecology and, as such, have received considerable attention in many introductory and advanced texts. We focus on them here in order to introduce the readers to the analysis of such models in **R** and **WinBUGS**, which we will translate directly to the analysis of SCR models in subsequent chapters.

Bayesian analysis is convenient for analyzing GLMMs because it allows us to work directly with the conditional model – i.e., the model that is conditional on the random effects, using computational methods known as Markov chain Monte Carlo (MCMC). Learning how to do Bayesian analysis of GLMs and GLMMs in **WinBUGS** is, in part, the purpose of this chapter. While we use **WinBUGS** to do the Bayesian computations, we organize and summarize our data and execute **WinBUGS** from within **R** using the useful package **R2WinBUGS**

(Sturtz et al., 2005). Kéry (2010), and Kéry and Schaub (2011) provide excellent introductions to the basics of Bayesian analysis and GLMs at an accessible level. We don't want to be too redundant with those books and so we avoid a detailed treatment of Bayesian methodology - instead just providing a cursory overview so that we can move on and attack the problems we're most interested in related to spatial capture-recapture. In addition, there are a number of texts that provide general introductions to Bayesian analysis, MCMC, and their applications in Ecology including McCarthy (2007), Kéry (2010), Link and Barker (2009), and King (2009).

While this chapter is about Bayesian analysis of GLMMs, such models are routinely analyzed using likelihood methods too, as discussed by Royle and Dorazio (2008), and Kéry (2010). Indeed, likelihood analysis of such models is the primary focus of many applied statistics texts, a good one being Zuur et al. (2009). Later in this book, we will use likelihood methods to analyze SCR models but, for now, we concentrate on providing a basic introduction to Bayesian analysis because that is the approach we will use in a majority of cases in later chapters.

2.1 Notation

We will sometimes use conventional “bracket notation” to refer to probability distributions. If y is a random variable the $[y]$ indicates its distribution or its probability density/mass function (pdf, pmf) depending on context. If x is another random variable then $[y|x]$ is the conditional distribution of y given x , and $[y, x]$ is the joint distribution of y and x . To differentiate specific distributions in some contexts we might label them $g(y)$, $g(y|\theta)$, $f(x)$, or similar. We will also write $y \sim \text{Normal}(\mu, \sigma^2)$ to indicate that y “is distributed as” a normal random variable with parameters μ and σ^2 . The expected value or mean of a random variable is $E[y] = \mu$, and $\text{Var}[y] = \sigma^2$ is the variance of y . To indicate specific observations we'll use an index such as “ i ”. So, y_i for $i = 1, 2, \dots, n$ indicates observations for n individuals. Finally, we write $\text{Pr}(y)$ to indicate specific probabilities, i.e., of events “ y ” or similar.

To illustrate these concepts and notation, suppose z is a binary outcome (e.g., species occurrence) and we might assume the model: $z \sim \text{Bern}(p)$ for observations. Under this model $\text{Pr}(z = 1) = \psi$, which is also the expected value $E[z] = \psi$. The variance is $\text{Var}[z] = \psi * (1 - \psi)$ and the probability mass function (pmf) is $[z] = \psi^z (1 - \psi)^{1-z}$. Sometimes we write $[z|\psi]$ when it is important to emphasize the conditional dependence of z on ψ . As another example, suppose y is a random variable denoting whether or not a species is detected if an occupied site is surveyed. In this case it might be natural to express the pmf of the observations y conditional on z . That is, $[y|z]$. In this case, $[y|z = 1]$ is the conditional pmf of y given that a site is occupied, and it is natural to assume that $[y|z = 1] = \text{Bern}(p)$ where p is the “detection probability” - the probability that we detect the species, given that it is present. The model for the observations y is completely specified once we describe the other conditional

pmf $[y|z = 0]$. For this conditional distribution it is sometimes reasonable to assume $\Pr(y = 1|z = 0) = 0$ (MacKenzie et al. (2002); see also Royle and Link (2006)). That is, if the species is absent, the probability of detection is 0. This implies that $\Pr(y = 0|z = 0) = 1$. To allow for situations in which the true state z is unobserved, we assume that $[z]$ is Bernoulli with parameter ψ . In this case, the marginal distribution of y is

$$[y] = [y|z = 1]Pr(z = 1) + [y|z = 0]Pr(z = 0)$$

because $[y|z = 0]$ is a point mass at $y = 0$, by assumption, then

$$\Pr(y = 1) = p\psi$$

And

$$\Pr(y = 0) = (1 - p) * \psi + (1 - \psi)$$

2.2 GLMs and GLMMs

We have asserted already that SCR models work out most of the time to be variations of GLMs and GLMMs. Some of you might therefore ask: What are GLMs and GLMMs, anyhow? These models are covered extensively in many very good applied statistics books and we refer the reader elsewhere for a detailed introduction. We think Kéry (2010), Kéry and Schaub (2011), and Zuur et al. (2009) are all accessible treatments of considerable merit. Here, we'll give the 1 minute treatment of GLMMs, not trying to be complete but rather only to preserve a coherent organization to the book.

The generalized linear model (GLM) is an extension of standard linear models by allowing the response variable to have some distribution from the exponential family of distributions (i.e., not just normal). This includes the normal distribution but also dozens of others such as the Poisson, binomial, gamma, exponential, and many more. In addition, GLMs allow the response variable to be related to the predictor variables (i.e., covariates) using a link function, which is usually nonlinear. Finally, GLMs typically accommodate a relationship between the mean and variance. The classical reference for GLMs is Nelder and Wedderburn (1972) and also McCullagh and Nelder (1989). The GLM consists of three components:

1. A probability distribution for the dependent variable y , from a class of probability distributions known as the exponential family.
2. A "linear predictor" $\eta = \mathbf{X}\beta$.
3. A link function g that relates $E[y]$ to the linear predictor, $E[y] = \mu = g^{-1}(\eta)$. Therefore $g(E[y]) = \eta$.

The dependent variable y is assumed to be an outcome from a distribution of the exponential family which includes many common distributions including

the normal, gamma, Poisson, binomial, and many others. The mean of the distribution of y is assumed to depend on predictor variables x according to

$$g(E[y]) = \mathbf{x}'\beta$$

where $E[y]$ is the expected value of y , and $\mathbf{x}'\beta$ is termed the *linear predictor*, i.e., a linear function of the predictor variables with unknown parameters β to be estimated. The function g is the link function. In standard GLMs, the variance of y is a function V of the mean of y : $\text{Var}(y) = V(\mu)$ (see below for examples).

A Poisson GLM posits that $y \sim \text{Poisson}(\lambda)$ with $E[y] = \lambda$ and usually the model for the mean is specified using the *log link function* by

$$\log(\lambda_i) = \beta_0 + \beta_1 * x_i$$

The variance function is $V(y_i) = \lambda_i$. The binomial GLM posits that $y_i \sim \text{Binomial}(K, p)$ where K is the fixed sample size parameter and $E[y_i] = K * p_i$. Usually the model for the mean is specified using the *logit link function* according to

$$\text{logit}(p_i) = \beta_0 + \beta_1 * x_i$$

Where $\text{logit}(u) = \log(u/(1-u))$. The inverse-logit function, g^{-1} , is a function we will refer to as “expit”, so that $\text{expit}(u) = \exp(u)/(1 + \exp(u))$.

A GLMM is the extension of GLMs to accommodate “random effects”. Often this involves adding a normal random effect to the linear predictor, and so a simple example is:

$$\log(\lambda_i) = \alpha_i + \beta_1 * x_i$$

where

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

2.3 Bayesian Analysis

Bayesian analysis is unfamiliar to many ecological researchers because older cohorts of ecologists were largely educated in the classical statistical paradigm of frequentist inference. But advances in technology and increasing exposure to benefits of Bayesian analysis are fast making Bayesians out of people or at least making Bayesian analysis an acceptable, general, alternative to classical, frequentist inference.

Conceptually, the main thing about Bayesian inference is that it uses probability directly to characterize uncertainty about things we don’t know. “Things”, in this case, are parameters of models and, just as it is natural to characterize uncertain outcomes of stochastic processes using probability, it seems natural also to characterize information about unknown “parameters” using probability. At least this seems natural to us and, we think, most ecologists either explicitly adopt that view or tend to fall into that point of view naturally. Conversely, frequentists use probability in many different ways, but never to characterize

uncertainty about parameters¹ Instead, frequentists use probability to characterize the behavior of *procedures* such as estimators or confidence intervals (see below), which can lead to some inelegant or unnatural interpretations of things. It is paradoxical that people readily adopt a philosophy of statistical inference in which the things you don't know (i.e., parameters) should *not* be regarded as random variables, so that, as a consequence, one cannot use probability to characterize one's state of knowledge about them.

2.3.1 Bayes Rule

As its name suggests, Bayesian analysis makes use of Bayes' rule in order to make direct probability statements about model parameters. Given two random variables z and y , Bayes rule relates the two conditional probability distributions $[z|y]$ and $[y|z]$ by the relationship:

$$[z|y] = [y|z][z]/[y]$$

Bayes' rule itself is a mathematical fact and there is no debate in the statistical community as to its validity and relevance to many problems. Generally speaking, these distributions are characterized as follows: $[y|z]$ is the conditional probability distribution of y *given* z , $[z]$ is the marginal distribution of z and $[y]$ is the marginal distribution of y . In the context of Bayesian inference we usually associate specific meanings in which $[y|z]$ is thought of as "the likelihood", $[z]$ as the "prior" and so on. We leave this for later because here the focus is on this expression of Bayes rule as a basic fact of probability.

As an example of a simple application of Bayes rule, consider the problem of determining species presence at a sample location based on imperfect survey information. Let z be a binary random variable that denotes species presence ($z = 1$) or absence ($z = 0$), let $\Pr(z = 1) = \psi$ where ψ is usually called occurrence probability, "occupancy" (MacKenzie et al., 2002) or "prevalence". Let y be the *observed* presence ($y = 1$) or absence ($y = 0$), and let p be the probability that a species is detected in a single survey at a site given that it is present. Thus, $\Pr(y = 1|z = 1) = p$. The interpretation of this is that, if the species is present, we will only observe presence with probability p . In addition, we assume here that $\Pr(y = 1|z = 0) = 0$. That is, the species cannot be detected if it is not present which is a conventional view adopted in most biological sampling problems (but see Royle and Link (2006)). If we survey a site T times but never detect the species, then this clearly does not imply that the species is not present ($z = 0$) at this site. Rather, our degree of belief in $z = 0$ should be made with a probabilistic statement $\Pr(z = 1|y_1 = 0, \dots, y_T = 0)$. If the T surveys are independent so that we might regard y_t as *iid* Bernoulli trials, then the total number of detections, say y , is Binomial with probability p then we can use Bayes rule to compute the probability that it is present given that

¹To hear this will be shocking to some readers perhaps.

179 it is not detected in T samples. In words, the expression we seek is:

$$\Pr(\text{present}|\text{not detected}) = \frac{\Pr(\text{not detected}|\text{present}) \Pr(\text{present})}{\Pr(\text{detected})}$$

180 Mathematically, this is

$$\Pr(z = 1|y = 0) = \Pr(y = 0|z = 1) \Pr(z = 1) / \Pr(y = 0) = [(1-p)^T \psi] / [(1-p)^T \psi + (1-\psi)].$$

181 To apply this, suppose that $T = 2$ surveys are done at a wetland for a species
 182 of frog, and the species is not detected there. Suppose further that $\psi = .8$ and
 183 $p = .5$ are obtained from a prior study. Then the probability that the species is
 184 present at this site is $.25 * .8 / (.25 * .8 + .2) = 0.50$. That is, there seems to be
 185 about a 50/50 chance that the site is occupied despite the fact that the species
 186 wasn't observed there.

187 In summary, Bayes' rule provides a simple linkage between the conditional
 188 probabilities $[y|z]$ and $[z|y]$ which is useful whenever one needs to deduce one
 189 from the other. Bayes' rule as a basic fact of probability is not disputed.

190 2.3.2 Bayesian Inference

191 What is controversial to some is the scope and manner in which Bayes rule is
 192 applied by Bayesian analysts. Bayesian analysts assert that Bayes rule is rele-
 193 vant, in general, to all statistical problems by regarding all unknown quantities
 194 of a model as realizations of random variables - this includes "data", latent
 195 variables, and also "parameters". Classical (non-Bayesian) analysts sometimes
 196 object to regarding "parameters" as outcomes of random variables. Classically,
 197 parameters are thought of as "fixed but unknown" (using the terminology of
 198 classical statistics). Of course, in Bayesian analysis they are also unknown
 199 and, in fact, there is a single data-generating value and so they are also fixed.
 200 The difference is that this fixed but unknown value is regarded as having been
 201 generated from some probability distribution. Specification of that probability
 202 distribution is necessary to carryout Bayesian analysis, but it is not required in
 203 classical frequentist inference.

204 To see the general relevance of Bayes rule in the context of statistical infer-
 205 ence, let y denote observations - i.e., "data" - and let $[y|\theta]$ be the observation
 206 model (often colloquially referred to as the "likelihood"). Suppose theta is a
 207 parameter of interest having (prior) probability distribution $[\theta]$. These are com-
 208 bined to obtain the posterior distribution using Bayes' rule, which is:

$$[\theta|y] = [y|\theta][\theta]/[y]$$

209 Asserting the general relevance of Bayes rule to all statistical problems, we
 210 can conclude that the two main features of Bayesian inference are that: (1)
 211 "parameters" θ are regarded as realizations of a random variable and, as a
 212 result, (2) inference is based on the probability distribution of the parameters
 213 given the data, $[\theta|y]$, which is called the posterior distribution. This is the

result of using Bayes rule to combine “the likelihood” and the prior distribution. The key concept is regarding parameters as realizations of a random variable because, once you admit this conceptual view, this leads directly to the posterior distribution, a very natural quantity upon which to base inference about things we don’t know - including parameters of statistical models. In particular, $[\theta|y]$ is a probability distribution for θ and therefore we can make direct probability statements to characterize uncertainty about θ .

The denominator of our invocation of Bayes rule, $[y]$, is the marginal distribution of the data y . We note without further remark right now that, in many practical problems, this can be an enormous pain to compute. The main reason that the Bayesian paradigm has become so popular in the last 20 years or so is because methods exist for characterizing the posterior distribution that do not require that we possess a mathematical understanding of $[y]$, i.e., we never have to compute it or know what it looks like, or know anything specific about it.

A common misunderstanding on the distinction between Bayesian and frequentist inference goes something like this “in frequentist inference parameters are fixed but unknown but in a Bayesian analysis parameters are random.” At best this is a sad caricature of the distinction and at worst it is downright wrong. What is true is that, to a Bayesian, parameters are random variables. However, a Bayesian assumes, just like a frequentist, that there was a single data-generating value of that parameter - a fixed, and unknown value that produced the given data set. The distinction between Bayesian and frequentist approaches is that Bayesians regard the parameter as a random variable, and its value as the outcome of a random value, on par with the observations. This allows Bayesians to use probability to make direct probability statements about parameters. Frequentist inference procedures do not permit direct probability statements to be made about parameter values – because parameters are not random variables!

While we can understand the conceptual basis of Bayesian inference merely by understanding Bayes rule – that’s really all there is to it – it is not so easy to understand the basis of classical “frequentist” inference which is mostly like² a “basket of methods” with little coherent organization. What is mostly coherent in frequentist inference is the manner in which items in this basket of methods are evaluated – the performance of a given procedure is evaluated by “averaging over” hypothetical realizations of y , regarding the *estimator* as a random variable. For example, if $\hat{\theta}$ is an estimator of θ then the frequentist is interested in $E_y[\hat{\theta}|y]$ which is used to characterize bias. If the expected value of $\hat{\theta}$, when averaged over realizations of y , is equal to θ , then $\hat{\theta}$ is unbiased.

The view of parameters as fixed constants and estimators as random variables leads to interpretations that are not so straightforward. For example confidence intervals having the interpretation “95% probability that the interval contains the true value” and p-values being “the probability of observing an outcome as extreme or more than the one observed.” These are far from intuitive interpretations to most people. Moreover, this is conceptually prob-

²Characterization from Sims REF XYZ

blematic to some because the hypothetical realizations that characterize the performance of our procedure we will never get to observe.

While we do tend to favor Bayesian inference for the conceptual simplicity (parameters are random, posterior inference), we mostly advocate for a pragmatic non-partisian approach to inference because, frankly, some of these “bucket of methods” are actually very convenient in certain situations as we will see in later chapters.

2.3.3 Prior distributions

The prior distribution $[\theta]$ is an important feature of Bayesian inference. As a conceptual matter, the prior distribution characterizes “prior beliefs” or “prior information” about a parameter. Indeed, an oft-touted benefit of Bayesian analysis is the ease with which prior information can be included in an analysis. However, more commonly, the prior is chosen to express a lack of prior information, even if previous studies have been done and even if the investigator does in fact know quite a bit about a parameter. This is because the manner in which prior information is embodied in a prior (and the amount of information) is usually very subjective and thus the result can wind up being very contentious, e.g., if different investigators might report different results based on subjective assessments of things. Thus it is usually better to “let the data speak” and use priors that reflect absence of information beyond the data set being analyzed.

But still the need occasionally arises to embody prior information or beliefs about a parameter formally into the estimation scheme. In SCR models we often have a parameter that is closely linked to “home range radius” and thus auxiliary information on the home range size of a species can be used as prior information (e.g., see Chandler and Royle (2012) ; also chapter XYZ).

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noninformative prior on one scale is informative on another scale. e.g., flat prior on $\logit(p)$ is very different from $\text{uniform}(0,1)$ on p ... show graphic.....

reference to non-invariance of prior distributions to transformation.....

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2.3.4 Posterior Inference

In Bayesian inference, we are not focusing on estimating a single point or interval but rather on characterizing a whole distribution – the posterior distribution – from which one can report any summary of interest. A point estimate might be the posterior mean, median, mode, etc.. In many applications in this book, we will compute 95% Bayesian intervals using the 2.5% and 97.5% quantiles of the posterior distribution. For such intervals, it is correct to say $\Pr(L < \theta < U) = 0.95$. That is, “the probability that θ is between L and U is 0.95”. It is not a subtle thing that this cannot be said using frequentist methods - although people tend to say it anyway and not really understand why it is wrong or even that it is wrong. This is actually a failing of frequentist ideas and the inability of frequentists to get people to overcome their natural tendency to use probability

- which is something that, as a frequentist, you simply cannot do in the manner that you would like to.

Posterior inference is the main practical element of Bayesian analysis. We get to make an inference conditional on the data that we actually observed - i.e., what we actually know. To us, this seems logical - to condition on what we know. Conversely, frequentist inference is based on considering average performance over hypothetical unobserved data sets (i.e., the “relative frequency” interpretation of probability). Frequentists know that their procedures work well when averaged over all hypothetical, unobserved, data sets but no one ever really knows how well they work for the specific data set analyzed. That seems like a relevant question to biologists who oftentimes only have their one, extremely valuable, data set. This distinction comes into play a lot in exposing philosophical biases in the peer review of statistical analyses in ecology in the sense that, despite these opposing conceptual views to inference (i.e. conditional on the data you have, or averaged over hypothetical realizations), those who conduct a Bayesian analysis are often (in ecology, almost always) required to provide a frequentist evaluation of their Bayesian procedure.

2.3.5 Small sample inference

Using Bayesian inference, we obtain an estimate of the posterior distribution which is an exhaustive summary of the state-of-knowledge about an unknown quantity. It is the posterior distribution - not an estimate of that thing. It is also not, usually, an approximation except to within Monte Carlo error (in cases where we use simulation to calculate it). One of the great virtues of Bayesian analysis which is not really appreciated is that it is completely valid for any particular sample size. i.e., it is $[\theta|y]$, as precise as we claim it to be based on our ability to do calculations, for the particular sample size and observations that we have even if we have only a single datum y . The same cannot be said for almost all frequentist procedures in which estimates or variances are very often (almost always in practice) based on “asymptotic approximations” to the procedure which is actually being employed.

There seems to be a prevailing view in statistical ecology that classical likelihood-based procedures are virtuous because of the availability of simple formulas and procedures for carrying out inference, such as calculating standard errors, doing model selection by AIC, and assessing goodness-of-fit. In large samples, this may be an important practical benefit, but the theoretical validity of these procedures cannot be asserted in most situations involving small samples. This is not a minor issue because it is typical in many wildlife sampling problems - especially in surveys of carnivores or rare/endangered species - to wind up with a small, sometimes extremely small, data set. For example, a recent paper on the fossa (*Cryptoprocta ferox*), an endangered carnivore in Madagascar, estimated an adult density of 0.18 adults / km sq based on 20 animals captured over 3 years (Hawkins and Racey, 2005). A similar paper on the endangered southern river otter (*Lontra provocax*) estimated a density of 0.25 animals per river km based on 12 individuals captured over 3 years (Sepúlveda

et al., 2007). Gardner et al. (2010) analyzed data from a study of the Pampas cat, a species for which very little is known, wherein only 22 individual cats were captured during the two year period. Trolle and Kéry (2005) reported only 9 individual ocelots captured and Jackson et al. (2006) captured 6 individual snow leopards using camera trapping. Thus, studies of rare and/or secretive carnivores necessarily and flagrantly violate one of Le Cam’s Basic Principles, that of “If you need to use asymptotic arguments, do not forget to let your number of observations tend to infinity.” (Le Cam, 1990).

The biologist thus faces a dilemma with such data. On one hand, these datasets, and the resulting inference, are often criticized as being poor and unreliable. Or, even worse³, “the data set is so small, this is a poor analysis.” On the other hand, such data may be all that is available for species that are extraordinarily important for conservation and management. The Bayesian framework for inference provides a valid, rigorous, and flexible framework that is theoretically justifiable in arbitrary sample sizes. This is not to say that one will obtain precise estimates of density or other parameters, just that your inference is coherent and justifiable from a conceptual and technical statistical point of view. That is, we report the posterior probability $\Pr(D|data)$ which is easily interpretable and just what it is advertised to be and we don’t need to do a simulation study to evaluate how well some approximate $\Pr(D|data)$ deviates from the actual $\Pr(D|data)$ because they are precisely the same quantity.

2.4 Characterizing posterior distributions by MCMC simulation

In practice, it is not really feasible to ever compute the marginal probability distribution $\Pr(y)$, the denominator resulting from application of Bayes’ rule. For decades this impeded the adoption of Bayesian methods by practitioners. Or, the few Bayesian analyses done were based on asymptotic normal approximations to the posterior distribution. While this was useful stuff from a theoretical and technical standpoint and, practically, it allowed people to make the probability statements that they naturally would like to make, it was kind of a bad joke around the Bayesian water-cooler to, on one hand, criticize classical statistics for being, essentially, completely ad hoc in their approach to things but then, on the other hand, have to devise various approximations to what they were trying to characterize. The advent of Markov chain Monte Carlo (MCMC) methods has made it easier to calculate posterior distributions for just about any problem to arbitrary levels of precision.

Broadly speaking, MCMC is a class of methods for drawing random numbers (sampling or simulating) from the target posterior distribution. Thus, even though we might not recognize the posterior as a named distribution or be able to analyze its features analytically, e.g., devise mathematical expressions for the mean and variance, we can use these MCMC methods to obtain a large sample

³Actual quote from a referee

from the posterior and then use that sample to characterize features of the posterior. What we do with the sample depends on our intentions – typically we obtain the mean or median for use as a point estimate, and take a confidence interval based on Monte Carlo estimates of the quantiles. These are estimates, but not like frequentist estimates. Rather, they are Monte Carlo estimates with an associated Monte Carlo error which is largely determined arbitrarily by the analyst. They are not estimates qualified by a sampling distribution as in classical statistics. If we run our MCMC long enough then our reported value of $E[\theta|y]$ or any feature of the posterior distribution is precisely what we say it is. There is no “sampling variation” in the frequentist sense of the word. In summary, the MCMC samples provide a Monte Carlo characterization of *the* posterior distribution.

2.5 What Goes on Under the MCMC Hood

We will develop and apply MCMC methods in some detail for spatial capture-recapture models in chapter 7. Here we provide a simple illustration of some basic ideas related to the practice of MCMC.

A type of MCMC method relevant to most problems is Gibbs sampling (REF XYZ XYZ), which is based on the idea of iterative simulation from the “full conditional” distributions (also called conditional posterior distributions). The full conditional distribution for an unknown quantity is the conditional distribution of that quantity given every other random variable in the model – the data and all other parameters. For example, for a normal regression model with $y \sim \text{Normal}(\alpha + \beta x, 1)$ then the two full conditionals are, in symbolic terms,

$$[\alpha|y, \beta]$$

and

$$[\beta|y, \alpha].$$

We might use our knowledge of probability to identify these mathematically. In particular, by Bayes’ Rule, $[\alpha|y, \beta] = [y|\alpha, \beta][\alpha|\beta]/[y|\beta]$ and similarly for $[\beta|y, \alpha]$. For example, if we have priors for $[\alpha]$ and $[\beta]$ which are also normal distributions, some algebra reveals that XXXX COPY NOTATION FFROM CH. 6 XXXXX

$$[\alpha|y, \beta] = \text{Normal}(\text{ybar}, \dots \text{weightedvariancehere} \dots).$$

Similarly,

$$[\beta|y, \alpha] \text{ is normal}(\dots \dots \dots)$$

The MCMC algorithm for this model has us simulate in succession, repeatedly, from those two distributions. See Gelman et al. (2004) for more examples of Gibbs sampling for the normal model. A conceptual representation of the MCMC algorithm for this simple model is therefore: XXXX Check out ALGORITHM environment XXXXX

Algorithm

```

0. Initialize  $\alpha$  and  $\beta$ 

Repeat{
  1. Draw a new value of  $\alpha$  from Eq. \ref{xyz}
  2. Draw a new value of  $\beta$  from Eq. \ref{xyz}
}
```

As we just saw for this simple “normal-normal” model it is sometimes possible to specify the full conditional distributions analytically. In general, when certain so-called conjugate prior distributions are chosen, the form of full conditional distributions is similar to that of the observation model. In this normal-normal case, the normal distribution for the mean parameters is the conjugate prior under the normal model, and thus the full-conditional distributions are also normal. This is convenient because, in such cases, we can simulate directly from them using standard methods (or **R** functions). But, in practice, we don’t really ever need to know such things because most of the time we can get by using a simple algorithm, called the Metropolis-Hastings (henceforth “MH”) algorithm, to obtain samples from these full conditional distributions without having to recognize them as specific, named, distributions. This gives us enormous freedom in developing models and analyzing them without having to resolve them mathematically because to implement the MH algorithm we need only identify the full conditional distribution up to a constant of proportionality, that being the marginal distribution in the denominator (e.g., $[y|\beta]$ above).

We will talk about the Metropolis-Hastings algorithm shortly, and we will use it extensively in the analysis of SCR models (e.g., chapter 7).

2.5.1 Rules for constructing full conditional distributions

The basic strategy for constructing full-conditional distributions for devising MCMC algorithms can be reduced conceptually to a couple of basic steps summarized as follows:

- (step 1) Collect all stochastic components of the model;
- (step 2) Recognize and express the full conditional in question as proportional to the product of all components;
- (step 3) Remove the ones that don’t have the focal parameter in them.
- (step 4) Do some algebra on the result in order to identify the resulting pdf or pmf.

Of the 4 steps, the last of those is the main step that requires quite a bit of statistical experience and intuition because various algebraic tricks can be used to reshape the mess into something noticeable - i.e., a standard, named distribution.

But step 4 is not necessary if we decide instead to use the Metropolis-Hastings algorithm as described below.

To illustrate for computing $[\alpha|y, \beta]$ we first apply step 1 and identify the model components as: $[y|\alpha, \beta]$, $[\alpha]$ and $[\beta]$. Step 2 has us write $[\alpha|y, \beta] \propto [y|\alpha, \beta][\alpha][\beta]$. Step 3: We note that $[\beta]$ is not a function of alpha and therefore we remove it to obtain $[\alpha|y, \beta] \propto [y|\alpha, \beta][\alpha]$. Similarly we obtain $[\beta|y, \alpha] \propto [y|\alpha, \beta][\beta]$. We apply step 4 and manipulate these algebraically to arrive at the result or, alternatively, we can sample them indirectly using the Metropolis-Hastings algorithm (see below).

2.5.2 Metropolis-Hastings algorithm

The Metropolis-Hastings (MH) algorithm is a completely generic method for sampling from any distribution, say $f(\theta)$. In our applications, $f(\theta)$ will typically be the full conditional distribution of θ . While we sometimes use Gibbs sampling, we seldom use “pure” Gibbs sampling because we might use MH to sample from one or more of the full conditional distributions. When the MH algorithm is used to sample from full conditional distributions of a Gibbs sampler the resulting hybrid algorithm is called *Metropolized Gibbs sampling* or more commonly *Metropolis-within-Gibbs*. Shortly we will actually construct such an algorithm for a simple class of models.

The MH algorithm generates candidates from some proposal or candidate-generating distribution, that may be conditional on the current value of the parameter, denoted by $h(\theta^*|\theta^t)$. Here, θ^* is the *candidate* or proposed value and θ^t is the current value, i.e., at iteration t of the MCMC algorithm. The proposed value is accepted with probability XXXX check notation with Rahel XXXXXX

$$r = \frac{f(\theta^*)h(\theta^t|\theta^*)}{f(\theta^t)h(\theta^*|\theta^t)}$$

which we call the MH acceptance probability. This ratio can sometimes be > 1 in which case we set it equal to 1. It is useful to note that $h()$ can be anything at all. Absolutely anything! You can generate candidate values from a *normal*(0,1) distribution, from a *uniform*(-3455,3455) distribution, or anything of proper support. Note, however, that good choices of $h()$ are those that approximate the posterior distribution. Obviously if $h() = f(\theta|y)$ (i.e., the posterior) then you always accept the draw, and it stands to reason that proposals that are more similar to $f(\theta|y)$ will lead to higher acceptance probabilities. No matter the choice of $h()$, we can evaluate this ratio numerically because the marginal $f(y)$ cancels from both the numerator and denominator, which is the magic of the MH algorithm.

A special kind of $h()$ are those that are symmetric, which means that $h(a|b) = h(b|a)$ in which case $h(a|b)$ and $h(b|a)$ just cancel out from the MH acceptance probability and r is then just the ratio of the target density evaluated at the candidate value to that evaluated at the current value. A type of symmetric proposal useful in many situations is the so-called *random-walk* proposal distribution where candidate values are drawn from a normal distribution with

mean equal to the current value and some standard deviation, say δ , which is prescribed by the user. For parameters that have support on the real line, e.g., α in our example above, the random walk proposal generator has us generate $\alpha^* \sim \text{Normal}(\alpha^t, \delta)$. If we set δ very small we have a high probability of accepting the proposal and vice versa. In practice, we “tune” delta to achieve a compromise between acceptance rate and efficient mixing of the Markov chains (see below for an example) normally assessed by autocorrelation. Low δ increases the acceptance rate but will tend to produce Markov chains with high autocorrelation, and vice versa.

Parameters with bounded support: Many models contain parameters that have bounded support. E.g., variance parameters live on $[0, \infty]$, parameters that represent probabilities live on $[0, 1]$, etc.. In that case it is sometimes convenient to use a random walk proposal distribution that can generate any real number (e.g., a normal random walk proposal). In that case, we can just reject parameters that are outside of the parameter space (XXXX REF FOR THIS XXXX).

2.6 Practical Bayesian Analysis and MCMC

There are a number of really important practical issues to be considered in any Bayesian analysis and we cover some of these briefly here.

2.6.1 Choice of prior distributions

XXX integrate this material with previous section on prior distributions XXXXXX

Bayesian analysis requires that we choose prior distributions for all of the structural parameters of the model (we use the term structural parameter to mean all parameters that aren’t customary thought of as latent variables). We will strive to use priors that are meant to express little or no prior information - default or customary “non-informative” or diffuse priors. This will be $\text{Unif}(a, b)$ priors for parameters that have a natural bounded support and, for parameters that live on the real line we use either (1) diffuse normal priors; (2) “improper” uniform priors or (3) sometimes even a bounded $\text{Unif}(a, b)$ prior if that greatly improves the performance of **WinBUGS** or other software doing the MCMC for us. In **WinBUGS** a prior with low “precision”, τ , where $\tau = 1/\sigma^2$, such as $\text{Norm}(0, .01)$ will typically be used. Of course $\tau = 0.01$ ($\sigma^2 = 100$) might be very informative for a regression parameter that has a high variance. Therefore, we recommend that predictor variables *always* be standardized. Clearly there are a lot of choices for ostensibly non-informative priors, and the degree of non-informativeness depends on the parameterization. For example, a natural non-informative prior for the intercept of a logistic regression

$$\text{logit}(p_i) = \alpha + \beta x_i$$

Would be $[\alpha] = \text{const}$ which is the same as saying $a \sim \text{Unif}(\infty, \text{infty})$, the customary improper uniform prior. However, we might also use a prior on the parameter $p_0 = \text{logit}^{-1}(a)$, which is $\text{Pr}(y = 1)$ for the value $x = 0$. Since p_0 is a probability a natural choice is $p_0 \sim \text{Unif}(0, 1)$. These two priors can affect results (see Chapter 3.XYZ), yet they are both sensible non-informative priors. Choice of priors and parameterization is very much problem-specific and often largely subjective. Moreover, it also affects the behavior of MCMC algorithms and therefore the analyst needs to pay some attention to this issue and possibly try different things out. XXX REFS on prior distributions XXXXX

2.6.2 Convergence and so-forth

Once we have carried-out an analysis by MCMC, there are many other practical issues that we have to confront. One of the most important is “have the chains converged?” Most MCMC algorithms only guarantee that, eventually, the samples being generated will be from the target posterior distribution. So-called “convergence” of the Markov chain is achieved when that happens. Typically a period of transience is observed in the early part of the MCMC algorithm, and this is usually discarded as the “burn-in” period.

The quick diagnostic to whether convergence has been achieved is that your Markov chains look “grassy” – see Fig. 2.5 below. Another way to check convergence is to update the parameters some more and see if the posterior changes. It is good to confirm convergence using the “R-hat” statistic (\hat{R}) or Brooks-Gelman-Rubin statistic (Gelman et al., 1996) which should be close to 1 if the Markov chains have converged and sufficient posterior samples have been obtained. In practice, $\hat{R} = 1.2$ is probably good enough for some problems. For some models you can’t actually realize a low \hat{R} . E.g., if the posterior is a discrete mixture of distributions then you can be misled into thinking that your Markov chains have not converged when in fact the chains are just jumping back and forth in the posterior state-space. So, for example, using model selection methods (section XYZ) sometimes suggests non-convergence. Another situation is when one of the parameters is on the boundary of the parameter space which might appear to be very poor mixing, but all within some extreme region of the parameter space.⁴ This kind of stuff is normally ok and you need to think really hard about the context of the model and the problem before you conclude that your MCMC algorithm is ill-behaved.

Some models exhibit “poor mixing” of the Markov chains or what people might also say “have not covered” (or “slow convergence”) which is a term we would disagree with because the samples might well be from the posterior (i.e., the Markov chains have converged to the proper stationary distribution) but simply mix around the posterior rather slowly. Anyway, poor mixing can happen for a huge number of reasons – when parameters are highly correlated (even confounded), or barely identified from the data, or the algorithms are

⁴it would be nice if we could compile examples of this later in the book and reference back to this point

very terrible and probably many other reasons. Slow mixing equates to high autocorrelation in the Markov chain - the successive draws are highly correlated, and thus we need to run the MCMC algorithm much longer to get an effective sample size that is sufficient for estimation - or to reduce the MC error to a tolerable level. A strategy often used to reduce autocorrelation is “thinning” - i.e., keep every m^{th} value of the Markov chain output. However, thinning is necessarily inefficient from the stand point of inference - you can always get more precise posterior estimates by using all of the MCMC output regardless of the level of autocorrelation (MacEachern and Berliner, 1994). Practical considerations might necessitate thinning, even though it is statistically inefficient. For example, in models with many parameters or other unknowns being tabulated, the output files might be enormous and unwieldy to work with. In such cases, thinning is perfectly reasonable. In many cases, how well the Markov chains mix is strongly influenced by parameterization, standardization of covariates, and the prior distributions being used. Some things work better than others, and the investigator should experiment with different settings and remain calm when things don’t work out perfectly. MCMC is an art, and a science.

Is the posterior sample large enough? A good rule of thumb is that you should never report MCMC results to more than 2 decimal places - because they will always be different! Look at the MC error which is printed by default in summaries of BUGS output. You want that to be smallish relative to the magnitude of the parameter and this might depend on the purpose of the analysis. For a preliminary analysis you might settle for a few percent whereas for a final analysis then certainly less than 1% is called for, but you can run your MCMC algorithm as long as it takes. Note that MC error in summaries of the posterior is not the same as having an “approximate” solution in a standard likelihood analysis or similar. The approximate SE in likelihood inference is actually wrong in its actual value.... XYZ.

2.6.3 Bayesian confidence intervals

The 95% Bayesian interval based on percentiles of the posterior is not a unique interval - there are many of them - and the so-called “highest posterior density” (HPD) interval is the narrowest interval. We might compute that frequently because it is easy to do with an integer parameter which N is (See the next chapter). The 95 % HPD is not often exactly 95% but usually slightly more conservative than nominal because it is the narrowest interval that contains at least 95% of the posterior mass.

2.6.4 Estimating functions of parameters

A benefit of analysis by MCMC is that we can seamlessly estimate functions of parameters by simply tabulating the desired function of the simulated posterior draws. For example, if θ is the parameter of interest and let $\theta^{(i)}$ for $i = 1, 2, \dots, M$ be the posterior samples of θ . Let $\eta = \exp(\theta)$, then a posterior sample of η can be obtained simply by computing $\exp(\theta^{(i)})$ for $i = 1, 2, \dots, M$.

We give another example in section 2.7.2 below and throughout this book. Almost all SCR models in this book involve at least 1 derived parameter. For example, density D is a derived parameter, being a function of population size N and the area A of the underlying state-space of the point process (see chapter 4).

2.7 Bayesian Analysis using WinBUGS

We won't be too concerned with devising our own MCMC algorithms for every analysis although we will do that a few times for fun. More often, we will rely on the freely available software package **WinBUGS** or **JAGS** for doing this. We will always execute these **BUGS** engines from within **R** using the **R2WinBUGS** (REF XYZ XYZ) or **rjags** packages. **WinBUGS** and **JAGS** are MCMC black boxes that takes a pseudo-code description (i.e., written in the **BUGS** language) of all of the relevant stochastic and deterministic elements of a model and generates an MCMC algorithm for that model. But you never get to see the algorithm. Instead, **WinBUGS/JAGS** will run the algorithm and just return the Markov chain output - the posterior samples of model parameters.

The great thing about using the **BUGS** language is that it forces you to become intimate with your statistical model - you have to write each element of the model down, admit (explicitly) all of the various assumptions, understand what the actual probability assumptions are and how data relate to latent variables and data and latent variables relate to parameters, and how parameters relate to one another.

While we normally use **WinBUGS** or **JAGS** in this book, we note that **OpenBUGS** is the current active development tree of the **BUGS** language. See Kéry (2010, ch.xyz) and Kéry and Schaub (2011, appendix xyz) for more on practical analysis in **WinBUGS**. That book should also be consulted for a more comprehensive introduction to using **WinBUGS**. In this example, we're going to accelerate pretty fast.

2.7.1 Linear Regression in WinBUGS

We provide a brief introductory example of a normal regression model using a small simulated data set. The following commands are executed from within your R workspace, the command line being indicated by '`>`'. First, simulate a covariate x and observations y having prescribed intercept, slope and variance:

```
> x<-rnorm(10)
> mu<- -3.2+ 1.5*x
> y<-rnorm(10,mu,sd=4)
```

The **BUGS** model specification for a normal regression model is written within **R** as a character string input to the command `cat()` and then dumped to a text file named `normal.txt`:

```

661 > cat("
662 model {
663   for (i in 1:10){
664     y[i]~dnorm(mu[i],tau)           # the "likelihood"
665     mu[i]<- beta0 + beta1*x[i]      # the linear predictor
666   }
667   beta0~dnorm(0,.01)               # prior distributions
668   beta1~dnorm(0,.01)
669   sigma~dunif(0,100)
670   tau<-1/(sigma*sigma)             # tau is a derived parameter
671 }
672 ",file="normal.txt")

```

Alternatively, you can write the model specifications directly within a text file and save it in your current working directory, but we do not usually take that approach in this book.

Remarks: **1. WinBUGS** parameterizes the normal in terms of the mean and inverse-variance, called the precision. Thus, `dnorm(0,.01)` implies a variance of 100; **2.** We typically use diffuse normal priors for mean parameters, β_0 and β_1 in this case, but sometimes we might use uniform priors with suitable bounds $-B$ and $+B$. **3.** We typically use a `Unif(0, B)` prior on standard deviation parameters (Gelman XXX 2006 XXXX). But sometimes we might use a gamma prior on the precision parameter τ . **4.** In a **WinBUGS** model file, every variable referenced in the model description has to be either data, which will be input (see below), a random variable which must have a probability distribution associated with it using the “~”, or it has to be a derived parameter connected to variables and data using “<-”.

To fit the model, we need to describe various data objects to **WinBUGS**. In particular, we create an **R** list object called `data` which are the data objects identified in the BUGS model file. In the example, the data consist of two objects which exist as y and x in the **R** workspace and also in the **WinBUGS** model definition. We also have to create an **R** function that produces a list of starting values `inits` that get sent to **WinBUGS**. Finally, we identify the names of the parameters (labeled correspondingly in the **WinBUGS** model specification) that we want **WinBUGS** to save the MCMC output for. In this example, we will “monitor” the parameters β_0 , β_1 , σ and τ . **WinBUGS** is executed using the **R** command `bugs()`. We set the option `debug=TRUE` if we want the **WinBUGS** GUI to stay open (useful for analyzing MCMC output and looking at the **WinBUGS** error log). Also, we set `working.dir=getwd()` so that **WinBUGS** output files and the log file are saved in the current **R** working directory. All of these activities look like this:

```

701 library("R2WinBUGS")    # "attach" the R2WinBUGS library
702 data <- list ( "y","x")
703 inits <- function()
704   list ( beta1=rnorm(1),beta0=rnorm(1),sigma=runif(1,0,2) )
705 parameters <- c("beta0","beta1","sigma","tau")
706 out<-bugs (data, inits, parameters, "normal.txt", n.thin=2, n.chains=2,

```

```

707         n.burnin=2000, n.iter=6000, debug=TRUE,working.dir=getwd())

```

708 **Remarks:** A common question is “how should my data be formatted?”
709 That depends on how you describe the model in the **BUGS** language, how
710 your data are input into **R** and subsequently formatted. There is no unique
711 way to describe any particular model and so you have some flexibility. We
712 talk about data format further in the context of capture-recapture models and
713 **SCR** models in chapter 4 and elsewhere. In general, starting values are optional
714 but we recommend to always provide reasonable starting values for structural
715 parameters, but are not always necessary for random effects. Note that the pre-
716 viously created objects defining data, initial values and parameters to monitor
717 are passed to the function `bugs()`. In addition, various other things are de-
718 clared: The number of Markov chains (`n.chains`), the thinning rate (`n.thin`),
719 the number of burn-in iterations (`n.burnin`) and the total number of iterations
720 (`n.iter`). To develop a detailed understanding of the various parameters and
721 settings used for MCMC, consult a basic reference such as Kéry (2010).

722 You should execute all of the commands given above and then look at the
723 resulting output. Kill the **WinBUGS** GUI and the data will be read back
724 into **R** (or specify `debug=FALSE`). We don’t want to give instructions on how
725 to navigate and use the GUI - see XYZ REF (XYZ) for that. The object `out`
726 prints important summaries by default (this is slightly edited):

```

727 > print(out,digits=2)
728 Inference for Bugs model at "normal.txt", fit using WinBUGS,
729 2 chains, each with 6000 iterations (first 2000 discarded), n.thin = 2
730 n.sims = 4000 iterations saved
731      mean   sd  2.5%  25%   50%   75%  97.5% Rhat n.eff
732 beta0  -2.43 1.84 -6.21 -3.50 -2.42 -1.34  1.27   1  4000
733 beta1   2.62 1.54 -0.42  1.68  2.62  3.57  5.67   1  4000
734 sigma   5.29 1.66  3.11  4.14  4.95  6.05  9.39   1  4000
735 tau     0.05 0.02  0.01  0.03  0.04  0.06  0.10   1  4000
736 deviance 59.85 3.24 56.18 57.47 59.00 61.37 68.32   1   840
737
738 For each parameter, n.eff is a crude measure of effective sample size,
739 and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
740
741 DIC info (using the rule, pD = Dbar-Dhat)
742 pD = 2.6 and DIC = 62.4

```

743 **Remarks:** (1) convergence is assessed using the \hat{R} statistic – which we
744 might sometimes write “*Rhat*”. A value of *Rhat* near 1 indicates convergence;
745 (2) DIC is the “deviance information criterion” (Spiegelhalter et al., 2002) (see
746 section 2.8) which some people use in a manner similar to AIC although it is
747 recognized to have some problems in hierarchical models (Millar, 2009). We
748 evaluate this in the context of **SCR** models in chapter XYZ XYZ.

2.7.2 Inference about functions of model parameters

Using the MCMC draws for a given model we can easily obtain the posterior distribution of any function of model parameters. We showed this in the above example by providing the posterior of τ when the model was parameterized in terms of standard deviation σ . As another example, suppose that the normal regression model above had a quadratic response function of the form

$$E(y_i) = \beta_0 + \beta_1 x_i + \beta_2 x_i^2$$

Then the optimum value of x , i.e., that corresponding to the optimal expected response, can be found by setting the derivative of this function to 0 and solving for x . We find that

$$df/dx = \beta_1 + 2 * \beta_2 x = 0$$

yields that $x_{opt} = -\beta_1/(2 * \beta_2)$. We can just take our posterior draws for β_1 and β_2 and obtain a posterior sample of x_{opt} by this simple calculation. As an exercise, take the normal model above and simulate a quadratic response and then describe the posterior distribution of x_{opt} .

2.8 Model Checking and Selection

In general terms model checking - or assessing the adequacy of the model - and model selection are quite thorny issues and, despite contrary and, sometimes, strongly held belief among practitioners, there are not really definitive, general solutions to either problem. We're against dogma on these issues and think people need to be open-minded about such things and recognize that models can be useful whether or not they pass certain statistical tests. Some models are intrinsically better than others because they make more biological sense or foster understanding or achieve some objective that some bootstrap or other goodness-of-fit test can't decide for you. That said, it gives you some confidence if your model seems adequate and we try to provide some fit assessment in most real applications of SCR models. We provide a very brief overview of concepts here, but provide more detailed coverage in chapter 8. See also Kéry (2010, ch. xyz) and Link and Barker (2009, ch. xyz) for specific context related to Bayesian model checking and selection.

2.8.1 Goodness-of-fit

Goodness-of-fit testing is an important element of any analysis because our model represents a general set of hypotheses about the ecological and observation processes that generated our data. Thus, if our model "fits" in some statistical or scientific sense, then we believe it to be consistent with the hypotheses that went into the model. More formally, we would conclude that the data are *not inconsistent* with the hypotheses, or that the model appears adequate. If we have enough data, then of course we will reject any set of statistical hypotheses. Conversely, we can always come up with a model that fits

by making the model extremely complex. Despite this paradox, it seems to us that simple models that you can understand should usually be preferred even if they don't fit, for example if they embody essential mechanisms central to our understanding of things, or if we think that some contributing factors to lack-of-fit are minor or irrelevant to the scientific context and intended use of the model. In other words, models can be useful irrespective of whether they fit according to some formal statistical test of fit. Yet the tension is there to obtain fitting models, and this comes naturally at the expense of models that can be easily interpreted and studied and effectively used. Moreover, conducting goodness-of-fit tests is not always so easy to do. Moreover, it is never really easy (or especially convenient) to decide if your goodness-of-fit test is worth anything. It might have 0 power! Despite this, we recommend attempting to assess model fit in real applications, as a general rule, and we provide some basic guidance here and some more specific to SCR models in chapter 8.

To evaluate goodness-of-fit in Bayesian analyses, we will most often use the Bayesian p-value (Gelman et al., 1996). The basic idea is to define a fit statistic or “discrepancy measure” and compare the posterior distribution of that statistic to the posterior predictive distribution of that statistic for hypothetical perfect data sets for which the model is known to be correct. For example, with count frequency data, a standard measure of fit is the sum of squares of the “Pearson residuals”,

$$D(y_i, \theta) = \frac{(y_i - E(y_i))^2}{Var(y_i)}$$

The fit statistic based on the squared residuals is

$$FIT = \sum_i D(y_i, \theta)^2$$

which can be computed at each iteration of a MCMC algorithm given the current values of parameters that determine the response distribution. At the same time (i.e., at each MCMC iteration), the equivalent statistic is computed for a “new” data set, simulated using the current parameter values. The Bayesian p-value is simply the posterior probability $\Pr(\text{Fit} > \text{Fit}_{new})^5$ which should be close to 0.50 for a good model – one that “fits” in the sense that the observed data set is consistent with realizations simulated under the model being fitted to the observed data. In practice we judge “close to 0.50” as being “not too close to 0 or 1” and, as always, closeness is somewhat subjective. We're happy with anything $> .1$ and $< .9$ but might settle for $> .05$ and < 0.95 . In summary, the Bayesian p-value seems like a bootstrap idea, is easy to compute, and widely used as a result.

Another useful fit statistic is the Freeman-Tukey statistic⁶, in which

$$D(\mathbf{y}, \theta) = \sum_i (\sqrt{y_i} - \sqrt{e_i})^2$$

⁵Check this definition!

⁶Ref for this?

(Brooks et al., 2000), where y_i is the observed value of observation i and e_i its expected value. In contrast to a chi-square discrepancy, the Freeman-Tukey statistic removes the need to pool cells with small expected values.

2.8.2 Model Selection

For model selection we typically use three different methods: First is, let's say, common sense. If a parameter has posterior mass concentrated away from 0 then it seems like it should be regarded as important - that is, it is "significant." This approach seems to have fallen out of favor with all of the interest over the last 10 or 15 years on model selection in ecology. It seems reasonable to us.

For regression problems we sometimes use the factor weighting idea which is to introduce a set of binary variables w_k for variable k , and express the model as, e.g., for a single covariate model:

$$E(y_i) = \alpha + w\beta x_i$$

where w is given a Bernoulli prior distribution with some prescribed probability. E.g., $w \sim \text{Bern}(0.50)$ to provide a prior probability of 0.50 that variable x should be an element of the linear predictor. The posterior probability of the event $w = 1$ is a gauge of the importance of the variable x . i.e., high values of $\text{Pr}(w = 1)$ indicate stronger evidence to support that " x is in the model" whereas values of $\text{Pr}(w = 1)$ close to 0 suggest that x is less important.

This idea seems to be due to Kuo and Mallick (1998)⁷ and see Royle and Dorazio (2008, ch. XXXX) for an example in the context of logistic regression. This approach seems to even work sometimes with fairly complex hierarchical models of a certain form. E.g., Royle (2008) applied it to a random effects model to evaluate the importance of the random effect component of the model. The main problem with this approach is that its effectiveness and results will typically be highly sensitive to the prior distribution on the structural parameters (e.g., see Royle and Dorazio (2008, table xyz)). The reason for this is obvious: If $w = 0$ for the current iteration of the MCMC algorithm, so that β is sampled from the prior distribution, and the prior distribution is very diffuse, then extreme values of β are likely. Consequently, when the current value of β is far away from the mass of the posterior when $w = 1$, then the Markov chain may only jump from $w = 0$ to $w = 1$ infrequently. One seemingly reasonable solution to this problem (Aitken XYZ FIND THIS XXXXX⁸) is to fit the full model to obtain posterior distributions for all parameters, and then use those as prior distributions in a "model selection" run of the MCMC algorithm. This seems preferable to more-or-less arbitrary restriction of the prior support to improve the performance of the MCMC algorithm.

A third method that that we advocate is subject-matter context. It seems that there are some situations - some models - where one should not have to do model selection because it is necessitated by the specific context of the

⁷Is this also what people call Zellner's G-priors?

⁸see Royle 2008 paper for reference

problem, thus rendering a formal hypothesis test pointless (Johnson, 1999). SCR models are such an example. In SCR models, we will see that “spatial location” of individuals is an element of the model. The simpler, reduced, model is an ordinary capture-recapture model which is not spatially explicit (i.e., chapter 3), but it seems silly and pointless to think about actually using the reduced model even if we could concoct some statistical test to refute the more complex model. The simpler model is manifestly wrong but, more importantly, not even a plausible data-generating model! Other examples are when effort, area or sample rate is used as a covariate. One might prefer to have such things in models regardless of whether or not they pass some statistical litmus test (although one can always find referees to argue for pedantic procedure over thinking).

Many problems can be approached using one of these methods but there are also broad classes of problems that can’t and, for those, you’re on your own. In later chapters we will address model selection in specific contexts and we hope those will prove useful for a majority of the situations you encounter.

2.9 Poisson GLMs

The Poisson GLM (also known as “Poisson regression”) is probably the most relevant and important class of models in all of ecology. The basic model assumes observations $y(i); i = 1, 2, \dots, n$ follow a Poisson distribution with mean lambda which we write

$$y(i) \sim \text{Poisson}(\lambda)$$

Commonly $y(i)$ is a count of animals or plants at some point in space and lambda might depend on i . For example, i might index point count locations in a forest, BBS route centers, or sample quadrats, or similar. If covariates are available it is typical to model them as linear effects on the log mean. If $x(i)$ is some measured covariate associated with observation i . Then,

$$\log(x(i)) = \alpha + \beta * x(i)$$

While we only specify the mean of the Poisson model directly, the Poisson model (and all GLMs) has a “built-in” variance which is directly related to the mean. In this case, $\text{Var}(y) = E(y) = \lambda$. Thus the model accommodates a linear increase in variance with the mean. Another extremely useful feature of the Poisson model is the property of “compound additivity”. If $y(1)$ and $y(2)$ are Poisson random variables with means $\lambda[1]$ and $\lambda[2]$, then $y(1) + y(2)$ is Poisson with mean $(\lambda[1] + \lambda[2])$. Thus, if the observations can be viewed as an aggregate of counts over some finer scale, then the mean aggregates in a corresponding manner. Multinomial random variables have a direct relationship to Poisson random variables. If $y(1)$ and $y(2)$ are *iid* Poisson then, conditional on their total $T = y(1) + y(2)$, they have a multinomial distribution with sample size T and cell probabilities $\lambda[1]/(\lambda[1] + \lambda[2])$ and $\lambda[2]/(\lambda[1] + \lambda[2])$. These are some of the reasons the Poisson distribution is extremely useful in ecology.

2.9.1 Example: Breeding Bird Survey Data

As an example we consider a classical situation in ecology where counts of an organism are made at a collection of spatial locations. In this particular example, we have mourning dove counts made along North American Breeding Bird Survey (BBS) routes in Pennsylvania, USA. A route consists of 50 stops separated by 0.5 mile. For the purposes here we are defining $y[i]$ = route total count and the sample location will be marked by the center point of the BBS route. The survey is run annually and the data set we have is 1966-1998. BBS data can be obtained online at <http://...xyz.xyz.xyz>. We will make use of the whole data set shortly but for now we're going to focus on a specific year of counts - 1990 - for no particular reason. For 1990 there were 77 active routes. We have the data stored in a .csv file where rows index the unique route, column 1 is the route ID, columns 2-3 are the route coordinates (longitude/latitude), column 4 is a habitat covariate "forest cover" (standardized, see below) and the remaining columns are the yearly counts. Years for which a route was not run are coded as "NA" in the data matrix. We imagine that this will be a typical format for many ecological studies, perhaps with more columns representing covariates. To read in the data and display the first few elements of this matrix, do this:

```
> a<-read.csv("pa-bbsdovedata-all.csv")
> data[1:2,1:6]
      X      lon      lat      habitat X66 X67
1 72002 -80.445 41.501 -0.3871372  NA  24
2 72003 -80.347 41.214 -1.0171629  NA  NA
```

It is useful to display the pattern in counts. For that we use a spatial dot plot - where we plot the coordinates of the observations and mark the color of the plotting symbol based on the magnitude of the count. We have a special plotting function for that which is called `spatial.plot()` and it is available with the supplemental materials. Actually, what we want to do here is plot the log-count (+1 of course!) which displays a notable pattern that could be related to something. We can ponder the potential effects that might lead to dove counts being high....Corn fields, telephone wires, barn roofs along with misidentification of pigeons, these could all correlated reasonably well with these counts for all we know. Unfortunately we don't have any of that information.

We do have a measure of forest cover in the vicinity of each point which is contained in the data set ("habitat"). This was derived from a larger GIS coverage of the state (provided in the data file "pahabdata") which can be plotted using the `spatial.plot` function using the following commands

```
> map('state',regions="penn",lwd=2)
> spatial.plot(pahabdata[,2:3],pahabdata[, "dfor"],cx=2)
> map('state',regions="penn",lwd=2,add=TRUE)
```

We see a prominent pattern that indicates high forest coverage in the central part of the state and low forest cover in the SE. Inspecting the previous figure

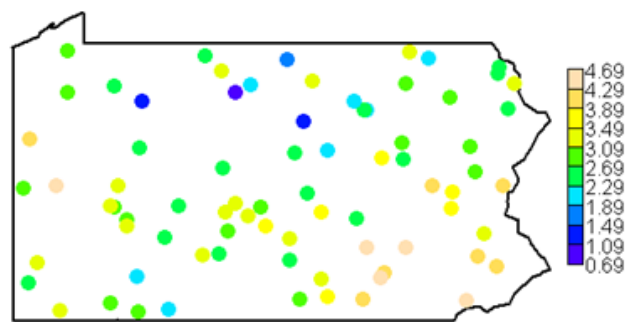


Figure 2.1: Needs a caption

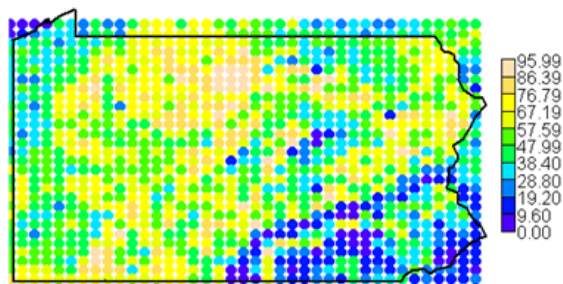


Figure 2.2: Needs a caption

of log-counts suggests a relationship between counts and forest cover which is not surprising.

2.9.2 Doing it in WinBUGS

Here we demonstrate how to fit a Poisson GLM in WinBUGS using the covariate $x(i)$ = forest cover. It is advisable that $x(i)$ be standardized in most cases as this will improve mixing of the Markov chains. Recall that the data we have stored include a standardized covariate (forest cover) and so we don't have to worry about that here. To read the BBS data into R and get things set up for WinBUGS we issue the following commands:

```
data<-read.csv("pa-bbsdovedata-all.csv")
y<-data[,29] # pick out 1990
notna<-!is.na(y)
y<-y[notna]
habitat<-data[notna,4]
library("R2WinBUGS")
data <- list ( "y","M","habitat")
```

Now we write out the Poisson model specification in WinBUGS pseudo-code, provide initial values, identify parameters to be monitored and then execute WinBUGS:

```
cat("
model {
  for (i in 1:M){
    y[i]~dpois(lam[i])
    log(lam[i])<- beta0+beta1*habitat[i]
  }
  beta0~dunif(-5,5)
  beta1~dunif(-5,5)
}
",file="PoissonGLM.txt")

inits <- function() list ( beta0=rnorm(1),beta1=rnorm(1))
parameters <- c("beta0","beta1")
out<-bugs (data, inits, parameters, "PoissonGLM.txt", n.thin=2, n.chains=2, n.burnin=2000)
```

Remarks: (1) Note the close correspondence in how the model is specified here compared with the normal regression model previously. As an exercise you should discuss the specific differences between the BUGS model specifications for the normal and Poisson models.

```
> print(out,digits=3)
Inference for Bugs model at
'PoissonGLM.txt', fit using WinBUGS,
2 chains, each with 4000 iterations (first 1000 discarded), n.thin = 2
```

```

983 n.sims = 3000 iterations saved
984      mean      sd      2.5%      25%      50%      75%      97.5%  Rhat n.eff
985 beta0      3.151  0.025      3.102      3.135      3.151      3.168      3.199 1.001 2300
986 beta1     -0.498  0.021     -0.539     -0.512     -0.498     -0.484     -0.457 1.001 3000
987 fit       869.930 19.856    835.500    855.700    868.600    881.900    913.602 1.002 1600
988 fitnew     76.709 12.519     54.098     68.107     76.215     84.510    102.602 1.001 3000
989 deviance  1116.605  2.014   1115.000   1115.000   1116.000   1117.000   1122.000
990 1.001 3000

```

991 We might wonder whether this model provides an adequate fit to our data.
 992 To evaluate that, we used a Bayesian p-value analysis with fit statistic based
 993 on the Freeman-Tukey residual by replacing the model specification above with
 994 this:

```

995 cat("
996 model {
997   for (i in 1:M){
998     y[i]~dpois(lam[i])
999     log(lam[i])<- beta0+beta1*habitat[i]
1000     d[i]<- pow(pow(y[i],0.5)-pow(lam[i],0.5),2)    #
1001
1002     ynew[i]~dpois(lam[i])
1003     dnew[i]<-pow( pow(ynew[i],0.5)-pow(lam[i],0.5),2)
1004
1005   }
1006   fit<-sum(d[])
1007   fitnew<-sum(dnew[])
1008   beta0~dunif(-5,5)
1009   beta1~dunif(-5,5)
1010 }
1011
1012
1013 ",file="PoissonGLM.txt")

```

1014 The Bayesian p-value is the proportion of times *fitnew* > *fit* which, for this
 1015 data set, is 0, which was 1.0 in this case (calculation omitted). This suggests
 1016 that the basic Poisson model does not fit well.

1017 2.9.3 Constructing your own MCMC algorithm

1018 It will be helpful for people to suffer through a couple examples building a
 1019 custom MCMC algorithm. So, here, we build a basic one for the Poisson regres-
 1020 sion model using a Metropolis-within-Gibbs approach. First, we will assume
 1021 that the two parameters have diffuse normal priors, say $[\alpha] = \text{norm}(0, 100)$ and
 1022 $[\beta] = \text{norm}(0, 100)$. We need to collect the relevant elements of the model which
 1023 are the likelihood $[y|\alpha, \beta] = \text{prod}_i [y[i]|\alpha\beta]$ which is, mathematically, the prod-
 1024 uct of the Poisson pmf evaluated at $y[i]$, given particular values of β_0 and β_1 .

1025 The priors are $[\alpha]$ and $[\beta]$. We identify the full conditionals which are $[\alpha|\beta, y]$
 1026 and $[\beta|\alpha, y]$. We use the all-purpose rule for constructing full conditionals to
 1027 discover that:

$$\begin{aligned} & [\alpha|\beta, y] \propto [y|\alpha, \beta][\alpha] \\ & [\beta|\alpha, y] \propto [y|\alpha, \beta][\beta] \end{aligned}$$

1029 Remember we could replace the “propto” with “equals” if we simply put $[y|\beta]$
 1030 or $[y|\alpha]$ in the denominator. But, in general, $[y|\alpha]$ or $[y|\beta]$ will be quite a
 1031 pain to compute and, more importantly, it is a constant as far as the operative
 1032 parameter (beta or alpha, respectively) goes so we can just as well ignore it
 1033 because, recall, the MH acceptance probability will be the ratio of the full-
 1034 conditional evaluated at a candidate draw to that evaluated at the current
 1035 draw. So, the denominator required to change α to $=$ winds up canceling from
 1036 the MH acceptance probability. Here we will use the random walk candidate
 1037 generator. The “Metropolis within Gibbs” algorithm for a Poisson regression is
 1038 remarkably simple:

1039 I would break this code up into more lines and have objects called “prior” and “pri

1040 You could also mention that this is a random walk M-H. It would help lots of people out

```

1041 # put random number seed here
1042 out<-matrix(NA,nrow=1000,ncol=2)    # matrix to store the output
1043 beta0<- -1                          # starting values
1044 beta1<- -.8
1045
1046 # begin the MCMC loop ; do 1000 iterations
1047 for(i in 1:1000){
1048
1049   # update the beta0 parameter
1050   lik.curr<- sum(log(dpois(y,exp(beta0+beta1*habitat))))
1051   prior.curr<- log(dnorm(beta0,0,100))
1052   beta0c<-rnorm(1,beta0,.25)         # generate candidate
1053   lik.cand<- sum(log(dpois(y,exp(beta0c+beta1*habitat))))
1054   prior.cand<- log(dnorm(beta0c,0,100))
1055   if(runif(1)< exp(lik.cand+prior.cand-lik.curr-prior.curr)) beta0<-beta0c
1056
1057   # update the beta1 parameter
1058   lik.curr<- sum(log(dpois(y,exp(beta0+beta1*habitat))))
1059   prior.curr<- log(dnorm(beta1,0,100))
1060   beta1c<-rnorm(1,beta1,.25)
1061   lik.cand<- sum(log(dpois(y,exp(beta0+beta1c*habitat))))
1062   prior.cand<- log(dnorm(beta1c,0,100))
1063   if(runif(1)< exp(lik.cand+prior.cand-lik.curr-prior.curr)) beta1<-beta1c
1064   out[i,]<-c(beta0,beta1)             # save the current values
1065 }
1066

```

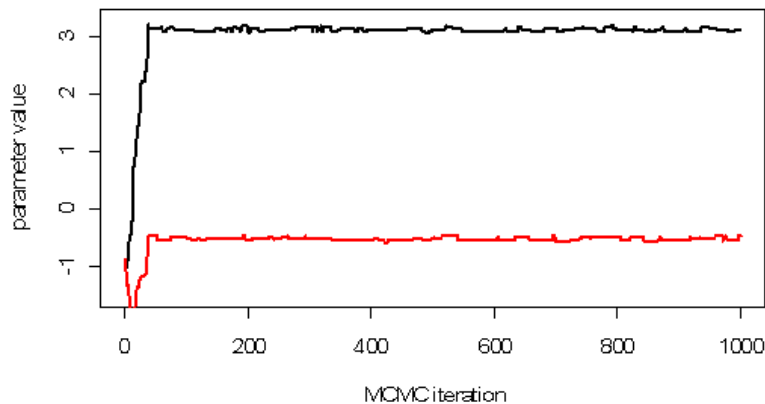


Figure 2.3: Needs a caption

Look at the output (beta0 in red, beta1 in black). You might not like the appearance of this output too much but a couple of things are evident: The Markov chains clearly stabilize - “converge” – after about 100 iterations. They also appear to mix very slowly, although this is not so clear given the scale of the y-axis.

We decreased the variance for candidate generating distribution and re-ran the MCMC algorithm producing the history plots below. We see that the burn-in takes longer but it seems to mix better.

Fig. XYZ shows a longer MCMC run (10,000 total iterations) for beta1 based on discarding the first 400 samples as burn-in. The “grassy” look of the MCMC history is diagnostic of Markov chains that are well-mixing.

Remarks: We used a specific set of starting values for these simulations. It should be clear that starting values closer to the mass of the posterior distribution might cause burn-in to occur faster. As an exercise, evaluate that. (2) Clearly the influence of the proposal variance term is important. Small values lead to much better mixing but it should be noted that values that are too small will lead to very slow mixing. We saw that values that were too large tended to get the parameters stuck in one spot. This suggests there is an optimal value of the Metropolis-Hastings tuning parameter⁹. As an exercise you should find that optimal value. (3) For the flat normal prior distributions here we could leave the prior contribution out of the full conditional evaluation since it is “locally constant”. Note also that we have used a different prior than in our WinBUGS model specification. As an exercise, evaluate whether this seems to affect the

⁹Defined previously?

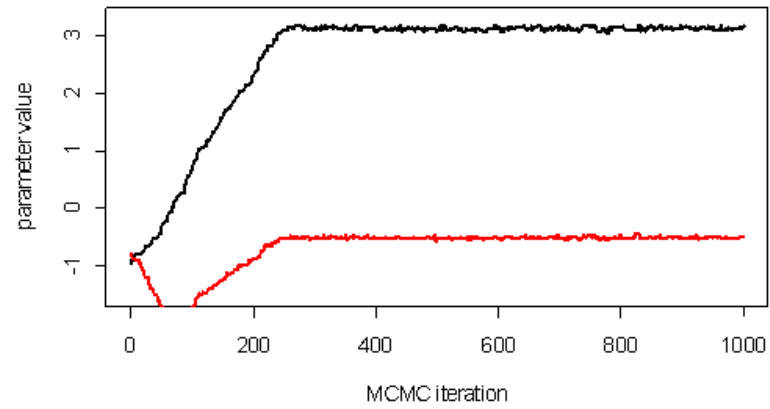


Figure 2.4: Needs a caption

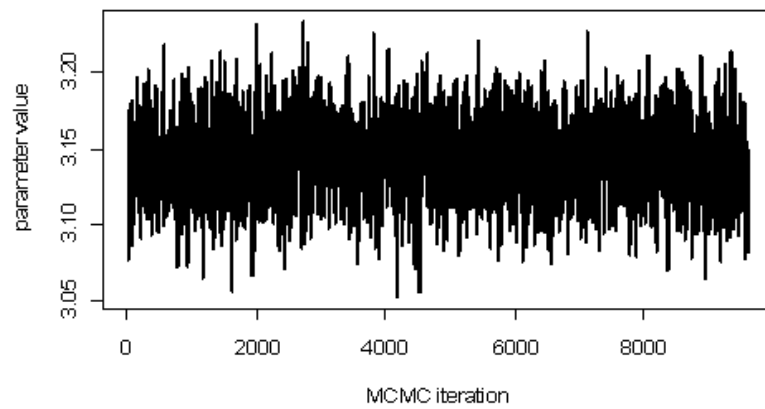


Figure 2.5: nice grassy mcmc output

1091 result.

1092 2.10 Poisson GLM with Random Effects

1093 What we will be doing in most of this book is dealing with random effects
1094 in GLM-like models - models that are usually referred to as generalized linear
1095 mixed models (GLMMs).

1096 **The Log-Normal mixture:** The classical situation involves a GLM with
1097 a normally distributed random effect. The linear predictor of the Poisson model
1098 is extended simply by adding a noise term, say:

$$\log(\lambda(i)) = \alpha + \beta * x(i) + \eta[i]$$

1099 where $\eta[i] \sim \text{normal}(0, \sigma^2)$. A natural alternative is to have $\exp(\eta[i]) / \sim \gamma(a, b)$
1100 which would correspond to a negative binomial kind of over-dispersion whereas
1101 the normal noise has a different mean/variance relationship (the interested
1102 reader should work that out). Choosing between such possibilities is not a
1103 topic we will get into here because it doesn't seem possible to provide general
1104 guidance on it. Anyhow, it is really amazingly simple to express this model in
1105 WinBUGS and have WinBUGS draw samples from the posterior distribution
1106 using the following code for the BBS dove counts:

```
1107 data<-read.csv("pa-bbsdovedata-all.csv")
1108 locs<-data[,2:3]
1109 habitat<-data[,4]
1110 y<-data[,29]
1111 notna<-!is.na(y) # to remove missing values
1112 y<-y[notna]
1113 locs<-locs[notna,]
1114 habitat<-habitat[notna]
1115 M<-length(y)
1116
1117 cat("
1118 model {
1119     for (i in 1:M){
1120         y[i]~dpois(lam[i])
1121         log(lam[i])<- beta0+beta1*habitat[i] + eta[i]
1122         eta[i] ~ dnorm(0,tau)
1123     }
1124     beta0~dunif(-5,5)
1125     beta1~dunif(-5,5)
1126     sigma~dunif(0,10)
1127     tau<-1/(sigma*sigma)
1128 }
```

1129 I have removed the final several R commands which package up the data and
1130 execute WinBUGS as those commands are largely redundant with the previous

demo. The summary results are:

```

1132 > print(out,digits=3)
1133 Inference for Bugs model at "model.txt", fit using WinBUGS,
1134 2 chains, each with 5000 iterations (first 1000 discarded), n.thin = 2
1135 n.sims = 4000 iterations saved
1136      mean      sd    2.5%    25%    50%    75%   97.5%  Rhat  n.eff
1137 beta0      2.967  0.076   2.817   2.915   2.969   3.020   3.111 1.006   430
1138 beta1     -0.518  0.073  -0.657  -0.566  -0.517  -0.470  -0.374 1.008 4000
1139 sigma      0.598  0.059   0.491   0.556   0.594   0.634   0.725 1.004   640
1140 tau       2.883  0.569   1.904   2.489   2.836   3.233   4.149 1.004   640
1141 fit       19.885  3.190  14.119  17.670  19.705  21.902  26.610 1.001 4000
1142 fitnew     20.043  3.422  14.100  17.630  19.770  22.292  27.360 1.001 4000
1143 deviance  446.255 12.290 424.000 437.700 445.600 454.100 472.302 1.001 4000
1144
1145 For each parameter, n.eff is a crude measure of effective sample size,
1146 and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
1147
1148 DIC info (using the rule, pD = Dbar-Dhat)
1149 pD = 66.0 and DIC = 512.2
1150 DIC is an estimate of expected predictive error (lower deviance is better).
1151 >
1152

```

The Bayesian p-value for this model is

```

1154 > mean(out$sims.list$fit>out$sims.list$fitnew)
1155 [1] 0.473
1156 >

```

indicating a pretty good fit. Given the site-level random effect, it would be surprising for this model to not fit! One thing we notice is that the posterior standard deviations of the regression parameters are much higher, a result of the excess variation. (we would also notice much less precise predictions of hypothetical new observations).

2.11 Binomial GLMs

Another class of statistical models that are very important in ecology are binomial models. We use binomial models for count data whenever the observations are counts or frequencies and it is natural to condition on a “sample size” - the maximum frequency possible in a sample, say K (i.e., K is known). The random variable, y/leK , is then the frequency of occurrences out of K . The parameter of the binomial models is p , often called “success probability” which is related to the expected value of y by $E[y] = pK$. Binomial GLMs or binomial regression models are often referred to as logistic regression, but that term really

only applies when the logistic link is used to model the relationship between p and covariates (see below).

One of the most typical Binomial GLMs occurs when the sample size equals 1 and the outcome, y , is “presence” ($y = 1$) or “absence” ($y = 0$) of a species. This is a classical “species distribution” modeling situation. A special situation occurs when presence/absence is observed with error (MacKenzie et al., 2002; MacKenzie, 2006; Kéry et al., 2010). In that case, $K > 1$ samples are usually required in order to estimate model parameters effectively. In standard binomial regression problems the sample size is fixed by design but interesting models also arise when the sample size is itself a random variable. These are the N-mixture models (Royle, 2004; Kéry et al., 2005; Royle and Dorazio, 2008; Kéry, 2010) ch. 22) and related models (in this case, N being the sample size which we labeled K above). This is actually a little bit confusing because the binomial index is usually referred to as “sample size” but in this context N is actually a “population size”. A useful situation in which the binomial sample size is “fixed” is closed population capture-recapture models in which a population of individuals is sampled K times. The number of times each individual is encountered is a binomial outcome with parameter - encounter probability - p , based on a sample of size K . We consider such models in the following chapter.

2.11.1 Binomial regression

In binomial models, covariates are modeled on a suitable transformation (the link function) of the binomial success probability, p . Let x_i denote some measured covariate for sample unit i and let p_i be the success probability for unit i . The standard choice is the “logit” link function which is:

$$\log(p[i]/(1 - p[i])) = \alpha + \beta * x[i]$$

with inverse “expit”

$$p[i] = \text{expit}(\alpha + \beta * x[i]) = \exp(\alpha + \beta * x[i]) / (1 + \exp(\alpha + \beta * x[i]))$$

There are many other possible link functions. However, ecologists seem to blindly adopt the logit link function without question to such an extent that you are likely to be questioned by referees and associate editors if you use some alternative link (unless you are doing species distribution modeling, in which case any explicit link function will be questioned by some referees). We sometimes use the “complementary log-log” (= “cloglog”) link function in ecological applications because it can often be justified based on subject-matter considerations (Royle and Dorazio (2008); section XYZ) or natural scaling relationships germane to the problem. For example, the cloglog link arises as the “probability of a count greater than 0” under a Poisson model. That is, $\Pr(y > 0) = 1 - \exp(-\lambda)$ in which case

$$\text{cloglog}(p) = \log(-\log(1 - p)) = \log(\lambda)$$

So that if you have covariates in your linear predictor for $E[y]$ under a Poisson model then they are linear on the complementary log-log link of p . We will use the cloglog link in some analyses of SCR models in Chapter 4 and elsewhere.

A natural situation in which the cloglog link arises is modeling occupancy in which $N \sim \text{Poisson}(A * \lambda)$ and you have site area, A , measured for every sample. In this case the probability that the site is occupied, ψ , is related to area on the cloglog scale. i.e.,

$$\text{cloglog}(\psi) = \log(A) + \log(\lambda).$$

There seems to be perennial debate over whether site area should be a covariate on “detection” or “occupancy” and the above argument suggests the latter.

2.11.2 Example: Waterfowl Banding Data

It would be easy to consider a standard “distribution modeling” application where $K = 1$ and the outcome is occurrence ($y = 1$) or not ($y = 0$) of some species. Such examples abound in books (e.g., Royle and Dorazio (2008), ch. 3; Kéry (2010), chapter 21 XYZ?; Kéry and Schaub (2011), chapter XYZ) and in the literature (see Kéry et al. (2010); Kéry et al. (2010) XYZ). Instead, we will consider an example involving band returns of waterfowl which were analyzed by Royle and Dubovsky (200X)¹⁰.

For these data, $y[i]$ is the number of waterfowl bands recovered out of $B[i]$ birds banded at some location $s[i]$. In this case $B[i]$ is fixed. Thinking about recovery rate as being proportional to harvest rate, we wanted to explore geographic gradients in recovery rate resulting from variability in harvest pressure experienced by populations depending on their migration ecology. As such, we fit a basic binomial GLM with a linear response to geographic coordinates (including an interaction term). The data are provided on the web supplement along with an R script to do the post-processing. Here we just provide the part of the script for creating the model and calling WinBUGS:

```
sink("model.txt")
cat("
model {
  for(t in 1:5){
    for (i in 1:nobs){
      m[i,t] ~ dbin(p[i,t], R[i,t])
      logit(p[i,t]) <- alpha0[t] + alpha1*X[i,1] + alpha2*X[i,2] + alpha3*X[i,1]*X[i,2]
    }
  }
  alpha1~dnorm(0,.001)
  alpha2~dnorm(0,.001)
  alpha3~dnorm(0,.001)
  for(t in 1:5){
    alpha0[t] ~ dnorm(0,.001)
  }
}
```

¹⁰not happy about this example. Anyone got a better one?

```

1249 ",fill=TRUE)
1250 sink()
1251
1252 data <- list('R', 'm', 'nobs','X')
1253 inits <- function(){
1254   list(alpha0=rnorm(5),alpha1=0,alpha2=0,alpha3=0)
1255 }
1256 parms <- list('alpha0','alpha1','alpha2','alpha3')
1257 out <- bugs(data,inits, parms,"model.txt",n.chains=3,
1258   n.iter=2000,n.burnin=1000,
1259   n.thin=2, debug=TRUE)

```

1260 Posterior summaries of model parameters are as follows:

```

1261 Inference for Bugs model at "model.txt", fit using WinBUGS,
1262 3 chains, each with 2000 iterations (first 1000 discarded), n.thin = 2
1263 n.sims = 1500 iterations saved

```

	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
1264 alpha0[1]	-2.346	0.036	-2.417	-2.370	-2.346	-2.323	-2.277	1.001	1500
1265 alpha0[2]	-2.356	0.032	-2.420	-2.379	-2.356	-2.335	-2.292	1.001	1500
1266 alpha0[3]	-2.220	0.035	-2.291	-2.244	-2.219	-2.197	-2.153	1.001	1500
1267 alpha0[4]	-2.144	0.039	-2.225	-2.169	-2.143	-2.116	-2.068	1.000	1500
1268 alpha0[5]	-1.925	0.034	-1.990	-1.949	-1.924	-1.901	-1.856	1.004	570
1269 alpha1	-0.023	0.003	-0.028	-0.025	-0.023	-0.022	-0.018	1.001	1500
1270 alpha2	0.020	0.006	0.009	0.016	0.020	0.024	0.031	1.001	1500
1271 alpha3	0.000	0.001	-0.002	-0.001	0.000	0.000	0.002	1.001	1500
1272 deviance	1716.001	4.091	1710.000	1713.000	1715.000	1718.000	1726.000	1.001	1500

```

1273
1274
1275 For each parameter, n.eff is a crude measure of effective sample size,
1276 and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
1277
1278 DIC info (using the rule, pD = Dbar-Dhat)
1279 pD = 7.9 and DIC = 1723.9
1280 DIC is an estimate of expected predictive error (lower deviance is better).

```

1281 The basic result suggests a negative east-west gradient and a positive south
 1282 to north gradient but no interaction. A map of the response surface is given
 1283 below. We could use DIC to do some model selection - i.e., try models with-
 1284 out the interaction term, or models with a quadratic term, or with a constant
 1285 intercept, etc., but we don't pursue that here. We did an MCMC run where
 1286 we saved the binomial parameter p and computed the Bayesian p -value [double
 1287 use of " p " here is confusing!] using a fit statistic based on the Freeman-Tukey
 1288 statistic (see Section XXX above). The result indicates that the linear response
 1289 surface model does not provide an adequate fit of the data. The reader should
 1290 contemplate whether this invalidates the basic interpretation of the result.

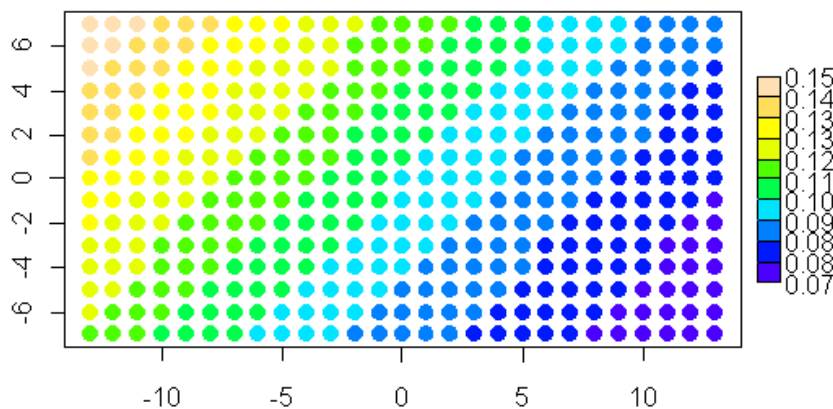


Figure 2.6: Needs a caption

2.12 Stuff on hierarchical models here?

2.13 Summary and Outlook

GLMs and GLMMs are the most useful statistical methods in all of ecology. The principles and procedures underlying these methods are relevant to nearly all modeling and analysis problems in every branch of ecology. Moreover, understanding how to analyze these models is crucial in a huge number of diverse problems. If you understand and can conduct classical likelihood and Bayesian analysis of Poisson and binomial GLM(M)s, then you will be successful analyzing and understanding more complex classes of models that arise. We will see shortly that spatial capture-recapture models are just a type of GLMM (i.e., a GLM with a random effect) and thus having a basic understanding of the conceptual origins and formulation of GLMs and their analysis is extremely useful. We note that GLMs are routinely analyzed by likelihood methods but we have focused on Bayesian analysis here in order to develop the tools that are less familiar to most ecologists. In particular, Bayesian analysis of GLMs with random effects (i.e., GLMMs) is relatively straightforward because the models are easy to analyze conditional on the random effect, using methods of MCMC. Thus, we will often analyze SCR models in later chapters by MCMC, explicitly adopting a Bayesian inference framework.

In that regard, BUGS engines are enormously useful because they provides a straightforward way to carry out analyses by MCMC by just describing the model, and not having to worry about how to actually build MCMC algorithms.

1313 That said, the BUGS language is more important than just to the extent that
1314 it enables one to do MCMC - it is useful as a modeling tool because it fosters
1315 understanding, in the sense that it forces you to become intimate with your
1316 model. You have to write down all of the probability assumptions, the relation-
1317 ships between observations and latent variables and parameters. This is really
1318 a great learning paradigm that you can grow with. Skills gained in Bayesian
1319 analysis of the GLMMs covered in this chapter will be directly transferrable and
1320 useful for the SCR models addressed subsequently. Before getting to that, how-
1321 ever, it will be useful to talk about more basic, conventional closed population
1322 capture-recapture models and these are the topic of the next Chapter.

1323 Chapter 3

1324 Closed population models

1325 **Chapter 4**

1326 **Fully Spatial**
1327 **Capture-Recapture Models**

1328 Chapter 5

1329 Other observation models

1330 Chapter 6

1331 Maximum likelihood 1332 estimation

¹³³³ **Chapter 7**

¹³³⁴ **MCMC details**

1335 Chapter 8

1336 Goodness of Fit and stuff

1337 Chapter 9

1338 Covariate models

1339 **Chapter 10**

1340 **Inhomogeneous Point**
1341 **Process**

1342 Chapter 11

1343 Open models

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