Chapter 10: Nonconjugate priors and Metropolis-Hastings algorithms

Contents

Generalized linear models

Poisson + logistic. No conjugate priors.

Metropolis algorithm

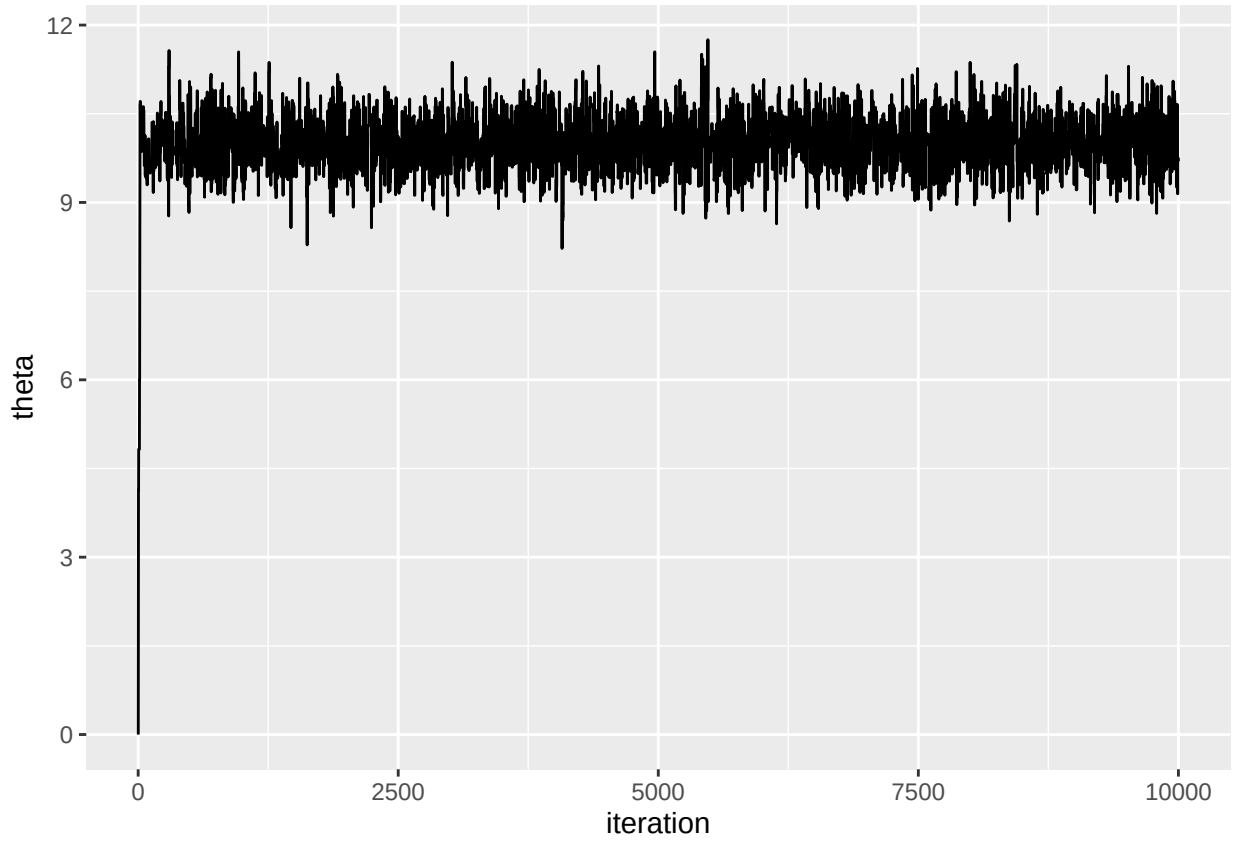
```
s2 = 1; t2 = 10; mu = 5
y = c(9.37, 10.18, 9.16, 11.60, 10.33)
theta = 0
delta2 = 2
S = 10000
THETA = rep(NA, S)
set.seed(1)
# theta - current sample
# theta.star - proposed sample according to proposal distribution
# log.r - acceptance ratio
for (s in 1:S) {
  theta.star = rnorm(1, theta, sqrt(delta2))
  log.r = (sum(dnorm(y, theta.star, sqrt(s2), log = TRUE)) +
             dnorm(theta.star, mu, sqrt(t2), log = TRUE)) -
    (sum(dnorm(y, theta, sqrt(s2), log = TRUE)) +
       dnorm(theta, mu, sqrt(t2), log = TRUE))

  if (log(runif(1)) < log.r) theta = theta.star

  THETA[s] = theta
}
```

```
theta.df = data.frame(
  iteration = 1:S,
  theta = THETA
```

```
)
ggplot(theta.df, aes(x = iteration, y = theta)) +
  geom_line()
```

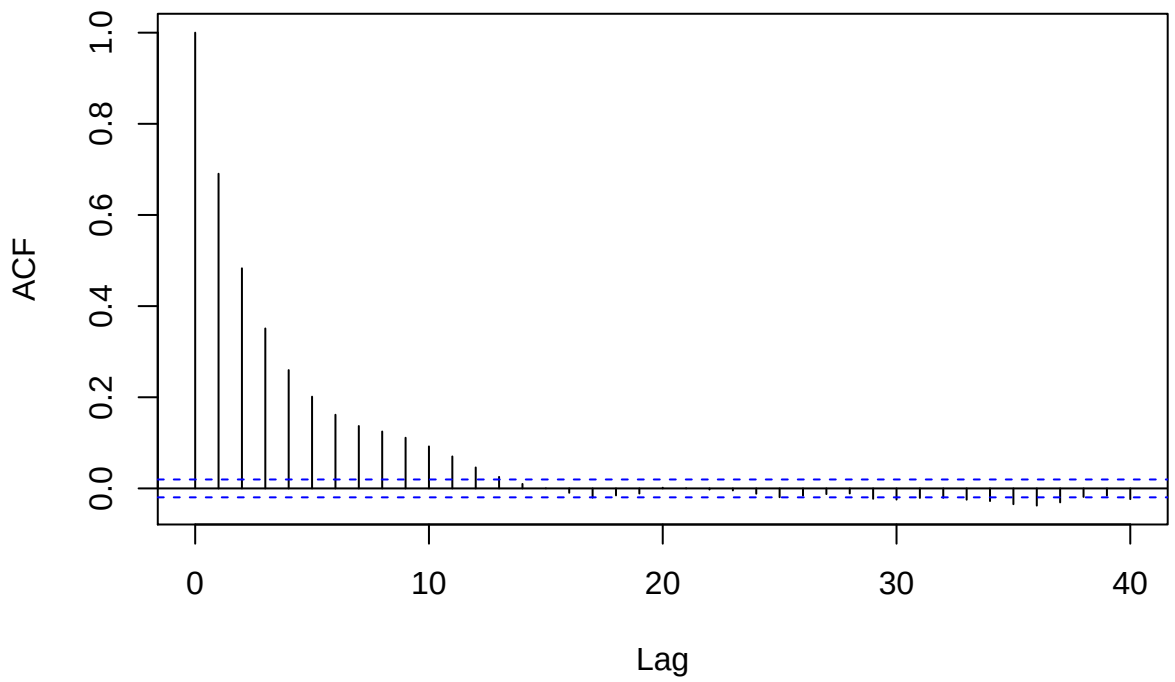


Interestingly, the effective sample sizes is quite low, only in the low thousands:

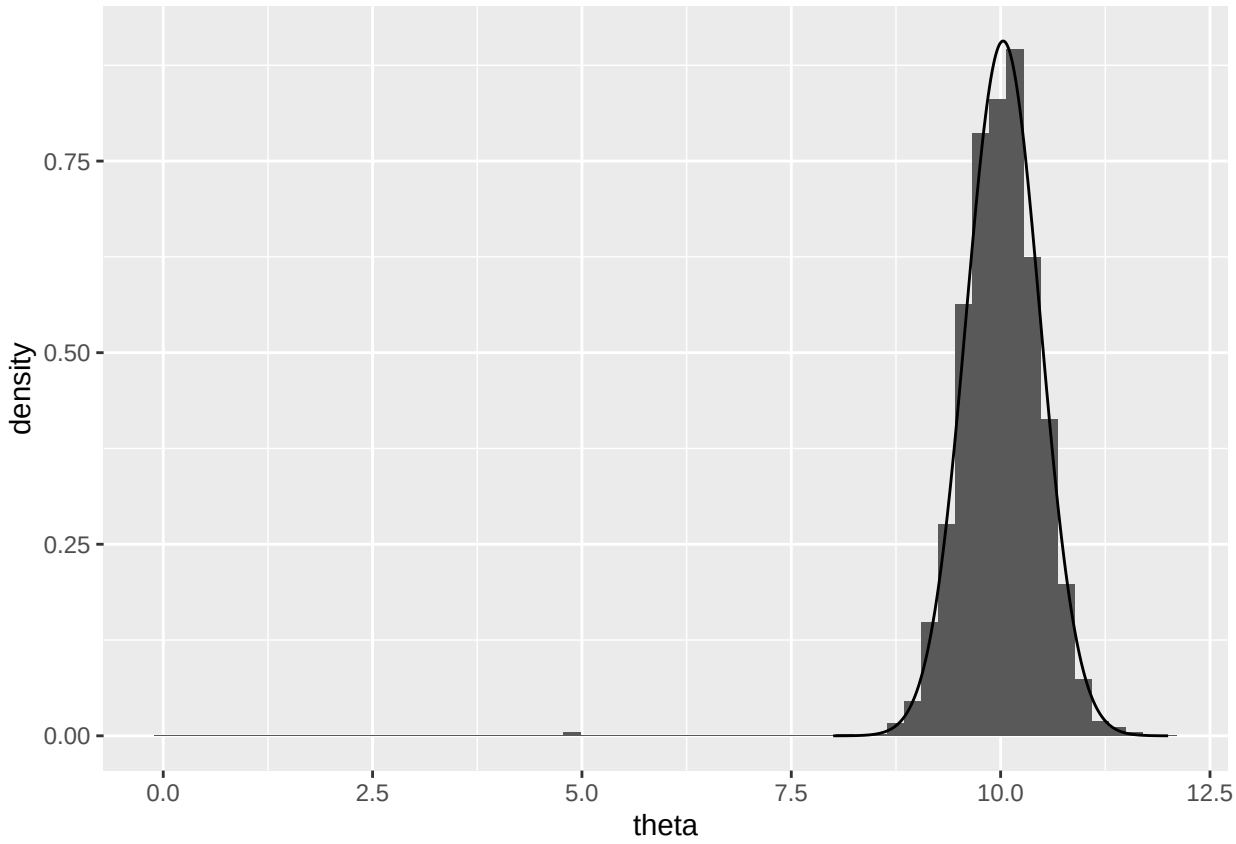
```
library(coda)
effectiveSize(THETA)
```

```
##     var1
## 1427.451
```

```
acf(THETA)
```




```
real.df = data.frame(
  theta = seq(8, 12, length = 500),
  density = dnorm(seq(8, 12, length = 500), 10.03, .44)
)
ggplot(theta.df) +
  geom_histogram(aes(x = theta, y = ..density..), bins = 60) +
  geom_line(data = real.df, mapping = aes(x = theta, y = density))
```




```
# outs[, 4]
# distribution looks different if we include 25000 vs ...  1000
```

Output of the Metropolis algorithm

Need to run until stationarity

Different proposal distributions. Delta as a tradeoff between rate of approach towards the HPD region versus overshooting (like learning rate in gradient descent, etc)

Acceptance rate of between 20 and 50% is good. Control length

Combining Metropolis and Gibbs algorithms

Since proposal distributions for different parameters can all be different - could use Gibbs for some parameters (where Gibbs is just a special case of Metropolis-Hastings)

A regression model with correlated errors

Here I explore the idea of running multiple independent MCMC chains, then combining the data (which is theoretically OK). In `icecore_parallel.R` I take the MH algorithm for analyzing the icecore data and distribute it across multiple cores with `parallel::mclapply`. That file creates `icecore_mcmc` which is analyzed here.

```r
if (!file.exists('./icecore_mcmc')) {
  stop("Run icecore_parallel.R first to get MCMC data")
}
load('./icecore_mcmc')
# Should have "outs" now
# TODO: put colnames in icecore_parallel
colnames(outs) = c('b1', 'b2', 's2', 'phi')
plot(density(outs[seq(1, 80000), 'phi']))
plot(density(outs[seq(1, 80000, by = 25), 'phi']))
outs.df = data.frame(outs)
outs.df$iteration = 1:nrow(outs.df)
message(nrow(outs.df), " samples in ./icecore_mcmc")
ggplot(outs.df, aes(x = iteration, y = phi)) +
  geom_line()
effectiveSize(outs.df$phi)
```

Exercises

10.2

```r
msparrownest = read.table(url('http://www.stat.washington.edu/people/pdhoff/Book/Data/hwdata/msparrownes
```

For convenience let $\theta_i = P(Y_i = 1 \mid \alpha, \beta, x_i)$. Now we solve for θ_i in our model

$$\log\left(\frac{\theta_i}{1-\theta_i}\right) = \alpha + \beta x_i \tag{1}$$

$$\implies \frac{\theta_i}{1-\theta_i} = \exp(\alpha + \beta x_i) \tag{2}$$

$$\implies \theta_i = \exp(\alpha + \beta x_i) - \theta_i \exp(\alpha + \beta x_i) \tag{3}$$

$$\implies \theta_i = \frac{\exp(a + \beta x_i)}{1 + \exp(\alpha + \beta x_i)} \tag{4}$$

So we know $Y_i \sim \text{Bernoulli}\,(p_i)$ where $p_i = \frac{\exp(a+\beta x_i)}{1+\exp(a+\beta x_i)}$ and thus

$$p(y_i \mid \alpha, \beta, x_i) = p_i^{y_i}(1-p_i)^{1-y_i}$$

a

Let $z_i = \exp(\alpha + \beta x_i)$ for simplicity.

$$
\begin{aligned}
p(\boldsymbol{y} \mid \alpha, \beta, x_i) &= \prod_{i=1}^{n} p(y_i \mid \alpha, \beta, x_i) && (5)\\
&= \prod_{i=1}^{n} p_i^{y_i}(1-p_i)^{1-y_i} && (6)\\
&= \prod_{i=1}^{n} \left(\frac{z_i}{1+z_i}\right)^{y_i} \left(1 - \frac{z_i}{1+z_i}\right)^{1-y_i} && (7)\\
&= \prod_{i=1}^{n} \left(\frac{z_i}{1+z_i}\right)^{y_i} \left(\frac{1+z_i}{1+z_i} - \frac{z_i}{1+z_i}\right)^{1-y_i} && (8)\\
&= \prod_{i=1}^{n} \left(\frac{z_i}{1+z_i}\right)^{y_i} \left(\frac{1}{1+z_i}\right)^{1-y_i} && (9)\\
&= \prod_{i=1}^{n} \frac{z_i^{y_i}}{(1+z_i)^{y_i}} \frac{1}{(1+z_i)^{1-y_i}} && (10)\\
&= \prod_{i=1}^{n} \frac{z_i^{y_i}}{1+z_i} && (11)\\
&= \prod_{i=1}^{n} \frac{\exp(y_i(\alpha+\beta x_i))}{1+\exp(\alpha+\beta x_i)} && (12)\\
& && (13)
\end{aligned}
$$

and I don't think that can be simplified further.

b

It's helpful (I think) to think about this in terms of the log-odds i.e. log-odds$(\theta_i) = a + \beta x_i$. If we have an uniformative prior where we by default assume no interaction between wingspan x_i and nesting, then we should center our prior for β around 0. If we also want to be uninformative about our prior proportion of nesting birds regardless of wingspan, then we should center our prior for α around 0 as well, our prior expectation regardless of x_i is log-odds$(\theta_i) = 0 + 0x_i = 0$ (so not favoring nesting or not).

The question is what to use for a prior distribution and how diffuse to make our priors. We would like priors for α and β to be symmetric, so normal distributions for both make sense. And we want our prior to be uninformative, so we should set the variance of these normals high.

If α is always 0, then as x moves from 10 to 15, we want our possible values of β to allow for a change in the log-odds ratio from approximately 0 to 1. Notice the log-odds ratio of some sufficiently small number e.g. `1e-5` is -11.5129155 which is roughly 10. Since x at a minimum is 10, it makes sense to have most of our prior on β in the range $[-10/10, 10/10] = [-1, 1]$, so I'll set the standard deviation of the β prior to 0.5 and the variance to 0.25.

Similarly I'll let the standard deviation of our α prior to be 5 and the variance 25, so that, if $\beta = 0$, the most of the α prior falls in the log-odds interval $[-10, 10]$.

So

$$
\begin{aligned}
\alpha &\sim \mathcal{N}(0, 25) && (14)\\
\beta &\sim \mathcal{N}(0, 0.25) && (15)\\
& && (16)
\end{aligned}
$$

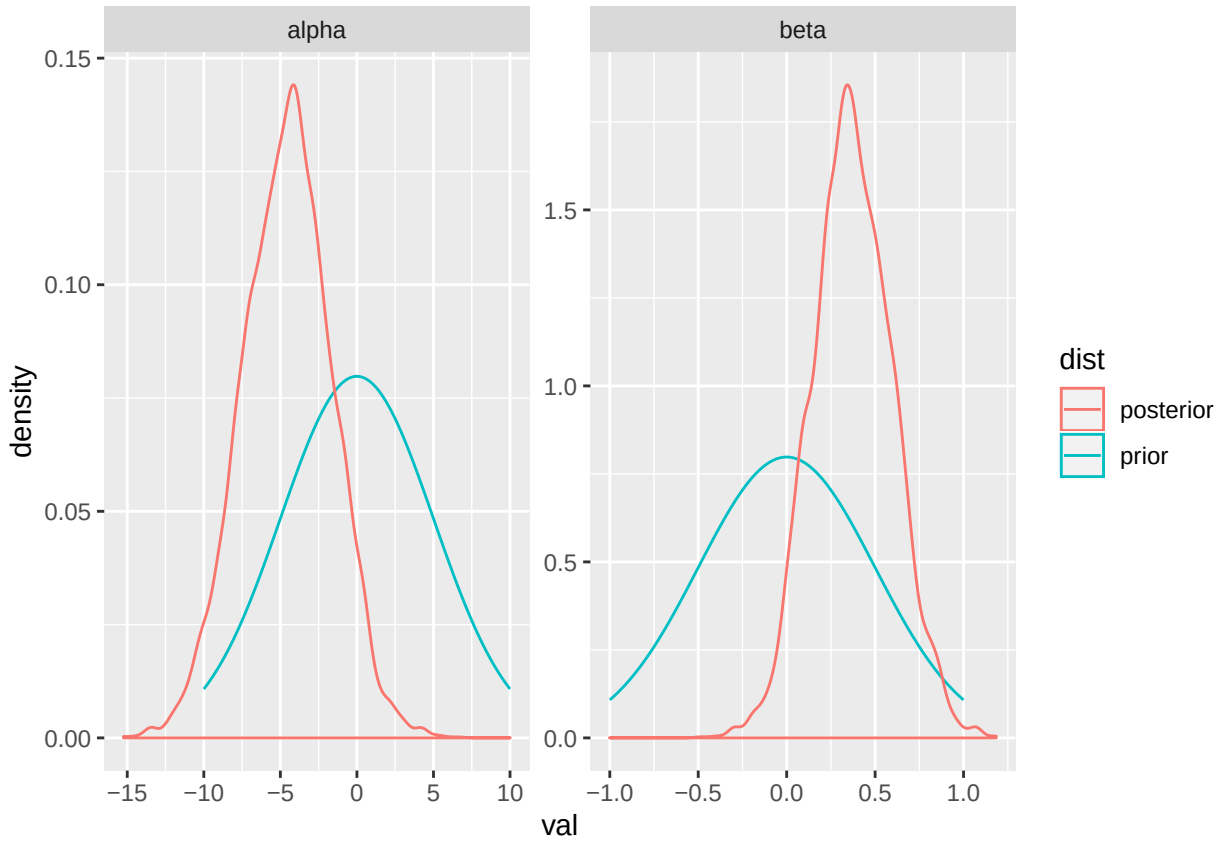
c

```
library(MASS)
inv = solve
# In this sampling scheme, when we sample, we keep the values together
# ($\theta$). But when I store the values, I split them (ALPHA, BETA).
S = 10000
burnin = 5000
y = msparrownest[, 1]
n = length(y)
# Use linear regression format, where column 1 is 1 (for alpha) and column 2 is
# the wingspan
x = cbind(rep(1, n), msparrownest[, 2])
# Start with X^T X but increase until acceptance ratio between 30% - 50%
var.prop = 7 * inv(t(x) %*% x)
# Prior parameters
pmn.theta = c(0, 0)
psd.theta = sqrt(c(25, 0.25))
# Where to store values
ALPHA = numeric(S + burnin)
BETA = numeric(S + burnin)
# Acceptances
acs = 0
# Initial estimates
theta = c(0, 0)
# For calculating likelihood ratio
log.p.y = function(x, y, theta) {
  exp_term = exp(x %*% theta)
  p = exp_term / (1 + exp_term)
  sum(dbinom(y, 1, p, log = TRUE))
}
p.theta = function(theta) {
  sum(dnorm(theta, pmn.theta, psd.theta, log = TRUE))
}
for (s in 1:(S + burnin)) {
  theta.star = mvrnorm(1, theta, var.prop)
  lhr = log.p.y(x, y, theta.star) +
    p.theta(theta.star) -
    log.p.y(x, y, theta) -
    p.theta(theta)
  if (log(runif(1)) < lhr) {
    theta = theta.star
    if (s > burnin) {
      acs = acs + 1
    }
  }
  ALPHA[s] = theta[1]
  BETA[s] = theta[2]
}
ALPHA = ALPHA[burnin:length(ALPHA)]
BETA = BETA[burnin:length(BETA)]
message("Acceptance ratio: ", acs / S) # Good to go
c(effectiveSize(ALPHA), effectiveSize(BETA))
```

```
##     var1     var1
## 1569.255 1549.445
```

d

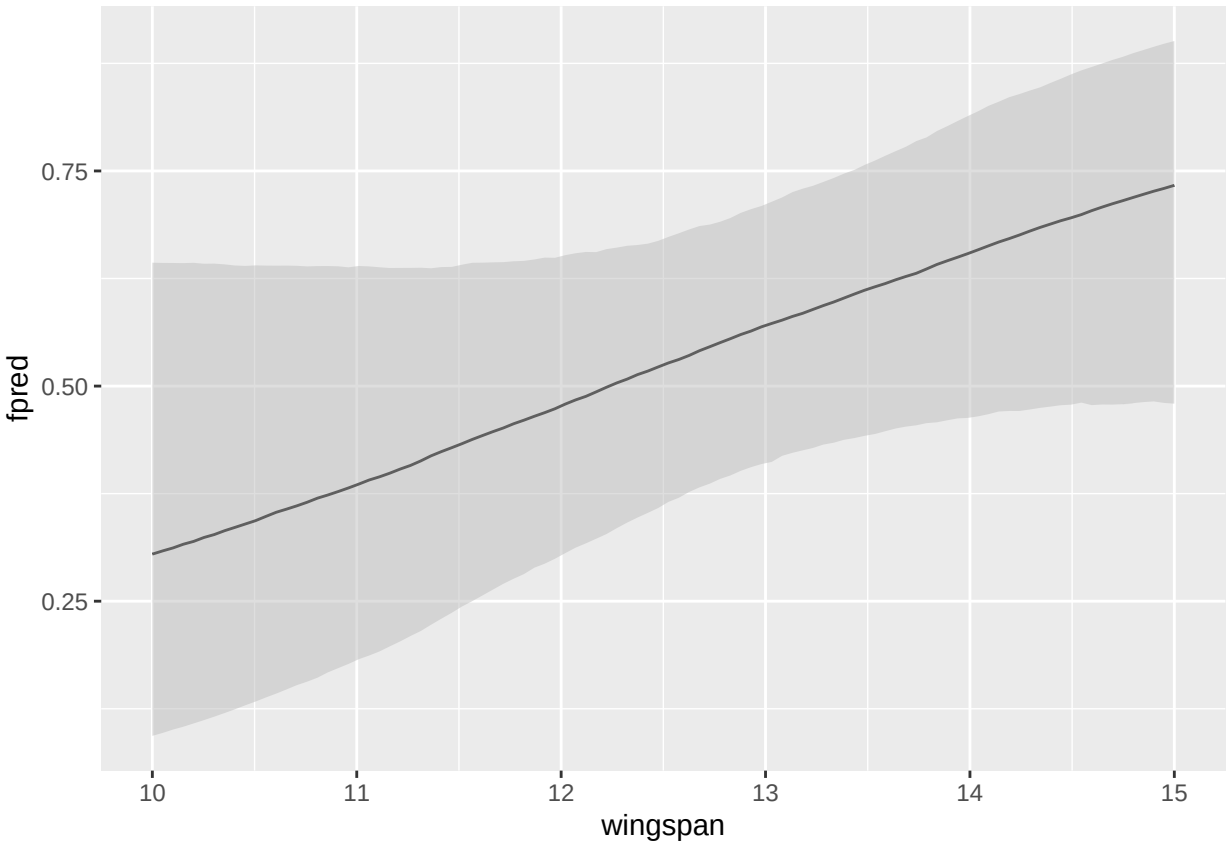
```
alpha_prior = data.frame(
  val = seq(-10, 10, length.out = 1000),
  density = dnorm(seq(-10, 10, length.out = 1000), 0, 5),
  var = 'alpha',
  dist = 'prior'
)
beta_prior = data.frame(
  val = seq(-1, 1, length.out = 1000),
  density = dnorm(seq(-1, 1, length.out = 1000), 0, 0.5),
  var = 'beta',
  dist = 'prior'
)
prior_df = rbind(alpha_prior, beta_prior)
alpha_post = data.frame(
  val = ALPHA,
  var = 'alpha',
  dist = 'posterior'
)
beta_post = data.frame(
  val = BETA,
  var = 'beta',
  dist = 'posterior'
)
post_df = rbind(alpha_post, beta_post)
ggplot(prior_df, aes(x = val, y = density, color = dist)) +
  geom_line() +
  geom_density(data = post_df, mapping = aes(x = val, y = ..density..)) +
  facet_wrap(~ var, scales = 'free')
```



e

Using the samples of α and β, simply compute a distribution on $f_{\alpha\beta}(x)$. We can then construct confidence intervals around this distribution. However, we need to do this for many x values:

```
x_seq = seq(10, 15, length = 100)
quantiles = sapply(x_seq, function(x) {
  exp_term = exp(ALPHA + BETA * x)
  fab = exp_term / (1 + exp_term)
  quantile(fab, probs = c(0.025, 0.5, 0.975))
})
fab_df = data.frame(
  wingspan = x_seq,
  ymin = quantiles[1, ],
  fpred = quantiles[2, ],
  ymax = quantiles[3, ]
)
ggplot(fab_df, aes(x = wingspan, y = fpred, ymin = ymin, ymax = ymax)) +
  geom_line() +
  geom_ribbon(fill = 'grey', alpha = 0.5)
```



This is the logistic regressions' approximate probability of nesting based on wingspan, although the confidence intervals are quite wide.