Bayesian Modeling Using Stan

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Contents

Chapter 1

Introduction to the brms Package

In **Probability and Bayesian Modeling**, the JAGS software is illustrated to fit various Bayesian models by Markov Chain Monte Carlo (MCMC) methods. JAGS consists of a mix of conjugate, Gibbs sampling, and Metropolis algorithms. In recent years, Hamiltonian sampling and the associated Stan software are becoming popular in fitting Bayesian models by MCMC.

The purpose of this supplement is to illustrate Bayesian fitting of common models using the `brms` package which is a popular interface for the Stan software.

1.1 Installing the `brms` package

Basic information about installing the `brms` package is available at https://github.com/paul-buerkner/brms

Since the package is an interface to the Stan software, a C++ compiler is required.

1.2 One Bayesian fitting function `brm()`

One attractive feature of the `brms` package is that one function `brm()` can be used to fit all of the models described in **Probability and Bayesian Modeling**.

The basic function syntax of the `brm()` function is:

```
brm(model_description,
    data = my_data,
    family = the_family,
```

```
    prior = the_prior)
```

where

- `model_description` is the description of the regression model including any random effects similar to the notation used in the `glm()` and `glmer` functions
- `my_data` is the data frame containing the data
- `family` is the sampling family (normal, binomial, Poisson, etc)
- `prior` is the specification of the prior on the regression terms and the error standard deviation

The output of the `brm()` function is an object of class brmsfit that contains the posterior samples and other information about the model.

Chapter 2

Binomial Modeling

2.1 Packages for example

```
library(ProbBayes)
library(brms)
library(dplyr)
library(ggplot2)
```

2.2 Example

Suppose a sample of $n = 20$ college students are asked if they plan on wearing masks while attending class. Let p denote the proportion of all students who plan on wearing masks.

2.3 Prior on proportion

Suppose you believe that $p = 0.40$ and you are 90 percent sure that $p < 0.60$.

Use `beta.select()` from the `ProbBayes` package to find the shape parameters of the matching beta curve prior.

```
beta.select(list(x = 0.4, p = 0.5),
            list(x = 0.6, p = 0.9))
```

```
## [1] 4.31 6.30
```

A beta(4.31, 6.30) prior represents one's beliefs about the proportion p.

2.4 Prior on the logit parameter

Since we will writing a model in terms of the logit function

$$\theta = \log\left(\frac{p}{1-p}\right)$$

We want to find a corresponding normal prior on θ.

A simple way of doing this is by simulation ...

1. Simulate 1000 draws from the beta prior on p.
2. Compute θ on these simulated draws of p.
3. Find the sample mean and standard deviation of these draws – those will be estimates of the mean and standard deviation of the normal prior on θ.

```
set.seed(123)
p_sim <- rbeta(1000, 4.31, 6.30)
theta_sim <- log(p_sim / (1 - p_sim))
c(mean(theta_sim), sd(theta_sim))
```

```
## [1] -0.4000904  0.6540093
```

The corresponding prior on the logit parameter θ is assumed to be normal with mean -0.400 and standard deviation 0.654.

2.5 Fitting the model

The model is $y_1, ..., y_{20}$ are a random sample from a Bernoulli distribution with probability p where p has the logistic representation.

$$\log\left(\frac{p}{1-p}\right) = \theta$$

where $\theta \sim N(-0.400, 0.654)$.

We put the twenty binary responses in a data frame.

```
bdata <- data.frame(y = c(1, 0, 1, 0, 0, 0, 1,
0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0))
```

We use the `brm()` function from the `brms` package to fit the model.

```
fit <- brm(data = bdata,
           family = bernoulli,
           y  ~ 0 + Intercept,
           prior = c(prior(normal(-0.400, 0.654),
                           coef = Intercept)),
```

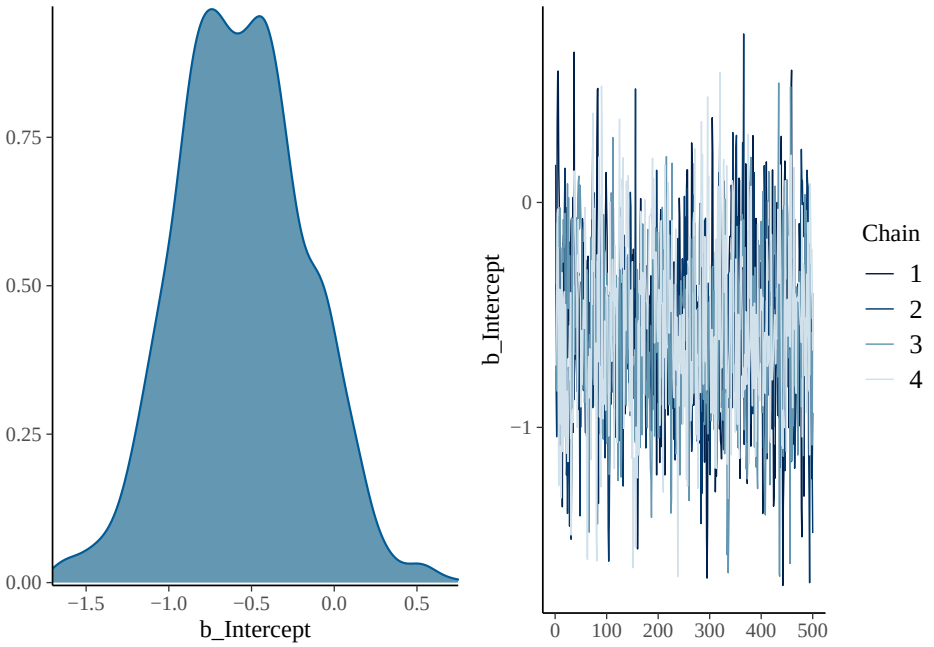
```
            iter = 1000,
            refresh = 0)
```

```
## Compiling the C++ model
```

```
## Start sampling
```

The `plot()` function will display a density plot and a trace plot of the intercept θ.

```
plot(fit)
```



The `summary()` function provides summary statistics for θ.

```
summary(fit)
```

```
##  Family: bernoulli
##   Links: mu = logit
## Formula: y ~ 0 + Intercept
##    Data: bdata (Number of observations: 20)
## Samples: 4 chains, each with iter = 1000; warmup = 500; thin = 1;
##          total post-warmup samples = 2000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    -0.56      0.39    -1.29     0.17 1.01      684     1111
##
```

```
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

The `posterior_samples()` function will display the simulated draws of θ.

```
post <- posterior_samples(fit)
head(post)
```

```
##   b_Intercept      lp__
## 1  -0.3644459 -13.59560
## 2  -0.4101895 -13.54451
## 3  -0.5691616 -13.48236
## 4   0.3479299 -16.35609
## 5   0.5788761 -18.04030
## 6   0.5842954 -18.08432
```

2.6 Inferences about the proportion

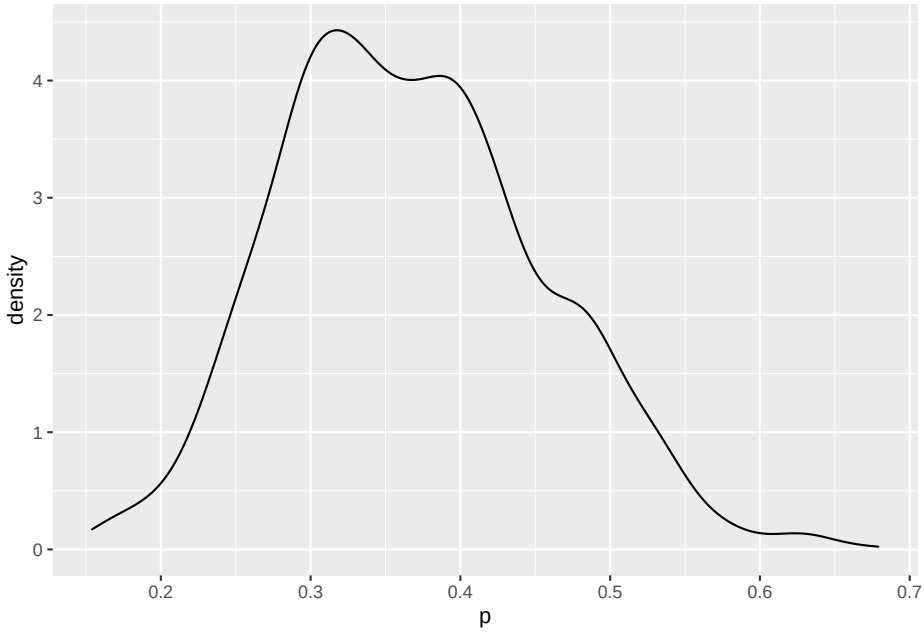
To obtain a sample of draws from the posterior distribution on p, one can use the inverse logit transformation on the simulated draws of θ.

$$p = \frac{\exp(\theta)}{1 + \exp(\theta)}$$

```
post %>%
  mutate(p = exp(b_Intercept) / (1 + exp(b_Intercept))) -> post
```

The posterior density for p is found by constructing a density plot of the simulated draws of p.

```
ggplot(post, aes(p)) +
  geom_density()
```



A 90% posterior interval estimate is found by selecting particular quantiles from the simulated values of p.

```
quantile(post$p, c(.05, .95))
```

```
##        5%       95%
## 0.2378037 0.5192776
```

Chapter 3

Normal Modeling

3.1 Packages for example

```
library(ProbBayes)
library(brms)
```

3.2 Normal sampling model

Assume that $y_1, ..., y_n$ are a sample from a normal distribution with mean μ and standard deviation σ.

For a prior, we assume that μ and σ are independent where μ is assigned a normal prior and σ is assigned a uniform prior on an interval.

3.3 Data and prior

We consider the variable `time` from the dataset `federer_time_to_serve` that contains the time to serve for 20 serves of Roger Federer.

We place a weakly informative prior on the parameters. We assume the mean time-to-serve μ is N(15, 5) and assume the standard deviation σ is uniform on the interval (0, 20).

3.4 Bayesian fitting

We use the `brm()` function with the family = gaussian option. Note how the prior is specified by the prior argument.

```
fit <- brm(data = federer_time_to_serve,
           family = gaussian,
           time ~ 1,
    prior = c(prior(normal(15, 5), class = Intercept),
              prior(uniform(0, 20), class = sigma)),
    iter = 1000, refresh = 0, chains = 4)
```

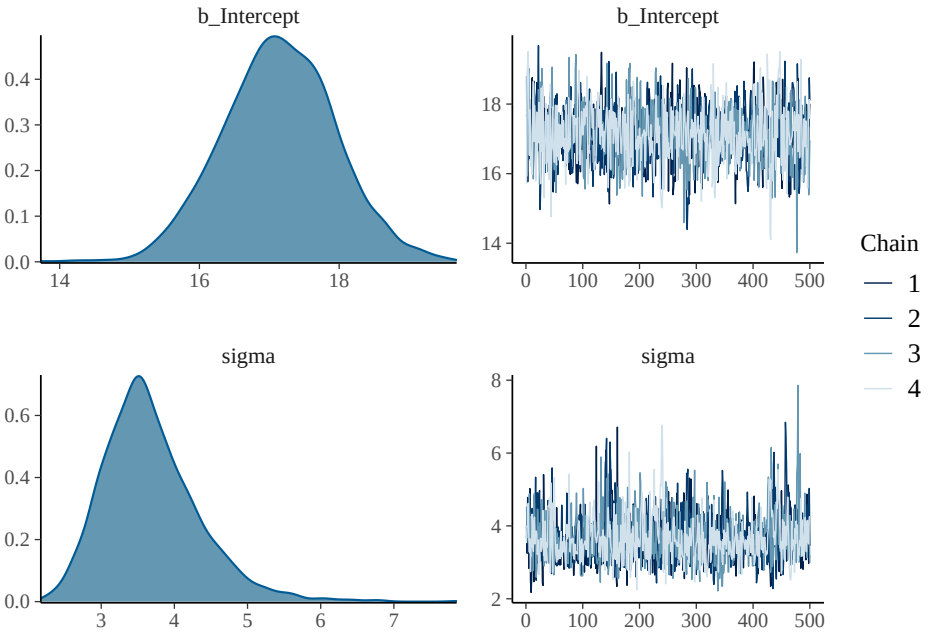
```
## Warning: It appears as if you have specified an upper bounded prior on a parameter t
## If this is really what you want, please specify argument 'ub' of 'set_prior' appropr
## Warning occurred for prior
## sigma ~ uniform(0, 20)
```

```
## Compiling the C++ model
```

```
## Start sampling
```

One obtains density plots and trace plots for μ and σ by the `plot()` function.

```
plot(fit)
```



One obtains posterior summaries for each parameter by the `summary()` function.

```
summary(fit)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: time ~ 1
##    Data: federer_time_to_serve (Number of observations: 20)
```

```
## Samples: 4 chains, each with iter = 1000; warmup = 500; thin = 1;
##          total post-warmup samples = 2000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    17.14      0.80    15.58    18.70 1.00     1394     1053
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     3.68      0.66     2.64     5.21 1.00     1137      878
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

One can obtain a matrix of simulated draws by the `posterior_samples()` function.

```
post <- posterior_samples(fit)
head(post)
```

```
##   b_Intercept    sigma      lp__
## 1    17.69829 3.989865 -57.47744
## 2    17.47939 3.252316 -57.01475
## 3    15.76746 4.781054 -59.40308
## 4    17.62919 4.469536 -58.14521
## 5    16.42508 2.837153 -58.30991
## 6    18.14501 3.504918 -57.70406
```

Chapter 4

Poisson Modeling

4.1 Packages for example

```
library(ProbBayes)
library(brms)
```

4.2 Poisson log-linear model

Here we observe counts $y_1, ..., y_n$ distributed according to a Poisson distribution with mean λ.

Write a model in terms of the logarithm of the mean:

$$\theta = \log \lambda$$

Complete the model by assigning a $N(\mu, \sigma)$ prior to the log mean parameter θ.

4.3 Learning about website counts

In the `ProbBayes` package, the variable `Count` in the dataset `web_visits` contains counts of daily visits to a blog website. We are interested in learning about the mean count of visits λ.

We place a N(0, 10) prior on $\theta = \log \lambda$ reflecting weak prior information about the location of this paramter.

4.4 Bayesian Fitting

In this run of the `brm()` function, we assume Poisson sampling and a normal prior with mean 0 and standard deviation 10 placed on the log mean $\theta = \log \lambda$.

```
fit <- brm(Count ~ 0 + Intercept,
           data = web_visits,
           family = poisson,
            refresh = 0,
          prior = prior(normal(0, 10),
                        class = b,
                        coef = "Intercept"))
```

```
## Compiling the C++ model
```

```
## Start sampling
```

We confirm the prior with the `prior_summary()` function.

```
prior_summary(fit)
```

```
##           prior class      coef group resp dpar nlpar bound
## 1                     b
## 2 normal(0, 10)     b Intercept
```

The `summary()` function provides summaries of the posterior of θ.

```
summary(fit)
```

```
##  Family: poisson
##   Links: mu = log
## Formula: Count ~ 0 + Intercept
##    Data: web_visits (Number of observations: 28)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     4.59      0.02     4.55     4.62 1.00     1574     2209
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

The `posterior_samples()` function outputs the posterior simulations of θ.

```
post <- posterior_samples(fit)
head(post)
```

```
##   b_Intercept      lp__
## 1    4.556476 -136.7185
```

```
## 2    4.562960 -136.2752
## 3    4.560979 -136.3987
## 4    4.598670 -135.8759
## 5    4.594855 -135.7515
## 6    4.590376 -135.6570
```

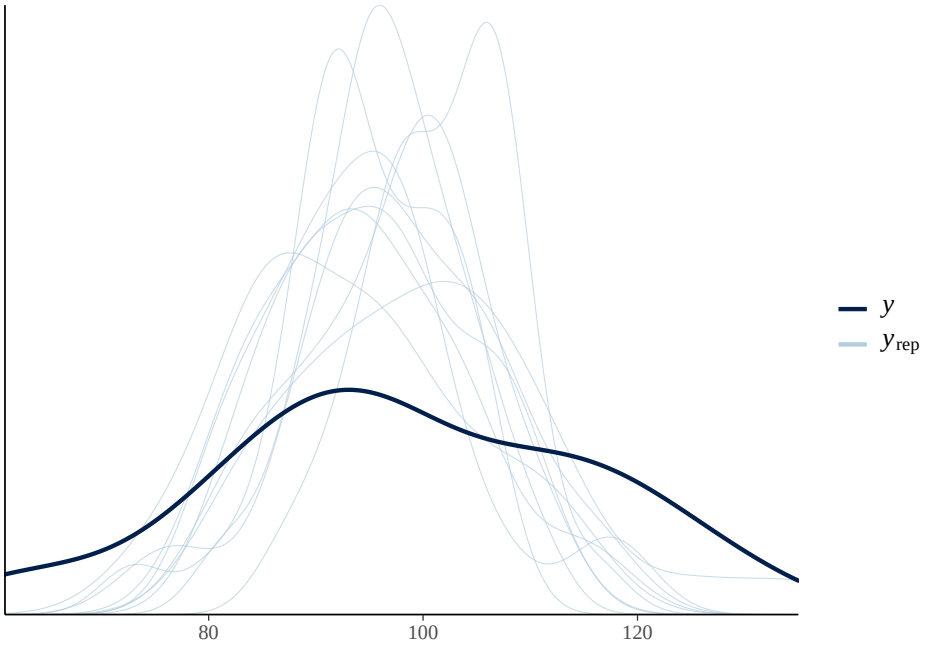
4.5 Posterior predictive model checks

Actual this is a poor model for these data. One can see that by several posterior predictive checks.

The `pp_check()` shows density plots of 10 replicated datasets from the posterior predictive distribution. Note that these replicated datasets look different (smaller variation) than the observed data.

```
pp_check(fit)
```

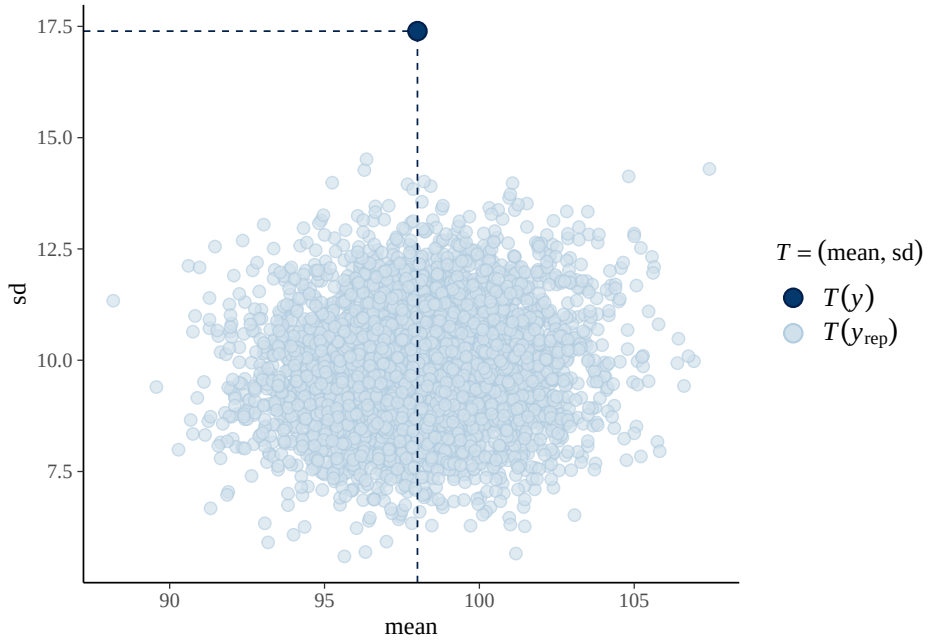
```
## Using 10 posterior samples for ppc type 'dens_overlay' by default.
```



The `pp_check()` function will implement a posterior predictive check using various checking functions. Here we are using $(\bar{y}, s)$ as a bivariate checking function. The scatterplot represents values of $(\bar{y}, s)$ from the simulated predictive distributions and the observed values of $(\bar{y}, s)$ is displayed. The takeaway is that the observed data has more variation than predicted from the Poisson model.

```
pp_check(fit, type = "stat_2d")
```

```
## Using all posterior samples for ppc type 'stat_2d' by default.
```



Chapter 5

Comparing Proportions

5.1 Packages for example

```
library(ProbBayes)
library(brms)
library(dplyr)
library(ggplot2)
```

5.2 Facebook use example

In Chapter 9, we consider the following comparison of proportions example. A sample of students were asked their gender and the average number of times they visited Facebook in a day.

Of n_M males sampled, y_M had a high number of Facebook visits, and of n_F females sampled, y_F had a high number of visits.

Suppose the data is organized as a data frame as follows:

Gender	Sample_size	Visits
male	n_M	y_M
female	n_F	y_F

5.3 Sampling model

Suppose we have two independent samples where y_M is binomial(n_M, p_M) and y_F is binomial(n_F, p_F).

Write the proportions using a logistic model:

$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 I(Gender = Male)$$

Note for females, the logit of p_F is given by

$$\log\left(\frac{p}{1-p}\right) = \beta_0$$

and for males the logit for p_M is given by

$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1$$

5.4 The data

Here's the observed data:

```
fb_data <- data.frame(Gender = c("male", "female"),
                      Sample_Size = c(93, 151),
                      Visits = c(39, 75))
```

5.5 Priors

In this model, β_0 is the logit of the proportion of women who are high Facebook users and β_1 represents the difference in the logits of the proportions for men and women.

Assume that you don't know much about the location of β_0, but you believe men and women are similar in their use of Facebook. So you assign a N(0, 31.6) prior to β_0 with a high standard deviation, reflecting little knowledge. To reflect the belief that β_1 is close to 0, you use a N(0, 0.71) prior.

The `get_prior()` function lists all parameters to define priors on for this particular model, assigning the result to `prior`. Then the two components of `prior` are assigned that reflect the statements above.

```
(my_prior <- get_prior(family = binomial,
          Visits | trials(Sample_Size) ~ Gender,
          data = fb_data))
```

```
##                 prior     class       coef group resp dpar nlpar bound
## 1                             b
## 2                             b Gendermale
## 3 student_t(3, 0, 2.5) Intercept
```

```
my_prior$prior[3] <- "normal(0, 31.6)"
my_prior$prior[2] <- "normal(0, 0.71)"
```

5.6 Posterior sampling

Here is the run of `brm()` where I use the prior specification in `my_prior`.

```
fit <- brm(family = binomial,
           Visits | trials(Sample_Size) ~ Gender,
           data = fb_data,
           prior = my_prior,
           iter = 1000,
           refresh = 0)
```

```
## Compiling the C++ model
```

```
## Start sampling
```

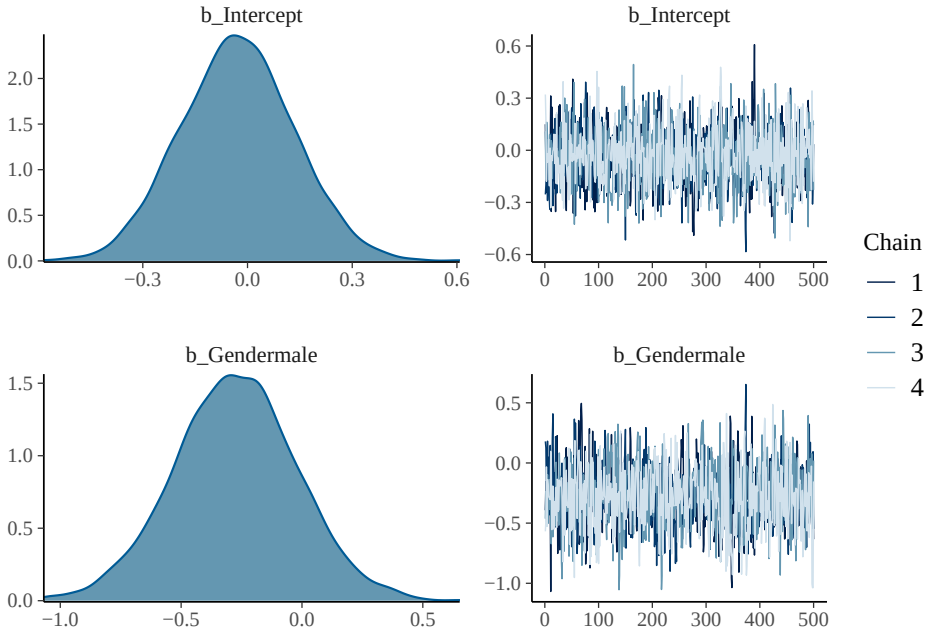
One obtains the matrix of simulated values of the parameters by the `posterior_samples()` function.

```
post <- posterior_samples(fit)
head(post)
```

```
##    b_Intercept b_Gendermale      lp__
## 1  0.149825204   -0.3929578 -10.89798
## 2 -0.077477237   -0.1550768 -10.36612
## 3  0.014914205   -0.2591160 -10.32287
## 4 -0.244104208   -0.2079800 -11.39275
## 5 -0.006092644   -0.2035093 -10.36111
## 6  0.012292753   -0.4538551 -10.53464
```

The `plot()` function provides trace plots and density plots of each parameter.

```
plot(fit)
```



Posterior summaries are provided by the `print()` function.

```
print(fit)
```

```
##  Family: binomial
##   Links: mu = logit
## Formula: Visits | trials(Sample_Size) ~ Gender
##    Data: fb_data (Number of observations: 2)
## Samples: 4 chains, each with iter = 1000; warmup = 500; thin = 1;
##          total post-warmup samples = 2000
##
## Population-Level Effects:
##            Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     -0.03      0.16    -0.34     0.28 1.00     2198     1576
## Gendermale    -0.28      0.25    -0.78     0.23 1.01     1525     1121
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Chapter 6

Comparing Rates

6.1 Packages for example

```
library(ProbBayes)
library(brms)
library(dplyr)
```

6.2 Comparing two Poisson Rates

Suppose we observe two independent samples: $x_1, ..., x_m$ are a random sample from a Poisson distribution with mean λ_x, and $w_1, ..., w_n$ are a random sample from a Poisson distribution with mean λ_y. We are interested in learning about the ratio of Poisson means

$$\theta = \frac{\lambda_x}{\lambda_y}$$

6.3 Write as a log-linear model

Suppose we collect the observations

$$y = c(x_1, ..., x_m, w_1, ..., w_n)$$

and let `group2` be an indicator variable for the second group.

$$group2 = c(0, 0, ..., 0, 1, 1, ..., 1)$$

Then we can represent the model as

$$y_1, \cdots, y_{m+n}$$

independent from Poisson distributions with means $\lambda_1, ..., \lambda_{m_n}$ where the means follow the log-linear model

$$\log \lambda_j = \beta_0 + \beta_1 group2$$

In this model, $\beta_0 = \log \lambda_x$, and $\beta_0 + \beta_1 = \log \lambda_y$. So $\beta_1 = \log(\lambda_y) - \log(\lambda_x)$ represents the increase in the means on the log scale.

6.4 The data

We collect web count visits for a number of days stored in the data frame `web_visits` in the `ProbBayes` package. The key variables are `Day`, the day of the week, and `Count`, the website visit count. We define a new variable `Type` that is either "weekend" or "weekday".

We are interested in comparing the mean visit counts for weekdays and weekend days.

```
web_visits %>%
  mutate(Type = ifelse(Day %in%
      c("Fri", "Sat", "Sun"), "weekend", "weekday")) -> web_visits
```

6.5 Priors

Here we are assume weakly informative priors on the regression parameters β_0 and β_1.

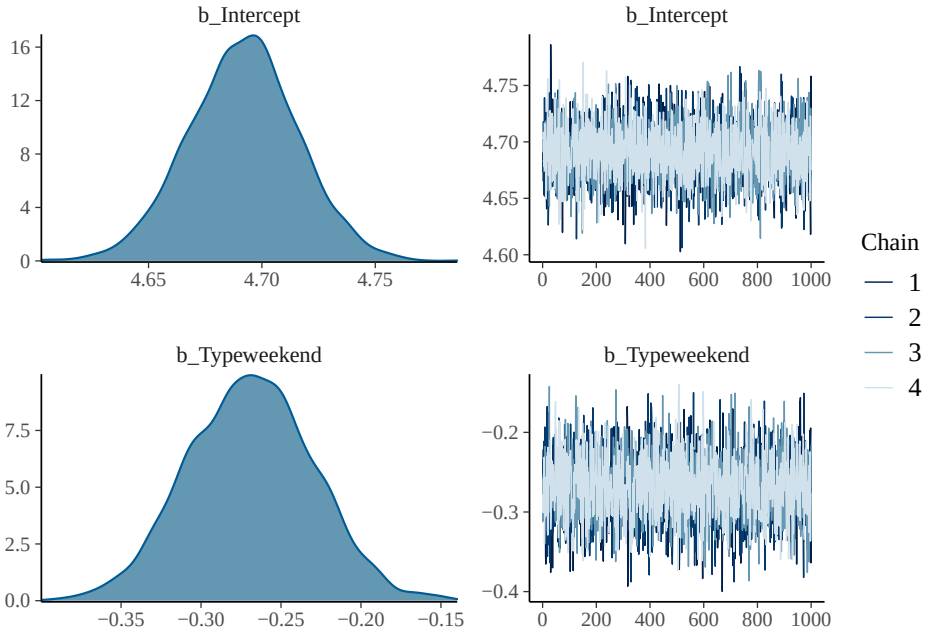
6.6 Bayesian fitting

```
fit <- brm(Count ~ Type,
           family = poisson,
           data = web_visits,
           refresh = 0)
```

```
## Compiling the C++ model

## Start sampling
```

```
plot(fit)
```




```
summary(fit)
```

```
##  Family: poisson
##   Links: mu = log
## Formula: Count ~ Type
##    Data: web_visits (Number of observations: 28)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Population-Level Effects:
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept       4.69      0.02     4.64     4.74 1.00     3888     2663
## Typeweekend    -0.27      0.04    -0.35    -0.19 1.00     3292     2805
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
sim_draws <- posterior_samples(fit)
head(sim_draws)
```

```
##   b_Intercept b_Typeweekend      lp__
## 1    4.683972    -0.3003928 -111.6071
## 2    4.690432    -0.2403990 -111.1721
## 3    4.665176    -0.2213930 -111.6114
## 4    4.683088    -0.2696015 -110.9016
```

```
## 5    4.678049    -0.2929583 -111.6562
## 6    4.699903    -0.2566505 -111.0721
```

Chapter 7

Multilevel Modeling of Proportions

7.1 Packages for example

```
library(ProbBayes)
library(tidyverse)
library(brms)
```

7.2 Hospital Study

Table 10.2 gives the number of cases and number of deaths from heart attacks for 13 hospitals in New York City. This data is contained in the data frame `DeathHeartAttackManhattan` in the `ProbBayes` package.

7.3 A Multilevel Model

We consider a different formulation of the hierarchical model described in Section 10.3.

Sampling

We first assume that y_j, the number of deaths for the jth hospital, is binomial with sample size n_j and probability p_j. Let $\theta_j = \log(p_j/(1-p_j))$ denote the logit for the jth hospital.

Write $\theta_j = \beta + \gamma_j$.

Prior

1. We assume the intercept β has a student t distribution with mean 0, scale parameter 2.5 and 3 degrees of freedom.
2. We assume $\gamma_1, ..., \gamma_N$ have a normal distribution with mean 0 and standard deviation σ.
3. The standard deviation σ is assumed to have a t density with mean 0 and standard deviation 3.5.

7.4 Fitting the Bayesian model

We fit the multilevel model using the 'brm() function. Note the use of the "family = binomial" argument to indicate the sampling distribution. The "(1 | Hospital)" component indicates that the γ_j have a random distribution.

```
fit <- brm(data = DeathHeartAttackManhattan,
           family = binomial,
           Deaths | trials(Cases) ~ 1 + (1 | Hospital),
           refresh = 0)
```

```
## Compiling the C++ model
```

```
## Start sampling
```

We didn't specify priors, but there are default priors behind the scenes. The prior_summary() function displays the priors.

```
prior_summary(fit)
```

```
##                 prior     class      coef    group resp dpar nlpar bound
## 1 student_t(3, 0, 2.5) Intercept
## 2 student_t(3, 0, 2.5)        sd
## 3                             sd           Hospital
## 4                             sd Intercept Hospital
```

7.5 Posterior summaries of β and σ

The summary() function shows posterior summaries of β (the intercept) and the standard deviation σ.

```
summary(fit)
```

```
##  Family: binomial
##   Links: mu = logit
## Formula: Deaths | trials(Cases) ~ 1 + (1 | Hospital)
##    Data: DeathHeartAttackManhattan (Number of observations: 13)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
```

```
## Group-Level Effects:
## ~Hospital (Number of levels: 13)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.19      0.15     0.01     0.56 1.00      913     1675
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    -2.60      0.11    -2.82    -2.37 1.00     2555     1376
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

7.6 Posterior summaries of hospital effects

The `posterior_samples()` function produces a large matrix of simulated draws where the column corresponds to the parameter and the row corresponds to the iteration number.

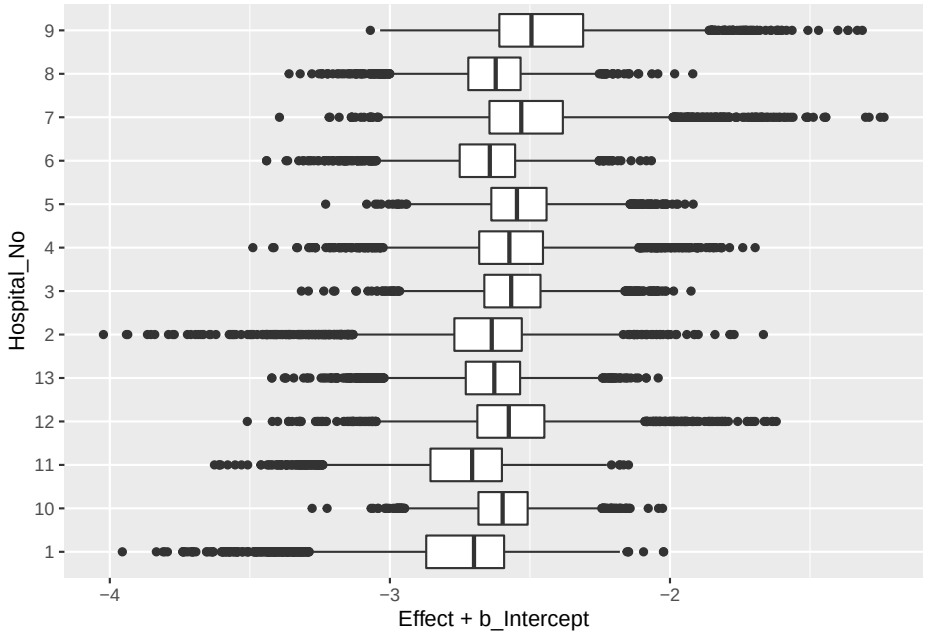
By use of the `pivot_longer()` function, I reformat the simulation matrix where there is a new variable `Hospital` indicating the name of the hospital and `Effect` is the simulated value of γ_j. Also I create a new variable that is the number of the hospital from 1 to 13.

```
posterior_samples(fit) %>%
  pivot_longer(starts_with("r_Hospital"),
               names_to = "Hospital",
               values_to = "Effect") -> post
post$Hospital_No <- as.character(as.numeric(factor(post$Hospital)))
```

Below is a graph of the posterior distribution of the parameters $\{\beta + \gamma_j\}$ for all 13 hospitals.

These are graphed on the logit scale. By taking the inverse logit function, one could find the posterior distributions of the death rates $p_1, ..., p_N$.

```
ggplot(post, aes(Hospital_No, Effect + b_Intercept)) +
  geom_boxplot() +
  coord_flip()
```


Hospital_No
9
8
7
6
5
4
3
2
13
12
11
10
1
−4
−3
−2
Effect + b_Intercept

Chapter 8

Multilevel Modeling of Means

8.1 Packages for example

```
library(ProbBayes)
library(tidyverse)
library(brms)
```

8.2 Movie Ratings Study

Table 10.1 gives summaries of the ratings for eight different animation movies. The table includes the number of ratings, the mean and the standard deviation of the ratings. The data is contained in the data frame `animation_ratings` in the `ProbBayes` package.

8.3 The Multilevel Model

Sampling

Let y_{ij} denote the rating of the ith individual for the jth movie.

We assume that $y_{ij} \sim N(\mu_j, \sigma)$.

Prior

The parameters $\mu_1, ..., \mu_8$ represent the mean ratings for the eight movies. Write

$$\mu_j = \beta + \gamma_j$$

1. The intercept parameter β has a student t distribution with mean 4, scale parameter 2.5, and 3 degrees of freedom.
2. We assume the effect parameters $\gamma_1, ..., \gamma_8$ have a normal distribution with mean 0 and standard deviation τ.
3. There are two standard deviations, the sampling standard deviation σ and the between-means standard deviation *tau*. Each of these standard deviations are given weakly informative student t distributions with mean 0, scale 2.5 and 3 degrees of freedom.

8.4 Bayesian Fitting

The model is fit by use of the `brm()` function. By default, this function assumes a Gaussian (normal) sampling distribution. The "(1 | movieID)" argument indicates that the $\mu_1, ..., \mu_8$ have a random distribution.

```
fit <- brm(rating ~ (1 | movieId),
           data = animation_ratings,
           refresh = 0)
```

```
## Compiling the C++ model
```

```
## Start sampling
```

```
## Warning: There were 6 divergent transitions after warmup. Increasing adapt_delta abo
## http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup
```

```
## Warning: Examine the pairs() plot to diagnose sampling problems
```

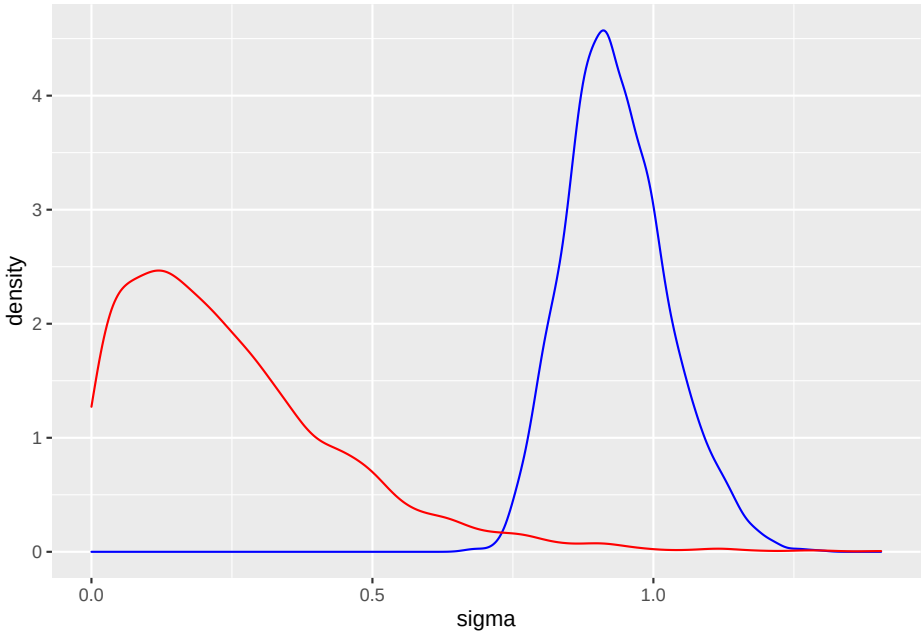
One can check the default priors by use of the `prior_summary()` function.

```
prior_summary(fit)
```

```
##                  prior     class      coef   group resp dpar nlpar bound
## 1 student_t(3, 4, 2.5) Intercept
## 2 student_t(3, 0, 2.5)        sd
## 3                             sd           movieId
## 4                             sd Intercept movieId
## 5 student_t(3, 0, 2.5)     sigma
```

The posterior matrix of simulated draws is available by use of the `posterior_samples()` function. Below I construct density estimates of the two standard deviation parameters σ (blue) and τ (red).

```
ggplot(posterior_samples(fit),
       aes(sigma)) +
  geom_density(color = "blue") +
  geom_density(aes(sd_movieId__Intercept),
               color = "red")
```

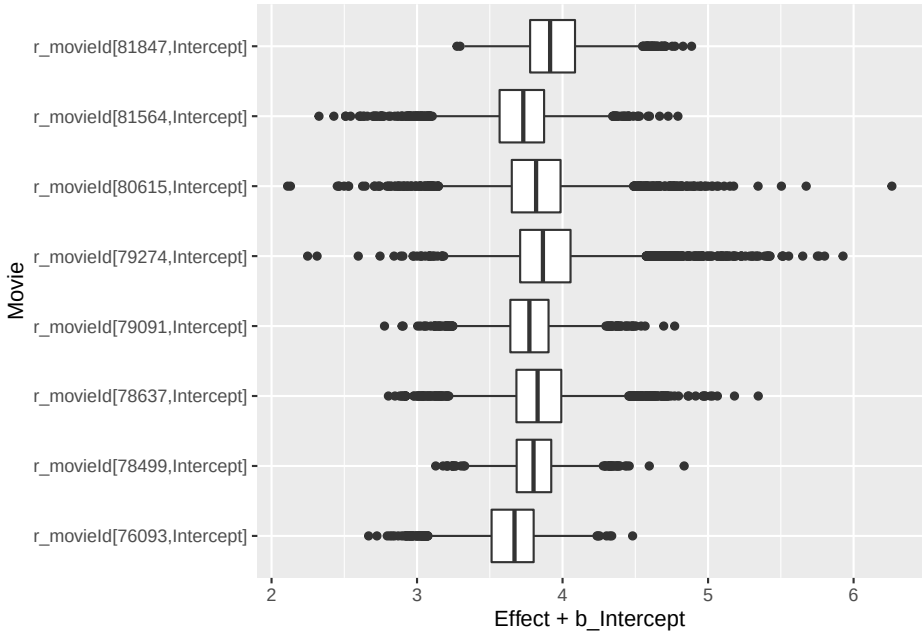


To show the posterior distributions of the means, I reshape the matrix of simulated draws by use of the `pivot_longer()` function.

```
posterior_samples(fit) %>%
  pivot_longer('r_movieId[76093,Intercept]':'r_movieId[81847,Intercept]',
               names_to = "Movie",
               values_to = "Effect") -> post
```

Remember that we represented the movie ratings mean as $\mu_j = \beta + \gamma_j$. Below are parallel boxplots of the posterior distributions of $\mu_1, ..., \mu_8$.

```
ggplot(post, aes(Movie, Effect + b_Intercept)) +
  geom_boxplot() +
  coord_flip()
```


r_movieId[81847,Intercept]
r_movieId[81564,Intercept]
r_movieId[80615,Intercept]
r_movieId[79274,Intercept]
r_movieId[79091,Intercept]
r_movieId[78637,Intercept]
r_movieId[78499,Intercept]
r_movieId[76093,Intercept]
Movie
2
3
4
5
6
Effect + b_Intercept

Chapter 9

Multilevel Regression

9.1 Packages for example

```
library(tidyverse)
library(brms)
```

9.2 Some baseball data

The function `get_onbase_data()` function collects on-base data for all players born in the year 1977 who have had at least 1000 career plate appearances.

```
source("get_onbase_data.R")
d78 <- get_onbase_data(1977, 1000)
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## `summarise()` regrouping output by 'playerID' (override with `.groups` argument)
```

```
unique(d78$nameLast)
```

```
##  [1] "Beltran"    "Bergeron"   "Bigbie"     "Bloomquist" "Byrd"
##  [6] "Caruso"     "Chavez"     "Davis"      "Ellis"      "Everett"
## [11] "Fukudome"   "Furcal"     "Gerut"      "Gibbons"    "Gonzalez"
## [16] "Hafner"     "Hinske"     "Hudson"     "Inge"       "Jimenez"
## [21] "Jones"      "Monroe"     "Munson"     "Nieves"     "Overbay"
## [26] "Pierre"     "Punto"      "Quinlan"    "Redman"     "Roberts"
## [31] "Ross"       "Rowand"     "Sanchez"    "Thames"     "Tyner"
## [36] "Wigginton"  "Wilkerson"  "Wilson"
```

9.3 Quadratic aging model

Let y_{ij} denote the number of on-base events in n_{ij} opportunities (plate appearances) of the ith batter in the jth season. Assume that y_{ij} is binomial with sample size n_{ij} and probability of success p_{ij}.

Assume that the on-base probabilities for the ith player satisfy the logistic model

$$\log\left(\frac{p_{ij}}{1-p_{ij}}\right) = \beta_{i0} + \beta_{i1} D_{ij} + \beta_{i2} D_{ij}^2$$

where $D_{ij} = x_{ij} - 30$, x_{ij} is the age of the ith player in the jth season.

9.4 Multilevel Prior

The ith player's trajectory is described by the regression vector $\beta_i = (\beta_{i0}, \beta_{i1}, \beta_{i2})$. We place a two-stage prior on the trajectories $\beta_1, ..., \beta_N$:

1. $\beta_1, ..., \beta_N$ are a sample from a multivariate normal density with mean β and variance-covariance matrix Σ.
2. The second-stage parameters β and Σ are independent with weakly informative priors.

9.5 Bayesian fitting

The fitting of this model is done using the `brm()` function.

```
fit <- brm(OB | trials(PA) ~ AgeD + I(AgeD ^ 2) +
             (AgeD + I(AgeD ^  2) | Player),
           data = filter(d78, PA > 0),
           family = binomial("logit"),
           refresh = 0)
```

```
## Compiling the C++ model
```

```
## Start sampling
```

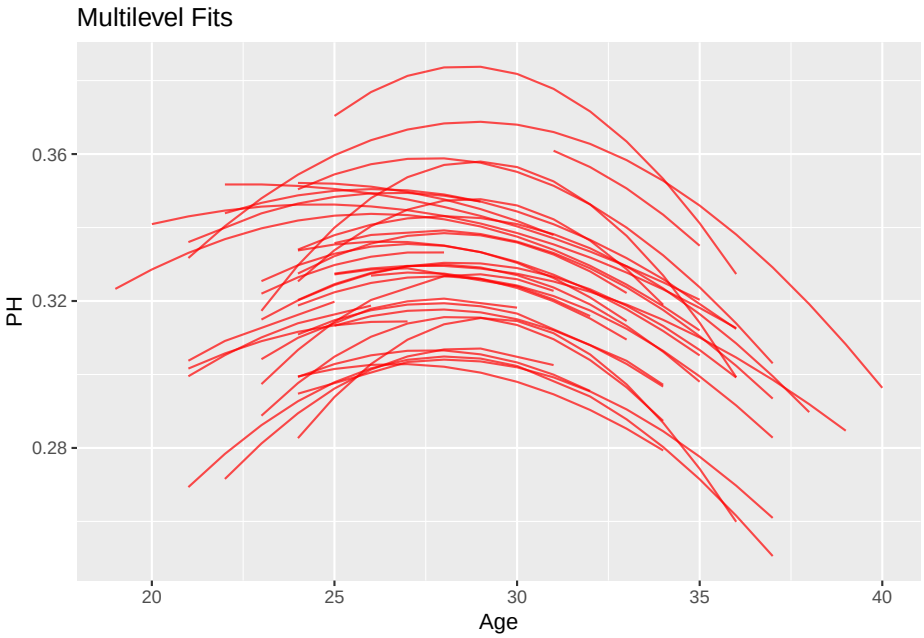
I find posterior means of the fitted trajectories for all players.

```
Player_Fits <- coef(fit)$Player[, "Estimate", ] %>%
  as.data.frame() %>%
    mutate(Player = 1:max(d78$Player))
```

```
d78 <- inner_join(d78, Player_Fits, by = "Player")
```

```
d78 %>%
  mutate(PH = plogis(Intercept + AgeD.y * AgeD.x +
                       IAgeDE2 * AgeD.x ^ 2)) -> d78
```

```
ggplot(d78, aes(Age, PH, group = Player)) +
  geom_line(color = "red", alpha = 0.7) +
  ggtitle("Multilevel Fits")
```



For a given player, define the peak age

$$Age_j = 30 - \frac{\beta_{j1}}{2\beta_{j2}}.$$

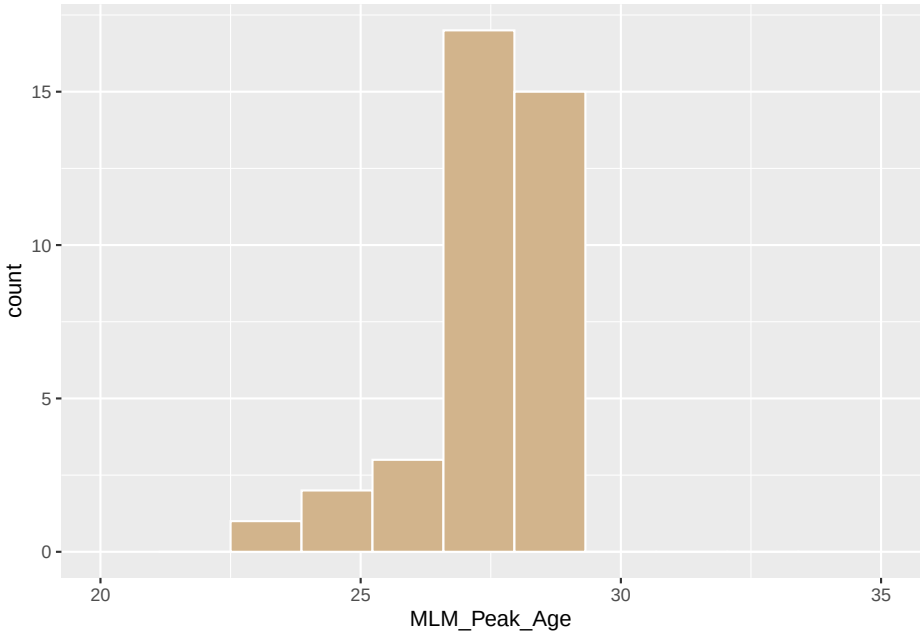
the age at which the player achieves peak performance.

The following graph shows the posterior distributions of the peak ages for all players.

```
d78  %>% group_by(Player) %>%
  summarize(b0 = first(Intercept),
            b1 = first(AgeD.y),
            b2 = first(IAgeDE2)) %>%
  mutate(MLM_Peak_Age = 30 - b1 / 2 / b2)  %>%
  ggplot(aes(MLM_Peak_Age)) +
  geom_histogram(bins = 12,
                 color = "white", fill = "tan") +
  xlim(20, 35)
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```


15
10
5
0
count
20
25
30
35
MLM_Peak_Age