Week 6: Visualizing the Bayesian Workflow

23/02/23

Introduction

This lab will be looking at trying to replicate some of the visualizations in the lecture notes, involving prior and posterior predictive checks, and LOO model comparisons.

The dataset is a 0.1% of all births in the US in 2017. I've pulled out a few different variables, but as in the lecture, we'll just focus on birth weight and gestational age.

The data

Read it in, along with all our packages.

```
library(tidyverse)
library(here)
# for bayes stuff
library(rstan)
library(bayesplot)
library(loo)
library(tidybayes)

ds <- read_rds(here("data","births_2017_sample.RDS"))
head(ds)
```

```
# A tibble: 6 x 8
  mager mracehisp meduc   bmi sex   combgest  dbwt ilive
  <dbl>     <dbl> <dbl> <dbl> <chr>    <dbl> <dbl> <chr>
1    16         2     2  23   M           39  3.18 Y
2    25         7     2  43.6 M           40  4.14 Y
```

```
3    27         2     3  19.5 F           41  3.18 Y
4    26         1     3  21.5 F           36  3.40 Y
5    28         7     2  40.6 F           34  2.71 Y
6    31         7     3  29.3 M           35  3.52 Y
```

Brief overview of variables:

- `mager` mum's age
- `mracehisp` mum's race/ethnicity see here for codes: https://data.nber.org/natality/2017/natl2017.pdf page 15
- `meduc` mum's education see here for codes: https://data.nber.org/natality/2017/natl2017.pdf page 16
- `bmi` mum's bmi
- `sex` baby's sex
- `combgest` gestational age in weeks
- `dbwt` birth weight in kg
- `ilive` alive at time of report y/n/ unsure

I'm going to rename some variables, remove any observations with missing gestational age or birth weight, restrict just to babies that were alive, and make a preterm variable.

```
ds <- ds %>%
  rename(birthweight = dbwt, gest = combgest) %>%
  mutate(preterm = ifelse(gest<32, "Y", "N")) %>%
  filter(ilive=="Y",gest< 99, birthweight<9.999)
```

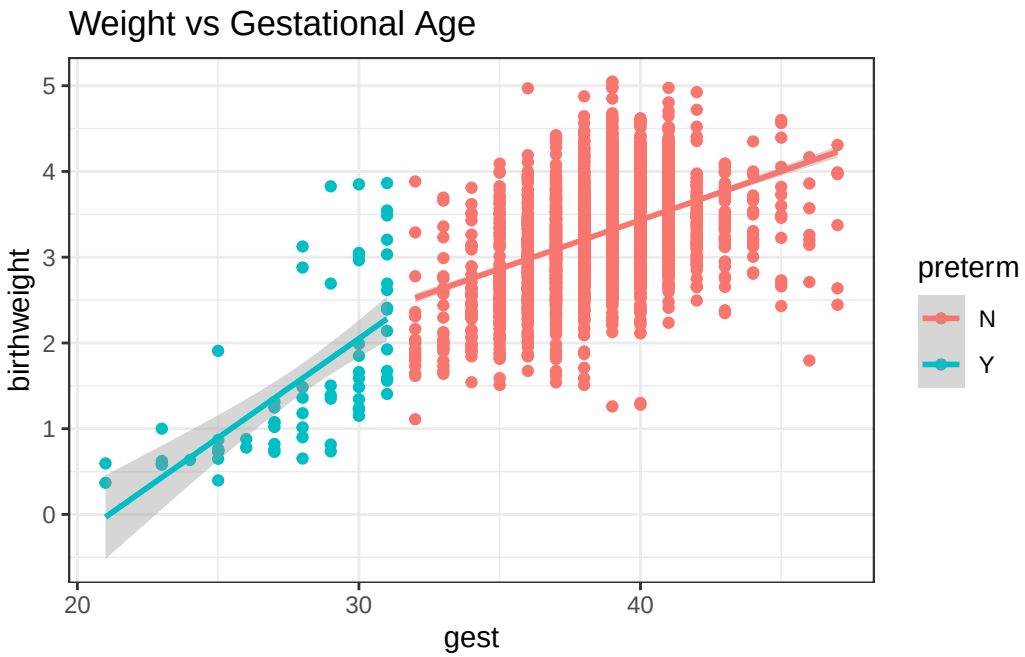
Question 1

Use plots or tables to show three interesting observations about the data. Remember:

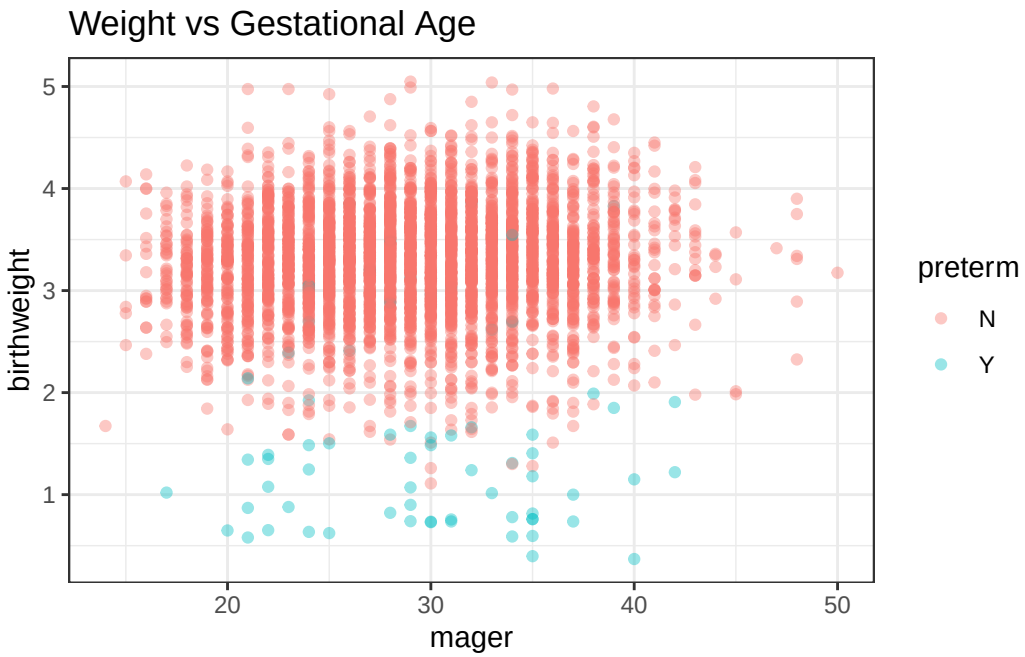
- Explain what your graph/ tables show
- Choose a graph type that's appropriate to the data type
- If you use `geom_smooth`, please also plot the underlying data

Feel free to replicate one of the scatter plots in the lectures as one of the interesting observations, as those form the basis of our models.

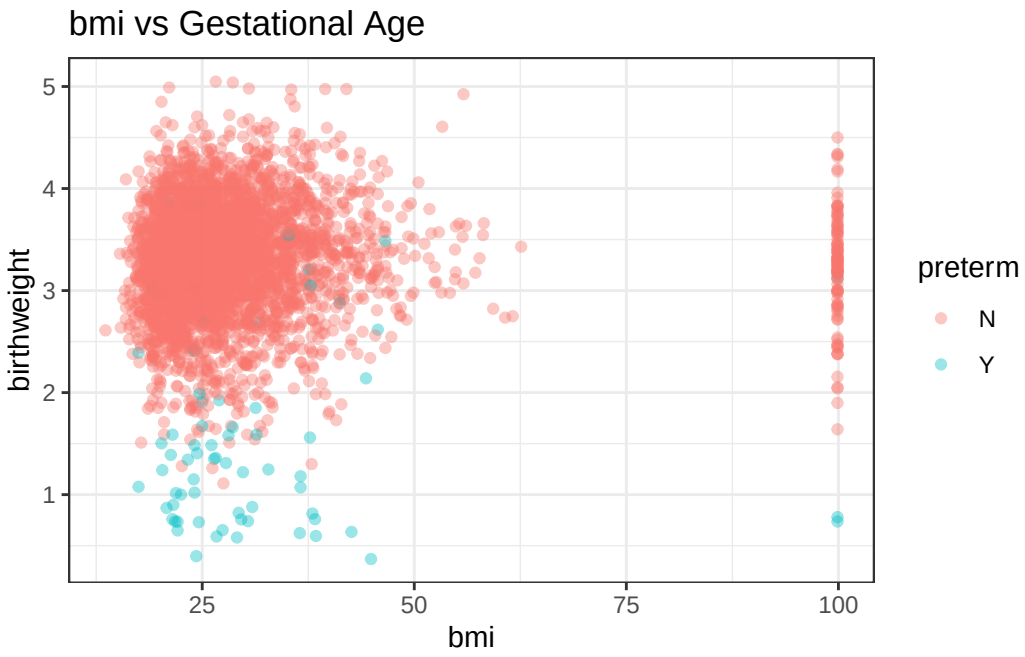
```
ds %>% ggplot() + aes(x = gest, y = birthweight, color = preterm, group = preterm) +
  geom_point() +
  theme_bw() +
  geom_smooth(method = "lm") +
  labs(title = "Weight vs Gestational Age")
```




```
ds %>% ggplot() + aes(x = mager, y = birthweight, color = preterm) +
  geom_point(alpha = 0.4) +
  theme_bw() +
  labs(title = "Weight vs Gestational Age")
```




```
ds %>% ggplot() + aes(x = bmi, y = birthweight, color = preterm) +
  geom_point(alpha = 0.4) +
  theme_bw() +
  labs(title = "bmi vs Gestational Age")
```



The model

As in lecture, we will look at two candidate models

Model 1 has log birth weight as a function of log gestational age

$$\log(y_i) \sim N(\beta_1 + \beta_2 \log(x_i), \sigma^2)$$

Model 2 has an interaction term between gestation and prematurity

$$\log(y_i) \sim N(\beta_1 + \beta_2 \log(x_i) + \beta_2 z_i + \beta_3 \log(x_i) z_i, \sigma^2)$$

- y_i is weight in kg
- x_i is gestational age in weeks, CENTERED AND STANDARDIZED
- z_i is preterm (0 or 1, if gestational age is less than 32 weeks)

Prior predictive checks

Let's put some weakly informative priors on all parameters i.e. for the βs

$$\beta \sim N(0, 1)$$

and for σ

$$\sigma \sim N^{+}(0, 1)$$

where the plus means positive values only i.e. Half Normal.

Let's check to see what the resulting distribution of birth weights look like given Model 1 and the priors specified above, assuming we had no data on birth weight (but observations of gestational age).

Question 2

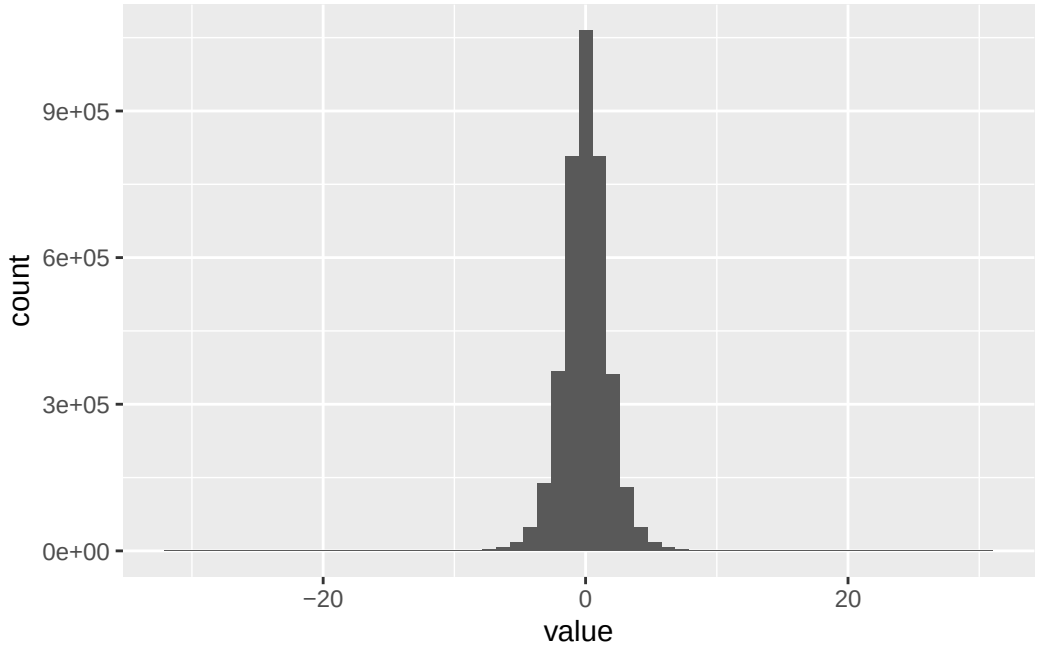
For Model 1, simulate values of βs and σ based on the priors above. Do 1000 simulations. Use these values to simulate (log) birth weights from the likelihood specified in Model 1, based on the set of observed gestational weights. **Remember the gestational weights should be centered and standardized**.

- Plot the resulting distribution of simulated (log) birth weights.
- Plot ten simulations of (log) birthweights against gestational age.

```
set.seed(1)
beta1 = rnorm(1000)
beta2 = rnorm(1000)
sigma = abs(rnorm(1000))
gestational <- ds %>% mutate(log_z_gest = scale(log(gest))) %>% select(log_z_gest)

for (i in 1:1000){
  mu <- beta1[i] + beta2[i] * gestational$log_z_gest
  gestational[i+1] =  rnorm(3842, mean = mu, sd = sigma[i])
}
```

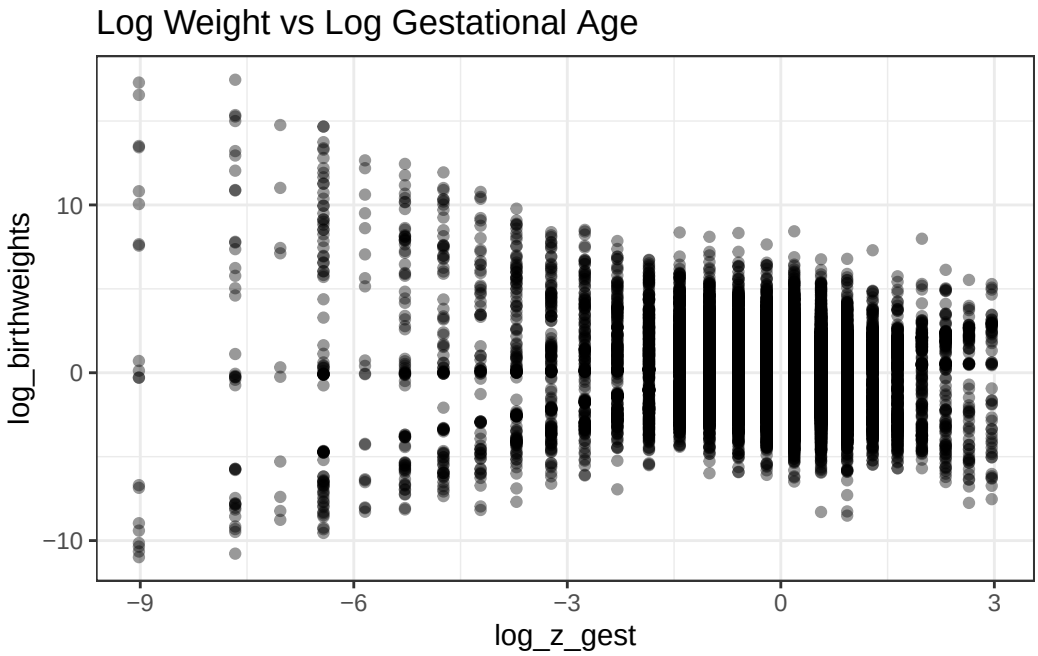
```
gestational %>% select(-log_z_gest) %>% pivot_longer(cols = everything()) %>%
  ggplot(aes(x= value)) +
  geom_histogram(bins = 60)
```




```
sim10 <- gestational[1:11] %>%
  pivot_longer(cols = starts_with("..."), names_to = "Sim_num",
               values_to = "log_birthweights")
sim10
```

```
# A tibble: 38,420 x 3
   log_z_gest[,1] Sim_num log_birthweights
            <dbl> <chr>              <dbl>
 1          0.188 ...2               0.242
 2          0.188 ...3              -0.916
 3          0.188 ...4              -5.15
 4          0.188 ...5               2.23
 5          0.188 ...6               0.305
 6          0.188 ...7               0.136
 7          0.188 ...8               0.649
 8          0.188 ...9               1.07
 9          0.188 ...10             -0.0466
10          0.188 ...11              0.306
# ... with 38,410 more rows
```

```
sim10 %>% ggplot() + aes(x = log_z_gest, y = log_birthweights) +
  geom_point(alpha = 0.4) +
  theme_bw() +
  labs(title = "Log Weight vs Log Gestational Age")
```



Run the model

Now we're going to run Model 1 in Stan. The stan code is in the `code/models` folder.

First, get our data into right form for input into stan.

```
ds$log_weight <- log(ds$birthweight)
ds$log_gest_c <- (log(ds$gest) - mean(log(ds$gest)))/sd(log(ds$gest))

# put into a list
stan_data <- list(N = nrow(ds),
                  log_weight = ds$log_weight,
                  log_gest = ds$log_gest_c)
```

Now fit the model

```r
mod1 <- stan(data = stan_data,
             file = here("code/models/simple_weight.stan"),
             iter = 500,
             seed = 243)
```

```
SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 0.000274 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 2.74 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:   1 / 500 [  0%]  (Warmup)
Chain 1: Iteration:  50 / 500 [ 10%]  (Warmup)
Chain 1: Iteration: 100 / 500 [ 20%]  (Warmup)
Chain 1: Iteration: 150 / 500 [ 30%]  (Warmup)
Chain 1: Iteration: 200 / 500 [ 40%]  (Warmup)
Chain 1: Iteration: 250 / 500 [ 50%]  (Warmup)
Chain 1: Iteration: 251 / 500 [ 50%]  (Sampling)
Chain 1: Iteration: 300 / 500 [ 60%]  (Sampling)
Chain 1: Iteration: 350 / 500 [ 70%]  (Sampling)
Chain 1: Iteration: 400 / 500 [ 80%]  (Sampling)
Chain 1: Iteration: 450 / 500 [ 90%]  (Sampling)
Chain 1: Iteration: 500 / 500 [100%]  (Sampling)
Chain 1:
Chain 1:  Elapsed Time: 0.393 seconds (Warm-up)
Chain 1:                0.317 seconds (Sampling)
Chain 1:                0.71 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2:
Chain 2: Gradient evaluation took 0.000158 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 1.58 seconds.
Chain 2: Adjust your expectations accordingly!
Chain 2:
Chain 2:
Chain 2: Iteration:   1 / 500 [  0%]  (Warmup)
Chain 2: Iteration:  50 / 500 [ 10%]  (Warmup)
Chain 2: Iteration: 100 / 500 [ 20%]  (Warmup)
Chain 2: Iteration: 150 / 500 [ 30%]  (Warmup)
```

```
Chain 2: Iteration: 200 / 500 [ 40%]  (Warmup)
Chain 2: Iteration: 250 / 500 [ 50%]  (Warmup)
Chain 2: Iteration: 251 / 500 [ 50%]  (Sampling)
Chain 2: Iteration: 300 / 500 [ 60%]  (Sampling)
Chain 2: Iteration: 350 / 500 [ 70%]  (Sampling)
Chain 2: Iteration: 400 / 500 [ 80%]  (Sampling)
Chain 2: Iteration: 450 / 500 [ 90%]  (Sampling)
Chain 2: Iteration: 500 / 500 [100%]  (Sampling)
Chain 2:
Chain 2:  Elapsed Time: 0.377 seconds (Warm-up)
Chain 2:                0.346 seconds (Sampling)
Chain 2:                0.723 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 0.000137 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 1.37 seconds.
Chain 3: Adjust your expectations accordingly!
Chain 3:
Chain 3:
Chain 3: Iteration:   1 / 500 [  0%]  (Warmup)
Chain 3: Iteration:  50 / 500 [ 10%]  (Warmup)
Chain 3: Iteration: 100 / 500 [ 20%]  (Warmup)
Chain 3: Iteration: 150 / 500 [ 30%]  (Warmup)
Chain 3: Iteration: 200 / 500 [ 40%]  (Warmup)
Chain 3: Iteration: 250 / 500 [ 50%]  (Warmup)
Chain 3: Iteration: 251 / 500 [ 50%]  (Sampling)
Chain 3: Iteration: 300 / 500 [ 60%]  (Sampling)
Chain 3: Iteration: 350 / 500 [ 70%]  (Sampling)
Chain 3: Iteration: 400 / 500 [ 80%]  (Sampling)
Chain 3: Iteration: 450 / 500 [ 90%]  (Sampling)
Chain 3: Iteration: 500 / 500 [100%]  (Sampling)
Chain 3:
Chain 3:  Elapsed Time: 0.366 seconds (Warm-up)
Chain 3:                0.31 seconds (Sampling)
Chain 3:                0.676 seconds (Total)
Chain 3:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4:
Chain 4: Gradient evaluation took 0.000147 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 1.47 seconds.
```

```
Chain 4: Adjust your expectations accordingly!
Chain 4:
Chain 4:
Chain 4: Iteration:   1 / 500 [  0%]  (Warmup)
Chain 4: Iteration:  50 / 500 [ 10%]  (Warmup)
Chain 4: Iteration: 100 / 500 [ 20%]  (Warmup)
Chain 4: Iteration: 150 / 500 [ 30%]  (Warmup)
Chain 4: Iteration: 200 / 500 [ 40%]  (Warmup)
Chain 4: Iteration: 250 / 500 [ 50%]  (Warmup)
Chain 4: Iteration: 251 / 500 [ 50%]  (Sampling)
Chain 4: Iteration: 300 / 500 [ 60%]  (Sampling)
Chain 4: Iteration: 350 / 500 [ 70%]  (Sampling)
Chain 4: Iteration: 400 / 500 [ 80%]  (Sampling)
Chain 4: Iteration: 450 / 500 [ 90%]  (Sampling)
Chain 4: Iteration: 500 / 500 [100%]  (Sampling)
Chain 4:
Chain 4:  Elapsed Time: 0.361 seconds (Warm-up)
Chain 4:                0.371 seconds (Sampling)
Chain 4:                0.732 seconds (Total)
Chain 4:
```

```r
summary(mod1)$summary[c("beta[1]", "beta[2]", "sigma"),]
```

```
            mean      se_mean          sd      2.5%       25%       50%
beta[1] 1.1624783 8.160385e-05 0.002856578 1.1570200 1.1604786 1.1625011
beta[2] 0.1437529 8.295075e-05 0.002912236 0.1381284 0.1416970 0.1436747
sigma   0.1690330 1.113724e-04 0.001902828 0.1652694 0.1677842 0.1690763
             75%     97.5%     n_eff      Rhat
beta[1] 1.1644669 1.1681028 1225.3801 0.9978044
beta[2] 0.1456716 0.1495180 1232.5721 0.9998714
sigma   0.1702528 0.1727953  291.9066 1.0146111
```

Question 3

Based on model 3, give an estimate of the expected birthweight of a baby who was born at a gestational age of 37 weeks.

```r
exp((log(37)- mean(log(ds$gest)))/sd(log(ds$gest))*0.1437529 + 1.1624783)
```

```
[1] 2.935874
```

Using the estimated posterior mean, the expected birth weight of a baby who was born at a gestational age of 37 weeks is 2.935kg

Question 4

Write a stan model to run Model 2, and run it.

```
preterm <- ifelse(ds$preterm == "Y", 1, 0)

stan_data <- list(N = nrow(ds),
                  log_weight = ds$log_weight,
                  log_gest = ds$log_gest_c,
                  preterm = ifelse(ds$preterm == "Y", 1, 0),
                  interaction = ds$log_gest_c*preterm)

mod2 <- stan(data = stan_data,
file = here("code/models/simple_weight_q4.stan"),
iter = 1000,
seed = 243)
```

```
SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 0.000886 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 8.86 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 1: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 1: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 1: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 1: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 1: Iteration: 500 / 1000 [ 50%]  (Warmup)
Chain 1: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 1: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 1: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 1: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 1: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 1: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 1:
```

```
Chain 1:  Elapsed Time: 3.99 seconds (Warm-up)
Chain 1:                2.858 seconds (Sampling)
Chain 1:                6.848 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2:
Chain 2: Gradient evaluation took 0.000466 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 4.66 seconds.
Chain 2: Adjust your expectations accordingly!
Chain 2:
Chain 2:
Chain 2: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 2: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 2: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 2: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 2: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 2: Iteration: 500 / 1000 [ 50%]  (Warmup)
Chain 2: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 2: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 2: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 2: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 2: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 2: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 2:
Chain 2:  Elapsed Time: 4.004 seconds (Warm-up)
Chain 2:                4.052 seconds (Sampling)
Chain 2:                8.056 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 0.000475 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 4.75 seconds.
Chain 3: Adjust your expectations accordingly!
Chain 3:
Chain 3:
Chain 3: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 3: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 3: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 3: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 3: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 3: Iteration: 500 / 1000 [ 50%]  (Warmup)
```

```
Chain 3: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 3: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 3: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 3: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 3: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 3: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 3:
Chain 3:  Elapsed Time: 4.075 seconds (Warm-up)
Chain 3:                4.002 seconds (Sampling)
Chain 3:                8.077 seconds (Total)
Chain 3:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4:
Chain 4: Gradient evaluation took 0.000471 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 4.71 seconds.
Chain 4: Adjust your expectations accordingly!
Chain 4:
Chain 4:
Chain 4: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 4: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 4: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 4: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 4: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 4: Iteration: 500 / 1000 [ 50%]  (Warmup)
Chain 4: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 4: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 4: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 4: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 4: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 4: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 4:
Chain 4:  Elapsed Time: 4.02 seconds (Warm-up)
Chain 4:                4.256 seconds (Sampling)
Chain 4:                8.276 seconds (Total)
Chain 4:
```

```
summary(mod2)$summary[c("beta[1]", "beta[2]", "beta[3]", "beta[4]", "sigma"),]
```

```
             mean      se_mean          sd       2.5%        25%       50%
beta[1] 1.1695606 5.259778e-05 0.002619877 1.16440944 1.16793892 1.1696211
```

```
beta[2] 0.1019187 7.460161e-05 0.003372707 0.09534751 0.09970971 0.1019299
beta[3] 0.5617196 3.024670e-03 0.063523319 0.43251124 0.51932707 0.5633255
beta[4] 0.1980411 6.329651e-04 0.013271075 0.17020939 0.18952383 0.1979300
sigma   0.1612523 5.496825e-05 0.001828663 0.15774082 0.16005586 0.1612095
              75%     97.5%     n_eff      Rhat
beta[1] 1.1712320 1.1748836 2481.0005 0.9994273
beta[2] 0.1041208 0.1085593 2043.9053 0.9994972
beta[3] 0.6054852 0.6841378  441.0729 1.0125540
beta[4] 0.2071063 0.2238445  439.5949 1.0107559
sigma   0.1624835 0.1648295 1106.7345 1.0016836
```

Question 5

For reference I have uploaded some model 2 results. Check your results are similar.

```
load(here("output", "mod2.Rda"))
summary(mod2)$summary[c(paste0("beta[", 1:4, "]"), "sigma"),]
```

```
             mean      se_mean          sd       2.5%        25%       50%
beta[1] 1.1697241 1.385590e-04 0.002742186 1.16453578 1.16767109 1.1699278
beta[2] 0.5563133 5.835253e-03 0.058054991 0.43745504 0.51708255 0.5561553
beta[3] 0.1020960 1.481816e-04 0.003669476 0.09459462 0.09997153 0.1020339
beta[4] 0.1967671 1.129799e-03 0.012458398 0.17164533 0.18817091 0.1974114
sigma   0.1610727 9.950037e-05 0.001782004 0.15784213 0.15978020 0.1610734
              75%     97.5%     n_eff      Rhat
beta[1] 1.1716235 1.1750167 391.67359 1.0115970
beta[2] 0.5990427 0.6554967  98.98279 1.0088166
beta[3] 0.1044230 0.1093843 613.22428 0.9978156
beta[4] 0.2064079 0.2182454 121.59685 1.0056875
sigma   0.1623019 0.1646189 320.75100 1.0104805
```

The result is similar.

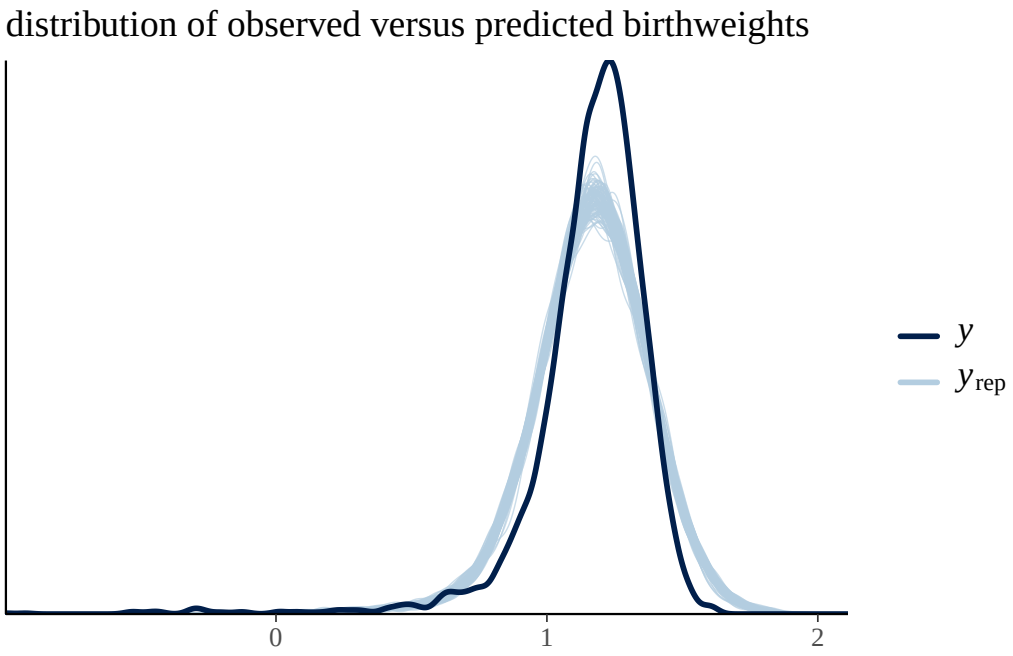
PPCs

Now we've run two candidate models let's do some posterior predictive checks. The `bayesplot` package has a lot of inbuilt graphing functions to do this. For example, let's plot the distribution of our data (y) against 100 different datasets drawn from the posterior predictive distribution:

```
set.seed(1856)
y <- ds$log_weight
yrep1 <- extract(mod1)[["log_weight_rep"]]
yrep2 <- extract(mod2)[["log_weight_rep"]]
dim(yrep1)
```

```
[1] 1000 3842
```

```
samp100 <- sample(nrow(yrep1), 100)
ppc_dens_overlay(y, yrep1[samp100, ])  + ggtitle("distribution of observed versus predicte
```

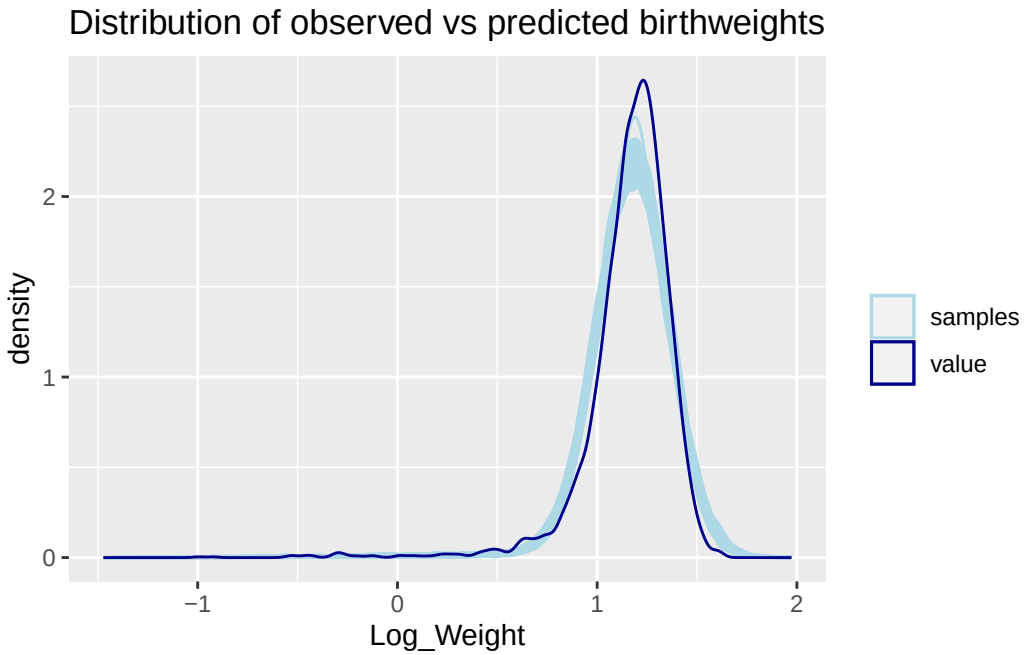


Question 6

Make a similar plot to the one above but for model 2, and **not** using the bayes plot in built function (i.e. do it yourself just with `geom_density`)

```
samp100_2 <- sample(nrow(yrep2), 100)
samples <- as_tibble(t(yrep2[samp100_2, ]))
log_weight <- as_tibble(ds$log_weight)
samples <- cbind(log_weight, samples)
```

```r
samples %>%
  pivot_longer( everything(), names_to = "simulate", values_to = "Log_Weight" ) %>%
  ggplot(aes(Log_Weight, group = simulate)) +
  geom_density(alpha = 0.2, aes(color = "samples")) +
  geom_density(data = ds %>% mutate(simulate = "value"), aes(x = log(birthweight), col = "
  scale_color_manual(name = "", values = c("value" = "darkblue", "samples" = "lightblue"))
  ggtitle("Distribution of observed vs predicted birthweights")
```

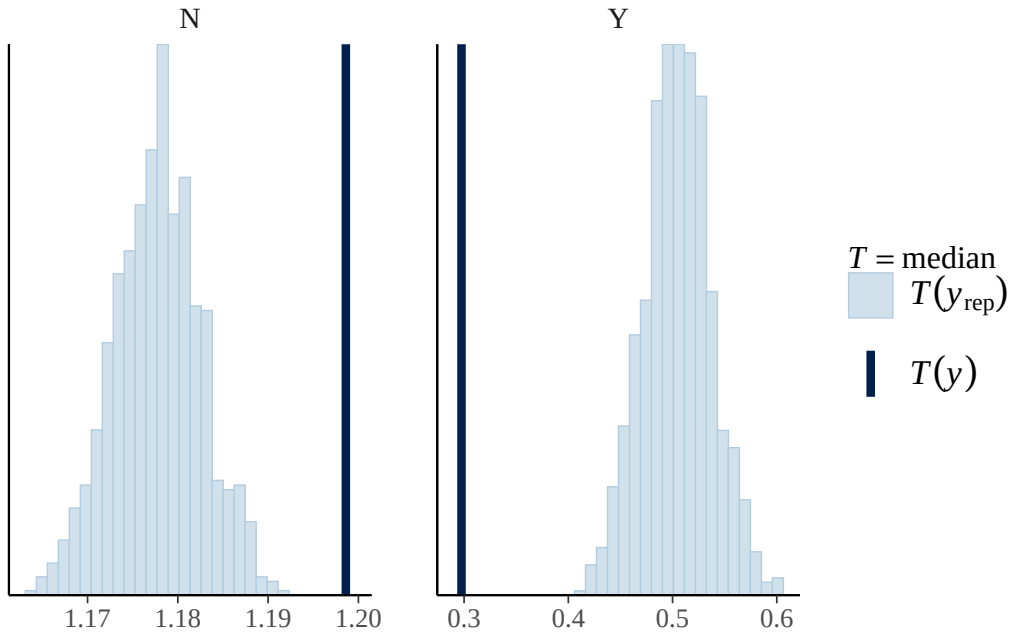


Test statistics

We can also look at some summary statistics in the PPD versus the data, again either using `bayesplot` – the function of interest is `ppc_stat` or `ppc_stat_grouped` – or just doing it ourselves using ggplot.

E.g. medians by prematurity for Model 1

```r
ppc_stat_grouped(ds$log_weight, yrep1, group = ds$preterm, stat = 'median')
```



Question 7

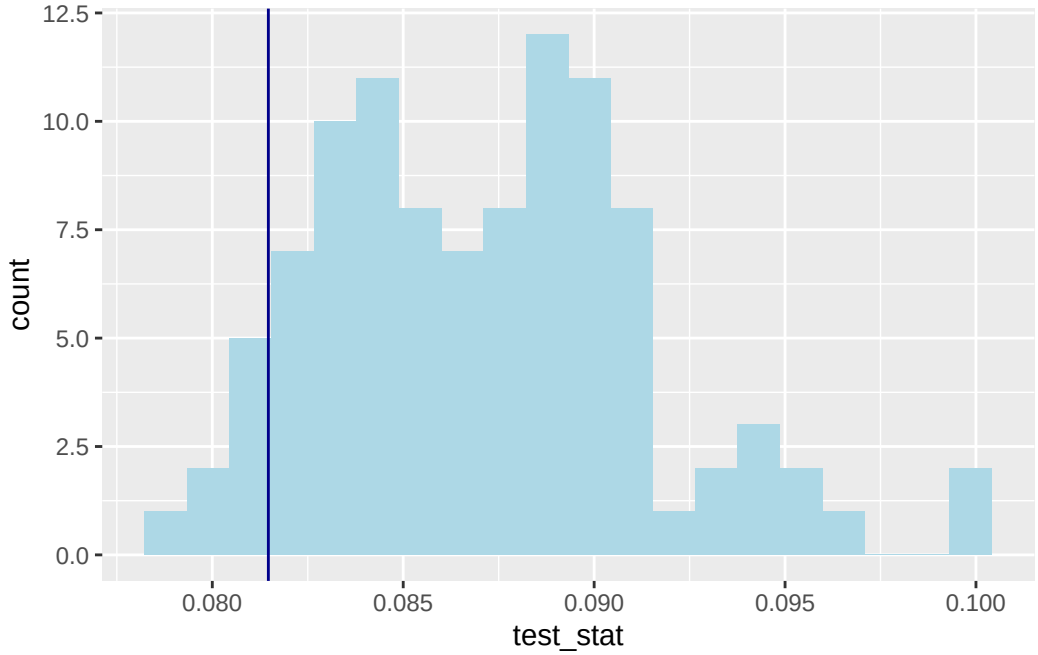
Use a test statistic of the proportion of births under 2.5kg. Calculate the test statistic for the data, and the posterior predictive samples for both models, and plot the comparison (one plot per model).

```
mean(ds$birthweight < 2.5)
```

```
[1] 0.08146799
```

Model 2:

```
samples %>%
  pivot_longer( everything(), names_to = "simulate", values_to = "Log_Weight" ) %>%
  group_by(simulate) %>%
  summarize(test_stat = mean(exp(Log_Weight) < 2.5)) %>%
  ggplot(aes(x = test_stat)) +
  geom_histogram(bins = 20, fill = "lightblue") +
  geom_vline(xintercept = mean(ds$birthweight < 2.5), color = "darkblue")
```

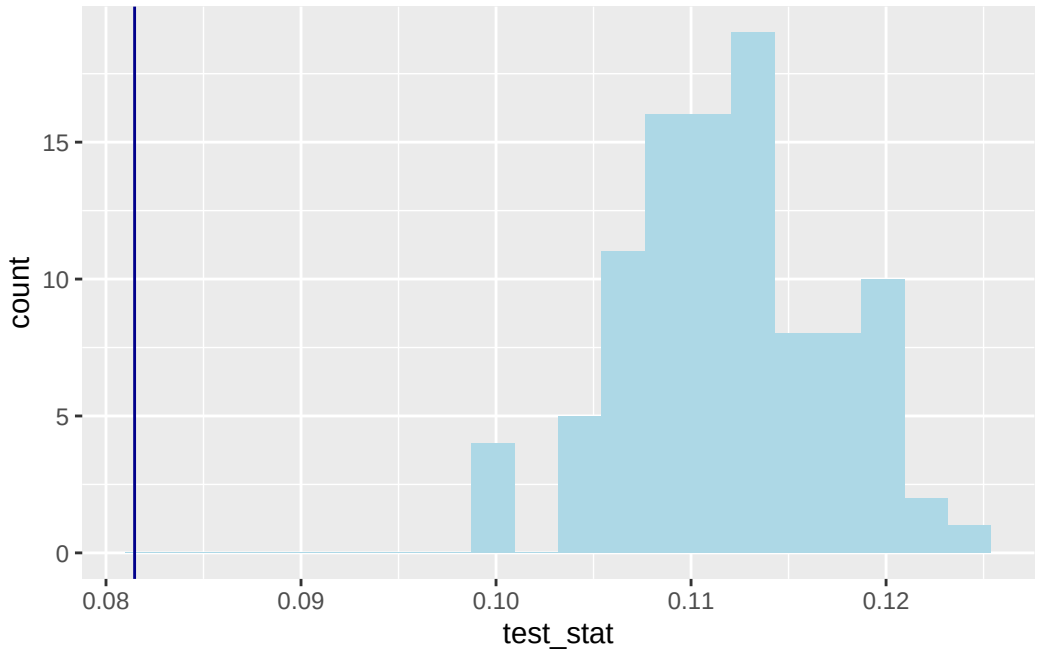


Model 1:

```
samp100_1 <- sample(nrow(yrep1), 100)
samp100_1
```

```
  [1]   42  737  241  327   44  335  744  743  583  670  220  379  229  947  695
 [16]  405  767  142  300  689  599  173  952  746  532  305  425  484  204  288
 [31]   92  370  772  575  864  750  146  501  215  253   97  295  243  298  569
 [46]  414  728  625  888  334   88  893  182   94  742  258   81  765  272  589
 [61]  429  672   52  129  970  457  139  357  398  358  769  990  726  603  541
 [76] 1000  475  526  165  813   59  997  533  107  988  535  321  100  462  360
 [91]  417  829  668  711  860  149  958  119  896  175
```

```
samples1 <- as_tibble(t(yrep1[samp100_1, ]))
samples1 %>%
  pivot_longer( everything(), names_to = "simulate", values_to = "Log_Weight" ) %>%
  group_by(simulate) %>%
  summarize(test_stat = mean(exp(Log_Weight) < 2.5)) %>%
  ggplot(aes(x = test_stat)) +
  geom_histogram(bins = 20, fill = "lightblue") +
  geom_vline(xintercept = mean(ds$birthweight < 2.5), color = "darkblue")
```



LOO

Finally let's calculate the LOO elpd for each model and compare. The first step of this is to get the point-wise log likelihood estimates from each model:

```
loglik1 <- extract(mod1)[["log_lik"]]
loglik2 <- extract(mod2)[["log_lik"]]
```

And then we can use these in the `loo` function to get estimates for the elpd. Note the `save_psis = TRUE` argument saves the calculation for each simulated draw, which is needed for the LOO-PIT calculation below.

```
loo1 <- loo(loglik1, save_psis = TRUE)
loo2 <- loo(loglik2, save_psis = TRUE)
```

Look at the output:

```
loo1
```

```
Computed from 1000 by 3842 log-likelihood matrix
```

```
         Estimate    SE
elpd_loo   1377.0  72.4
p_loo         9.8   1.4
looic     -2754.1 144.8
------
Monte Carlo SE of elpd_loo is 0.1.

All Pareto k estimates are good (k < 0.5).
See help('pareto-k-diagnostic') for details.
```

```
loo2
```

```
Computed from 500 by 3842 log-likelihood matrix

         Estimate    SE
elpd_loo   1552.8  70.0
p_loo        14.8   2.3
looic     -3105.6 139.9
------
Monte Carlo SE of elpd_loo is 0.2.

All Pareto k estimates are good (k < 0.5).
See help('pareto-k-diagnostic') for details.
```

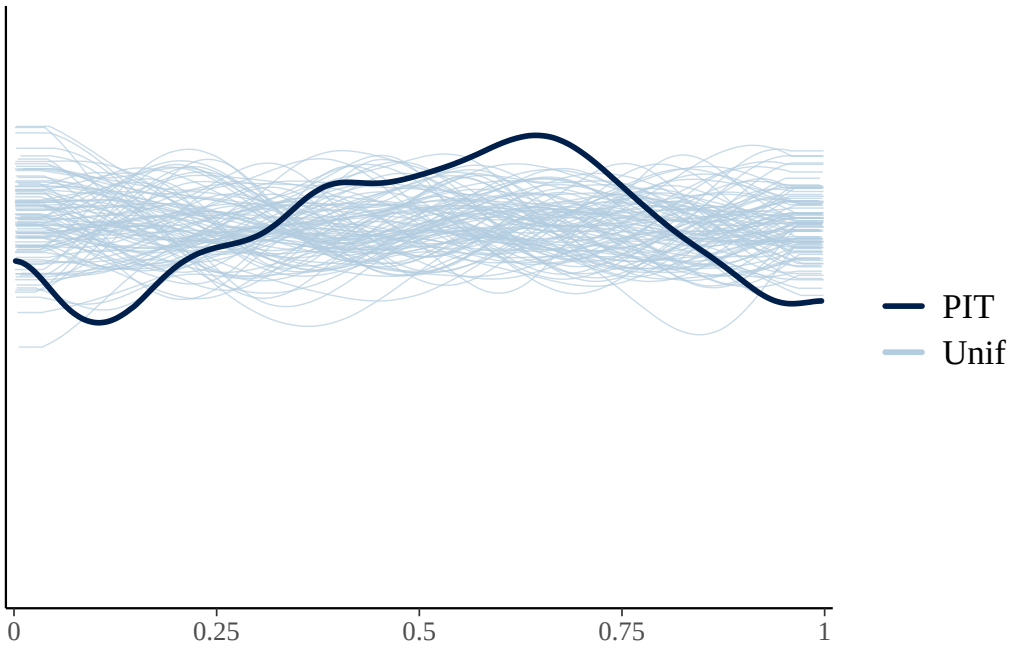
Comparing the two models tells us Model 2 is better:

```
loo_compare(loo1, loo2)
```

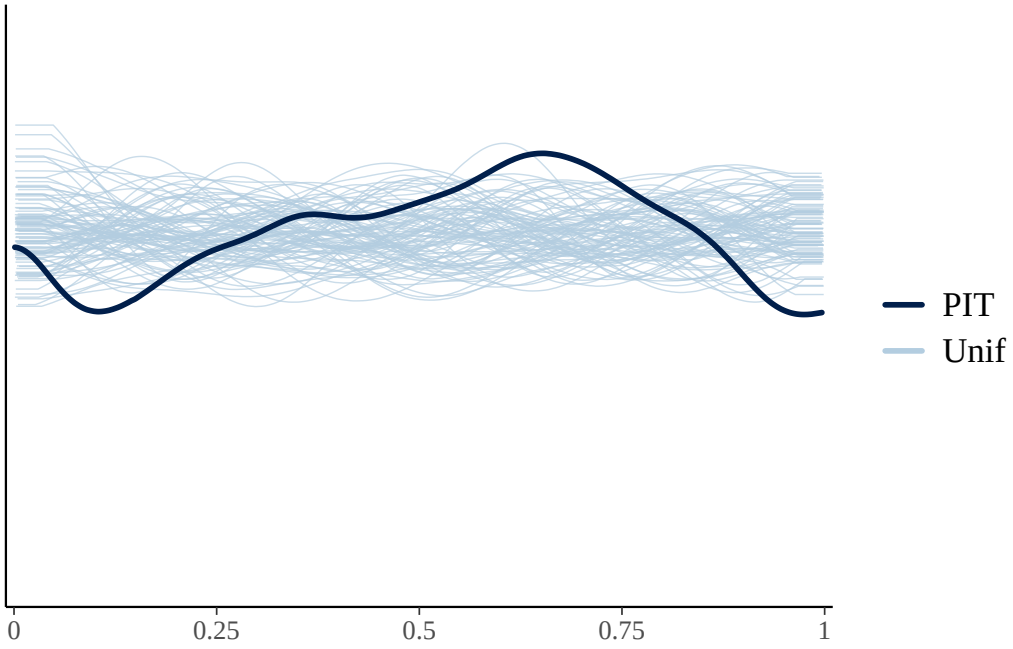
```
       elpd_diff se_diff
model2    0.0       0.0
model1 -175.8      36.2
```

We can also compare the LOO-PIT of each of the models to standard uniforms. The both do pretty well.

```
ppc_loo_pit_overlay(yrep = yrep1, y = y, lw = weights(loo1$psis_object))
```




```
ppc_loo_pit_overlay(yrep = yrep2, y = y, lw = weights(loo2$psis_object))
```



Bonus question (not required)

Create your own PIT histogram "from scratch" for Model 2.

Question 8

Based on the original dataset, choose one (or more) additional covariates to add to the linear regression model. Run the model in Stan, and compare with Model 2 above on at least 2 posterior predictive checks.

Adding mother's age as covariate to the model.

```
stan_data <- list(N = nrow(ds),
                  log_weight = ds$log_weight,
                  log_gest = ds$log_gest_c,
                  preterm = ifelse(ds$preterm == "Y", 1, 0),
                  interaction = ds$log_gest_c*preterm,
                  age = ds$mager)

mod3 <- stan(data = stan_data,file = here("code/models/simple_weight_q8.stan"),iter = 1000
```

```
SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 0.001126 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 11.26 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 1: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 1: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 1: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 1: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 1: Iteration: 500 / 1000 [ 50%]  (Warmup)
Chain 1: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 1: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 1: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 1: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 1: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 1: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 1:
```

```
Chain 1:  Elapsed Time: 24.128 seconds (Warm-up)
Chain 1:                42.119 seconds (Sampling)
Chain 1:                66.247 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2:
Chain 2: Gradient evaluation took 0.00067 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 6.7 seconds.
Chain 2: Adjust your expectations accordingly!
Chain 2:
Chain 2:
Chain 2: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 2: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 2: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 2: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 2: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 2: Iteration: 500 / 1000 [ 50%]  (Warmup)
Chain 2: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 2: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 2: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 2: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 2: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 2: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 2:
Chain 2:  Elapsed Time: 44.183 seconds (Warm-up)
Chain 2:                52.22 seconds (Sampling)
Chain 2:                96.403 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 0.000624 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 6.24 seconds.
Chain 3: Adjust your expectations accordingly!
Chain 3:
Chain 3:
Chain 3: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 3: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 3: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 3: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 3: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 3: Iteration: 500 / 1000 [ 50%]  (Warmup)
```

```
Chain 3: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 3: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 3: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 3: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 3: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 3: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 3:
Chain 3:  Elapsed Time: 38.533 seconds (Warm-up)
Chain 3:                44.568 seconds (Sampling)
Chain 3:                83.101 seconds (Total)
Chain 3:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4:
Chain 4: Gradient evaluation took 0.000631 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 6.31 seconds.
Chain 4: Adjust your expectations accordingly!
Chain 4:
Chain 4:
Chain 4: Iteration:   1 / 1000 [  0%]  (Warmup)
Chain 4: Iteration: 100 / 1000 [ 10%]  (Warmup)
Chain 4: Iteration: 200 / 1000 [ 20%]  (Warmup)
Chain 4: Iteration: 300 / 1000 [ 30%]  (Warmup)
Chain 4: Iteration: 400 / 1000 [ 40%]  (Warmup)
Chain 4: Iteration: 500 / 1000 [ 50%]  (Warmup)
Chain 4: Iteration: 501 / 1000 [ 50%]  (Sampling)
Chain 4: Iteration: 600 / 1000 [ 60%]  (Sampling)
Chain 4: Iteration: 700 / 1000 [ 70%]  (Sampling)
Chain 4: Iteration: 800 / 1000 [ 80%]  (Sampling)
Chain 4: Iteration: 900 / 1000 [ 90%]  (Sampling)
Chain 4: Iteration: 1000 / 1000 [100%]  (Sampling)
Chain 4:
Chain 4:  Elapsed Time: 31.339 seconds (Warm-up)
Chain 4:                47.681 seconds (Sampling)
Chain 4:                79.02 seconds (Total)
Chain 4:
```

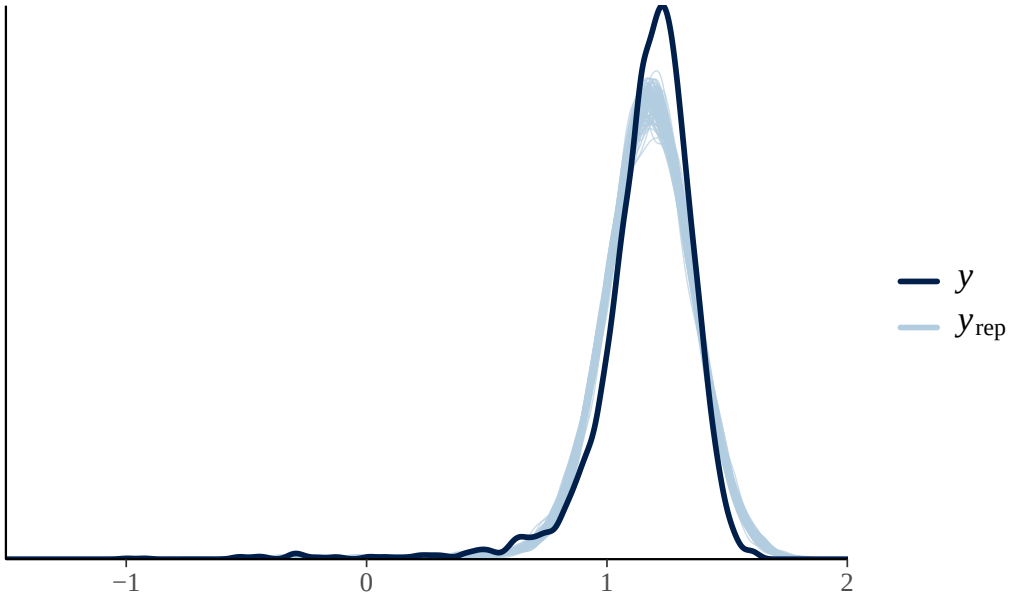
```r
summary(mod3)$summary[c("beta[1]", "beta[2]", "beta[3]", "beta[4]", "beta[5]", "sigma"),]
```

```
              mean      se_mean           sd        2.5%         25%
beta[1] 1.096836370 4.513563e-04 0.0130752067 1.071660621 1.087970125
```

```
beta[2] 0.102709090 8.283478e-05 0.0035119139 0.095662968 0.100369058
beta[3] 0.561859604 2.057254e-03 0.0622485677 0.440921574 0.519266917
beta[4] 0.197865269 4.422943e-04 0.0129336267 0.172965608 0.189173903
beta[5] 0.002516418 1.519570e-05 0.0004455417 0.001655092 0.002189443
sigma   0.160547116 6.541354e-05 0.0019870883 0.156676091 0.159195915
                50%        75%       97.5%     n_eff     Rhat
beta[1] 1.096889452 1.10610288 1.121422248  839.1856 1.007480
beta[2] 0.102716600 0.10513781 0.109474416 1797.4724 1.000943
beta[3] 0.561041715 0.60459695 0.688527149  915.5513 1.003016
beta[4] 0.197770659 0.20687603 0.223405544  855.1020 1.004142
beta[5] 0.002510789 0.00281973 0.003374534  859.6772 1.007356
sigma   0.160548712 0.16182020 0.164601763  922.7818 1.000615
```

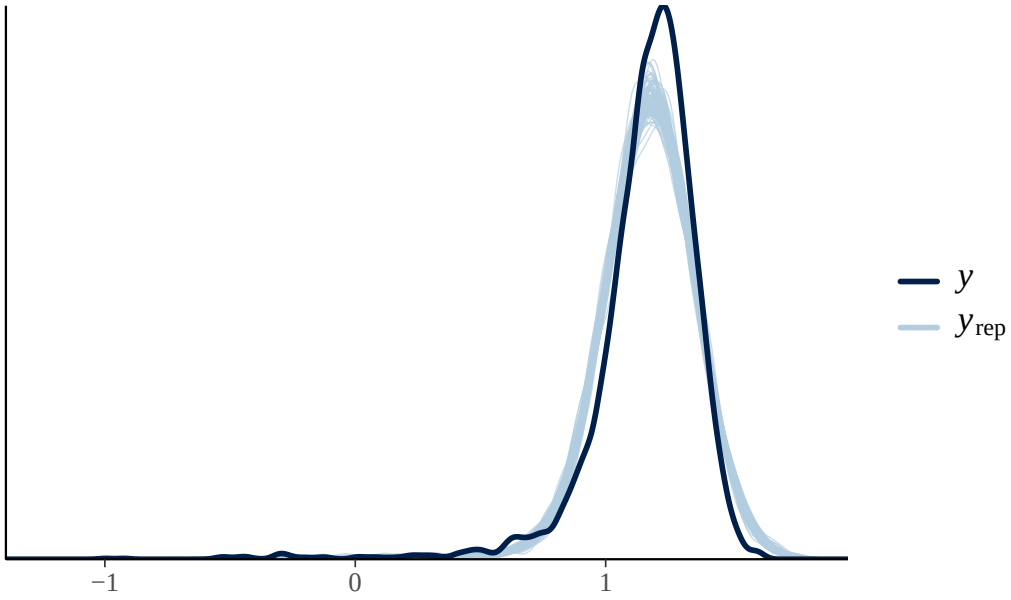
```
y <- ds$log_weight
yrep3 <- extract(mod3)[["log_weight_rep"]]
samp100 <- sample(nrow(yrep3), 100)
ppc_dens_overlay(y, yrep3[samp100, ])  + ggtitle("Model 3: distribution of observed versus
```

Model 3: distribution of observed versus predicted birthweights

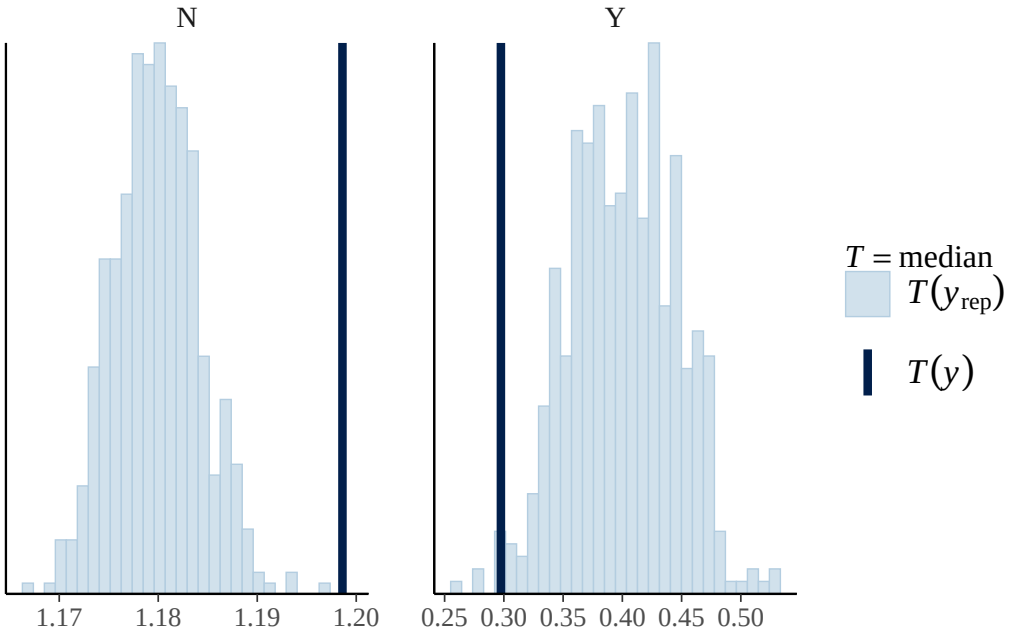



```
yrep2 <- extract(mod2)[["log_weight_rep"]]
samp100 <- sample(nrow(yrep2), 100)
ppc_dens_overlay(y, yrep2[samp100, ])  + ggtitle("Model 2:distribution of observed versus
```

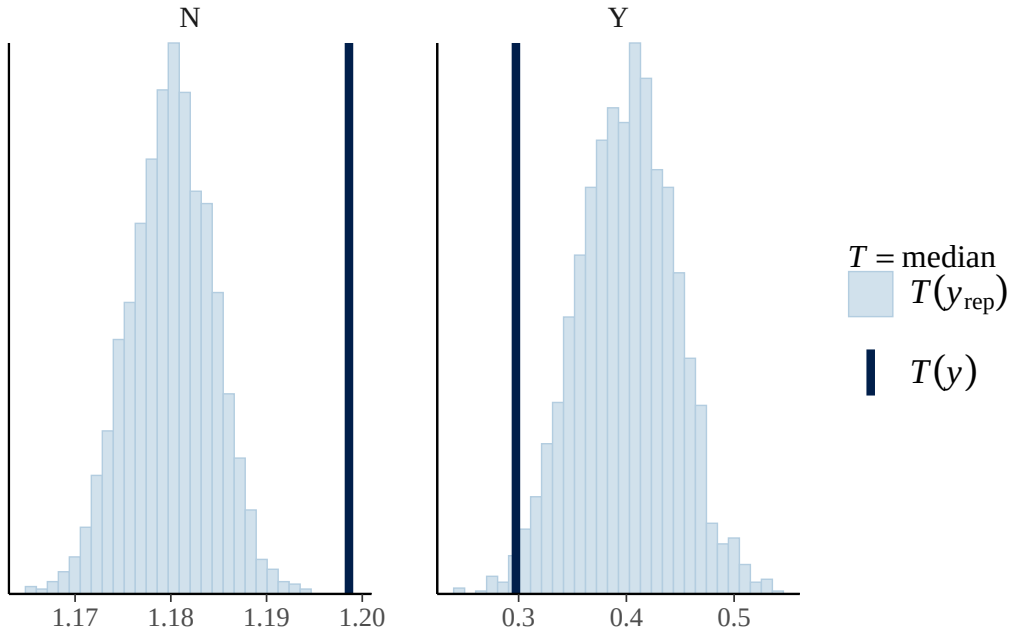
Model 2:distribution of observed versus predicted birthweights




```
ppc_stat_grouped(ds$log_weight, yrep2, group = ds$preterm, stat = 'median')
```



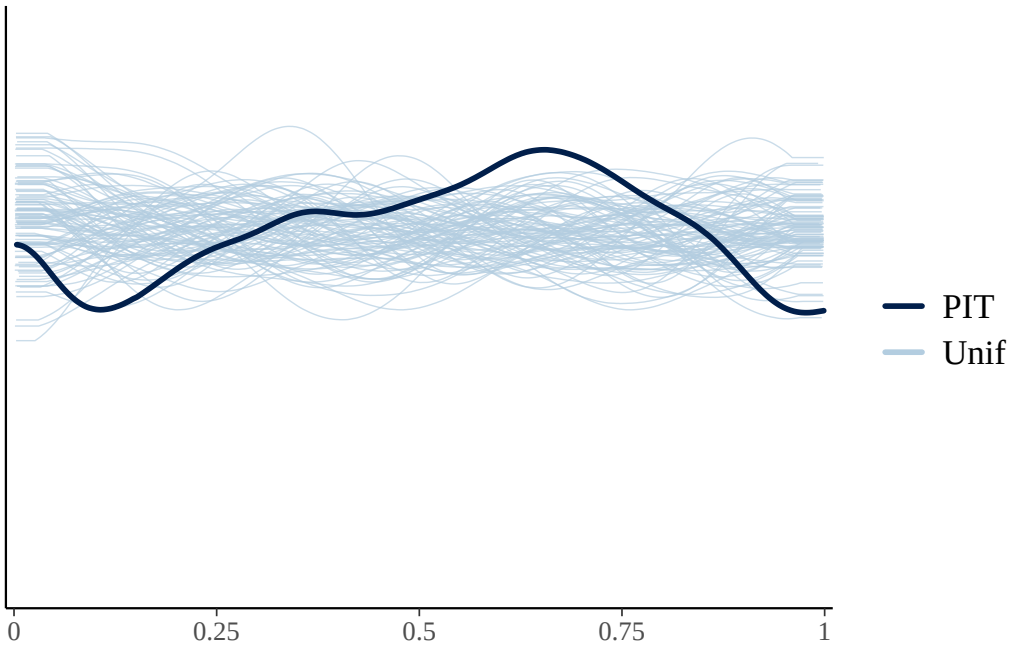
```
ppc_stat_grouped(ds$log_weight, yrep3, group = ds$preterm, stat = 'median')
```




```
loglik3 <- extract(mod3)[["log_lik"]]
loo3 <- loo(loglik3, save_psis = TRUE)
loo_compare(loo2, loo3)
```

```
       elpd_diff se_diff
model2   0.0       0.0
model1 -15.1       5.6
```

```
ppc_loo_pit_overlay(yrep = yrep2, y = y, lw = weights(loo2$psis_object))
```




```
ppc_loo_pit_overlay(yrep = yrep3, y = y, lw = weights(loo3$psis_object))
```