Lab 6

```
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)
```

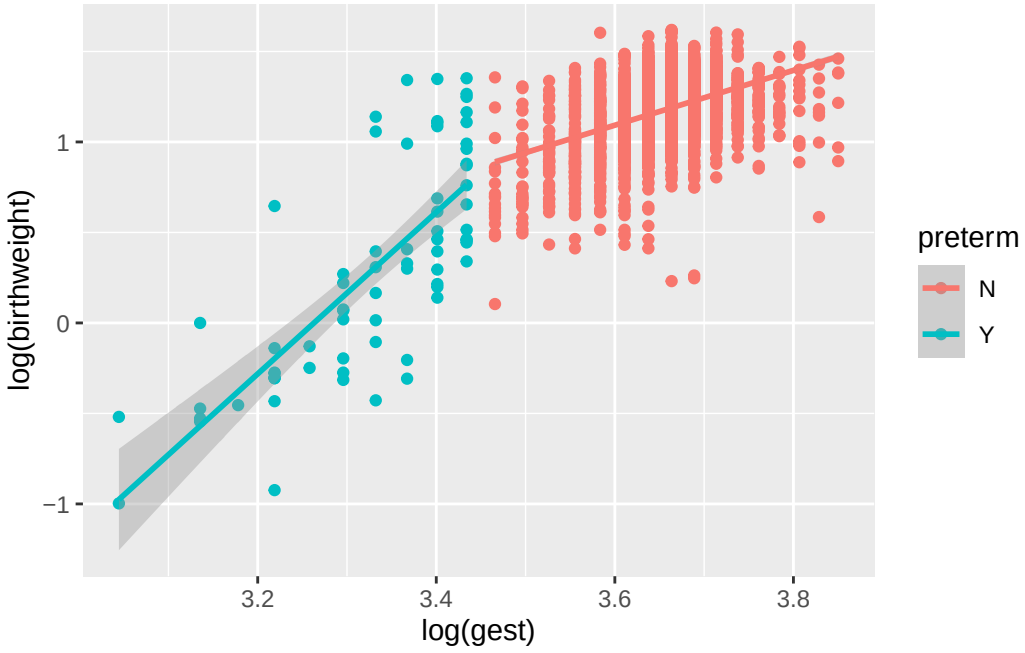
```
# A tibble: 6 x 8
  mager mracehisp meduc   bmi sex   combgest  dbwt ilive
  <dbl>     <dbl> <dbl> <dbl> <chr>    <dbl> <dbl> <chr>
1    16         2     2  23   M           39  3.18 Y
2    25         7     2  43.6 M           40  4.14 Y
3    27         2     3  19.5 F           41  3.18 Y
4    26         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
```

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

Question 1

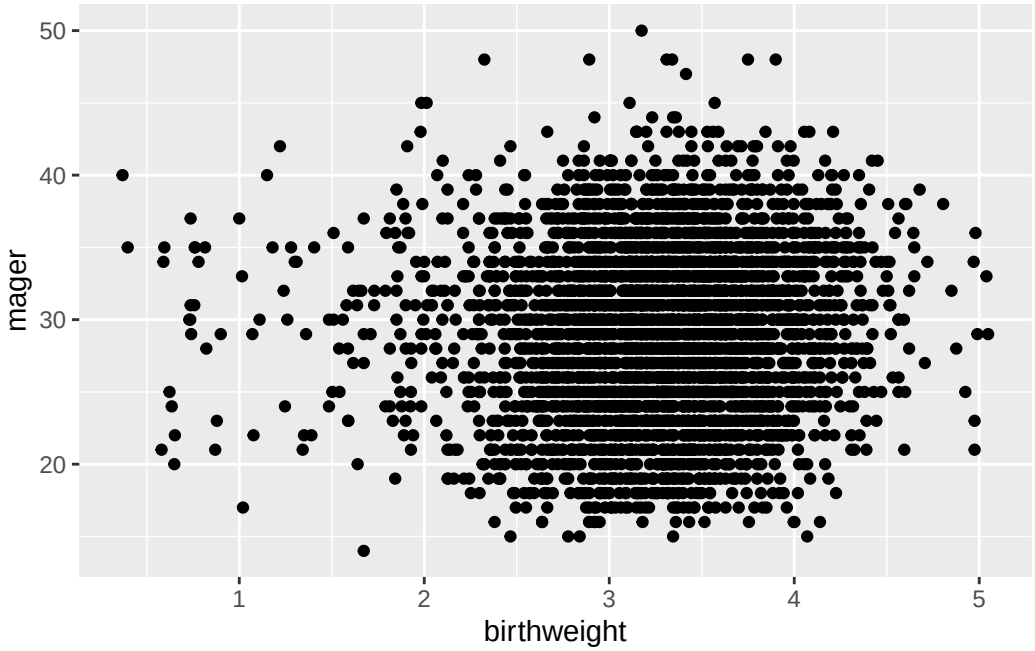
```
ggplot(ds,aes(x=log(gest),y=log(birthweight),color = preterm))+geom_point()+geom_smooth(me
```

```
`geom_smooth()` using formula = 'y ~ x'
```



The first interest point is that as gestational age increases, the infant's weight increases, and in the preterm period, the baby's body weight increases more rapidly.

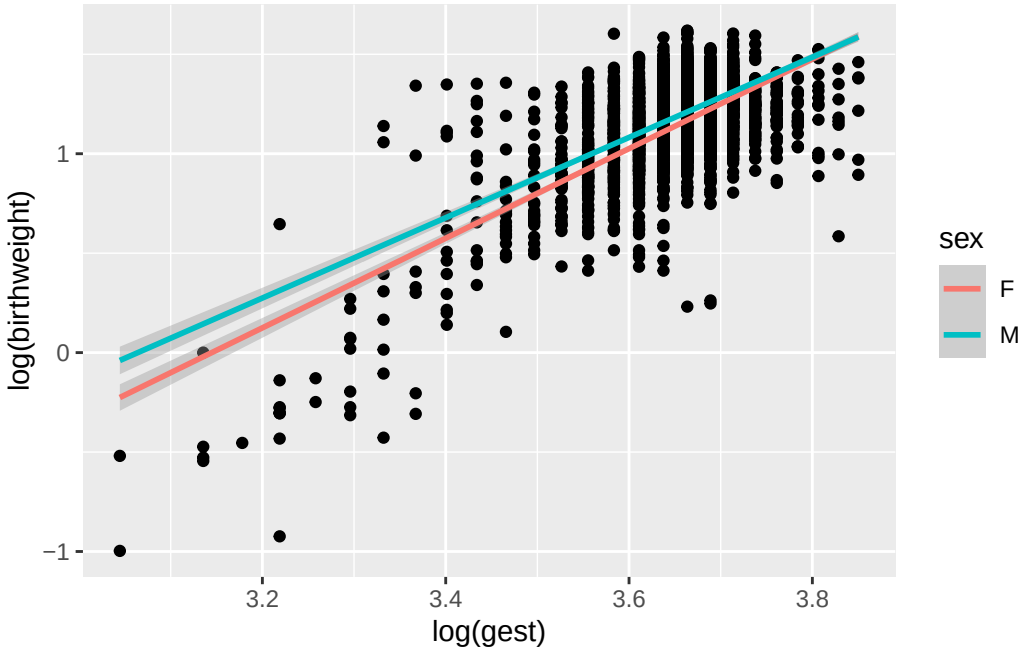
```
ggplot(ds,aes(x=birthweight,y=mager))+geom_point()
```



The second interest point is that there does not seem to be a strong relationship between the baby's weight and the mother's age.

```
ggplot(ds,aes(x=log(gest),y=log(birthweight)))+geom_point()+geom_smooth(method=lm,aes(colo
```

```
`geom_smooth()` using formula = 'y ~ x'
```

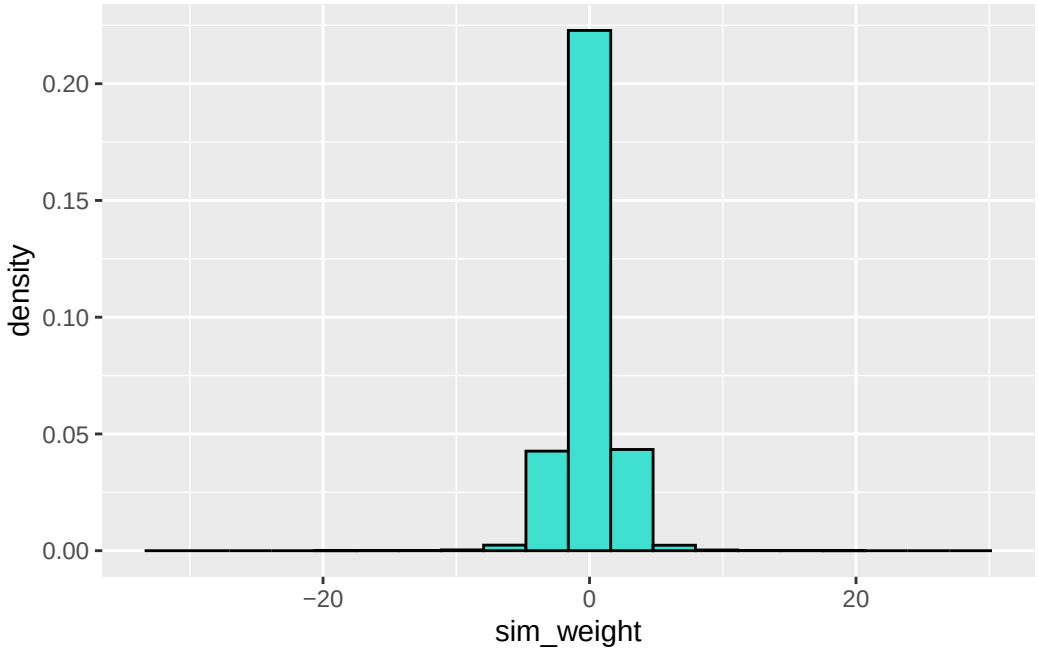


The third interest point is that as the gestational age increases, the birth weight increase for both baby boys and baby girls, and increase rate is slightly higher in baby girls than baby boys.

Question 2

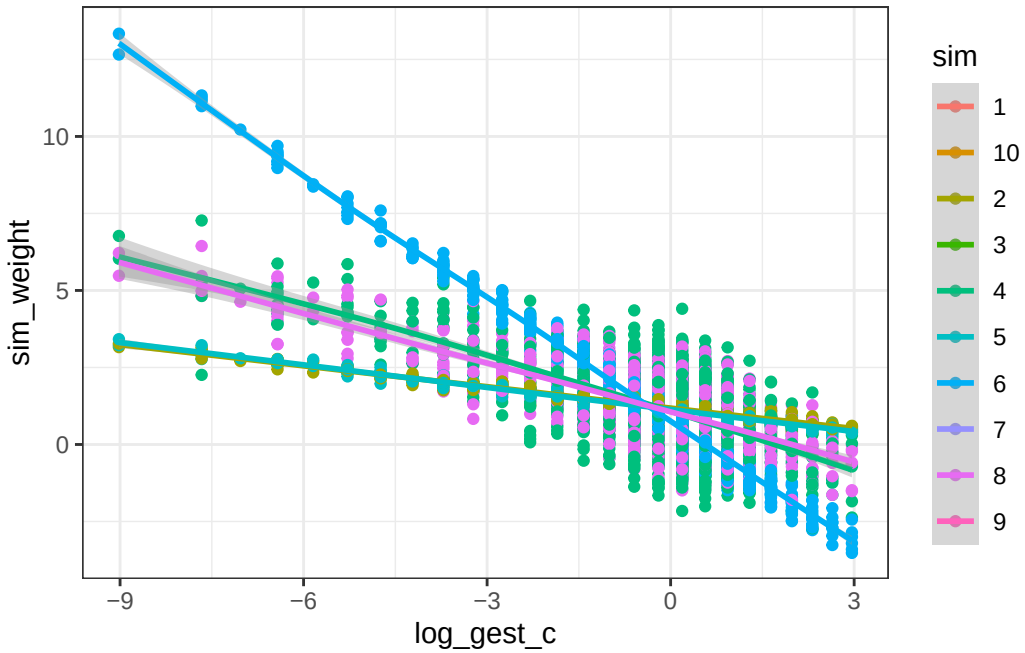
```
set.seed(100)
nsims <- 1000
sigma <- rnorm(nsims, 0, 1)
beta0 <- rnorm(nsims, 0, 1)
beta1 <- rnorm(nsims, 0, 1)

dsims <- tibble(log_gest_c = (log(ds$gest)-mean(log(ds$gest)))/sd(log(ds$gest)))

for(i in 1:nsims){
  this_mu <- beta0[i] + beta1[i]*dsims$log_gest_c
  dsims[paste0(i)] <- this_mu + rnorm(nrow(dsims), 0, sigma[i])
}

dsl <- dsims %>%
  pivot_longer(`1`:`1000`, names_to = "sim", values_to = "sim_weight")
```

```
dsl %>%
  ggplot(aes(sim_weight)) + geom_histogram(aes(y = ..density..), bins = 20, fill = "turquo
```




```
dsl10 <- dsims %>%
  pivot_longer(`1`:`10`, names_to = "sim", values_to = "sim_weight")
ggplot(dsl10,aes(x=log_gest_c,y=sim_weight,color=sim))+geom_point()+geom_smooth()+theme_bw
```

```
`geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
```



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

```
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 0.000284 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 2.84 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: 0.336 seconds (Warm-up)
Chain 1:                0.276 seconds (Sampling)
Chain 1:                0.612 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2:
Chain 2: Gradient evaluation took 0.000112 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 1.12 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: 0.335 seconds (Warm-up)
Chain 2:                0.31 seconds (Sampling)
Chain 2:                0.645 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 0.000123 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 1.23 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: 0.331 seconds (Warm-up)
Chain 3:                0.282 seconds (Sampling)
Chain 3:                0.613 seconds (Total)
Chain 3:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4:
Chain 4: Gradient evaluation took 0.000125 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 1.25 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: 0.352 seconds (Warm-up)
Chain 4:                0.301 seconds (Sampling)
Chain 4:                0.653 seconds (Total)
Chain 4:
```

```
Warning: Bulk Effective Samples Size (ESS) is too low, indicating posterior means and medians
Running the chains for more iterations may help. See
https://mc-stan.org/misc/warnings.html#bulk-ess
```

```
Warning: Tail Effective Samples Size (ESS) is too low, indicating posterior variances and tai
Running the chains for more iterations may help. See
https://mc-stan.org/misc/warnings.html#tail-ess
```

```
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

```
est_37 <- (log(37)-mean(log(ds$gest)))/sd(log(ds$gest))
est_beta0 <- 1.1624783
est_beta1 <- 0.1437529
exp(est_beta0+est_beta1*est_37)
```

```
[1] 2.935874
```

Question 4

```
stan_data_mod2 <- list(N = nrow(ds),
                   log_weight = ds$log_weight,
                   log_gest = ds$log_gest_c,
                   preterm = ifelse(ds$preterm=="Y",1,0))

mod2 <- stan(data = stan_data_mod2,
             file ="Lab6mod2.stan",
             iter = 500,
             seed = 243)
```

```
SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 0.000874 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 8.74 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: 1.287 seconds (Warm-up)
Chain 1:                1.065 seconds (Sampling)
Chain 1:                2.352 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
```

```
Chain 2:
Chain 2: Gradient evaluation took 0.000281 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 2.81 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: 1.261 seconds (Warm-up)
Chain 2:                1.141 seconds (Sampling)
Chain 2:                2.402 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 0.000285 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 2.85 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: 1.308 seconds (Warm-up)
Chain 3:                1.042 seconds (Sampling)
Chain 3:                2.35 seconds (Total)
Chain 3:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4:
Chain 4: Gradient evaluation took 0.000297 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 2.97 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: 1.24 seconds (Warm-up)
Chain 4:                1.083 seconds (Sampling)
Chain 4:                2.323 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] 1.1696329 8.021297e-05 0.002705139 1.16410383 1.16791913 1.1695478
beta[2] 0.1018545 1.111662e-04 0.003424916 0.09508969 0.09961365 0.1019319
beta[3] 0.5620695 3.406560e-03 0.062560942 0.43112646 0.52265217 0.5614275
beta[4] 0.1982641 6.964438e-04 0.012807594 0.17144797 0.18979854 0.1986269
sigma   0.1611971 8.785429e-05 0.001825790 0.15774991 0.15994557 0.1611909
              75%     97.5%     n_eff     Rhat
beta[1] 1.1714725 1.1748162 1137.3388 1.000638
```

```
beta[2] 0.1040358 0.1087724  949.1923 1.002232
beta[3] 0.6039584 0.6839901  337.2675 1.015352
beta[4] 0.2062635 0.2232005  338.1917 1.013325
sigma   0.1623667 0.1649513  431.8927 1.004553
```

Question 5

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

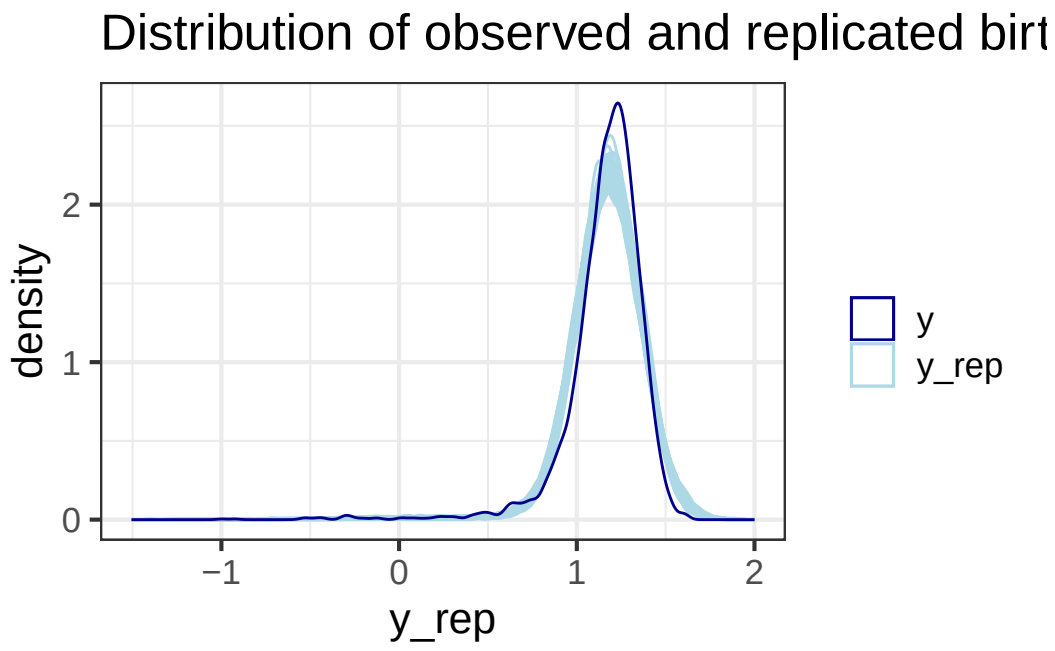
```
             mean      se_mean          sd       2.5%        25%       50%
beta[1] 1.1697241 1.385590e-04 0.002742186 1.16453578 1.16767109 1.1699278
beta[2] 0.5563133 5.835253e-03 0.058054991 0.43745504 0.51708255 0.5561553
beta[3] 0.1020960 1.481816e-04 0.003669476 0.09459462 0.09997153 0.1020339
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
```

Based on the summary, the coefficients are similar after flipping beta[2] and beta[3].

Question 6

```
N = nrow(ds)
yrep2 <- extract(mod2)[['log_weight_rep']]
samp2 <- sample(nrow(yrep2),100)
# first, get into a tibble
rownames(yrep2) <- 1:nrow(yrep2)
dr <- as_tibble(t(yrep2))
dr <- dr %>% bind_cols(i = 1:N, log_weight_obs = log(ds$birthweight))

# turn into long format; easier to plot
dr <- dr %>%
  pivot_longer(-(i:log_weight_obs), names_to = "sim", values_to ="y_rep")
```

```r
# filter to just include 100 draws and plot!
dr %>%
  filter(sim %in% samp2) %>%
  ggplot(aes(y_rep, group = sim)) +
  geom_density(alpha = 0.2, aes(color = "y_rep")) +
  geom_density(data = ds %>% mutate(sim = 1),
               aes(x = log(birthweight), col = "y")) +
  scale_color_manual(name = "",
                     values = c("y" = "darkblue",
                                "y_rep" = "lightblue")) +
  ggtitle("Distribution of observed and replicated birthweights") +
  theme_bw(base_size = 16)
```



Question 7

```r
yrep1 <- extract(mod1)[["log_weight_rep"]]
```

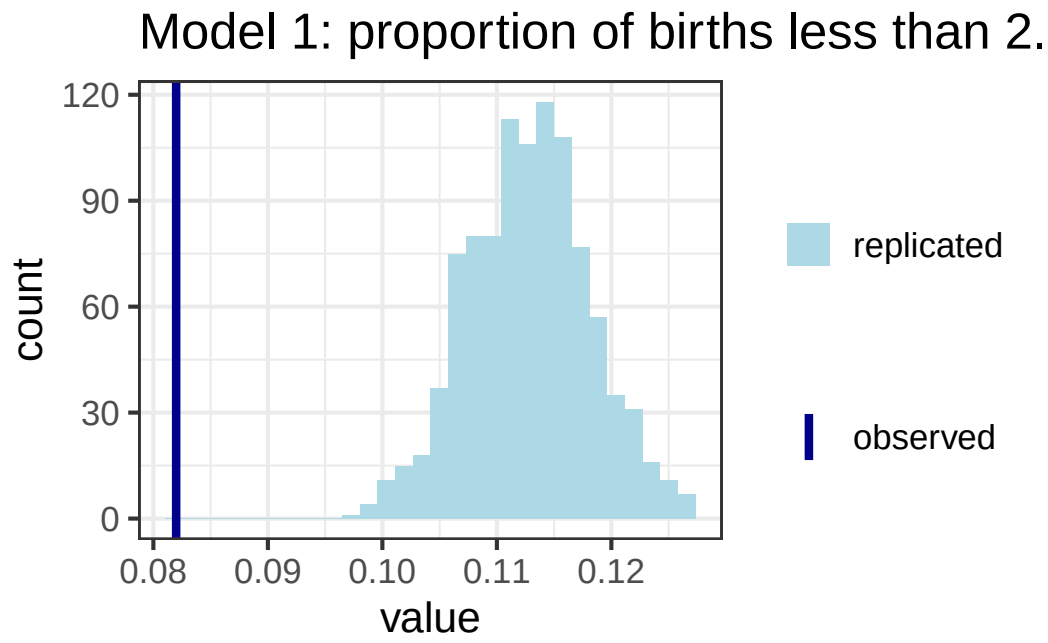
```r
y <- ds$log_weight
t_y <- mean(y<=log(2.5))
t_y_rep <- sapply(1:nrow(yrep1), function(i) mean(yrep1[i,]<=log(2.5)))
```

```
t_y_rep_2 <- sapply(1:nrow(yrep2), function(i) mean(yrep2[i,]<=log(2.5)))
```

```
ggplot(data = as_tibble(t_y_rep), aes(value)) +
    geom_histogram(aes(fill = "replicated")) +
    geom_vline(aes(xintercept = t_y, color = "observed"), lwd = 1.5) +
  ggtitle("Model 1: proportion of births less than 2.5kg") +
  theme_bw(base_size = 16) +
  scale_color_manual(name = "",
                     values = c("observed" = "darkblue"))+
  scale_fill_manual(name = "",
                     values = c("replicated" = "lightblue"))
```

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```

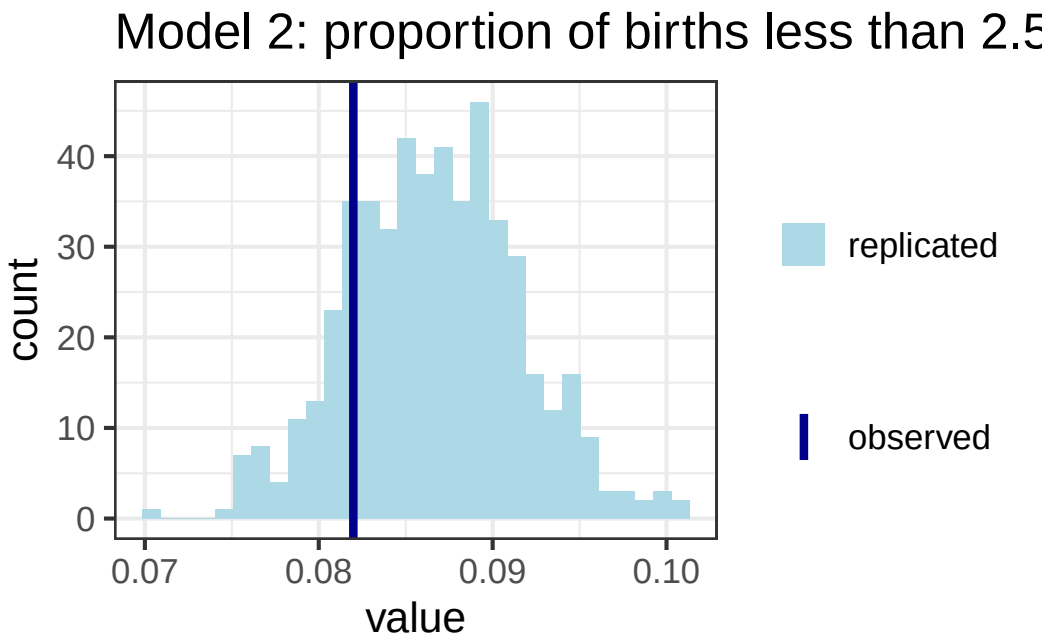
```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
ggplot(data = as_tibble(t_y_rep_2), aes(value)) +
    geom_histogram(aes(fill = "replicated")) +
```

```
  geom_vline(aes(xintercept = t_y, color = "observed"), lwd = 1.5) +
ggtitle("Model 2: proportion of births less than 2.5kg") +
theme_bw(base_size = 16) +
scale_color_manual(name = "",
                   values = c("observed" = "darkblue"))+
scale_fill_manual(name = "",
                   values = c("replicated" = "lightblue"))
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Question 8

Based on the EDA, add sex as an additional covariates to the linear regression model. Then, the model become:

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

where
- y_i is weight in kg
- x_i is gestational age in weeks, CENTERED AND STANDARDIZED
- s_i is sex (0 for female and 1 for male)

```r
stan_data_mod3 <- list(N = nrow(ds),
                       log_weight = ds$log_weight,
                       log_gest = ds$log_gest_c,
                       sex = ifelse(ds$sex=="M",1,0))
mod3 <- stan(data = stan_data_mod3,
             file ="Lab6mod3.stan",
             iter = 500,
             seed = 243)
```

```
SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 0.000447 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 4.47 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: 0.727 seconds (Warm-up)
Chain 1:                0.627 seconds (Sampling)
Chain 1:                1.354 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2:
Chain 2: Gradient evaluation took 0.000247 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 2.47 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: 0.679 seconds (Warm-up)
Chain 2:                0.676 seconds (Sampling)
Chain 2:                1.355 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 0.000246 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 2.46 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: 0.697 seconds (Warm-up)
Chain 3:                0.598 seconds (Sampling)
Chain 3:                1.295 seconds (Total)
Chain 3:
```

```
SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4:
Chain 4: Gradient evaluation took 0.000248 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 2.48 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: 0.695 seconds (Warm-up)
Chain 4:                0.658 seconds (Sampling)
Chain 4:                1.353 seconds (Total)
Chain 4:

Warning: Bulk Effective Samples Size (ESS) is too low, indicating posterior means and medians
Running the chains for more iterations may help. See
https://mc-stan.org/misc/warnings.html#bulk-ess

Warning: Tail Effective Samples Size (ESS) is too low, indicating posterior variances and tai
Running the chains for more iterations may help. See
https://mc-stan.org/misc/warnings.html#tail-ess
```

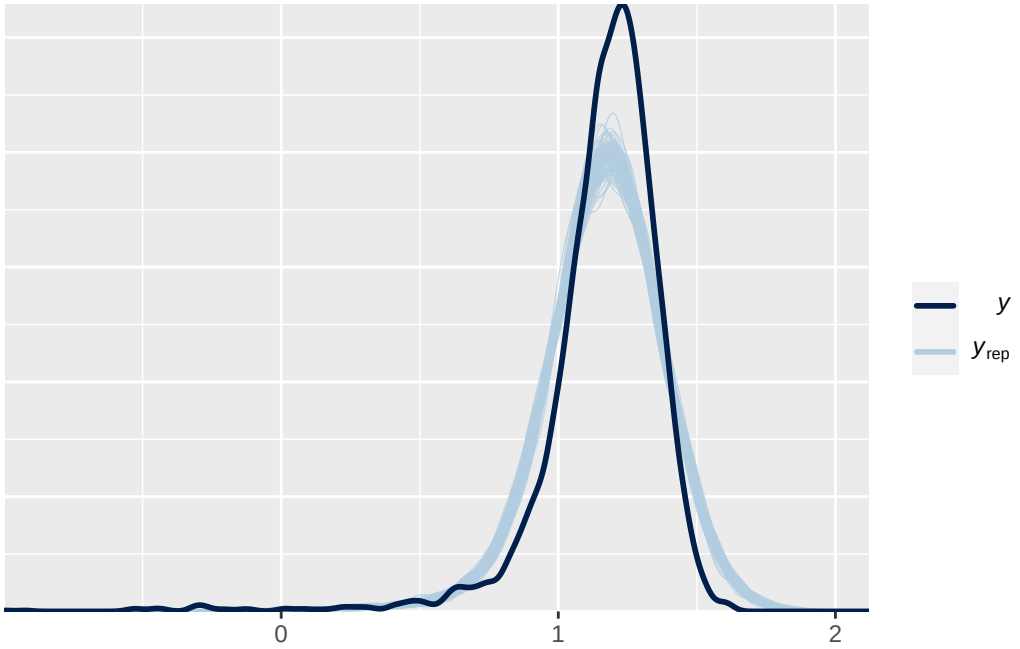
```
summary(mod3)$summary[c("beta[1]", "beta[2]","beta[3]", "sigma"),]
```

```
             mean      se_mean          sd       2.5%        25%        50%
beta[1] 1.14028996 1.493403e-04 0.003754554 1.13285962 1.13779512 1.14018814
beta[2] 0.14414166 9.454262e-05 0.002773616 0.13860941 0.14230469 0.14404814
beta[3] 0.04436215 2.183887e-04 0.005392706 0.03392679 0.04069144 0.04438335
sigma   0.16739711 1.090949e-04 0.002013758 0.16359394 0.16609752 0.16731626
              75%      97.5%    n_eff      Rhat
```

```
beta[1] 1.14287688 1.14764264 632.0665 0.9998937
beta[2] 0.14592509 0.15018203 860.6716 1.0007940
beta[3] 0.04802888 0.05480015 609.7522 1.0006674
sigma   0.16868116 0.17155964 340.7265 0.9974656
```

1. Comparing the 100 simulated datasets drawn from the posterior predictive distribution to the actual data.

```
yrep3 <- extract(mod3)[['log_weight_rep']]
samp3 <- sample(nrow(yrep3),100)
ppc_dens_overlay(y,yrep3[samp3,])
```

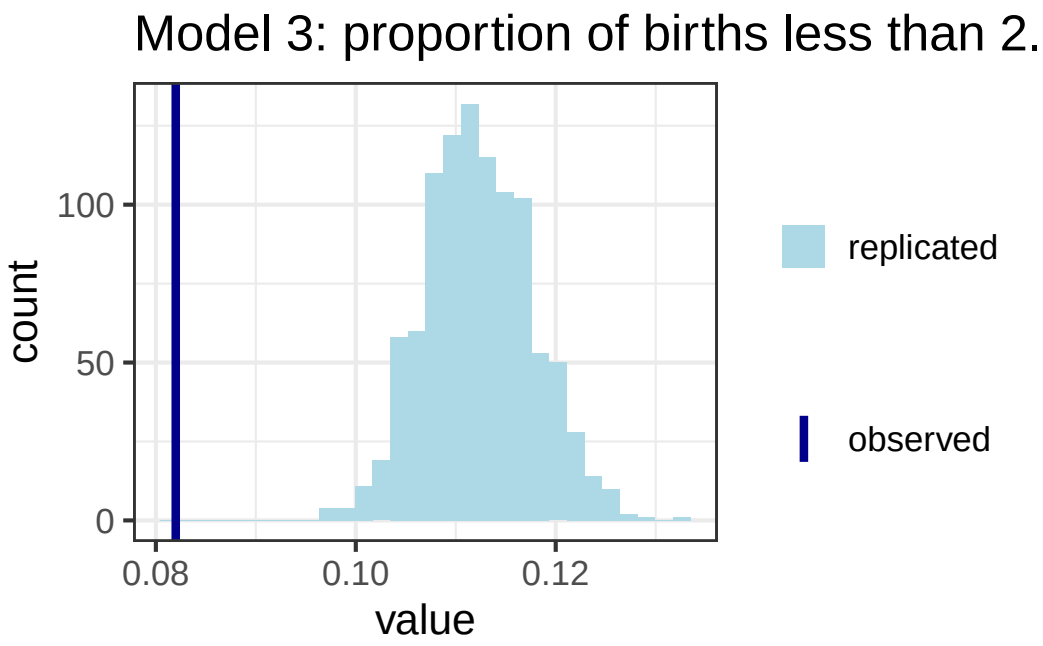


2. Calculate the test statistic for the data, and the posterior predictive samples for both models, and plot the comparison.

```
t_y_rep_3 <- sapply(1:nrow(yrep3), function(i) mean(yrep3[i,]<=log(2.5)))
ggplot(data = as_tibble(t_y_rep_3), aes(value)) +
    geom_histogram(aes(fill = "replicated")) +
    geom_vline(aes(xintercept = t_y, color = "observed"), lwd = 1.5) +
  ggtitle("Model 3: proportion of births less than 2.5kg") +
  theme_bw(base_size = 16) +
  scale_color_manual(name = "",
```

```
                      values = c("observed" = "darkblue"))+
    scale_fill_manual(name = "",
                      values = c("replicated" = "lightblue"))
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Thus, the result shows that comparing to model 3, model 2 is better.