Bayesian Statistics with Stan

Packages for this section

```
library(tidyverse)
# library(rstan)
library(cmdstanr)
library(posterior)
library(bayesplot)
```

Installation 1/2

- `cmdstanr`:

```
install.packages("cmdstanr",
                 repos = c("https://mc-stan.org/r-packages/",
                           getOption("repos")))
```

- `posterior` and `bayesplot`, from the same place:

```
install.packages("posterior",
                 repos = c("https://mc-stan.org/r-packages/",
                           getOption("repos")))
install.packages("bayesplot",
                 repos = c("https://mc-stan.org/r-packages/",
                           getOption("repos")))
```

Installation 2/2

Then, to check that you have the C++ stuff needed to compile Stan code:

```
check_cmdstan_toolchain()
```

```
## The C++ toolchain required for CmdStan is setup properly!
```

and then:

```
install_cmdstan(cores = 2)
```

If you happen to know how many cores (processors) your computer has, insert the appropriate number. (My laptop has 4 and my desktop 6.)

All of this is done once. If you have problems, go here (link).

Bayesian and frequentist inference

- The inference philosophy that we have learned so far says that:
  - parameters to be estimated are *fixed* but *unknown*
  - Data random; if we took another sample we'd get different data.
- This is called "frequentist" or "repeated-sampling" inference.
- Bayesian inference says:
  - *parameters* are random, *data* is *given*
- Ingredients:
  - **prior distribution**: distribution of parameters before seeing data.
  - **likelihood**: model for data if the parameters are known
  - **posterior distribution**: distribution of parameters *after* seeing data.

Distribution of parameters

- Instead of having a point or interval estimate of a parameter, we have an entire distribution
- so in Bayesian statistics we can talk about eg.
  - probability that a parameter is bigger than some value
  - probability that a parameter is close to some value
  - probability that one parameter is bigger than another
- Name comes from Bayes' Theorem, which here says *posterior is proportional to likelihood times prior*

- more discussion about this is in **a blog post**.

An example

- Suppose we have these (integer) observations:

```
(x <- c(0, 4, 3, 6, 3, 3, 2, 4))
```

```
## [1] 0 4 3 6 3 3 2 4
```

- Suppose we believe that these come from a Poisson distribution with a mean λ that we want to estimate.
- We need a prior distribution for λ. I will (for some reason) take a $Weibull$ distribution with parameters 1.1 and 6, that has quartiles 2 and 6. Normally this would come from your knowledge of the data-generating *process*.
- The Poisson likelihood can be written down (see over).

Some algebra

- We have $n = 8$ observations x_i, so the Poisson likelihood is proportional to

$$\prod_{i=1}^{n} e^{-\lambda} \lambda^{x_i} = e^{-n\lambda} \lambda^{S},$$

where $S = \sum_{i=1}^{n} x_i$.

- then you write the Weibull prior density (as a function of λ):

$$C(\lambda/6)^{0.1} e^{-(\lambda/6)^{1.1}}$$

where C is a constant.

- and then you multiply these together and try to recognize the distributional form. Only, here you can't. The powers 0.1 and 1.1 get in the way.

Sampling from the posterior distribution

- Wouldn't it be nice if we could just *sample* from the posterior distribution? Then we would be able to compute it as accurately as we want.
- Metropolis and Hastings: devise a Markov chain (C62) whose limiting distribution is the posterior you want, and then sample from that Markov chain (easy), allowing enough time to get close enough to the limiting distribution.
- Stan: uses a modern variant that is more efficient (called Hamiltonian Monte Carlo), implemented in R packages `cmdstanr`.
- Write Stan code in a file, compile it and sample from it.

Components of Stan code: the model

```
model {
  // likelihood
  x ~ poisson(lambda);
}
```

This is how you say "X has a Poisson distribution with mean λ". **Note that lines of Stan code have semicolons on the end.**

Components of Stan code: the prior distribution

```
model {
  // prior
  lambda ~ weibull(1.1, 6);
  // likelihood
  x ~ poisson(lambda);
}
```

Components of Stan code: data and parameters

- first in the Stan code:

```
data {
  int x[8];
}

parameters {
  real<lower=0> lambda;
}
```

Compile and sample from the model

- compile

```
poisson1 <- cmdstan_model("poisson1.stan")
```

- set up data

```
poisson1_data <- list(x = x)
```

- sample

```
poisson1_fit <- poisson1$sample(data = poisson1_data)
```

```
## Running MCMC with 4 sequential chains...
##
## Chain 1 Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 2000 [  5%]  (Warmup)
## Chain 1 Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 1 Iteration:  300 / 2000 [ 15%]  (Warmup)
## Chain 1 Iteration:  400 / 2000 [ 20%]  (Warmup)
```

The output

```
poisson1_fit
```

```
##  variable mean median   sd  mad   q5  q95 rhat
##    lp__   3.75   4.03 0.71 0.31 2.36 4.26 1.00
##    lambda 3.19   3.15 0.63 0.61 2.24 4.31 1.00
##  ess_bulk ess_tail
##      1827     2086
##      1443     1807
```

Comments

- This summarizes the posterior distribution of λ
- the posterior mean is 3.19
- with a 90% posterior interval of 2.24 to 4.31.
- The probability that λ is between these two values really is 90%.

Making the code more general

- The coder in you is probably offended by hard-coding the sample size and the parameters of the prior distribution. More generally:

```
data {
  int<lower=1> n;
  real<lower=0> a;
  real<lower=0> b;
  int x[n];
}
...
model {
// prior
lambda ~ weibull(a, b);
// likelihood
x ~ poisson(lambda);
}
```

Set up again and sample:

- Compile again:

```
poisson2 <- cmdstan_model("poisson2.stan")
poisson2
```

```
## // Estimating Poisson mean
##
## data {
##   int<lower=1> n;
##   real<lower=0> a;
##   real<lower=0> b;
##   int x[n];
## }
##
## parameters {
##   real<lower=0> lambda;
## }
```

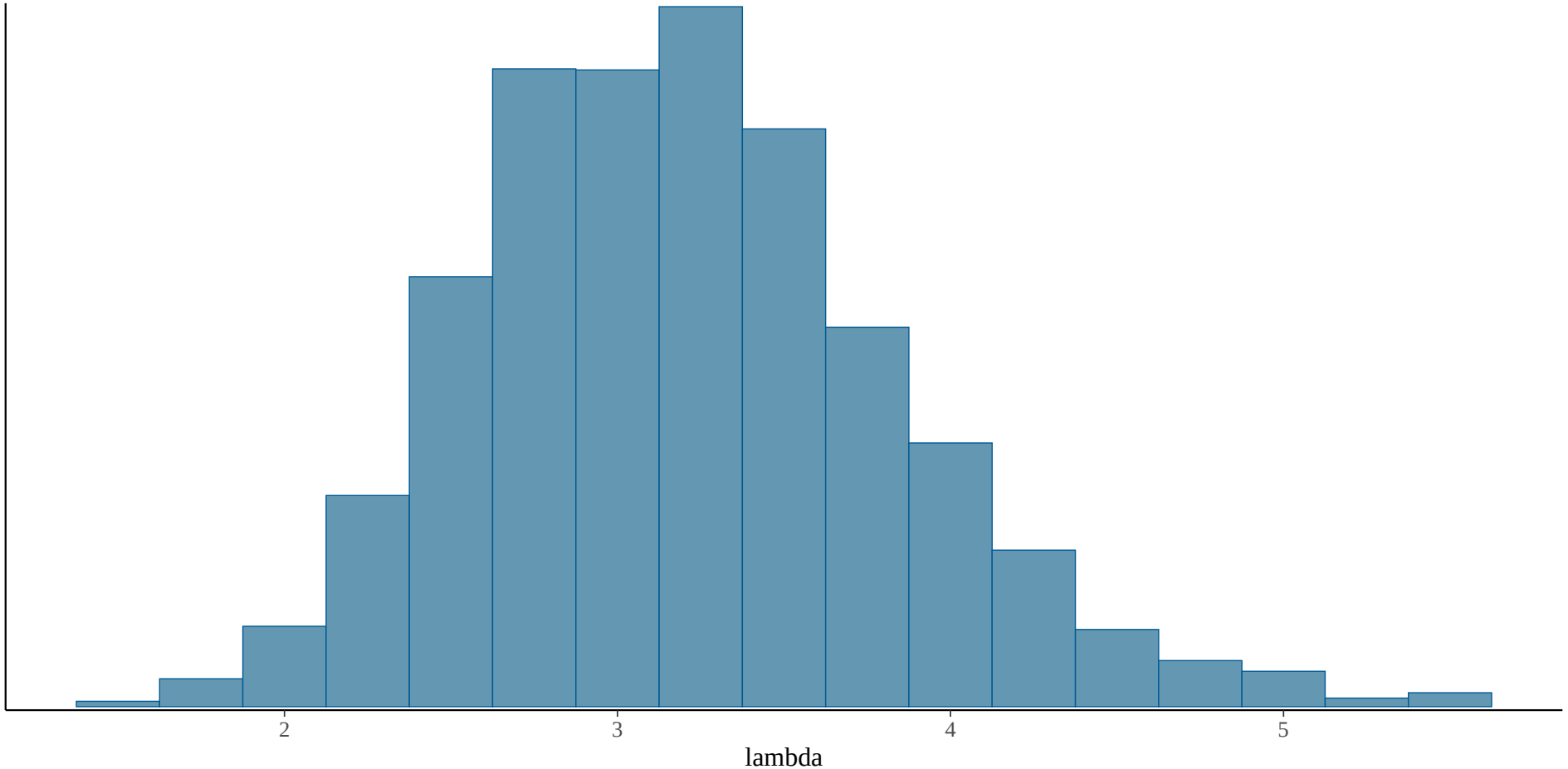
output should be the same (to within randomness)

```
poisson2_fit
```

```
##  variable mean median   sd  mad   q5  q95 rhat
##     lp__   3.76   4.03 0.72 0.31 2.31 4.26 1.00
##     lambda 3.21   3.16 0.63 0.60 2.29 4.30 1.00
##  ess_bulk ess_tail
##      1707     1844
##      1429     1830
```

Picture of posterior

```
mcmc_hist(poisson2_fit$draws("lambda"), binwidth = 0.25)
```



Extracting actual sampled values

A little awkward at first:

```
poisson2_fit$draws()
```

```
## # A draws_array: 1000 iterations, 4 chains, and 2 variables
## , , variable = lp__
##
##          chain
## iteration   1   2   3   4
##         1 4.2 3.6 3.9 4.0
##         2 4.2 3.5 4.1 4.0
##         3 3.9 3.8 4.1 3.6
##         4 4.0 3.1 3.8 4.2
##         5 4.0 4.0 4.0 4.2
##
## , , variable = lambda
##
```

Sampled values as dataframe

```
as_draws_df(poisson2_fit$draws()) %>%
  as_tibble() -> poisson2_draws
poisson2_draws
```

```
## # A tibble: 4,000 x 5
##      lp__ lambda .chain .iteration .draw
##     <dbl>  <dbl>  <int>      <int> <int>
##  1  4.20   2.99       1          1     1
##  2  4.20   2.99       1          2     2
##  3  3.93   3.72       1          3     3
##  4  4.04   3.62       1          4     4
##  5  4.02   3.64       1          5     5
##  6  3.74   3.87       1          6     6
##  7  1.70   4.82       1          7     7
##  8  4.07   2.83       1          8     8
##  9  4.16   3.47       1          9     9
## 10  4.22   3.02       1         10    10
```

Posterior predictive distribution

- Another use for the actual sampled values is to see what kind of *response* values we might get in the future. This should look something like our data. For a Poisson distribution, the response values are integers:

```
poisson2_draws %>%
  rowwise() %>%
  mutate(xsim = rpois(1, lambda)) -> d
d
```

```
## # A tibble: 4,000 x 6
##      lp__ lambda .chain .iteration .draw  xsim
##     <dbl>  <dbl>  <int>      <int> <int> <int>
##  1  4.20   2.99       1          1     1     2
##  2  4.20   2.99       1          2     2     3
##  3  3.93   3.72       1          3     3     2
##  4  4.04   3.62       1          4     4     5
```

Comparison

Our actual data values were these:

```
x
```

```
## [1] 0 4 3 6 3 3 2 4
```

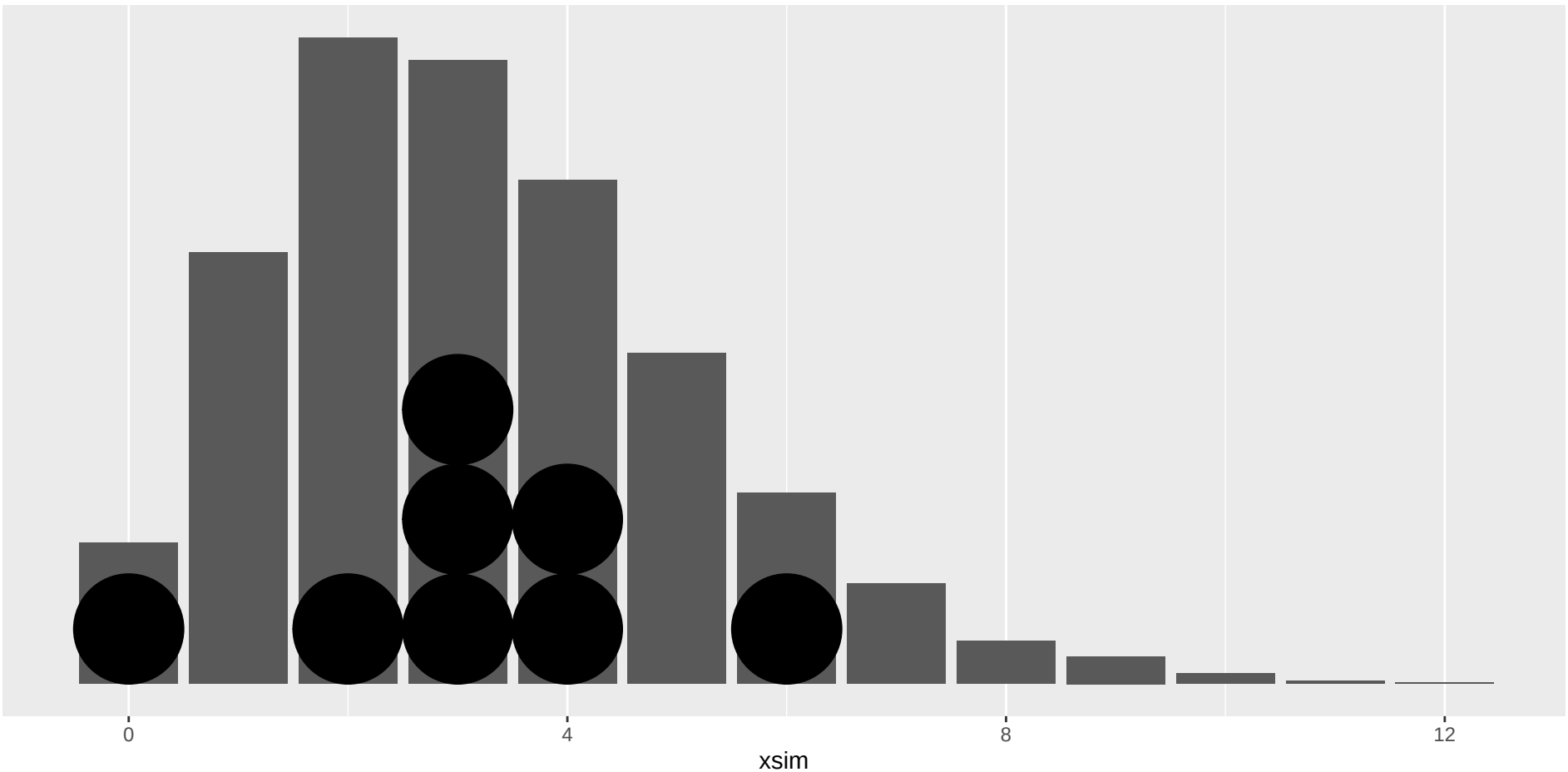
- None of these are very unlikely according to our posterior predictive distribution, so our model is believable.
- Or make a plot: a bar chart with the data on it as well (over):

```
ggplot(d, aes(x = xsim)) + geom_bar() +
  geom_dotplot(data = tibble(x), aes(x = x), binwidth = 1) +
  scale_y_continuous(NULL, breaks = NULL) -> g
```

- This also shows that the distribution of the data conforms well enough to the posterior predictive distribution (over).

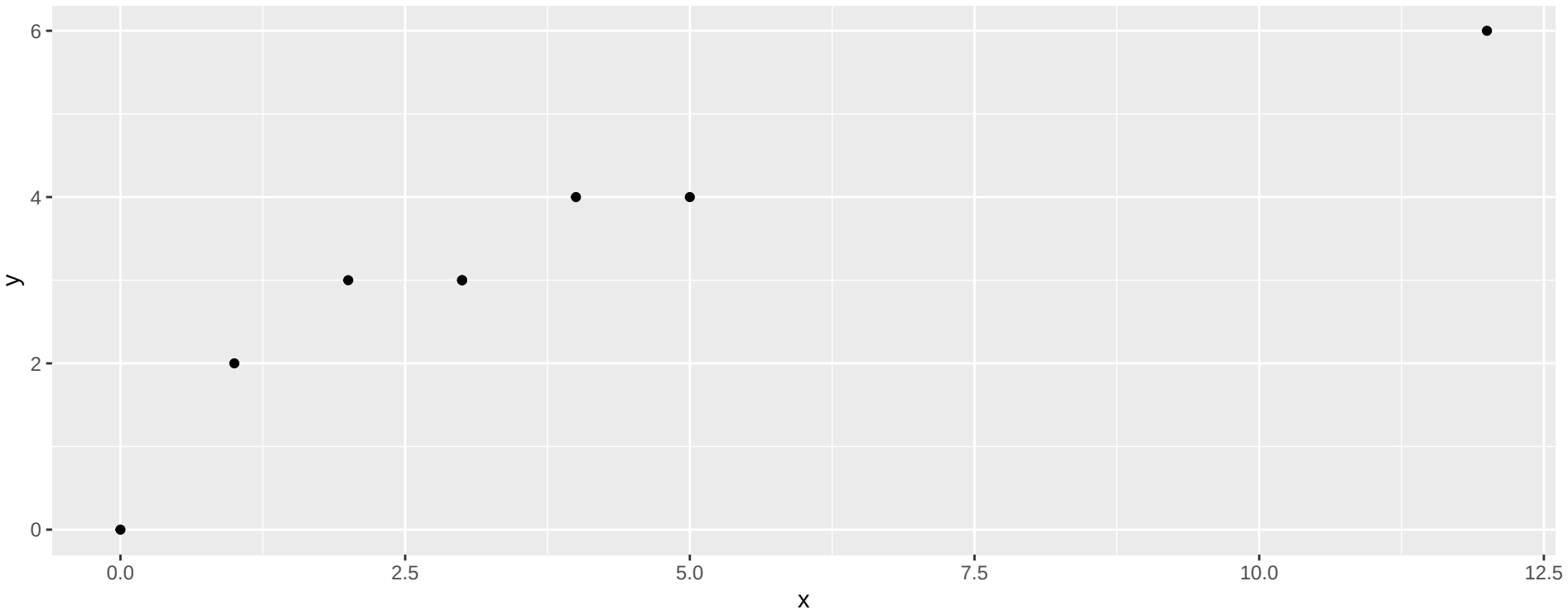
The plot

```
g
```



Do they have the same distribution?

```
qqplot(d$xsim, x, plot.it = F) %>% as_tibble() -> dd
ggplot(dd, aes(x=x, y=y)) + geom_point()
```



the observed zero is a bit too small compared to expected (from the posterior), but the other points seem pretty well on a line.

Analysis of variance, the Bayesian way

Recall the jumping rats data:

```
my_url <-
  "http://www.utsc.utoronto.ca/~butler/c32/jumping.txt"
rats0 <- read_delim(my_url, " ")
rats0
```

```
## # A tibble: 30 x 2
##    group   density
##    <chr>     <dbl>
##  1 Control     611
##  2 Control     621
##  3 Control     614
##  4 Control     593
##  5 Control     593
##  6 Control     653
##  7 Control     600
```

Our aims here

- Estimate the mean bone density of all rats under each of the experimental conditions
- Model: given the group means, each observation normally distributed with common variance σ^2
- Three parameters to estimate, plus the common variance.
- Obtain posterior distributions for the group means.
- Ask whether the posterior distributions of these means are sufficiently different.

Numbering the groups

- Stan doesn't handle categorical variables (everything is `real` or `int`).
- Turn the groups into group *numbers* first.
- Take opportunity to put groups in logical order:

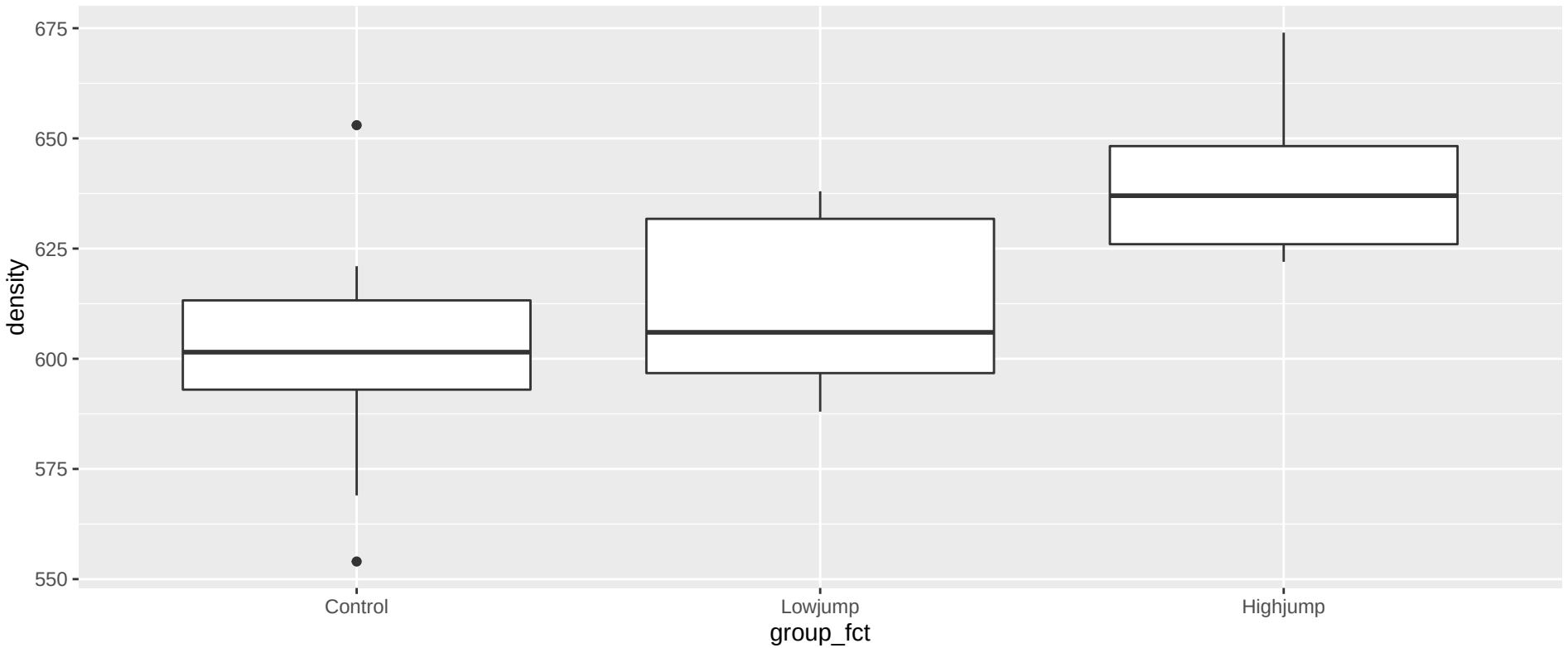
```
rats0 %>% mutate(
  group_fct = fct_inorder(group),
  group_no = as.integer(group_fct)
) -> rats
rats
```

```
## # A tibble: 30 x 4
##    group   density group_fct group_no
##    <chr>     <dbl> <fct>         <int>
##  1 Control     611 Control           1
##  2 Control     621 Control           1
##  3 Control     614 Control           1
##  4 Control     593 Control           1
```

Plotting the data 1/2

Most obviously, boxplots:

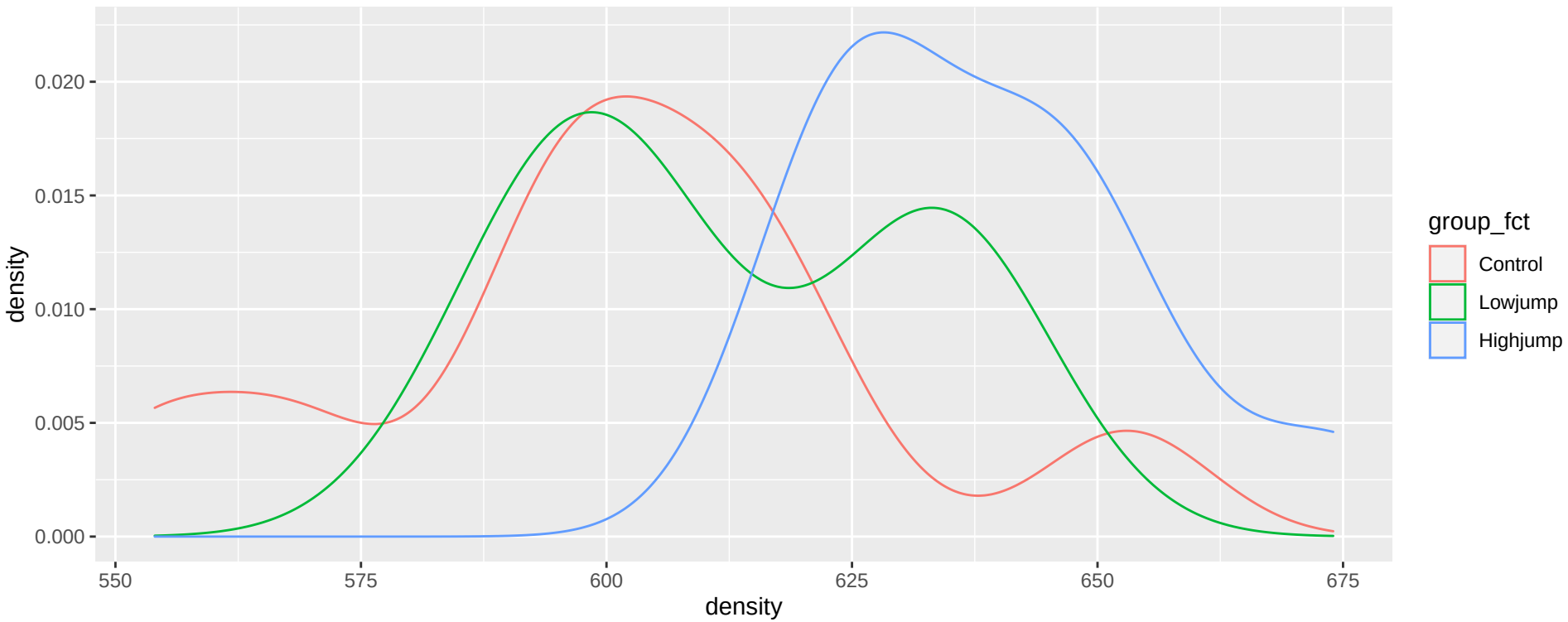
```
ggplot(rats, aes(x = group_fct, y = density)) +
  geom_boxplot()
```



Plotting the data 2/2

Another way: density plot (smoothed out histogram); can distinguish groups by colours:

```
ggplot(rats, aes(x = density, colour = group_fct)) +
  geom_density()
```



The procedure

- For each observation, find out which (numeric) group it belongs to,
- then model it as having a normal distribution with that group's mean and the common variance.
- Stan does `for` loops.

The model part

Suppose we have `n_obs` observations:

```
model {
  // likelihood
  for (i in 1:n_obs) {
    g=group_no[i];
    density[i] ~ normal(mu[g], sigma);
  }
}
```

The variables here

- `n_obs` is data.
- `g` is a temporary integer variable only used here
- `i` is only used in the loop (integer) and does not need to be declared
- `density` is data, a real vector of length `n_obs`
- `mu` is a parameter, a real vector of length 3 (3 groups)
- `sigma` is a real parameter

`mu` and `sigma` need prior distributions:

- for `mu`, each component independently normal with mean 600 and SD 50 (my guess at how big and variable they will be)
- for `sigma`, chi-squared with 50 df (my guess at typical amount of variability from obs to obs)

Complete the `model` section:

```
model {
  int g;
  // priors
  mu ~ normal(600, 50);
  sigma ~ chi_square(50);
  // likelihood
  for (i in 1:n_obs) {
    g=group_no[i];
    density[i] ~ normal(mu[g], sigma);
  }
}
```

Parameters

The elements of `mu`, one per group, and also `sigma`, scalar, lower limit zero:

```
parameters {
  real mu[n_group];
  real<lower=0> sigma;
}
```

- Declare `sigma` to have lower limit zero here, so that the sampling runs smoothly.
- declare `n_group` in data section

Data

Everything else:

```
data {
  int n_obs;
  int n_group;
  real density[n_obs];
  int<lower=1, upper=n_group> group_no[n_obs];
}
```

Compile

Arrange these in order data, parameters, model in file `anova.stan`, then:

```
anova <- cmdstan_model("anova.stan")
```

Set up data and sample

Supply values for *everything* declared in `data`:

```
anova_data <- list(
  n_obs = 30,
  n_group = 3,
  density = rats$density,
  group_no = rats$group_no
)
anova_fit <- anova$sample(data = anova_data)
```

```
## Running MCMC with 4 sequential chains...
##
## Chain 1 Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 1 Iteration:  100 / 2000 [  5%]  (Warmup)
## Chain 1 Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 1 Iteration:  300 / 2000 [ 15%]  (Warmup)
## Chain 1 Iteration:  400 / 2000 [ 20%]  (Warmup)
```

Check that the sampling worked properly

```
anova_fit$cmdstan_diagnose()
```

```
## Processing csv files: /tmp/Rtmpdoovb9/anova-202104211944-1-126537.csv, /tmp/Rtmp
202104211944-2-126537.csv, /tmp/Rtmpdoovb9/anova-202104211944-3-126537.csv, /tmp/Rt
202104211944-4-126537.csv
##
## Checking sampler transitions treedepth.
## Treedepth satisfactory for all transitions.
##
## Checking sampler transitions for divergences.
## No divergent transitions found.
##
## Checking E-BFMI - sampler transitions HMC potential energy.
## E-BFMI satisfactory for all transitions.
##
## Effective sample size satisfactory.
##
## Split R-hat values satisfactory all parameters.
##
## Processing complete, no problems detected.
```

Look at the results

```
anova_fit
```

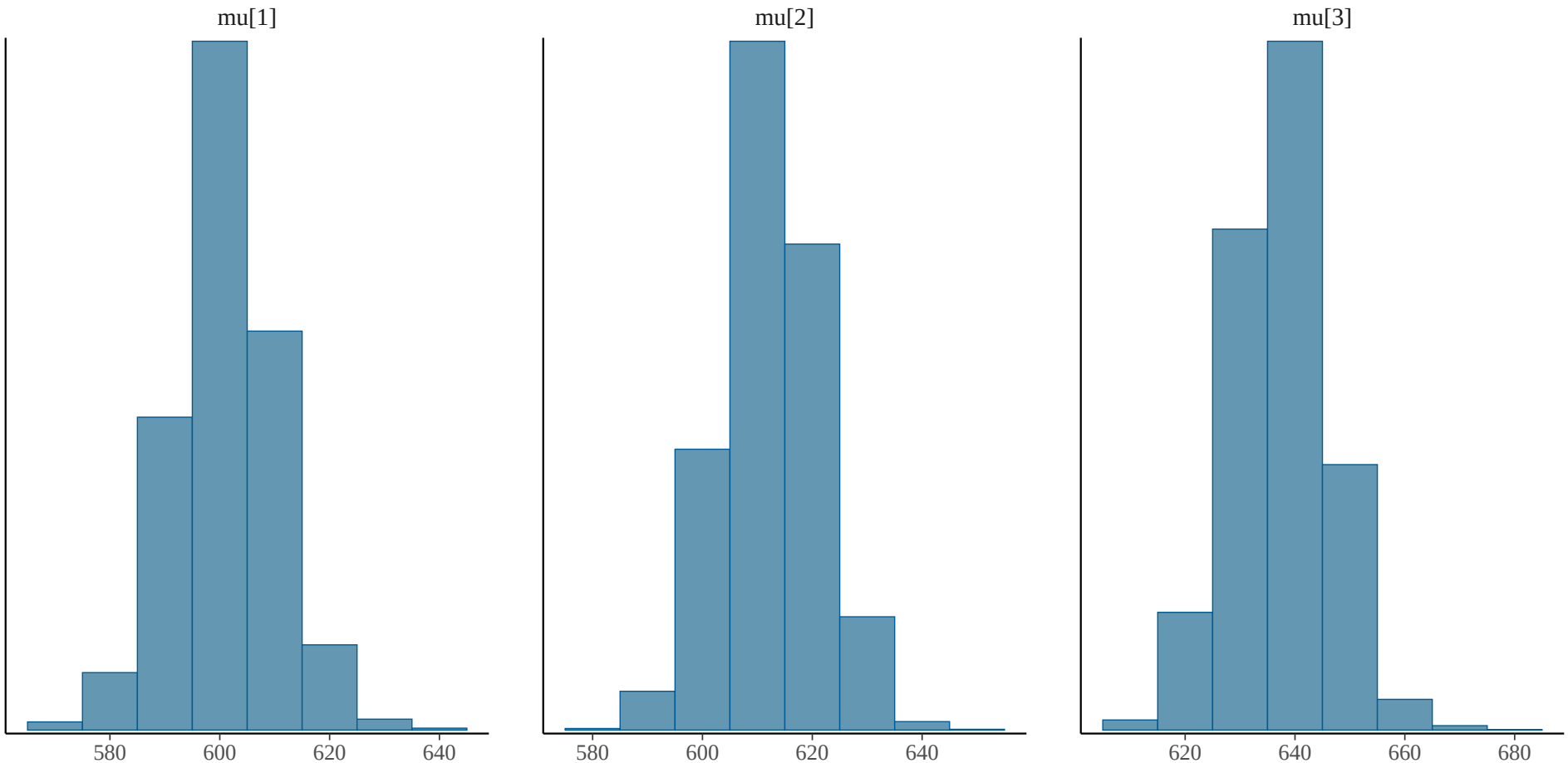
```
##  variable   mean median   sd  mad     q5    q95
##     lp__  -40.99 -40.62 1.52 1.24 -43.89 -39.29
##     mu[1] 600.93 600.81 9.19 8.53 586.06 616.02
##     mu[2] 612.36 612.29 8.80 8.55 598.09 626.98
##     mu[3] 637.38 637.49 8.81 8.77 622.74 651.45
##     sigma  28.48  28.13 4.19 4.04  22.51  35.84
##  rhat ess_bulk ess_tail
##  1.00     1999     2522
##  1.00     4064     2624
##  1.00     4171     2984
##  1.00     3688     2652
##  1.00     3339     2868
```

Comments

- The posterior 95% intervals for control (group 1) and highjump (group 3) do not quite overlap, suggesting that these exercise groups really are different.
- Bayesian approach does not normally do tests: look at posterior distributions and decide whether they are different enough to be worth treating as different.

Plotting the posterior distributions for the mu

```
mcmc_hist(anova_fit$draws("mu"), binwidth = 10)
```



Extract the sampled values

```
as_draws_df(anova_fit$draws()) %>% as_tibble() -> anova_draws
anova_draws
```

```
## # A tibble: 4,000 x 8
##      lp__ `mu[1]` `mu[2]` `mu[3]` sigma .chain
##     <dbl>   <dbl>   <dbl>   <dbl> <dbl>  <int>
##  1 -40.5    597.    605.    631.  23.1       1
##  2 -40.6    592.    620.    630.  25.5       1
##  3 -41.9    617.    604.    641.  24.3       1
##  4 -40.2    601.    613.    633.  33.1       1
##  5 -42.4    596.    606.    624.  37.1       1
##  6 -39.3    601.    614.    631.  27.8       1
##  7 -41.4    596.    624.    651.  29.6       1
##  8 -39.5    595.    610.    640.  29.4       1
##  9 -39.4    607.    614.    636.  24.8       1
## 10 -39.4    607.    614.    636.  24.8       1
## # … with 3,990 more rows, and 2 more variables:
```

estimated probability that $\mu_3 > \mu_1$

```
anova_draws %>%
  count(`mu[3]`>`mu[1]`) %>%
  mutate(prob = n/sum(n))
```

```
## # A tibble: 2 x 3
##   `\`mu[3]\` > \`mu[1]\``     n   prob
##   <lgl>                   <int>  <dbl>
## 1 FALSE                      14 0.0035
## 2 TRUE                     3986 0.996
```

High jumping group almost certainly has larger mean than control group.

More organizing

- for another plot
  - make longer
  - give group values their proper names back

```
anova_draws %>%
  pivot_longer(starts_with("mu"),
               names_to = "group",
               values_to = "bone_density") %>%
  mutate(group = fct_recode(group,
    Control = "mu[1]",
    Lowjump = "mu[2]",
    Highjump = "mu[3]"
  )) -> sims
```

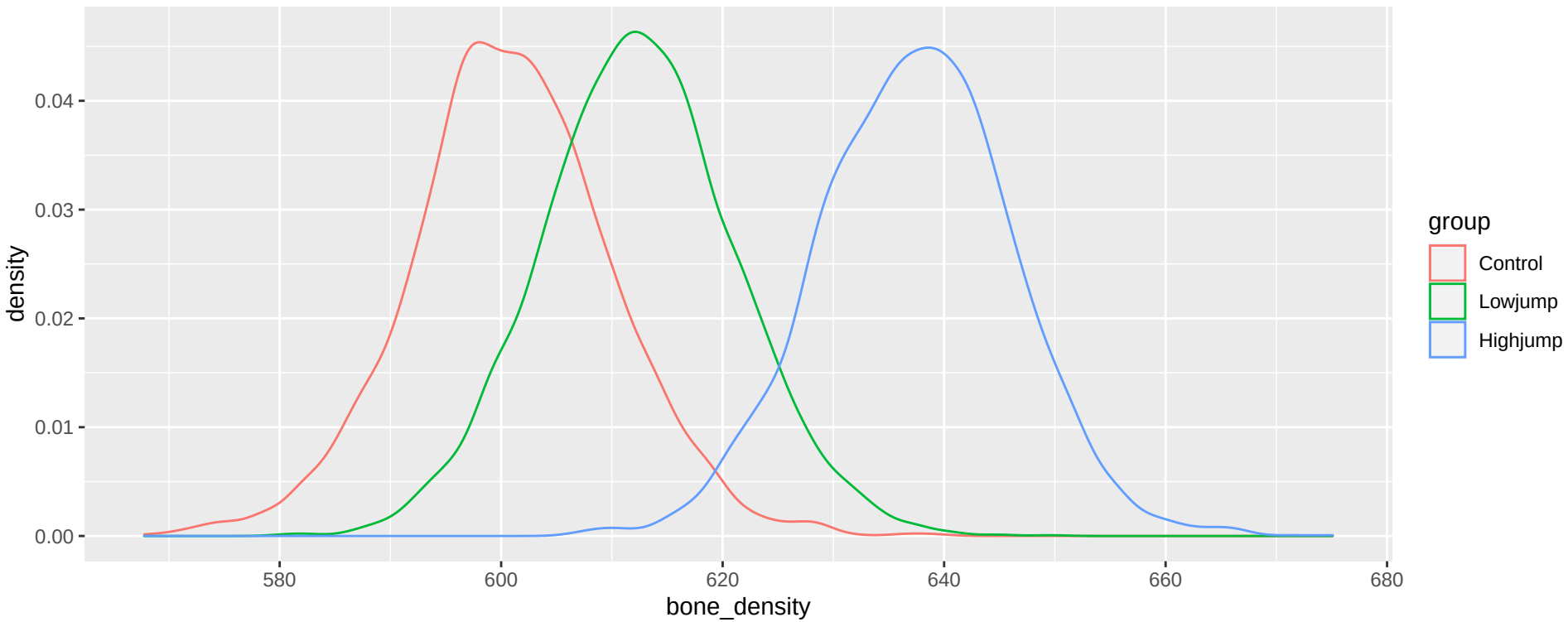
What we have now:

```
sims %>% sample_n(8)
```

```
## # A tibble: 8 x 7
##    lp__ sigma .chain .iteration .draw group
##   <dbl> <dbl>  <int>      <int> <int> <fct>
## 1 -42.8  33.7      4        302  3302 Highjump
## 2 -41.3  24.5      3        422  2422 Highjump
## 3 -40.7  26.2      3        438  2438 Lowjump
## 4 -39.7  27.6      1        780   780 Control
## 5 -39.9  27.3      4        895  3895 Control
## 6 -42.2  37.8      2         58  1058 Lowjump
## 7 -40.4  28.0      2        558  1558 Lowjump
## 8 -42.8  34.7      3        761  2761 Lowjump
## # ... with 1 more variable: bone_density <dbl>
```

Density plots of posterior mean distributions

```
ggplot(sims, aes(x = bone_density, colour = group)) + geom_den
```



Posterior predictive distributions

Randomly sample from posterior means and SDs in `sims`. There are 12000 rows in `sims`:

```
sims %>% mutate(sim_data = rnorm(12000, bone_density, sigma))
ppd
```

```
## # A tibble: 12,000 x 8
##      lp__ sigma .chain .iteration .draw group
##     <dbl> <dbl>  <int>      <int> <int> <fct>
##  1 -40.5  23.1      1          1     1 Control
##  2 -40.5  23.1      1          1     1 Lowjump
##  3 -40.5  23.1      1          1     1 Highjump
##  4 -40.6  25.5      1          2     2 Control
##  5 -40.6  25.5      1          2     2 Lowjump
##  6 -40.6  25.5      1          2     2 Highjump
##  7 -41.9  24.3      1          3     3 Control
##  8 -41.9  24.3      1          3     3 Lowjump
```

Compare posterior predictive distribution with actual data

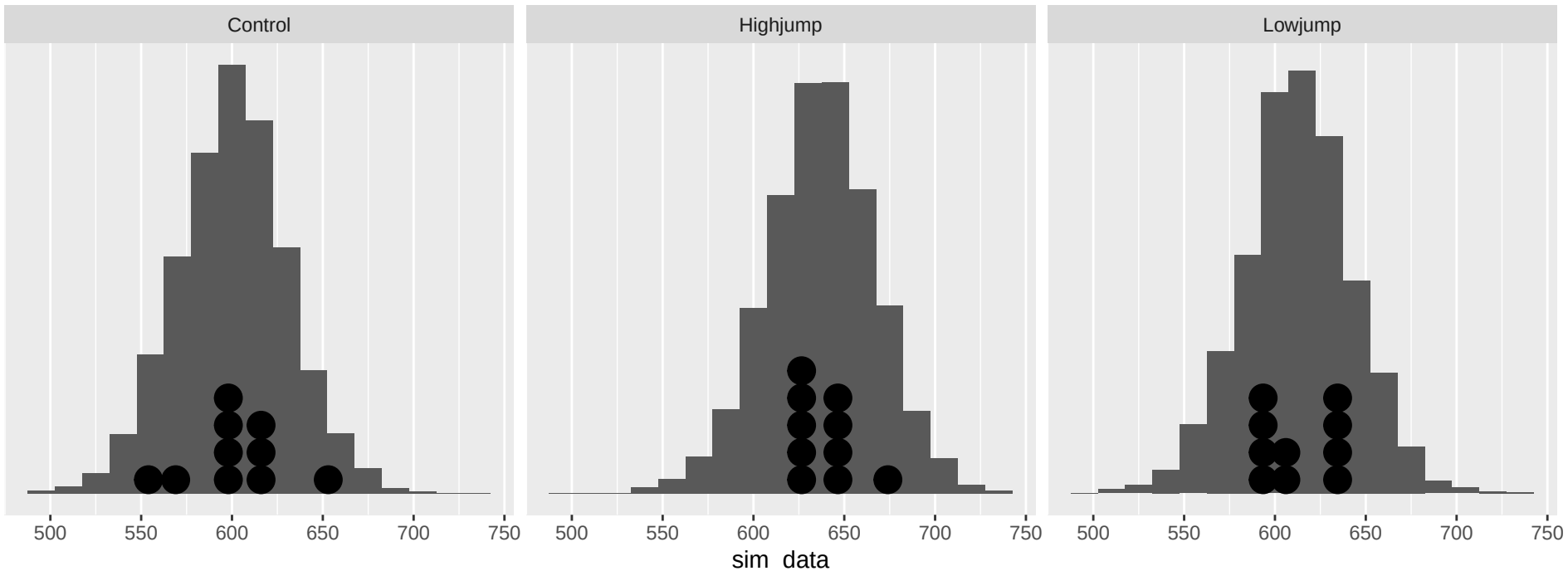
- Check that the model works: distributions of data similar to what we'd predict
- Idea: make plots of posterior predictive distribution, and plot actual data as points on them
- Use facets, one for each treatment group:

```
my_binwidth <- 15
ggplot(ppd, aes(x = sim_data)) +
  geom_histogram(binwidth = my_binwidth) +
  geom_dotplot(
    data = rats, aes(x = density),
    binwidth = my_binwidth
  ) +
  facet_wrap(~group) +
  scale_y_continuous(NULL, breaks = NULL) -> g
```

- See (over) that the data values are mainly in the middle of the predictive distributions.
- Even for the control group that had outliers.

The plot

```
g
```



Extensions

- if you want a different model other than normal, change distribution in `model` section
- if you want to allow unequal spreads, create `sigma[n_group]` and in model `density[i] ~ normal(mu[g], sigma[g]);`
- Stan will work just fine after you recompile
- very flexible.
- Typical modelling strategy: start simple, add complexity as warranted by data.