

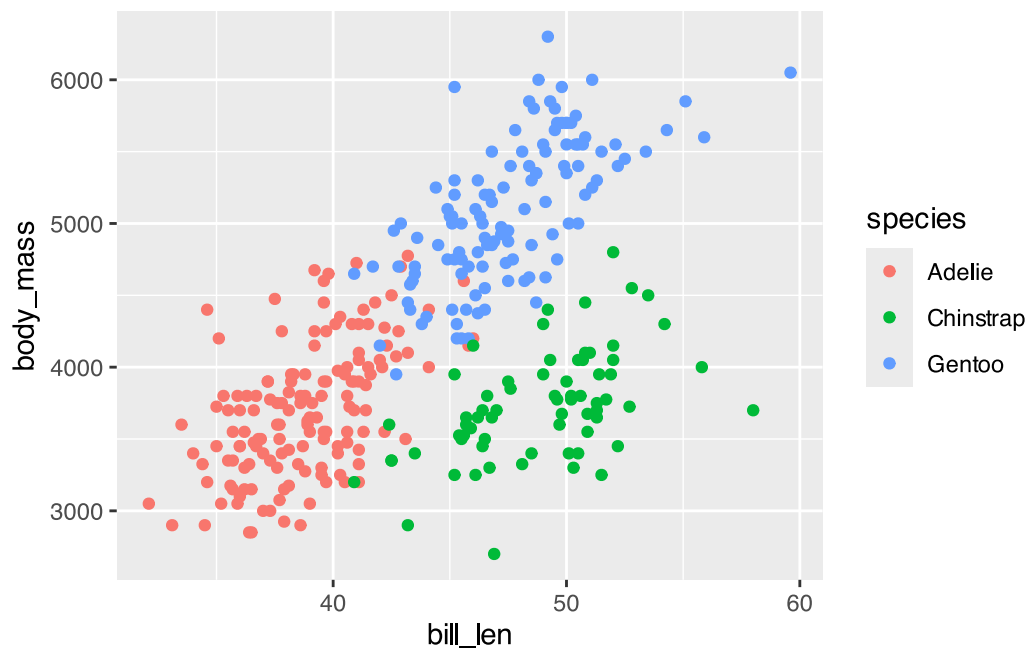
## Analysis

```
library(tidyverse)
library(tidybayes)
library(targets)
library(marginaleffects)
library(modelsummary)
library(parameters)
library(patchwork)

tar_load(penguins)
tar_load(c(model1_bayes, model2_bayes))
```

### Look at data

```
ggplot(penguins, aes(x = bill_len, y = body_mass, color = species)) +
  geom_point()
```



### Look at models

Here is model 1

```
model_parameters(model1_bayes, verbose = FALSE)
```

```
# Fixed Effects
```

| Parameter   | Median | 95% CI            | pd     | Rhat  | ESS  |
|-------------|--------|-------------------|--------|-------|------|
| (Intercept) | 394.74 | [-203.64, 962.24] | 90.33% | 1.000 | 3888 |
| bill_len    | 86.72  | [ 73.86, 100.09]  | 100%   | 1.000 | 3907 |

```
# sigma Parameters
```

| Parameter | Median | 95% CI           | pd   | Rhat  | ESS  |
|-----------|--------|------------------|------|-------|------|
| sigma     | 653.05 | [604.48, 708.34] | 100% | 1.000 | 3630 |

Here are both:

```
modelsummary(list(model1_bayes, model2_bayes), statistic = "[{conf.low},
{conf.high}]",
  ci_method = "hdi",
  metrics = c("R2"), fmt = 1)
```

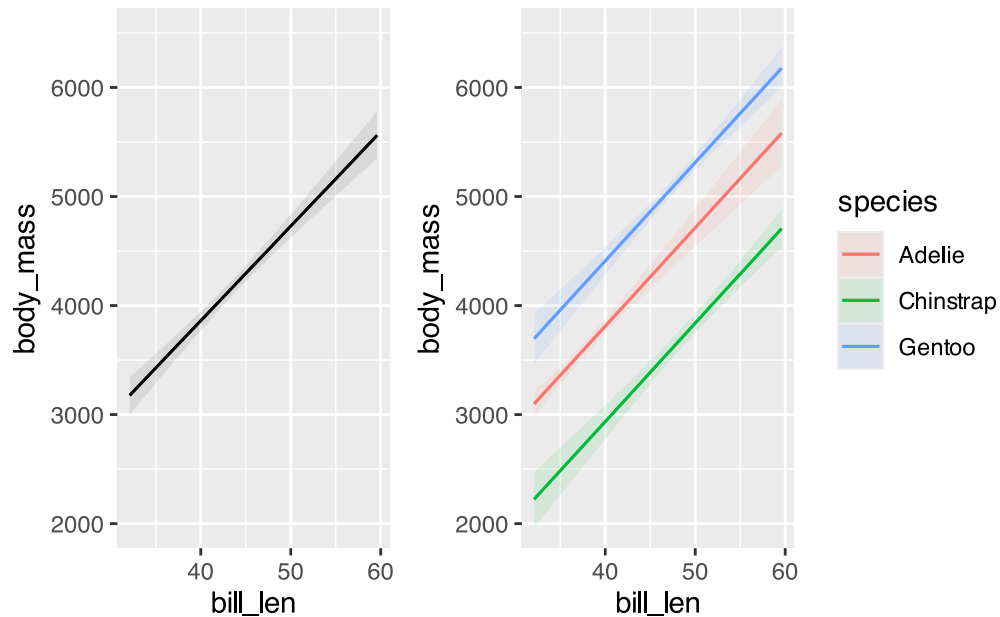
|                    | (1)             | (2)               |
|--------------------|-----------------|-------------------|
| b_Intercept        | 394.7           | 201.7             |
|                    | [-209.7, 948.8] | [-332.1, 775.9]   |
| b_bill_len         | 86.7            | 90.3              |
|                    | [74.1, 100.2]   | [76.0, 104.4]     |
| sigma              | 653.1           | 375.5             |
|                    | [601.1, 703.9]  | [347.0, 404.5]    |
| b_speciesChinstrap |                 | -876.2            |
|                    |                 | [-1054.5, -700.1] |
| b_speciesGentoo    |                 | 599.3             |
|                    |                 | [443.2, 753.3]    |
| Num.Obs.           | 333             | 333               |
| R2                 | 0.347           | 0.784             |

```
p1 <- model1_bayes |>
  plot_predictions(condition = c("bill_len")) +
```

```
coord_cartesian(ylim = c(2000, 6500))

p2 <- model2_bayes |>
  plot_predictions(condition = c("bill_len", "species")) +
  coord_cartesian(ylim = c(2000, 6500))

p1 | p2
```



```
bill_len_model_1 <- model1_bayes |>
  gather_draws(b_bill_len) |>
  mutate(model = "Model 1")

bill_len_model_2 <- model2_bayes |>
  gather_draws(b_bill_len) |>
  mutate(model = "Model 2")

bind_rows(bill_len_model_1, bill_len_model_2) |>
  ggplot(aes(x = .value, y = model, fill = model)) +
  stat_halfeye() +
  guides(fill = "none") +
  labs(x = "bill_len")
```

