```r
library(rstan)
library(rstanarm)
library(tidyverse)
```

```r
m333 <- read_csv("../data/subsets/dat_small.csv") %>%
  filter(province == "M333")
```

```
## Warning: Missing column names filled in: 'X1' [1]

## Parsed with column specification:
## cols(
##   .default = col_double(),
##   subsection = col_character(),
##   section = col_character(),
##   province = col_character()
## )

## See spec(...) for full column specifications.
```

```r
mod <- stan_lmer(BIOLIVE_TPA ~ 1 + nlcd11 + (1 | subsection),
                 data = m333,
                 verbose = FALSE)
```

```
##
## SAMPLING FOR MODEL 'continuous' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0.000367 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 3.67 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 1: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 1: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 1: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 1: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 1: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 1: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 1: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 1: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 1: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 1: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 7.49884 seconds (Warm-up)
## Chain 1:                3.58094 seconds (Sampling)
## Chain 1:                11.0798 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'continuous' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 0.000142 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 1.42 seconds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
## Chain 2: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 2: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 2: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 2: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 2: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 2: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 2: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 2: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 2: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 2: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 2: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 2: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 2:
## Chain 2:  Elapsed Time: 9.36712 seconds (Warm-up)
## Chain 2:                3.60665 seconds (Sampling)
## Chain 2:                12.9738 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'continuous' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 0.000216 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 2.16 seconds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 3: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 3: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 3: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 3: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 3: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 3: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 3: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 3: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 3: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 3: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 3: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 3:
## Chain 3:  Elapsed Time: 9.9175 seconds (Warm-up)
## Chain 3:                2.74855 seconds (Sampling)
## Chain 3:                12.6661 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'continuous' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 0.000275 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 2.75 seconds.
## Chain 4: Adjust your expectations accordingly!
## Chain 4:
## Chain 4:
```

```
## Chain 4: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 4: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 4: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 4: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 4: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 4: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 4: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 4: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 4: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 4: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 4: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 4: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 4:
## Chain 4:  Elapsed Time: 9.08662 seconds (Warm-up)
## Chain 4:                3.79536 seconds (Sampling)
## Chain 4:                12.882 seconds (Total)
## Chain 4:
```

```
# ggplot(m333, aes(x = nlcd11,
#                  y = BIOLIVE_TPA)) +
#   geom_point() +
#   facet_wrap(~subsection)


mod_df <- data.frame(
  fitted = mod$fitted.values,
  subsection = m333 %>% dplyr::select(subsection),
  true = mod$y
)

mod_df %>%
  yardstick::metrics(truth = true,
                     estimate = fitted)
```

```
## # A tibble: 3 x 3
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 rmse    standard      29.4
## 2 rsq     standard       0.461
## 3 mae     standard      20.7
```

```
sub_mean <- mod_df %>%
  group_by(subsection) %>%
  summarize(mean_y = mean(true))
```

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

```
bayes_cv <- mod_df %>%
  group_by(subsection) %>%
  yardstick::rmse(truth = true,
                  estimate = fitted) %>%
  left_join(sub_mean) %>%
```

```r
  group_by(subsection) %>%
  summarize(cv = .estimate / mean_y)
```

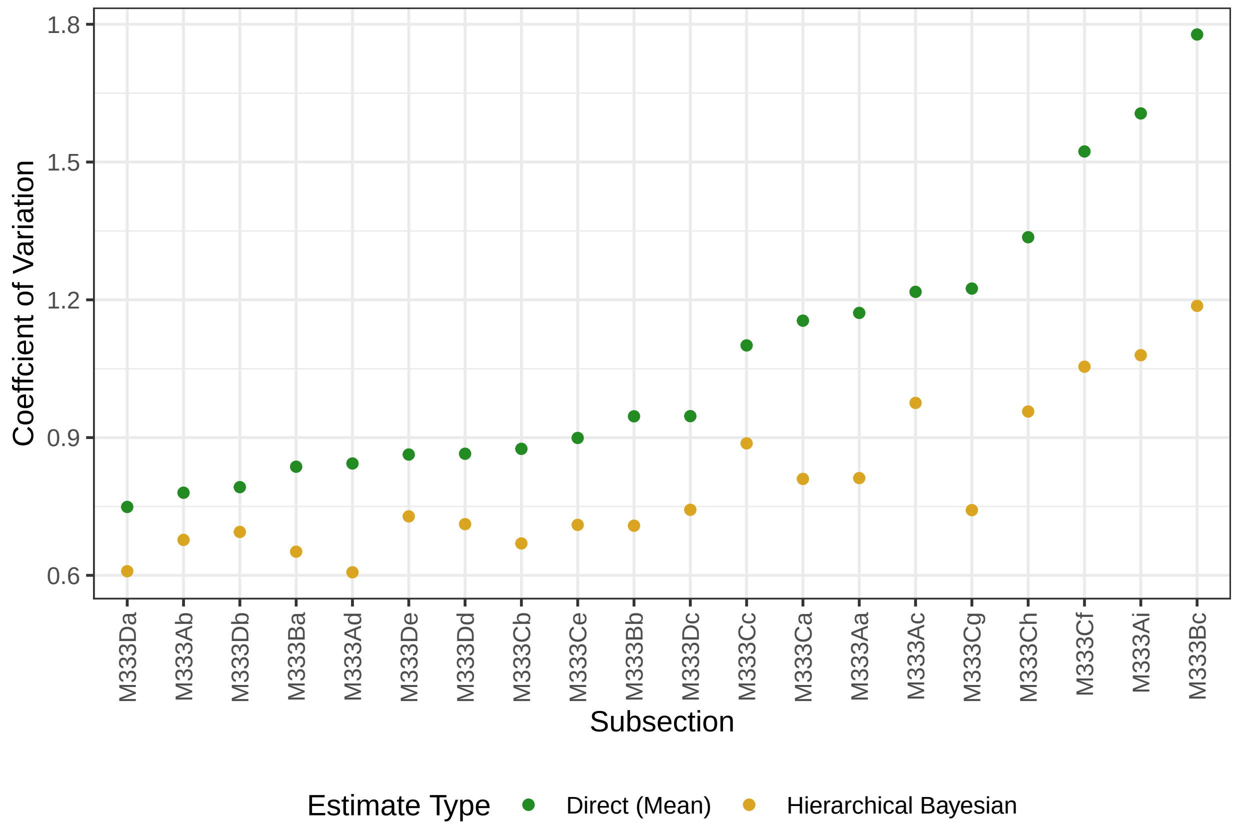
```
## Joining, by = "subsection"

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

```r
mod_df %>%
  group_by(subsection) %>%
  summarize(direct_cv = sd(true) / mean(true)) %>%
  left_join(bayes_cv) %>%
  mutate(subsection = fct_reorder(subsection, direct_cv)) %>%
  ggplot(aes(x = subsection)) +
  geom_point(aes(y = cv, color = "goldenrod")) +
  geom_point(aes(y = direct_cv, color = "forestgreen")) +
  theme_bw() +
  scale_color_manual(
    name = 'Estimate Type',
    values = c('goldenrod' = 'goldenrod',
               'forestgreen' = 'forestgreen'),
    labels = c('Direct (Mean)', 'Hierarchical Bayesian'),
    guide = "legend"
  ) +
  theme(axis.text.x = element_text(
    angle = 90,
    vjust = 0.5,
    hjust = 1
  ),
  legend.position = "bottom") +
  labs(x = "Subsection",
      y = "Coeffcient of Variation")
```

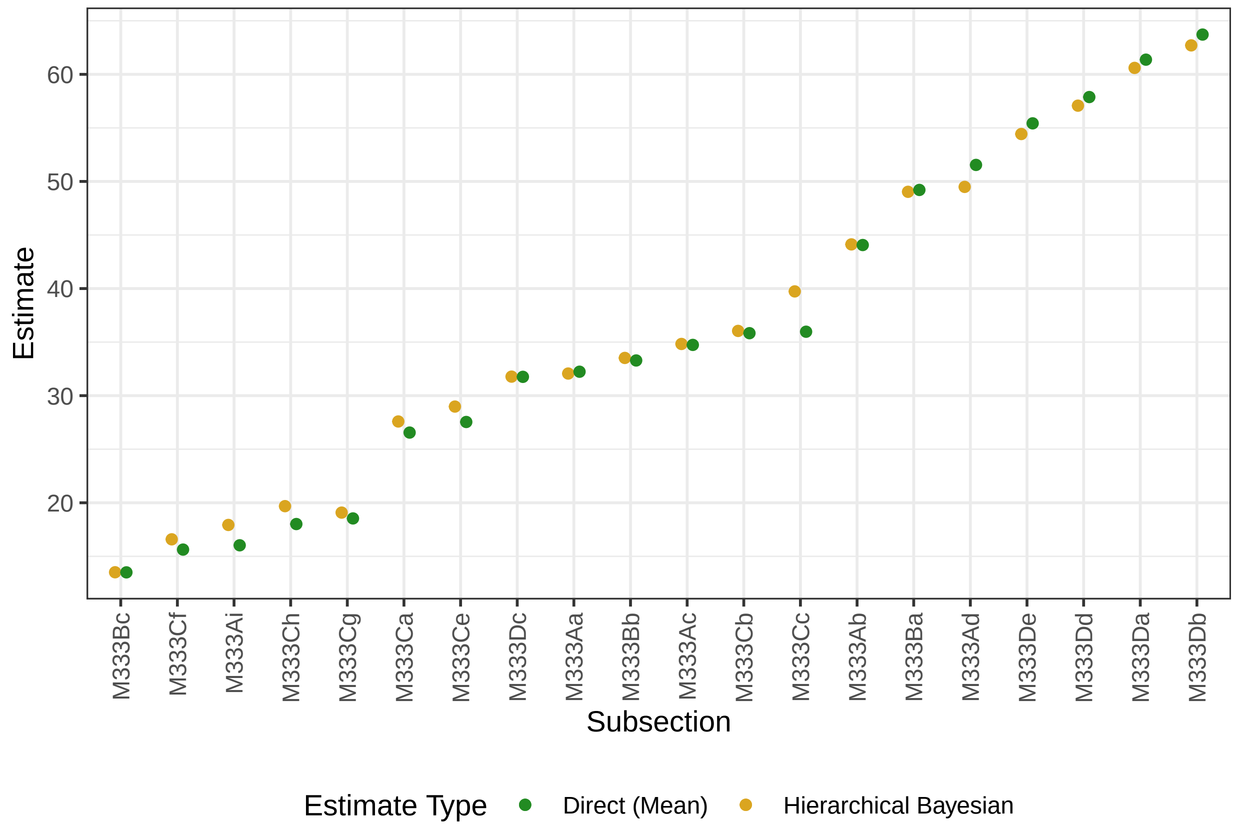
```
## `summarise()` ungrouping output (override with `.groups` argument)

## Joining, by = "subsection"
```



```
mod_df %>%
  group_by(subsection) %>%
  summarize(mean_direct = mean(true),
            mean_bayes = mean(fitted)) %>%
  mutate(subsection = fct_reorder(subsection, mean_direct)) %>%
  ggplot(aes(x = subsection)) +
  geom_point(aes(y = mean_bayes,
                 color = "goldenrod"),
             position = position_nudge(x = -0.1)) +
  geom_point(aes(y = mean_direct,
                 color = "forestgreen"),
             position = position_nudge(x = 0.1)) +
  theme_bw() +
  scale_color_manual(
    name = 'Estimate Type',
    values = c('goldenrod' = 'goldenrod',
               'forestgreen' = 'forestgreen'),
    labels = c('Direct (Mean)', 'Hierarchical Bayesian'),
    guide = "legend"
  ) +
  theme(axis.text.x = element_text(
    angle = 90,
    vjust = 0.5,
    hjust = 1
  ),
  legend.position = "bottom") +
  labs(x = "Subsection",
       y = "Estimate")
```

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



All the provinces

```
df <- read_csv("../data/subsets/dat_small.csv")
```

```
## Warning: Missing column names filled in: 'X1' [1]
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   subsection = col_character(),
##   section = col_character(),
##   province = col_character()
## )
```

```
## See spec(...) for full column specifications.
```

```r
df <- df %>%
  mutate(id = province) %>%
  group_by(id) %>%
  nest()

models_df <- list()
cv <- c()
models <- readRDS("models.rds")
for(i in 1:14) {
  # models[[i]] <- stan_lmer(BIOLIVE_TPA ~ 1 + nlcd11 + (1 | subsection),
  #                  data = df[[i,2]][[1]],
  #                  verbose = FALSE)

  models_df[[i]] <- data.frame(
  fitted = models[[i]]$fitted.values,
  subsection = df[[i,2]][[1]] %>% dplyr::select(subsection),
  true = models[[i]]$y
  ) }


cv <- list()
for(i in 1:14){

cv[i] <- models_df[[i]] %>%
  group_by(subsection) %>%
  summarize(bayes_cv = sd(fitted, na.rm = TRUE) / mean(fitted, na.rm = TRUE),
            direct_cv = sd(true, na.rm = TRUE) / mean(true, na.rm = TRUE)) %>%
 summarize(median(bayes_cv / direct_cv, na.rm = TRUE))
}
```

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

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```

```r
unlist(cv)
```

```
##  [1] 0.7874218 0.6088884 0.7469403 0.2930950 0.7840197 0.7830745 0.6622711
##  [8] 0.6516997 0.7034978 0.6956291 0.6941903 0.6490448 0.9724442 0.7304559
```

```r
mean(unlist(cv))
```

```
## [1] 0.6973338
```