

Untitled

Make data into long format

```
estimates_long <- results %>%
  pivot_longer(cols = c("est_hb_unit", "est_hb_area", "est_freq_unit", "est_freq_area", "est_dirmean"),
               names_to = "estimator",
               values_to = "estimate") %>%
  dplyr::select(-cov_hb_unit, -cov_hb_area, -cov_freq_unit, -cov_freq_area, -cov_dirmean) %>%
  mutate(estimator = stringr::str_sub(estimator, start = 5))

cov_long <- results %>%
  pivot_longer(cols = c("cov_hb_unit", "cov_hb_area", "cov_freq_unit", "cov_freq_area", "cov_dirmean"),
               names_to = "estimator",
               values_to = "cov") %>%
  dplyr::select(-est_hb_unit, -est_hb_area, -est_freq_unit, -est_freq_area, -est_dirmean) %>%
  mutate(estimator = stringr::str_sub(estimator, start = 5))

results_long <- estimates_long %>%
  full_join(cov_long) %>%
  mutate(
    section = str_remove_all(subsection, "[:lower:]"),
    province = str_sub(section, end = -2)
  )
```

```
## Joining, by = c("subsection", "response", "estimator")
```

```
dat_summary <- dat %>%
  group_by(subsection) %>%
  summarize(mean_forprob = mean(forprob, na.rm = T))
```

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

```
results_long <- results_long %>%
  full_join(dat_summary)
```

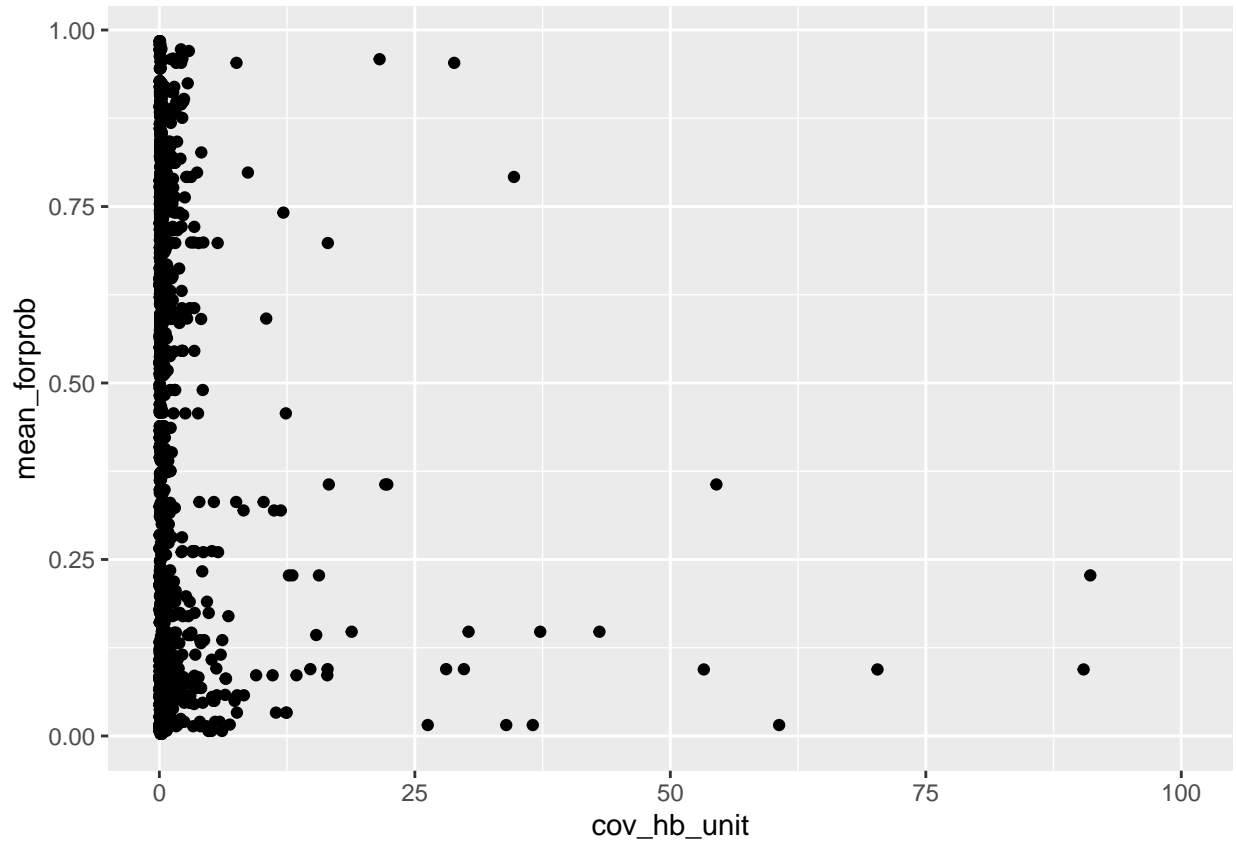
```
## Joining, by = "subsection"
```

```
results <- results %>%
  full_join(dat_summary)
```

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

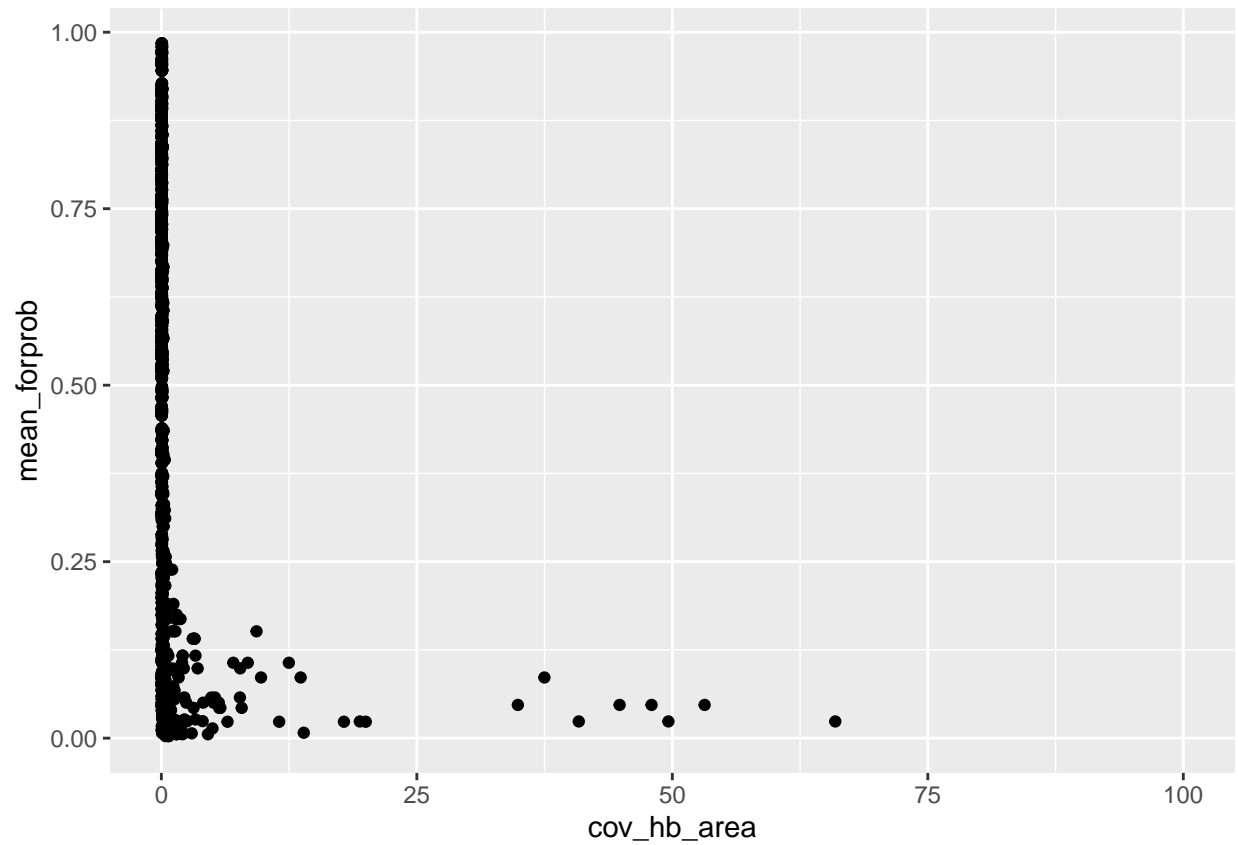
```
ggplot(results, aes(x = cov_hb_unit,
                    y = mean_forprob)) +
  geom_point() +
  xlim(0,100)
```

Warning: Removed 59 rows containing missing values (geom_point).



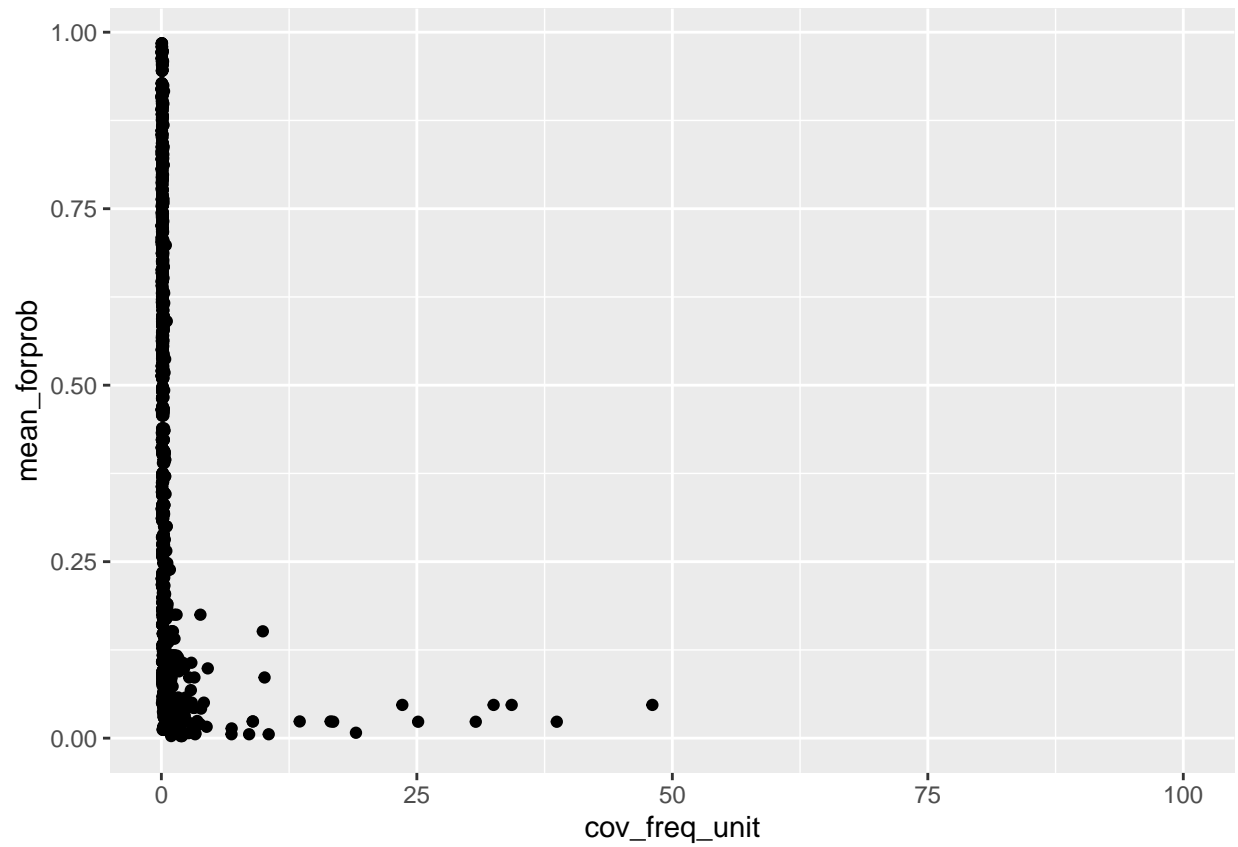
```
ggplot(results, aes(x = cov_hb_area,
                    y = mean_forprob)) +
  geom_point() +
  xlim(0,100)
```

Warning: Removed 52 rows containing missing values (geom_point).



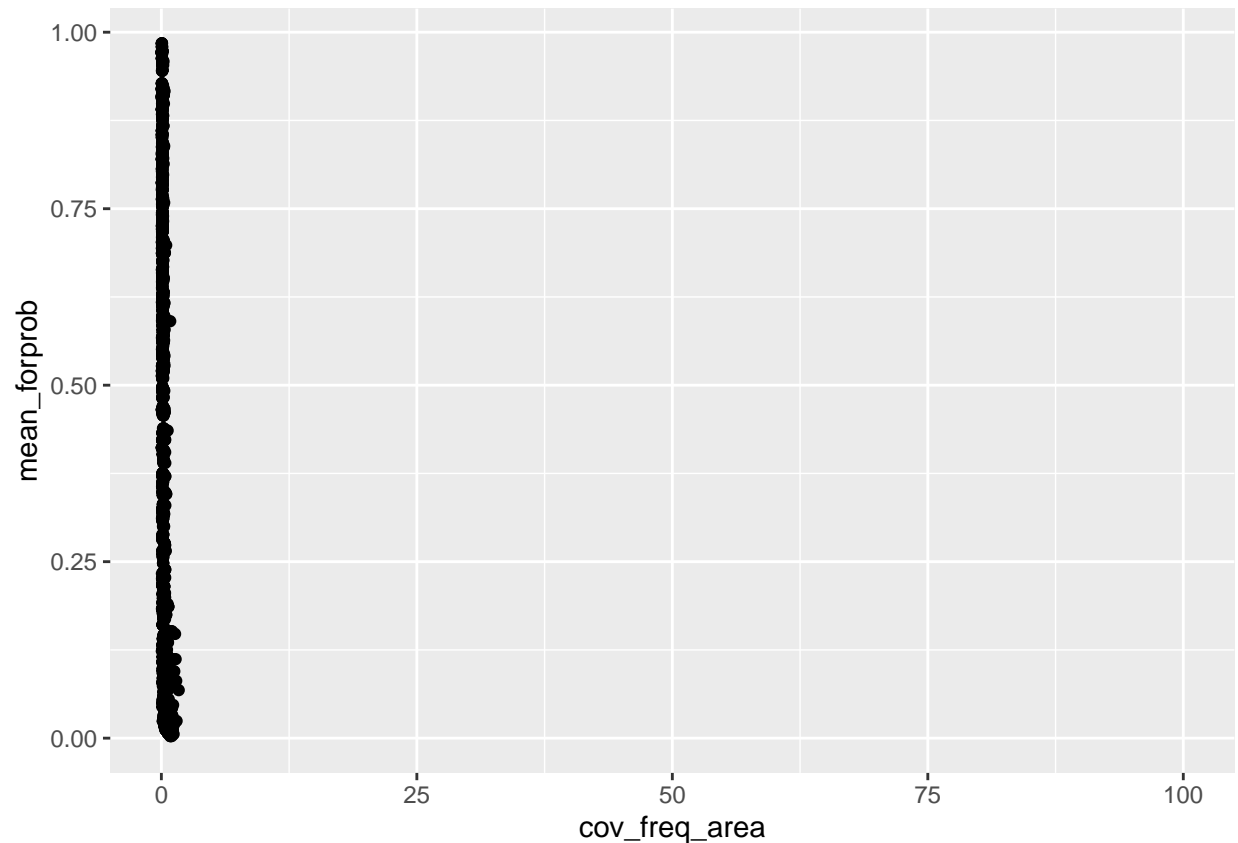
```
ggplot(results, aes(x = cov_freq_unit,
                    y = mean_forprob)) +
  geom_point() +
  xlim(0,100)
```

Warning: Removed 52 rows containing missing values (geom_point).



```
ggplot(results, aes(x = cov_freq_area,  
                    y = mean_forprob)) +  
  geom_point() +  
  xlim(0,100)
```

```
## Warning: Removed 52 rows containing missing values (geom_point).
```



```
results_long %>%
  # filter(mean_forprob >= 0.25) %>%
  group_by(estimator) %>%
  summarize(mean = mean(cov),
            median = median(cov))
```

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

```
## # A tibble: 6 x 3
##   estimator    mean  median
##   <chr>      <dbl>  <dbl>
## 1 dirmean    0.270  0.190
## 2 freq_area  0.238  0.153
## 3 freq_unit  0.489  0.132
## 4 hb_area    0.503  0.0557
## 5 hb_unit    1.99   0.156
## 6 <NA>      NA     NA
```

```
median((results$est_hb_unit - results$est_freq_unit) / results$est_freq_unit, na.rm = T)
```

```
## [1] -0.006743596
```

```
median((results$est_hb_area - results$est_freq_area) / results$est_freq_area, na.rm = T)
```

```
## [1] 0.1330755
```

Plot some results

```
m333_long_basal <- results_long %>%
  filter(province == "M333",
         response == "BALIVE_TPA")

m333_basal <- results %>%
  filter(subsection %in% m333_long_basal$subsection,
         response == "BALIVE_TPA")

m333_long_basal <- m333_basal %>%
  dplyr::select("subsection", "est_dirmean") %>%
  full_join(m333_long_basal, by = "subsection") %>%
  mutate(sd = cov * estimate)

m333_long_basal_hbarea <- m333_long_basal %>%
  filter(estimator == "hb_area")

p1 <- ggplot(m333_long_basal,
            aes(
              x = stringr::str_sub(subsection, 5),
              y = cov,
              color = estimator
            )) +
  geom_point() +
  scale_color_manual(
    values = c("goldenrod", "maroon", "red", "navyblue", "steelblue"),
    labels = c(
      "Mean",
      "Freq. Area-level",
      "Freq. Unit-level",
      "Bayesian Area-level",
      "Bayesian Unit-level"
    )
  ) +
  theme_bw() +
  theme(legend.position = "bottom") +
  labs(
    y = "Coefficient of Variation",
    x = "Ecological Subsection",
    color = "Estimator:",
    title = "Coefficent of Variation of Estimators in the Northern Rocky Forest (M333)"
  )

p2 <- ggplot(m333_long_basal,
            aes(
```

```

      x = stringr::str_sub(subsection, 5),
      y = estimate,
      color = estimator
    )) +
  geom_point() +
  scale_color_manual(
    values = c("goldenrod", "maroon", "red", "navyblue", "steelblue"),
    labels = c(
      "Mean",
      "Freq. Area-level",
      "Freq. Unit-level",
      "Bayesian Area-level",
      "Bayesian Unit-level"
    )
  ) +
  theme_bw() +
  theme(legend.position = "bottom") +
  labs(
    y = "Basal Area (sq ft)",
    x = "Ecological Subsection",
    color = "Estimator:",
    title = "Basal Area Model Results in the Northern Rocky Forest (M333)"
  )
)

p3 <- ggplot(m333_long_basal,
  aes(
    x = stringr::str_sub(subsection, 5),
    y = estimate,
    color = estimator
  )) +
  geom_point() +
  geom_errorbar(data = m333_long_basal_hbarea,
    aes(ymin = estimate - 2*sd, ymax = estimate + 2*sd)) +
  scale_color_manual(
    values = c("goldenrod", "maroon", "red", "navyblue", "steelblue"),
    labels = c(
      "Mean",
      "Freq. Area-level",
      "Freq. Unit-level",
      "Bayesian Area-level",
      "Bayesian Unit-level"
    )
  ) +
  theme_bw() +
  theme(legend.position = "bottom") +
  labs(
    y = "Basal Area (sq ft)",
    x = "Ecological Subsection",
    color = "Estimator:",
    title = "Basal Area Model Results in the Northern Rocky Forest (M333)"
  )
)

```