Example of Using Modeling Functions

First, you need to load the functions in the this folder:

```r
source("direct_CoV.R")
source("direct_estimate.R")
source("freq_area.R")
source("freq_area_CoV.R")
source("freq_unit.R")
source("freq_unit_CoV.R")
source("hb_area.R")
source("hb_CoV.R")
source("hb_unit.R")
```

Now, let's pick a province

```r
m333 <- df %>%
  dplyr::filter(province == "M333")
```

Let's fit the 5 models:

```r
# Direct
direct <- direct_estimate(m333, "BIOLIVE_TPA", "subsection")

# Frequentist models
freq_unit_mod <- freq_unit(m333, BIOLIVE_TPA ~ nlcd11, "subsection")
freq_area_mod <- freq_area(m333, BIOLIVE_TPA ~ nlcd11, "subsection")

# Hierarchical Bayesian models
bayes_unit <- hb_unit(m333, BIOLIVE_TPA ~ nlcd11, "subsection")
```

```
## numerical integration of f(x) (normalization constant): 1.802e+15 with absolute error < 2.4e+07
## numerical integration of x*f(x): 1.869e+14 with absolute error < 927610
```

posterior density for σ_v^2/σ_e^2
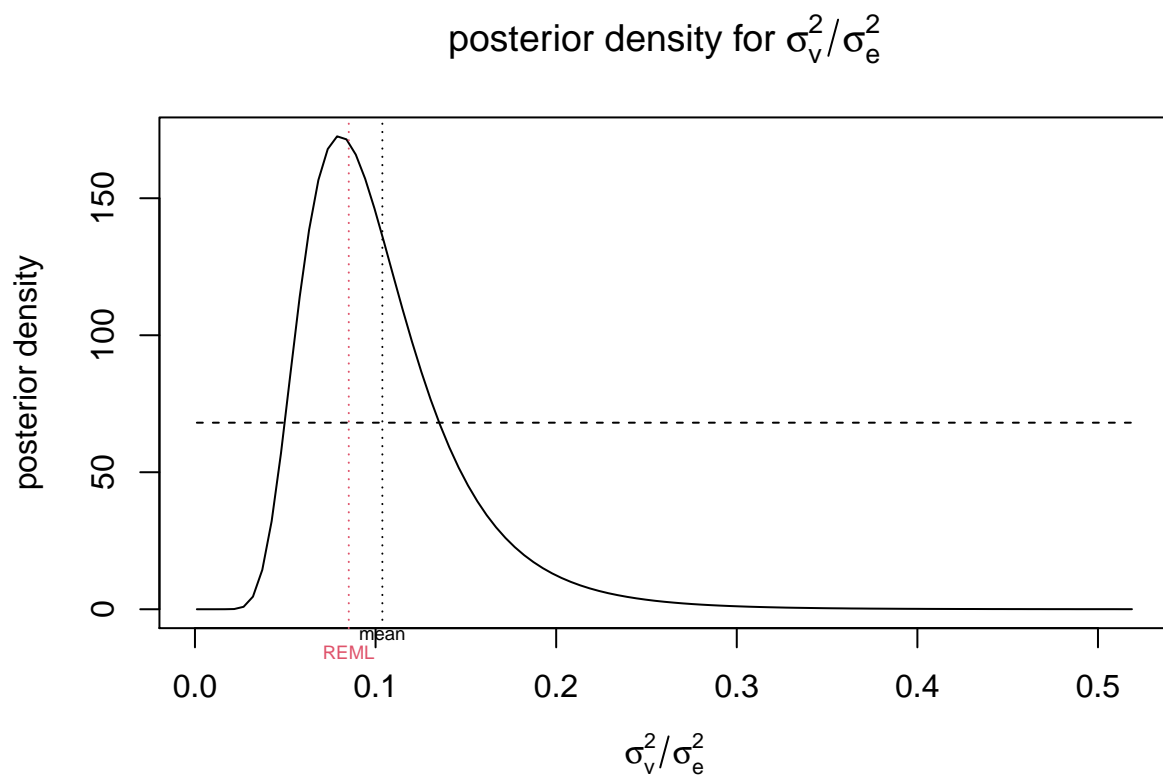

```r
bayes_area <- hb_area(m333, BIOLIVE_TPA ~ nlcd11, "subsection")
```

```
## numerical integration of f(x) (normalization constant): 3.917 with absolute error < 1.6e-08
## numerical integration of x*f(x): 340.5 with absolute error < 4.2e-06
```

posterior density for σ_v^2/σ_e^2
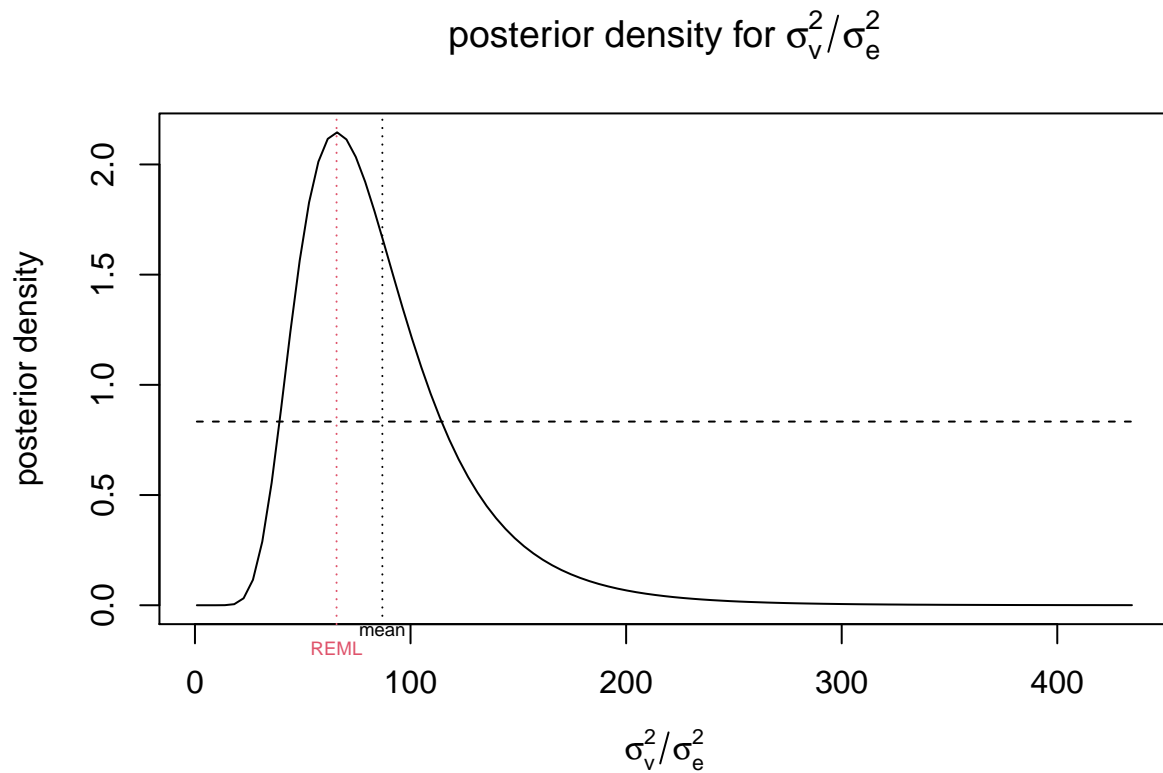
Let's get their CoV's:

```r
# Direct
dicov <- direct_CoV(direct)

# Freq
fucov <- freq_unit_CoV(m333, BIOLIVE_TPA ~ nlcd11, "subsection")
```

```
## [1] 1
## [1] 51
```

```r
facov <- freq_area_CoV(m333, BIOLIVE_TPA ~ nlcd11, "subsection")
```

```
## [1] 1
## [1] 51
```

```r
# Bayes
bucov <- hb_CoV(bayes_unit)
bacov <- hb_CoV(bayes_area)
```

Summarize CoV's:

```r
mean(dicov)
```

```
## [1] 0.1107611
```

```r
mean(fucov)
```

```
## [1] 0.1129852
```

```r
mean(facov)
```

```
## [1] 0.102314
```

```r
mean(bucov)
```

```
## [1] 0.09904166
```

```r
mean(bacov)
```

```
## [1] 0.06679799
```

Let's plot them:

```r
cov_df <- data.frame(unitbayes = bucov,
                     areabayes = bacov,
                     unitfreq = fucov,
                     areafreq = facov,
                     direct = dicov)
cov_df <- cov_df %>%
  mutate(subsection = rownames(cov_df))

cov_df %>%
  mutate(subsection = fct_reorder(subsection, direct)) %>%
  ggplot(aes(x = subsection)) +
  geom_point(aes(y = unitbayes,
                 color = "goldenrod")) +
  geom_point(aes(y = areabayes,
                 color = "forestgreen")) +
  geom_point(aes(y = unitfreq,
                 color = "steelblue")) +
  geom_point(aes(y = areafreq,
                 color = "maroon")) +
  geom_point(aes(y = direct,
                 color = "deeppink")) +
  theme_bw() +
  scale_color_manual(
    name = 'Estimate Type',
    values = c('goldenrod' = 'goldenrod',
               'forestgreen' = 'forestgreen',
               "steelblue" = "steelblue",
               "maroon" = "maroon",
               "deeppink" = "deeppink"),
    labels = c('Direct (Mean)', 'HB Area', "HB Unit", "Freq Area", "Freq Unit"),
    guide = "legend"
  ) +
```

```
theme(axis.text.x = element_text(
  angle = 90,
  vjust = 0.5,
  hjust = 1
),
legend.position = "bottom") +
labs(x = "Subsection",
     y = "Estimate")
```