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```
popdat <- m333 %>%  
  group_by(subsection) %>%  
  summarize(  
    '(Intercept)' = n(),  
    nlcd11 = mean(nlcd11))
```

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

```
popdat <- as.data.frame(popdat)
```

```
xpop <- m333 %>%  
  group_by(subsection) %>%  
  summarize(  
    nlcd11 = mean(nlcd11)  
  ) %>%  
  as.data.frame()
```

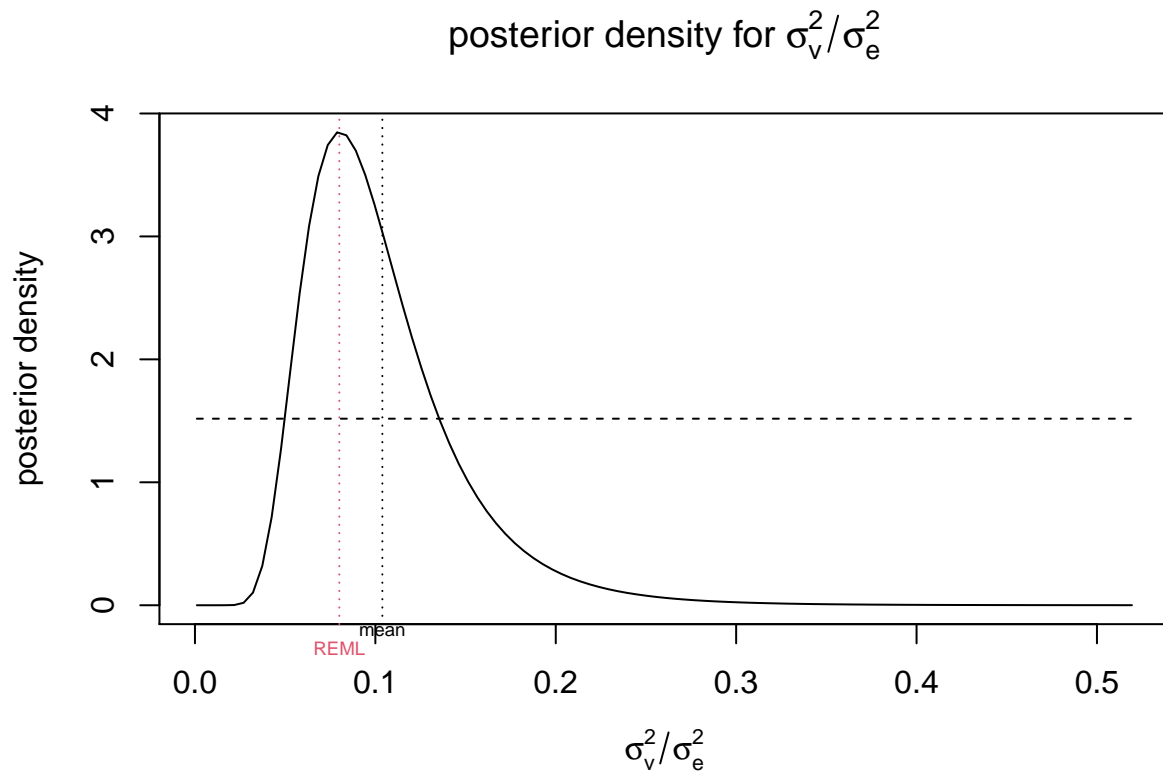
```
## 'summarise()' ungrouping output (override with '.groups' argument)
```

```
rownames(xpop) <- xpop$subsection  
  
xpop <- xpop %>% select(nlcd11)  
  
unit_mod <- fSAE.Unit(y = m333$BIOLIVE_TPA,  
  X = m333 %>% dplyr::select(nlcd11),  
  area = m333$subsection,  
  Narea = popdat$'(Intercept)',  
  Xpop = xpop,  
  fpc = FALSE,  
  nu0 = 2,  
  s20 = 10)
```

```
## REML estimate of variance ratio: 0.08002
```

```
## numerical integration of f(x) (normalization constant): 60.69 with absolute error < 3.3e-07  
## numerical integration of x*f(x): 6.305 with absolute error < 6.2e-08
```

```
## posterior mean for variance ratio: 0.1039
```



```
anova <- aov(BIOLIVE_TPA ~ subsection, data = m333)
summary <- summary(anova)
```

```
lambda <- summary(anova)[[1]]["subsection", "F value"]
```

```
freq_mod <- fSAE.Unit(y = m333$BIOLIVE_TPA,
  X = m333 %>% dplyr::select(nlcd11),
  area = m333$subsection,
  Narea = popdat$`(Intercept)`,
  Xpop = xpop,
  fpc = FALSE,
  method = "BLUP",
  lambda0 = lambda)
```

```
SE(unit_mod) / m333_area$meanbio
```

```
##      M333Aa      M333Ab      M333Ac      M333Ad      M333Ai      M333Ba      M333Bb
## 0.08321000 0.06950407 0.07894010 0.09477250 0.26643264 0.03927688 0.04448655
##      M333Bc      M333Ca      M333Cb      M333Cc      M333Ce      M333Cf      M333Cg
## 0.13013963 0.11685367 0.04357960 0.13569412 0.11316135 0.20417707 0.17035954
##      M333Ch      M333Da      M333Db      M333Dc      M333Dd      M333De
## 0.18852056 0.03178039 0.03081893 0.06035469 0.03701514 0.04089723
```

```
dat <- data.frame(
  mean = m333_area$meanbio,
```

```

    est = EST(unit_mod),
    subsection = m333_area$subsection,
    freq = EST(freq_mod)
  )

dat %>%
  mutate(subsection = fct_reorder(subsection, mean)) %>%
  ggplot(aes(x = subsection)) +
  geom_point(aes(y = est,
                 color = "goldenrod"),
             position = position_nudge(x = -0.1)) +
  geom_point(aes(y = mean,
                 color = "forestgreen"),
             position = position_nudge(x = 0.1)) +
  geom_point(aes(y = freq,
                 color = "steelblue"),
             position = position_nudge(x = 0.2)) +
  theme_bw() +
  scale_color_manual(
    name = 'Estimate Type',
    values = c('goldenrod' = 'goldenrod',
               'forestgreen' = 'forestgreen',
               "steelblue" = "steelblue"),
    labels = c('Direct (Mean)', 'Hierarchical Bayesian', "BLUP"),
    guide = "legend"
  ) +
  theme(axis.text.x = element_text(
    angle = 90,
    vjust = 0.5,
    hjust = 1
  )),
  legend.position = "bottom" +
  labs(x = "Subsection",
       y = "Estimate")

```

