

## Back to hbsae

```
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

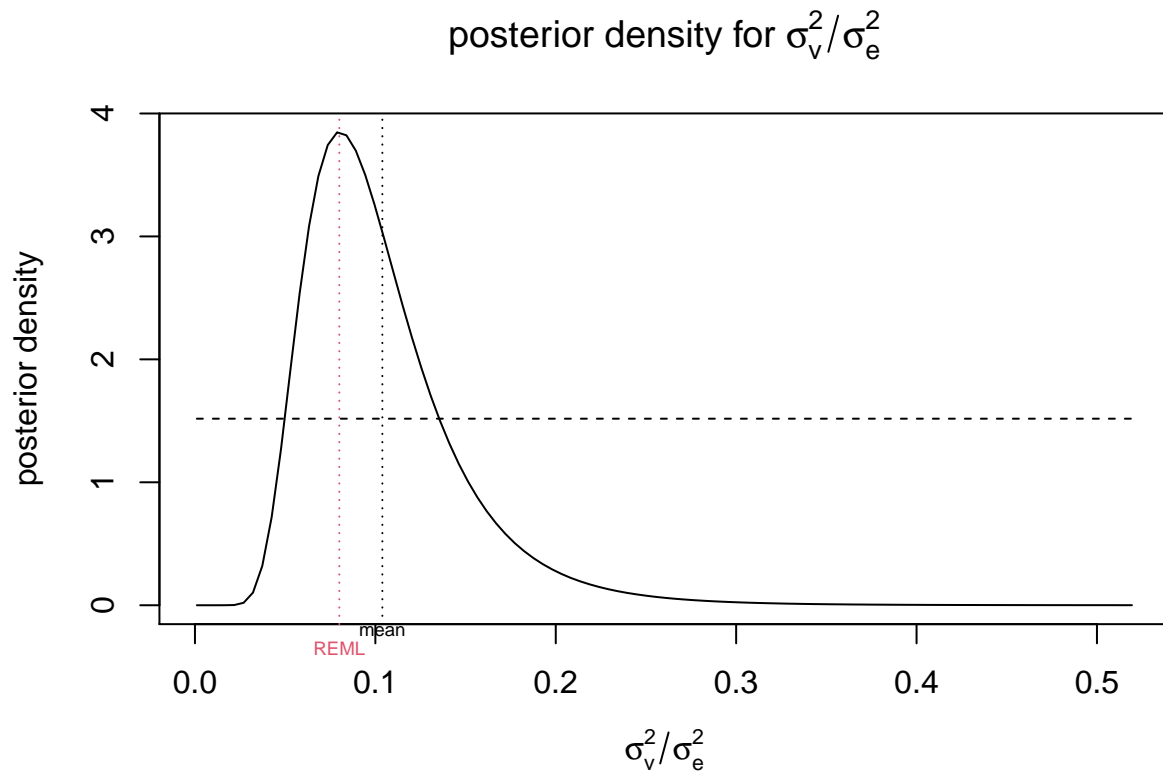
xpop <- xpop %>% select(nlcd11)

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
```



```
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
)

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)) +
  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")

```

