Suggested model based packages: sae, JoSae, yalmpute

```r
library(hbsae)
library(tidyverse)
```

```
## -- Attaching packages ------------------------------------------------------ tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.3     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## -- Conflicts --------------------------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
dat_small <- 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
mod <- fSAE.Unit(
  y = dat_small$BIOLIVE_TPA,
  X = dat_small %>% select(forbio),
  area = dat_small$subsection
)
```

```
## REML estimate of variance ratio: 0.1857
```

```
## numerical integration of f(x) (normalization constant): 7.594e+29 with absolute error < 6.3e+21
## numerical integration of x*f(x): 1.424e+29 with absolute error < 1.3e+19
```

```
## posterior mean for variance ratio: 0.1875
```

posterior density for σ_v^2/σ_e^2