

1. Start a new R session, go Session>Restart R then Session>Clear Workspace
2. Go to Github and click where it says *Direct Data Download*
3. Drag the file into data/raw/
4. Name the file breastcancer.txt
5. Open and Run R/EDA.Rmd
6. Open and Run R/Model.Rmd
7. Open and Run R/Diagnostics and R/Posterior
8. Open and Run R/Clustering.Rmd

Packages needed (these are in EDA.Rmd): broom, knitr, tidyverse, dplyr, ggplot2, stringr, ggthemes, scales, brms, bayesplot, rstan, caret, sjPlot, tidyr, mclust

#### RUNTIME NOTES:

Rstan requires C++ compiler, try both rstan and cmdstan if errors exist

```
...
```

```
rstan_options(auto_write = TRUE)
options(mc.cores = parallel::detectCores())
...
```