

1. Place the ZIP file into a new folder on your desktop, and unzip it
2. Start a new R session, go Session>Restart R then Session>Clear Workspace
3. Go to Github (<https://github.com/JonathanMa03/bayesproject-MaZhuFeng-FA25>) and click where it says *Direct Data Download*
4. Drag the file into data/raw/
5. Name the file breastcancer.txt
6. Open and Run R/EDA.Rmd
7. Open and Run R/Model.Rmd
8. Open and Run R/Diagnostics and R/Posterior
9. 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())  
...
```