Exercises: k-fold cross validation and LOO (Vasishth/Nicenboim)

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1 Exercise 1

Run the full 10-fold cross validation procedure for the Chinese RC data (in the code provided in the lecture notes, we only ran 2 folds to illustrate the procedure).

2 Exercise 2

Load the Chinese replication experiment.

```
crit_rep<-read.table("data/gibsonwu2012datarepeat.txt")</pre>
head(crit_rep)
##
     subj item condition pos
                             rt
                                    region
## 9
      1m1 15 obj-ext 8 832 head noun
## 20 1m1 8 subj-ext 8 2131 head noun
## 33 1m1 11 obj-ext 8 553 head noun
     1m1 10 subj-ext 8 1091 head noun
## 46
## 62
      1m1 16 subj-ext 8 598 head noun
## 75
           14 subj-ext
                          8 645 head noun
     1m1
colnames(crit_rep)[3]<-"type"</pre>
crit_rep < -crit_rep[, c(1,2,3,5)]
head(crit_rep)
##
     subj item
                   type
                         rt
## 9
      1m1 15 obj-ext 832
## 20 1m1 8 subj-ext 2131
## 33 1m1 11 obj-ext
                       553
## 46
      1m1 10 subj-ext 1091
      1m1 16 subj-ext
## 62
                         598
## 75
      1m1 14 subj-ext
```

Find out whether M0 or M1 has a better predictive performance on this data.

3 Exercise 3

Load the English relative clause data and preprocess it to get to the critical data:

```
library(tidyverse)
## -- Attaching packages ----- tidyverse 1.2.1 --
## v tibble 2.0.1
                     v purrr 0.2.5
## v tidyr 0.8.2
                    v dplyr 0.7.8
## v readr 1.1.1
                    v stringr 1.3.1
## v tibble 2.0.1
                     v forcats 0.3.0
## Warning: package 'tibble' was built under R version 3.5.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::laq()
                    masks stats::laq()
## Grodner and Gibson, this is a comma separated vector file
gge1<-read.csv("data/GrodnerGibson2005E1.csv", header=TRUE)
gge1 <- gge1 %>% filter(item != 0)
gge1 <- gge1 %>% mutate(word_positionnew = ifelse(item != 15 &
                       word_position > 10, word_position-1,
                       word_position))
## isolate critical data:
rDat3 <- subset(gge1, (condition == "objgap" & word_position == 6) |
            ( condition == "subjgap" & word_position == 4 ))
```

Determine whether M0 or M1 is the better model using PSIS-LOO, and do the same comparison using the k-fold cross-validation procedure. Check whether both methods give the same conclusion.

4 Exercise 4

Optional: Generate fake data that actually has a mixture distribution (use the function I provide for generating fake data), and then test if the M1 model comes out showing a better fit than M0 using k-fold cross validation and PSIS-loo.