3.4.1: R - Model Validation Stat 5100: Dr. Bean

Project 2 is focused on using information regarding Tinder profiles to predict the genuineness of the user. Information regarding the total set of variables are included in the project 2 description. For purposes of illustration, only a subset of variables are considered here.

```
# Set a seed so that results are reproducible
set.seed(222)
library(stat5100)
# If you run this code, you will have to import the data differently. This
# particular dataset is not included in the stat5100 package for copyright
# reasons, hence why I load it locally here.
tinder <- read.csv("../../../data_csv/tinder.csv", na.strings = ".",</pre>
                   stringsAsFactors = FALSE)
# All the column names in the tinder dataset
names(tinder)
   [1] "ID"
                                                            "InstPrivConc"
##
                         "Genuine"
                                          "SocPrivConc"
                         "SelfEsteem"
   [5] "Narcissism"
                                          "Loneliness"
                                                            "Hookup"
   [9] "Friends"
                         "Partner"
                                          "Travel"
                                                            "SelfValidation"
                                          "Gender"
## [13] "Entertainment" "Orientation"
                                                           "Education"
## [17] "Income"
                         "Employment"
                                          "Age"
                                                            "ImpFitness"
## [21] "ImpEnergy"
                         "ImpAttractive"
apply(tinder, 2, class)
##
               ID
                         Genuine
                                    SocPrivConc
                                                  InstPrivConc
                                                                   Narcissism
                     "character"
                                                   "character"
                                                                   "character"
##
      "character"
                                    "character"
      SelfEsteem
                    Loneliness
                                         Hookup
                                                       Friends
                                                                      Partner
##
                     "character"
                                   "character"
                                                   "character"
      "character"
                                                                   "character"
##
          Travel SelfValidation Entertainment
##
                                                   Orientation
                                                                        Gender
##
      "character" "character" "character"
                                                   "character"
                                                                   "character"
       Education
                                    Employment
                                                                  ImpFitness
##
                        Income
                                                          Age
                   "character"
                                    "character"
                                                 "character"
      "character"
                                                                   "character"
##
        ImpEnergy ImpAttractive
##
##
      "character"
                     "character"
# These columns by default are set as factors, which are categorical variables.
# To make this work out for a continuous response variable, we need to convert
# some of the columns to numeric values.
numeric_columns <- c("Genuine", "SocPrivConc", "InstPrivConc", "Narcissism",</pre>
                     "SelfEsteem", "Loneliness", "Hookup", "Friends", "Partner",
                     "Travel", "SelfValidation", "Entertainment", "Age",
                     "ImpFitness", "ImpEnergy", "ImpAttractive")
for (nc in numeric_columns) {
  tinder[[nc]] <- as.numeric(tinder[[nc]])</pre>
```

```
# Some of the variables we want to be factors (for example, different gender
# classes, sexual orientations, etc.)
factor_columns <- c("Orientation", "Gender", "Education", "Income", "Employment")</pre>
for (fc in factor_columns) {
 tinder[[fc]] <- as.factor(tinder[[fc]])</pre>
# Separate the data into training and test sets. Here we will withhold 20%
# for validation.
n <- nrow(tinder)</pre>
training_index <- sample(1:n, size = 0.20 * n)</pre>
tinder_train <- tinder[training_index, ]</pre>
tinder_test <- tinder[-training_index, ]</pre>
# Fit one model with 4 variables
tinder_lm1 <- lm(Genuine ~ SocPrivConc + InstPrivConc + Narcissism + SelfEsteem,
                 data = tinder_train)
# Fit another model with more variables
tinder_lm2 <- lm(Genuine ~ SocPrivConc + InstPrivConc + Narcissism +
                    SelfEsteem + Loneliness + Hookup + Friends + Partner +
                    Travel + SelfValidation + Entertainment, data = tinder_train)
# To fit a third model with no predictors, we simply use the average of the
# response variable (Genuine). Having this third "model" can help us decide
# if there is any significant improvement using the predictors over simply
# quessing the average.
tinder_lm3 <- lm(Genuine ~ 1, data = tinder_train)</pre>
```

Calculate MSPR for each model

```
# To do this, we make predictions with the testing dataset and then compare
# it to the known value of the response variable Genuine in the testing dataset.
tinder_test_pred1 <- predict(tinder_lm1, newdata = tinder_test)
tinder_test_pred2 <- predict(tinder_lm2, newdata = tinder_test)
tinder_test_pred3 <- predict(tinder_lm3, newdata = tinder_test)

mspr1 <- mean((tinder_test_pred1 - tinder_test$Genuine)^2, na.rm = T)
mspr2 <- mean((tinder_test_pred2 - tinder_test$Genuine)^2, na.rm = T)
mspr3 <- mean((tinder_test_pred3 - tinder_test$Genuine)^2, na.rm = T)

# Show results
data.frame(mspr1, mspr2, mspr3)

## mspr1 mspr2 mspr3
## 1 2.701384 2.329362 2.747672

# Based upon the MSPR, it looks like models 1 and 3 perform roughly the same
# on the testing dataset, but model 2 does better.</pre>
```