TODD GARNER

DS 6306 WEEK 7 PART 2

FEBRUARY 14. 2023

PART 2, #1

- Read in the data, add sex, run code as below with seed(4), view results.

```r
# Read in the training set.  Check to "View" the full file to make sure it's what we want.
Titanic <- read.csv(file.choose(), header = TRUE)
View(Titanic)
```

We won't need to run that piece of code again so I'm isolating it.

```r
#Titanic$SurvivedF <- factor(Titanic$Survived, labels = c("Died", "Survived"))
Titanic$MF <- factor(Titanic$Sex, labels = c("0", "1")) #male = 1, female = 0
head(Titanic$MF)
head(Titanic)
Titanic_sub <- Titanic %>% filter(!is.na(Age) & !is.na(Pclass) & !is.na(MF))
Titanic_Sub_filter <- Titanic_sub %>% select(Age, Pclass, Survived, MF)
head(Titanic_Sub_filter)
model <- naiveBayes(Titanic_Sub_filter[((Titanic_Sub_filter$Age) & (Titanic_Sub_filter$Pclass) & (Titanic_Sub_filter$MF)), c("Age", "Pclass",
"MF")], Titanic_Sub_filter$Survived, laplace = 1)
Titanic_clean = Titanic %>% filter(!is.na(Age) & !is.na(Pclass) & !is.na(MF))
set.seed(4)
trainIndices = sample(seq(1:length(Titanic_clean$MF)),round(.7*length(Titanic_clean$MF)))
trainTitanic = Titanic_clean[trainIndices,]
testTitanic = Titanic_clean[-trainIndices,]
head(trainTitanic)
dim(trainTitanic)
head(testTitanic)
dim(testTitanic)
model <- naiveBayes(trainTitanic,as.factor(trainTitanic$Survived) , laplace = 1)
summary(model)
dim(model)
#head(model)
df <- data.frame(testTitanic)
nrow(df)
x <- round(predict(model, df, type = "raw"), digits = 0)
y <- x[,2]
y
dim(df$Survived)
nrow(df$Survived)
table(y, df$Survived)
confusionMatrix(table(y, df$Survived))
```

```
Confusion Matrix and Statistics


y     0   1
  0 128   0
  1   0  86

               Accuracy : 1
                 95% CI : (0.9829, 1)
    No Information Rate : 0.5981
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 1

 Mcnemar's Test P-Value : NA

            Sensitivity : 1.0000
            Specificity : 1.0000
         Pos Pred Value : 1.0000
         Neg Pred Value : 1.0000
             Prevalence : 0.5981
         Detection Rate : 0.5981
   Detection Prevalence : 0.5981
      Balanced Accuracy : 1.0000

       'Positive' Class : 0
```

- Perhaps I'm missing the point, but this looks identical to the prior exercise.

P2 #2, WRITE LOOP(100) AND GATHER RESULTS

Code:

```r
```{r}
Titanic_clean = Titanic %>% filter(!is.na(Age) & !is.na(Pclass) & !is.na(MF))
iterations = 100
master_sens <- 0
master_spec <- 0
master_acc <- 0
master_sens <- data.frame(master_sens)
master_spec <- data.frame(master_spec)
master_acc <- data.frame(master_acc)

for(i in 1:iterations) {
set.seed(i)
trainIndices = sample(seq(1:length(Titanic_clean$MF)),round(.7*length(Titanic_clean$MF)))
trainTitanic = Titanic_clean[trainIndices,]
testTitanic = Titanic_clean[-trainIndices,]

model <- naiveBayes(trainTitanic,as.factor(trainTitanic$Survived) , laplace = 1)
df <- data.frame(testTitanic)
x <- round(predict(model, df, type = "raw"), digits = 0)
y <- x[,2]
y
master_sens[,i] = sensitivity(factor(y), factor(df$Survived))
master_spec[,i] = specificity(factor(y), factor(df$Survived))
z <- table(factor(y), factor(df$Survived))
CM <- confusionMatrix(z, k = i)
master_acc[,i] = CM$overall[1]

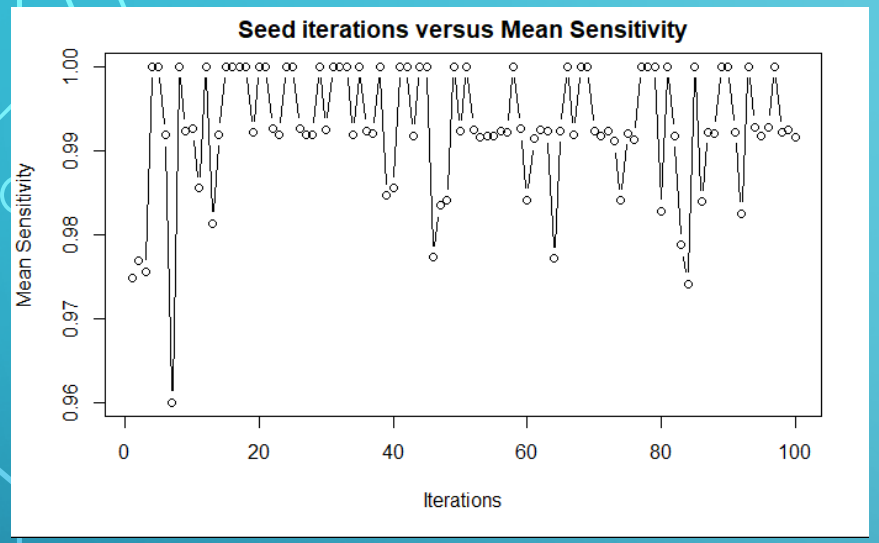
}
mean_sens = colMeans(master_sens)
mean_spec = colMeans(master_spec)
mean_acc = colMeans(master_acc)

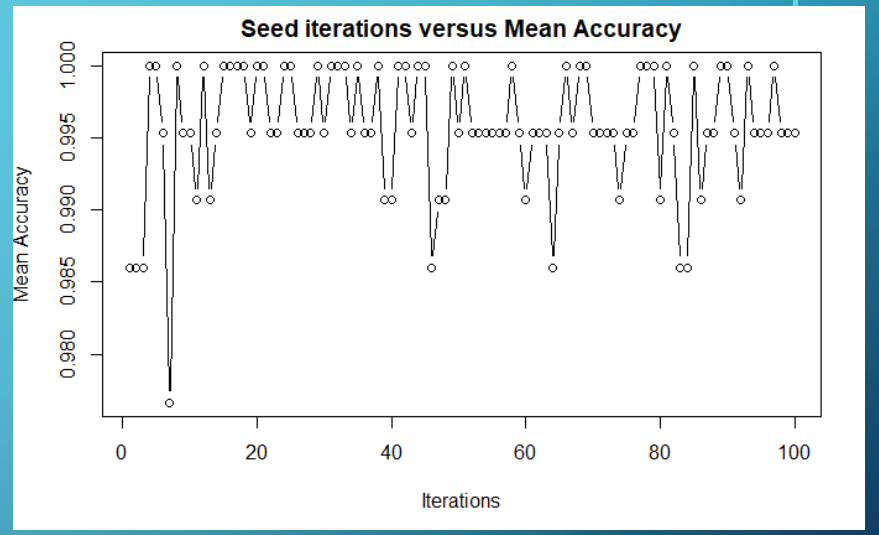
which.max(mean_sens)
max(mean_sens)
which.max(mean_spec)
max(mean_spec)
which.max(mean_acc)
max(mean_acc)

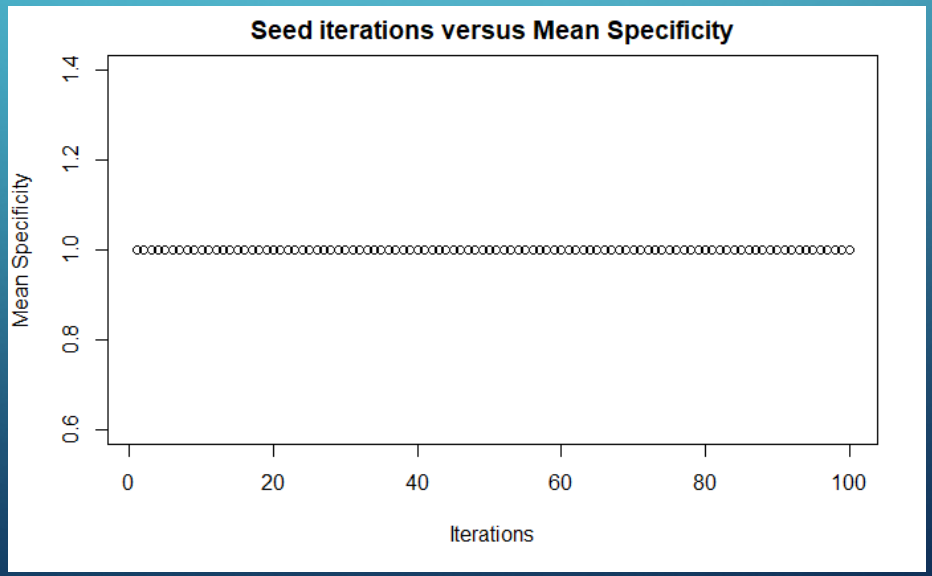

plot(mean_sens,xlab = "Iterations", ylab = "Mean Sensitivity", main = "Seed iterations versus Mean Sensitivity", type = "b")
plot(mean_spec,xlab = "Iterations", ylab = "Mean Specificity", main = "Seed iterations versus Mean Specificity",type = "b")
plot(mean_acc, xlab = "Iterations", ylab = "Mean Accuracy", main = "Seed iterations versus Mean Accuracy",type = "b")
```
```

P2 #3, PLOTS OF ACCURACY, SENSITIVITY, SPECIFICITY

- Means were all identical: 1







P2 IRIS, CROSS VALIDATION SEPAL LENGTH & WIDTH

I must say I was stumped by this one. My code is found below. Perhaps in Live Session we can go through it to find out what I'm doing wrong?

```
# Part 2, Iris

```{r}
#View(iris)
iris_clean = iris %>% filter(!is.na(Sepal.Length) & !is.na(Sepal.Width))
iterations = 100

for(i in 1:iterations) {
set.seed(i)
trainiris = sample(seq(1:length(iris_clean$Sepal.Length)),round(.7*length(iris_clean$Sepal.Length)))
trainIris = iris_clean[trainiris,]
testIris = iris_clean[-trainiris,]
head(trainiris)
head(testIris)

model <- naiveBayes(trainIris,as.factor(trainIris$Sepal.Length & trainIris$Sepal.Width), laplace = 1) # & trainIris$Sepal.Width
head(model)
df <- data.frame(testIris)
head(df)
x <- round(predict(model, df, type = "raw"), digits = 1)
x
y <- x[,2]
y
master_sens[,i] = sensitivity(factor(y), factor(df$Sepal.Length))
master_spec[,i] = specificity(factor(y), factor(df$Sepal.Length))
CM <- confusionMatrix(factor(y), factor(df$Sepal.Length), k = i)
master_acc[,i] = CM$overall
}

mean_sens = colMeans(master_sens)
mean_spec = colMeans(master_spec)
mean_acc = colMeans(master_acc)

which.max(mean_sens)
max(mean_sens)
which.max(mean_spec)
max(mean_spec)
which.max(mean_acc)
max(mean_acc)
```
```

QUESTIONS

Questions:

1. I'm not sure I fully grasped the concept on the last question. How does one use two variables to predict an outcome?
2. Can you provide a real-world example of how this scheme would work? In what industry might this be used? And on what type of question might it answer? I read the example of medical testing. How might this be used in the oil and gas industry?
3. I got 100% accuracy on Part 2. I can't help but feel that may be an error. I checked and rechecked the inputs and I believe I've done it correctly. What are the odds of obtaining a 100% accuracy in "the real world?"

KEY TAKEAWAYS

- This (machine learning) is why I am pursuing the data science degree. I presume I can anticipate learning much more in machine learning 1 & 2. Are there any books out there or resources that might allow me to take a deep dive? (guess this is actually a question)