Practice Problems 3

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1. Download the data set for the tutorial.

```
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------------------------------------------------------
```

```
## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.0.3     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
origin_prostate <- read.csv("prostate_cancer.csv", stringsAsFactors = FALSE)
prostate <- origin_prostate
head(prostate)
```

```
##   id diagnosis_result radius texture perimeter area smoothness compactness
## 1  1                M     23      12       151  954      0.143       0.278
## 2  2                B      9      13       133 1326      0.143       0.079
## 3  3                M     21      27       130 1203      0.125       0.160
## 4  4                M     14      16        78  386      0.070       0.284
## 5  5                M      9      19       135 1297      0.141       0.133
## 6  6                B     25      25        83  477      0.128       0.170
##   symmetry fractal_dimension
## 1    0.242             0.079
## 2    0.181             0.057
## 3    0.207             0.060
## 4    0.260             0.097
## 5    0.181             0.059
## 6    0.209             0.076
```

2. Follow this tutorial on applying kNN to prostate cancer detection and implement all of the steps in an R Notebook. Make sure to explain each step and what it does. (*Note*: The data set provided as part of this assignment has been slightly modified from the one used in the tutorial, so small deviations in the result can be expected.)'

Step 1: Data Collection

See Question 1

Step 2: Preparing and Exploring the Data

```
# remove the first variable (id) from the dataset
prostate <- prostate[-1]

# get table of number of patients based on diagnosis
table(prostate$diagnosis_result)
```

```
##
##  B  M
## 38 62
```

```
# Rename B and M to Benign and Malignant
prostate$diagnosis <- factor(prostate$diagnosis_result, levels = c("B", "M"),
                             labels = c("Benign", "Malignant"))
# Get percentage of B/M diagnoses
round(prop.table(table(prostate$diagnosis)) * 100, digits = 1)
```

```
##
##    Benign Malignant
##        38        62
```

Normalize Numeric Data

```
normalize <- function(x) {
  return ((x - min(x)) / (max(x) - min(x))) }
norm_prostate <- as.data.frame(lapply(prostate[2:9], normalize))
summary(norm_prostate$radius)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0000  0.1875  0.5000  0.4906  0.7500  1.0000
```

Create test and training data set

```
# Split training and test dataset by 65/35
prostate_train <- norm_prostate[1:65,]
prostate_test <- norm_prostate[66:100,]

# Target variable is 'diagnosis_result', which is not in the training/test datasets
train_labels <- prostate[1:65, 1]
test_labels <- prostate[66:100, 1]
```

Step 3 - Train the model on data

```
library(class)
prc_test_pred <- knn(train = prostate_train,
                     test = prostate_test,
                     cl = train_labels,
                     k=10)
```

Step 4 - Evaluate the model performance

```
library(gmodels)
CrossTable(x = test_labels, y = prc_test_pred, prop.chisq = FALSE)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  35
##
##
##              | prc_test_pred
##  test_labels |         B |         M | Row Total |
## -------------|-----------|-----------|-----------|
##            B |         6 |        13 |        19 |
##              |     0.316 |     0.684 |     0.543 |
##              |     0.857 |     0.464 |           |
##              |     0.171 |     0.371 |           |
## -------------|-----------|-----------|-----------|
##            M |         1 |        15 |        16 |
##              |     0.062 |     0.938 |     0.457 |
##              |     0.143 |     0.536 |           |
##              |     0.029 |     0.429 |           |
## -------------|-----------|-----------|-----------|
## Column Total |         7 |        28 |        35 |
##              |     0.200 |     0.800 |           |
## -------------|-----------|-----------|-----------|
##
##
```

Step 5 - Improve the performance of the model, change the k-value

```r
# k=8
prc_test_pred <- knn(train = prostate_train,
                     test = prostate_test,
                     cl = train_labels,
                     k = 8)
CrossTable(x = test_labels, y = prc_test_pred, prop.chisq = FALSE)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  35
##
##
##              | prc_test_pred
##  test_labels |         B |         M | Row Total |
## -------------|-----------|-----------|-----------|
##            B |         9 |        10 |        19 |
##              |     0.474 |     0.526 |     0.543 |
##              |     1.000 |     0.385 |           |
##              |     0.257 |     0.286 |           |
## -------------|-----------|-----------|-----------|
##            M |         0 |        16 |        16 |
##              |     0.000 |     1.000 |     0.457 |
##              |     0.000 |     0.615 |           |
##              |     0.000 |     0.457 |           |
## -------------|-----------|-----------|-----------|
## Column Total |         9 |        26 |        35 |
##              |     0.257 |     0.743 |           |
## -------------|-----------|-----------|-----------|
##
##
```

```r
# k=9
prc_test_pred <- knn(train = prostate_train,
                     test = prostate_test,
                     cl = train_labels,
                     k = 9)
CrossTable(x = test_labels, y = prc_test_pred, prop.chisq = FALSE)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
```

```
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  35
##
##
##              | prc_test_pred
##  test_labels |         B |         M | Row Total |
## -------------|-----------|-----------|-----------|
##            B |         8 |        11 |        19 |
##              |     0.421 |     0.579 |     0.543 |
##              |     1.000 |     0.407 |           |
##              |     0.229 |     0.314 |           |
## -------------|-----------|-----------|-----------|
##            M |         0 |        16 |        16 |
##              |     0.000 |     1.000 |     0.457 |
##              |     0.000 |     0.593 |           |
##              |     0.000 |     0.457 |           |
## -------------|-----------|-----------|-----------|
## Column Total |         8 |        27 |        35 |
##              |     0.229 |     0.771 |           |
## -------------|-----------|-----------|-----------|
##
##
```

```r
# k=11
prc_test_pred <- knn(train = prostate_train,
                     test = prostate_test,
                     cl = train_labels,
                     k = 11)
CrossTable(x = test_labels, y = prc_test_pred, prop.chisq = FALSE)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  35
##
##
##              | prc_test_pred
##  test_labels |         B |         M | Row Total |
## -------------|-----------|-----------|-----------|
##            B |         5 |        14 |        19 |
##              |     0.263 |     0.737 |     0.543 |
```

```
##              |     1.000 |     0.467 |           |
##              |     0.143 |     0.400 |           |
## -------------|-----------|-----------|-----------|
##            M |         0 |        16 |        16 |
##              |     0.000 |     1.000 |     0.457 |
##              |     0.000 |     0.533 |           |
##              |     0.000 |     0.457 |           |
## -------------|-----------|-----------|-----------|
## Column Total |         5 |        30 |        35 |
##              |     0.143 |     0.857 |           |
## -------------|-----------|-----------|-----------|
##
##
```

```r
# k=12
prc_test_pred <- knn(train = prostate_train,
                     test = prostate_test,
                     cl = train_labels,
                     k = 12)
CrossTable(x = test_labels, y = prc_test_pred, prop.chisq = FALSE)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  35
##
##
##              | prc_test_pred
##  test_labels |         B |         M | Row Total |
## -------------|-----------|-----------|-----------|
##            B |         5 |        14 |        19 |
##              |     0.263 |     0.737 |     0.543 |
##              |     1.000 |     0.467 |           |
##              |     0.143 |     0.400 |           |
## -------------|-----------|-----------|-----------|
##            M |         0 |        16 |        16 |
##              |     0.000 |     1.000 |     0.457 |
##              |     0.000 |     0.533 |           |
##              |     0.000 |     0.457 |           |
## -------------|-----------|-----------|-----------|
## Column Total |         5 |        30 |        35 |
##              |     0.143 |     0.857 |           |
## -------------|-----------|-----------|-----------|
##
##
```

k=9 produced the least amount of false positives and most accurate results overall, so I would use k=9 for kNN for this dataset.

3. Once you have complete the tutorial, try another kNN implementation from another package, such as the **caret** package. Compare the accuracy of the two implementations.'

```
library(caret)
```

```
## Loading required package: lattice
```

```
##
## Attaching package: 'caret'
```

```
## The following object is masked from 'package:purrr':
##
##     lift
```

Sampling

```
# Split data as training and test set. Using createDataPartition() function from caret
indxTrain <- createDataPartition(y = prostate$diagnosis_result,p = 0.75,list = FALSE)
training <- prostate[indxTrain,]
testing <- prostate[-indxTrain,]

# Check distibution in original data and partitioned data
prop.table(table(prostate$diagnosis_result)) * 100
```

```
##
##  B  M
## 38 62
```

```
prop.table(table(testing$diagnosis_result)) * 100
```

```
##
##    B    M
## 37.5 62.5
```

```
prop.table(table(prostate$diagnosis_result)) * 100
```

```
##
##  B  M
## 38 62
```

Preprocessing

```r
trainX <- training[,names(training) != "diagnosis_result"]
preProcValues <- preProcess(x = trainX, method = c("center", "scale"))
preProcValues
```

```
## Created from 76 samples and 9 variables
##
## Pre-processing:
##   - centered (8)
##   - ignored (1)
##   - scaled (8)
```

Training and train control

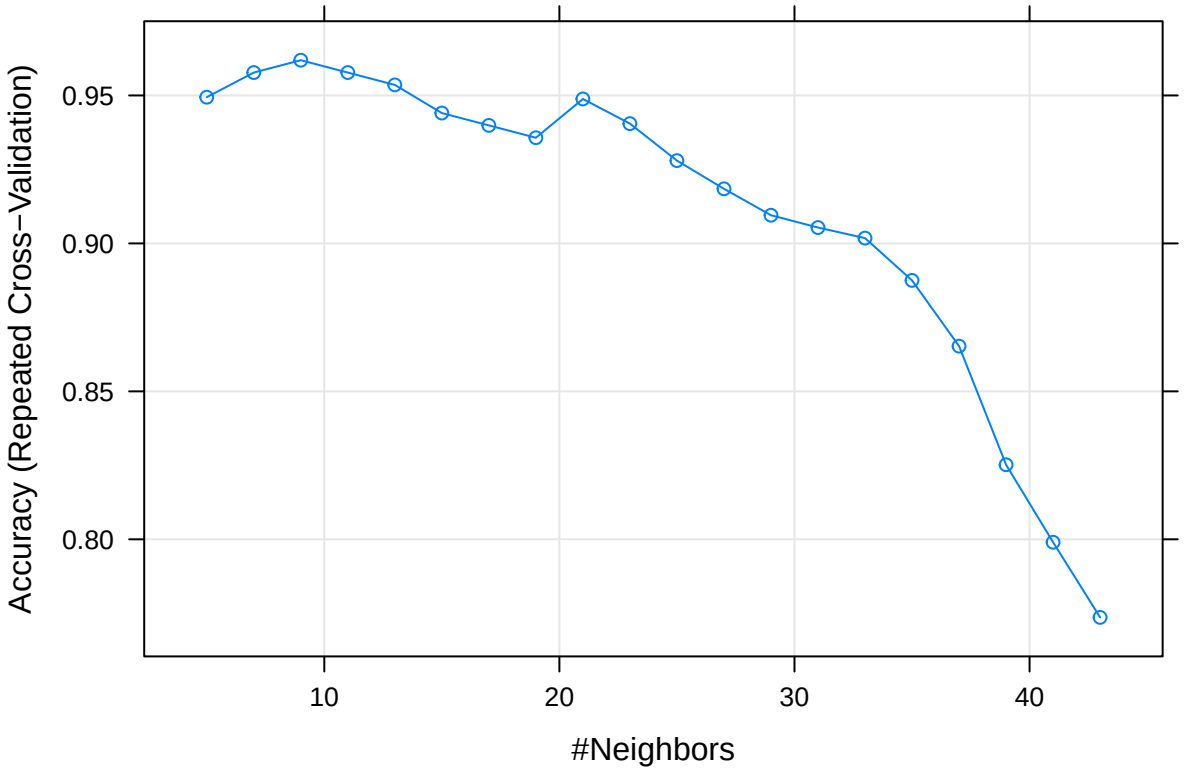
```r
set.seed(400)
ctrl <- trainControl(method="repeatedcv", repeats = 3)
knnFit <- train(diagnosis_result ~ .,
                data = training,
                method = "knn",
                trControl = ctrl,
                preProcess = c("center","scale"),
                tuneLength = 20)

# kNNFit output
knnFit
```

```
## k-Nearest Neighbors
##
## 76 samples
##  9 predictor
##  2 classes: 'B', 'M'
##
## Pre-processing: centered (9), scaled (9)
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 69, 69, 68, 68, 68, 69, ...
## Resampling results across tuning parameters:
##
##   k   Accuracy   Kappa
##    5  0.9494048  0.8785822
##    7  0.9577381  0.8976298
##    9  0.9619048  0.9071536
##   11  0.9577381  0.8976298
##   13  0.9535714  0.8881060
##   15  0.9440476  0.8678162
##   17  0.9398810  0.8568271
##   19  0.9357143  0.8473033
##   21  0.9488095  0.8779611
##   23  0.9404762  0.8589135
##   25  0.9279762  0.8274116
##   27  0.9184524  0.8071218
##   29  0.9095238  0.7874530
```

```
##    31  0.9053571  0.7764640
##    33  0.9017857  0.7627994
##    35  0.8875000  0.7314424
##    37  0.8652778  0.6790614
##    39  0.8251984  0.5763410
##    41  0.7990079  0.5033357
##    43  0.7736111  0.4469255
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was k = 9.
```

```
#Plot yields Number of Neighbors Vs accuracy (based on repeated cross validation)
plot(knnFit)
```



4. Try the *confusionMatrix* function from the **caret** package to determine the accuracy of both algorithms.

```
knnPredict <- predict(knnFit, newdata = testing)

# Get the confusion matrix to see accuracy value and other parameter values
confusionMatrix(knnPredict, as.factor(testing$diagnosis_result))
```

```
## Confusion Matrix and Statistics
##
##           Reference
```

```
## Prediction  B  M
##          B  7  0
##          M  2 15
##
##                Accuracy : 0.9167
##                  95% CI : (0.73, 0.9897)
##     No Information Rate : 0.625
##     P-Value [Acc > NIR] : 0.001448
##
##                   Kappa : 0.814
##
##  Mcnemar's Test P-Value : 0.479500
##
##             Sensitivity : 0.7778
##             Specificity : 1.0000
##          Pos Pred Value : 1.0000
##          Neg Pred Value : 0.8824
##              Prevalence : 0.3750
##          Detection Rate : 0.2917
##    Detection Prevalence : 0.2917
##       Balanced Accuracy : 0.8889
##
##        'Positive' Class : B
##
```

```
mean(knnPredict == testing$diagnosis_result)
```

```
## [1] 0.9166667
```

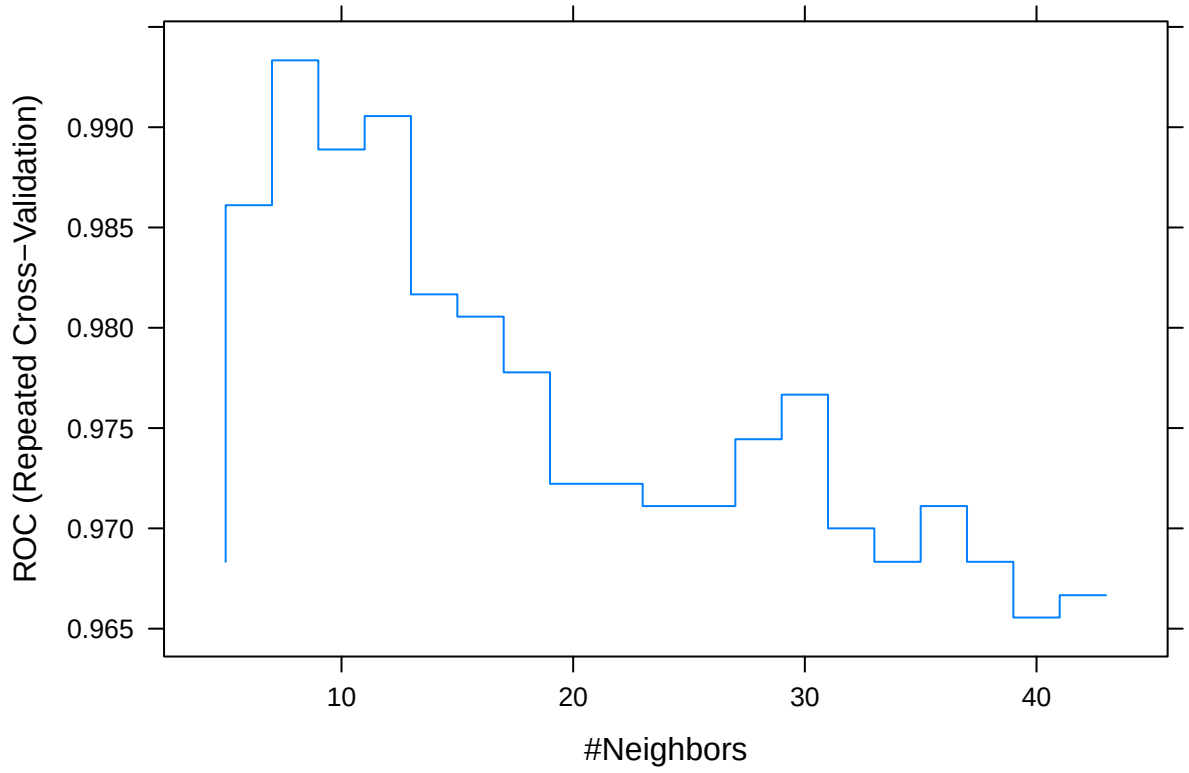
```
# Verify 2 class summary function
ctrl <- trainControl(method="repeatedcv",
                     repeats = 3,
                     classProbs = TRUE,
                     summaryFunction = twoClassSummary)
knnFit <- train(diagnosis_result ~ .,
                data = training,
                method = "knn",
                trControl = ctrl,
                preProcess = c("center","scale"),
                tuneLength = 20)

knnFit
```

```
## k-Nearest Neighbors
##
## 76 samples
##  9 predictor
##  2 classes: 'B', 'M'
##
## Pre-processing: centered (9), scaled (9)
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 68, 68, 68, 69, 70, 69, ...
## Resampling results across tuning parameters:
```

```
##
##    k   ROC        Sens       Spec
##    5  0.9683333  0.9055556  1
##    7  0.9861111  0.8944444  1
##    9  0.9933333  0.8944444  1
##   11  0.9888889  0.8944444  1
##   13  0.9905556  0.8722222  1
##   15  0.9816667  0.8722222  1
##   17  0.9805556  0.8388889  1
##   19  0.9777778  0.8611111  1
##   21  0.9722222  0.8611111  1
##   23  0.9722222  0.8500000  1
##   25  0.9711111  0.8388889  1
##   27  0.9711111  0.8166667  1
##   29  0.9744444  0.7833333  1
##   31  0.9766667  0.7833333  1
##   33  0.9700000  0.7888889  1
##   35  0.9683333  0.8055556  1
##   37  0.9711111  0.7111111  1
##   39  0.9683333  0.6000000  1
##   41  0.9655556  0.4666667  1
##   43  0.9666667  0.3888889  1
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was k = 9.
```

```
plot(knnFit, print.thres = 0.5, type="S")
```




```
knnPredict <- predict(knnFit,newdata = testing)

# Get the confusion matrix to see accuracy value and other parameter values
confusionMatrix(knnPredict, as.factor(testing$diagnosis_result))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##          B  7  0
##          M  2 15
##
##                Accuracy : 0.9167
##                  95% CI : (0.73, 0.9897)
##     No Information Rate : 0.625
##     P-Value [Acc > NIR] : 0.001448
##
##                   Kappa : 0.814
##
##  Mcnemar's Test P-Value : 0.479500
##
##             Sensitivity : 0.7778
##             Specificity : 1.0000
##          Pos Pred Value : 1.0000
##          Neg Pred Value : 0.8824
```

```
##              Prevalence : 0.3750
##          Detection Rate : 0.2917
##    Detection Prevalence : 0.2917
##       Balanced Accuracy : 0.8889
##
##        'Positive' Class : B
##
```

```r
mean(knnPredict == testing$diagnosis_result)
```

```
## [1] 0.9166667
```