```r
# set working directory
setwd("C:/Users/jaosi/Desktop/DS-Projects/graduate-project/prostate-cancer")

# load dataset
APPENC05 <- read.csv("./data/processed/APPENC05.txt")
mydata <- APPENC05
summary(mydata)
```

```
##       Obs     Y_HighGradeCancer    PSALevel          CancerVol
##  Min.   : 1   Min.   :0.0000    Min.   :-2.53370   Min.   :-2.30258
##  1st Qu.:25   1st Qu.:0.0000    1st Qu.:-0.65227   1st Qu.:-0.71613
##  Median :49   Median :0.0000    Median : 0.09702   Median : 0.08555
##  Mean   :49   Mean   :0.2165    Mean   : 0.00000   Mean   : 0.00000
##  3rd Qu.:73   3rd Qu.:0.0000    3rd Qu.: 0.50654   3rd Qu.: 0.66550
##  Max.   :97   Max.   :1.0000    Max.   : 2.70223   Max.   : 2.10683
##      Weight             Age          BenignProstaticHyperplasia
##  Min.   :-2.5953   Min.   :-3.0872   Min.   :-0.8406
##  1st Qu.:-0.5519   1st Qu.:-0.5220   1st Qu.:-0.8406
##  Median :-0.0663   Median : 0.1531   Median :-0.3929
##  Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000
##  3rd Qu.: 0.4597   3rd Qu.: 0.5582   3rd Qu.: 0.7375
##  Max.   : 4.9712   Max.   : 2.0433   Max.   : 2.5678
##  SeminalVesicleInvasion CapsularPenetration
##  Min.   :0.0000         Min.   :-0.5966
##  1st Qu.:0.0000         1st Qu.:-0.5966
##  Median :0.0000         Median :-0.4772
##  Mean   :0.2165         Mean   : 0.0000
##  3rd Qu.:0.0000         3rd Qu.: 0.2681
##  Max.   :1.0000         Max.   : 4.2321
```

```r
View(mydata)
names(mydata)
```

```
## [1] "Obs"                       "Y_HighGradeCancer"
## [3] "PSALevel"                  "CancerVol"
## [5] "Weight"                    "Age"
## [7] "BenignProstaticHyperplasia" "SeminalVesicleInvasion"
## [9] "CapsularPenetration"
```

```r
# load packages
library(caTools)
library(ROCR)
library(ResourceSelection)
```

```
## Warning: package 'ResourceSelection' was built under R version 4.0.3
## ResourceSelection 0.3-5 2019-07-22
```

```r
library(car)
```

```
## Warning: package 'car' was built under R version 4.0.3
## Loading required package: carData
## Warning: package 'carData' was built under R version 4.0.3
```

```r
# declare SeminalVesicleInvasion a categorical variable (SeminalVesicleInvasion == [0, 1])
mydata$SeminalVesicleInvasion <- factor(mydata$SeminalVesicleInvasion)
```

```r
# create training and testing subsets
myseed <- 123
set.seed(myseed)
split <- sample.split(mydata, SplitRatio=0.8)
train <- subset(mydata, split=="TRUE")
test <- subset(mydata, split=="FALSE")

View(train)
View(test)

# write train & test datasets to CSV files
write.csv(train, "./data/processed/train.txt")
write.csv(test, "./data/processed/test.txt")


###################################
### Building Helpful Functions ###
###################################

freq <- function(data) {
  ### function requires one input parameter: data.
  ### this function will display the table of Y_HighGradeCancer counts (frequency table);
  # i.e. the counts of 0's and 1's in the input data.
  ### the function will then display the proportion of 0 to 1 (I already know via
  # previous analysis that the counts of 0's greatly outweigh the count of 1's).
  ### we can consider this proportion to be a "base accuracy" for model comparison;
  # i.e. if the model just predicted 0's (most frequent classification),
  # for all cases.

  name <- deparse(substitute(data))

  if (name=='train') {
    cat('TRAINING DATA\n')
  }
  else {
    cat('TESTING DATA\n')
  }

  freq_tab <- table(data$Y_HighGradeCancer)
  most_freq_prop <- round(sum(freq_tab[1])/sum(freq_tab), 4)
  less_freq_pop <- round(sum(freq_tab[2])/sum(freq_tab), 4)

  # print out both the table, and calculated base accuracy
  cat('Frequency Table:\n')
  print(freq_tab)
  cat('\nThe proportion of 0 to 1 is:', most_freq_prop, '\n')
  cat('The proportion of 1 to 0 is:', less_freq_pop)
}


accuracy <- function(model, data, val=0.50) {
  ### function requires three input parameters: model, data, and decision value boundry
  # (optional); defualt 50%.
```

```
  ### this function will first apply the fitted model and create classifications,
  # then compare to real values (which we know).
  ### the confusion matrix and accuracy score will output to the terminal.
  ### idealy we want the accuracy score to be greater than the base score calculated
  # previously (this indicates the logistic model is a better fit).
  ### decision boundry value may require analysis and adjustments/optimizations afterwards.

  name <- deparse(substitute(data))

  if (name=='train') {
    cat('TRAINING DATA\n')
  }
  else {
    cat('TESTING DATA\n')
  }

  res <- predict(model, data, type="response")
  tab <- table(ActualValue=data$Y_HighGradeCancer, PredictedValue=res>=val)
  err <- round((1-(sum(diag(tab))/sum(tab)))*100, 1)
  acc <- round(sum(diag(tab))/sum(tab)*100, 1)

  # print out confusion matrix, and calculated accuracy
  cat('Prediction Rule:', val, '\n')
  cat('Confusion Matrix:\n', '\n')
  print(tab)
  cat('\nThe calculated error is:', err, '%')
  cat('\nThe calculated accuracy is:', acc, '%')
}



############################
###                      ###
###    Model Fitting     ###
###                      ###
############################

################################################
### Second-Order Polynomial Logistic Models ###
################################################

# fit full second-order logistic model
logit_poly <- glm(Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(CancerVol, 2) +
                    poly(Weight, 2) + poly(Age, 2) + poly(BenignProstaticHyperplasia, 2) +
                    SeminalVesicleInvasion + poly(CapsularPenetration, 2),
                  data=train, family="binomial")
summary(logit_poly)

##
## Call:
## glm(formula = Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(CancerVol,
##     2) + poly(Weight, 2) + poly(Age, 2) + poly(BenignProstaticHyperplasia,
##     2) + SeminalVesicleInvasion + poly(CapsularPenetration, 2),
##     family = "binomial", data = train)
```

```
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.56947  -0.29292  -0.11807  -0.02792   2.70547
##
## Coefficients:
##                                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)                         -3.1879     1.1911  -2.676  0.00744 **
## poly(PSALevel, 2)1                   8.8748     9.4300   0.941  0.34664
## poly(PSALevel, 2)2                   9.9300     9.7971   1.014  0.31079
## poly(CancerVol, 2)1                  9.0626    12.3092   0.736  0.46158
## poly(CancerVol, 2)2                  3.7797     8.9295   0.423  0.67209
## poly(Weight, 2)1                    -1.7984     8.8561  -0.203  0.83908
## poly(Weight, 2)2                   -22.1802    19.1499  -1.158  0.24676
## poly(Age, 2)1                        3.0558     5.5976   0.546  0.58513
## poly(Age, 2)2                        6.6241     4.6130   1.436  0.15102
## poly(BenignProstaticHyperplasia, 2)1   8.0033     7.2503   1.104  0.26966
## poly(BenignProstaticHyperplasia, 2)2   6.8035     6.3958   1.064  0.28745
## SeminalVesicleInvasion1             -0.9176     1.1728  -0.782  0.43397
## poly(CapsularPenetration, 2)1        2.4574     3.9676   0.619  0.53568
## poly(CapsularPenetration, 2)2       -7.9544     4.4302  -1.795  0.07258 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 72.613  on 75  degrees of freedom
## Residual deviance: 33.998  on 62  degrees of freedom
## AIC: 61.998
##
## Number of Fisher Scoring iterations: 8

step(logit_poly, direction="backward")

## Start:  AIC=62
## Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(CancerVol, 2) +
##     poly(Weight, 2) + poly(Age, 2) + poly(BenignProstaticHyperplasia,
##     2) + SeminalVesicleInvasion + poly(CapsularPenetration, 2)
##
##                                     Df Deviance    AIC
## - poly(CancerVol, 2)                 2   35.756 59.756
## - poly(BenignProstaticHyperplasia, 2)  2   35.913 59.913
## - SeminalVesicleInvasion             1   34.644 60.644
## - poly(Weight, 2)                    2   36.698 60.698
## <none>                                   33.998 61.998
## - poly(CapsularPenetration, 2)       2   38.078 62.078
## - poly(Age, 2)                       2   38.511 62.511
## - poly(PSALevel, 2)                  2   40.072 64.072
##
## Step:  AIC=59.76
## Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(Weight, 2) + poly(Age,
##     2) + poly(BenignProstaticHyperplasia, 2) + SeminalVesicleInvasion +
##     poly(CapsularPenetration, 2)
##
```

```
##                                       Df Deviance    AIC
## - poly(BenignProstaticHyperplasia, 2)  2   37.400 57.400
## - poly(Weight, 2)                      2   38.191 58.191
## - SeminalVesicleInvasion               1   36.552 58.552
## <none>                                     35.756 59.756
## - poly(Age, 2)                         2   39.906 59.906
## - poly(CapsularPenetration, 2)         2   42.124 62.124
## - poly(PSALevel, 2)                    2   47.961 67.961
##
## Step:  AIC=57.4
## Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(Weight, 2) + poly(Age,
##     2) + SeminalVesicleInvasion + poly(CapsularPenetration, 2)
##
##                                Df Deviance    AIC
## - poly(Weight, 2)               2   38.338 54.338
## - SeminalVesicleInvasion        1   38.128 56.128
## <none>                              37.400 57.400
## - poly(Age, 2)                  2   43.065 59.065
## - poly(CapsularPenetration, 2)  2   43.734 59.734
## - poly(PSALevel, 2)             2   48.695 64.695
##
## Step:  AIC=54.34
## Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(Age, 2) + SeminalVesicleInvasion +
##     poly(CapsularPenetration, 2)
##
##                                Df Deviance    AIC
## - SeminalVesicleInvasion        1   38.900 52.900
## <none>                              38.338 54.338
## - poly(Age, 2)                  2   44.099 56.099
## - poly(CapsularPenetration, 2)  2   46.605 58.605
## - poly(PSALevel, 2)             2   51.230 63.230
##
## Step:  AIC=52.9
## Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(Age, 2) + poly(CapsularPenetration,
##     2)
##
##                                Df Deviance    AIC
## <none>                              38.900 52.900
## - poly(Age, 2)                  2   44.200 54.200
## - poly(CapsularPenetration, 2)  2   46.739 56.739
## - poly(PSALevel, 2)             2   51.888 61.888
##
## Call:  glm(formula = Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(Age,
##     2) + poly(CapsularPenetration, 2), family = "binomial", data = train)
##
## Coefficients:
##                   (Intercept)             poly(PSALevel, 2)1
##                        -2.604                         12.807
##            poly(PSALevel, 2)2                 poly(Age, 2)1
##                         7.005                          2.768
##                 poly(Age, 2)2  poly(CapsularPenetration, 2)1
##                         6.363                          4.741
## poly(CapsularPenetration, 2)2
```

```
##                       -8.417
##
## Degrees of Freedom: 75 Total (i.e. Null);  69 Residual
## Null Deviance:     72.61
## Residual Deviance: 38.9  AIC: 52.9
```

```
# use second-order reduced model setup for quick analysis of adding/removing predictors
logit_poly_red <- glm(Y_HighGradeCancer ~
                        poly(PSALevel, 2)
                      + poly(CancerVol, 2)
                      # + poly(Weight, 2)
                      # + poly(Age, 2)
                      # + poly(BenignProstaticHyperplasia, 2)
                      # + poly(SeminalVesicleInvasion, 2)
                      #  + poly(CapsularPenetration, 2)
                      , data=train, family="binomial")
summary(logit_poly_red)
```

```
##
## Call:
## glm(formula = Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(CancerVol,
##     2), family = "binomial", data = train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.65643  -0.46122  -0.20861  -0.01794   2.41869
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -2.9802     1.2771  -2.334   0.0196 *
## poly(PSALevel, 2)1    9.0035     8.1120   1.110   0.2670
## poly(PSALevel, 2)2    0.6259     7.4678   0.084   0.9332
## poly(CancerVol, 2)1  17.9731    14.8783   1.208   0.2270
## poly(CancerVol, 2)2  -3.3028    10.0734  -0.328   0.7430
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 72.613  on 75  degrees of freedom
## Residual deviance: 44.511  on 71  degrees of freedom
## AIC: 54.511
##
## Number of Fisher Scoring iterations: 8
```

```
step(logit_poly_red, direction="backward")
```

```
## Start:  AIC=54.51
## Y_HighGradeCancer ~ poly(PSALevel, 2) + poly(CancerVol, 2)
##
##                      Df Deviance    AIC
## - poly(PSALevel, 2)   2   48.120 54.120
## <none>                    44.511 54.511
## - poly(CancerVol, 2)  2   50.767 56.767
##
```

```
## Step:  AIC=54.12
## Y_HighGradeCancer ~ poly(CancerVol, 2)
##
##                       Df Deviance    AIC
## <none>                     48.120 54.120
## - poly(CancerVol, 2)  2   72.613 74.613
##
## Call:  glm(formula = Y_HighGradeCancer ~ poly(CancerVol, 2), family = "binomial",
##     data = train)
##
## Coefficients:
##         (Intercept)  poly(CancerVol, 2)1  poly(CancerVol, 2)2
##             -2.6364              20.0802              -0.4743
##
## Degrees of Freedom: 75 Total (i.e. Null);  73 Residual
## Null Deviance:     72.61
## Residual Deviance: 48.12  AIC: 54.12
```

```
####################################
### First-Order Logistic Models ###
####################################

# fit full first-order logistic model
logit_full <- glm(Y_HighGradeCancer ~ PSALevel + CancerVol + Weight +
                    Age + BenignProstaticHyperplasia +
                    SeminalVesicleInvasion + CapsularPenetration, data=train,
                  family="binomial")
summary(logit_full)
```

```
##
## Call:
## glm(formula = Y_HighGradeCancer ~ PSALevel + CancerVol + Weight +
##     Age + BenignProstaticHyperplasia + SeminalVesicleInvasion +
##     CapsularPenetration, family = "binomial", data = train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.66861  -0.39211  -0.18721  -0.02467   2.17445
##
## Coefficients:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -2.84305    0.75774  -3.752 0.000175 ***
## PSALevel                    1.28155    0.74609   1.718 0.085856 .
## CancerVol                   1.40464    0.90103   1.559 0.119014
## Weight                     -0.17618    0.75535  -0.233 0.815567
## Age                         0.56784    0.43547   1.304 0.192245
## BenignProstaticHyperplasia  0.07823    0.54237   0.144 0.885320
## SeminalVesicleInvasion1    -0.38818    1.04075  -0.373 0.709164
## CapsularPenetration         0.25330    0.44939   0.564 0.572988
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
```

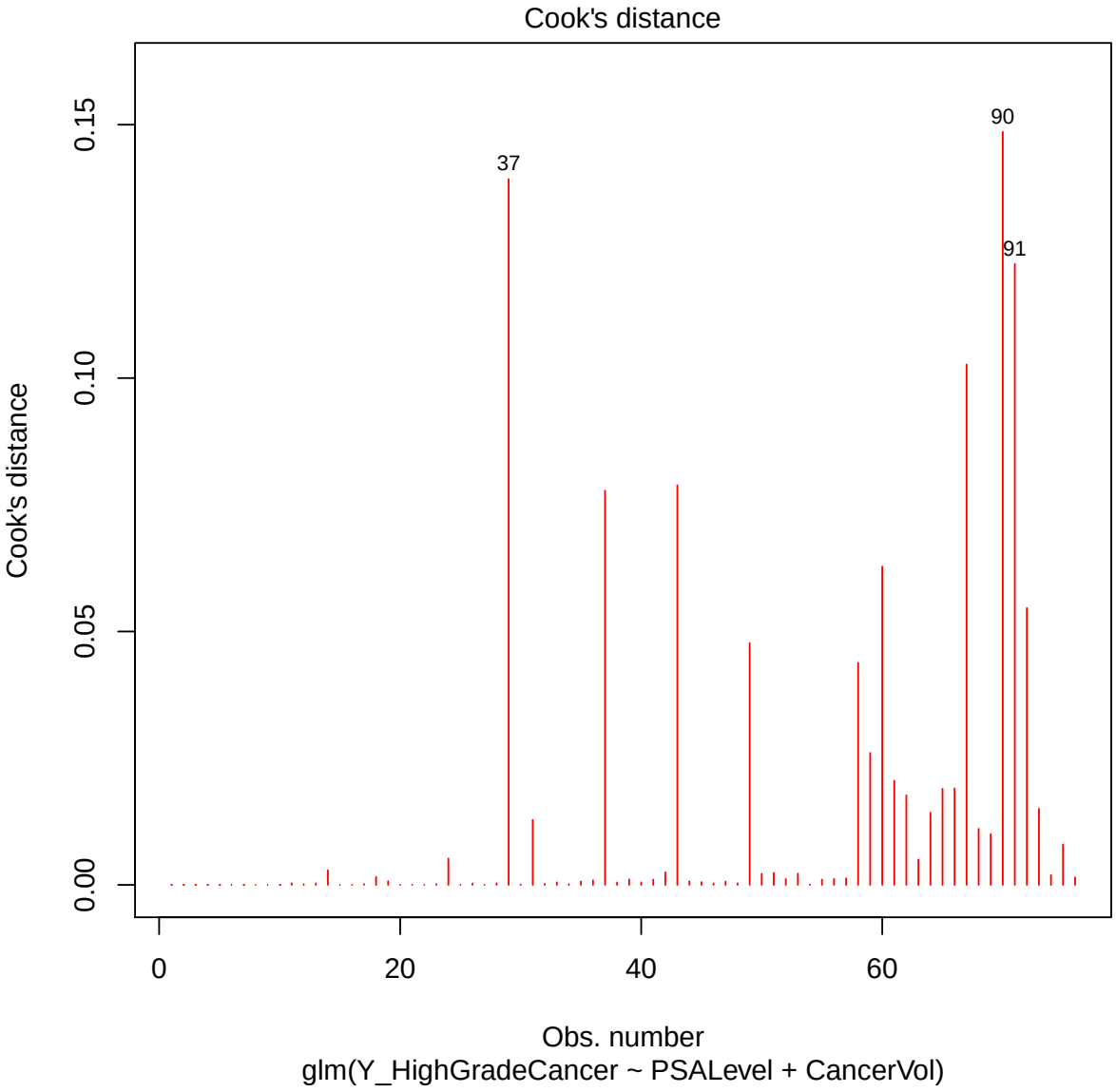
```
##     Null deviance: 72.613  on 75  degrees of freedom
## Residual deviance: 42.303  on 68  degrees of freedom
## AIC: 58.303
##
## Number of Fisher Scoring iterations: 7
```

```
step(logit_full, direction="backward")
```

```
## Start:  AIC=58.3
## Y_HighGradeCancer ~ PSALevel + CancerVol + Weight + Age + BenignProstaticHyperplasia +
##     SeminalVesicleInvasion + CapsularPenetration
##
##                              Df Deviance    AIC
## - BenignProstaticHyperplasia  1   42.324 56.324
## - Weight                      1   42.358 56.358
## - SeminalVesicleInvasion      1   42.444 56.444
## - CapsularPenetration         1   42.627 56.627
## - Age                         1   43.954 57.954
## <none>                            42.303 58.303
## - CancerVol                   1   45.225 59.225
## - PSALevel                    1   45.903 59.903
##
## Step:  AIC=56.32
## Y_HighGradeCancer ~ PSALevel + CancerVol + Weight + Age + SeminalVesicleInvasion +
##     CapsularPenetration
##
##                          Df Deviance    AIC
## - Weight                  1   42.358 54.358
## - SeminalVesicleInvasion  1   42.499 54.499
## - CapsularPenetration     1   42.695 54.695
## - Age                     1   44.044 56.044
## <none>                        42.324 56.324
## - CancerVol               1   45.389 57.389
## - PSALevel                1   46.031 58.031
##
## Step:  AIC=54.36
## Y_HighGradeCancer ~ PSALevel + CancerVol + Age + SeminalVesicleInvasion +
##     CapsularPenetration
##
##                          Df Deviance    AIC
## - SeminalVesicleInvasion  1   42.522 52.522
## - CapsularPenetration     1   42.755 52.755
## - Age                     1   44.151 54.151
## <none>                        42.358 54.358
## - CancerVol               1   45.390 55.390
## - PSALevel                1   46.059 56.059
##
## Step:  AIC=52.52
## Y_HighGradeCancer ~ PSALevel + CancerVol + Age + CapsularPenetration
##
##                       Df Deviance    AIC
## - CapsularPenetration  1   42.780 50.780
## - Age                  1   44.168 52.168
## <none>                     42.522 52.522
```

```
## - CancerVol            1   45.558 53.558
## - PSALevel             1   46.285 54.285
##
## Step:  AIC=50.78
## Y_HighGradeCancer ~ PSALevel + CancerVol + Age
##
##             Df Deviance    AIC
## - Age        1   44.628 50.628
## <none>           42.780 50.780
## - PSALevel   1   46.445 52.445
## - CancerVol  1   48.777 54.777
##
## Step:  AIC=50.63
## Y_HighGradeCancer ~ PSALevel + CancerVol
##
##             Df Deviance    AIC
## <none>           44.628 50.628
## - PSALevel   1   48.123 52.123
## - CancerVol  1   50.767 54.767
##
## Call:  glm(formula = Y_HighGradeCancer ~ PSALevel + CancerVol, family = "binomial",
##     data = train)
##
## Coefficients:
## (Intercept)     PSALevel    CancerVol
##      -2.687        1.058        1.550
##
## Degrees of Freedom: 75 Total (i.e. Null);  73 Residual
## Null Deviance:     72.61
## Residual Deviance: 44.63  AIC: 50.63

# use reduced model setup for quick analysis of adding/removing predictors
logit_red <- glm(Y_HighGradeCancer ~
                   PSALevel
                 + CancerVol
                 # + Weight
                 # + Age
                 # + BenignProstaticHyperplasia
                 # + SeminalVesicleInvasion
                 # + CapsularPenetration
                 , data=train, family="binomial")
summary(logit_red)

##
## Call:
## glm(formula = Y_HighGradeCancer ~ PSALevel + CancerVol, family = "binomial",
##     data = train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.73560  -0.43637  -0.23378  -0.03521   2.42555
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)  -2.6867     0.6186  -4.343 1.41e-05 ***
## PSALevel      1.0577     0.6198   1.707   0.0879 .
## CancerVol     1.5502     0.6859   2.260   0.0238 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 72.613  on 75  degrees of freedom
## Residual deviance: 44.628  on 73  degrees of freedom
## AIC: 50.628
##
## Number of Fisher Scoring iterations: 6

########################################
###                                  ###
###    Model Checking and Validation   ###
###                                  ###
########################################

#####################################################################
### Cook's Distance Diagnostics for Influential Observations ###
#####################################################################
plot(logit_red, pch=18, col="red", which=c(4))
```




```
myCDs <- sort(round(cooks.distance(logit_red), 5), decreasing=TRUE)
myCDs
```

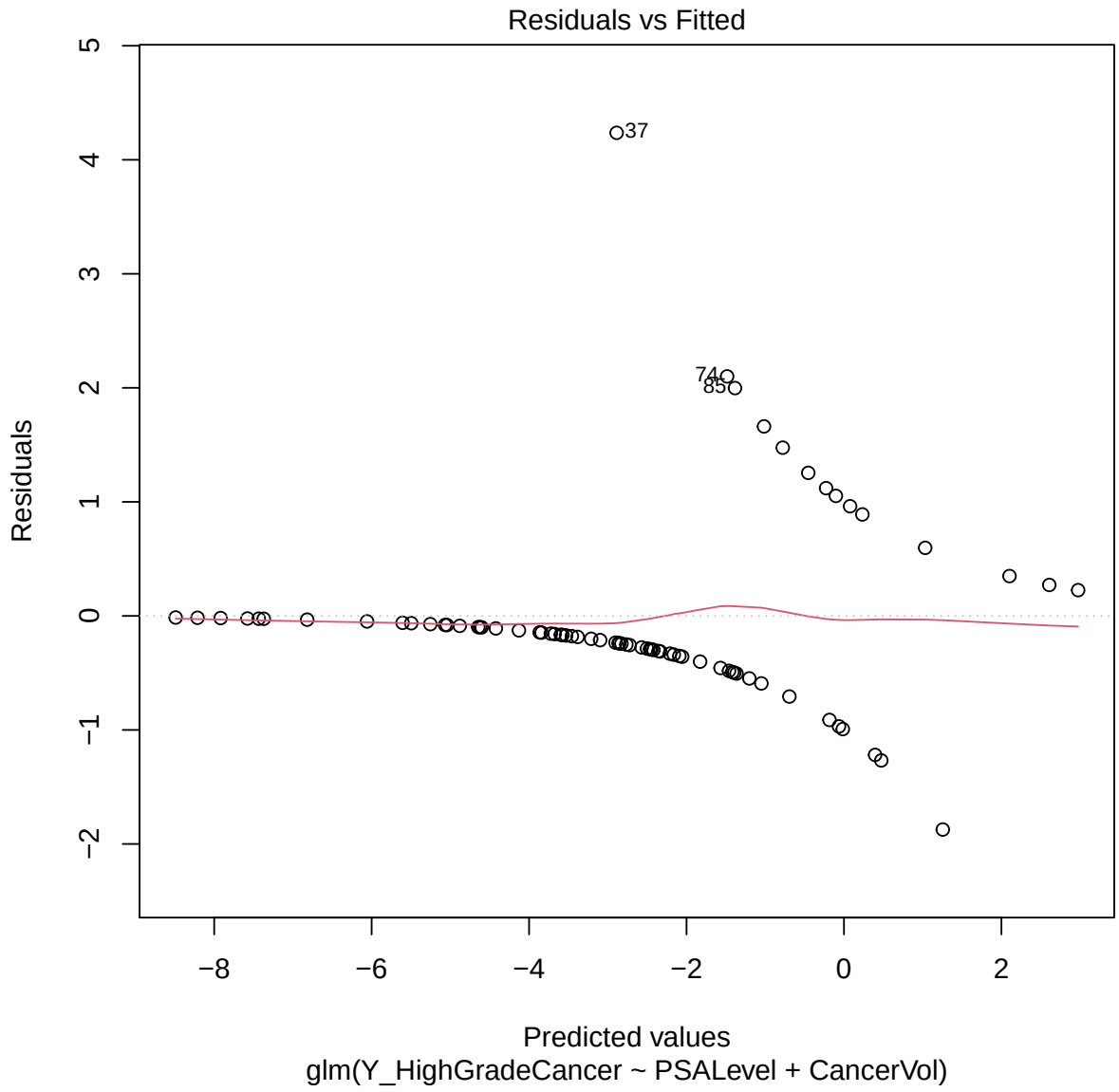
```
##      90      37      91      85      55      47      76      92      63      74
## 0.14859 0.13928 0.12254 0.10270 0.07886 0.07780 0.06282 0.05464 0.04771 0.04380
##      75      78      84      83      79      93      82      39      87      88
## 0.02604 0.02058 0.01905 0.01897 0.01768 0.01504 0.01424 0.01284 0.01107 0.01004
##      96      30      81      18      54      65      67      64      94      22
## 0.00797 0.00521 0.00500 0.00290 0.00251 0.00238 0.00224 0.00221 0.00196 0.00158
##      97      73      72      66      49      70      52      46      24      56
## 0.00149 0.00131 0.00119 0.00116 0.00110 0.00106 0.00105 0.00092 0.00073 0.00071
##      45      60      57      42      51      48      13      36      16      61
## 0.00069 0.00066 0.00057 0.00052 0.00052 0.00048 0.00034 0.00033 0.00032 0.00031
##      33      58      40      21      29      15      43      38      69      27
```

```
## 0.00029 0.00028 0.00018 0.00015 0.00015 0.00014 0.00014 0.00009 0.00008 0.00005
##      25      31      34       7      20      10      11      28       1       2
## 0.00004 0.00004 0.00003 0.00002 0.00002 0.00001 0.00001 0.00001 0.00000 0.00000
##       3       4       6       9      12      19
## 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000
```

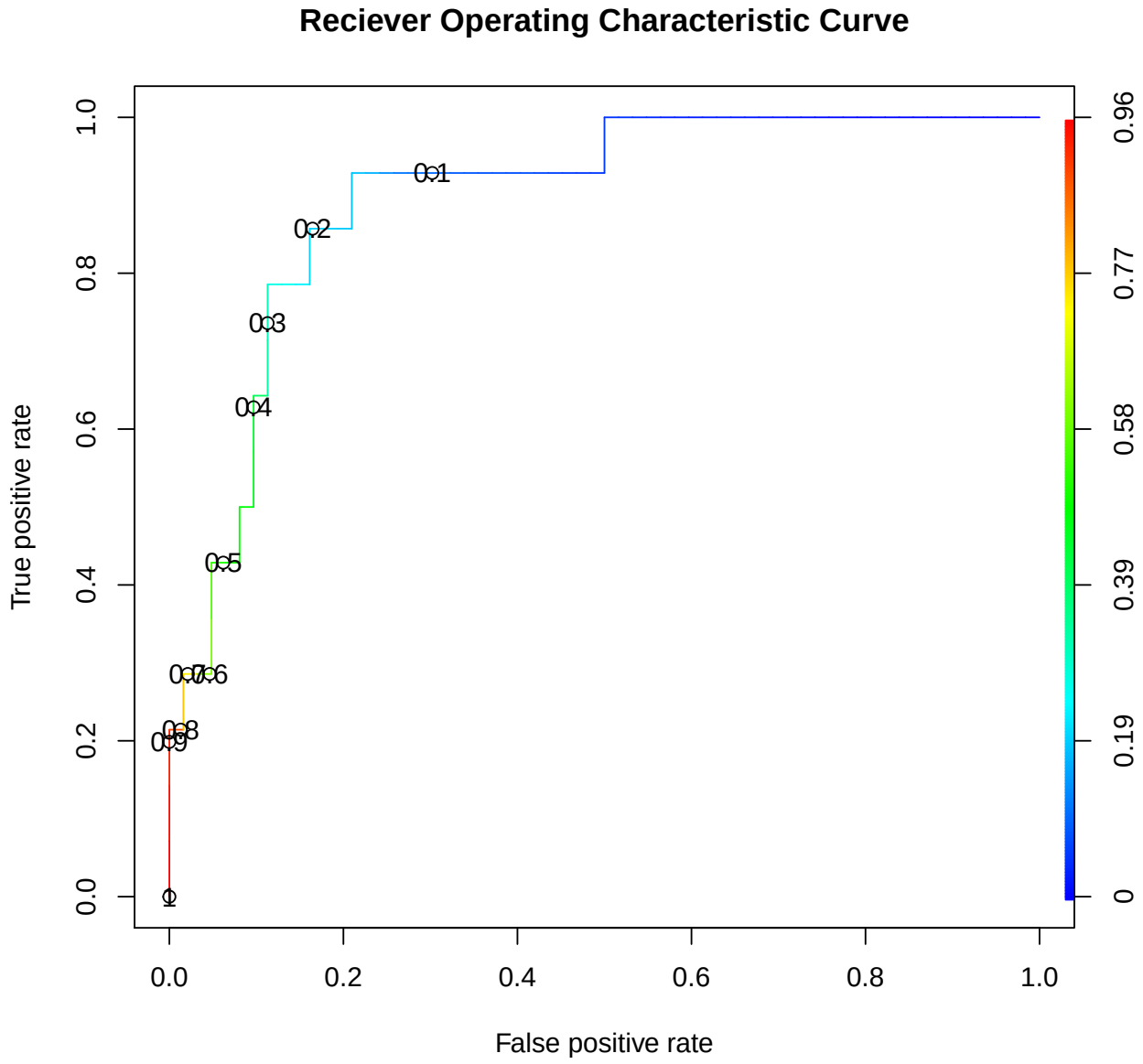
```
# drop rows for model building (influential observations)
# this step will be visited within Coook's Distance analysis
train_trim <- subset(train, Obs != 90
                     #  & Obs != 37
                     #  & Obs != 91
)

# view the trimmed data
View(train_trim)

# write train_trim dataset to csv file
write.csv(train_trim, "./data/processed/train_trim.txt")

# re-fit the logistic model
logit_red_trim <- glm(Y_HighGradeCancer ~
                        PSALevel
                      + CancerVol
                      # + Weight
                      # + Age
                      # + BenignProstaticHyperplasia
                      # + SeminalVesicleInvasion
                      # + CapsularPenetration
                      , data=train_trim, family="binomial")
summary(logit_red_trim)
```

```
##
## Call:
## glm(formula = Y_HighGradeCancer ~ PSALevel + CancerVol, family = "binomial",
##     data = train_trim)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.71156  -0.43371  -0.20855  -0.03378   2.46797
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.9030     0.6907  -4.203 2.63e-05 ***
## PSALevel      0.7495     0.6120   1.225   0.2207
## CancerVol     1.9077     0.7711   2.474   0.0134 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 69.170  on 74  degrees of freedom
## Residual deviance: 41.576  on 72  degrees of freedom
## AIC: 47.576
##
```

```
## Number of Fisher Scoring iterations: 6

# RESULT: the removal of these rows did not improve the model.
# continue forward with original logit_red model

##############################################
### Hosmer-Lemeshow Goodness of Fit Test ###
##############################################

gof <- hoslem.test(logit_red$y, fitted(logit_red), g=5) # choosing 5 groups
cbind(gof$expected, gof$observed)

##                         yhat0      yhat1 y0 y1
## [0.000206,0.00973] 15.941605 0.05839507 16  0
## (0.00973,0.0521]   14.592690 0.40730980 15  0
## (0.0521,0.103]     13.898096 1.10190404 14  1
## (0.103,0.333]      11.889917 3.11008275 11  4
## (0.333,0.951]       5.677692 9.32230835  6  9

gof

##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  logit_red$y, fitted(logit_red)
## X-squared = 0.83815, df = 3, p-value = 0.8403

#######################
### vizualizations ###
#######################

# Residuals vs. Fitted
# Normal Q-Q
# scale-location (Predicted Values vs. sqrt[Std. Pearson Residuals])
# Residuals vs. Leverage
# residualPlot(logit_red, type="pearson")
plot(logit_red, which=c(1))
```




```
### build and plot ROC curve ###
pred <- predict(logit_red, train, type="response")
ROCRPred <- prediction(pred, train$Y_HighGradeCancer)
ROCRPref <- performance(ROCRPred, "tpr", "fpr")
plot(ROCRPref, colorize=TRUE, print.cutoffs.at=seq(0.1, by=0.1),
     main="Reciever Operating Characteristic Curve")
```




```
###################################
### Accuracy Model Comparisons ###
###################################

### invoke functions ###
freq(train)

## TRAINING DATA
## Frequency Table:
##
##  0  1
## 62 14
##
## The proportion of 0 to 1 is: 0.8158
```

```
## The proportion of 1 to 0 is: 0.1842
```

```
accuracy(logit_red, train, 0.184) # starting point prediction rule
```

```
## TRAINING DATA
## Prediction Rule: 0.184
## Confusion Matrix:
##
##             PredictedValue
## ActualValue FALSE TRUE
##           0    49   13
##           1     1   13
##
## The calculated error is: 18.4 %
## The calculated accuracy is: 81.6 %
```

```
accuracy(logit_red, train, 0.20) # final prediction rule
```

```
## TRAINING DATA
## Prediction Rule: 0.2
## Confusion Matrix:
##
##             PredictedValue
## ActualValue FALSE TRUE
##           0    52   10
##           1     2   12
##
## The calculated error is: 15.8 %
## The calculated accuracy is: 84.2 %
```

```
#########################
###                   ###
###    Final Model    ###
###                   ###
#########################

# no changes have been made from the reduced model
logit_final <- logit_red
summary(logit_final)
```

```
##
## Call:
## glm(formula = Y_HighGradeCancer ~ PSALevel + CancerVol, family = "binomial",
##     data = train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.73560  -0.43637  -0.23378  -0.03521   2.42555
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.6867     0.6186  -4.343 1.41e-05 ***
## PSALevel      1.0577     0.6198   1.707   0.0879 .
## CancerVol     1.5502     0.6859   2.260   0.0238 *
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 72.613  on 75  degrees of freedom
## Residual deviance: 44.628  on 73  degrees of freedom
## AIC: 50.628
##
## Number of Fisher Scoring iterations: 6

########################################
###                                  ###
###    Model Validation: Test Data   ###
###                                  ###
########################################

###################################
### Accuracy Model Comparisons ###
###################################

### invoke functions ###
freq(test)

## TESTING DATA
## Frequency Table:
##
##  0  1
## 14  7
##
## The proportion of 0 to 1 is: 0.6667
## The proportion of 1 to 0 is: 0.3333

accuracy(logit_final, test, 0.20)

## TESTING DATA
## Prediction Rule: 0.2
## Confusion Matrix:
##
##            PredictedValue
## ActualValue FALSE TRUE
##           0    13    1
##           1     2    5
##
## The calculated error is: 14.3 %
## The calculated accuracy is: 85.7 %
```