## Classification

Tyler Frankenberg 3/20/2022

# Import packages

```
library(tidyverse)
library(pROC)
library(caret)
```

# Import and examine data

```
url <- "https://raw.githubusercontent.com/curdferguson/data621/main/datasets/classification-outp
ut-data.csv"

class_raw <- read_csv(url, col_names = TRUE)
head(class_raw)</pre>
```

```
## # A tibble: 6 x 11
     pregnant glucose diastolic skinfold insulin
##
                                                  bmi pedigree
                                                                  age class
                                                          <dbl> <dbl> <dbl>
        <dbl>
                          <dbl>
                                  <dbl>
                                          <dbl> <dbl>
##
               <dbl>
                 124
                                      33
                                             215 25.5
                                                          0.161
                                                                   37
## 1
## 2
            2
                 122
                            76
                                      27
                                            200 35.9
                                                         0.483
                                                                  26
                                                                          0
## 3
            3
                  107
                                      13
                                            48 22.9
                                                                   23
                            62
                                                          0.678
                                                                          1
## 4
            1
                   91
                            64
                                      24
                                              0 29.2
                                                          0.192
                                                                  21
## 5
            4
                   83
                            86
                                      19
                                              0 29.3
                                                          0.317
                                                                   34
## 6
            1
                  100
                            74
                                      12
                                             46 19.5
                                                          0.149
                                                                  28
## # ... with 2 more variables: scored.class <dbl>, scored.probability <dbl>
```

```
summary(class_raw)
```

```
diastolic
                                                         skinfold
##
       pregnant
                        glucose
   Min. : 0.000
                            : 57.0
                                            : 38.0
                                                             : 0.0
##
                     Min.
                                     Min.
                                                      Min.
    1st Qu.: 1.000
                     1st Qu.: 99.0
                                     1st Qu.: 64.0
                                                      1st Qu.: 0.0
##
   Median : 3.000
##
                     Median :112.0
                                     Median : 70.0
                                                     Median :22.0
         : 3.862
   Mean
                            :118.3
                                            : 71.7
##
                     Mean
                                     Mean
                                                      Mean
                                                             :19.8
    3rd Qu.: 6.000
                     3rd Qu.:136.0
                                     3rd Qu.: 78.0
                                                      3rd Qu.:32.0
                            :197.0
##
   Max.
           :15.000
                     Max.
                                     Max.
                                            :104.0
                                                      Max.
                                                             :54.0
##
       insulin
                          bmi
                                        pedigree
                                                            age
   Min.
         : 0.00
                                             :0.0850
##
                     Min.
                            :19.40
                                     Min.
                                                       Min.
                                                              :21.00
##
    1st Qu.: 0.00
                     1st Qu.:26.30
                                     1st Qu.:0.2570
                                                       1st Qu.:24.00
   Median: 0.00
                                     Median :0.3910
                     Median :31.60
                                                       Median:30.00
##
   Mean
         : 63.77
                            :31.58
                                     Mean
                                             :0.4496
                                                              :33.31
##
                     Mean
                                                       Mean
    3rd Qu.:105.00
                     3rd Qu.:36.00
                                     3rd Qu.:0.5800
                                                       3rd Qu.:41.00
##
##
   Max.
           :543.00
                     Max.
                            :50.00
                                     Max.
                                             :2.2880
                                                       Max.
                                                              :67.00
##
        class
                      scored.class
                                      scored.probability
   Min.
                                              :0.02323
##
           :0.0000
                     Min.
                            :0.0000
                                      Min.
   1st Qu.:0.0000
                     1st Qu.:0.0000
                                      1st Qu.:0.11702
##
   Median :0.0000
                     Median :0.0000
                                      Median :0.23999
##
                            :0.1768
   Mean
         :0.3149
##
                     Mean
                                      Mean
                                              :0.30373
    3rd Qu.:1.0000
                     3rd Qu.:0.0000
                                      3rd Qu.:0.43093
   Max.
           :1.0000
                     Max.
                            :1.0000
                                              :0.94633
##
                                      Max.
```

### **Contingency Function**

```
contingency <- function(df) {</pre>
    df1 <- data_frame(df)</pre>
    colnames(df1) <- c("class", "scored.class", "scored.prob")</pre>
    ct <- with(df1, table(df1$class, df1$scored.class, dnn= c("class", "scored.class")))</pre>
    cat("Contingency Table:", "\n")
    cat("\n")
    print(ct)
    tp <- ct[2, 2]
    tn <- ct[1, 1]
    fp <- ct[1, 2]
    fn <- ct[2, 1]
    total <- sum(ct)
    acc <- (tp + tn) / total
    err <- (fp + fn) / total
    cat("\n")
    cat("Accuracy: ", acc, "\n")
    cat("Classification Error Rate: ", err, "\n")
    if (acc + err != 1) {
      cat("\n")
      cat("...")
      cat("ERROR: Accuracy and Error do not sum to 1")
      break
    } else {
      prec <- tp / (tp + fp)</pre>
      sens <- tp / (tp + fn)
      spec <- tn / (tn + fp)
      f1 <- (2 * prec * sens) / (prec + sens)
      cat("...", "\n")
      cat("Precision: ", prec, "\n")
      cat("Sensitivity: ", sens, "\n")
      cat("Specificity: ", spec, "\n")
      cat("F1 Score: ", f1, "\n")
    }
}
class_df <- data_frame(as_factor(class_raw$class),</pre>
                        as_factor(class_raw$scored.class),
                   class_raw$scored.probability)
colnames(class_df) <- c("class", "scored.class", "scored.prob")</pre>
contingency(class_df)
```

```
## Contingency Table:
##
##
        scored.class
## class
           0
              1
##
       0 119
              5
       1 30 27
##
##
## Accuracy:
               0.8066298
## Classification Error Rate: 0.1933702
## ...
## Precision:
                0.84375
## Sensitivity: 0.4736842
## Specificity: 0.9596774
## F1 Score:
                 0.6067416
```

confusionMatrix(class\_df\$scored.class, reference=class\_df\$class)

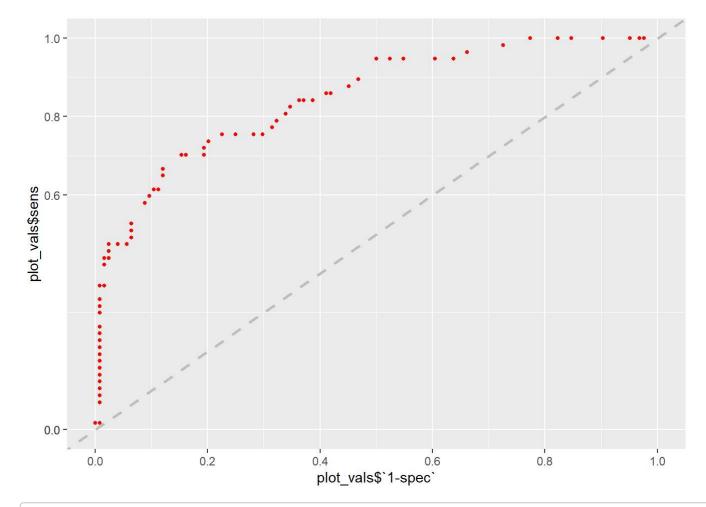
```
## Confusion Matrix and Statistics
##
##
             Reference
## Prediction
                0
                    1
##
            0 119
                   30
                   27
##
##
##
                  Accuracy : 0.8066
                    95% CI : (0.7415, 0.8615)
##
       No Information Rate: 0.6851
##
##
       P-Value [Acc > NIR] : 0.0001712
##
##
                     Kappa : 0.4916
##
##
    Mcnemar's Test P-Value : 4.976e-05
##
               Sensitivity: 0.9597
##
               Specificity: 0.4737
##
##
            Pos Pred Value : 0.7987
            Neg Pred Value: 0.8438
##
                Prevalence: 0.6851
##
##
            Detection Rate: 0.6575
##
      Detection Prevalence : 0.8232
##
         Balanced Accuracy: 0.7167
##
          'Positive' Class : 0
##
##
```

#### **ROC Curve Function**

```
df2 <- data_frame(class_df)</pre>
colnames(df2) <- c("class", "scored.class", "scored.prob")</pre>
scored.class_list <- lapply(seq(0.03, 0.94, 0.01), function(i) {</pre>
  i = if_else(df2$scored.prob >= i, 1, 0) })
ct_list <- lapply(scored.class_list, function(j) {</pre>
  table(df2$class, j, dnn= c("class", paste0("scored.class_")))
})
tp_list <- lapply(seq(1, 92, 1), function(k) {</pre>
  ct_list[[k]][4]
})
tn_list <- lapply(seq(1, 92, 1), function(k) {</pre>
  ct_list[[k]][1]
})
fp_list <- lapply(seq(1, 92, 1), function(k) {</pre>
 ct_list[[k]][3]
})
fn_list <- lapply(seq(1, 92, 1), function(k) {</pre>
  ct list[[k]][2]
})
plot_vals <- data_frame(index = seq(3, 94, 1),</pre>
                         threshold = seq(0.03, 0.94, 0.01),
                         tp = unlist(tp_list),
                         tn = unlist(tn list),
                         fp = unlist(fp_list),
                         fn = unlist(fn_list),
                         sens = tp / (tp + fn),
                         spec = tn / (tn + fp),
                         `1-spec` = 1 - spec)
roc_plot <- ggplot(plot_vals, aes(x=plot_vals$`1-spec`, y=plot_vals$sens)) +</pre>
        geom_point(col="red", size = 1) +
        scale x continuous(limits=c(0.0, 1.0), breaks=c(0, 0.20, 0.40, 0.60, 0.80, 1)) +
        scale_y_continuous(limits=c(0.0, 1.0), breaks=c(0, 0,20, 0,40, 0.60, 0.80, 1)) +
        geom_abline(slope = 1, intercept = 0, col="gray", size=1, linetype="dashed")
roc plot
```

```
## Warning: Use of `plot_vals$`1-spec`` is discouraged. Use `1-spec` instead.
```

## Warning: Use of `plot\_vals\$sens` is discouraged. Use `sens` instead.



## Setting direction: controls > cases

auc(rocCurve)

## Area under the curve: 0.8503

plot.roc(rocCurve)

