# My Document

Me

### Today

```
1<-load("recovery.Rdata")</pre>
dat <- eval(parse(text = 1))%>%
 mutate(study = factor(study))
head(dat)
    id age gender race smoking height weight bmi hypertension diabetes SBP LDL
           0
                                                                0 120 97
## 1 1 56
                  1
                          2 170.2 78.7 27.2 0
                                                   1 0 134 112
1 0 131 88
0 0 115 87
0 0 127 118
0 0 129 104
## 2 2 70
                                   73.1 25.4
             1 1
                           1 169.6
## 3 3 57
             1 1
                           0 168.4 77.4 27.3
             0 1
## 4 4 53
                          0 166.7
                                   76.1 27.4
                                   70.2 23.3
## 5 5 59
             1 1
                           2 173.6
## 6 6 60
              1 3
                           1 162.8 75.1 28.4
## vaccine severity study recovery_time
## 1
      0
            O A
## 2
        0
                O A
                                   44
## 3
        1
                                 29
                1 A
O A
## 4
        0
                                  47
## 5
         1
                                   40
## 6
                                   34
set.seed(5296)
data.1 <- dat[sample(1:10000, 2000),]</pre>
set.seed(5095)
data.2 <- dat[sample(1:10000, 2000),]</pre>
reco.data<-rbind(data.1, data.2)%>%
 unique.array()%>%
 dplyr::select(-id)
head(reco.data)
       age gender race smoking height weight bmi hypertension diabetes SBP LDL
## 6338 61
                          0 171.5
                                   73.9 25.1
               0
                   1
                                                  1
                                                                0 133 118
                                                 0 0 127 120
1 0 133 118
1 0 134 124
1 0 135 141
               1 1
## 6800 57
                           0 169.7
                                    74.5 25.9
                         0 165.9
## 4395 56
             1 1
                                   92.1 33.5
## 4128 68
             1 3
                         0 177.7 84.5 26.8
             1 4 0 165.2
                                   83.5 30.6
## 6589 61
```

```
## 7384 62 1 1 0 175.0 86.1 28.1
                                                   1 0 144 88
##
       vaccine severity study recovery_time
## 6338
          0
                    0
## 6800
                      0
                             В
                                         28
              1
                             В
## 4395
              0
                      0
                                         109
## 4128
              1
                      0 B
                                         24
## 6589
              1
                      0
                            В
                                          98
## 7384
                      0
              1
                             В
                                           8
reco.data.bin<-reco.data%>%
  mutate(recovery_time = factor(ifelse(recovery_time>30, "long", "short")))
set.seed(2023)
rowtrain <- createDataPartition(y=reco.data.bin$recovery_time, p=0.8, list=FALSE)</pre>
training_set.bin <- reco.data.bin[rowtrain,]</pre>
test_set.bin <- reco.data.bin[-rowtrain,]</pre>
x_train.bin <- model.matrix(recovery_time~.,training_set.bin)[,-1]</pre>
y_train.bin <- training_set.bin$recovery_time</pre>
x_test.bin <- model.matrix(recovery_time~.,test_set.bin)[,-1]</pre>
y_test.bin <- test_set.bin$recovery_time</pre>
```

#### EDA

```
table(y_train.bin)

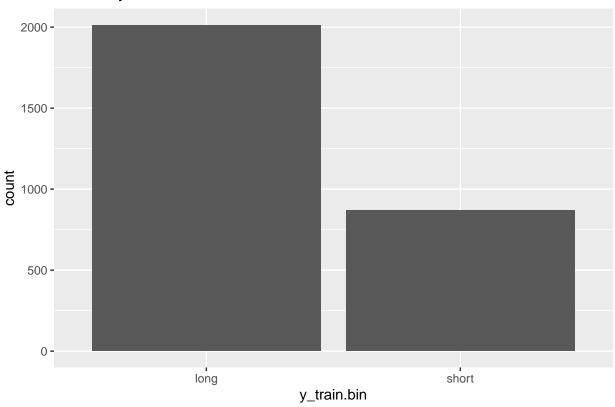
## y_train.bin

## long short

## 2012 870

ggplot(training_set.bin, aes(y_train.bin)) +
    geom_bar()+
    ggtitle("Recovery")
```

## Recovery



```
p1 <- ggplot(training_set.bin,aes(x = recovery_time, y = age)) +
    geom_boxplot()
p2 <- ggplot(training_set.bin,aes(x = recovery_time, y = bmi)) +
    geom_boxplot()
p5 <- ggplot(training_set.bin,aes(x = recovery_time, y = height)) +
    geom_boxplot()
p6 <- ggplot(training_set.bin,aes(x = recovery_time, y = weight)) +
    geom_boxplot()
p3 <- ggplot(training_set.bin,aes(x = recovery_time, y = SBP)) +
    geom_boxplot()
p4 <- ggplot(training_set.bin,aes(x = recovery_time, y = LDL)) +
    geom_boxplot()
arrange = ggarrange(p1,p2,p5,p6, p3,p4, ncol = 3, nrow = 2)
ggsave("arrangedplot3.png", arrange)</pre>
```

## Saving 6.5 x 4.5 in image

### Modeling

logistic Regression

# # Performance coef(logit.fit\$finalModel)%>%knitr::kable()

	X
(Intercept)	77.9377809
age	-0.0014737
gender	0.2872523
race2	0.0049070
race3	0.1832813
race4	0.1183182
smoking1	-0.3491295
smoking2	-0.5142643
height	-0.4556903
weight	0.4958408
bmi	-1.5094498
hypertension	-0.2501449
diabetes	0.0040744
SBP	0.0000674
LDL	-0.0000503
vaccine	0.5584663
severity	-0.6682278
studyB	1.1348875
studyC	0.0696563

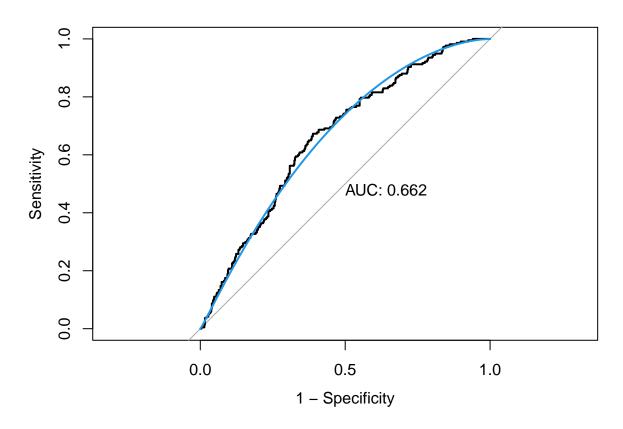
```
# ROC Curve

pred.logit.1 <- predict(logit.fit, newdata = x_test.bin, type = "prob")[,2]
roc.logit <- roc(y_test.bin, pred.logit.1)

## Setting levels: control = long, case = short

## Setting direction: controls < cases

plot(roc.logit, legacy.axes = TRUE, print.auc = TRUE)
plot(smooth(roc.logit), col = 4, add = TRUE)</pre>
```



```
## Confusion Matrix and Statistics
##
##
             Reference
## Prediction long short
##
        long
               447
                     169
        short
                55
                      48
##
##
##
                  Accuracy : 0.6885
                    95% CI : (0.6532, 0.7222)
##
##
       No Information Rate: 0.6982
       P-Value [Acc > NIR] : 0.7299
##
##
                     Kappa : 0.1312
##
##
##
    Mcnemar's Test P-Value: 4.348e-14
##
##
               Sensitivity: 0.8904
               Specificity: 0.2212
##
            Pos Pred Value: 0.7256
##
##
            Neg Pred Value: 0.4660
```

```
## Prevalence : 0.6982
## Detection Rate : 0.6217
## Detection Prevalence : 0.8567
## Balanced Accuracy : 0.5558
##
## 'Positive' Class : long
##
```

The accuracy of logistic regression with the best tunning parameter is 0.6885

#### MARS

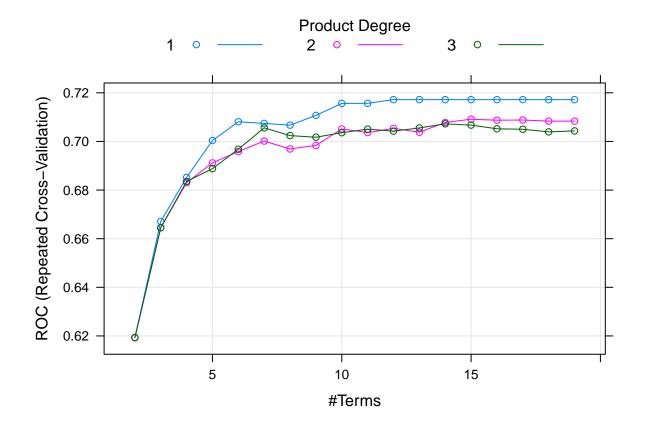
## 载入需要的程辑包: Formula

## 载入需要的程辑包: plotmo

## 载入需要的程辑包: plotrix

## 载入需要的程辑包: TeachingDemos

```
#performance
plot(mars.fit)
```



#### mars.fit\$bestTune

## nprune degree ## 11 12 1

#### coef(mars.fit\$finalModel)%>%knitr::kable()

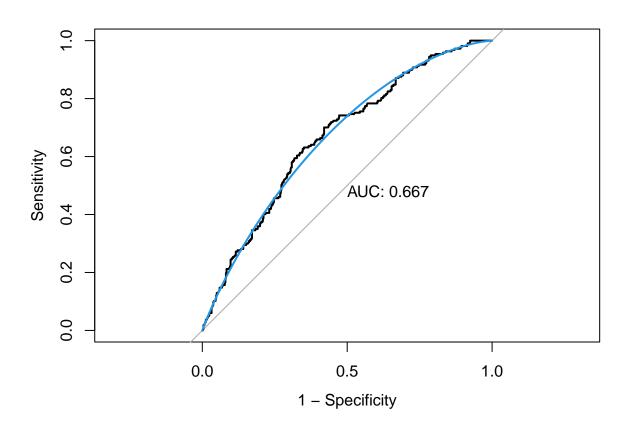
	X
(Intercept)	0.1116993
studyB	1.1310163
h(27.7-bmi)	-0.4801829
vaccine	0.5724142
severity	-0.7050607
gender	0.3084459
smoking2	-0.5517739
smoking1	-0.3567230
h(SBP-146)	-0.2366423
h(bmi-24)	-0.3634087
hypertension	-0.2360256

```
# ROC Curve
pred.mars.1 <- predict(mars.fit, newdata = x_test.bin, type = "prob")[,2]
mars.roc <- roc(y_test.bin, pred.mars.1)</pre>
```

```
## Setting levels: control = long, case = short

## Setting direction: controls < cases

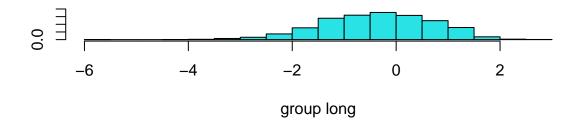
plot(mars.roc, legacy.axes = TRUE, print.auc = TRUE)
plot(smooth(mars.roc), col = 4, add = TRUE)</pre>
```

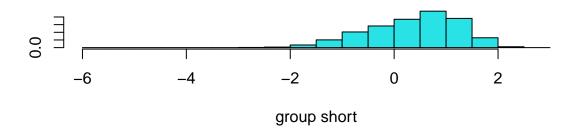


```
## Confusion Matrix and Statistics
##
##
             Reference
## Prediction long short
##
               444
                     160
        long
##
        short
                58
                      57
##
##
                  Accuracy : 0.6968
##
                    95% CI : (0.6618, 0.7302)
##
       No Information Rate: 0.6982
       P-Value [Acc > NIR] : 0.5506
##
##
```

```
##
                     Kappa : 0.1698
##
##
   Mcnemar's Test P-Value : 7.887e-12
##
               Sensitivity: 0.8845
##
##
               Specificity: 0.2627
            Pos Pred Value : 0.7351
##
            Neg Pred Value: 0.4957
##
##
                Prevalence : 0.6982
            Detection Rate : 0.6175
##
##
      Detection Prevalence : 0.8401
##
         Balanced Accuracy: 0.5736
##
##
          'Positive' Class : long
##
```

#### LDA





# #Performance coef(lda.fit\$finalModel)

```
##
                           LD1
                -0.0006725142
## age
## gender
                 0.3916442927
                 0.0152252625
## race2
                 0.2532393459
## race3
## race4
                 0.1636328407
                -0.4481450169
## smoking1
## smoking2
                -0.6835692462
## height
                -0.4834816425
## weight
                 0.5229986644
                -1.6020430301
## bmi
## hypertension -0.3290637233
## diabetes
                 0.0210963168
## SBP
                -0.0007270520
## LDL
                -0.0001418491
## vaccine
                 0.7648376558
## severity
                -0.8301518980
## studyB
                  1.5041801769
## studyC
                 0.0747323482
```

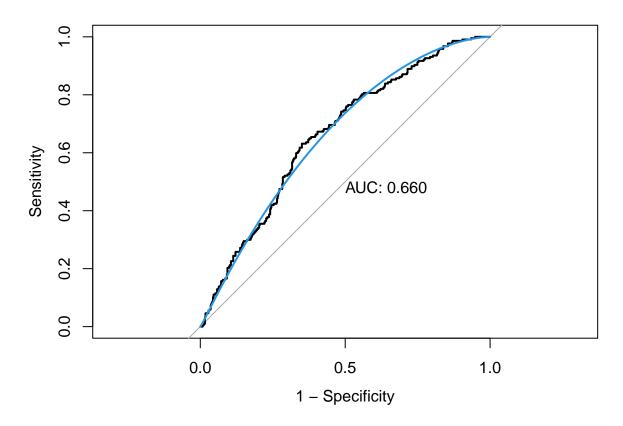
```
# ROC Curve
```

```
pred.lda.1 <- predict(lda.fit, newdata = x_test.bin, type = "prob")[,2]
lda.roc <- roc(y_test.bin, pred.lda.1)</pre>
```

```
## Setting levels: control = long, case = short

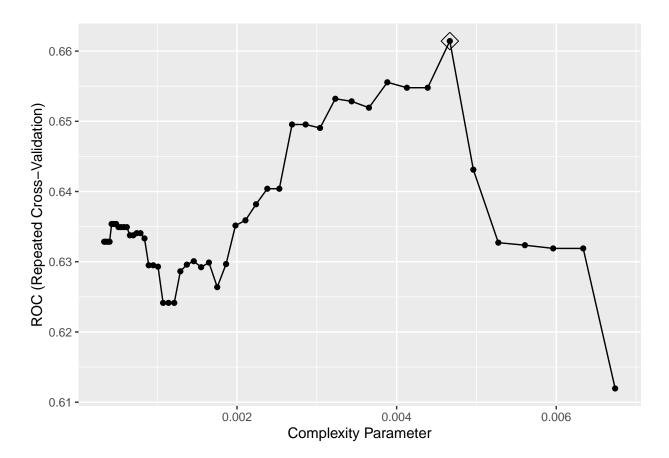
## Setting direction: controls < cases

plot(lda.roc, legacy.axes = TRUE, print.auc = TRUE)
plot(smooth(lda.roc), col = 4, add = TRUE)</pre>
```



```
## Confusion Matrix and Statistics
##
##
             Reference
## Prediction long short
##
        long
               452
                     172
##
        short
                50
                      45
##
##
                  Accuracy : 0.6912
##
                    95% CI : (0.656, 0.7249)
##
       No Information Rate: 0.6982
```

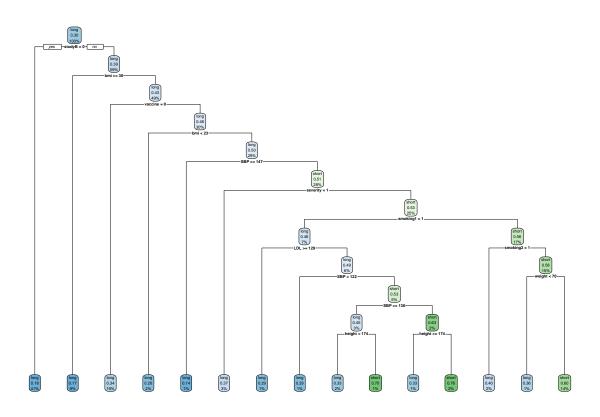
```
P-Value [Acc > NIR] : 0.674
##
##
                     Kappa: 0.1282
##
##
    Mcnemar's Test P-Value : 4.624e-16
##
##
##
               Sensitivity: 0.9004
               Specificity: 0.2074
##
##
            Pos Pred Value : 0.7244
##
            Neg Pred Value: 0.4737
##
                Prevalence: 0.6982
            Detection Rate: 0.6287
##
##
      Detection Prevalence: 0.8679
##
         Balanced Accuracy: 0.5539
##
##
          'Positive' Class : long
##
```



#### rpart.fit\$bestTune

```
## cp
## 44 0.004666495
```

rpart.plot(rpart.fit\$finalModel)



```
# Performance

# ROC Curve

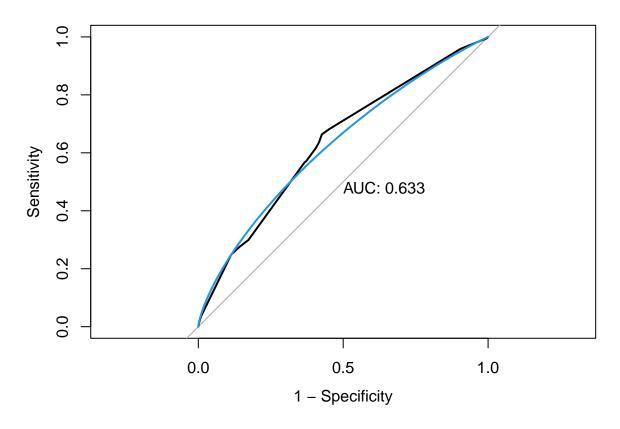
pred.rpart.1 <- predict(rpart.fit, newdata = x_test.bin, type = "prob")[,2]

rpart.roc <- roc(y_test.bin, pred.rpart.1)

## Setting levels: control = long, case = short

## Setting direction: controls < cases

plot(rpart.roc, legacy.axes = TRUE, print.auc = TRUE)
plot(smooth(rpart.roc), col = 4, add = TRUE)</pre>
```



```
## Confusion Matrix and Statistics
##
##
             Reference
## Prediction long short
        long
               445
##
        short
                57
                      54
##
##
##
                  Accuracy: 0.694
                    95% CI : (0.6589, 0.7275)
##
##
       No Information Rate: 0.6982
       P-Value [Acc > NIR] : 0.6138
##
##
                     Kappa : 0.1571
##
##
##
    Mcnemar's Test P-Value : 1.451e-12
##
##
               Sensitivity: 0.8865
               Specificity: 0.2488
##
            Pos Pred Value: 0.7319
##
##
            Neg Pred Value: 0.4865
```

```
## Prevalence : 0.6982
## Detection Rate : 0.6189
## Detection Prevalence : 0.8456
## Balanced Accuracy : 0.5677
##
## 'Positive' Class : long
##
```

#### Model Comparison

```
set.seed(2023)
res <- caret::resamples(list(Logit = logit.fit, Mars = mars.fit, lda = lda.fit, rpart=rpart.fit),metric</pre>
                 method = "cv",index = createFolds(trainData$binary_outcome, k = 10))
summary(res)
##
## Call:
## summary.resamples(object = res)
## Models: Logit, Mars, lda, rpart
## Number of resamples: 10
##
## ROC
##
                     1st Qu.
                                Median
                                             Mean
                                                    3rd Qu.
## Logit 0.6423694 0.6762452 0.6944587 0.6949499 0.7155744 0.7381928
## Mars 0.6708774 0.6934223 0.7138732 0.7171922 0.7356822 0.7727893
         0.6523703 0.6795763 0.6929409 0.6944544 0.7013972 0.7444387
                                                                          0
## rpart 0.6146852 0.6356794 0.6648653 0.6614290 0.6753588 0.7230283
##
## Sens
##
              Min.
                     1st Qu.
                                Median
                                             Mean
                                                    3rd Qu.
## Logit 0.8855721 0.9017413 0.9230703 0.9209891 0.9427861 0.9552239
## Mars 0.8366337 0.8967662 0.9079602 0.9021033 0.9203980 0.9356436
         0.9059406 \ 0.9104478 \ 0.9131570 \ 0.9239717 \ 0.9303483 \ 0.9701493
## rpart 0.8514851 0.8793532 0.8955224 0.8966159 0.9092040 0.9504950
                                                                          0
##
## Spec
##
                      1st Qu.
                                 Median
                                                     3rd Qu.
               Min.
                                              Mean
## Logit 0.14942529 0.1522989 0.1781609 0.2011494 0.2241379 0.3563218
## Mars 0.20689655 0.2183908 0.2758621 0.2770115 0.3103448 0.4137931
                                                                           0
         0.09195402\ 0.1752874\ 0.1954023\ 0.1896552\ 0.2183908\ 0.2643678
                                                                           0
## rpart 0.14942529 0.2126437 0.2873563 0.2597701 0.2988506 0.3563218
                                                                           0
```