R version 4.0.2 (2020-06-22) -- "Taking Off Again"

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Platform: x86\_64-w64-mingw32/x64 (64-bit)

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Natural language support but running in an English locale

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Type 'q()' to quit R.

> knitr::opts\_chunk$set(echo = TRUE)

> ## Set the working directory to the root of your DSC 520 directory

> setwd("C:/Users/binay/Documents/GitHub/dsc520/")

The working directory was changed to C:/Users/binay/Documents/GitHub/dsc520 inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.>

> ## Load the `foreign` library

> library(foreign)

>

> ## Load the `data/ThoraricSurgery.arff` to

> thoracic\_surgery\_df <- read.arff('data/ThoraricSurgery.arff')

> head(thoracic\_surgery\_df)

>

>

> # Since Risk1Y = True means patient died and we want to predict whether patient survived.

> # We should set baseline category as True, (which means Not Survived)

> # otherwise default will be taken as False due to alphabetical order

> # This means T = 0 and F = 1

> thoracic\_surgery\_df$Risk1Yr<-relevel(thoracic\_surgery\_df$Risk1Yr, "T")

>

> # Could also split this df using split function to training set and test set.

> # However leaving it for this exercise, assuming all dataset is training dataset.

>

> # This model includes all other parameters as dependent

> lrmodel.1 <- glm(Risk1Yr ~ . , family ='binomial' , data = thoracic\_surgery\_df)

> summary(lrmodel.1)

Call:

glm(formula = Risk1Yr ~ ., family = "binomial", data = thoracic\_surgery\_df)

Deviance Residuals:

Min 1Q Median 3Q Max

-2.4929 0.2762 0.4199 0.5439 1.6084

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 1.655e+01 2.400e+03 0.007 0.99450

DGNDGN2 -1.474e+01 2.400e+03 -0.006 0.99510

DGNDGN3 -1.418e+01 2.400e+03 -0.006 0.99528

DGNDGN4 -1.461e+01 2.400e+03 -0.006 0.99514

DGNDGN5 -1.638e+01 2.400e+03 -0.007 0.99455

DGNDGN6 -4.089e-01 2.673e+03 0.000 0.99988

DGNDGN8 -1.803e+01 2.400e+03 -0.008 0.99400

PRE4 2.272e-01 1.849e-01 1.229 0.21909

PRE5 3.030e-02 1.786e-02 1.697 0.08971 .

PRE6PRZ1 4.427e-01 5.199e-01 0.852 0.39448

PRE6PRZ2 2.937e-01 7.907e-01 0.371 0.71030

PRE7T -7.153e-01 5.556e-01 -1.288 0.19788

PRE8T -1.743e-01 3.892e-01 -0.448 0.65419

PRE9T -1.368e+00 4.868e-01 -2.811 0.00494 \*\*

PRE10T -5.770e-01 4.826e-01 -1.196 0.23185

PRE11T -5.162e-01 3.965e-01 -1.302 0.19295

PRE14OC12 -4.394e-01 3.301e-01 -1.331 0.18318

PRE14OC13 -1.179e+00 6.165e-01 -1.913 0.05580 .

PRE14OC14 -1.653e+00 6.094e-01 -2.713 0.00668 \*\*

PRE17T -9.266e-01 4.445e-01 -2.085 0.03709 \*

PRE19T 1.466e+01 1.654e+03 0.009 0.99293

PRE25T 9.789e-02 1.003e+00 0.098 0.92227

PRE30T -1.084e+00 4.990e-01 -2.172 0.02984 \*

PRE32T 1.398e+01 1.645e+03 0.008 0.99322

AGE 9.506e-03 1.810e-02 0.525 0.59944

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 395.61 on 469 degrees of freedom

Residual deviance: 341.19 on 445 degrees of freedom

AIC: 391.19

Number of Fisher Scoring iterations: 15

>

> # Trying out another model

> # This model includes only DGN parameters as dependent

> lrmodel.2 <- glm(Risk1Yr ~ DGN , family ='binomial' , data = thoracic\_surgery\_df)

>

> summary(lrmodel.2)

Call:

glm(formula = Risk1Yr ~ DGN, family = "binomial", data = thoracic\_surgery\_df)

Deviance Residuals:

Min 1Q Median 3Q Max

-2.0464 0.5128 0.5128 0.5128 1.1774

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 1.557e+01 1.455e+03 0.011 0.991

DGNDGN2 -1.436e+01 1.455e+03 -0.010 0.992

DGNDGN3 -1.360e+01 1.455e+03 -0.009 0.993

DGNDGN4 -1.382e+01 1.455e+03 -0.009 0.992

DGNDGN5 -1.543e+01 1.455e+03 -0.011 0.992

DGNDGN6 1.300e-08 1.627e+03 0.000 1.000

DGNDGN8 -1.557e+01 1.455e+03 -0.011 0.991

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 395.61 on 469 degrees of freedom

Residual deviance: 379.79 on 463 degrees of freedom

AIC: 393.79

Number of Fisher Scoring iterations: 14

>

>

> result <- predict(lrmodel.1,thoracic\_surgery\_df,type = "response")

> # result

> # validating - putting the actual value and counts of Predicted values in a matrix

> # Since T = 0 and F = 1, so if result < 0.5, it should be T

> confmatrix <- table(ActualValue=thoracic\_surgery\_df$Risk1Yr, PredictedValue = result < 0.5)

> confmatrix

PredictedValue

ActualValue FALSE TRUE

T 67 3

F 390 10

> # accuracy - Cases where we predicted correctly by Total Predictions

> # from matrix, we see when Actual Value is T, confmatrix needs to pick 1,2

> # and when F it should pick 2,1

> (confmatrix[1,2]+confmatrix[2,1])/sum(confmatrix)

[1] 0.8361702

>

>