Hospital Readmission sample solution

This chunk reads in the data, relevels factors, and prints a summary.

```
# Loading data
readmission <- read.csv(file="readmission.csv")

vars <- colnames(readmission)[c(2,3,5,9)] #variables to relevel
for (i in vars){
  table <- as.data.frame(table(readmission[,i]))
  max <- which.max(table[,2])
  level.name <- as.character(table[max,1])
  readmission[,i] <- relevel(readmission[,i], ref = level.name)
}
summary(readmission)
```

```
##  Readmission.Status Gender          Race             ER
##  Min.   :0.0000     F:38011   White   :56124   Min.   :0.0000
##  1st Qu.:0.0000     M:28771   Black   : 7099   1st Qu.:0.0000
##  Median :0.0000               Hispanic: 1286   Median :0.0000
##  Mean   :0.1259               Others  : 2273   Mean   :0.5083
##  3rd Qu.:0.0000                                3rd Qu.:1.0000
##  Max.   :1.0000                                Max.   :9.0000
##    DRG.Class          LOS              Age          HCC.Riskscore
##  MED    :35771   Min.   : 1.000   Min.   : 24.00   Min.   : 0.079
##  SURG   :30447   1st Qu.: 3.000   1st Qu.: 67.00   1st Qu.: 1.107
##  UNGROUP:  564   Median : 5.000   Median : 75.00   Median : 1.865
##                  Mean   : 6.693   Mean   : 73.64   Mean   : 2.345
##                  3rd Qu.: 8.000   3rd Qu.: 83.00   3rd Qu.: 3.173
##                  Max.   :36.000   Max.   :101.00   Max.   :12.307
##       DRG.Complication
##  MedicalMCC.CC:18110
##  MedicalNoC   :12310
##  Other        : 9345
##  SurgMCC.CC   :15468
##  SurgNoC      :11549
##
```

Task 1

I have elected to make a table for ER and histograms for the other three variables.

```
library(ggplot2)
```

```
## Warning: replacing previous import by 'rlang:::=' when loading 'dplyr'

## Warning: replacing previous import by 'rlang::.data' when loading 'dplyr'

## Warning: replacing previous import by 'rlang::as_label' when loading
## 'dplyr'

## Warning: replacing previous import by 'rlang::as_name' when loading 'dplyr'

## Warning: replacing previous import by 'rlang::dots_n' when loading 'dplyr'
```

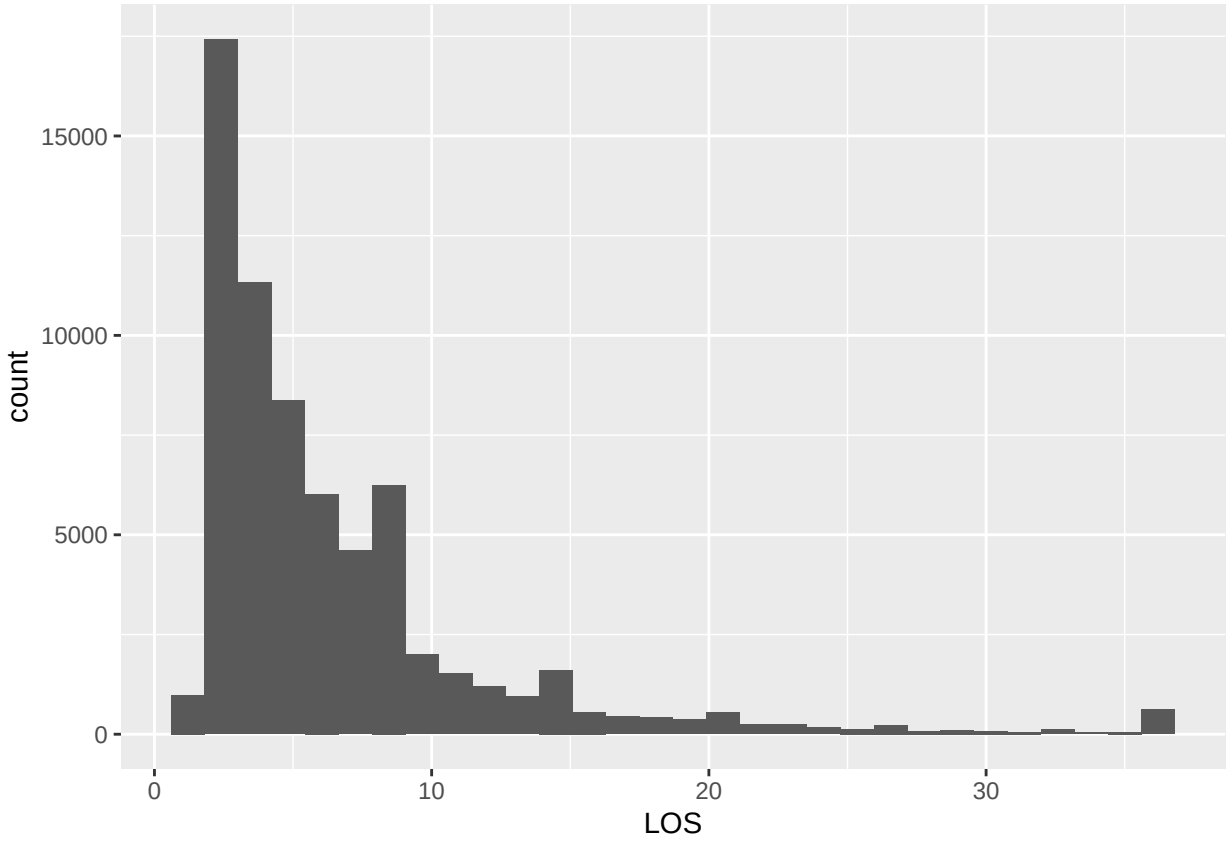
```
## Warning: replacing previous import by 'rlang::enquo' when loading 'dplyr'
## Warning: replacing previous import by 'rlang::enquos' when loading 'dplyr'
## Warning: replacing previous import by 'rlang::expr' when loading 'dplyr'
## Warning: replacing previous import by 'rlang::sym' when loading 'dplyr'
## Warning: replacing previous import by 'rlang::syms' when loading 'dplyr'
```

```
table(readmission$ER)
```

```
##
##     0     1     2     3     4     5     6     7     9
## 43086 16280  5286  1572   438   105    10     3     2
```

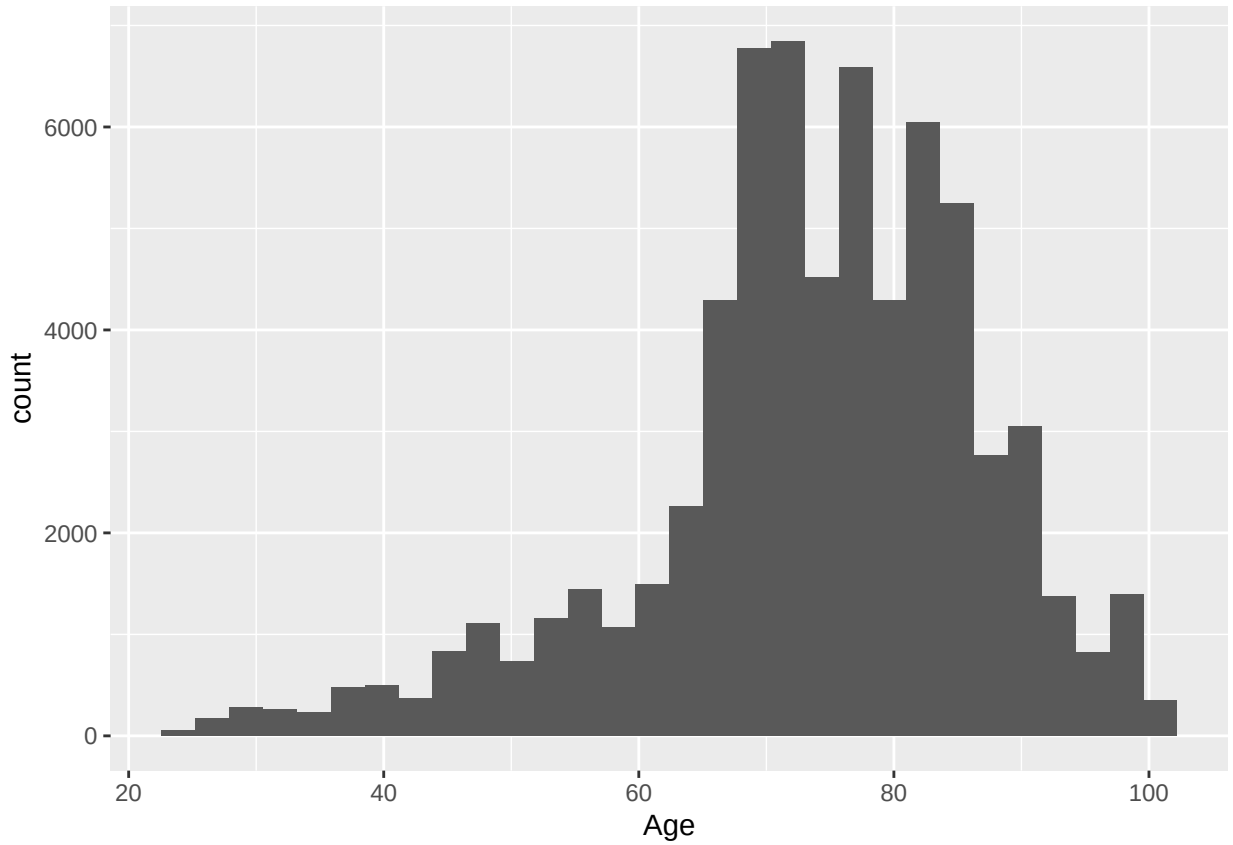
```
ggplot(readmission,aes(x=LOS))+geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



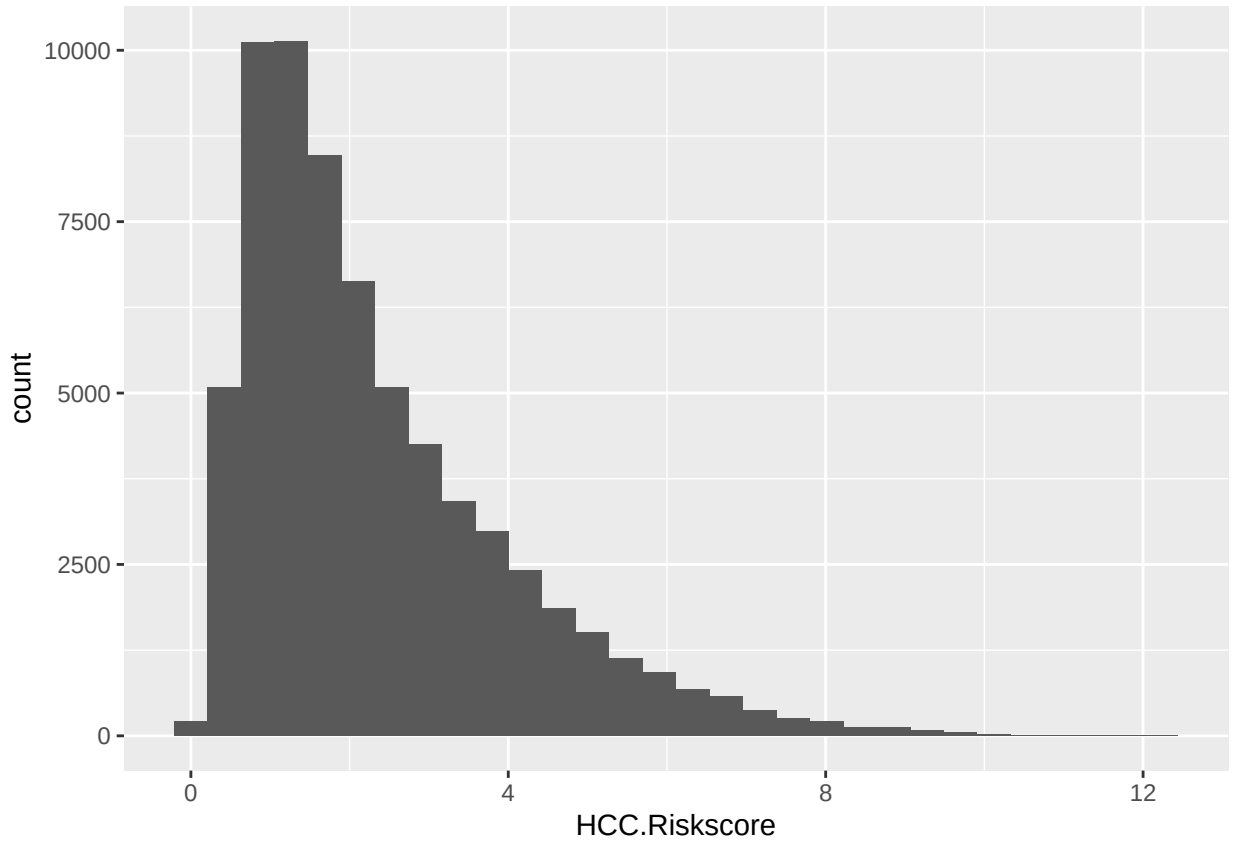

```
ggplot(readmission,aes(x=Age))+geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
ggplot(readmission,aes(x=HCC.Riskscore))+geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



I will use log transformations of the LOS and HCC.Riskscore variables. I also create an indicator variables for those under age 65. The following chunk does these.

```
#two log transforms and removal of original variables
readmission$logLOS <- log(readmission$LOS)
readmission$logRiskscore <- log(readmission$HCC.Riskscore)
readmission$LOS <- NULL
readmission$HCC.Riskscore <- NULL
readmission$Under65 <- ifelse(readmission$Age < 65, 1, 0)
summary(readmission)
```

```
##  Readmission.Status Gender          Race             ER
##  Min.   :0.0000     F:38011   White   :56124   Min.   :0.0000
##  1st Qu.:0.0000     M:28771   Black   : 7099   1st Qu.:0.0000
##  Median :0.0000               Hispanic: 1286   Median :0.0000
##  Mean   :0.1259               Others  : 2273   Mean   :0.5083
##  3rd Qu.:0.0000                                3rd Qu.:1.0000
##  Max.   :1.0000                                Max.   :9.0000
##    DRG.Class          Age              DRG.Complication     logLOS
##  MED    :35771   Min.   : 24.00   MedicalMCC.CC:18110   Min.   :0.000
##  SURG   :30447   1st Qu.: 67.00   MedicalNoC   :12310   1st Qu.:1.099
##  UNGROUP:  564   Median : 75.00   Other        : 9345   Median :1.609
##                  Mean   : 73.64   SurgMCC.CC   :15468   Mean   :1.653
##                  3rd Qu.: 83.00   SurgNoC      :11549   3rd Qu.:2.079
##                  Max.   :101.00                         Max.   :3.584
##   logRiskscore        Under65
##  Min.   :-2.5383   Min.   :0.0000
##  1st Qu.: 0.1017   1st Qu.:0.0000
```

```
##  Median : 0.6235   Median :0.0000
##  Mean   : 0.5999   Mean   :0.1684
##  3rd Qu.: 1.1547   3rd Qu.:0.0000
##  Max.   : 2.5102   Max.   :1.0000
```

Task 2

This chunk creates a tabular view of the two variables.

```
table(readmission$DRG.Class,readmission$DRG.Complication)
```

```
##
##           MedicalMCC.CC MedicalNoC Other SurgMCC.CC SurgNoC
##   MED             18104      12310  5357          0       0
##   SURG                6          0  3424      15468   11549
##   UNGROUP             0          0   564          0       0
```

Six items will be deleted and the two existing variables recoded as a single factor variable. The following code does that.

```
readmission.new <- readmission #preserve the original data until the work can be checked
readmission.new <- readmission.new[!(readmission.new$DRG.Complication=="MedicalMCC.CC" & readmission.new
readmission.new$DRG <- ifelse(readmission.new$DRG.Complication=="MedicalMCC.CC","Med.C",
                       ifelse(readmission.new$DRG.Complication=="MedicalNoC","Med.NoC",
                              ifelse(readmission.new$DRG.Complication=="SurgMCC.CC","Surg.C",
                                     ifelse(readmission.new$DRG.Complication=="SurgNoC","Surg.NoC",
                                            ifelse(readmission.new$DRG.Class=="UNGROUP","UNGROUP",
                                                   ifelse(readmission.new$DRG.Complication=="Other"&rea
readmission.new$DRG <- as.factor(readmission.new$DRG)
table(readmission.new$DRG)
```

```
##
##     Med.C   Med.NoC  OtherMED OtherSURG    Surg.C  Surg.NoC   UNGROUP
##     18104     12310      5357      3424     15468     11549       564
```

```
readmission.new$DRG.Class <- NULL
readmission.new$DRG.Complication <- NULL
```

Relevel the new variable.

```
table <- as.data.frame(table(readmission.new[,"DRG"]))
  max <- which.max(table[,2])
  level.name <- as.character(table[max,1])
  readmission.new[,"DRG"] <- relevel(readmission.new[,"DRG"], ref = level.name)
table(readmission.new$DRG)
```

```
##
##     Med.C   Med.NoC  OtherMED OtherSURG    Surg.C  Surg.NoC   UNGROUP
##     18104     12310      5357      3424     15468     11549       564
```

Accept the new dataframe by renaming it back to readmission.

```
readmission <- readmission.new
readmission.new <- NULL
summary(readmission)
```

```
##  Readmission.Status Gender          Race             ER
##  Min.   :0.0000     F:38005   White   :56120   Min.   :0.0000
```

```
##  1st Qu.:0.0000     M:28771   Black   : 7097   1st Qu.:0.0000
##  Median :0.0000               Hispanic: 1286   Median :0.0000
##  Mean   :0.1259               Others  : 2273   Mean   :0.5083
##  3rd Qu.:0.0000                                3rd Qu.:1.0000
##  Max.   :1.0000                                Max.   :9.0000
##
##       Age             logLOS       logRiskscore        Under65
##  Min.   : 24.00   Min.   :0.000   Min.   :-2.5383   Min.   :0.0000
##  1st Qu.: 67.00   1st Qu.:1.099   1st Qu.: 0.1017   1st Qu.:0.0000
##  Median : 75.00   Median :1.609   Median : 0.6238   Median :0.0000
##  Mean   : 73.64   Mean   :1.653   Mean   : 0.6000   Mean   :0.1684
##  3rd Qu.: 83.00   3rd Qu.:2.079   3rd Qu.: 1.1547   3rd Qu.:0.0000
##  Max.   :101.00   Max.   :3.584   Max.   : 2.5102   Max.   :1.0000
##
##         DRG
##  Med.C    :18104
##  Med.NoC  :12310
##  OtherMED : 5357
##  OtherSURG: 3424
##  Surg.C   :15468
##  Surg.NoC :11549
##  UNGROUP  :  564
```

Task 3

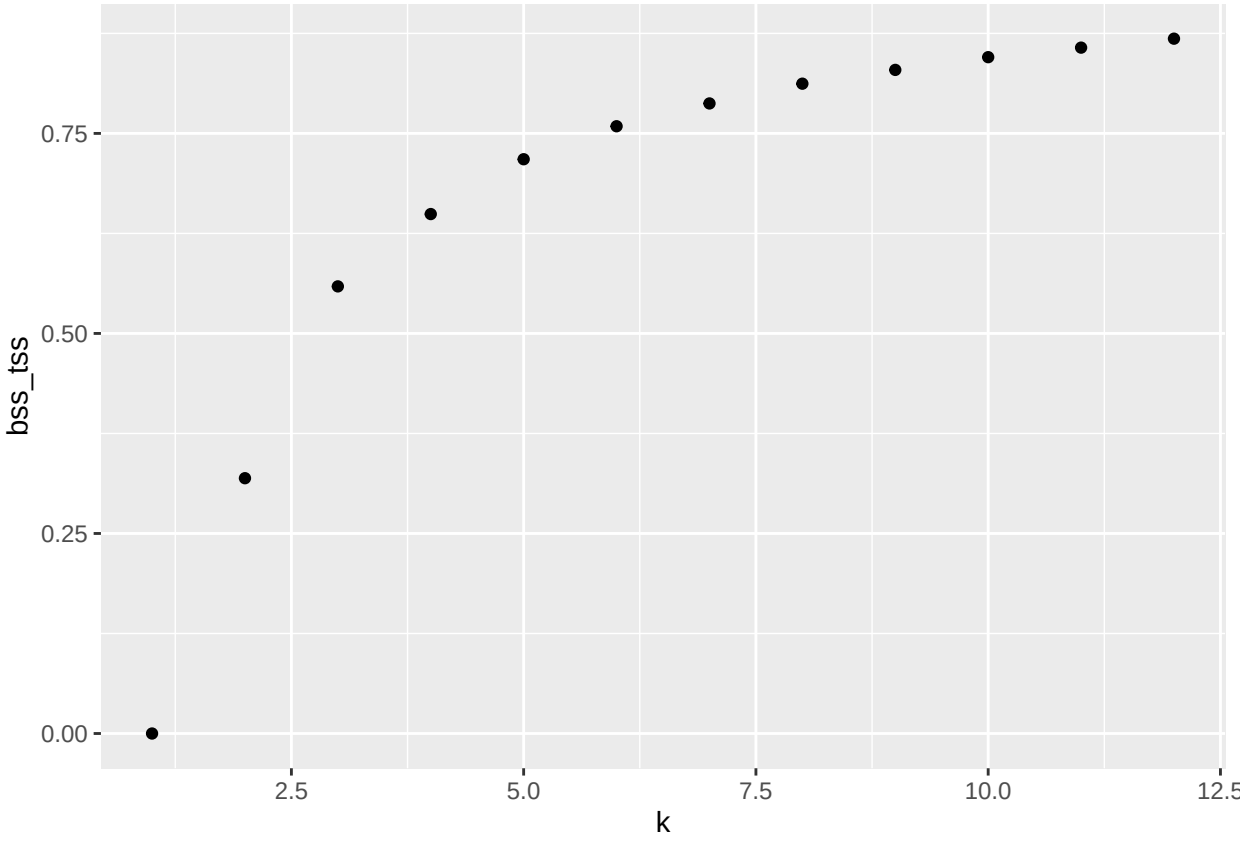
This code performs cluster analysis for from 1 to 12 clusters and constructs an elbow plot.

```
nstart.val <- 20
cluster_vars <- readmission[c('logLOS','Age')]
for(i in 1:ncol(cluster_vars)){
  cluster_vars[,i] <- scale(cluster_vars[,i])
}
km1 <- kmeans(cluster_vars,centers=1,nstart=nstart.val)
km2 <- kmeans(cluster_vars,centers=2,nstart=nstart.val)
km3 <- kmeans(cluster_vars,centers=3,nstart=nstart.val)
km4 <- kmeans(cluster_vars,centers=4,nstart=nstart.val)
km5 <- kmeans(cluster_vars,centers=5,nstart=nstart.val)
km6 <- kmeans(cluster_vars,centers=6,nstart=nstart.val)
km7 <- kmeans(cluster_vars,centers=7,nstart=nstart.val)
km8 <- kmeans(cluster_vars,centers=8,nstart=nstart.val)
km9 <- kmeans(cluster_vars,centers=9,nstart=nstart.val)
km10 <- kmeans(cluster_vars,centers=10,nstart=nstart.val)
km11 <- kmeans(cluster_vars,centers=11,nstart=nstart.val)
km12 <- kmeans(cluster_vars,centers=12,nstart=nstart.val)

var.exp <- data.frame(k = c(1:12),
                      bss_tss = c(km1$betweenss/km1$totss,
                                  km2$betweenss/km2$totss,
                                  km3$betweenss/km3$totss,
                                  km4$betweenss/km4$totss,
                                  km5$betweenss/km5$totss,
                                  km6$betweenss/km6$totss,
                                  km7$betweenss/km7$totss,
                                  km8$betweenss/km8$totss,
```

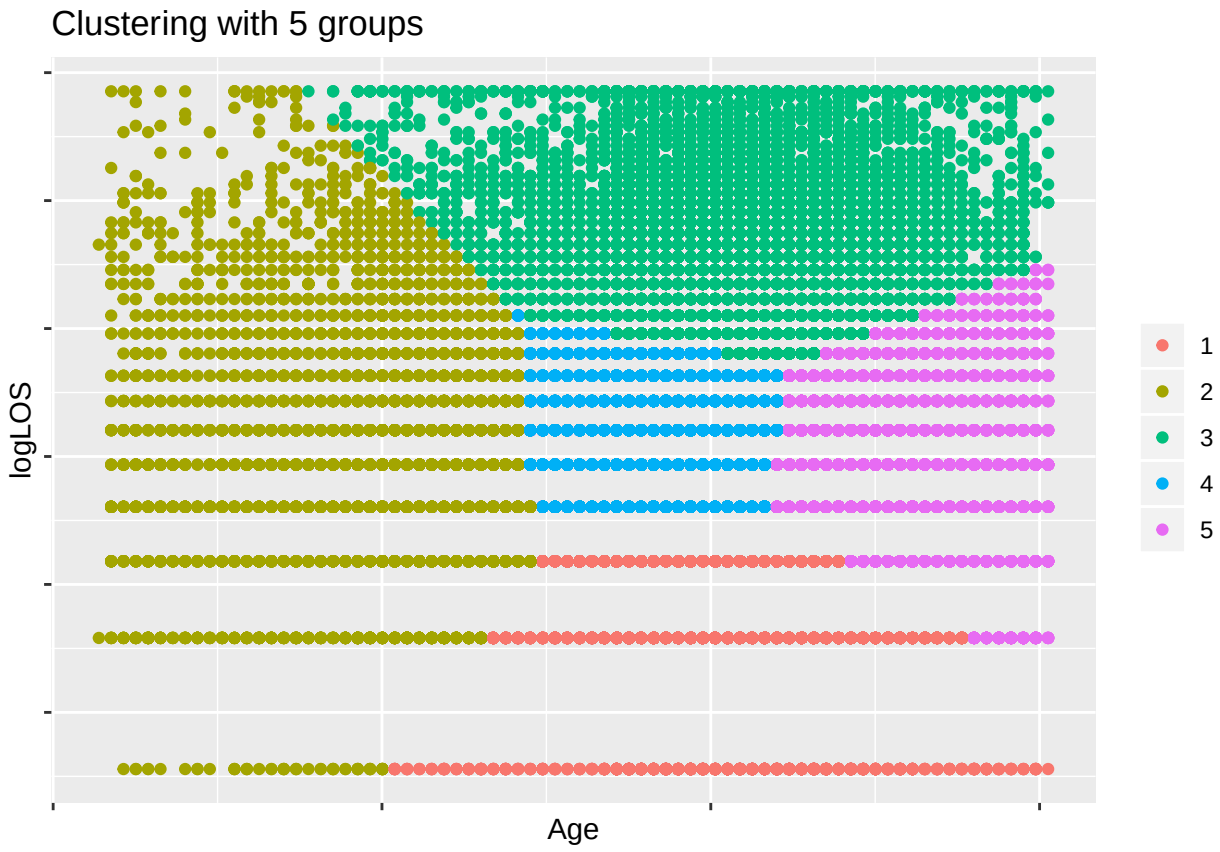
```
                                km9$betweenss/km9$totss,
                                km10$betweenss/km10$totss,
                                km11$betweenss/km11$totss,
                                km12$betweenss/km12$totss))

ggplot(var.exp,aes(x=k,y=bss_tss))+geom_point()
```



The following chunk creates the new variable based on 5 clusters.

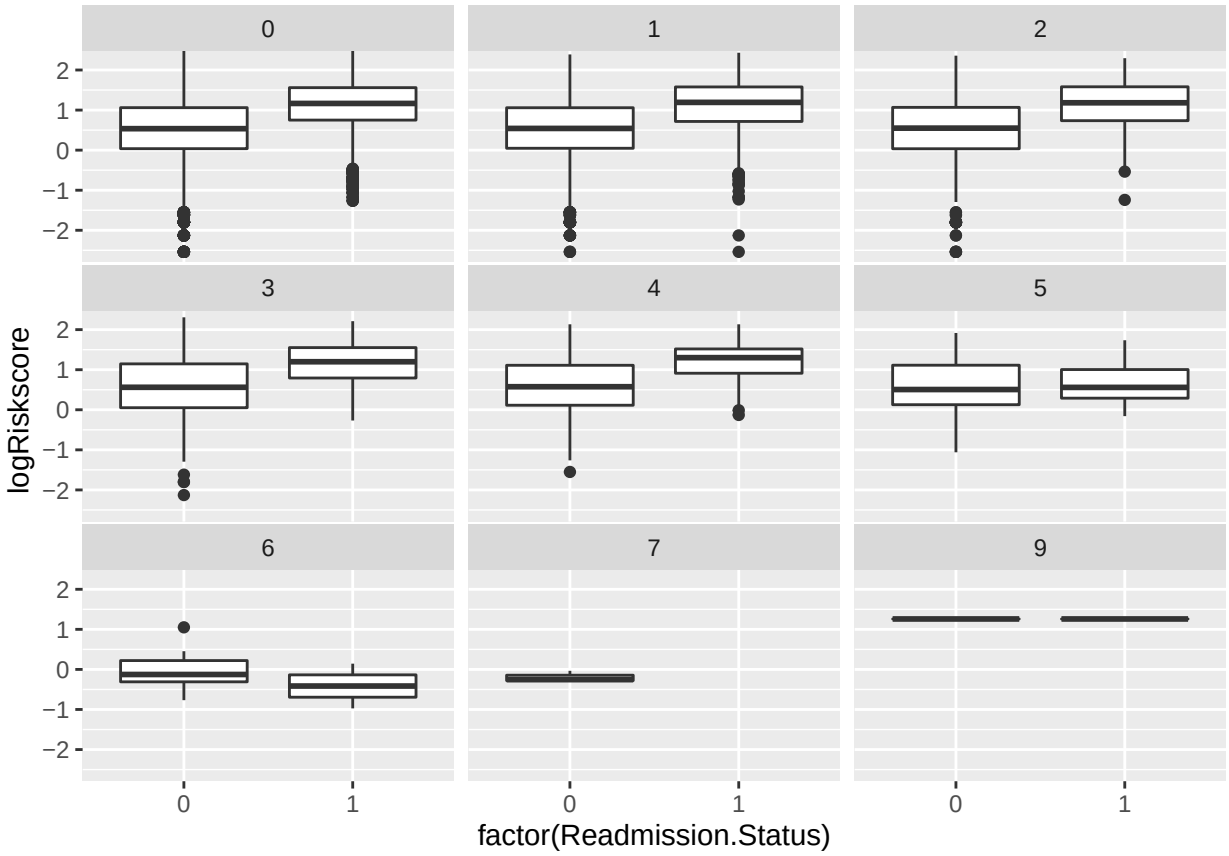
```
LOS_Age_Clust <- as.factor(km5$cluster) #This creates a new variable based on having 5 clusters.
cluster_vars$LOS_Age_Clust <- LOS_Age_Clust
ggplot(data = cluster_vars, aes(x = Age, y = logLOS, col = LOS_Age_Clust)) + geom_point() + theme(axis.
```



Task 4

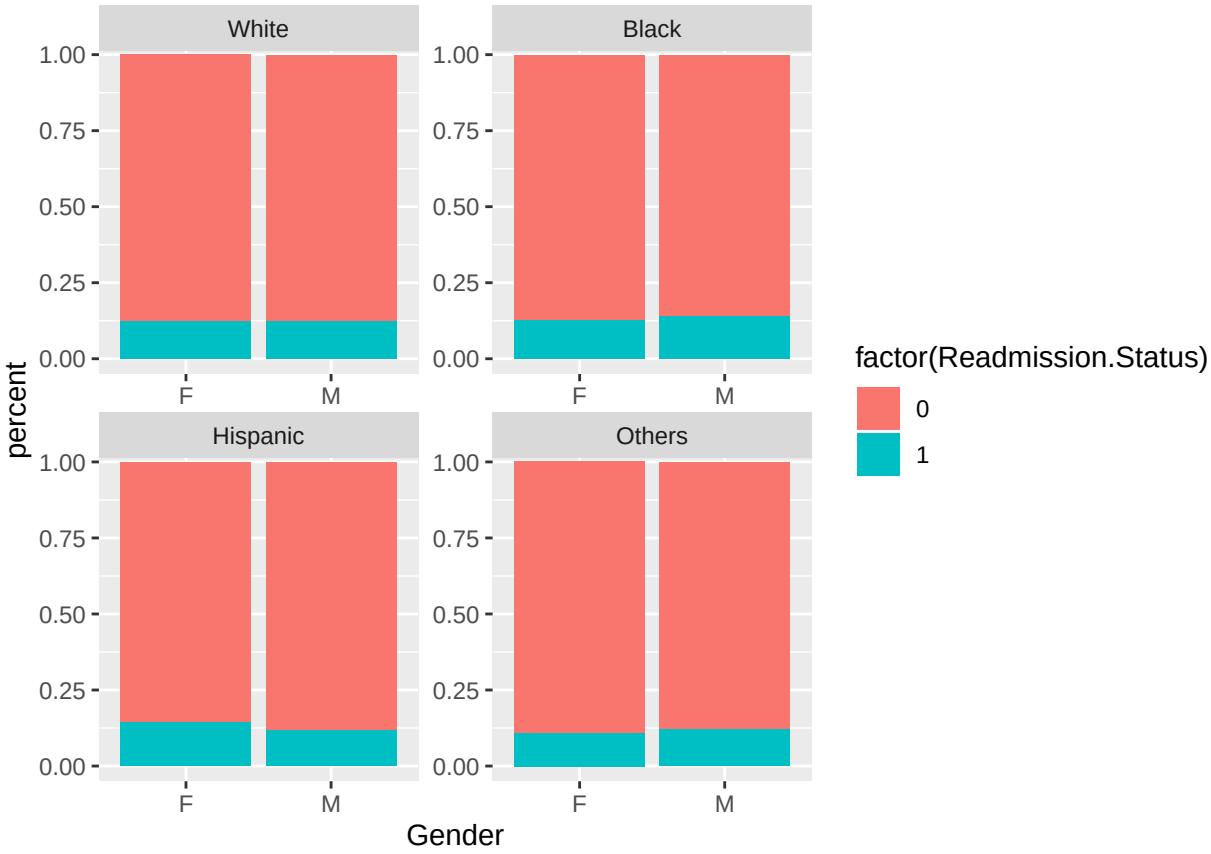
My first look is at ER and logRiskscore.

```
ggplot(readmission,aes(x=factor(Readmission.Status),y=logRiskscore)) + geom_boxplot() +facet_wrap(~facto
```



Trying again with Race and Gender.

```
ggplot(readmission,aes(Gender,fill=factor(Readmission.Status))) + geom_bar(position = "fill") +
  facet_wrap(~Race,ncol=2,scales="free")+scale_y_continuous()+ylab("percent")
```



Task 5

Before fitting a GLM, I will split the data into training and test sets.

```
#Create train and test sets
library(caret)
```

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

```
## Warning: replacing previous import by 'rlang::!!' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::as_character' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::call2' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::exec' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::expr' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::f_lhs' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::f_rhs' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::is_empty' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::is_quosure' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::na_dbl' when loading
```

```
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::names2' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::quo' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::quo_get_expr' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::quo_squash' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::quo_text' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'rlang::quos' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::sym' when loading 'recipes'
```

```
## Warning: replacing previous import by 'rlang::syms' when loading 'recipes'
```

```
## Warning: replacing previous import by 'tibble::tibble' when loading
## 'recipes'
```

```
## Warning: replacing previous import by 'plyr::ddply' when loading 'caret'
```

```
## Warning: replacing previous import by 'recipes::all_outcomes' when loading
## 'caret'
```

```
## Warning: replacing previous import by 'recipes::all_predictors' when
## loading 'caret'
```

```
## Warning: replacing previous import by 'recipes::bake' when loading 'caret'
```

```
## Warning: replacing previous import by 'recipes::has_role' when loading
## 'caret'
```

```
## Warning: replacing previous import by 'recipes::juice' when loading 'caret'
```

```
## Warning: replacing previous import by 'recipes::prep' when loading 'caret'
```

```
set.seed(4321)
partition <- createDataPartition(readmission[,1], list = FALSE, p = .75) #The partition will stratify u
train <- readmission[partition, ]
test <- readmission[-partition, ]

print("TRAIN")
```

```
## [1] "TRAIN"
```

```
mean(train$Readmission.Status)
```

```
## [1] 0.1269518
```

```
print("TEST")
```

```
## [1] "TEST"
```

```
mean(test$Readmission.Status)
```

```
## [1] 0.1228585
```

I will now run a glm using the binomial distribution and logit link and add the desired interaction.

```r
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```r
glmlogit <- glm(Readmission.Status ~ . + Gender*Race, data=train, family = binomial(link="logit"))

summary(glmlogit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ . + Gender * Race, family = binomial(link = "logit"),
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3460  -0.5643  -0.3911  -0.2544   3.0541
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -2.603997   0.136923 -19.018  < 2e-16 ***
## GenderM              -0.021739   0.031186  -0.697  0.48575
## RaceBlack             0.050490   0.059038   0.855  0.39244
## RaceHispanic          0.142477   0.129136   1.103  0.26989
## RaceOthers           -0.127669   0.113611  -1.124  0.26112
## ER                   -0.005826   0.017218  -0.338  0.73508
## Age                  -0.007438   0.001617  -4.598 4.26e-06 ***
## logLOS                0.065528   0.020390   3.214  0.00131 **
## logRiskscore          1.330490   0.023717  56.100  < 2e-16 ***
## Under65              -0.064840   0.057945  -1.119  0.26314
## DRGMed.NoC           -0.040421   0.042587  -0.949  0.34254
## DRGOtherMED           0.125416   0.054738   2.291  0.02195 *
## DRGOtherSURG          0.103201   0.065984   1.564  0.11781
## DRGSurg.C             0.007461   0.039946   0.187  0.85184
## DRGSurg.NoC          -0.010876   0.043732  -0.249  0.80360
## DRGUNGROUP            0.134489   0.139704   0.963  0.33571
## GenderM:RaceBlack     0.003736   0.090470   0.041  0.96706
## GenderM:RaceHispanic -0.321541   0.213049  -1.509  0.13124
## GenderM:RaceOthers    0.237410   0.158452   1.498  0.13405
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33955  on 50063  degrees of freedom
## AIC: 33993
##
## Number of Fisher Scoring iterations: 5
```

```r
predslogit <- predict(glmlogit,newdat=test,type="response")

roclogit <- roc(test$Readmission.Status,predslogit)
```

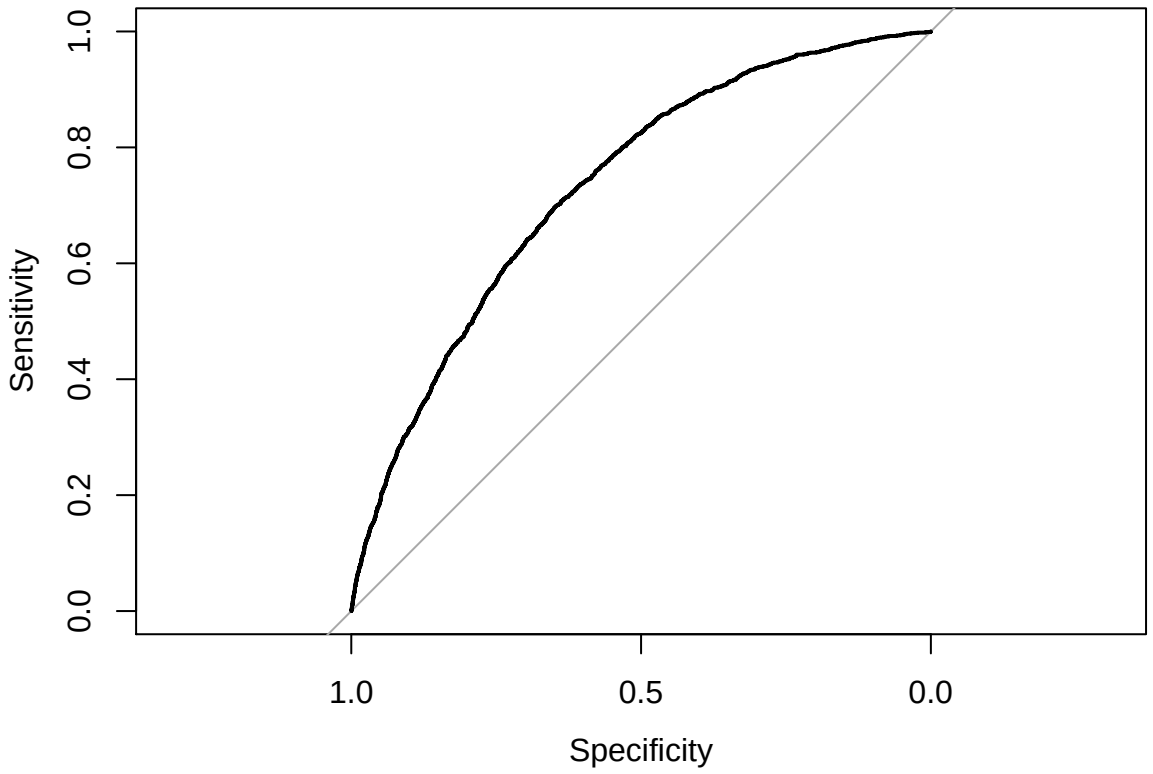
```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```r
confusionMatrix(factor(1*(predslogit>.5)),factor(test$Readmission.Status))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction     0     1
##          0 14630  2042
##          1    13     9
##
##                Accuracy : 0.8769
##                  95% CI : (0.8718, 0.8818)
##     No Information Rate : 0.8771
##     P-Value [Acc > NIR] : 0.5434
##
##                   Kappa : 0.0061
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.999112
##             Specificity : 0.004388
##          Pos Pred Value : 0.877519
##          Neg Pred Value : 0.409091
##              Prevalence : 0.877141
##          Detection Rate : 0.876363
##    Detection Prevalence : 0.998682
##       Balanced Accuracy : 0.501750
##
##        'Positive' Class : 0
##
```

```r
plot(roclogit)
```




```
auc(roclogit)
```

```
## Area under the curve: 0.7324
```

The same code is now run with the probit link.

```
library(pROC)
glmprobit <- glm(Readmission.Status ~ . + Gender*Race, data=train, family = binomial(link="probit"))

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ . + Gender * Race, family = binomial(link = "probit"),
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2689  -0.5756  -0.3944  -0.2384   3.2478
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -1.4371865  0.0741325 -19.387  < 2e-16 ***
## GenderM             -0.0138744  0.0168726  -0.822  0.41090
## RaceBlack            0.0237364  0.0321619   0.738  0.46050
## RaceHispanic         0.0763654  0.0711823   1.073  0.28335
## RaceOthers          -0.0712955  0.0606013  -1.176  0.23941
## ER                  -0.0025486  0.0093214  -0.273  0.78454
## Age                 -0.0045131  0.0008786  -5.137 2.79e-07 ***
## logLOS               0.0343572  0.0112270   3.060  0.00221 **
## logRiskscore         0.7121243  0.0124659  57.126  < 2e-16 ***
```

```
## Under65              -0.0408896  0.0314227  -1.301  0.19316
## DRGMed.NoC           -0.0216338  0.0230263  -0.940  0.34746
## DRGOtherMED           0.0679331  0.0298657   2.275  0.02293 *
## DRGOtherSURG          0.0540437  0.0362048   1.493  0.13551
## DRGSurg.C             0.0086575  0.0215849   0.401  0.68835
## DRGSurg.NoC          -0.0045170  0.0236140  -0.191  0.84830
## DRGUNGROUP            0.0704562  0.0778915   0.905  0.36571
## GenderM:RaceBlack     0.0159955  0.0493390   0.324  0.74579
## GenderM:RaceHispanic -0.1665655  0.1147644  -1.451  0.14668
## GenderM:RaceOthers    0.1305341  0.0854834   1.527  0.12676
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33928  on 50063  degrees of freedom
## AIC: 33966
##
## Number of Fisher Scoring iterations: 5
```

```
predsprobit <- predict(glmprobit,newdat=test,type="response")

rocprobit <- roc(test$Readmission.Status,predsprobit)
```

```
## Setting levels: control = 0, case = 1
```

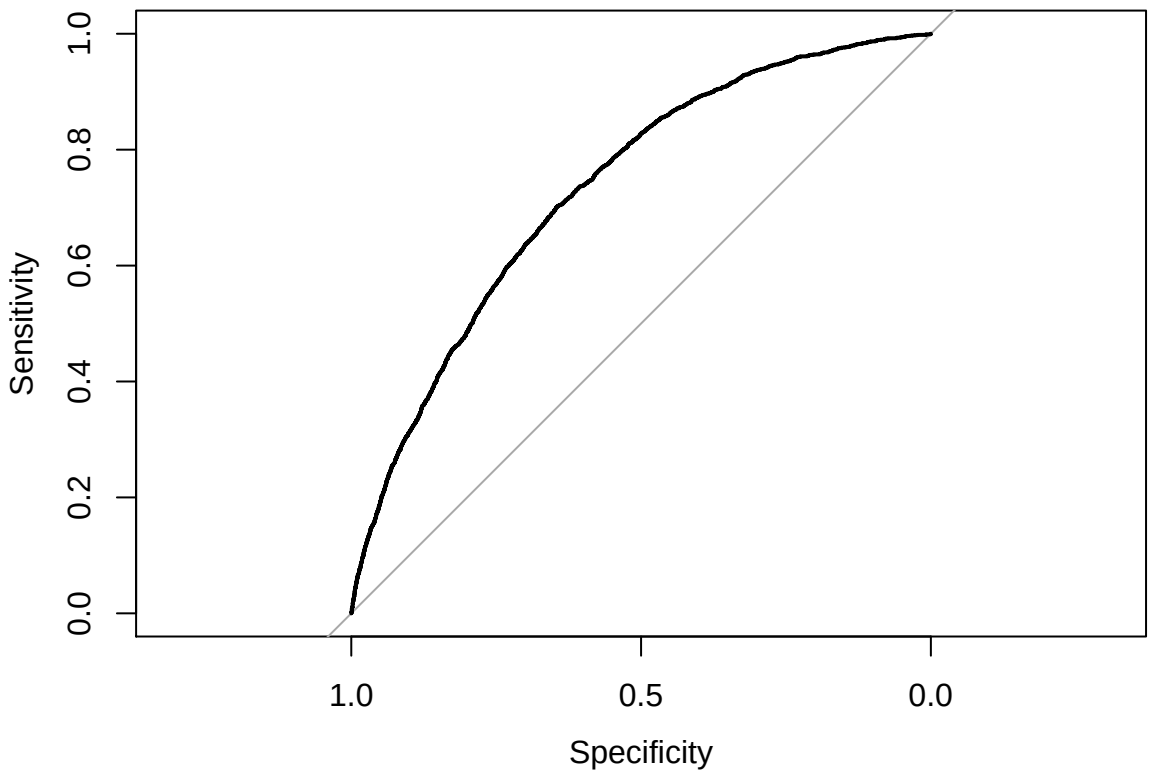
```
## Setting direction: controls < cases
```

```
confusionMatrix(factor(1*(predsprobit>.5)),factor(test$Readmission.Status))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction     0     1
##          0 14638  2048
##          1     5     3
##
##                Accuracy : 0.877
##                  95% CI : (0.8719, 0.882)
##     No Information Rate : 0.8771
##     P-Value [Acc > NIR] : 0.5247
##
##                   Kappa : 0.002
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.999659
##             Specificity : 0.001463
##          Pos Pred Value : 0.877262
##          Neg Pred Value : 0.375000
##              Prevalence : 0.877141
##          Detection Rate : 0.876842
##    Detection Prevalence : 0.999521
##       Balanced Accuracy : 0.500561
##
```

```
##        'Positive' Class : 0
##
```

```
plot(rocprobit)
```




```
auc(rocprobit)
```

```
## Area under the curve: 0.7324
```

Task 6

A new dataframe is created that drops logLOS and Age and adds LOS_Age_Clust. It must then be partitioned.

```
readmission.cluster <- readmission
readmission.cluster$Age <- NULL
readmission.cluster$logLOS <- NULL
readmission.cluster$LOS_Age_Clust <- LOS_Age_Clust
table(readmission.cluster$LOS_Age_Clust)
```

```
##
##     1     2     3     4     5
## 14231  7640 10811 18296 15798
```

```
train.cluster <- readmission.cluster[partition, ]
test.cluster <- readmission.cluster[-partition, ]
```

This code reruns the probit regression using the cluster variable.

```
library(pROC)
glmprobit.clust <- glm(Readmission.Status ~ . + Gender*Race, data=train.cluster, family = binomial(link=
```

```r
summary(glmprobit.clust)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ . + Gender * Race, family = binomial(link = "probit"),
##     data = train.cluster)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2352  -0.5764  -0.3958  -0.2390   3.2774
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -1.764757   0.025668 -68.754  < 2e-16 ***
## GenderM              -0.009280   0.016857  -0.551 0.581972
## RaceBlack             0.029904   0.032122   0.931 0.351880
## RaceHispanic          0.081615   0.071134   1.147 0.251238
## RaceOthers           -0.064763   0.060541  -1.070 0.284736
## ER                   -0.002681   0.009317  -0.288 0.773505
## logRiskscore          0.708164   0.012367  57.262  < 2e-16 ***
## Under65               0.078550   0.033476   2.346 0.018954 *
## DRGMed.NoC           -0.021906   0.023018  -0.952 0.341244
## DRGOtherMED           0.069296   0.029842   2.322 0.020229 *
## DRGOtherSURG          0.056222   0.036180   1.554 0.120192
## DRGSurg.C             0.007818   0.021579   0.362 0.717132
## DRGSurg.NoC          -0.004116   0.023607  -0.174 0.861582
## DRGUNGROUP            0.072082   0.077943   0.925 0.355068
## LOS_Age_Clust2        0.030645   0.042490   0.721 0.470763
## LOS_Age_Clust3        0.083453   0.025226   3.308 0.000939 ***
## LOS_Age_Clust4        0.050077   0.023290   2.150 0.031541 *
## LOS_Age_Clust5        0.004006   0.023922   0.167 0.867013
## GenderM:RaceBlack     0.014296   0.049321   0.290 0.771932
## GenderM:RaceHispanic -0.164691   0.114652  -1.436 0.150875
## GenderM:RaceOthers    0.128235   0.085419   1.501 0.133291
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33948  on 50061  degrees of freedom
## AIC: 33990
##
## Number of Fisher Scoring iterations: 5
```

```r
predsprobit.clust <- predict(glmprobit.clust,newdat=test.cluster,type="response")

rocprobit.clust <- roc(test.cluster$Readmission.Status,predsprobit.clust)
```

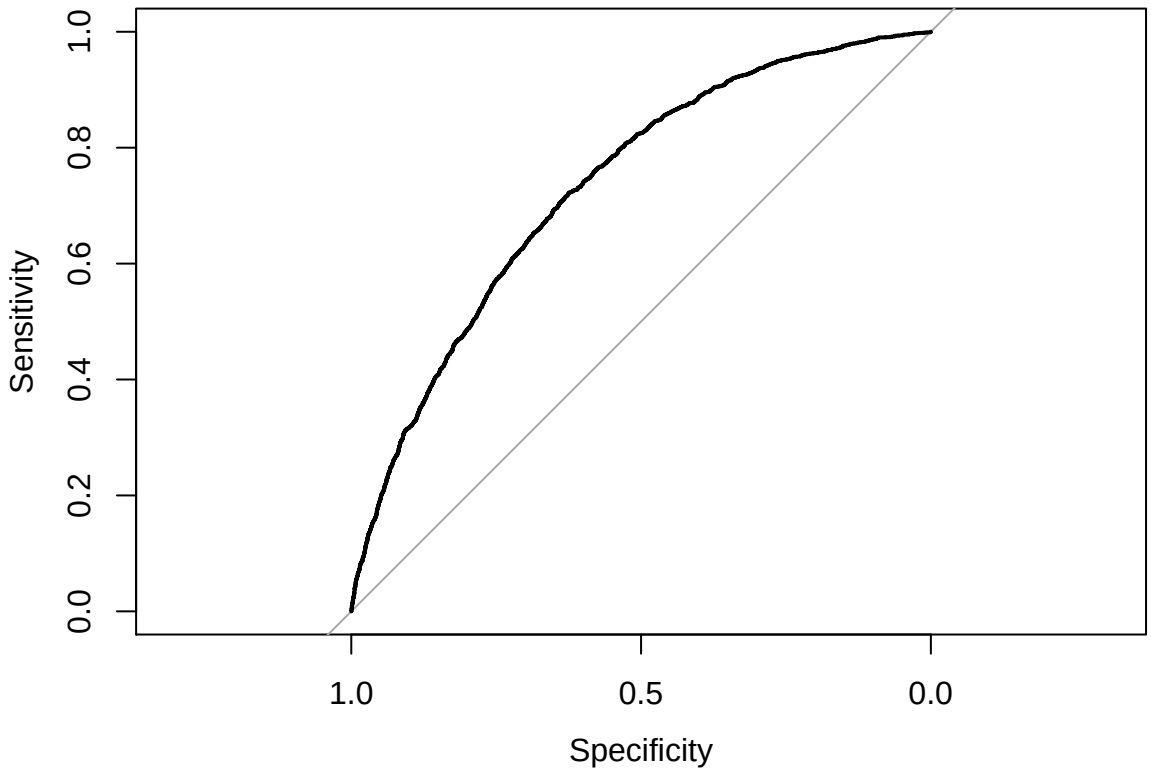
```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```r
confusionMatrix(factor(1*(predsprobit.clust>.5)),factor(test.cluster$Readmission.Status))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction     0     1
##          0 14639  2049
##          1     4     2
##
##                Accuracy : 0.877
##                  95% CI : (0.8719, 0.882)
##     No Information Rate : 0.8771
##     P-Value [Acc > NIR] : 0.5247
##
##                   Kappa : 0.0012
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.9997268
##             Specificity : 0.0009751
##          Pos Pred Value : 0.8772172
##          Neg Pred Value : 0.3333333
##              Prevalence : 0.8771415
##          Detection Rate : 0.8769019
##    Detection Prevalence : 0.9996406
##       Balanced Accuracy : 0.5003510
##
##        'Positive' Class : 0
##
```

```
plot(rocprobit.clust)
```



```r
auc(rocprobit.clust)
```

```
## Area under the curve: 0.7321
```

Task 7

The first step is to binarize the factor levels that have more than two levels. fullRank is set to FALSE so that all levels get binarized. The interaction variable is also a factor variable and must be binarized as well. In each case the base level will then need to be deleted. I do it this way becasue if fullRank is TRUE I can't be sure about which level becomes the base.

```r
#Add the interaction variable to the data frame
readmission$RaceGender <- factor(paste0(readmission$Race,readmission$Gender))
summary(readmission$RaceGender)
```

```
##    BlackF    BlackM HispanicF HispanicM   OthersF   OthersM    WhiteF
##      4157      2940       751       535      1206      1067     31891
##    WhiteM
##     24229
```

```r
factor_names <- c("Race","DRG","RaceGender")
factor_vars <- readmission[,factor_names]
for (var in factor_names) {
  factor_vars[, var] <- as.character(factor_vars[, var])
}


binarizer <- caret::dummyVars(paste("~", paste(factor_names, collapse = "+")) , data = factor_vars, full
binarized_vars <- data.frame(predict(binarizer, newdata = factor_vars))
head(binarized_vars)
```

```
##   RaceBlack RaceHispanic RaceOthers RaceWhite DRGMed.C DRGMed.NoC
## 1         0            0          0         1        0          0
## 2         0            0          0         1        0          0
## 3         0            0          0         1        0          0
## 4         0            0          0         1        0          1
## 5         0            0          0         1        0          1
## 6         0            0          0         1        0          0
##   DRGOtherMED DRGOtherSURG DRGSurg.C DRGSurg.NoC DRGUNGROUP
## 1           1            0         0           0          0
## 2           0            0         0           1          0
## 3           0            0         0           1          0
## 4           0            0         0           0          0
## 5           0            0         0           0          0
## 6           0            0         1           0          0
##   RaceGenderBlackF RaceGenderBlackM RaceGenderHispanicF
## 1                0                0                   0
## 2                0                0                   0
## 3                0                0                   0
## 4                0                0                   0
## 5                0                0                   0
## 6                0                0                   0
##   RaceGenderHispanicM RaceGenderOthersF RaceGenderOthersM RaceGenderWhiteF
## 1                   0                 0                 0                 0
```

```
## 2                   0                 0                 0                 0
## 3                   0                 0                 0                 0
## 4                   0                 0                 0                 0
## 5                   0                 0                 0                 0
## 6                   0                 0                 0                 0
##   RaceGenderWhiteM
## 1                1
## 2                1
## 3                1
## 4                1
## 5                1
## 6                1
```

Now delete the three base variables.

```
binarized_vars$RaceWhite <- NULL
binarized_vars$DRGMed.C <- NULL
binarized_vars$RaceGenderWhiteF <- NULL
head(binarized_vars)
```

```
##   RaceBlack RaceHispanic RaceOthers DRGMed.NoC DRGOtherMED DRGOtherSURG
## 1         0            0          0          0           1            0
## 2         0            0          0          0           0            0
## 3         0            0          0          0           0            0
## 4         0            0          0          1           0            0
## 5         0            0          0          1           0            0
## 6         0            0          0          0           0            0
##   DRGSurg.C DRGSurg.NoC DRGUNGROUP RaceGenderBlackF RaceGenderBlackM
## 1         0           0          0                0                0
## 2         0           1          0                0                0
## 3         0           1          0                0                0
## 4         0           0          0                0                0
## 5         0           0          0                0                0
## 6         1           0          0                0                0
##   RaceGenderHispanicF RaceGenderHispanicM RaceGenderOthersF
## 1                   0                   0                0
## 2                   0                   0                0
## 3                   0                   0                0
## 4                   0                   0                0
## 5                   0                   0                0
## 6                   0                   0                0
##   RaceGenderOthersM RaceGenderWhiteM
## 1                 0                1
## 2                 0                1
## 3                 0                1
## 4                 0                1
## 5                 0                1
## 6                 0                1
```

I now attach the binarized variables and remove the three original factor variables. A new dataframe is created so the old one is preserved.

```
readmission.bin <- cbind(readmission,binarized_vars)
readmission.bin$DRG <- NULL
readmission.bin$Race <- NULL
readmission.bin$RaceGender <- NULL
```

```
summary(readmission.bin)
```

```
##  Readmission.Status Gender          ER              Age
##  Min.   :0.0000     F:38005   Min.   :0.0000   Min.   : 24.00
##  1st Qu.:0.0000     M:28771   1st Qu.:0.0000   1st Qu.: 67.00
##  Median :0.0000               Median :0.0000   Median : 75.00
##  Mean   :0.1259               Mean   :0.5083   Mean   : 73.64
##  3rd Qu.:0.0000               3rd Qu.:1.0000   3rd Qu.: 83.00
##  Max.   :1.0000               Max.   :9.0000   Max.   :101.00
##      logLOS       logRiskscore        Under65         RaceBlack
##  Min.   :0.000   Min.   :-2.5383   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:1.099   1st Qu.: 0.1017   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :1.609   Median : 0.6238   Median :0.0000   Median :0.0000
##  Mean   :1.653   Mean   : 0.6000   Mean   :0.1684   Mean   :0.1063
##  3rd Qu.:2.079   3rd Qu.: 1.1547   3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :3.584   Max.   : 2.5102   Max.   :1.0000   Max.   :1.0000
##   RaceHispanic       RaceOthers        DRGMed.NoC      DRGOtherMED
##  Min.   :0.00000   Min.   :0.00000   Min.   :0.0000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000
##  Median :0.00000   Median :0.00000   Median :0.0000   Median :0.00000
##  Mean   :0.01926   Mean   :0.03404   Mean   :0.1843   Mean   :0.08022
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.00000   Max.   :1.0000   Max.   :1.00000
##   DRGOtherSURG       DRGSurg.C       DRGSurg.NoC      DRGUNGROUP
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.000   Min.   :0.000000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:0.000000
##  Median :0.00000   Median :0.0000   Median :0.000   Median :0.000000
##  Mean   :0.05128   Mean   :0.2316   Mean   :0.173   Mean   :0.008446
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.000   3rd Qu.:0.000000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.000   Max.   :1.000000
##  RaceGenderBlackF  RaceGenderBlackM  RaceGenderHispanicF
##  Min.   :0.00000   Min.   :0.00000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.00000
##  Median :0.00000   Median :0.00000   Median :0.00000
##  Mean   :0.06225   Mean   :0.04403   Mean   :0.01125
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.00000   Max.   :1.00000
##  RaceGenderHispanicM RaceGenderOthersF RaceGenderOthersM RaceGenderWhiteM
##  Min.   :0.000000    Min.   :0.00000   Min.   :0.00000   Min.   :0.0000
##  1st Qu.:0.000000    1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.0000
##  Median :0.000000    Median :0.00000   Median :0.00000   Median :0.0000
##  Mean   :0.008012    Mean   :0.01806   Mean   :0.01598   Mean   :0.3628
##  3rd Qu.:0.000000    3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:1.0000
##  Max.   :1.000000    Max.   :1.00000   Max.   :1.00000   Max.   :1.0000
```

I need to again split the data into train and test sets.

```
train.bin <- readmission.bin[partition, ]
test.bin <- readmission.bin[-partition, ]
```

I next run the GLM on the binarized data. In doing so, I recognized that the interaction variable created combinations that were redundant. I need to remove all the interactions with male and then re-partition the data.

```
readmission.bin$RaceGenderOthersM <- NULL
readmission.bin$RaceGenderWhiteM <- NULL
readmission.bin$RaceGenderHispanicM <- NULL
readmission.bin$RaceGenderBlackM <- NULL
summary(readmission.bin)
```

```
##  Readmission.Status Gender          ER              Age
##  Min.   :0.0000     F:38005   Min.   :0.0000   Min.   : 24.00
##  1st Qu.:0.0000     M:28771   1st Qu.:0.0000   1st Qu.: 67.00
##  Median :0.0000               Median :0.0000   Median : 75.00
##  Mean   :0.1259               Mean   :0.5083   Mean   : 73.64
##  3rd Qu.:0.0000               3rd Qu.:1.0000   3rd Qu.: 83.00
##  Max.   :1.0000               Max.   :9.0000   Max.   :101.00
##      logLOS       logRiskscore        Under65         RaceBlack
##  Min.   :0.000   Min.   :-2.5383   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:1.099   1st Qu.: 0.1017   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :1.609   Median : 0.6238   Median :0.0000   Median :0.0000
##  Mean   :1.653   Mean   : 0.6000   Mean   :0.1684   Mean   :0.1063
##  3rd Qu.:2.079   3rd Qu.: 1.1547   3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :3.584   Max.   : 2.5102   Max.   :1.0000   Max.   :1.0000
##   RaceHispanic       RaceOthers        DRGMed.NoC      DRGOtherMED
##  Min.   :0.00000   Min.   :0.00000   Min.   :0.0000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000
##  Median :0.00000   Median :0.00000   Median :0.0000   Median :0.00000
##  Mean   :0.01926   Mean   :0.03404   Mean   :0.1843   Mean   :0.08022
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.00000   Max.   :1.0000   Max.   :1.00000
##   DRGOtherSURG       DRGSurg.C       DRGSurg.NoC      DRGUNGROUP
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.000   Min.   :0.000000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:0.000000
##  Median :0.00000   Median :0.0000   Median :0.000   Median :0.000000
##  Mean   :0.05128   Mean   :0.2316   Mean   :0.173   Mean   :0.008446
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.000   3rd Qu.:0.000000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.000   Max.   :1.000000
##  RaceGenderBlackF  RaceGenderHispanicF RaceGenderOthersF
##  Min.   :0.00000   Min.   :0.00000     Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000     1st Qu.:0.00000
##  Median :0.00000   Median :0.00000     Median :0.00000
##  Mean   :0.06225   Mean   :0.01125     Mean   :0.01806
##  3rd Qu.:0.00000   3rd Qu.:0.00000     3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.00000     Max.   :1.00000
```

```
train.bin <- readmission.bin[partition, ]
test.bin <- readmission.bin[-partition, ]
```

```
glmprobit <- glm(Readmission.Status ~ . , data=train.bin, family = binomial(link="probit"))

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ ., family = binomial(link = "probit"),
##     data = train.bin)
##
## Deviance Residuals:
```

```
##     Min       1Q   Median       3Q      Max
## -1.2689  -0.5756  -0.3944  -0.2384   3.2478
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -1.4371865  0.0741325 -19.387  < 2e-16 ***
## GenderM             -0.0138744  0.0168726  -0.822  0.41090
## ER                  -0.0025486  0.0093214  -0.273  0.78454
## Age                 -0.0045131  0.0008786  -5.137 2.79e-07 ***
## logLOS               0.0343572  0.0112270   3.060  0.00221 **
## logRiskscore         0.7121243  0.0124659  57.126  < 2e-16 ***
## Under65             -0.0408896  0.0314227  -1.301  0.19316
## RaceBlack            0.0397319  0.0378371   1.050  0.29368
## RaceHispanic        -0.0902001  0.0901389  -1.001  0.31698
## RaceOthers           0.0592385  0.0603545   0.982  0.32634
## DRGMed.NoC          -0.0216338  0.0230263  -0.940  0.34746
## DRGOtherMED          0.0679331  0.0298657   2.275  0.02293 *
## DRGOtherSURG         0.0540437  0.0362048   1.493  0.13551
## DRGSurg.C            0.0086575  0.0215849   0.401  0.68835
## DRGSurg.NoC         -0.0045170  0.0236140  -0.191  0.84830
## DRGUNGROUP           0.0704562  0.0778915   0.905  0.36571
## RaceGenderBlackF    -0.0159955  0.0493390  -0.324  0.74579
## RaceGenderHispanicF  0.1665655  0.1147644   1.451  0.14668
## RaceGenderOthersF   -0.1305341  0.0854834  -1.527  0.12676
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33928  on 50063  degrees of freedom
## AIC: 33966
##
## Number of Fisher Scoring iterations: 5
```

```
predsprobit <- predict(glmprobit,newdat=test.bin,type="response")

rocprobit <- roc(test.bin$Readmission.Status,predsprobit)
```

```
## Setting levels: control = 0, case = 1
```

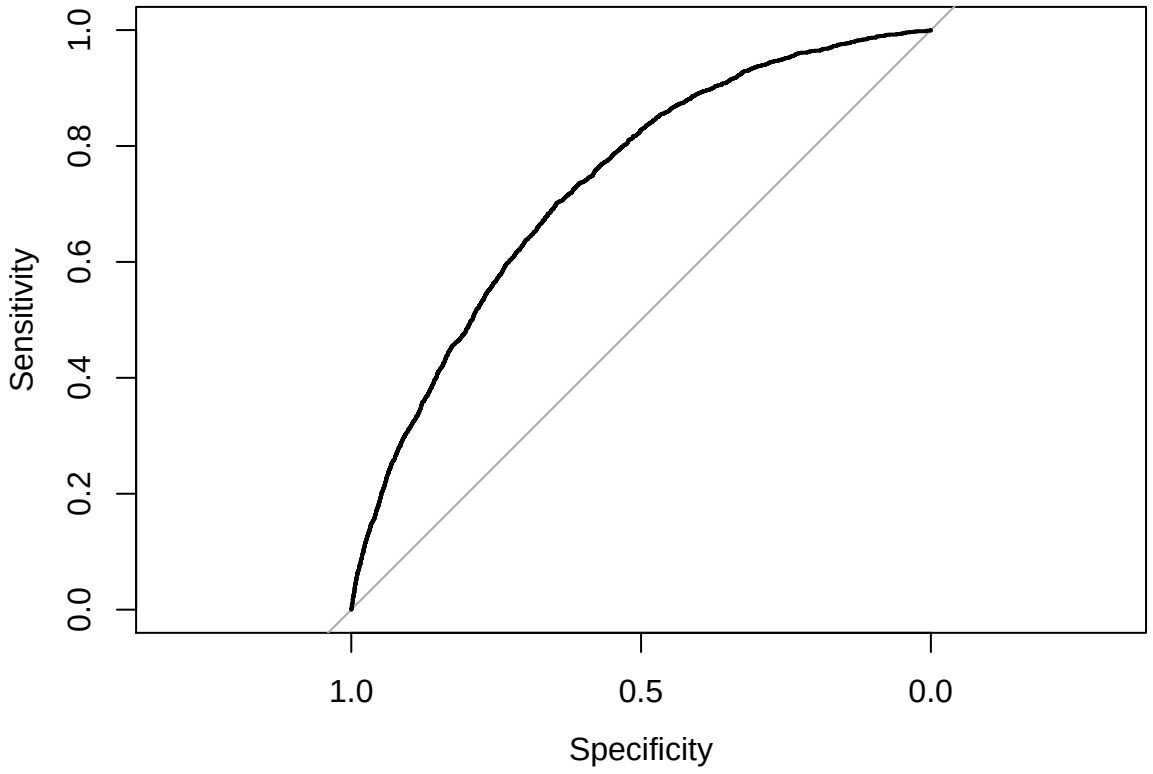
```
## Setting direction: controls < cases
```

```
confusionMatrix(factor(1*(predsprobit>.5)),factor(test.bin$Readmission.Status))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction     0     1
##          0 14638  2048
##          1     5     3
##
##                Accuracy : 0.877
##                  95% CI : (0.8719, 0.882)
##     No Information Rate : 0.8771
##     P-Value [Acc > NIR] : 0.5247
```

```
##
##                  Kappa : 0.002
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.999659
##             Specificity : 0.001463
##          Pos Pred Value : 0.877262
##          Neg Pred Value : 0.375000
##              Prevalence : 0.877141
##          Detection Rate : 0.876842
##    Detection Prevalence : 0.999521
##       Balanced Accuracy : 0.500561
##
##        'Positive' Class : 0
##
```

```
plot(rocprobit)
```




```
auc(rocprobit)
```

```
## Area under the curve: 0.7324
```

The next step is to run stepAIC on this model.

```
library(MASS)
stepAIC(glmprobit)
```

```
## Start:  AIC=33965.61
## Readmission.Status ~ Gender + ER + Age + logLOS + logRiskscore +
##     Under65 + RaceBlack + RaceHispanic + RaceOthers + DRGMed.NoC +
```

```
##     DRGOtherMED + DRGOtherSURG + DRGSurg.C + DRGSurg.NoC + DRGUNGROUP +
##     RaceGenderBlackF + RaceGenderHispanicF + RaceGenderOthersF
##
##                        Df Deviance   AIC
## - DRGSurg.NoC           1    33928 33964
## - ER                    1    33928 33964
## - RaceGenderBlackF      1    33928 33964
## - DRGSurg.C             1    33928 33964
## - Gender                1    33928 33964
## - DRGUNGROUP            1    33928 33964
## - DRGMed.NoC            1    33928 33964
## - RaceOthers            1    33929 33965
## - RaceHispanic          1    33929 33965
## - RaceBlack             1    33929 33965
## - Under65               1    33929 33965
## <none>                       33928 33966
## - RaceGenderHispanicF   1    33930 33966
## - DRGOtherSURG          1    33930 33966
## - RaceGenderOthersF     1    33930 33966
## - DRGOtherMED           1    33933 33969
## - logLOS                1    33937 33973
## - Age                   1    33954 33990
## - logRiskscore          1    37741 37777
##
## Step:  AIC=33963.65
## Readmission.Status ~ Gender + ER + Age + logLOS + logRiskscore +
##     Under65 + RaceBlack + RaceHispanic + RaceOthers + DRGMed.NoC +
##     DRGOtherMED + DRGOtherSURG + DRGSurg.C + DRGUNGROUP + RaceGenderBlackF +
##     RaceGenderHispanicF + RaceGenderOthersF
##
##                        Df Deviance   AIC
## - ER                    1    33928 33962
## - RaceGenderBlackF      1    33928 33962
## - DRGSurg.C             1    33928 33962
## - Gender                1    33928 33962
## - DRGUNGROUP            1    33929 33963
## - DRGMed.NoC            1    33929 33963
## - RaceOthers            1    33929 33963
## - RaceHispanic          1    33929 33963
## - RaceBlack             1    33929 33963
## - Under65               1    33929 33963
## <none>                       33928 33964
## - RaceGenderHispanicF   1    33930 33964
## - RaceGenderOthersF     1    33930 33964
## - DRGOtherSURG          1    33930 33964
## - DRGOtherMED           1    33934 33968
## - logLOS                1    33937 33971
## - Age                   1    33954 33988
## - logRiskscore          1    37742 37776
##
## Step:  AIC=33961.73
## Readmission.Status ~ Gender + Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + RaceHispanic + RaceOthers + DRGMed.NoC + DRGOtherMED +
##     DRGOtherSURG + DRGSurg.C + DRGUNGROUP + RaceGenderBlackF +
```

```
##     RaceGenderHispanicF + RaceGenderOthersF
##
##                        Df Deviance   AIC
## - RaceGenderBlackF      1    33928 33960
## - DRGSurg.C             1    33928 33960
## - Gender                1    33928 33960
## - DRGUNGROUP            1    33929 33961
## - DRGMed.NoC            1    33929 33961
## - RaceOthers            1    33929 33961
## - RaceHispanic          1    33929 33961
## - RaceBlack             1    33929 33961
## - Under65               1    33929 33961
## <none>                       33928 33962
## - RaceGenderHispanicF   1    33930 33962
## - RaceGenderOthersF     1    33930 33962
## - DRGOtherSURG          1    33930 33962
## - DRGOtherMED           1    33934 33966
## - logLOS                1    33937 33969
## - Age                   1    33954 33986
## - logRiskscore          1    37742 37774
##
## Step:  AIC=33959.83
## Readmission.Status ~ Gender + Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + RaceHispanic + RaceOthers + DRGMed.NoC + DRGOtherMED +
##     DRGOtherSURG + DRGSurg.C + DRGUNGROUP + RaceGenderHispanicF +
##     RaceGenderOthersF
##
##                        Df Deviance   AIC
## - DRGSurg.C             1    33928 33958
## - Gender                1    33928 33958
## - DRGUNGROUP            1    33929 33959
## - DRGMed.NoC            1    33929 33959
## - RaceOthers            1    33929 33959
## - RaceHispanic          1    33929 33959
## - RaceBlack             1    33929 33959
## - Under65               1    33930 33960
## <none>                       33928 33960
## - RaceGenderHispanicF   1    33930 33960
## - RaceGenderOthersF     1    33930 33960
## - DRGOtherSURG          1    33930 33960
## - DRGOtherMED           1    33934 33964
## - logLOS                1    33937 33967
## - Age                   1    33954 33984
## - logRiskscore          1    37742 37772
##
## Step:  AIC=33958.11
## Readmission.Status ~ Gender + Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + RaceHispanic + RaceOthers + DRGMed.NoC + DRGOtherMED +
##     DRGOtherSURG + DRGUNGROUP + RaceGenderHispanicF + RaceGenderOthersF
##
##                        Df Deviance   AIC
## - Gender                1    33929 33957
## - DRGUNGROUP            1    33929 33957
## - RaceOthers            1    33929 33957
```

```
## - RaceHispanic         1    33929 33957
## - DRGMed.NoC           1    33929 33957
## - RaceBlack            1    33930 33958
## - Under65              1    33930 33958
## <none>                      33928 33958
## - RaceGenderHispanicF  1    33930 33958
## - RaceGenderOthersF    1    33930 33958
## - DRGOtherSURG         1    33930 33958
## - DRGOtherMED          1    33934 33962
## - logLOS               1    33937 33965
## - Age                  1    33954 33982
## - logRiskscore         1    37742 37770
##
## Step:  AIC=33956.68
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + RaceHispanic + RaceOthers + DRGMed.NoC + DRGOtherMED +
##     DRGOtherSURG + DRGUNGROUP + RaceGenderHispanicF + RaceGenderOthersF
##
##                       Df Deviance   AIC
## - RaceOthers           1    33929 33955
## - DRGUNGROUP           1    33929 33955
## - RaceHispanic         1    33930 33956
## - DRGMed.NoC           1    33930 33956
## - RaceBlack            1    33930 33956
## - Under65              1    33930 33956
## - RaceGenderOthersF    1    33931 33957
## <none>                      33929 33957
## - DRGOtherSURG         1    33931 33957
## - RaceGenderHispanicF  1    33931 33957
## - DRGOtherMED          1    33934 33960
## - logLOS               1    33938 33964
## - Age                  1    33955 33981
## - logRiskscore         1    37743 37769
##
## Step:  AIC=33955.42
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + RaceHispanic + DRGMed.NoC + DRGOtherMED + DRGOtherSURG +
##     DRGUNGROUP + RaceGenderHispanicF + RaceGenderOthersF
##
##                       Df Deviance   AIC
## - DRGUNGROUP           1    33930 33954
## - RaceGenderOthersF    1    33931 33955
## - RaceHispanic         1    33931 33955
## - DRGMed.NoC           1    33931 33955
## - RaceBlack            1    33931 33955
## - Under65              1    33931 33955
## <none>                      33929 33955
## - DRGOtherSURG         1    33932 33956
## - RaceGenderHispanicF  1    33932 33956
## - DRGOtherMED          1    33935 33959
## - logLOS               1    33939 33963
## - Age                  1    33956 33980
## - logRiskscore         1    37743 37767
##
```

```
## Step:  AIC=33954.19
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + RaceHispanic + DRGMed.NoC + DRGOtherMED + DRGOtherSURG +
##     RaceGenderHispanicF + RaceGenderOthersF
##
##                        Df Deviance   AIC
## - RaceGenderOthersF     1    33931 33953
## - RaceHispanic          1    33931 33953
## - RaceBlack             1    33932 33954
## - DRGMed.NoC            1    33932 33954
## - Under65               1    33932 33954
## <none>                       33930 33954
## - DRGOtherSURG          1    33932 33954
## - RaceGenderHispanicF   1    33933 33955
## - DRGOtherMED           1    33936 33958
## - logLOS                1    33940 33962
## - Age                   1    33956 33978
## - logRiskscore          1    37747 37769
##
## Step:  AIC=33953.39
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + RaceHispanic + DRGMed.NoC + DRGOtherMED + DRGOtherSURG +
##     RaceGenderHispanicF
##
##                        Df Deviance   AIC
## - RaceHispanic          1    33933 33953
## - DRGMed.NoC            1    33933 33953
## - RaceBlack             1    33933 33953
## - Under65               1    33933 33953
## <none>                       33931 33953
## - DRGOtherSURG          1    33934 33954
## - RaceGenderHispanicF   1    33934 33954
## - DRGOtherMED           1    33937 33957
## - logLOS                1    33941 33961
## - Age                   1    33957 33977
## - logRiskscore          1    37749 37769
##
## Step:  AIC=33952.59
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + DRGMed.NoC + DRGOtherMED + DRGOtherSURG + RaceGenderHispanicF
##
##                        Df Deviance   AIC
## - RaceGenderHispanicF   1    33934 33952
## - DRGMed.NoC            1    33934 33952
## - Under65               1    33934 33952
## - RaceBlack             1    33934 33952
## <none>                       33933 33953
## - DRGOtherSURG          1    33935 33953
## - DRGOtherMED           1    33938 33956
## - logLOS                1    33942 33960
## - Age                   1    33958 33976
## - logRiskscore          1    37751 37769
##
## Step:  AIC=33951.95
```

```
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + DRGMed.NoC + DRGOtherMED + DRGOtherSURG
##
##                Df Deviance   AIC
## - DRGMed.NoC    1    33935 33951
## - RaceBlack     1    33936 33952
## - Under65       1    33936 33952
## <none>               33934 33952
## - DRGOtherSURG  1    33936 33952
## - DRGOtherMED   1    33940 33956
## - logLOS        1    33943 33959
## - Age           1    33960 33976
## - logRiskscore  1    37754 37770
##
## Step:  AIC=33951.46
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     RaceBlack + DRGOtherMED + DRGOtherSURG
##
##                Df Deviance   AIC
## - RaceBlack     1    33937 33951
## - Under65       1    33937 33951
## <none>               33935 33951
## - DRGOtherSURG  1    33938 33952
## - DRGOtherMED   1    33942 33956
## - logLOS        1    33945 33959
## - Age           1    33961 33975
## - logRiskscore  1    37754 37768
##
## Step:  AIC=33951.02
## Readmission.Status ~ Age + logLOS + logRiskscore + Under65 +
##     DRGOtherMED + DRGOtherSURG
##
##                Df Deviance   AIC
## - Under65       1    33938 33950
## <none>               33937 33951
## - DRGOtherSURG  1    33940 33952
## - DRGOtherMED   1    33944 33956
## - logLOS        1    33946 33958
## - Age           1    33964 33976
## - logRiskscore  1    37759 37771
##
## Step:  AIC=33950.44
## Readmission.Status ~ Age + logLOS + logRiskscore + DRGOtherMED +
##     DRGOtherSURG
##
##                Df Deviance   AIC
## <none>               33938 33950
## - DRGOtherSURG  1    33941 33951
## - DRGOtherMED   1    33945 33955
## - logLOS        1    33948 33958
## - Age           1    33981 33991
## - logRiskscore  1    37765 37775
##
```

```
## Call:  glm(formula = Readmission.Status ~ Age + logLOS + logRiskscore +
##     DRGOtherMED + DRGOtherSURG, family = binomial(link = "probit"),
##     data = train.bin)
##
## Coefficients:
##  (Intercept)           Age        logLOS  logRiskscore   DRGOtherMED
##     -1.50930      -0.00371       0.03436       0.71158       0.07107
## DRGOtherSURG
##      0.05586
##
## Degrees of Freedom: 50081 Total (i.e. Null);  50076 Residual
## Null Deviance:       38120
## Residual Deviance: 33940     AIC: 33950
```

The probit model is now run using the five surviving variables.

```
glmprobit <- glm(Readmission.Status ~ logLOS + Age + logRiskscore + DRGOtherSURG + DRGOtherMED, data=tra

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ logLOS + Age + logRiskscore +
##     DRGOtherSURG + DRGOtherMED, family = binomial(link = "probit"),
##     data = train.bin)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2840  -0.5759  -0.3948  -0.2391   3.2705
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.5092975  0.0469985 -32.114  < 2e-16 ***
## logLOS        0.0343635  0.0112216   3.062   0.0022 **
## Age          -0.0037101  0.0005667  -6.547 5.88e-11 ***
## logRiskscore  0.7115770  0.0124458  57.174  < 2e-16 ***
## DRGOtherSURG  0.0558636  0.0341427   1.636   0.1018
## DRGOtherMED   0.0710677  0.0273260   2.601   0.0093 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33938  on 50076  degrees of freedom
## AIC: 33950
##
## Number of Fisher Scoring iterations: 5
```

```
predsprobit <- predict(glmprobit,newdat=test.bin,type="response")

rocprobit <- roc(test.bin$Readmission.Status,predsprobit)
```

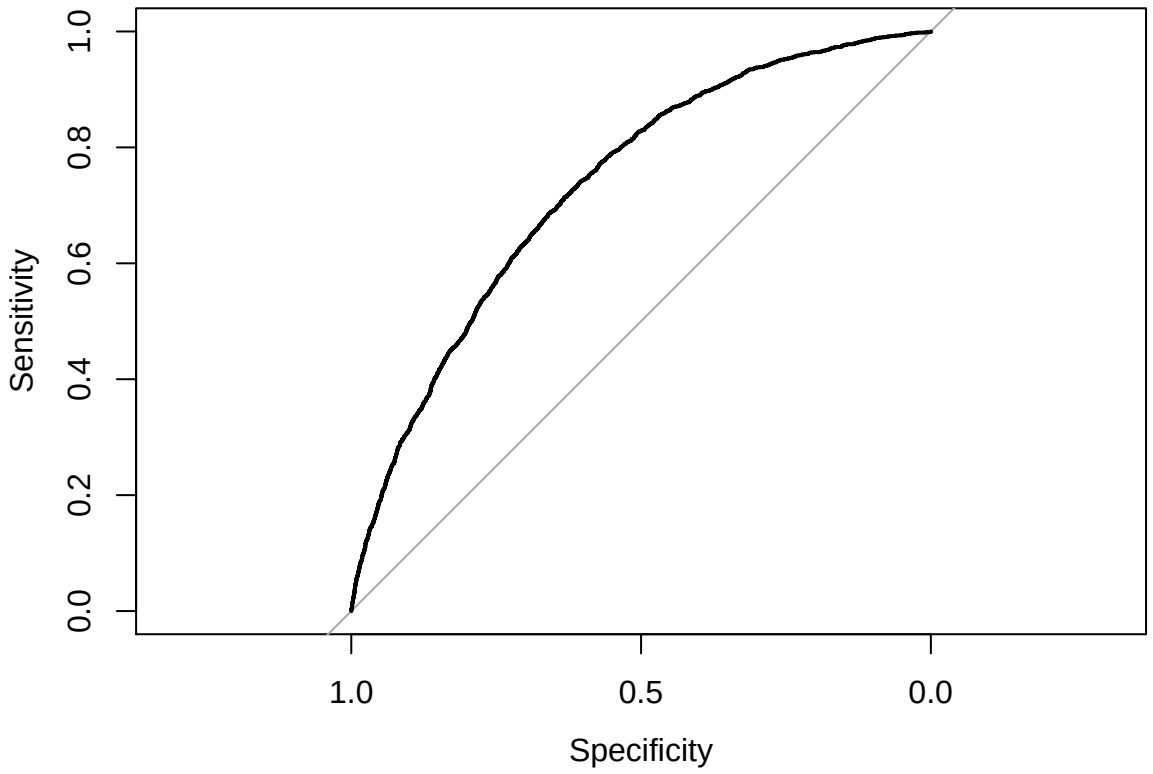
```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```r
confusionMatrix(factor(1*(predsprobit>.5)),factor(test.bin$Readmission.Status))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction     0     1
##          0 14639  2047
##          1     4     4
##
##                Accuracy : 0.8771
##                  95% CI : (0.8721, 0.8821)
##     No Information Rate : 0.8771
##     P-Value [Acc > NIR] : 0.5059
##
##                   Kappa : 0.0029
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.99973
##             Specificity : 0.00195
##          Pos Pred Value : 0.87732
##          Neg Pred Value : 0.50000
##              Prevalence : 0.87714
##          Detection Rate : 0.87690
##    Detection Prevalence : 0.99952
##       Balanced Accuracy : 0.50084
##
##        'Positive' Class : 0
##
```

```r
plot(rocprobit)
```




```
auc(rocprobit)
```

```
## Area under the curve: 0.7334
```

Task 8

I first run the model on the full dataset.

```
glmprobit <- glm(Readmission.Status ~ logLOS + Age + logRiskscore + DRGOtherSURG + DRGOtherMED, data=rea

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ logLOS + Age + logRiskscore +
##     DRGOtherSURG + DRGOtherMED, family = binomial(link = "probit"),
##     data = readmission.bin)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2680  -0.5747  -0.3952  -0.2421   3.9745
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.5026235  0.0407530 -36.871  < 2e-16 ***
## logLOS        0.0329948  0.0097365   3.389 0.000702 ***
## Age          -0.0036999  0.0004916  -7.526 5.25e-14 ***
## logRiskscore  0.7008229  0.0107283  65.325  < 2e-16 ***
## DRGOtherSURG  0.0560715  0.0293707   1.909 0.056250 .
```

```
## DRGOtherMED   0.0691546  0.0237996   2.906 0.003664 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 50559  on 66775  degrees of freedom
## Residual deviance: 45116  on 66770  degrees of freedom
## AIC: 45128
##
## Number of Fisher Scoring iterations: 5
```

I now create some arbitrary patients to learn how changing the values affects the predicted probability of readmission.

```
new.data <- data.frame("logLOS" = c(log(5),log(6),log(5),log(5),log(5),log(5)), "Age" = c(75,75,80,75,75
new.data
```

```
##     logLOS Age logRiskscore DRGOtherSURG DRGOtherMED
## 1 1.609438  75    0.6237971            0           0
## 2 1.791759  75    0.6237971            0           0
## 3 1.609438  80    0.6237971            0           0
## 4 1.609438  75    0.7193021            0           0
## 5 1.609438  75    0.6237971            1           0
## 6 1.609438  75    0.6237971            0           1
```

```
predict(glmprobit, newdat = new.data, type = "response")
```

```
##         1         2         3         4         5         6
## 0.09855331 0.09960192 0.09537932 0.11068247 0.10864481 0.11110281
```

Task 9

I rerun the model on the full dataset.

```
glmprobit <- glm(Readmission.Status ~ logLOS + Age + logRiskscore + DRGOtherSURG + DRGOtherMED, data=rea

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ logLOS + Age + logRiskscore +
##     DRGOtherSURG + DRGOtherMED, family = binomial(link = "probit"),
##     data = readmission.bin)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2680  -0.5747  -0.3952  -0.2421   3.9745
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.5026235  0.0407530 -36.871  < 2e-16 ***
## logLOS        0.0329948  0.0097365   3.389 0.000702 ***
## Age          -0.0036999  0.0004916  -7.526 5.25e-14 ***
## logRiskscore  0.7008229  0.0107283  65.325  < 2e-16 ***
## DRGOtherSURG  0.0560715  0.0293707   1.909 0.056250 .
```

```
## DRGOtherMED   0.0691546  0.0237996   2.906 0.003664 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 50559  on 66775  degrees of freedom
## Residual deviance: 45116  on 66770  degrees of freedom
## AIC: 45128
##
## Number of Fisher Scoring iterations: 5
```

```
predsprobit <- predict(glmprobit,newdat=readmission.bin,type="response")


confusionMatrix(factor(1*(predsprobit>.5)),factor(readmission.bin$Readmission.Status))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction     0     1
##          0 58356  8399
##          1    11    10
##
##                Accuracy : 0.8741
##                  95% CI : (0.8715, 0.8766)
##     No Information Rate : 0.8741
##     P-Value [Acc > NIR] : 0.5076
##
##                   Kappa : 0.0017
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.999812
##             Specificity : 0.001189
##          Pos Pred Value : 0.874182
##          Neg Pred Value : 0.476190
##              Prevalence : 0.874072
##          Detection Rate : 0.873907
##    Detection Prevalence : 0.999686
##       Balanced Accuracy : 0.500500
##
##        'Positive' Class : 0
##
```

This code calculates the cost for different cutoff values. I ran it at different values and am presting the final choice of 0.08.

```
cutoff <- 0.08
pred_readmit <- 1*(predsprobit > cutoff)
cm <- confusionMatrix(factor(pred_readmit),factor(readmission.bin$Readmission.Status))

no_intervention_cost <- 25*sum(readmission.bin$Readmission.Status == 1)
full_intervention_cost <- 2*nrow(readmission.bin)
modified_cost <- cm$table[2,1]*2+cm$table[2,2]*2+cm$table[1,2]*25
no_intervention_cost
```

```
## [1] 210225
```

```
full_intervention_cost
```

```
## [1] 133552
```

```
modified_cost
```

```
## [1] 106002
```

The final step is to get the confusion matrix.

```
cm
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction     0     1
##          0 26379  1096
##          1 31988  7313
##
##                Accuracy : 0.5046
##                  95% CI : (0.5008, 0.5084)
##     No Information Rate : 0.8741
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.125
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.4520
##             Specificity : 0.8697
##          Pos Pred Value : 0.9601
##          Neg Pred Value : 0.1861
##              Prevalence : 0.8741
##          Detection Rate : 0.3950
##    Detection Prevalence : 0.4115
##       Balanced Accuracy : 0.6608
##
##        'Positive' Class : 0
##
```

ALTERNATIVE FEATURE SELECTION

This section presents an alternative approach. It is based on using hypothesis tests to sequentially remove features. It begins by re-running the probit model on the training set using all the available features.

```
glmprobit <- glm(Readmission.Status ~ . + Race*Gender, data=train, family = binomial(link="probit"))

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ . + Race * Gender, family = binomial(link = "probit"),
##     data = train)
##
```

```
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2689  -0.5756  -0.3944  -0.2384   3.2478
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -1.4371865  0.0741325 -19.387  < 2e-16 ***
## GenderM               -0.0138744  0.0168726  -0.822  0.41090
## RaceBlack              0.0237364  0.0321619   0.738  0.46050
## RaceHispanic           0.0763654  0.0711823   1.073  0.28335
## RaceOthers            -0.0712955  0.0606013  -1.176  0.23941
## ER                    -0.0025486  0.0093214  -0.273  0.78454
## Age                   -0.0045131  0.0008786  -5.137 2.79e-07 ***
## logLOS                 0.0343572  0.0112270   3.060  0.00221 **
## logRiskscore           0.7121243  0.0124659  57.126  < 2e-16 ***
## Under65               -0.0408896  0.0314227  -1.301  0.19316
## DRGMed.NoC            -0.0216338  0.0230263  -0.940  0.34746
## DRGOtherMED            0.0679331  0.0298657   2.275  0.02293 *
## DRGOtherSURG           0.0540437  0.0362048   1.493  0.13551
## DRGSurg.C              0.0086575  0.0215849   0.401  0.68835
## DRGSurg.NoC           -0.0045170  0.0236140  -0.191  0.84830
## DRGUNGROUP             0.0704562  0.0778915   0.905  0.36571
## GenderM:RaceBlack      0.0159955  0.0493390   0.324  0.74579
## GenderM:RaceHispanic -0.1665655  0.1147644  -1.451  0.14668
## GenderM:RaceOthers     0.1305341  0.0854834   1.527  0.12676
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33928  on 50063  degrees of freedom
## AIC: 33966
##
## Number of Fisher Scoring iterations: 5
```

It is difficult to deal with a categorical interaction variable if the goal is to remove levels. With the interaction, there are actually 8 levels in play and they would need to be created as a new variable in order to merge some of them. Given that none of the three interaction terms appear to add value, I'll save time and go ahead and remove them.

```
glmprobit <- glm(Readmission.Status ~ ., data=train, family = binomial(link="probit"))

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ ., family = binomial(link = "probit"),
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2706  -0.5757  -0.3945  -0.2387   3.2499
##
## Coefficients:
```

```
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.4392073  0.0740620 -19.432  < 2e-16 ***
## GenderM      -0.0107974  0.0154547  -0.699  0.48477
## RaceBlack     0.0304827  0.0246611   1.236  0.21644
## RaceHispanic  0.0102060  0.0557975   0.183  0.85487
## RaceOthers   -0.0067658  0.0427270  -0.158  0.87418
## ER           -0.0025921  0.0093202  -0.278  0.78092
## Age          -0.0045021  0.0008785  -5.125 2.98e-07 ***
## logLOS        0.0343042  0.0112250   3.056  0.00224 **
## logRiskscore  0.7122625  0.0124642  57.145  < 2e-16 ***
## Under65      -0.0405129  0.0314153  -1.290  0.19719
## DRGMed.NoC   -0.0220462  0.0230238  -0.958  0.33830
## DRGOtherMED   0.0683215  0.0298592   2.288  0.02213 *
## DRGOtherSURG  0.0531373  0.0362010   1.468  0.14215
## DRGSurg.C     0.0083802  0.0215833   0.388  0.69782
## DRGSurg.NoC  -0.0045720  0.0236071  -0.194  0.84643
## DRGUNGROUP    0.0678532  0.0778955   0.871  0.38371
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33932  on 50066  degrees of freedom
## AIC: 33964
##
## Number of Fisher Scoring iterations: 5
```

Normally the next step would be combine Race-Others with Race-White (the base) but given the similarity to Race-Hispanic, both will be combined with Race-White. This is mostly done to save time.

```
readmission$RaceGender <- NULL #Need to remove this variable that was created earlier.

readmission2<-readmission

library(plyr)
var <- "Race"
var.levels <- levels(readmission2[,var])
readmission2[,var] <- mapvalues(readmission2[,var],var.levels,c("NonBlack","Black","NonBlack","NonBlack
#Relevel
table <- as.data.frame(table(readmission2[,var]))
  max <- which.max(table[,2])
  level.name <- as.character(table[max,1])
  readmission2[,var] <- relevel(readmission2[,var], ref = level.name)

table(readmission2[,var])
```

```
##
## NonBlack    Black
##    59679     7097
```

Running the model again, remembering to create new train and test sets. The same partition continues to be used to keep results consistent.

```
readmission <- readmission2
train <- readmission[partition,]
```

```
test <- readmission[-partition,]
glmprobit <- glm(Readmission.Status ~ ., data=train, family = binomial(link="probit"))

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ ., family = binomial(link = "probit"),
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2707  -0.5759  -0.3945  -0.2387   3.2495
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.439477   0.073950 -19.465  < 2e-16 ***
## GenderM      -0.010864   0.015453  -0.703  0.48201
## RaceBlack     0.030502   0.024555   1.242  0.21416
## ER           -0.002584   0.009320  -0.277  0.78156
## Age          -0.004499   0.000878  -5.124 2.98e-07 ***
## logLOS        0.034325   0.011224   3.058  0.00223 **
## logRiskscore  0.712279   0.012464  57.147  < 2e-16 ***
## Under65      -0.040346   0.031403  -1.285  0.19886
## DRGMed.NoC   -0.022075   0.023023  -0.959  0.33763
## DRGOtherMED   0.068353   0.029858   2.289  0.02206 *
## DRGOtherSURG  0.053060   0.036199   1.466  0.14271
## DRGSurg.C     0.008356   0.021583   0.387  0.69863
## DRGSurg.NoC  -0.004598   0.023606  -0.195  0.84556
## DRGUNGROUP    0.067814   0.077894   0.871  0.38397
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33932  on 50068  degrees of freedom
## AIC: 33960
##
## Number of Fisher Scoring iterations: 5
```

For similar reasons, we simultaneously merge the two insignificant DRG levels into the base.

```
readmission2<-readmission

var <- "DRG"
var.levels <- levels(readmission2[,var])
readmission2[,var] <- mapvalues(readmission2[,var],var.levels,c("DRGbase","Med.NoC","OtherMED","OtherSU
#Relevel
table <- as.data.frame(table(readmission2[,var]))
  max <- which.max(table[,2])
  level.name <- as.character(table[max,1])
  readmission2[,var] <- relevel(readmission2[,var], ref = level.name)

table(readmission2[,var])
```

```
##
##   DRGbase   Med.NoC  OtherMED OtherSURG   UNGROUP
##     45121     12310      5357      3424       564
```

```
readmission <- readmission2
train <- readmission[partition,]
test <- readmission[-partition,]
glmprobit <- glm(Readmission.Status ~ ., data=train, family = binomial(link="probit"))

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ ., family = binomial(link = "probit"),
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2706  -0.5759  -0.3946  -0.2387   3.2554
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.438216   0.073069 -19.683  < 2e-16 ***
## GenderM      -0.010833   0.015452  -0.701  0.48325
## RaceBlack     0.030546   0.024555   1.244  0.21350
## ER           -0.002595   0.009320  -0.278  0.78065
## Age          -0.004493   0.000878  -5.118 3.09e-07 ***
## logLOS        0.034320   0.011223   3.058  0.00223 **
## logRiskscore  0.712242   0.012463  57.147  < 2e-16 ***
## Under65      -0.040227   0.031401  -1.281  0.20017
## DRGMed.NoC   -0.023769   0.020119  -1.181  0.23744
## DRGOtherMED   0.066662   0.027689   2.408  0.01606 *
## DRGOtherSURG  0.051371   0.034428   1.492  0.13567
## DRGUNGROUP    0.066127   0.077090   0.858  0.39101
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33933  on 50070  degrees of freedom
## AIC: 33957
##
## Number of Fisher Scoring iterations: 5
```

Now remove ER.

```
glmprobit <- glm(Readmission.Status ~ Gender + Race + Age + logLOS + logRiskscore + Under65 + DRG, data=

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ Gender + Race + Age + logLOS +
```

```
##     logRiskscore + Under65 + DRG, family = binomial(link = "probit"),
##     data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2714  -0.5761  -0.3946  -0.2387   3.2566
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.439469   0.072930 -19.738  < 2e-16 ***
## GenderM      -0.010808   0.015452  -0.699  0.48426
## RaceBlack     0.030535   0.024555   1.244  0.21367
## Age          -0.004495   0.000878  -5.119 3.07e-07 ***
## logLOS        0.034349   0.011223   3.061  0.00221 **
## logRiskscore  0.712211   0.012463  57.148  < 2e-16 ***
## Under65      -0.040278   0.031400  -1.283  0.19959
## DRGMed.NoC   -0.023733   0.020119  -1.180  0.23815
## DRGOtherMED   0.066616   0.027688   2.406  0.01613 *
## DRGOtherSURG  0.051364   0.034428   1.492  0.13572
## DRGUNGROUP    0.066078   0.077092   0.857  0.39137
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33933  on 50071  degrees of freedom
## AIC: 33955
##
## Number of Fisher Scoring iterations: 5
```

Now remove Gender

```
glmprobit <- glm(Readmission.Status ~  Race + Age + logLOS + logRiskscore + Under65 + DRG, data=train, f

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ Race + Age + logLOS + logRiskscore +
##     Under65 + DRG, family = binomial(link = "probit"), data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2749  -0.5758  -0.3947  -0.2389   3.2608
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.4479936  0.0719116 -20.136  < 2e-16 ***
## RaceBlack     0.0308596  0.0245506   1.257  0.20876
## Age          -0.0044419  0.0008748  -5.078 3.82e-07 ***
## logLOS        0.0343108  0.0112223   3.057  0.00223 **
## logRiskscore  0.7120724  0.0124610  57.144  < 2e-16 ***
## Under65      -0.0395810  0.0313830  -1.261  0.20723
## DRGMed.NoC   -0.0237511  0.0201186  -1.181  0.23778
```

```
## DRGOtherMED   0.0667391  0.0276865   2.411  0.01593 *
## DRGOtherSURG  0.0515353  0.0344275   1.497  0.13441
## DRGUNGROUP    0.0658603  0.0770924   0.854  0.39294
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33933  on 50072  degrees of freedom
## AIC: 33953
##
## Number of Fisher Scoring iterations: 5
```

Rather than remove DRGUNGROUP at this stage, it will be combined with DRGOtherSURG. The difference in significance is likely due to sample sizes.

```
readmission2<-readmission

var <- "DRG"
var.levels <- levels(readmission2[,var])
readmission2[,var] <- mapvalues(readmission2[,var],var.levels,c("DRGbase","Med.NoC","OtherMED","OSUngrou
#Relevel
table <- as.data.frame(table(readmission2[,var]))
  max <- which.max(table[,2])
  level.name <- as.character(table[max,1])
  readmission2[,var] <- relevel(readmission2[,var], ref = level.name)

table(readmission2[,var])
```

```
##
##   DRGbase   Med.NoC  OtherMED OSUngroup
##     45121     12310      5357      3988
```

```
readmission <- readmission2
train <- readmission[partition,]
test <- readmission[-partition,]
glmprobit <- glm(Readmission.Status ~ Race + Age + logLOS + logRiskscore + Under65 + DRG, data=train, fa

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ Race + Age + logLOS + logRiskscore +
##     Under65 + DRG, family = binomial(link = "probit"), data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2749  -0.5758  -0.3947  -0.2390   3.2609
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.4480241  0.0719121 -20.136  < 2e-16 ***
## RaceBlack     0.0308837  0.0245501   1.258  0.20840
## Age          -0.0044420  0.0008748  -5.078 3.82e-07 ***
## logLOS        0.0343218  0.0112225   3.058  0.00223 **
```

```
## logRiskscore  0.7120944  0.0124602  57.149  < 2e-16 ***
## Under65      -0.0395813  0.0313827  -1.261  0.20722
## DRGMed.NoC   -0.0237522  0.0201187  -1.181  0.23776
## DRGOtherMED   0.0667366  0.0276866   2.410  0.01593 *
## DRGOSUngroup  0.0537795  0.0318155   1.690  0.09096 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33933  on 50073  degrees of freedom
## AIC: 33951
##
## Number of Fisher Scoring iterations: 5
```

Next to go is Med.NoC with the hightest p-value.

```
readmission2<-readmission

var <- "DRG"
var.levels <- levels(readmission2[,var])
readmission2[,var] <- mapvalues(readmission2[,var],var.levels,c("DRGbase","DRGbase","OtherMED","OSUngrou
#Relevel
table <- as.data.frame(table(readmission2[,var]))
  max <- which.max(table[,2])
  level.name <- as.character(table[max,1])
  readmission2[,var] <- relevel(readmission2[,var], ref = level.name)

table(readmission2[,var])
```

```
##
##   DRGbase  OtherMED OSUngroup
##     57431      5357      3988
```

```
readmission <- readmission2
train <- readmission[partition,]
test <- readmission[-partition,]
glmprobit <- glm(Readmission.Status ~ Race + Age + logLOS + logRiskscore + Under65 + DRG, data=train, fa

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ Race + Age + logLOS + logRiskscore +
##     Under65 + DRG, family = binomial(link = "probit"), data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2749  -0.5759  -0.3944  -0.2391   3.2651
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.4524752  0.0718246 -20.223  < 2e-16 ***
## RaceBlack     0.0305938  0.0245494   1.246  0.21269
## Age          -0.0044443  0.0008748  -5.081 3.76e-07 ***
```

```
## logLOS        0.0341318  0.0112210   3.042  0.00235 **
## logRiskscore  0.7119330  0.0124591  57.142  < 2e-16 ***
## Under65      -0.0394441  0.0313816  -1.257  0.20878
## DRGOtherMED   0.0718764  0.0273458   2.628  0.00858 **
## DRGOSUngroup  0.0589066  0.0315200   1.869  0.06164 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33935  on 50074  degrees of freedom
## AIC: 33951
##
## Number of Fisher Scoring iterations: 5
```

Now remove Race.

```
readmission <- readmission2
train <- readmission[partition,]
test <- readmission[-partition,]
glmprobit <- glm(Readmission.Status ~ Age + logLOS + logRiskscore + Under65 + DRG, data=train, family =

summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ Age + logLOS + logRiskscore +
##     Under65 + DRG, family = binomial(link = "probit"), data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2801  -0.5760  -0.3945  -0.2391   3.2626
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.4456943  0.0716320 -20.182  < 2e-16 ***
## Age          -0.0044962  0.0008739  -5.145 2.68e-07 ***
## logLOS        0.0340328  0.0112205   3.033  0.00242 **
## logRiskscore  0.7121407  0.0124577  57.165  < 2e-16 ***
## Under65      -0.0371728  0.0313192  -1.187  0.23527
## DRGOtherMED   0.0721155  0.0273450   2.637  0.00836 **
## DRGOSUngroup  0.0588470  0.0315197   1.867  0.06190 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33936  on 50075  degrees of freedom
## AIC: 33950
##
## Number of Fisher Scoring iterations: 5
```

Now remove Under65.

```
readmission <- readmission2
train <- readmission[partition,]
test <- readmission[-partition,]
glmprobit <- glm(Readmission.Status ~ Age + logLOS + logRiskscore + DRG, data=train, family = binomial(
summary(glmprobit)
```

```
##
## Call:
## glm(formula = Readmission.Status ~ Age + logLOS + logRiskscore +
##     DRG, family = binomial(link = "probit"), data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2838  -0.5759  -0.3948  -0.2391   3.2709
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.5099622  0.0470000 -32.127  < 2e-16 ***
## Age          -0.0037063  0.0005667  -6.540 6.15e-11 ***
## logLOS        0.0341991  0.0112199   3.048  0.00230 **
## logRiskscore  0.7114348  0.0124460  57.162  < 2e-16 ***
## DRGOtherMED   0.0719061  0.0273415   2.630  0.00854 **
## DRGOSUngroup  0.0590267  0.0315181   1.873  0.06110 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38117  on 50081  degrees of freedom
## Residual deviance: 33938  on 50076  degrees of freedom
## AIC: 33950
##
## Number of Fisher Scoring iterations: 5
```

Everything is now significant at the 10% level and we stop. If we wanted a lower significance level for decision making, the process would continue.