script_qviews.R

r439596

2022-05-09

```
# Title: qVIEWS
```

```
# Author: Jeronimo Moreno Cuesta
# Date: 4.5.2022

# Read data
data <- read.table("data.txt",header=T,sep="\t")
head(data)
```

```
##   study_number sreen_date group sex age ethnicity consent type_of_consent Total
## 1            1 23/07/2021     1   0  57         2       0               2     5
## 2            2 22/07/2021     1   0  26         2       1               1     5
## 3            3 25/07/2021     1   0  73         2       1               1    19
## 4            4 23/07/2021     1   0  63         3       0               2     7
## 5            5 02/08/2021     1   0  70         4       0               2    12
## 6            6 02/08/2021     1   1  55         3       0               2     8
##   rr sat air_oxygen sbp  hr avpu temp assessor1 assessor2 itu_admission
## 1 24  89          1 172 100    1 36.2         2        NA             1
## 2 24  95          1 114  78    1 37.0         1        NA             0
## 3 26  90          1  80 118    2 34.0         3        NA             1
## 4 26  98          1 139 100    1 39.0         2        NA             0
## 5 26  95          1  87 110    1 38.0         1         2             0
## 6 26  91          1 150  81    1 37.0         2         2             1
##   time_after_review outcome  X X.1
## 1                 0       0 NA  NA
## 2              <NA>       0 NA  NA
## 3                 0       0 NA  NA
## 4              <NA>       0 NA  NA
## 5                 1       0 NA  NA
## 6                 0       0 NA  NA
```

```
data <-data[1:254,-c(22,23)]
names(data)
```

```
##  [1] "study_number"      "sreen_date"        "group"
##  [4] "sex"               "age"               "ethnicity"
##  [7] "consent"           "type_of_consent"   "Total"
## [10] "rr"                "sat"               "air_oxygen"
## [13] "sbp"               "hr"                "avpu"
## [16] "temp"              "assessor1"         "assessor2"
## [19] "itu_admission"     "time_after_review" "outcome"
```

```
# Prepare data
str(data)
```

```
## 'data.frame':    254 obs. of  21 variables:
##  $ study_number     : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ sreen_date       : chr  "23/07/2021" "22/07/2021" "25/07/2021" "23/07/2021" ...
##  $ group            : int  1 1 1 1 1 1 0 1 1 0 ...
##  $ sex              : int  0 0 0 0 0 1 0 0 1 1 ...
##  $ age              : int  57 26 73 63 70 55 33 67 63 55 ...
##  $ ethnicity        : int  2 2 2 3 4 3 2 3 1 3 ...
##  $ consent          : int  0 1 1 0 0 0 0 1 1 0 ...
##  $ type_of_consent  : int  2 1 1 2 2 2 2 1 1 2 ...
##  $ Total            : int  5 5 19 7 12 8 0 7 5 2 ...
##  $ rr               : int  24 24 26 26 26 26 16 25 19 20 ...
##  $ sat              : int  89 95 90 98 95 91 98 96 96 96 ...
##  $ air_oxygen       : chr  "1" "1" "1" "1" ...
##  $ sbp              : int  172 114 80 139 87 150 150 122 170 139 ...
##  $ hr               : int  100 78 118 100 110 81 88 80 95 87 ...
##  $ avpu             : int  1 1 2 1 1 1 1 1 1 1 ...
##  $ temp             : num  36.2 37 34 39 38 37 36.5 36.7 37 36.7 ...
##  $ assessor1        : int  2 1 3 2 1 2 0 2 2 1 ...
##  $ assessor2        : int  NA NA NA NA 2 2 0 2 2 1 ...
##  $ itu_admission    : int  1 0 1 0 0 1 1 0 1 1 ...
##  $ time_after_review: chr  "0" NA "0" NA ...
##  $ outcome          : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
Rdate1 <- strptime(as.character(data$sreen_date),"%d/%m/%Y")
data <- data.frame(data,Rdate1)
data$group <- as.factor(data$group)
data$sex <- as.factor(data$sex)
data$ethnicity <- as.factor(data$ethnicity)
data$consent <- as.factor(data$consent)
data$type_of_consent <- as.factor(data$type_of_consent)
data$air_oxygen <- as.factor(data$air_oxygen)
data$avpu <- as.factor(data$avpu)
data$itu_admission <- as.factor(data$itu_admission)
data$time_after_review <- as.factor(data$time_after_review)
data$outcome <- as.factor(data$outcome)
summary(data)
```

```
##   study_number     sreen_date         group     sex          age
##  Min.   :  1.00   Length:254         0   :149   0:126   Min.   :18.00
##  1st Qu.: 64.25   Class :character   1   :104   1:128   1st Qu.:50.25
##  Median :127.50   Mode  :character   NA's:  1           Median :63.00
##  Mean   :127.50                                        Mean   :60.89
##  3rd Qu.:190.75                                        3rd Qu.:74.00
##  Max.   :254.00                                        Max.   :95.00
##
##  ethnicity  consent type_of_consent     Total              rr
##  1   : 15   0: 65   1   :174        Min.   : 0.000   Min.   :15.00
##  2   : 51   1:189   2   : 31        1st Qu.: 1.000   1st Qu.:18.00
##  3   :156           3   :  3        Median : 4.000   Median :20.00
##  4   : 25           4   : 14        Mean   : 4.157   Mean   :20.88
##  NA's:  7           5   :  8        3rd Qu.: 6.000   3rd Qu.:22.00
##                     6   : 19        Max.   :19.000   Max.   :45.00
##                     NA's:  5                         NA's   :1
##       sat         air_oxygen      sbp              hr         avpu
##  Min.   : 60.00   0   : 71   Min.   : 64.0   Min.   : 18.00   1:240
```

```
##  1st Qu.: 93.00   1   :164   1st Qu.:110.0   1st Qu.: 80.00   2:  9
##  Median : 95.00   1%  :  2   Median :122.0   Median : 90.00   3:  3
##  Mean   : 94.15   2   : 15   Mean   :125.2   Mean   : 91.59   4:  2
##  3rd Qu.: 96.00   NA's:  2   3rd Qu.:140.0   3rd Qu.:103.00
##  Max.   :100.00              Max.   :181.0   Max.   :192.00
##  NA's   :4                                   NA's   :1
##       temp        assessor1       assessor2     itu_admission time_after_review
##  Min.   :34.0   Min.   :0.000   Min.   :0.000   0   :118      0   :  8
##  1st Qu.:36.1   1st Qu.:1.000   1st Qu.:1.000   1   :127      1   :115
##  Median :36.5   Median :1.000   Median :1.000   NA's:  9      N/A :  1
##  Mean   :36.6   Mean   :1.319   Mean   :1.318                 NA's:130
##  3rd Qu.:37.0   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :39.0   Max.   :3.000   Max.   :3.000
##                 NA's   :3       NA's   :43
##  outcome     Rdate1
##  0:247   Min.   :2021-07-15 00:00:00
##  1:  7   1st Qu.:2021-11-23 00:00:00
##          Median :2022-01-28 12:00:00
##          Mean   :2022-01-16 05:40:09
##          3rd Qu.:2022-03-26 18:00:00
##          Max.   :2022-04-28 00:00:00
##
```

```
data$air_oxygen[data$air_oxygen=="1%"] <- 1
summary(data)
```

```
##   study_number     sreen_date         group     sex          age
##  Min.   :  1.00   Length:254         0   :149   0:126   Min.   :18.00
##  1st Qu.: 64.25   Class :character   1   :104   1:128   1st Qu.:50.25
##  Median :127.50   Mode  :character   NA's:  1           Median :63.00
##  Mean   :127.50                                        Mean   :60.89
##  3rd Qu.:190.75                                        3rd Qu.:74.00
##  Max.   :254.00                                        Max.   :95.00
##
##  ethnicity  consent type_of_consent     Total             rr
##  1   : 15   0: 65   1   :174        Min.   : 0.000   Min.   :15.00
##  2   : 51   1:189   2   : 31        1st Qu.: 1.000   1st Qu.:18.00
##  3   :156           3   :  3        Median : 4.000   Median :20.00
##  4   : 25           4   : 14        Mean   : 4.157   Mean   :20.88
##  NA's:  7           5   :  8        3rd Qu.: 6.000   3rd Qu.:22.00
##                     6   : 19        Max.   :19.000   Max.   :45.00
##                     NA's:  5                         NA's   :1
##       sat         air_oxygen      sbp             hr         avpu
##  Min.   : 60.00   0   : 71   Min.   : 64.0   Min.   : 18.00   1:240
##  1st Qu.: 93.00   1   :166   1st Qu.:110.0   1st Qu.: 80.00   2:  9
##  Median : 95.00   1%  :  0   Median :122.0   Median : 90.00   3:  3
##  Mean   : 94.15   2   : 15   Mean   :125.2   Mean   : 91.59   4:  2
##  3rd Qu.: 96.00   NA's:  2   3rd Qu.:140.0   3rd Qu.:103.00
##  Max.   :100.00              Max.   :181.0   Max.   :192.00
##  NA's   :4                                   NA's   :1
##       temp        assessor1       assessor2     itu_admission time_after_review
##  Min.   :34.0   Min.   :0.000   Min.   :0.000   0   :118      0   :  8
##  1st Qu.:36.1   1st Qu.:1.000   1st Qu.:1.000   1   :127      1   :115
##  Median :36.5   Median :1.000   Median :1.000   NA's:  9      N/A :  1
##  Mean   :36.6   Mean   :1.319   Mean   :1.318                 NA's:130
```

```
##  3rd Qu.:37.0   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :39.0   Max.   :3.000   Max.   :3.000
##                 NA's   :3       NA's   :43
##  outcome     Rdate1
##  0:247   Min.   :2021-07-15 00:00:00
##  1:  7   1st Qu.:2021-11-23 00:00:00
##          Median :2022-01-28 12:00:00
##          Mean   :2022-01-16 05:40:09
##          3rd Qu.:2022-03-26 18:00:00
##          Max.   :2022-04-28 00:00:00
##
```

```
data_consent <- data[data$consent=="1",]


# Table investigating assessor1 versus itu_admission
table(data_consent$assessor1,data_consent$itu_admission)
```

```
##
##      0  1
##   0 16 12
##   1 35 43
##   2 31 37
##   3  3  5
```

```
chisq.test(data_consent$assessor1,data_consent$itu_admission)
```

```
## Warning in chisq.test(data_consent$assessor1, data_consent$itu_admission): Chi-
## squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent$assessor1 and data_consent$itu_admission
## X-squared = 1.6373, df = 3, p-value = 0.651
```

```
# Table grouping assessor1 versus itu_admission
assessor1_group <- ifelse(data_consent$assessor1==0,0,9)
assessor1_group <- as.factor(assessor1_group)
ole <- table(assessor1_group,data_consent$itu_admission);ole
```

```
##
## assessor1_group  0  1
##               0 16 12
##               9 69 85
```

```
chisq.test(assessor1_group,data_consent$itu_admission)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  assessor1_group and data_consent$itu_admission
## X-squared = 0.99559, df = 1, p-value = 0.3184
```

```
# Sensitivity, specificity of assessor1 versus itu_admission in ole table
mx <- matrix(c(69,85,16,12),byrow=T,nrow=2)# Order is modified to allow FD as "a"
facial_display <- c("a","b")
rownames(mx) <- facial_display
```

```r
admission_names <- c("a","b")
colnames(mx) <- admission_names
mx
```

```
##    a  b
## a 69 85
## b 16 12
```

```r
library(caret)
```

```
## Loading required package: ggplot2
```

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

```r
confusionMatrix(mx)
```

```
## Confusion Matrix and Statistics
##
##    a  b
## a 69 85
## b 16 12
##
##                Accuracy : 0.4451
##                  95% CI : (0.3715, 0.5204)
##     No Information Rate : 0.533
##     P-Value [Acc > NIR] : 0.9928
##
##                   Kappa : -0.0614
##
##  Mcnemar's Test P-Value : 1.322e-11
##
##             Sensitivity : 0.8118
##             Specificity : 0.1237
##          Pos Pred Value : 0.4481
##          Neg Pred Value : 0.4286
##              Prevalence : 0.4670
##          Detection Rate : 0.3791
##    Detection Prevalence : 0.8462
##       Balanced Accuracy : 0.4677
##
##        'Positive' Class : a
##
```

```r
# Investigating if facial displays are better in predicting high risk group patients

data_consent_highrisk<- data_consent[data_consent$group=="1",]
table(data_consent_highrisk$assessor1,data_consent_highrisk$itu_admission)
```

```
##
##      0  1
##   0  3  1
##   1 14 11
##   2 17 15
##   3  3  5
```

```r
chisq.test(data_consent_highrisk$assessor1,data_consent_highrisk$itu_admission)
```

```
## Warning in chisq.test(data_consent_highrisk$assessor1,
## data_consent_highrisk$itu_admission): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_highrisk$assessor1 and data_consent_highrisk$itu_admission
## X-squared = 1.6312, df = 3, p-value = 0.6523
```

```
# Investigating if facial displays are better in predicitng low risk patients
data_consent_lowrisk<- data_consent[data_consent$group=="0",]
table(data_consent_lowrisk$assessor1,data_consent_lowrisk$itu_admission)
```

```
##
##      0  1
##   0 13 10
##   1 21 32
##   2 14 22
##   3  0  0
```

```
chisq.test(data_consent_lowrisk$assessor1,data_consent_lowrisk$itu_admission)
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_lowrisk$assessor1 and data_consent_lowrisk$itu_admission
## X-squared = 2.2115, df = 2, p-value = 0.331
```

```
#  Investigating if facial displays in women are better in predicitng admission to icu
data_consent_women <- data_consent[data_consent$sex=="0",]
table(data_consent_women$assessor1,data_consent_women$itu_admission)
```

```
##
##      0  1
##   0  5  7
##   1 20 11
##   2 20 16
##   3  0  4
```

```
chisq.test(data_consent_women$assessor1,data_consent_women$itu_admission)
```

```
## Warning in chisq.test(data_consent_women$assessor1,
## data_consent_women$itu_admission): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_women$assessor1 and data_consent_women$itu_admission
## X-squared = 6.849, df = 3, p-value = 0.07687
```

```
#  Investigating if facial displays in men are better in predicitng admission to icu
data_consent_men <- data_consent[data_consent$sex=="1",]
table(data_consent_men$assessor1,data_consent_men$itu_admission)
```

```
##
##      0  1
##   0 11  5
##   1 15 32
##   2 11 21
```

```
##   3  3  1
```

```
chisq.test(data_consent_men$assessor1,data_consent_men$itu_admission)
```

```
## Warning in chisq.test(data_consent_men$assessor1,
## data_consent_men$itu_admission): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_men$assessor1 and data_consent_men$itu_admission
## X-squared = 9.217, df = 3, p-value = 0.02654
```

```
# Investigating if facial displays according to ethnicity white are better in prediciting admission icu
data_consent_white <- data_consent[data_consent$ethnicity=="3",]
table(data_consent_white$assessor1,data_consent_white$itu_admission)
```

```
##
##      0  1
##   0 11  7
##   1 28 29
##   2 18 20
##   3  2  3
```

```
chisq.test(data_consent_white$assessor1,data_consent_white$itu_admission)
```

```
## Warning in chisq.test(data_consent_white$assessor1,
## data_consent_white$itu_admission): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_white$assessor1 and data_consent_white$itu_admission
## X-squared = 1.2117, df = 3, p-value = 0.7502
```

```
#  Investigating if facial displays according to ethnicity black are better in prediciting admission ic
data_consent_black <- data_consent[data_consent$ethnicity=="2",]
table(data_consent_black$assessor1,data_consent_black$itu_admission)
```

```
##
##      0  1
##   0  1  3
##   1  3  9
##   2  6 11
##   3  1  1
```

```
chisq.test(data_consent_black$assessor1,data_consent_black$itu_admission)
```

```
## Warning in chisq.test(data_consent_black$assessor1,
## data_consent_black$itu_admission): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_black$assessor1 and data_consent_black$itu_admission
## X-squared = 0.74476, df = 3, p-value = 0.8626
```

```
#  Investigating if facial displays according to ethnicity asian are better in prediciting admission ic
data_consent_asian <- data_consent[data_consent$ethnicity=="1",]
table(data_consent_asian$assessor1,data_consent_asian$itu_admission)
```

```
##
##     0 1
##   0 1 0
##   1 2 1
##   2 4 4
##   3 0 1
```

```
chisq.test(data_consent_asian$assessor1,data_consent_asian$itu_admission)
```

```
## Warning in chisq.test(data_consent_asian$assessor1,
## data_consent_asian$itu_admission): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_asian$assessor1 and data_consent_asian$itu_admission
## X-squared = 2.2698, df = 3, p-value = 0.5183
```

```
# Investigating if facial displays according to group age = Young are better in predicitn admission to
agecut <- cut(data_consent$age, breaks = 16+30*(0:3),labels=c("Young","Middle","Elderly"))
data_consent_age <- data.frame(data_consent,agecut)
data_consent_age_young <- data_consent_age[agecut=="Young",]
table(data_consent_age_young$assessor1,data_consent_age_young$itu_admission)
```

```
##
##     0 1
##   0 3 1
##   1 9 7
##   2 5 7
```

```
chisq.test(data_consent_age_young$assessor1,data_consent_age_young$itu_admission)
```

```
## Warning in chisq.test(data_consent_age_young$assessor1,
## data_consent_age_young$itu_admission): Chi-squared approximation may be
## incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_age_young$assessor1 and data_consent_age_young$itu_admission
## X-squared = 1.4641, df = 2, p-value = 0.4809
```

```
# Investigating if facial displays according to group age = Middle are better in predicitn admission to
data_consent_age_middle <- data_consent_age[agecut=="Middle",]
table(data_consent_age_middle$assessor1,data_consent_age_middle$itu_admission)
```

```
##
##      0  1
##   0 10 10
##   1 17 26
##   2 21 24
##   3  2  4
```

```
chisq.test(data_consent_age_middle$assessor1,data_consent_age_middle$itu_admission)
```

```
## Warning in chisq.test(data_consent_age_middle$assessor1,
## data_consent_age_middle$itu_admission): Chi-squared approximation may be
## incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_age_middle$assessor1 and data_consent_age_middle$itu_admission
## X-squared = 1.0469, df = 3, p-value = 0.7899
```

```
# Investigating if facial displays according to group age = Elderly are better in predicitn admission t
data_consent_age_elderly <- data_consent_age[agecut=="Elderly",]
table(data_consent_age_elderly$assessor1,data_consent_age_elderly$itu_admission)
```

```
##
##      0  1
##   0  3  1
##   1  9 10
##   2  5  6
##   3  1  1
```

```
chisq.test(data_consent_age_elderly$assessor1,data_consent_age_elderly$itu_admission)
```

```
## Warning in chisq.test(data_consent_age_elderly$assessor1,
## data_consent_age_elderly$itu_admission): Chi-squared approximation may be
## incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  data_consent_age_elderly$assessor1 and data_consent_age_elderly$itu_admission
## X-squared = 1.1435, df = 3, p-value = 0.7666
```

```
# logistic regression all data

mod1 <- glm(data_consent$itu_admission~data_consent$Total,family=binomial)
summary(mod1)
```

```
##
## Call:
## glm(formula = data_consent$itu_admission ~ data_consent$Total,
##     family = binomial)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.309  -1.231   1.051   1.106   1.415
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          0.30430    0.22660   1.343    0.179
## data_consent$Total -0.04464    0.04403  -1.014    0.311
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 254.29  on 183  degrees of freedom
## Residual deviance: 253.26  on 182  degrees of freedom
##   (5 observations deleted due to missingness)
## AIC: 257.26
##
## Number of Fisher Scoring iterations: 3
```

```
mod2 <- glm(data_consent$itu_admission~data_consent$assessor1+ data_consent$Total,family=binomial)
summary(mod2)
```

```
##
## Call:
## glm(formula = data_consent$itu_admission ~ data_consent$assessor1 +
##     data_consent$Total, family = binomial)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4984  -1.1903   0.9204   1.1024   1.3914
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)              0.01562    0.30279   0.052    0.959
## data_consent$assessor1   0.31215    0.20919   1.492    0.136
## data_consent$Total      -0.07437    0.04809  -1.546    0.122
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 251.51  on 181  degrees of freedom
## Residual deviance: 248.12  on 179  degrees of freedom
##   (7 observations deleted due to missingness)
## AIC: 254.12
##
## Number of Fisher Scoring iterations: 4
```

```
mod3 <- lm(data_consent$Total~data_consent$assessor1)
summary(mod3)
```

```
##
## Call:
## lm(formula = data_consent$Total ~ data_consent$assessor1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.0516 -2.3957 -0.3957  1.9484 12.2924
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)               1.7397     0.4571   3.806 0.000192 ***
## data_consent$assessor1    1.6560     0.2960   5.594 7.87e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.203 on 185 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1447, Adjusted R-squared:  0.1401
## F-statistic:  31.3 on 1 and 185 DF,  p-value: 7.869e-08
```

```
# Investigating facial displays by subgroup Low-Risk (LR) and High-Risk(HR)

names(data_consent)
```

```
##  [1] "study_number"      "sreen_date"        "group"
```

```
##  [4] "sex"               "age"               "ethnicity"
##  [7] "consent"           "type_of_consent"   "Total"
## [10] "rr"                "sat"               "air_oxygen"
## [13] "sbp"               "hr"                "avpu"
## [16] "temp"              "assessor1"         "assessor2"
## [19] "itu_admission"     "time_after_review" "outcome"
## [22] "Rdate1"
```

```
data_consent_LR <- data_consent[data_consent$group=="0",]
data_consent_HR <- data_consent[data_consent$group=="1",]

mod4 <- glm(data_consent_LR$itu_admission~data_consent_LR$Total,family=binomial)
summary(mod4)
```

```
##
## Call:
## glm(formula = data_consent_LR$itu_admission ~ data_consent_LR$Total,
##     family = binomial)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.357  -1.294   1.008   1.065   1.216
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            0.41364    0.29998   1.379    0.168
## data_consent_LR$Total -0.07212    0.12730  -0.567    0.571
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 155.78  on 113  degrees of freedom
## Residual deviance: 155.46  on 112  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 159.46
##
## Number of Fisher Scoring iterations: 4
```

```
mod5 <- glm(data_consent_LR$itu_admission~data_consent_LR$assessor1,family=binomial)
summary(mod5)
```

```
##
## Call:
## glm(formula = data_consent_LR$itu_admission ~ data_consent_LR$assessor1,
##     family = binomial)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4316  -1.2868   0.9429   1.0718   1.2086
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -0.07315    0.35176  -0.208    0.835
## data_consent_LR$assessor1   0.32664    0.26932   1.213    0.225
##
## (Dispersion parameter for binomial family taken to be 1)
```

```
##
##     Null deviance: 152.97  on 111  degrees of freedom
## Residual deviance: 151.48  on 110  degrees of freedom
##   (6 observations deleted due to missingness)
## AIC: 155.48
##
## Number of Fisher Scoring iterations: 4
```

```
mod6 <- glm(data_consent_LR$itu_admission~data_consent_LR$assessor1+ data_consent_LR$Total,family=binom
summary(mod6)
```

```
##
## Call:
## glm(formula = data_consent_LR$itu_admission ~ data_consent_LR$assessor1 +
##     data_consent_LR$Total, family = binomial)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5160  -1.2776   0.9091   1.0407   1.3086
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 0.08869    0.41237   0.215    0.830
## data_consent_LR$assessor1   0.33966    0.27057   1.255    0.209
## data_consent_LR$Total      -0.09798    0.12988  -0.754    0.451
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 152.97  on 111  degrees of freedom
## Residual deviance: 150.91  on 109  degrees of freedom
##   (6 observations deleted due to missingness)
## AIC: 156.91
##
## Number of Fisher Scoring iterations: 4
```

```
mod7 <- glm(data_consent_HR$itu_admission~data_consent_HR$Total,family=binomial)
summary(mod7)
```

```
##
## Call:
## glm(formula = data_consent_HR$itu_admission ~ data_consent_HR$Total,
##     family = binomial)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.290  -1.107  -1.057   1.249   1.438
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -0.59515    0.69964  -0.851    0.395
## data_consent_HR$Total  0.06116    0.08920   0.686    0.493
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 95.292  on 68  degrees of freedom
```

```
## Residual deviance: 94.813  on 67  degrees of freedom
##   (3 observations deleted due to missingness)
## AIC: 98.813
##
## Number of Fisher Scoring iterations: 4
```

```
mod8 <- glm(data_consent_HR$itu_admission~data_consent_HR$assessor1,family=binomial)
summary(mod8)
```

```
##
## Call:
## glm(formula = data_consent_HR$itu_admission ~ data_consent_HR$assessor1,
##     family = binomial)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3308  -1.1712  -0.8792   1.1837   1.5084
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -0.7512     0.5911  -1.271    0.204
## data_consent_HR$assessor1   0.3683     0.3256   1.131    0.258
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 95.292  on 68  degrees of freedom
## Residual deviance: 93.980  on 67  degrees of freedom
##   (3 observations deleted due to missingness)
## AIC: 97.98
##
## Number of Fisher Scoring iterations: 4
```

```
mod9 <- glm(data_consent_HR$itu_admission~data_consent_HR$assessor1+ data_consent_HR$Total,family=binom
summary(mod9)
```

```
##
## Call:
## glm(formula = data_consent_HR$itu_admission ~ data_consent_HR$assessor1 +
##     data_consent_HR$Total, family = binomial)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4017  -1.1345  -0.8859   1.1939   1.5143
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)               -0.92196    0.78422  -1.176    0.240
## data_consent_HR$assessor1  0.33124    0.34366   0.964    0.335
## data_consent_HR$Total      0.03154    0.09451   0.334    0.739
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 95.292  on 68  degrees of freedom
## Residual deviance: 93.867  on 66  degrees of freedom
##   (3 observations deleted due to missingness)
```

```
## AIC: 99.867
##
## Number of Fisher Scoring iterations: 4
#End of data analysis and end of script
```