A-novel-face-scale.R

r439596

2022-09-05

```
# Title: qVIEWS
```

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

# Read data
data <- read.table("data_final.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       1 NA  NA
## 4              <NA>       0 NA  NA
## 5                 1       0 NA  NA
## 6                 0       0 NA  NA
```

```
data <-data[1:398,-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':    398 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          : chr  "0" "0" "1" "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.   :  1.0   Length:398         0   :242   0:182   Min.   :18.00
##  1st Qu.:100.2   Class :character   1   :154   1:216   1st Qu.:51.00
##  Median :199.5   Mode  :character   2   :  1           Median :63.00
##  Mean   :199.5                      NA's:  1           Mean   :60.79
##  3rd Qu.:298.8                                         3rd Qu.:74.00
##  Max.   :398.0                                         Max.   :95.00
##
##  ethnicity  consent type_of_consent     Total              rr
##  1   : 26   0: 65   1   :294        Min.   : 0.000   Min.   :15.00
##  2   : 77   1:333   2   : 31        1st Qu.: 1.000   1st Qu.:18.00
##  3   :250           3   :  4        Median : 3.000   Median :20.00
##  4   : 38           4   : 14        Mean   : 3.947   Mean   :20.66
##  NA's:  7           5   :  8        3rd Qu.: 6.000   3rd Qu.:22.00
##                     6   : 42        Max.   :19.000   Max.   :45.00
##                     NA's:  5                         NA's   :1
##       sat         air_oxygen      sbp              hr         avpu
##  Min.   :  9.00   0   :128   Min.   : 64.0   Min.   : 18.00   1:383
```

```
##  1st Qu.: 93.00   1   :222   1st Qu.:110.0   1st Qu.: 78.00   2: 10
##  Median : 95.00   1%  :  2   Median :120.0   Median : 89.00   3:  3
##  Mean   : 94.08   2   : 44   Mean   :124.4   Mean   : 90.58   4:  2
##  3rd Qu.: 96.00   NA's:  2   3rd Qu.:140.0   3rd Qu.:102.00
##  Max.   :100.00              Max.   :197.0   Max.   :192.00
##  NA's   :4                                   NA's   :1
##       temp         assessor1       assessor2     itu_admission
##  Min.   :34.00   Min.   :0.000   Min.   :0.000   0   :204
##  1st Qu.:36.20   1st Qu.:1.000   1st Qu.:1.000   1   :180
##  Median :36.50   Median :1.000   Median :1.000   NA's: 14
##  Mean   :36.69   Mean   :1.367   Mean   :1.372
##  3rd Qu.:37.00   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :63.20   Max.   :3.000   Max.   :3.000
##                  NA's   :3       NA's   :43
##  time_after_review  outcome        Rdate1
##      :  2               :  1   Min.   :2021-07-15 00:00:00.00
##  0   : 93          0    :316   1st Qu.:2022-01-04 00:00:00.00
##  1   :168          1    : 52   Median :2022-03-31 00:00:00.00
##  N/A :  1          sill :  1   Mean   :2022-03-04 12:19:56.98
##  NA's:134          still: 28   3rd Qu.:2022-05-17 00:00:00.00
##                                Max.   :2022-06-27 00:00:00.00
##                                NA's   :1
```

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

```
##   study_number    sreen_date         group     sex          age
##  Min.   :  1.0   Length:398         0   :242   0:182   Min.   :18.00
##  1st Qu.:100.2   Class :character   1   :154   1:216   1st Qu.:51.00
##  Median :199.5   Mode  :character   2   :  1           Median :63.00
##  Mean   :199.5                      NA's:  1           Mean   :60.79
##  3rd Qu.:298.8                                         3rd Qu.:74.00
##  Max.   :398.0                                         Max.   :95.00
##
##  ethnicity  consent type_of_consent     Total             rr
##  1   : 26   0: 65   1   :294        Min.   : 0.000   Min.   :15.00
##  2   : 77   1:333   2   : 31        1st Qu.: 1.000   1st Qu.:18.00
##  3   :250           3   :  4        Median : 3.000   Median :20.00
##  4   : 38           4   : 14        Mean   : 3.947   Mean   :20.66
##  NA's:  7           5   :  8        3rd Qu.: 6.000   3rd Qu.:22.00
##                     6   : 42        Max.   :19.000   Max.   :45.00
##                     NA's:  5                         NA's   :1
##       sat         air_oxygen      sbp              hr         avpu
##  Min.   :  9.00   0   :128   Min.   : 64.0   Min.   : 18.00   1:383
##  1st Qu.: 93.00   1   :224   1st Qu.:110.0   1st Qu.: 78.00   2: 10
##  Median : 95.00   1%  :  0   Median :120.0   Median : 89.00   3:  3
##  Mean   : 94.08   2   : 44   Mean   :124.4   Mean   : 90.58   4:  2
##  3rd Qu.: 96.00   NA's:  2   3rd Qu.:140.0   3rd Qu.:102.00
##  Max.   :100.00              Max.   :197.0   Max.   :192.00
##  NA's   :4                                   NA's   :1
##       temp         assessor1       assessor2     itu_admission
##  Min.   :34.00   Min.   :0.000   Min.   :0.000   0   :204
##  1st Qu.:36.20   1st Qu.:1.000   1st Qu.:1.000   1   :180
##  Median :36.50   Median :1.000   Median :1.000   NA's: 14
##  Mean   :36.69   Mean   :1.367   Mean   :1.372
```

```
##  3rd Qu.:37.00   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :63.20   Max.   :3.000   Max.   :3.000
##                  NA's   :3       NA's   :43
##  time_after_review  outcome        Rdate1
##      :  2               :  1   Min.   :2021-07-15 00:00:00.00
##  0   : 93           0   :316   1st Qu.:2022-01-04 00:00:00.00
##  1   :168           1   : 52   Median :2022-03-31 00:00:00.00
##  N/A :  1           sill :  1   Mean   :2022-03-04 12:19:56.98
##  NA's:134           still: 28   3rd Qu.:2022-05-17 00:00:00.00
##                                 Max.   :2022-06-27 00:00:00.00
##                                 NA's   :1
```

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

# Inter-rater variability
class(data_consent$assessor1)
```

```
## [1] "integer"
```

```
class(data_consent$assessor2)
```

```
## [1] "integer"
```

```
db_agree <- as.data.frame (cbind(data_consent$assessor1,data_consent$assessor2))
library(irr)
```

```
## Loading required package: lpSolve
```

```
library(psych)
cohen.kappa(db_agree)# we use weighted estimates for nominal scales such as assessor
```

```
## Call: cohen.kappa1(x = x, w = w, n.obs = n.obs, alpha = alpha, levels = levels)
##
## Cohen Kappa and Weighted Kappa correlation coefficients and confidence boundaries
##                  lower estimate upper
## unweighted kappa  0.93     0.96  0.99
## weighted kappa    0.98     0.98  0.98
##
##  Number of subjects = 310
```

```
# Demography high-risk patients
data_consent_highrisk<- data_consent[data_consent$Total >= 5,]
summary(data_consent_highrisk)
```

```
##   study_number     sreen_date        group   sex         age        ethnicity
##  Min.   :  2.00   Length:120         0:  2   0:47   Min.   :19.00   1   :10
##  1st Qu.: 86.25   Class :character   1:118   1:73   1st Qu.:51.00   2   :24
##  Median :228.00   Mode  :character   2:  0          Median :64.00   3   :74
##  Mean   :210.98                                     Mean   :61.53   4   :10
##  3rd Qu.:325.50                                     3rd Qu.:74.00   NA's: 2
##  Max.   :396.00                                     Max.   :95.00
##
##  consent type_of_consent     Total             rr             sat
##  0:  0   1:98            Min.   : 5.000   Min.   :16.00   Min.   :79.00
##  1:120   2: 0            1st Qu.: 5.000   1st Qu.:20.00   1st Qu.:93.00
##          3: 0            Median : 7.000   Median :24.00   Median :95.00
##          4: 1            Mean   : 7.225   Mean   :23.71   Mean   :93.77
##          5: 0            3rd Qu.: 9.000   3rd Qu.:26.00   3rd Qu.:96.00
```

```
##          6:21            Max.   :19.000   Max.   :45.00   Max.   :99.00
##                                           NA's   :1       NA's   :1
##  air_oxygen      sbp              hr        avpu         temp
##  0   : 5    Min.   : 64.0   Min.   : 64.0   1:115   Min.   :34.00
##  1   :87    1st Qu.:103.8   1st Qu.: 88.0   2:  5   1st Qu.:36.40
##  1%  : 0    Median :118.0   Median :100.0   3:  0   Median :36.50
##  2   :27    Mean   :119.8   Mean   :101.1   4:  0   Mean   :37.05
##  NA's: 1    3rd Qu.:137.0   3rd Qu.:112.0           3rd Qu.:37.00
##             Max.   :197.0   Max.   :144.0           Max.   :63.20
##                             NA's   :1
##    assessor1       assessor2     itu_admission time_after_review  outcome
##  Min.   :0.000   Min.   :0.000   0   :68           : 1               : 1
##  1st Qu.:1.000   1st Qu.:1.000   1   :49       0   :34           0    :85
##  Median :2.000   Median :2.000   NA's: 3       1   :44           1    :23
##  Mean   :1.617   Mean   :1.613                 N/A : 0           sill : 1
##  3rd Qu.:2.000   3rd Qu.:2.000                 NA's:41           still:10
##  Max.   :3.000   Max.   :3.000
##                  NA's   :14
##      Rdate1
##  Min.   :2021-07-15 00:00:00.00
##  1st Qu.:2021-12-09 00:00:00.00
##  Median :2022-04-14 00:00:00.00
##  Mean   :2022-03-06 18:21:10.58
##  3rd Qu.:2022-05-27 00:00:00.00
##  Max.   :2022-06-25 00:00:00.00
##  NA's   :1
```

```
sd(data_consent_highrisk$age)
```

```
## [1] 17.00269
```

```
sd(data_consent_highrisk$Total)
```

```
## [1] 2.342384
```

```
sd(data_consent_highrisk$rr,na.rm=T)
```

```
## [1] 5.459175
```

```
sd(data_consent_highrisk$sat,na.rm=T)
```

```
## [1] 3.880497
```

```
sd(data_consent_highrisk$sbp,na.rm=T)
```

```
## [1] 25.82192
```

```
sd(data_consent_highrisk$hr,na.rm=T)
```

```
## [1] 18.75389
```

```
sd(data_consent_highrisk$temp,na.rm=T)
```

```
## [1] 2.654693
```

```
sd(data_consent_highrisk$assessor1,na.rm=T)
```

```
## [1] 0.7467952
```

```r
air_oxygen_factor <- as.factor(data_consent_highrisk$air_oxygen)
summary(air_oxygen_factor)
```

```
##    0    1   1%    2 NA's
##    5   87    0   27    1
```

```r
avpu_numeric <- as.numeric(data_consent_highrisk$avpu)
summary(avpu_numeric)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   1.000   1.042   1.000   2.000
```

```r
sd(avpu_numeric,na.rm=T)
```

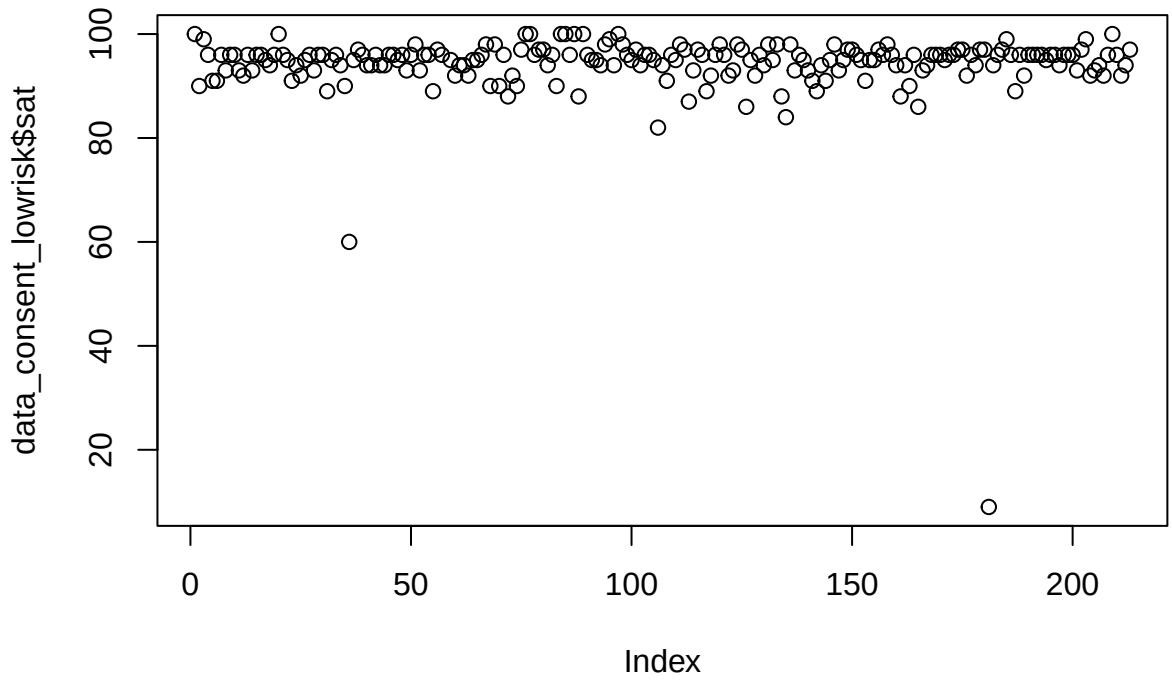
```
## [1] 0.2006642
```

```r
# Demography low-risk patients
data_consent_lowrisk<- data_consent[data_consent$Total <= 4,]
summary(data_consent_lowrisk)
```

```
##   study_number    sreen_date         group     sex          age
##  Min.   : 13.0   Length:213         0   :208   0: 96   Min.   :20.00
##  1st Qu.:158.0   Class :character   1   :  3   1:117   1st Qu.:51.00
##  Median :235.0   Mode  :character   2   :  1           Median :62.00
##  Mean   :227.9                      NA's:  1           Mean   :61.24
##  3rd Qu.:306.0                                         3rd Qu.:74.00
##  Max.   :398.0                                         Max.   :94.00
##
##  ethnicity  consent type_of_consent     Total             rr
##  1   : 14   0:  0   1:191           Min.   :0.000   Min.   :15.00
##  2   : 38   1:213   2:  0           1st Qu.:1.000   1st Qu.:18.00
##  3   :144           3:  1           Median :2.000   Median :18.00
##  4   : 14           4:  0           Mean   :1.831   Mean   :18.64
##  NA's:  3           5:  0           3rd Qu.:3.000   3rd Qu.:20.00
##                     6: 21           Max.   :4.000   Max.   :24.00
##
##       sat          air_oxygen      sbp              hr        avpu
##  Min.   :  9.00   0   :114   Min.   : 80.0   Min.   : 18.0   1:210
##  1st Qu.: 93.00   1   : 84   1st Qu.:110.0   1st Qu.: 72.0   2:  1
##  Median : 96.00   1%  :  0   Median :120.0   Median : 81.0   3:  0
##  Mean   : 94.16   2   : 14   Mean   :125.3   Mean   : 82.8   4:  2
##  3rd Qu.: 96.00   NA's:  1   3rd Qu.:139.0   3rd Qu.: 90.0
##  Max.   :100.00              Max.   :184.0   Max.   :130.0
##  NA's   :1
##       temp          assessor1       assessor2    itu_admission time_after_review
##  Min.   :36.00   Min.   :0.000   Min.   :0.00   0   :104          : 1
##  1st Qu.:36.20   1st Qu.:1.000   1st Qu.:1.00   1   :102      0   :54
##  Median :36.50   Median :1.000   Median :1.00   NA's:  7      1   :98
##  Mean   :36.49   Mean   :1.246   Mean   :1.26                 N/A : 1
##  3rd Qu.:36.60   3rd Qu.:2.000   3rd Qu.:2.00                 NA's:59
##  Max.   :39.00   Max.   :3.000   Max.   :3.00
##                  NA's   :2       NA's   :9
##   outcome        Rdate1
##       :  0   Min.   :2021-09-13 00:00:00.00
##  0    :178   1st Qu.:2022-02-23 00:00:00.00
##  1    : 17   Median :2022-04-18 00:00:00.00
```

```
##  sill :  0   Mean   :2022-03-31 08:47:19.44
##  still: 18   3rd Qu.:2022-05-21 00:00:00.00
##              Max.   :2022-06-27 00:00:00.00
##
```

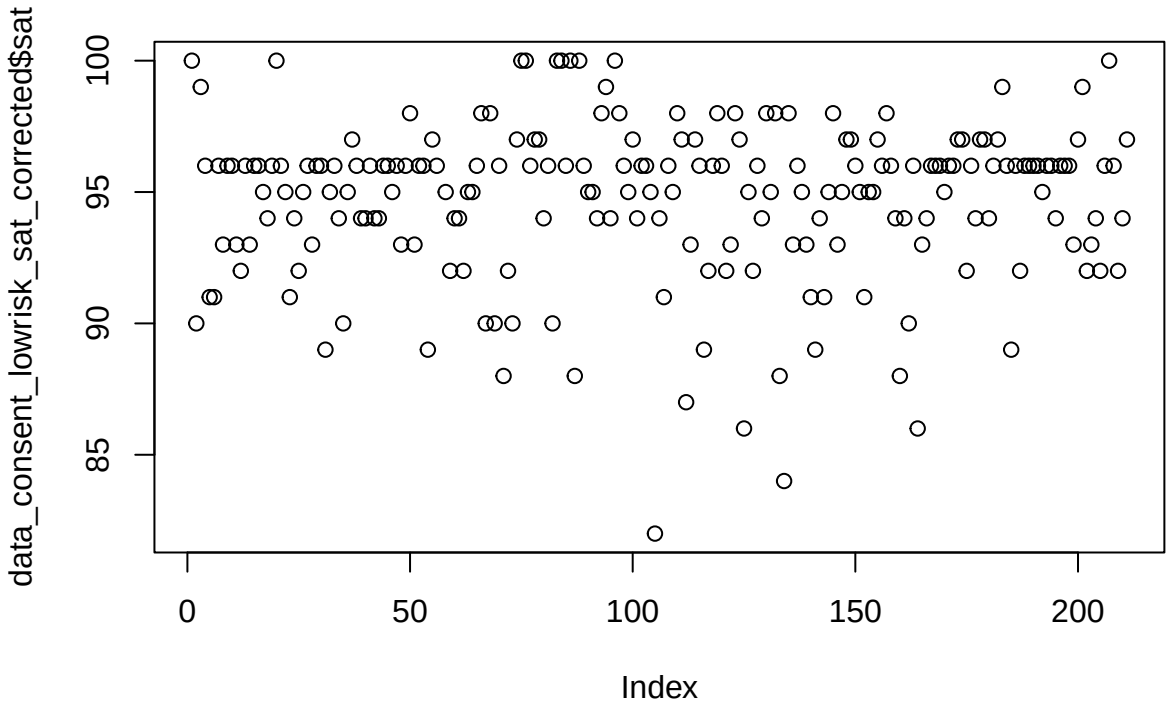
```
plot(data_consent_lowrisk$sat)# There are outliers / errors
```




```
which(data_consent_lowrisk$sat < 70)
```

```
## [1]  36 181
```

```
data_consent_lowrisk_sat_corrected <- data_consent_lowrisk[-c(36,181),]
plot(data_consent_lowrisk_sat_corrected$sat)# We checked rows 36 and 86 removed
```




```
summary(data_consent_lowrisk_sat_corrected$sat)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   82.00   93.00   96.00   94.72   96.00  100.00       1
```

```
sd(data_consent_lowrisk_sat_corrected$sat,na.rm=T)
```

```
## [1] 3.037234
```

```
sd(data_consent_lowrisk$age)
```

```
## [1] 16.97825
```

```
sd(data_consent_lowrisk$Total)
```

```
## [1] 1.414073
```

```
sd(data_consent_lowrisk$rr,na.rm=T)
```

```
## [1] 1.493512
```

```
sd(data_consent_lowrisk$sbp,na.rm=T)
```

```
## [1] 19.94701
```

```
sd(data_consent_lowrisk$hr,na.rm=T)
```

```
## [1] 15.63766
```

```
sd(data_consent_lowrisk$temp,na.rm=T)
```

```
## [1] 0.3832165
```

```
sd(data_consent_lowrisk$assessor1,na.rm=T)
```

```
## [1] 0.7341494
```

```r
air_oxygen_factor_lr <- as.factor(data_consent_lowrisk$air_oxygen)
summary(air_oxygen_factor_lr)
```

```
##    0    1   1%    2 NA's
##  114   84    0   14    1
```

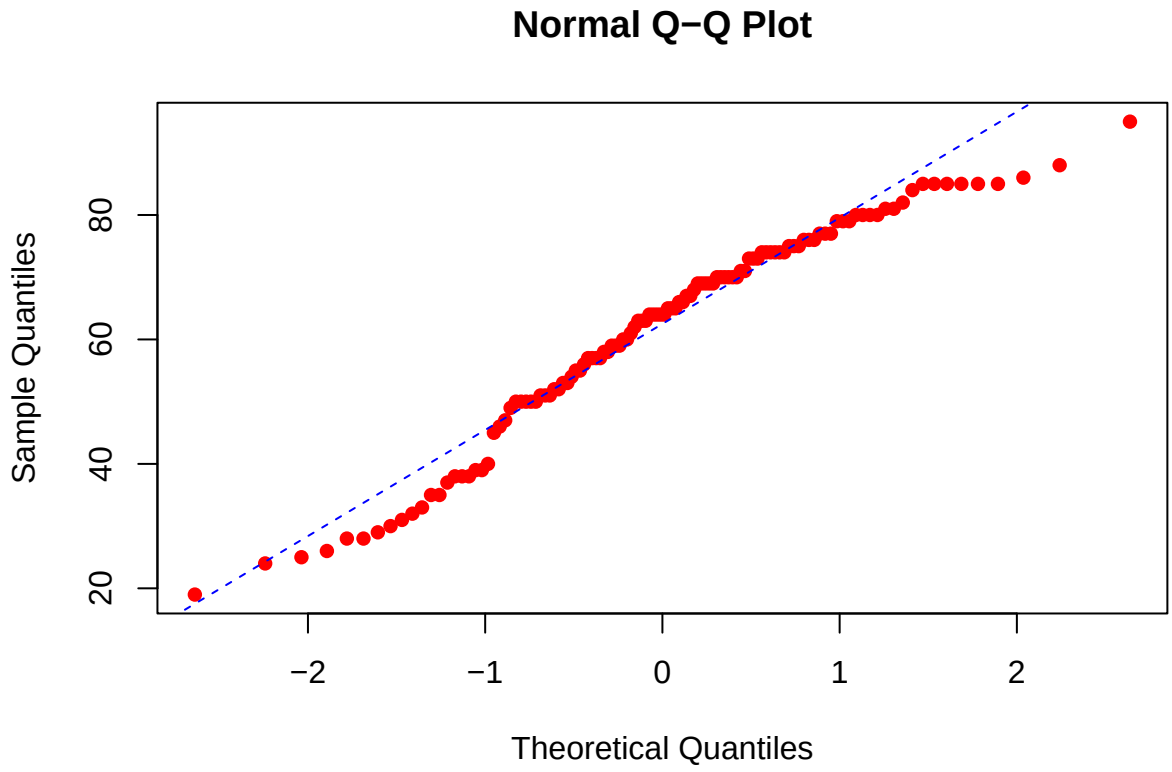
```r
avpu_numeric_lr <- as.numeric(data_consent_lowrisk$avpu)
summary(avpu_numeric_lr)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   1.000   1.033   1.000   4.000
```

```r
sd(avpu_numeric_lr,na.rm=T)
```

```
## [1] 0.2975525
```

```r
# Comparison demography high-risk and low-risk: FIRST ASSESSING NORMALITY OF VARIABLES
##Age
qqnorm(data_consent_highrisk$age,pch=16,col="red")
qqline(data_consent_highrisk$age,lty=2,col="blue")
```




```r
shapiro.test(data_consent_highrisk$age)# Age not normal, then we do Wilcoxon
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$age
## W = 0.95895, p-value = 0.001042
```

```r
wilcox.test(data_consent_highrisk$age,data_consent_lowrisk$age,paired=FALSE)
```

```
##
```

```
##  Wilcoxon rank sum test with continuity correction
##
## data:  data_consent_highrisk$age and data_consent_lowrisk$age
## W = 13038, p-value = 0.7596
## alternative hypothesis: true location shift is not equal to 0
```

```
#For table 1 then we use median and IQR
summary(data_consent_highrisk$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   19.00   51.00   64.00   61.53   74.00   95.00
```

```
summary(data_consent_lowrisk$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   20.00   51.00   62.00   61.24   74.00   94.00
```

```
##Sex: you have to create a group to compare vectors of different length
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"
```

```
group_corrected <- ifelse(data_consent$Total >= 5,1,0)# 1 = high-risk, 0=low-risk)
t1 <- table(group_corrected,data_consent$sex)
chisq.test(t1)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  t1
## X-squared = 0.86422, df = 1, p-value = 0.3526
```

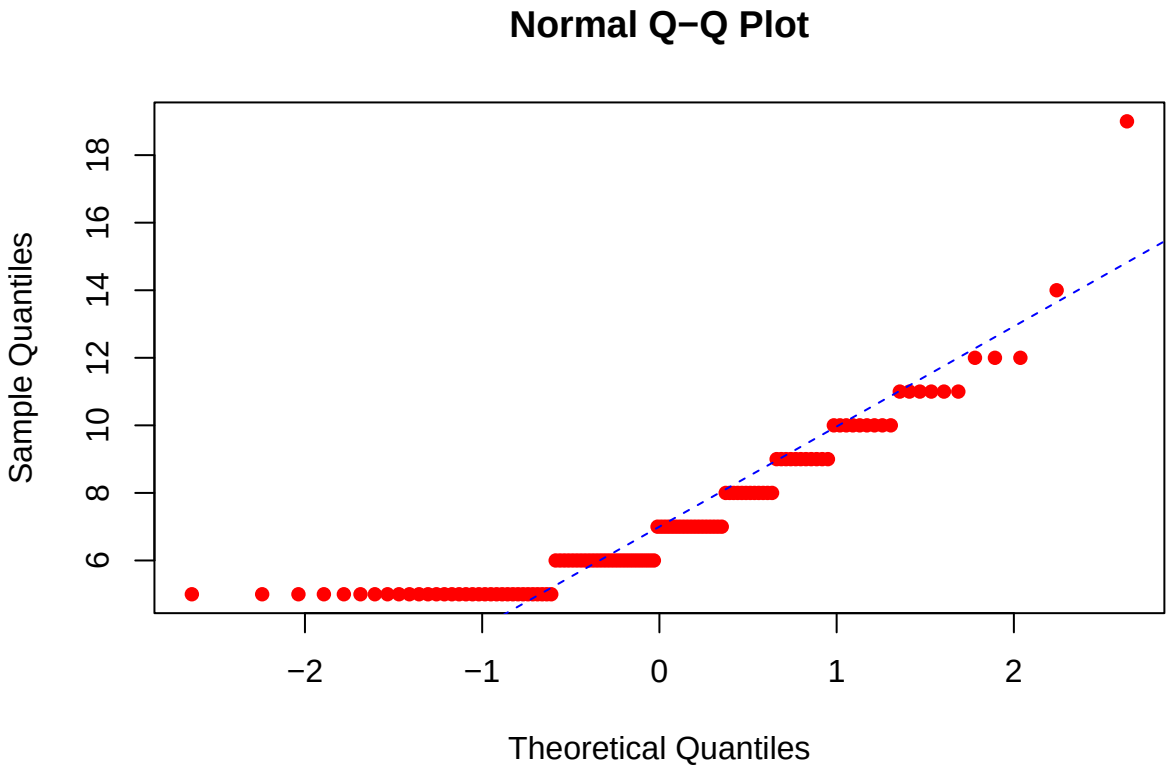
```
##Ethnicity
t2 <- table(group_corrected,data_consent$ethnicity);t2
```

```
##
## group_corrected   1   2   3   4
##               0  14  38 144  14
##               1  10  24  74  10
```

```
chisq.test(t2)
```

```
##
##  Pearson's Chi-squared test
##
## data:  t2
## X-squared = 1.2664, df = 3, p-value = 0.7371
```

```
##NEWS2 score
qqnorm(data_consent_highrisk$Total,pch=16,col="red")
qqline(data_consent_highrisk$Total,lty=2,col="blue")
```




```
shapiro.test(data_consent_highrisk$Total)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$Total
## W = 0.8362, p-value = 3.241e-10
```

```
wilcox.test(data_consent_highrisk$Total,data_consent_lowrisk$Total,paired=FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  data_consent_highrisk$Total and data_consent_lowrisk$Total
## W = 25560, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

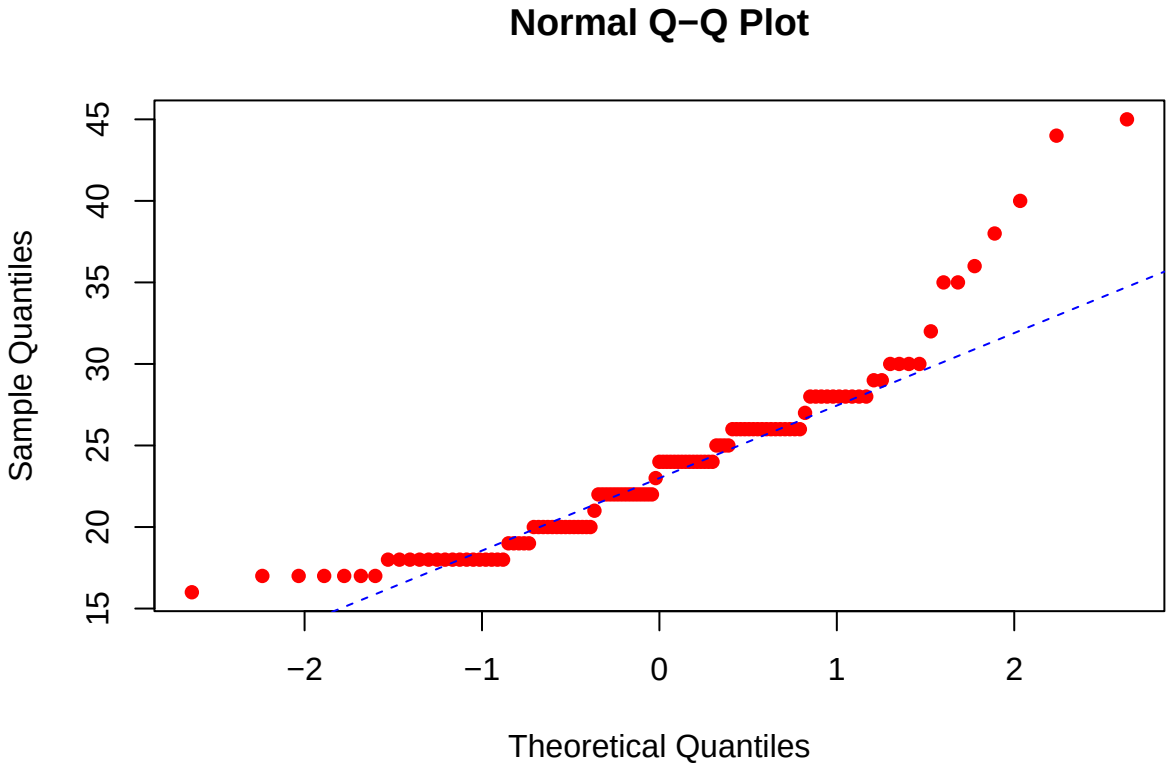
```
summary(data_consent_highrisk$Total)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   5.000   5.000   7.000   7.225   9.000  19.000
```

```
summary(data_consent_lowrisk$Total)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   1.000   2.000   1.831   3.000   4.000
```

```
## Respiratory rate
qqnorm(data_consent_highrisk$rr,pch=16,col="red")
qqline(data_consent_highrisk$rr,lty=2,col="blue")
```




```
shapiro.test(data_consent_highrisk$rr)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$rr
## W = 0.88752, p-value = 5.251e-08
```

```
wilcox.test(data_consent_highrisk$rr,data_consent_lowrisk$rr,paired=FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  data_consent_highrisk$rr and data_consent_lowrisk$rr
## W = 20789, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

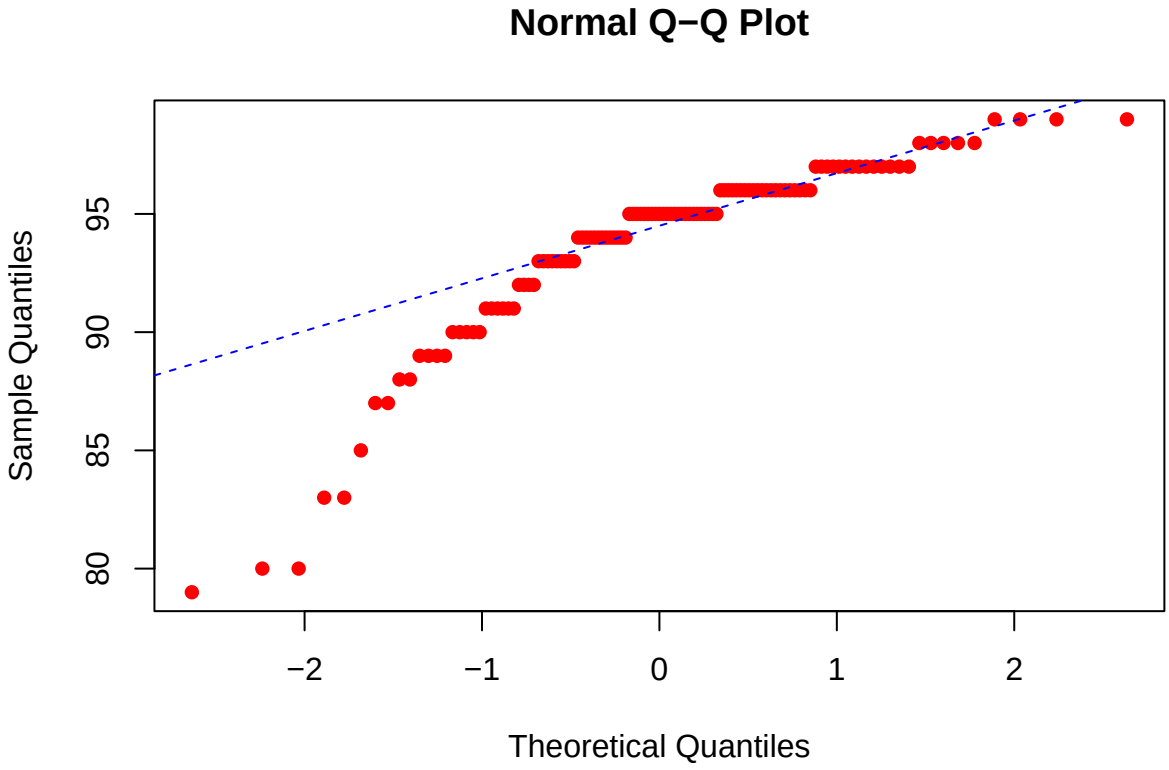
```
summary(data_consent_highrisk$rr)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   16.00   20.00   24.00   23.71   26.00   45.00       1
```

```
summary(data_consent_lowrisk$rr)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   15.00   18.00   18.00   18.64   20.00   24.00
```

```
## Oxygen saturation
qqnorm(data_consent_highrisk$sat,pch=16,col="red")
qqline(data_consent_highrisk$sat,lty=2,col="blue")
```




```
shapiro.test(data_consent_highrisk$sat)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$sat
## W = 0.83648, p-value = 3.736e-10
```

```
wilcox.test(data_consent_highrisk$sat,data_consent_lowrisk$sat,paired=FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  data_consent_highrisk$sat and data_consent_lowrisk$sat
## W = 11142, p-value = 0.07509
## alternative hypothesis: true location shift is not equal to 0
```

```
summary(data_consent_highrisk$sat)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   79.00   93.00   95.00   93.77   96.00   99.00       1
```

```
summary(data_consent_lowrisk$sat)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    9.00   93.00   96.00   94.16   96.00  100.00       1
```

```
##Oxygen administration. There is a misterious level called"1%" that has not value!
levels(data_consent$air_oxygen)[levels(data_consent$air_oxygen)== '1%'] <- NA # to remove it
t3 <- table(group_corrected,data_consent$air_oxygen);t3
```

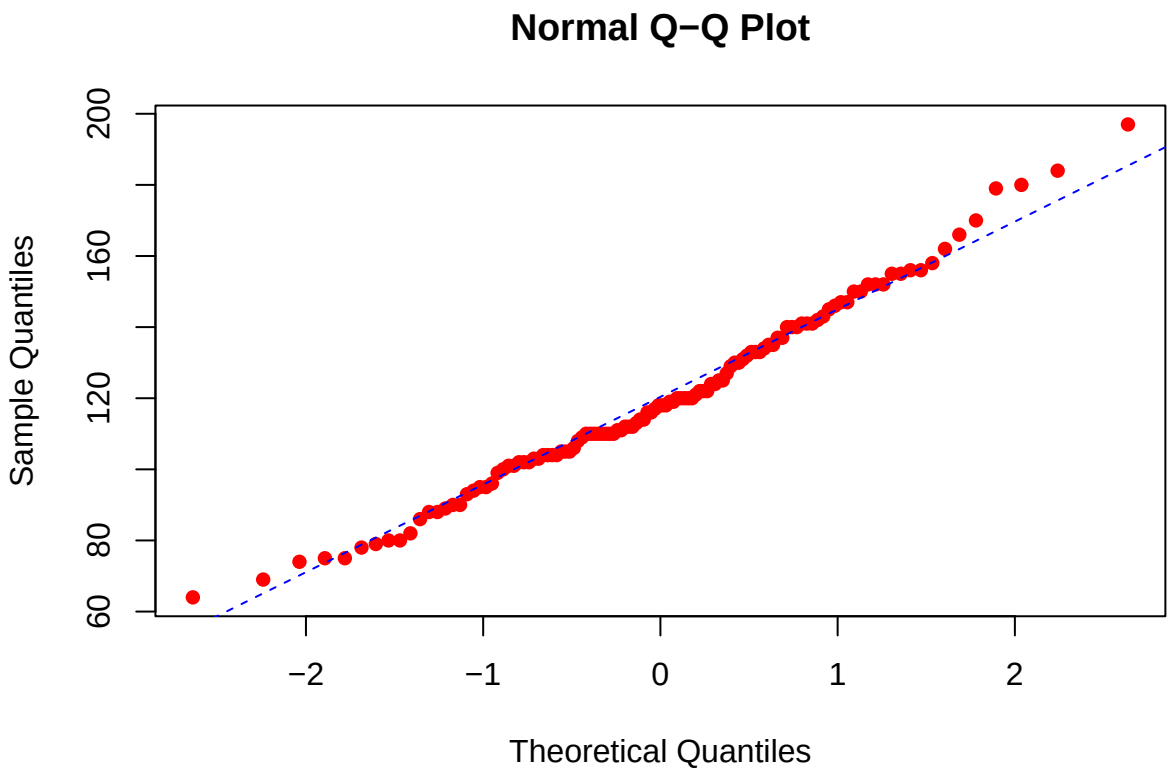
```
##
## group_corrected   0   1   2
```

```
##               0 114  84  14
##               1   5  87  27
```

```
chisq.test(t3)
```

```
##
##  Pearson's Chi-squared test
##
## data:  t3
## X-squared = 84.56, df = 2, p-value < 2.2e-16
```

```
## Systolic blood pressure
qqnorm(data_consent_highrisk$sbp,pch=16,col="red")
qqline(data_consent_highrisk$sbp,lty=2,col="blue")
```




```
shapiro.test(data_consent_highrisk$sbp)# It is normal, hence t-test
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$sbp
## W = 0.98656, p-value = 0.282
```

```
var.test(data_consent_highrisk$sbp,data_consent_lowrisk$sbp)# variance are different
```

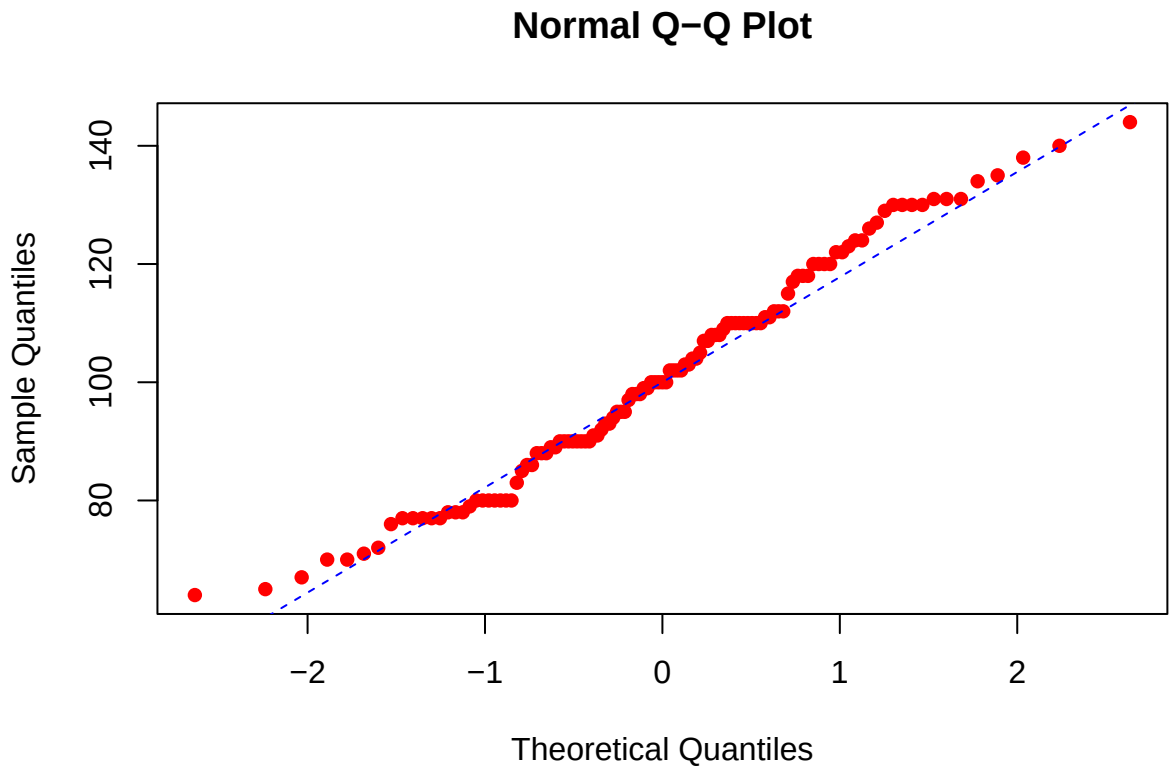
```
##
##  F test to compare two variances
##
## data:  data_consent_highrisk$sbp and data_consent_lowrisk$sbp
## F = 1.6758, num df = 119, denom df = 212, p-value = 0.00112
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
```

```
##  1.22723 2.32162
## sample estimates:
## ratio of variances
##           1.675796
```

```
t.test(data_consent_highrisk$sbp,data_consent_lowrisk$sbp,paired=FALSE,var.equal=FALSE,
conf.level =0.95,alternative="two.sided")
```

```
##
##  Welch Two Sample t-test
##
## data:  data_consent_highrisk$sbp and data_consent_lowrisk$sbp
## t = -2.008, df = 199.79, p-value = 0.04599
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -10.84426201  -0.09822625
## sample estimates:
## mean of x mean of y
##  119.7917  125.2629
```

```
##Heart rate
qqnorm(data_consent_highrisk$hr,pch=16,col="red")
qqline(data_consent_highrisk$hr,lty=2,col="blue")
```




```
shapiro.test(data_consent_highrisk$hr)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$hr
## W = 0.98046, p-value = 0.08097
```

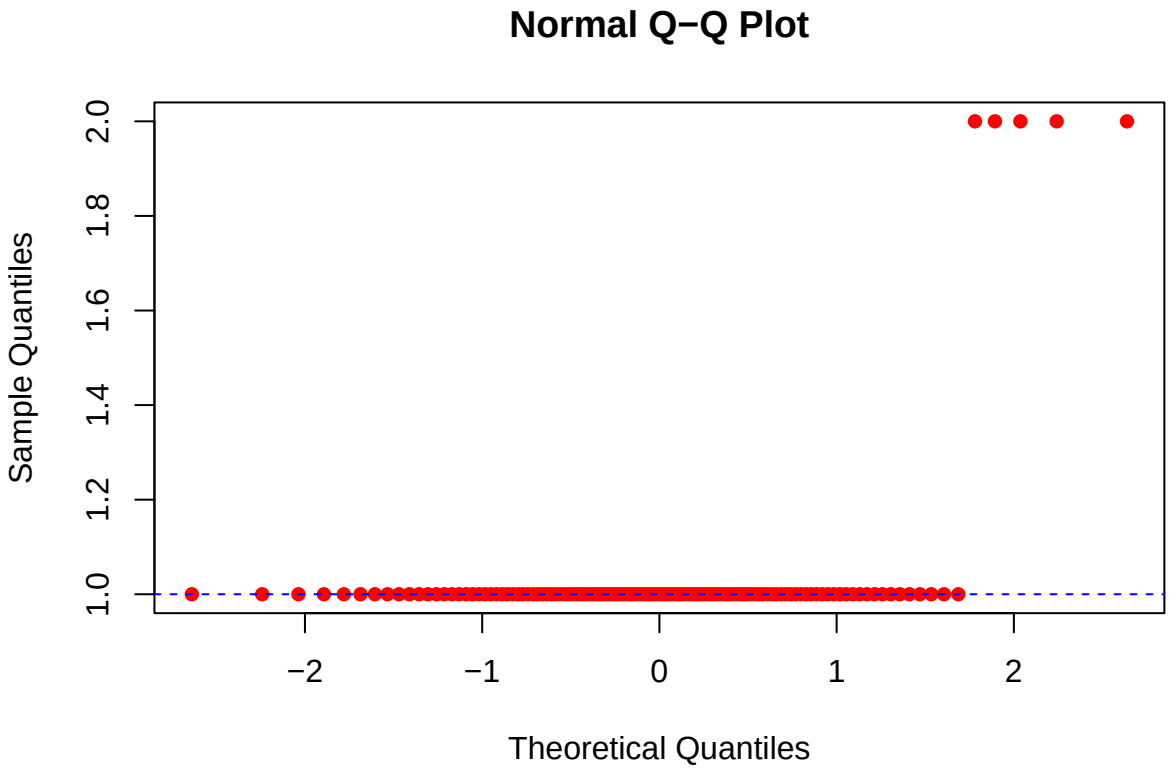
```r
var.test(data_consent_highrisk$hr,data_consent_lowrisk$hr)# Var are different
```

```
##
##  F test to compare two variances
##
## data:  data_consent_highrisk$hr and data_consent_lowrisk$hr
## F = 1.4383, num df = 118, denom df = 212, p-value = 0.02245
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  1.052508 1.994568
## sample estimates:
## ratio of variances
##           1.438266
```

```r
t.test(data_consent_highrisk$hr,data_consent_lowrisk$hr,paired=FALSE,var.equal=FALSE,
conf.level =0.95,alternative="two.sided")
```

```
##
##  Welch Two Sample t-test
##
## data:  data_consent_highrisk$hr and data_consent_lowrisk$hr
## t = 9.0369, df = 209.85, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  14.31303 22.29982
## sample estimates:
## mean of x mean of y
## 101.10924  82.80282
```

```r
##AVPU
avpu_numeric_highrisk <- as.numeric(data_consent_highrisk$avpu)
avpu_numeric_lowrisk <- as.numeric(data_consent_lowrisk$avpu)
qqnorm(avpu_numeric_highrisk,pch=16,col="red")
qqline(avpu_numeric_highrisk,lty=2,col="blue")
```




```
shapiro.test(avpu_numeric_highrisk)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  avpu_numeric_highrisk
## W = 0.19971, p-value < 2.2e-16
```

```
wilcox.test(avpu_numeric_highrisk,avpu_numeric_lowrisk,paired=FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  avpu_numeric_highrisk and avpu_numeric_lowrisk
## W = 13128, p-value = 0.1209
## alternative hypothesis: true location shift is not equal to 0
```

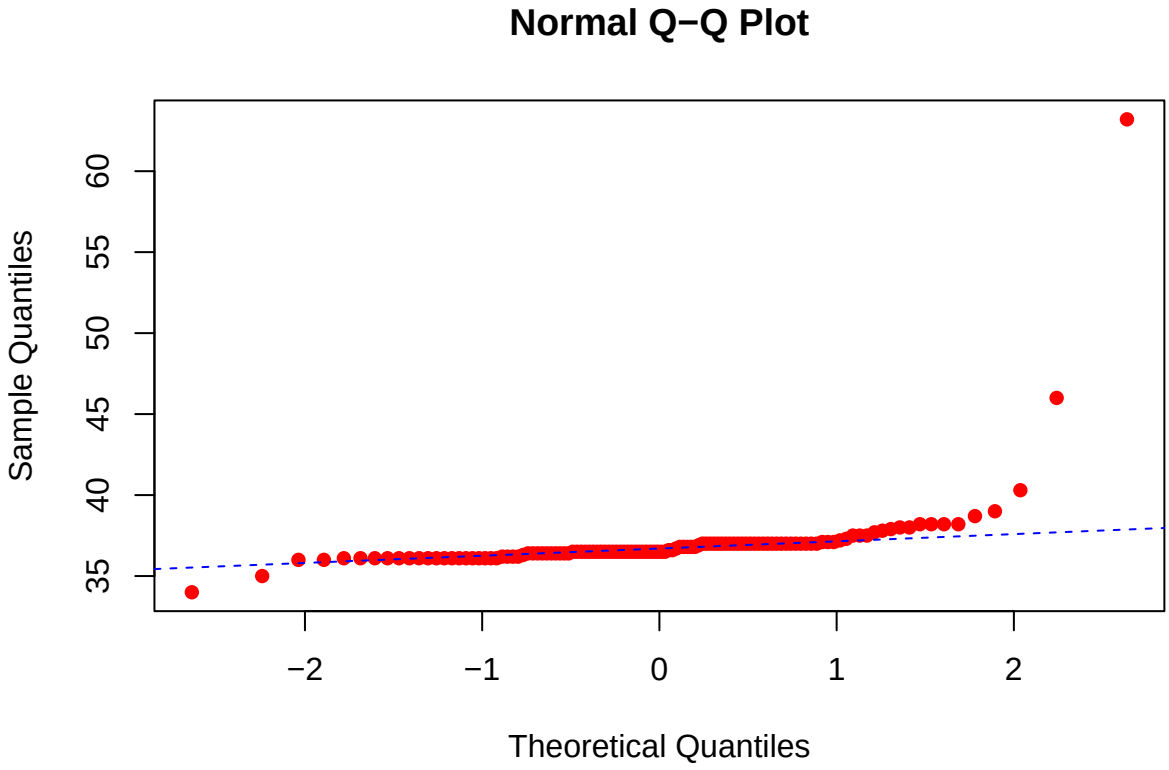
```
summary(avpu_numeric_highrisk)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   1.000   1.042   1.000   2.000
```

```
summary(avpu_numeric_lowrisk)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   1.000   1.033   1.000   4.000
```

```
##Temperature
qqnorm(data_consent_highrisk$temp,pch=16,col="red")
qqline(data_consent_highrisk$temp,lty=2,col="blue")
```




```
shapiro.test(data_consent_highrisk$temp)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$temp
## W = 0.28557, p-value < 2.2e-16
```

```
wilcox.test(data_consent_highrisk$temp,data_consent_lowrisk$temp,paired=FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  data_consent_highrisk$temp and data_consent_lowrisk$temp
## W = 16010, p-value = 0.0001056
## alternative hypothesis: true location shift is not equal to 0
```

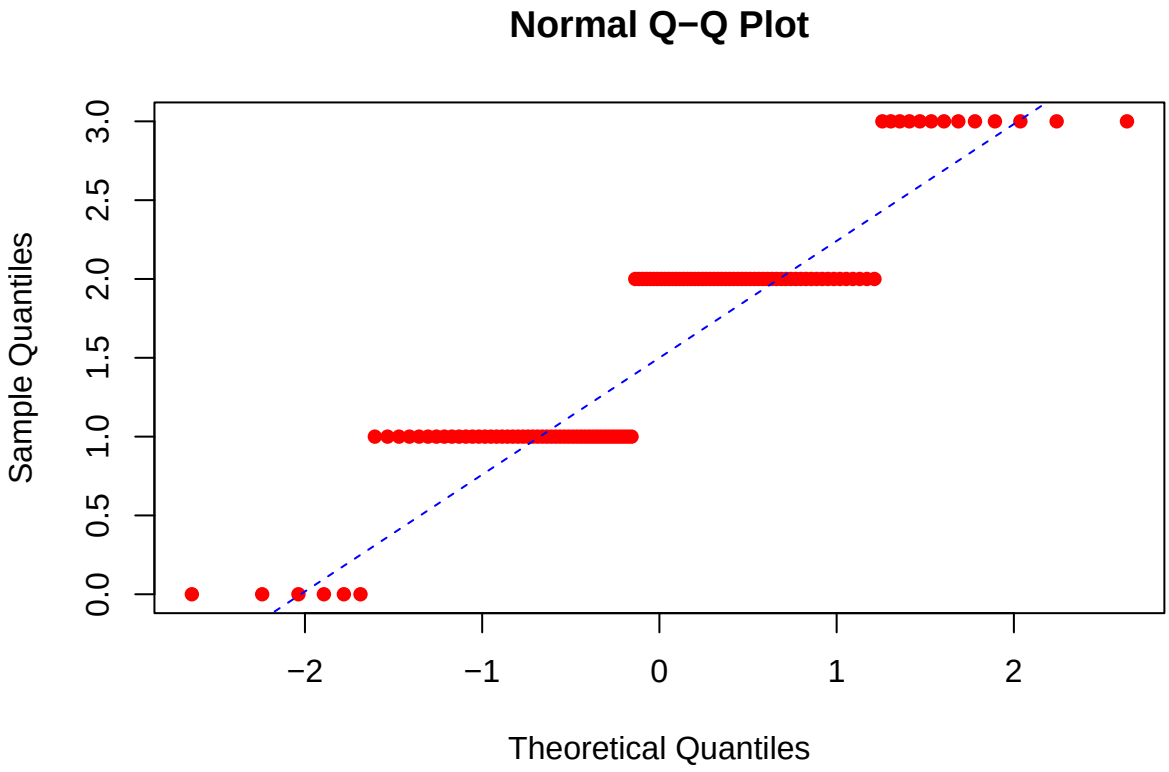
```
summary(data_consent_highrisk$temp)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   34.00   36.40   36.50   37.05   37.00   63.20
```

```
summary(data_consent_lowrisk$temp)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   36.00   36.20   36.50   36.49   36.60   39.00
```

```
#qVIEWS
qqnorm(data_consent_highrisk$assessor1,pch=16,col="red")
qqline(data_consent_highrisk$assessor1,lty=2,col="blue")
```




```
shapiro.test(data_consent_highrisk$assessor1)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data_consent_highrisk$assessor1
## W = 0.84567, p-value = 7.483e-10
```

```
wilcox.test(data_consent_highrisk$assessor1,data_consent_lowrisk$assessor1,paired=FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  data_consent_highrisk$assessor1 and data_consent_lowrisk$assessor1
## W = 15828, p-value = 4.121e-05
## alternative hypothesis: true location shift is not equal to 0
```

```
summary(data_consent_highrisk$assessor1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   1.000   2.000   1.617   2.000   3.000
```

```
summary(data_consent_lowrisk$assessor1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   0.000   1.000   1.000   1.246   2.000   3.000       2
```

```
## Preparing for Rigde regression
#Removing NA and selecting variables
data_consent <- data[data$consent=="1",]
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"
```

```
newdata <- data_consent[,c(4:6,10:17,19)]
names(newdata)
```

```
##  [1] "sex"           "age"           "ethnicity"     "rr"
##  [5] "sat"           "air_oxygen"    "sbp"           "hr"
##  [9] "avpu"          "temp"          "assessor1"     "itu_admission"
```

```
newdata <- na.omit(newdata)

#Looking for correlation between NEWS and qVIEWS all numerical variables
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"
```

```
str(data_consent)
```

```
## 'data.frame':    333 obs. of  22 variables:
##  $ study_number     : int  2 3 8 9 13 14 15 16 17 18 ...
##  $ sreen_date       : chr  "22/07/2021" "25/07/2021" "07/08/2021" "03/08/2021" ...
##  $ group            : Factor w/ 3 levels "0","1","2": 2 2 2 2 1 2 2 1 1 2 ...
##  $ sex              : Factor w/ 2 levels "0","1": 1 1 1 2 1 1 2 2 1 2 ...
##  $ age              : int  26 73 67 63 91 85 81 76 25 70 ...
##  $ ethnicity        : Factor w/ 4 levels "1","2","3","4": 2 2 3 1 3 3 3 3 2 3 ...
##  $ consent          : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ type_of_consent  : Factor w/ 6 levels "1","2","3","4",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Total            : int  5 19 7 5 2 7 4 0 5 7 ...
##  $ rr               : int  24 26 25 19 18 24 24 15 18 24 ...
##  $ sat              : int  95 90 96 96 100 95 90 99 94 92 ...
##  $ air_oxygen       : Factor w/ 4 levels "0","1","1%","2": 2 2 4 2 2 2 4 1 2 2 ...
##  $ sbp              : int  114 80 122 170 133 120 140 111 102 112 ...
##  $ hr               : int  78 118 80 95 70 111 78 90 88 102 ...
##  $ avpu             : Factor w/ 4 levels "1","2","3","4": 1 2 1 1 1 1 1 1 1 1 ...
##  $ temp             : num  37 34 36.7 37 37.1 37 36.4 37 37 37 ...
##  $ assessor1        : int  1 3 2 2 1 1 1 1 2 3 ...
##  $ assessor2        : int  NA NA 2 2 NA NA NA 1 NA 3 ...
##  $ itu_admission    : Factor w/ 2 levels "0","1": 1 2 1 2 1 1 2 2 2 2 ...
##  $ time_after_review: Factor w/ 4 levels "","0","1","N/A": NA 2 2 2 NA NA NA 3 3 NA ...
##  $ outcome          : Factor w/ 5 levels "","0","1","sill",..: 2 3 2 2 2 3 2 2 2 3 ...
##  $ Rdate1           : POSIXct, format: "2021-07-22" "2021-07-25" ...
```

```
data_consent$avpu <- as.numeric(data_consent$avpu)
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_numerical <- na.omit(data_consent)
XVars <- data_consent_numerical[,c(9,10,11,13,14,15,16,17)] # X numeric variables
round(cor(XVars), 2) # Correlation
```

```
##           Total    rr   sat   sbp    hr avpu  temp assessor1
## Total      1.00  0.54 -0.03 -0.18  0.54 0.10  0.19      0.27
## rr         0.54  1.00 -0.05  0.21  0.30 0.03  0.01      0.13
## sat       -0.03 -0.05  1.00 -0.18 -0.03 0.03  0.03     -0.02
## sbp       -0.18  0.21 -0.18  1.00  0.06 0.11 -0.05     -0.09
## hr         0.54  0.30 -0.03  0.06  1.00 0.15  0.11      0.12
## avpu       0.10  0.03  0.03  0.11  0.15 1.00  0.00      0.01
## temp       0.19  0.01  0.03 -0.05  0.11 0.00  1.00      0.21
## assessor1  0.27  0.13 -0.02 -0.09  0.12 0.01  0.21      1.00
```

```
## # to check if cor between Total News and qVIEWS is significant
cor.test(data_consent_numerical$Total,data_consent_numerical$assessor1)
```

```
##
##  Pearson's product-moment correlation
##
## data:  data_consent_numerical$Total and data_consent_numerical$assessor1
## t = 4.1868, df = 215, p-value = 4.126e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.146748 0.393366
## sample estimates:
##       cor
## 0.2745662
```

```
#RIDGE REGRESSION FOR NEWS variables alone
news_data1 <- newdata[,c(4:10,12)]
names(news_data1)
```

```
## [1] "rr"            "sat"           "air_oxygen"    "sbp"
## [5] "hr"            "avpu"          "temp"          "itu_admission"
```

```
##Splitting the sample (internal validation)

x1 <- model.matrix(news_data1$itu_admission~.,news_data1)[, -1]
y1 <- news_data1$itu_admission
set.seed(1)
train1 <- sample(1:nrow(x1),nrow(x1)/2)
test1 <- (-train1)
y.test1 <-y1[test1]
library(glmnet)
```

```
## Loading required package: Matrix
```

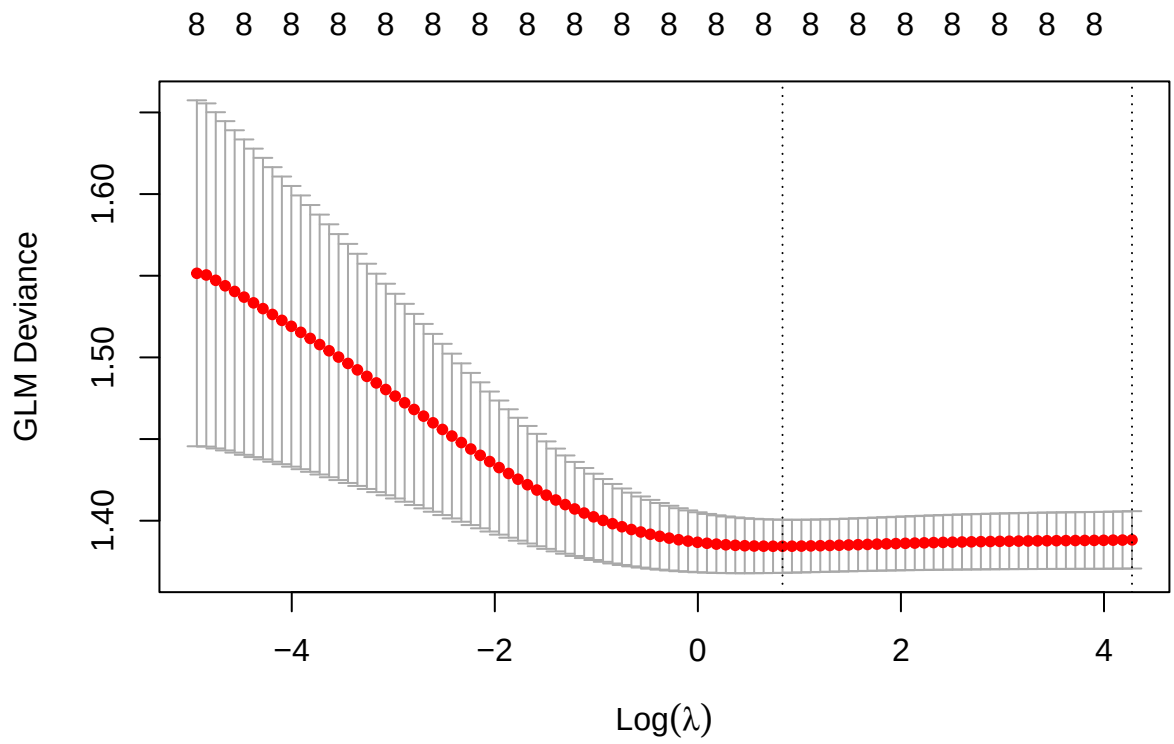
```
## Loaded glmnet 4.1-4
```

```
grid <- 10^seq(10,-2,length=100)

## Calculating best lambda
set.seed(1)
cv.out1 <- cv.glmnet(x1[train1,],y1[train1],alpha=0,family=binomial,type.measure="class")
```

```
## Warning: Only deviance, mse, mae available as type.measure for GLM models;
## deviance used instead
```

```
plot(cv.out1)
```




```
bestlam1 <- cv.out1$lambda.min
bestlam1
```

```
## [1] 2.301567
```

```
##Doing a ridge regression
out1 <- glmnet(x1[train1,],y1[train1],alpha=0,lamda=grid,family=binomial)
ridge.coeff1 <- predict(out1,s = bestlam1,newx = x1[test1 , ],type="coefficients")
ridge.coeff1
```

```
## 12 x 1 sparse Matrix of class "dgCMatrix"
##                            s1
## (Intercept)   1.1250538976
## rr           -0.0029238414
## sat          -0.0090857200
## air_oxygen1  -0.0133241501
## air_oxygen1% .
## air_oxygen2   0.0338682851
## sbp           0.0004122020
## hr           -0.0007236309
## avpu2        -0.0466924945
```

```
## avpu3          .
## avpu4          .
## temp          -0.0104529102
```

```
## Doing AUC for NEWS
ridge.coeff1 <- predict(out1,s = bestlam1,newx = x1[test1 , ],type="response")
library(pROC)
```

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

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

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

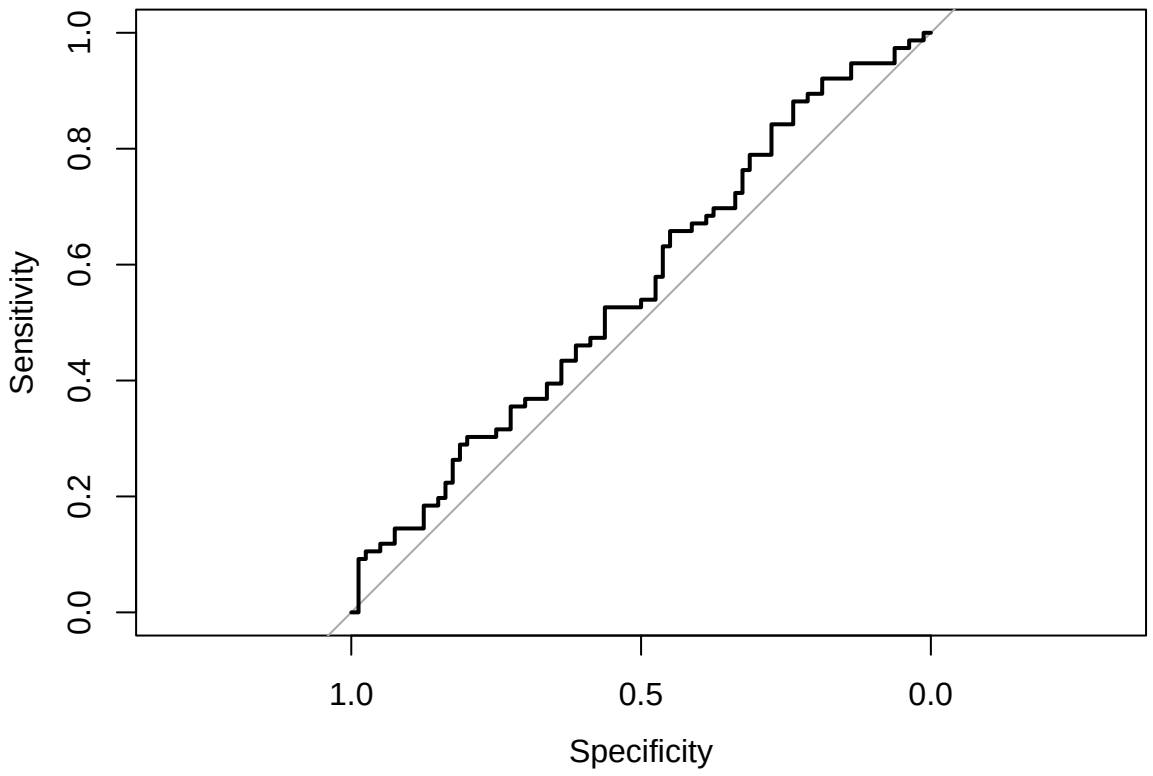
```
roccurve1 <- roc(y1[test1]~ ridge.coeff1)
```

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

```
## Warning in roc.default(response, predictors[, 1], ...): Deprecated use a matrix
## as predictor. Unexpected results may be produced, please pass a numeric vector.
```

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

```
plot(roccurve1)
```




```
auc(roccurve1)
```

```
## Area under the curve: 0.561
```

```
ci.auc(roccurve1)
```

```
## 95% CI: 0.4707-0.6514 (DeLong)
```

```
#RIDGE REGRESSION FOR NEWS variables + qVIEWS
news_data2 <- newdata[,c(4:12)]# Adding assessor1 which is qVIEWS
names(news_data2)
```

```
## [1] "rr"            "sat"           "air_oxygen"    "sbp"
## [5] "hr"            "avpu"          "temp"          "assessor1"
## [9] "itu_admission"
```

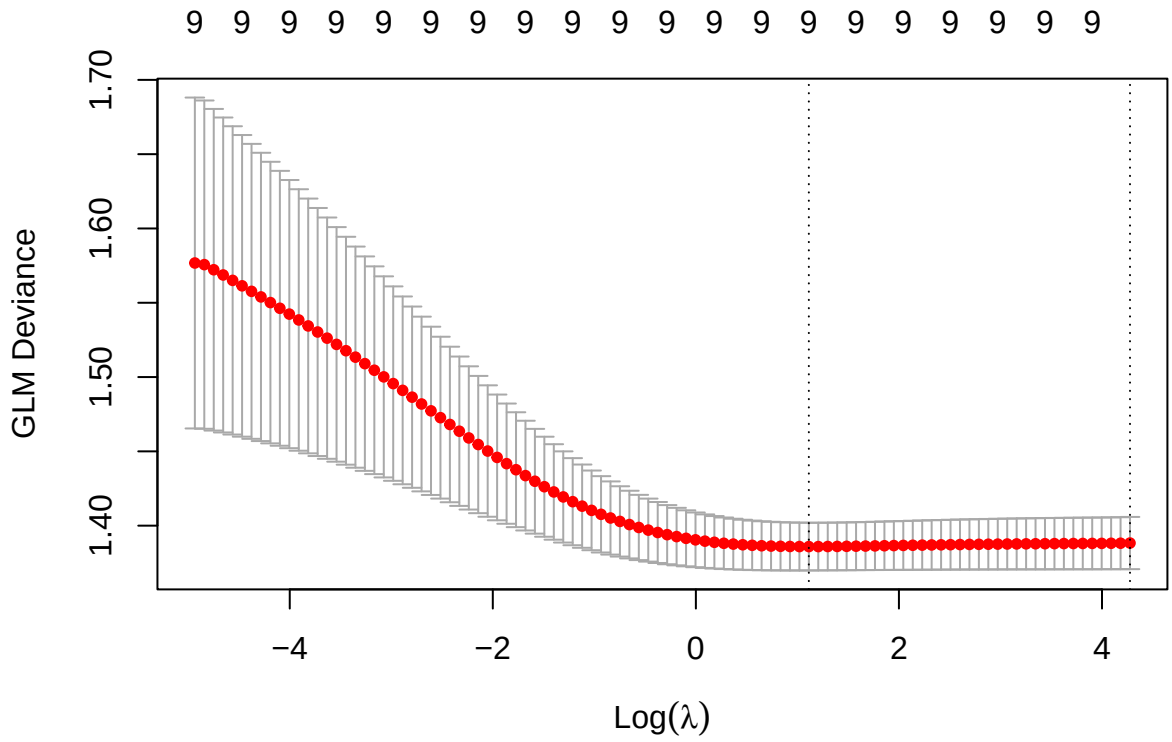
```
##Splitting the sample (internal validation)

x2 <- model.matrix(news_data2$itu_admission~.,news_data2)[, -1]
y2 <- news_data2$itu_admission
set.seed(1)
train2 <- sample(1:nrow(x2),nrow(x2)/2)
test2 <- (-train2)
y.test2 <-y2[test2]
library(glmnet)
grid <- 10^seq(10,-2,length=100)

## Calculating best lambda
set.seed(1)
cv.out2 <- cv.glmnet(x2[train2,],y2[train2],alpha=0,family=binomial,type.measure="class")
```

```
## Warning: Only deviance, mse, mae available as type.measure for GLM models;
## deviance used instead
```

```
plot(cv.out2)
```




```
bestlam2 <- cv.out2$lambda.min
bestlam2
```

```
## [1] 3.042536
```

```
##Doing a ridge regression
out2 <- glmnet(x2[train2,],y2[train2],alpha=0,lamda=grid,family=binomial)
ridge.coeff2 <- predict(out2,s = bestlam2,newx = x2[test2 , ],type="coefficients")
ridge.coeff2
```

```
## 13 x 1 sparse Matrix of class "dgCMatrix"
##                          s1
## (Intercept)   0.8360483349
## rr           -0.0022403986
## sat          -0.0070619480
## air_oxygen1  -0.0107636679
## air_oxygen1%  .
## air_oxygen2   0.0265976062
## sbp           0.0003219603
## hr           -0.0005645104
## avpu2        -0.0360369242
## avpu3         .
## avpu4         .
## temp         -0.0081027133
## assessor1    -0.0045762624
```

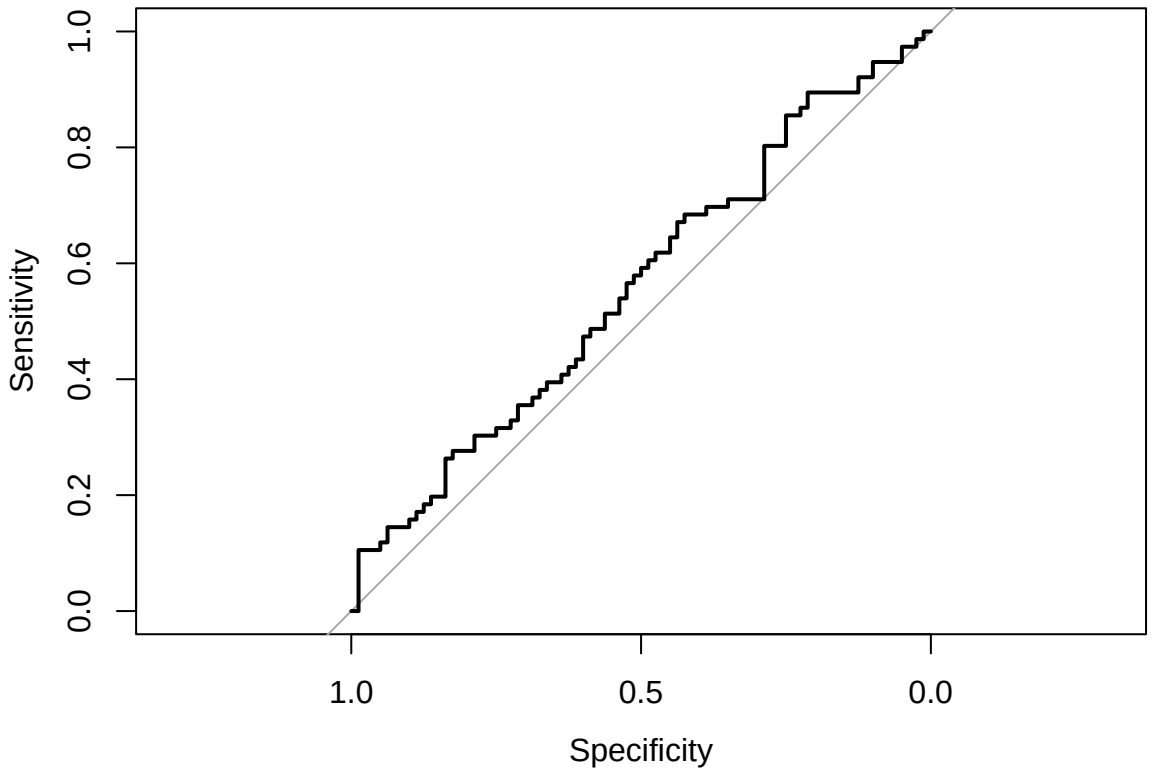
```
## Doing AUC for NEWS+qVIEWS
ridge.coeff2 <- predict(out2,s = bestlam2,newx = x2[test2, ],type="response")
library(pROC)
roccurve2 <- roc(y2[test2]~ ridge.coeff2)
```

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

```
## Warning in roc.default(response, predictors[, 1], ...): Deprecated use a matrix
## as predictor. Unexpected results may be produced, please pass a numeric vector.
```

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

```
plot(roccurve2)
```




```
auc(roccurve2)
```

```
## Area under the curve: 0.5584
```

```
ci.auc(roccurve2)
```

```
## 95% CI: 0.4679-0.6489 (DeLong)
```

```
#GRAPH THAT COMBINES BOTH AUROC
plot.roc(y2[test2]~ ridge.coeff2,percentage=T,col="red",smooth=T)# for NEWS+qVIEWS
```

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

```
## Warning in roc.default(response, predictor, plot = TRUE, ...): Deprecated use a
## matrix as predictor. Unexpected results may be produced, please pass a numeric
## vector.
```

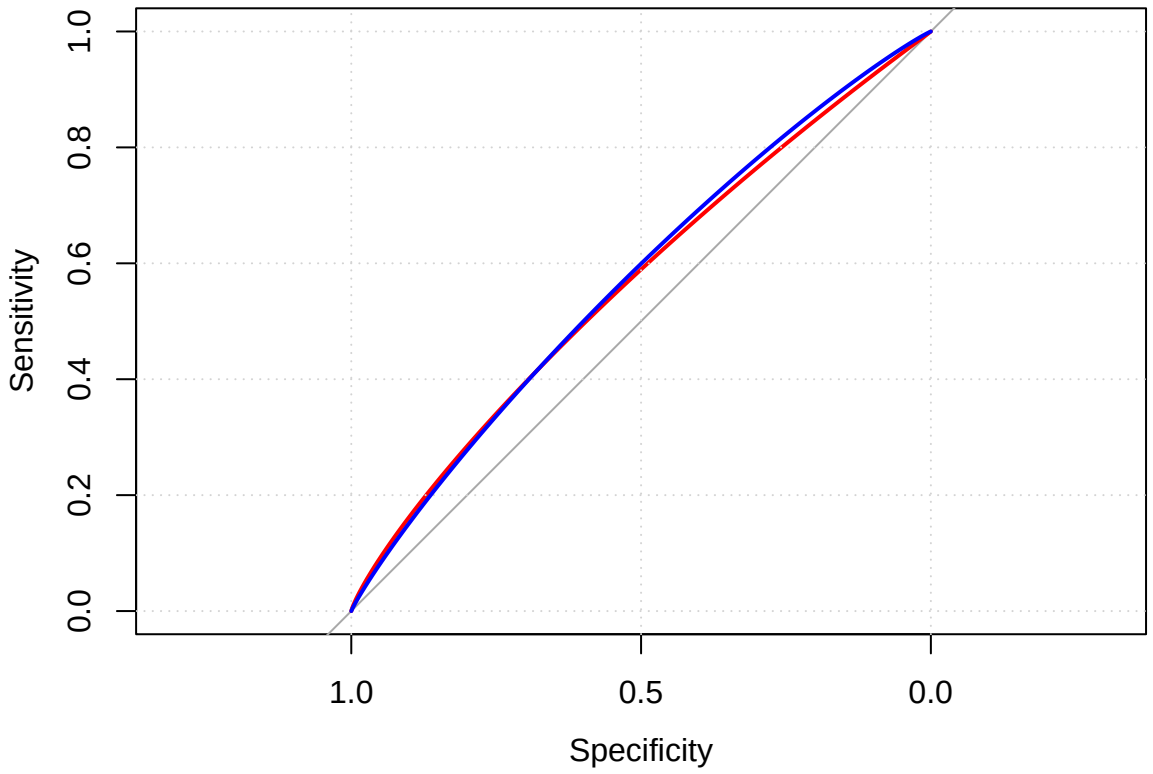
```
## Setting direction: controls < cases
```

```
grid(NULL,NULL,col = "lightgray", lty = "dotted",lwd = par("lwd"), equilogs = TRUE)
lines.roc(y1[test1]~ ridge.coeff1,percentage=T,col="blue",smooth=T)# For NEWS only
```

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

```
## Warning in roc.default(response, predictor, ...): Deprecated use a matrix as
## predictor. Unexpected results may be produced, please pass a numeric vector.
```

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




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

```
names(newdata)
```

```
##  [1] "sex"           "age"           "ethnicity"     "rr"
##  [5] "sat"           "air_oxygen"    "sbp"           "hr"
##  [9] "avpu"          "temp"          "assessor1"     "itu_admission"
```

```
newdata <- data_consent[,c(10:17,19)]

newdata <- na.omit(newdata)
names(newdata)
```

```
## [1] "rr"            "sat"           "air_oxygen"    "sbp"
## [5] "hr"            "avpu"          "temp"          "assessor1"
## [9] "itu_admission"
```

```
library(randomForest)
```

```
## randomForest 4.7-1.1
```

```
## Type rfNews() to see new features/changes/bug fixes.
##
## Attaching package: 'randomForest'
## The following object is masked from 'package:psych':
##
##     outlier
```

```
# Separate train and test sample
set.seed(1)
library(caTools)
sample <- sample.split(newdata$itu_admission,SplitRatio = 0.5)
train  <- subset(newdata,sample == TRUE)
testdata <- subset(newdata, sample == FALSE)
names(train)
```

```
## [1] "rr"            "sat"           "air_oxygen"    "sbp"
## [5] "hr"            "avpu"          "temp"          "assessor1"
## [9] "itu_admission"
```

```
names(testdata)
```

```
## [1] "rr"            "sat"           "air_oxygen"    "sbp"
## [5] "hr"            "avpu"          "temp"          "assessor1"
## [9] "itu_admission"
```

```
dim(train)
```

```
## [1] 158   9
```

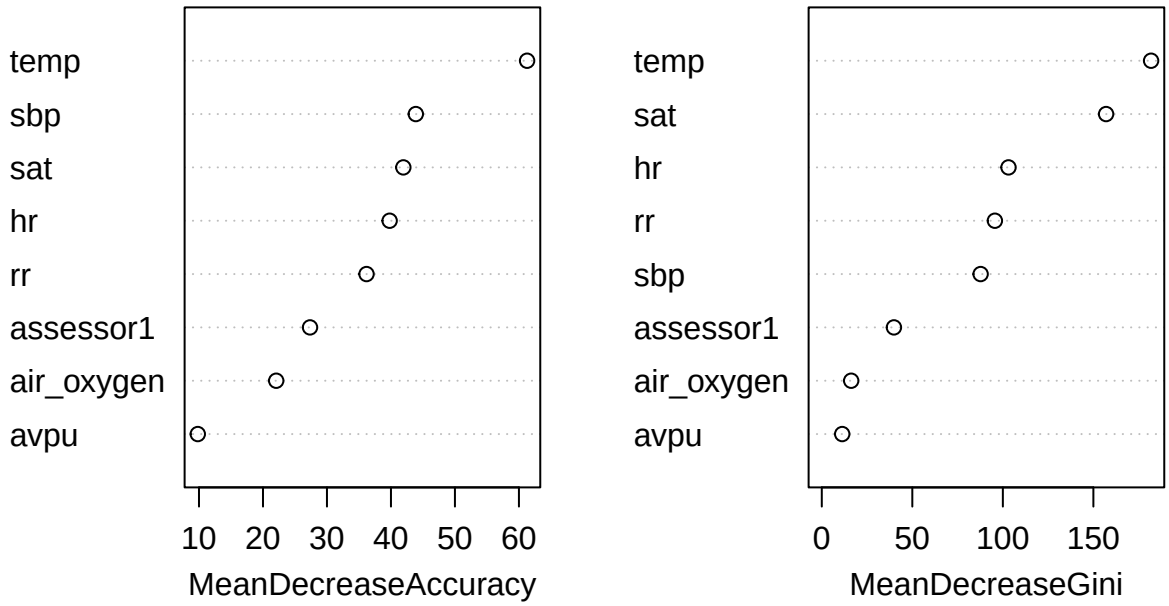
```
dim(testdata)
```

```
## [1] 158   9
```

```
# Random Forest
set.seed (1)
library(randomForest)
rf.newdata <- randomForest(newdata$itu_admission~.,data= newdata,subset=unlist(train),
mtry =3,importance = TRUE)
importance(rf.newdata)
```

```
##                    0         1 MeanDecreaseAccuracy MeanDecreaseGini
## rr         28.052253 31.944769            36.183033         95.59939
## sat        35.940974 31.147522            41.936336        157.01804
## air_oxygen 16.174831 20.221729            22.069342         16.24112
## sbp        34.589565 34.976893            43.887144         87.71821
## hr         31.947055 31.131106            39.793760        103.11545
## avpu        9.476563  6.726149             9.813107         11.27454
## temp       50.874434 45.062224            61.277081        181.86569
## assessor1  25.569541 18.791137            27.352904         39.84012
```

```
varImpPlot(rf.newdata)
```




```
##Random forest AUC
test.predictions <- predict(rf.newdata, newdata=testdata)
test.predictions <- as.numeric(test.predictions)
roccurve_forest <- roc(unlist(testdata$itu_admission)~ test.predictions)
```

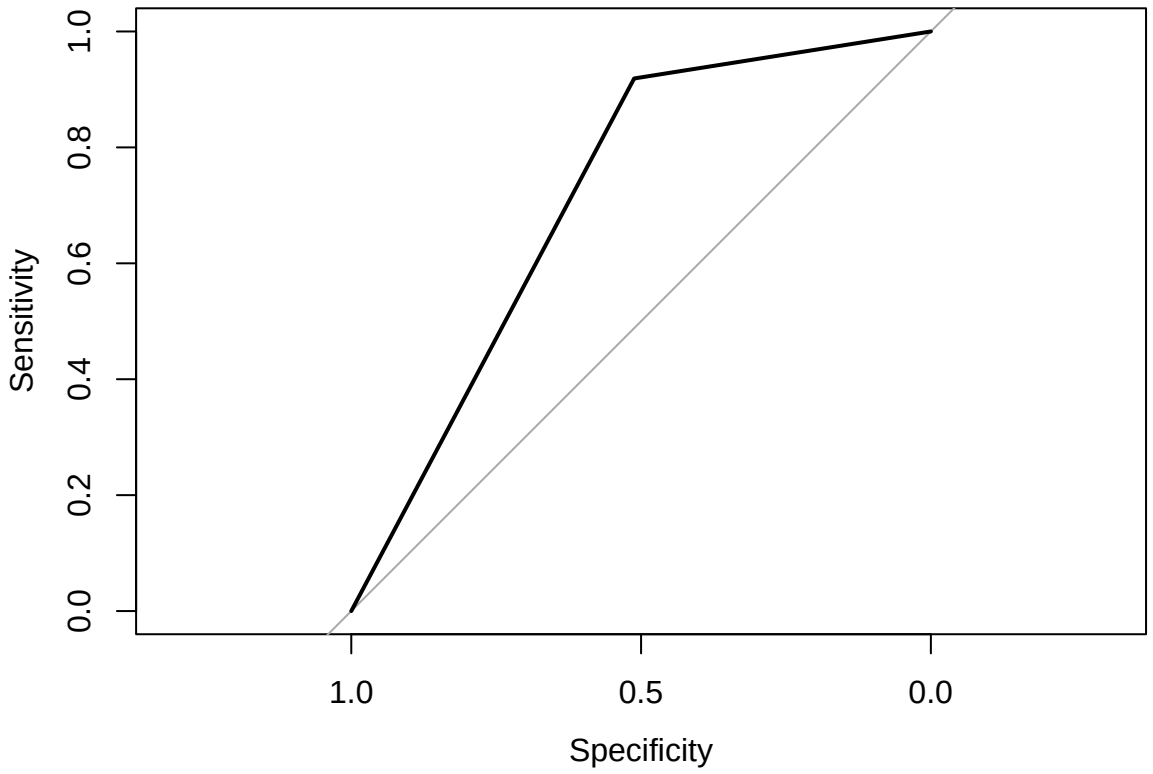
```
## Setting levels: control = 0, case = 1
```

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

```
auc(roccurve_forest)
```

```
## Area under the curve: 0.7154
```

```
plot(roccurve_forest)
```




```
ci.auc(roccurve_forest)
```

```
## 95% CI: 0.6532-0.7776 (DeLong)
```

```
# A better way to present the importance value as barplot
var.1 <- c("RR","SAT","AIR/OX","SBP","HR","AVPU",
"TEMP","qVIEWS")
Gini <- c(97.3,160.2,22.3,81.0,92.0,11.9,185.6,36.9)
Gini_per <- (Gini*100)/185.6
dt1 <- data.frame(var.1,Gini_per)
library(ggplot2)
```

```
##
## Attaching package: 'ggplot2'
```

```
## The following object is masked from 'package:randomForest':
##
##     margin
```

```
## The following objects are masked from 'package:psych':
##
##     %+%, alpha
```

```
library(reshape2)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
```

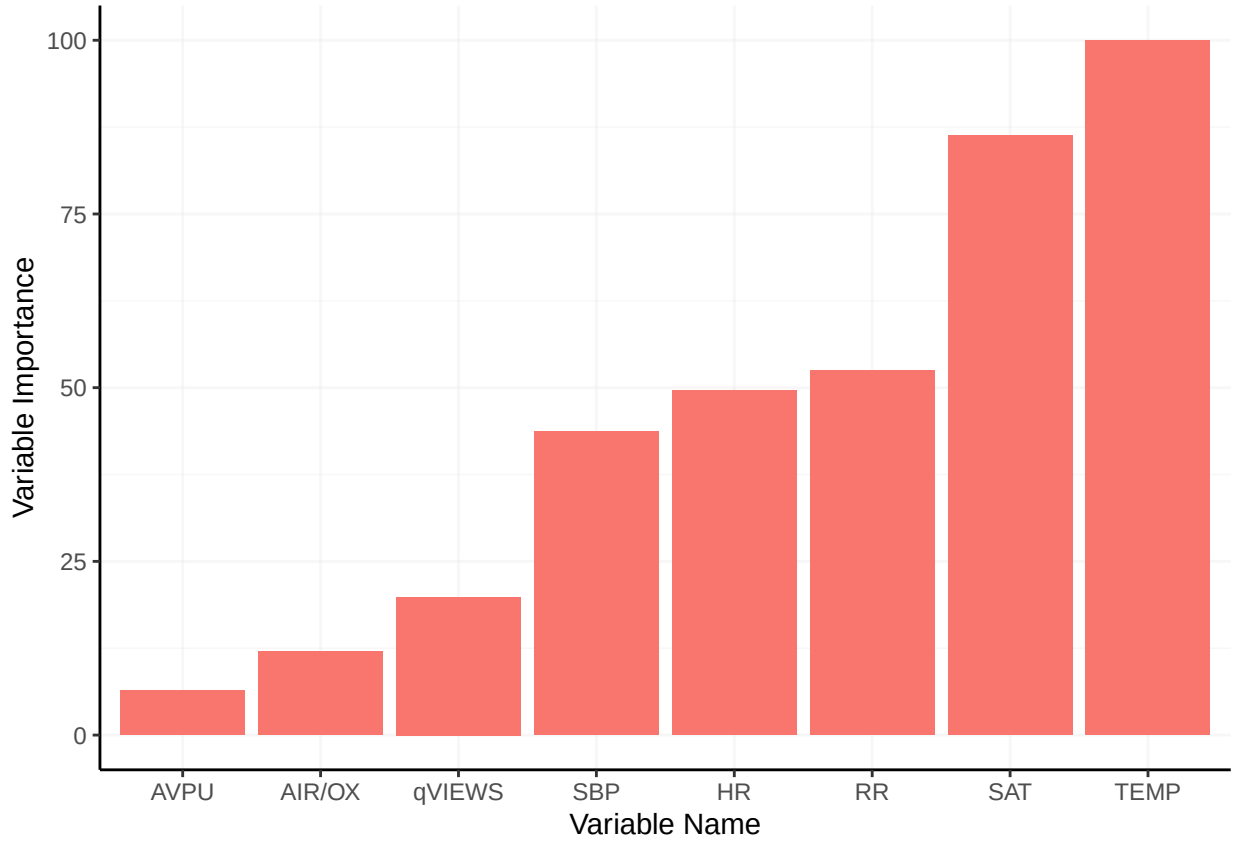
```
## v tibble  3.1.8     v dplyr   1.0.9
## v tidyr   1.2.0     v stringr 1.4.1
## v readr   2.1.2     v forcats 0.5.2
## v purrr   0.3.4
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
```

```
## x ggplot2::%+%()    masks psych::%+%()
## x ggplot2::alpha()  masks psych::alpha()
## x dplyr::combine()  masks randomForest::combine()
## x tidyr::expand()   masks Matrix::expand()
## x dplyr::filter()   masks stats::filter()
## x dplyr::lag()      masks stats::lag()
## x ggplot2::margin() masks randomForest::margin()
## x tidyr::pack()     masks Matrix::pack()
## x tidyr::unpack()   masks Matrix::unpack()
```

```
dt2 <- melt(dt1,id.vars='var.1')

col_grid <- rgb(235, 235, 235, 100, maxColorValue = 255)

ggplot(dt2, aes(fct_reorder(var.1,value),value, fill=variable))+
labs(y= "Variable Importance", x = "Variable Name")+
theme_bw()+
theme(panel.grid = element_line(color = col_grid))+
theme(legend.position="none")+
theme(panel.border = element_blank(), axis.line = element_line())+
geom_bar(stat='identity',position='dodge')
```




```
pred1 <- predict(rf.newdata,newdata=testdata,type="class")
table(pred1,testdata$itu_admission)
```

```
##
## pred1  0  1
##     0 43  6
```

```
##     1 41 68
```

```
(40+68)/158 # Correct predictions for around 68% of the locations in the test data set
```

```
## [1] 0.6835443
```

```
#Sensitivity, specificity of random forest prediction versus itu_admission in test sample
mx <- matrix(c(68,44,6,40),byrow=T,nrow=2)# Order is modified to allow itu_admission (1) as "1"
mx
```

```
##      [,1] [,2]
## [1,]   68   44
## [2,]    6   40
```

```
library(caret)
```

```
## Loading required package: lattice
##
## Attaching package: 'caret'
##
## The following object is masked from 'package:purrr':
##
##     lift
```

```
confusionMatrix(mx)
```

```
## Confusion Matrix and Statistics
##
##    A  B
## A 68 44
## B  6 40
##
##                Accuracy : 0.6835
##                  95% CI : (0.6049, 0.7551)
##     No Information Rate : 0.5316
##     P-Value [Acc > NIR] : 7.332e-05
##
##                   Kappa : 0.3834
##
##  Mcnemar's Test P-Value : 1.672e-07
##
##             Sensitivity : 0.9189
##             Specificity : 0.4762
##          Pos Pred Value : 0.6071
##          Neg Pred Value : 0.8696
##              Prevalence : 0.4684
##          Detection Rate : 0.4304
##    Detection Prevalence : 0.7089
##       Balanced Accuracy : 0.6976
##
##        'Positive' Class : A
##
```

```
# GRAPH THAT COMBINE RANDOM FOREST AND RIDGE AUC

plot.roc(y2[test2]~ ridge.coeff2,percentage=T,col="red",smooth=F)# for NEWS+qVIEWS
```

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

```
## Warning in roc.default(response, predictor, plot = TRUE, ...): Deprecated use a
## matrix as predictor. Unexpected results may be produced, please pass a numeric
## vector.
```

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

```
grid(NULL,NULL,col = "lightgray", lty = "dotted",lwd = par("lwd"), equilogs = TRUE)
lines.roc(y1[test1]~ ridge.coeff1,percentage=T,col="blue",smooth=F)# For NEWS only
```

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

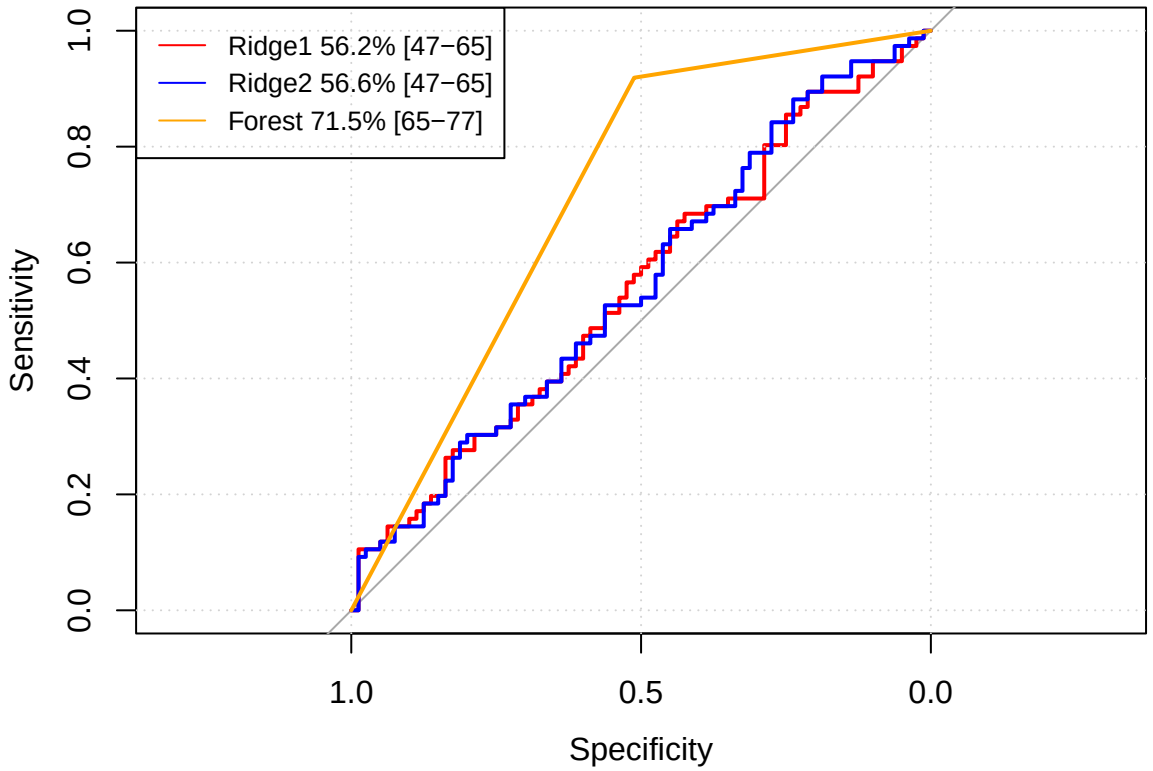
```
## Warning in roc.default(response, predictor, ...): Deprecated use a matrix as
## predictor. Unexpected results may be produced, please pass a numeric vector.
```

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

```
lines.roc(unlist(testdata$itu_admission)~ test.predictions,percentage=F,col="orange",smooth=F)
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```
legend("topleft", legend=c("Ridge1 56.2% [47-65]", "Ridge2 56.6% [47-65]","Forest 71.5% [65-77]"),
       col=c("red", "blue","orange"), lty=c(1,1,1), cex=0.8)
```




```
#End of data analysis and end of script
```