705604096_stats101c_hw4

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Question 1

```
kagtrain <- read.csv("TrainSAData2.csv")
kagtest <- read.csv("TestSAData2NoY.csv")
head(kagtrain)
```

```
##   ID    sex age height weight waistline sight_left sight_right hear_left
## 1  1   Male  75    160     NA        NA         NA         0.7    Normal
## 2  2 Female  50    160     60      74.0        1.0         1.2    Normal
## 3  3   Male  65    170     80      95.0        1.0         1.5    Normal
## 4  4   <NA>  65    155     55      81.0        0.3         0.4  Abnormal
## 5  5   Male  35    160     60      85.0        1.0         1.0    Normal
## 6  6 Female  50    160     70      73.2        0.3         0.4    Normal
##   hear_right SBP DBP BLDS tot_chole HDL_chole LDL_chole triglyceride hemoglobin
## 1     Normal  NA  76  136       215        33       143          193       15.0
## 2     Normal 118  70  125       207        85        NA          110       13.3
## 3     Normal 149  83  130       115        48        33          170       16.4
## 4   Abnormal 118  67   97       171        65        67          195       13.9
## 5     Normal  96  62   78       114        42        58           72       16.0
## 6     Normal 119  79  220       178        61        80          181       10.5
##   urine_protein serum_creatinine SGOT_AST SGOT_ALT gamma_GTP      BMI
## 1             3              0.9       28       23        36 23.43750
## 2             1              0.6       28       19        22 23.43750
## 3             1              1.4       41       64        53       NA
## 4             1              0.8       26       25        NA 22.89282
## 5             1              1.0       17       24        34       NA
## 6             1              0.5       36       NA        20 27.34375
##   BMI.Category AGE.Category Smoking.Status Alcoholic.Status
## 1      Healthy     Very Old  Still Smoking                Y
## 2         <NA>     Mid-aged   Never Smoked                Y
## 3   Overweight          Old  Still Smoking                Y
## 4         <NA>          Old   Never Smoked                N
## 5      Healthy     Mid-aged  Still Smoking                N
## 6   Overweight     Mid-aged   Never Smoked                N
```

```
head(kagtest)
```

```
##   ID    sex age height weight waistline sight_left sight_right hear_left
## 1  1   <NA>  40    175     NA        76        1.5         1.2    Normal
## 2  2 Female  55    150     55        81        1.0         0.9    Normal
## 3  3 Female  35    155     50        73        0.2         0.2    Normal
## 4  4 Female  60    155     50        79        1.0         1.0    Normal
## 5  5   Male  55    165     65        84         NA         0.9    Normal
## 6  6   Male  45    170     55        73        1.5         1.2    Normal
##   hear_right SBP DBP BLDS tot_chole HDL_chole LDL_chole triglyceride hemoglobin
## 1     Normal 118  78   89       160        49        75          181         NA
## 2     Normal  89  52  109       240        67       154           95       12.6
## 3     Normal 102  63   86        NA        48       120           63       12.0
## 4     Normal  NA  76   97       222        61       140          101       12.9
## 5     Normal 102  63   NA       198        46       112          200       17.1
## 6     Normal 120  80   98       152        NA        55          283       14.5
##   urine_protein serum_creatinine SGOT_AST SGOT_ALT gamma_GTP      BMI
## 1             1              1.1       18       13        15 22.85714
## 2             1              0.7       47       32        27 24.44444
## 3             1              0.8       14       10        10 20.81165
## 4             1              1.0       33       NA        64 20.81165
## 5             2              0.7       21       33        78 23.87511
## 6             1              1.0       17       25        26       NA
##   BMI.Category AGE.Category Smoking.Status
## 1      Healthy     Mid-aged  Still Smoking
## 2         <NA>          Old           <NA>
## 3      Healthy     Mid-aged           <NA>
## 4      Healthy          Old   Never Smoked
## 5      Healthy          Old   Never Smoked
## 6      Healthy     Mid-aged  Still Smoking
```

a.

```
dim(kagtrain)
```

```
## [1] 70000    28
```

```
dim(kagtest)
```

```
## [1] 30000    27
```

The training data set has 28 columns by 70,000 rows. The testing data set has 27 columns by 30,000 rows.

b. There are 21 numerical predictors. They include the variables ID, age, height, weight, waistline, sight_left, sight_right, SBP, DBP, BLDS, tot_chole, HDL_chole, LDL_chole, triglyceride, hemoglobin, urine_protein, serum_creatinine, SGOT_AST, SGOT_ALT, gamma_GTP, and BMI.

c. There are 7 categorical variables. They are sex, hear_left, hear_right, BMI.Category, AGE.Category, Smoking.Status, and Alcoholic.Status.

d.

```
(sapply(kagtrain, function(x) sum(is.na(x))) / 70000) * 100
```

```
##               ID              sex              age           height
##         0.000000         7.088571         6.967143         7.058571
##           weight        waistline       sight_left      sight_right
##         7.102857         7.057143         6.967143         7.000000
##        hear_left       hear_right              SBP              DBP
##         6.904286         6.981429         7.027143         6.992857
##             BLDS        tot_chole        HDL_chole        LDL_chole
##         6.887143         6.948571         6.880000         7.020000
##     triglyceride       hemoglobin    urine_protein serum_creatinine
##         6.967143         7.087143         6.998571         6.924286
##         SGOT_AST         SGOT_ALT        gamma_GTP              BMI
##         6.981429         6.990000         7.087143         7.095714
##     BMI.Category     AGE.Category   Smoking.Status Alcoholic.Status
##         6.962857        11.875714         6.970000         0.000000
```

```
((sapply(kagtest, function(x) sum(is.na(x)))) / 30000) * 100
```

```
##               ID              sex              age           height
##         0.000000         7.296667         7.103333         7.063333
##           weight        waistline       sight_left      sight_right
##         7.003333         7.183333         6.736667         7.146667
##        hear_left       hear_right              SBP              DBP
##         6.840000         6.800000         7.013333         7.056667
##             BLDS        tot_chole        HDL_chole        LDL_chole
##         7.050000         7.203333         7.026667         7.003333
##     triglyceride       hemoglobin    urine_protein serum_creatinine
##         6.680000         6.896667         6.830000         6.953333
##         SGOT_AST         SGOT_ALT        gamma_GTP              BMI
##         6.933333         7.076667         6.853333         7.200000
##     BMI.Category     AGE.Category   Smoking.Status
##         7.073333        11.730000         7.030000
```

e.

```
length(kagtrain$Alcoholic.Status[kagtrain$Alcoholic.Status == "Y"])
```

```
## [1] 34887
```

```
length(kagtrain$Alcoholic.Status[kagtrain$Alcoholic.Status == "N"])
```

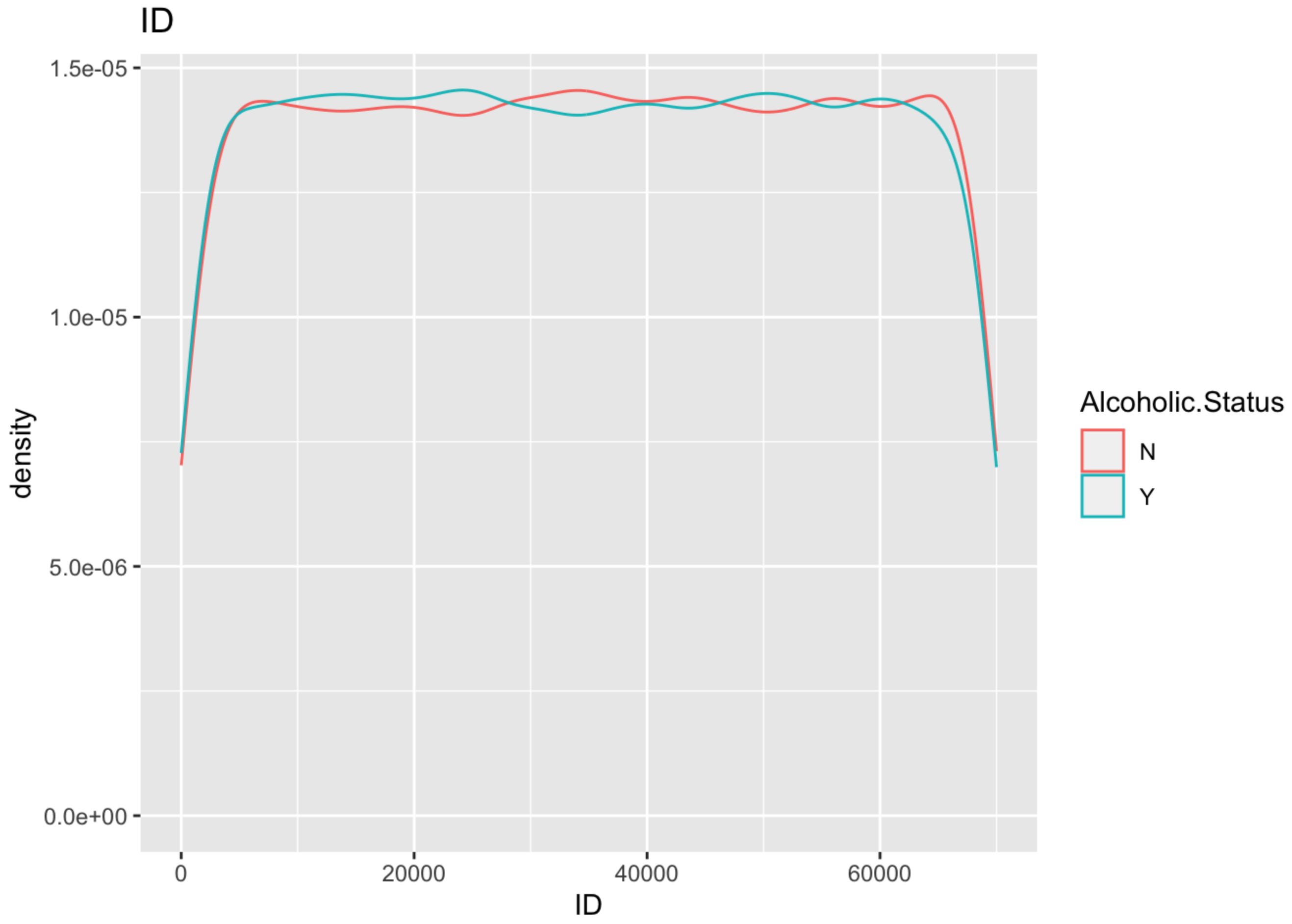
```
## [1] 35113
```

Our response variable is Alcoholic.Status that has two values, yes or no, denotes Y or N. Alcoholic.Status is Y 34887 times out of 70000 observations which is 49.84% and it is N 35113 times out of 70000 observations which is 50.16%. Our max error rate based on our training data is 49.84%.

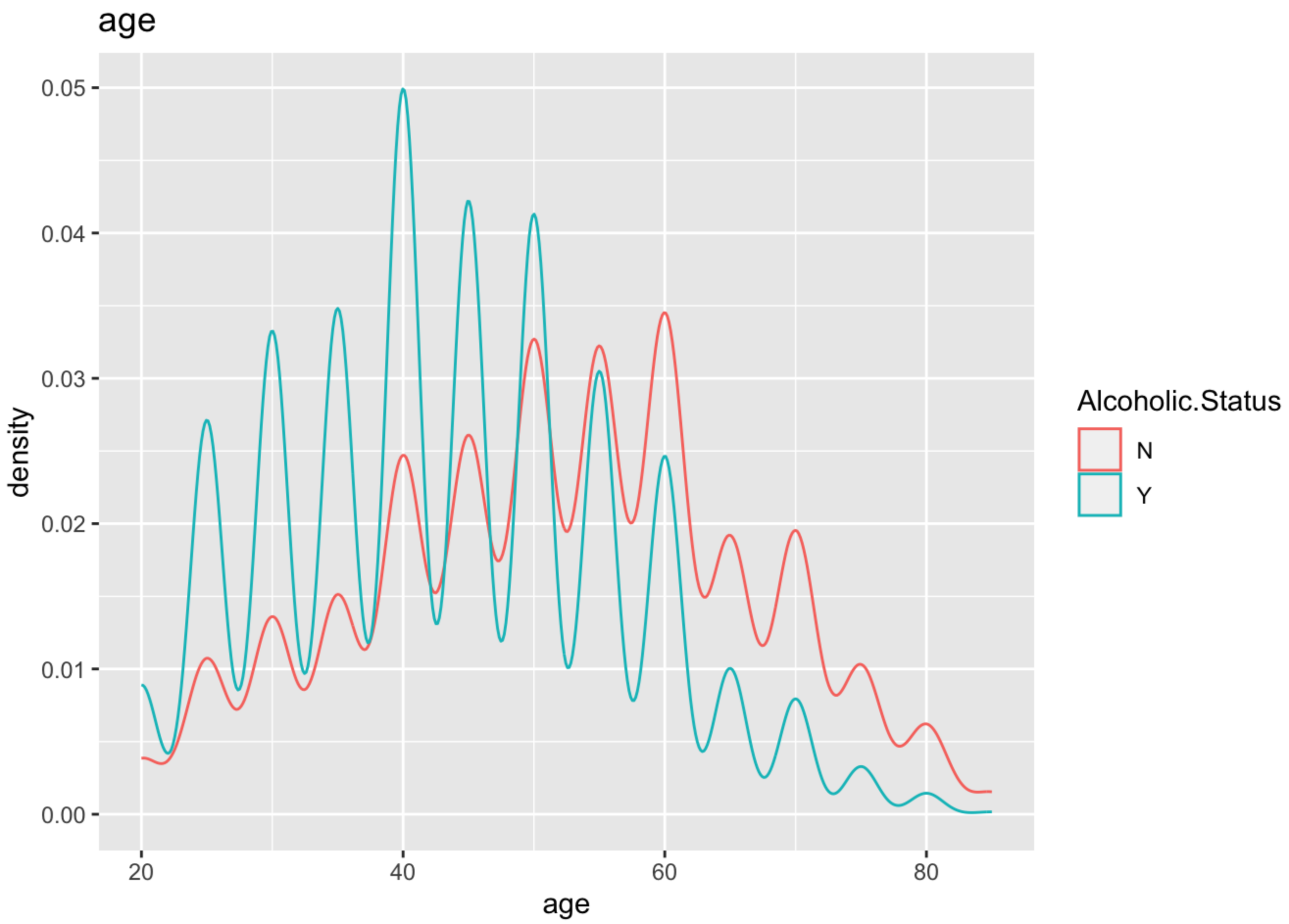
f.

```
num_names <- names(kagtrain[sapply(kagtrain, is.numeric)])
for(variable in num_names){
  plot <- ggplot(kagtrain, aes_string(variable, color = "Alcoholic.Status")) + geom_dens
ity() + ggtitle(variable)
  print(plot)
}
```

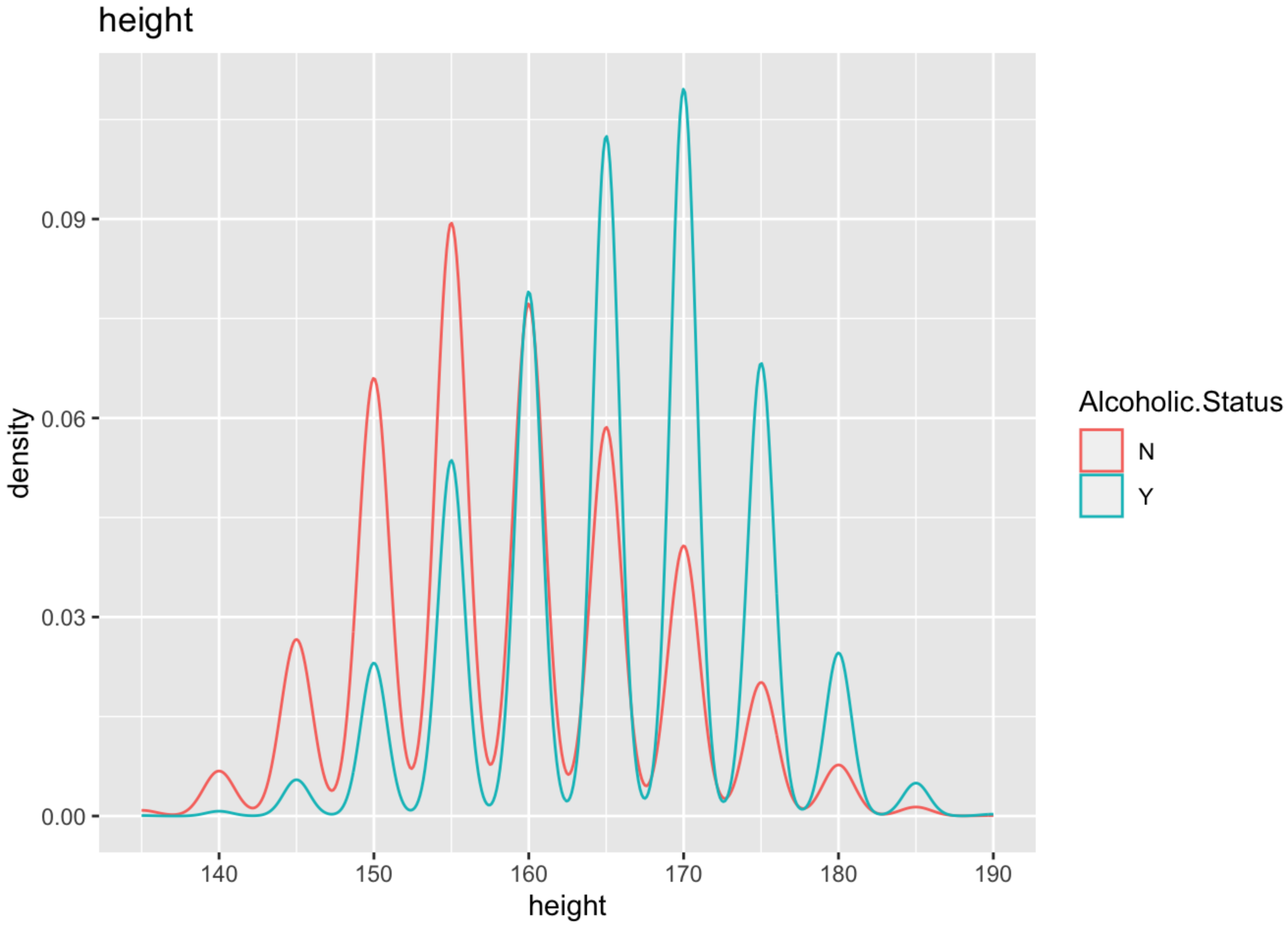
```
## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
## ℹ Please use tidy evaluation idioms with `aes()`.
## ℹ See also `vignette("ggplot2-in-packages")` for more information.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



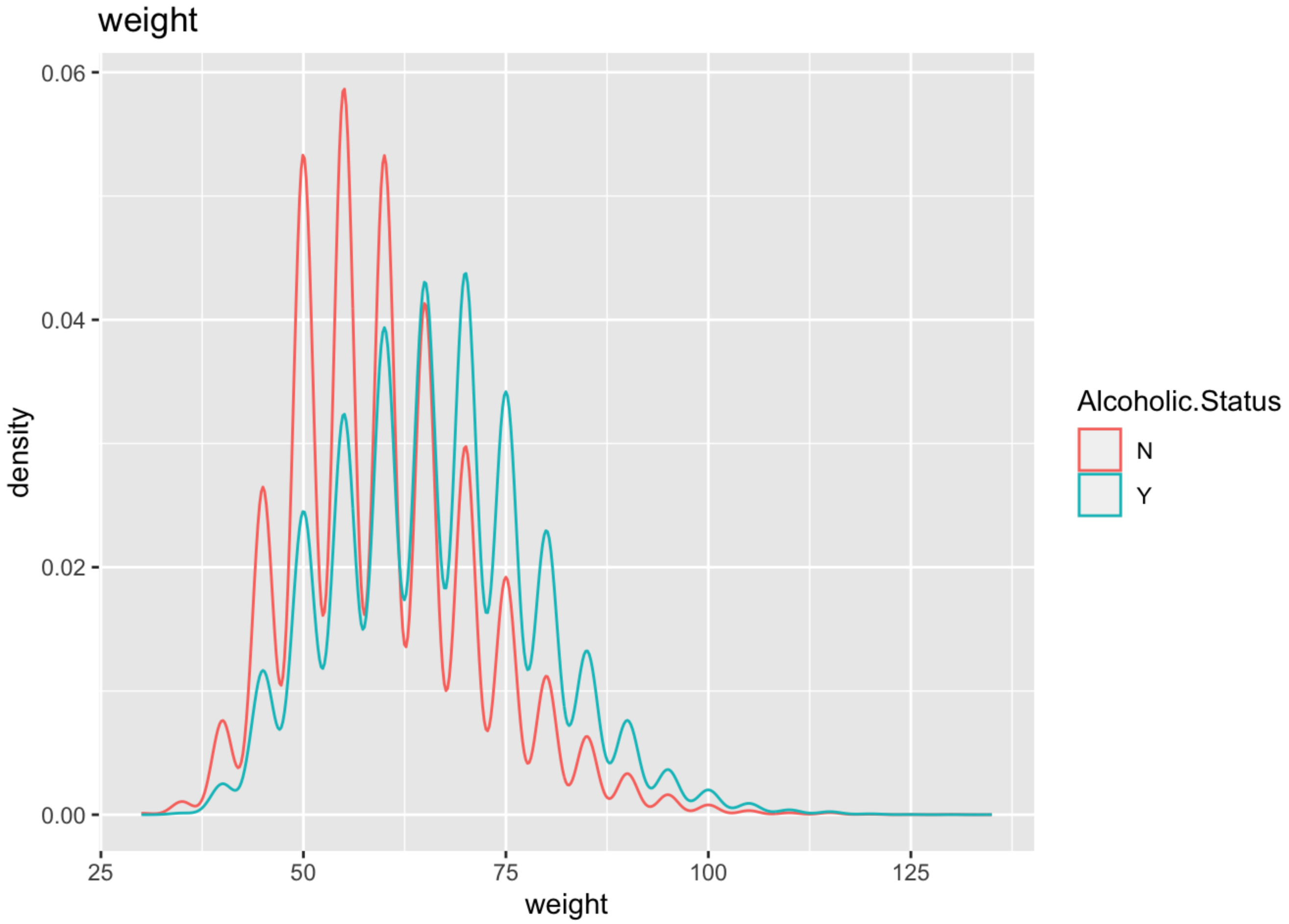
```
## Warning: Removed 4877 rows containing non-finite values (`stat_density()`).
```



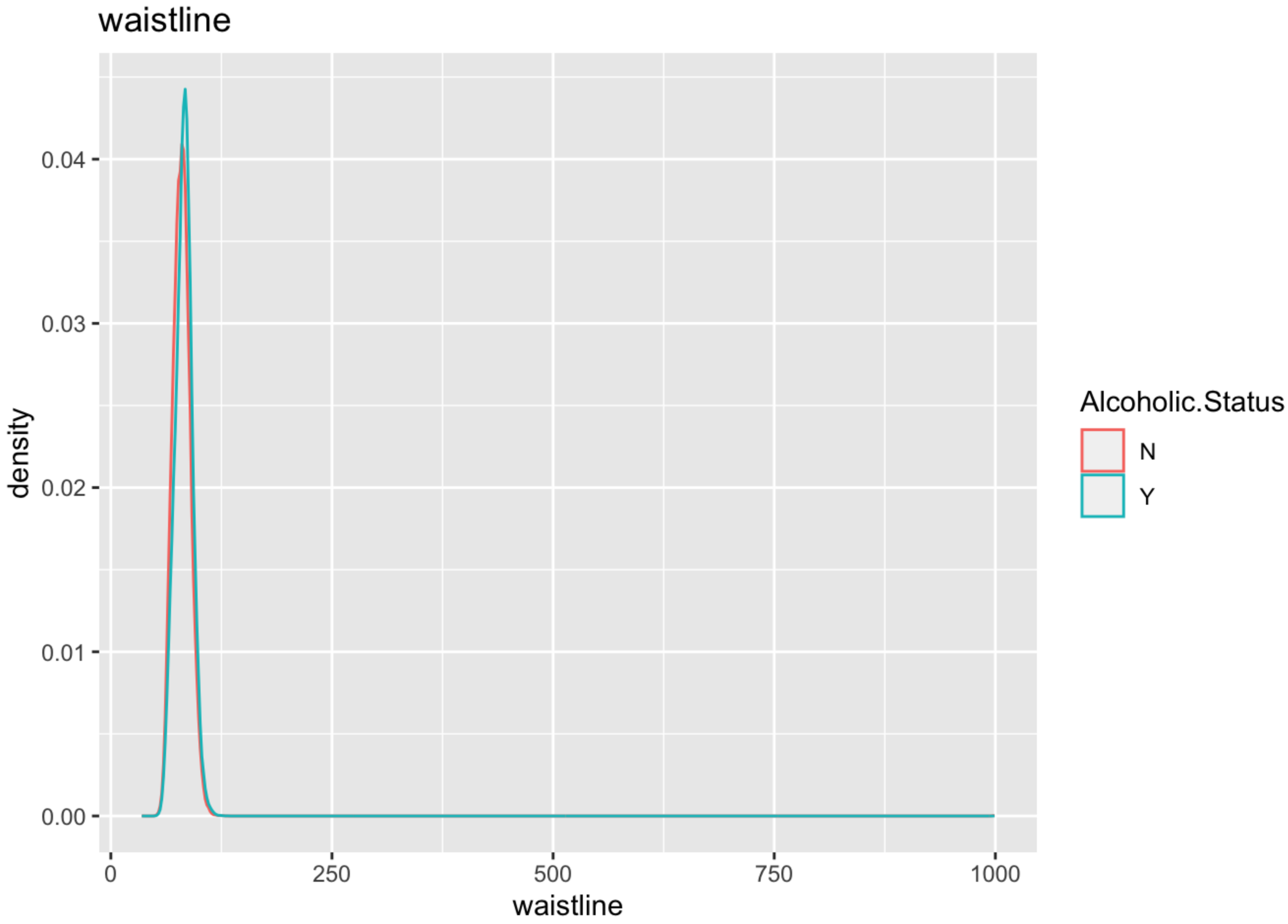
```
## Warning: Removed 4941 rows containing non-finite values (`stat_density()`).
```



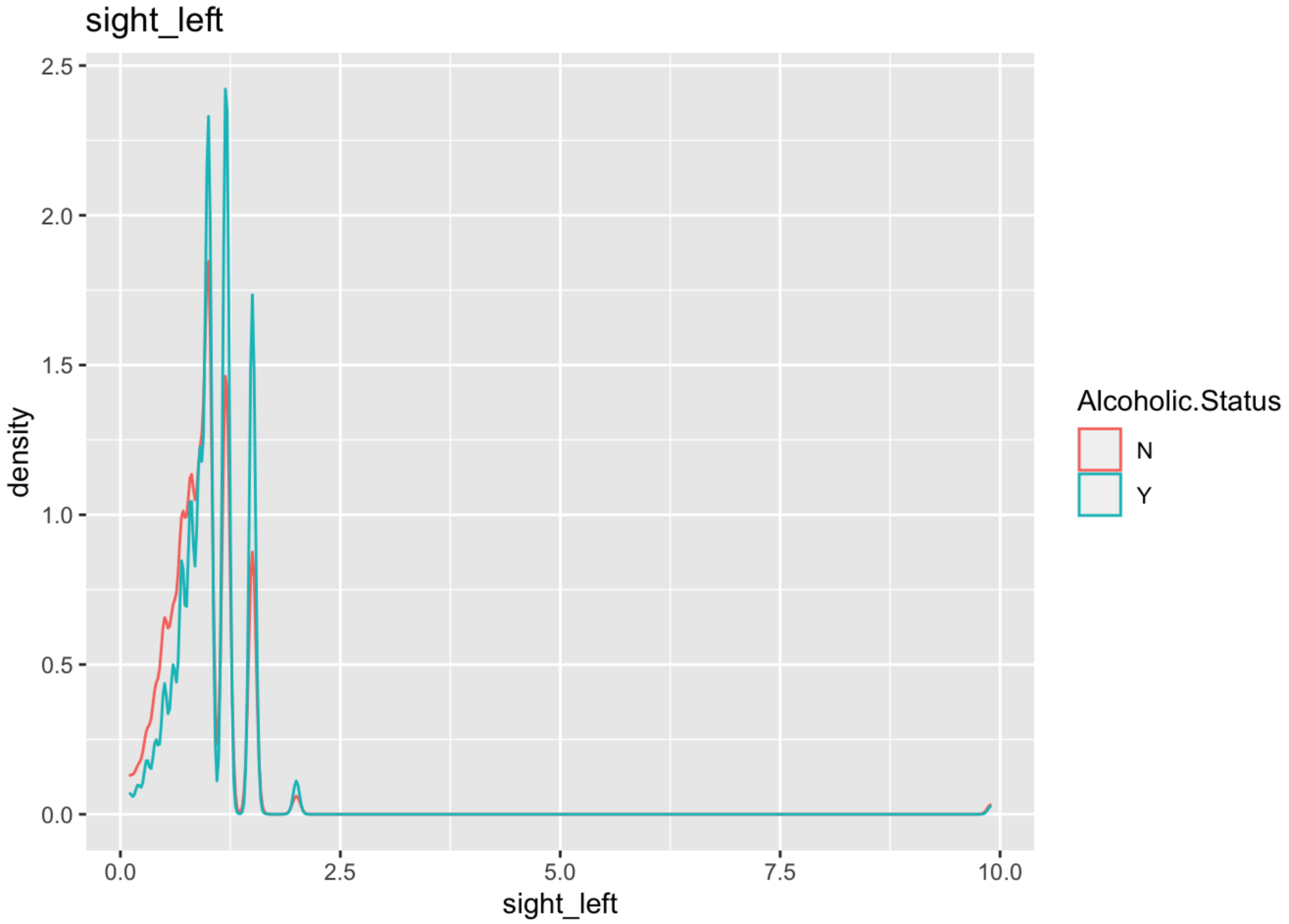
```
## Warning: Removed 4972 rows containing non-finite values (`stat_density()`).
```



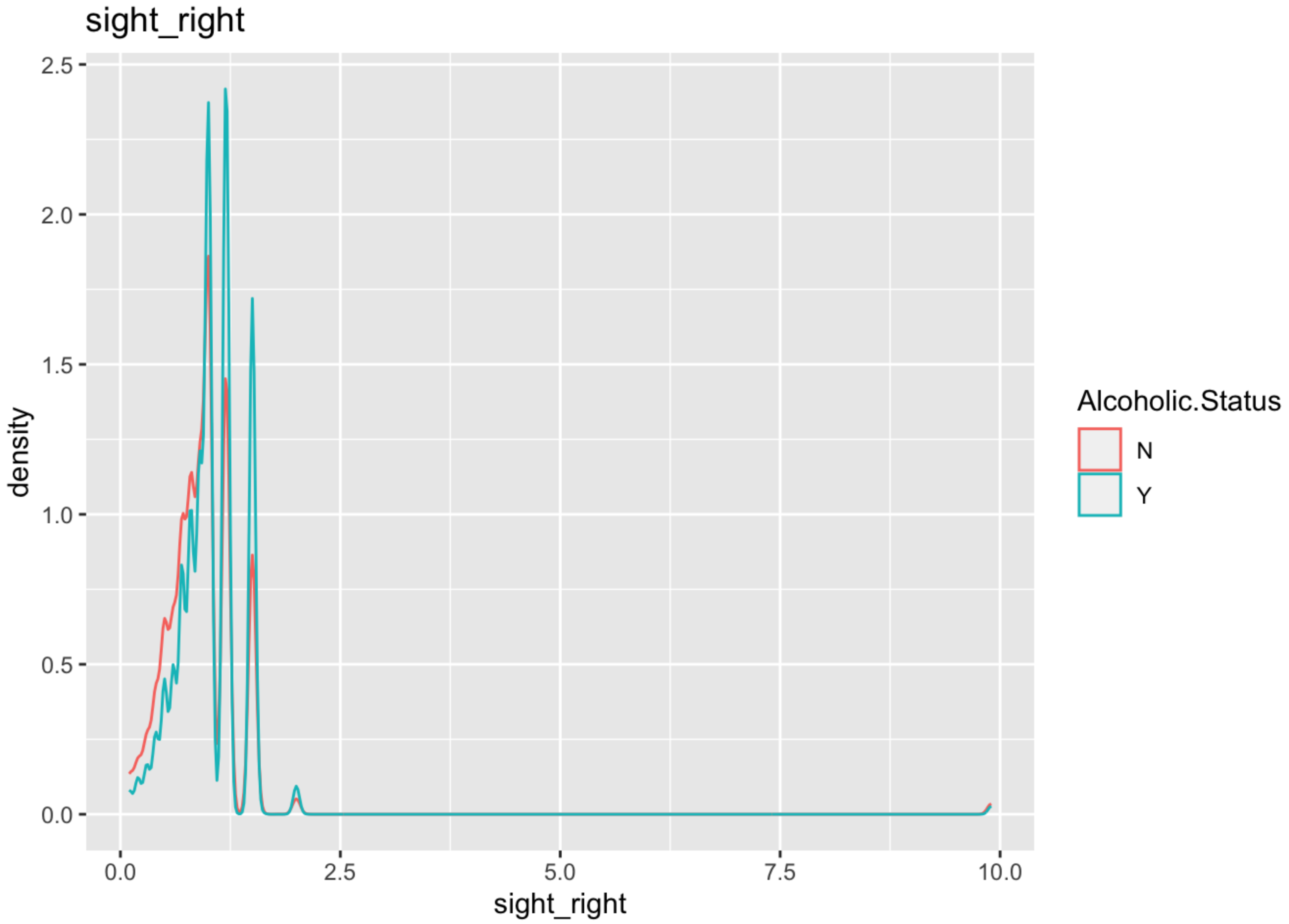
```
## Warning: Removed 4940 rows containing non-finite values (`stat_density()`).
```



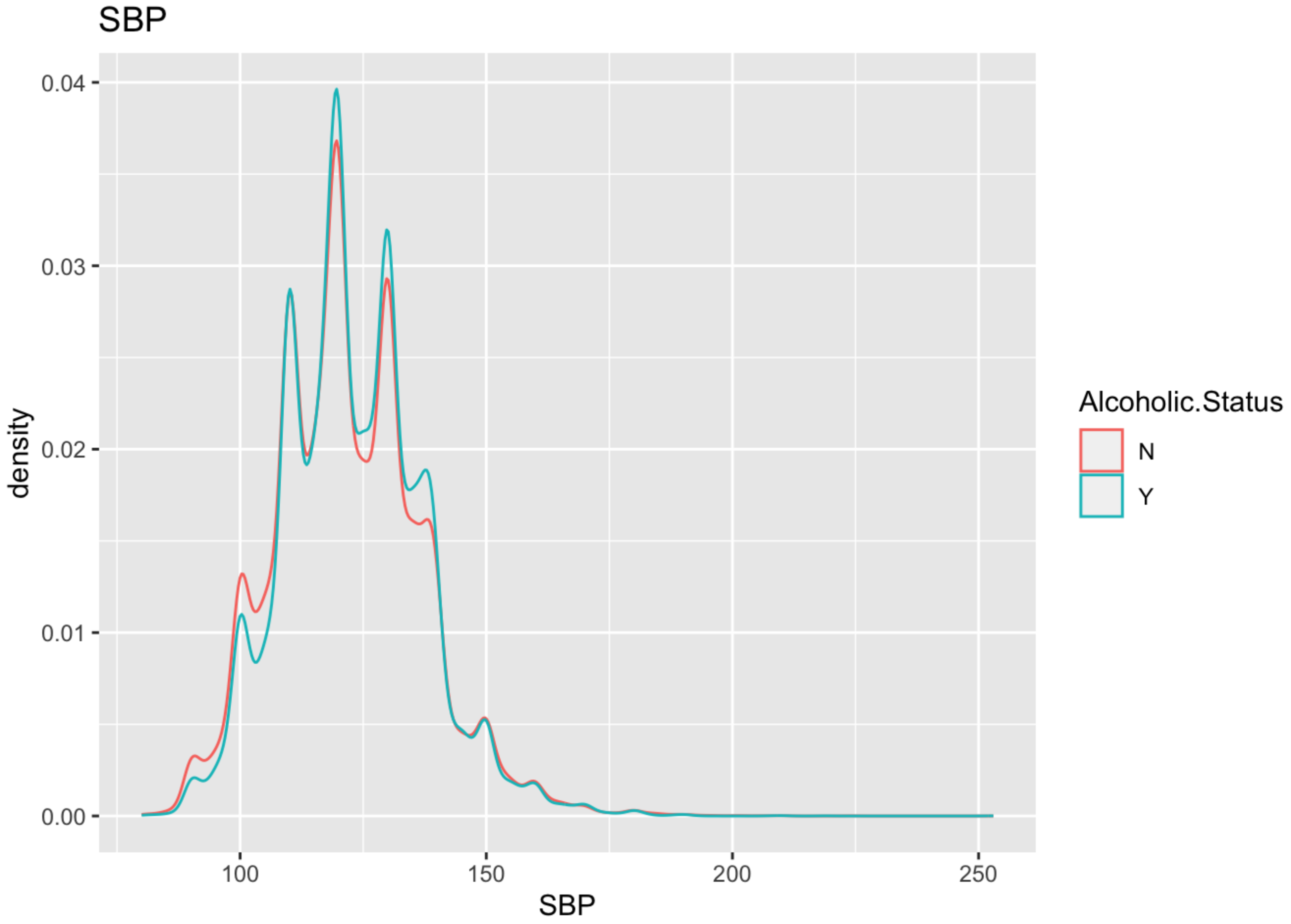
```
## Warning: Removed 4877 rows containing non-finite values (`stat_density()`).
```



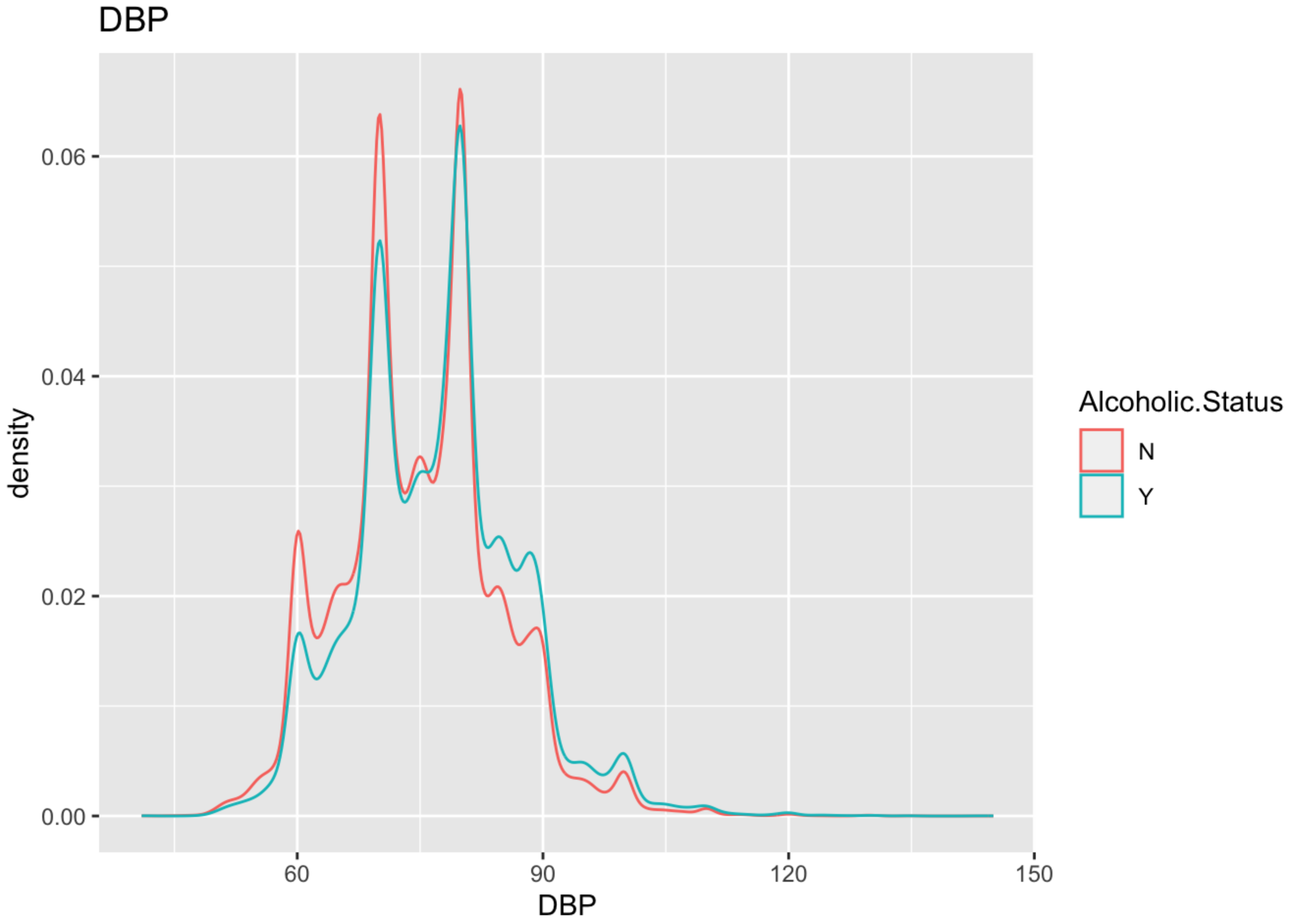
```
## Warning: Removed 4900 rows containing non-finite values (`stat_density()`).
```



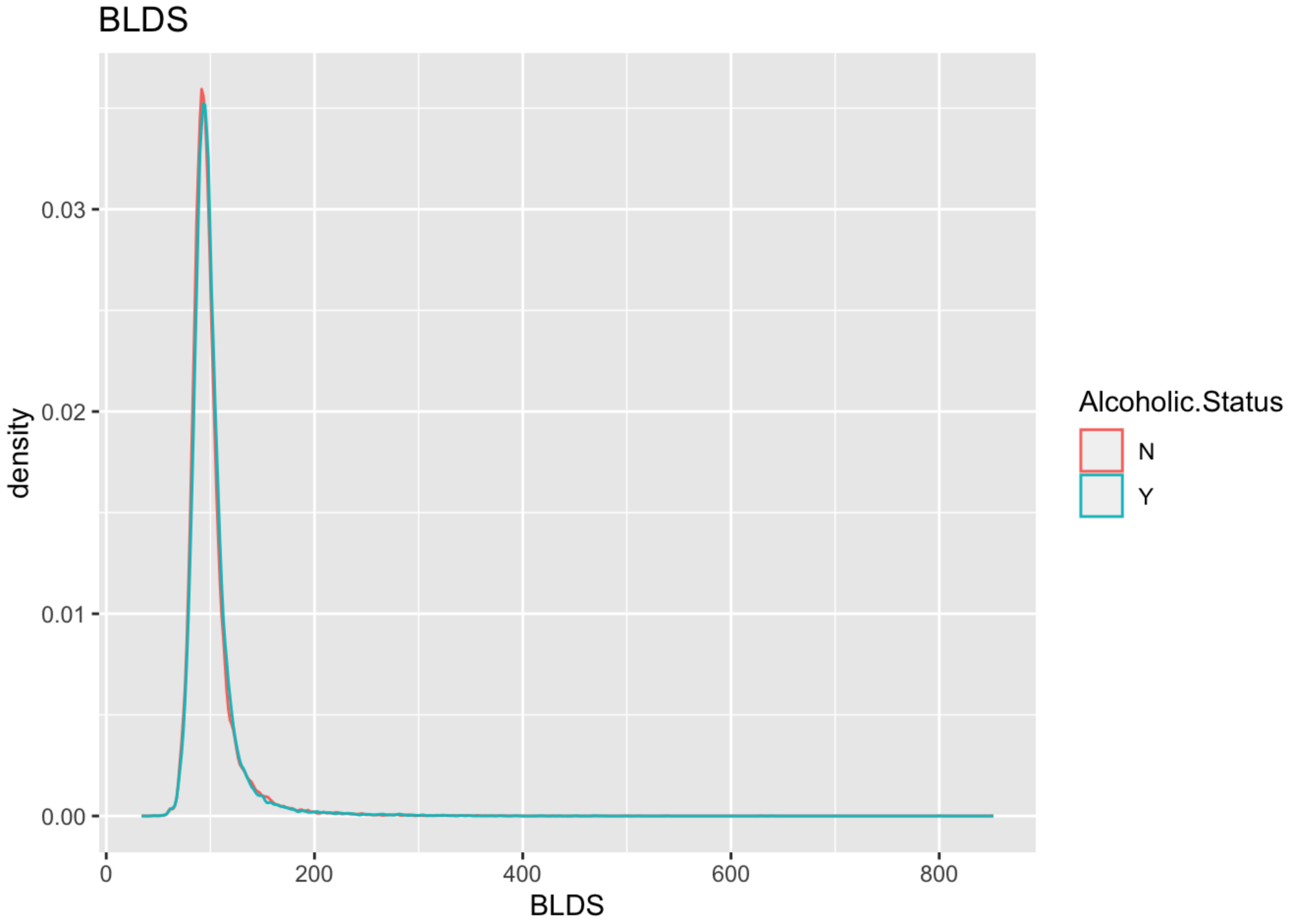
```
## Warning: Removed 4919 rows containing non-finite values (`stat_density()`).
```



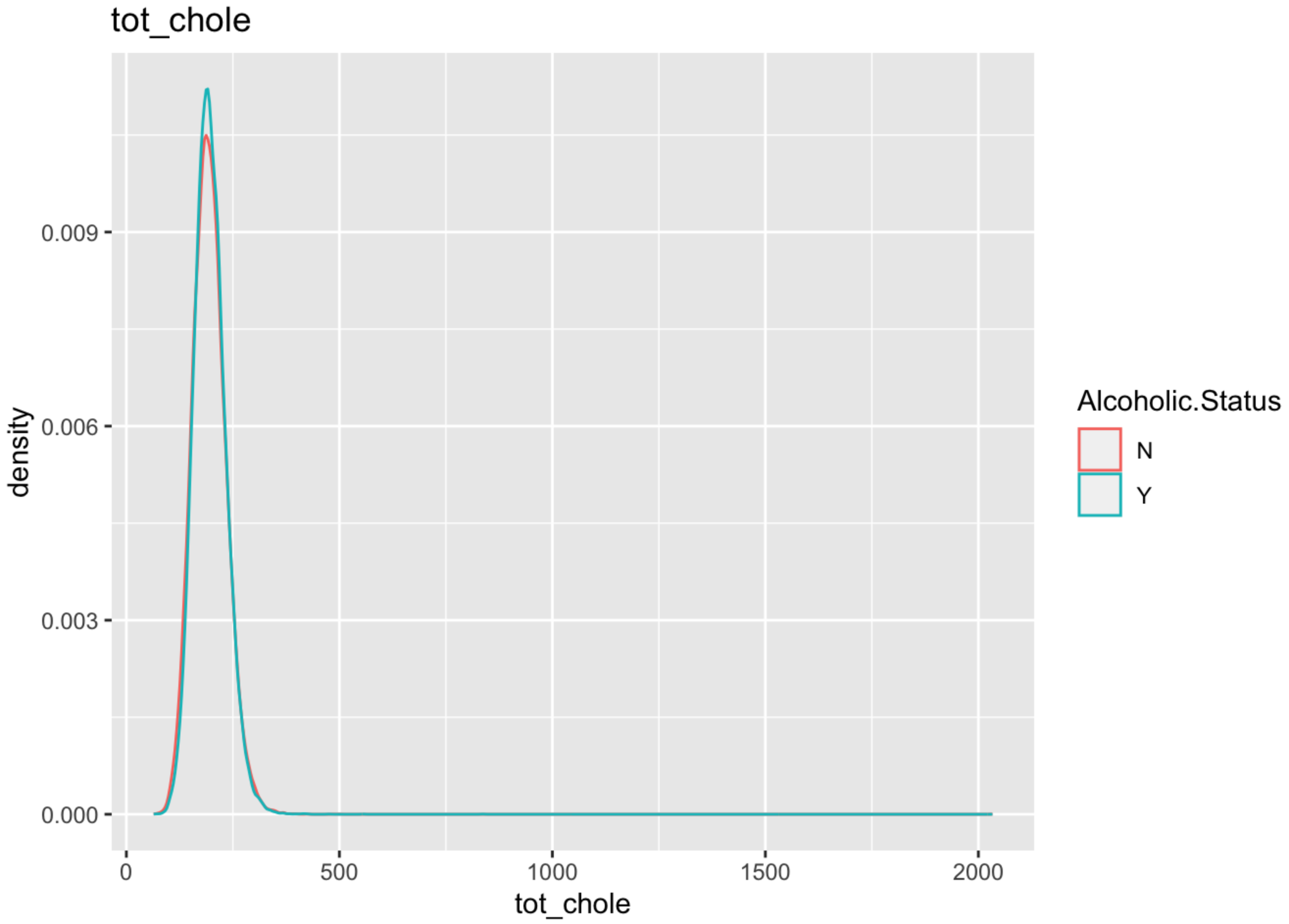
```
## Warning: Removed 4895 rows containing non-finite values (`stat_density()`).
```



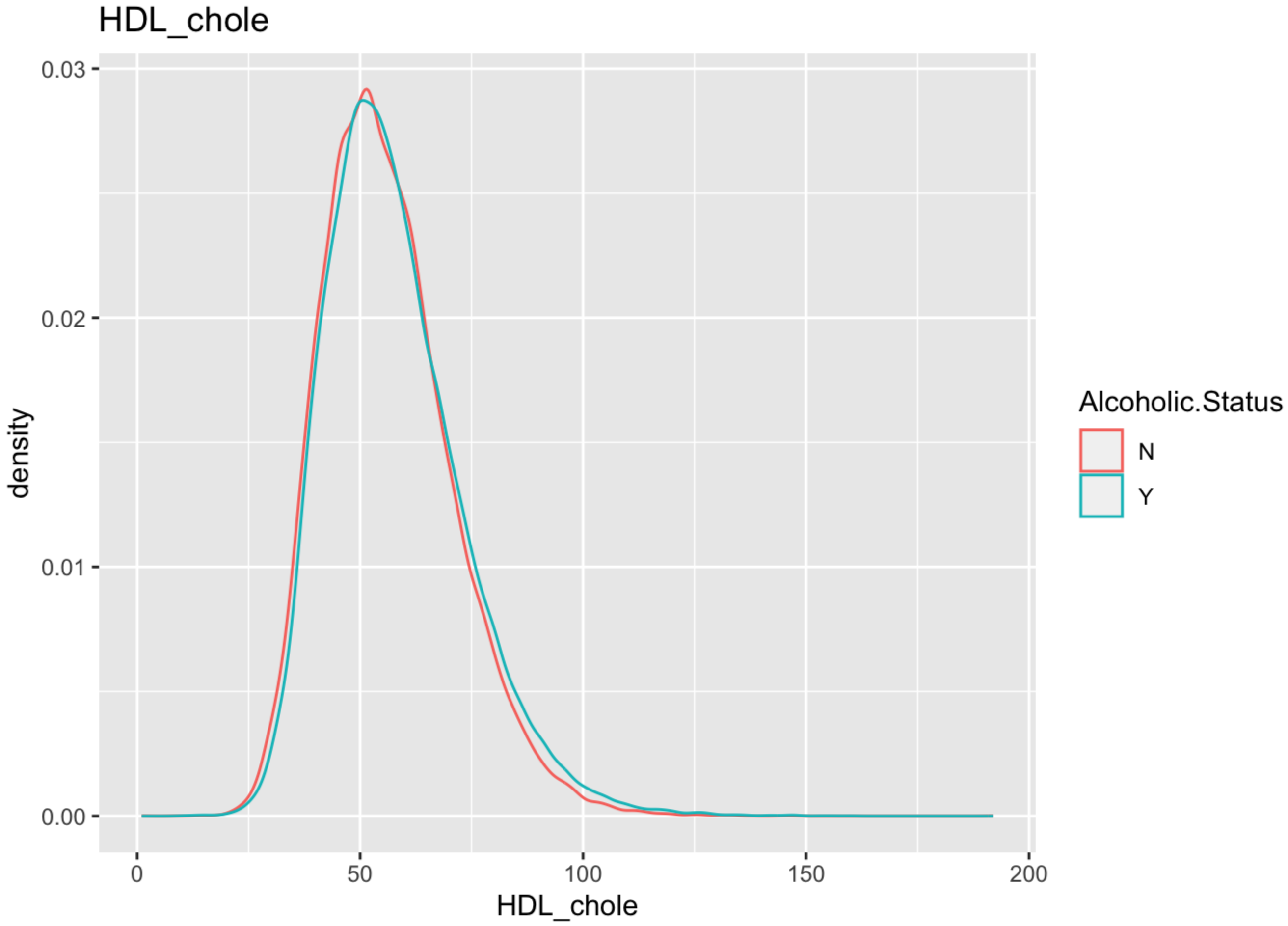
```
## Warning: Removed 4821 rows containing non-finite values (`stat_density()`).
```



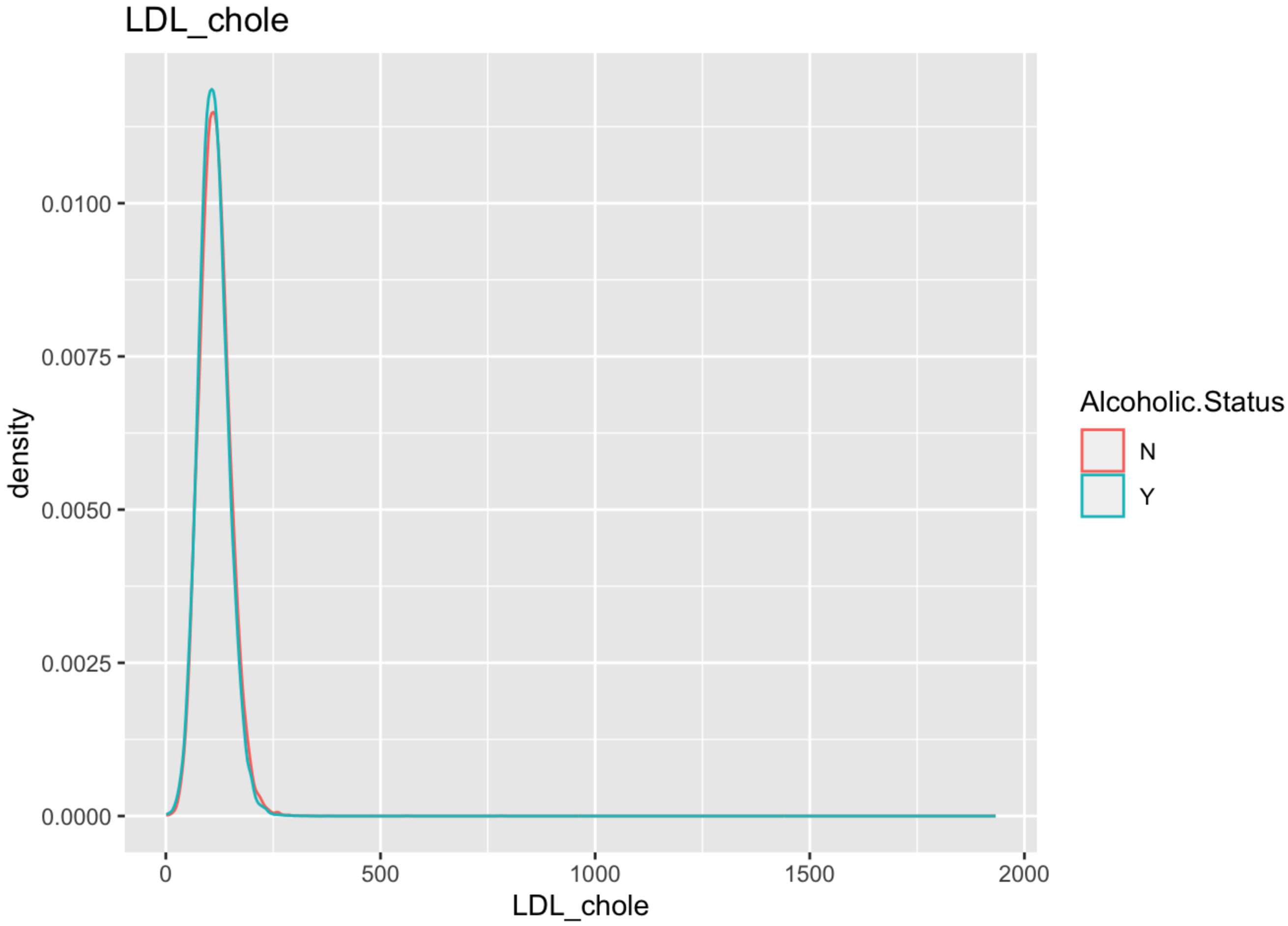
```
## Warning: Removed 4864 rows containing non-finite values (`stat_density()`).
```



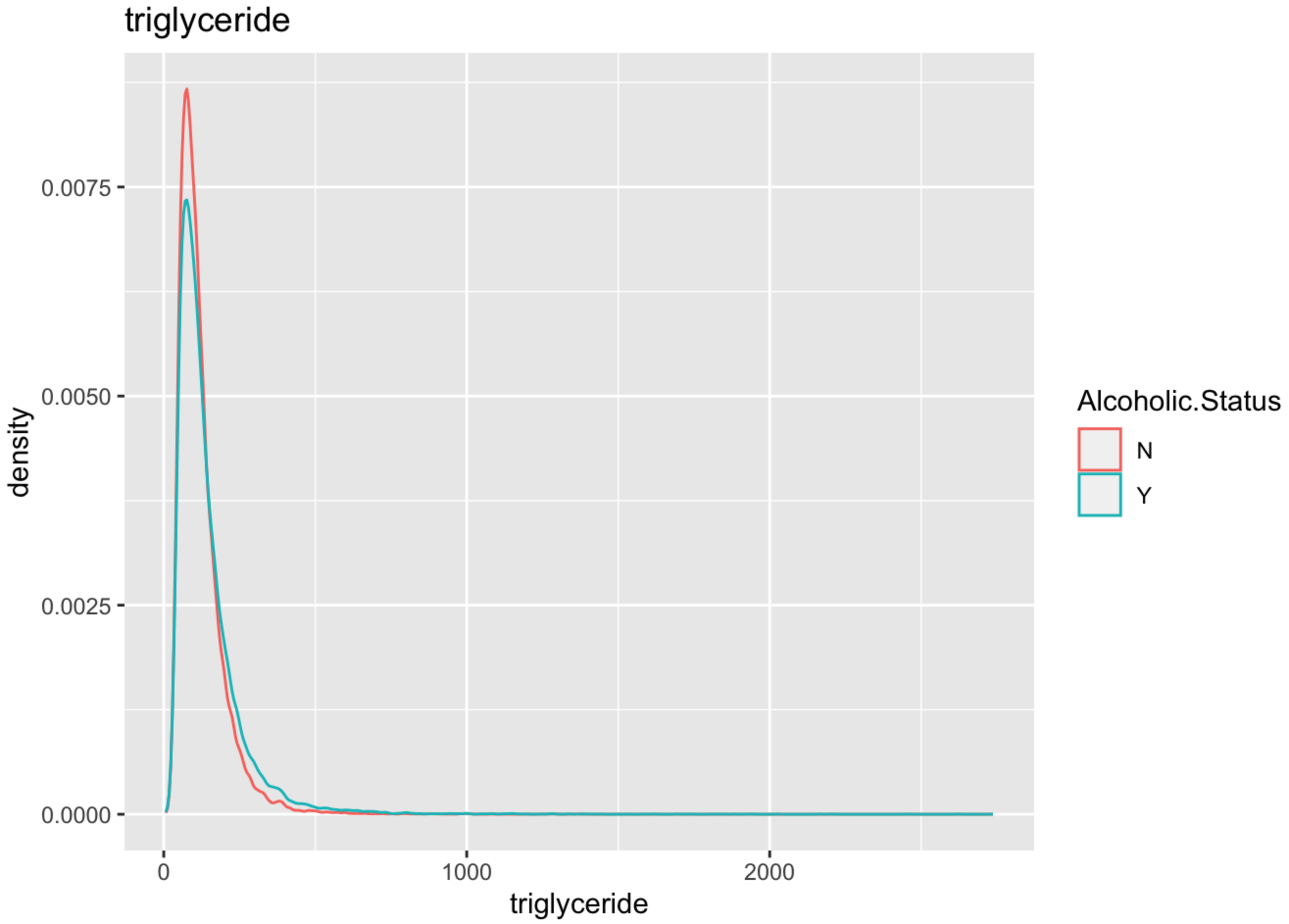
```
## Warning: Removed 4816 rows containing non-finite values (`stat_density()`).
```



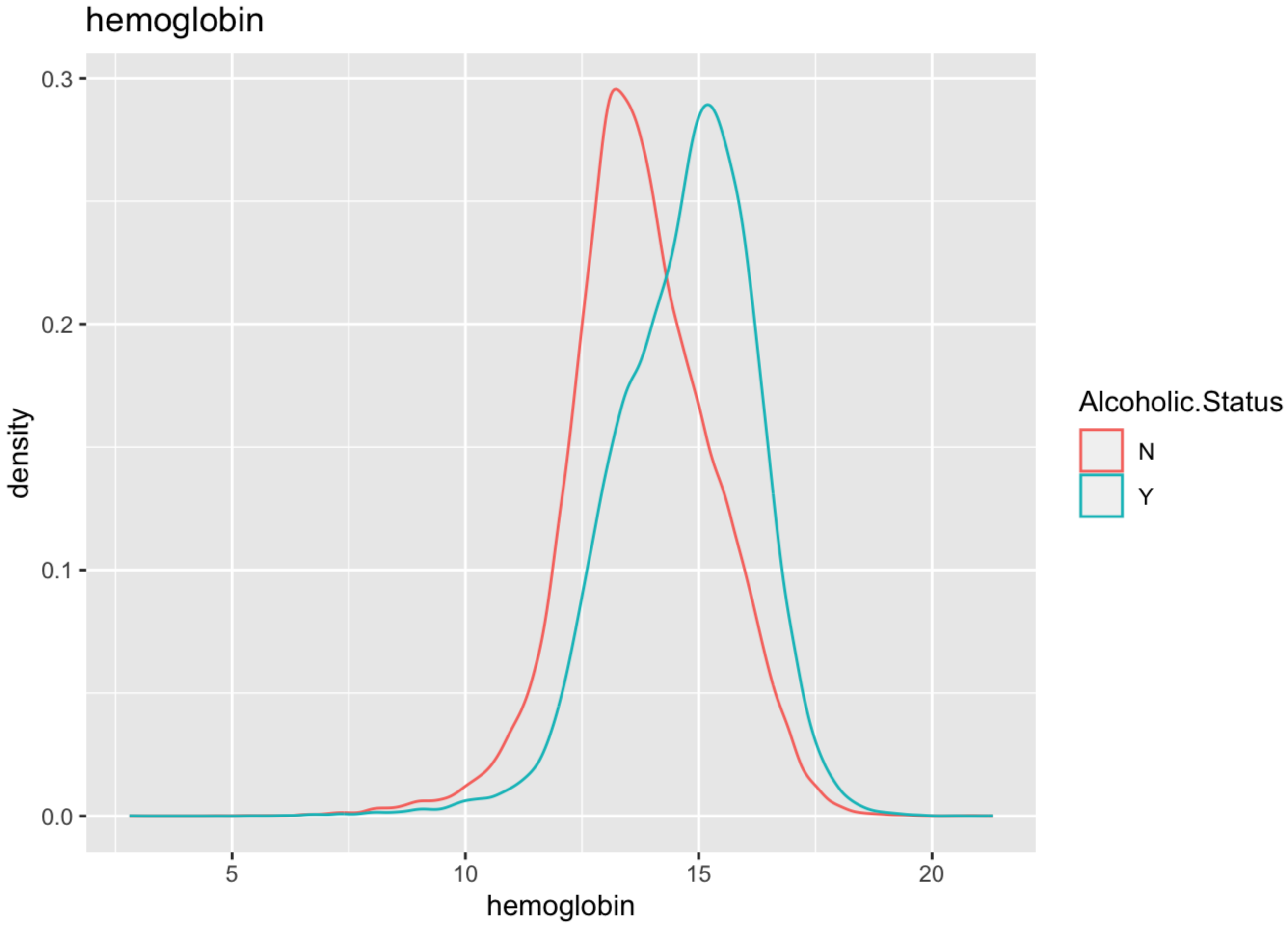
```
## Warning: Removed 4914 rows containing non-finite values (`stat_density()`).
```



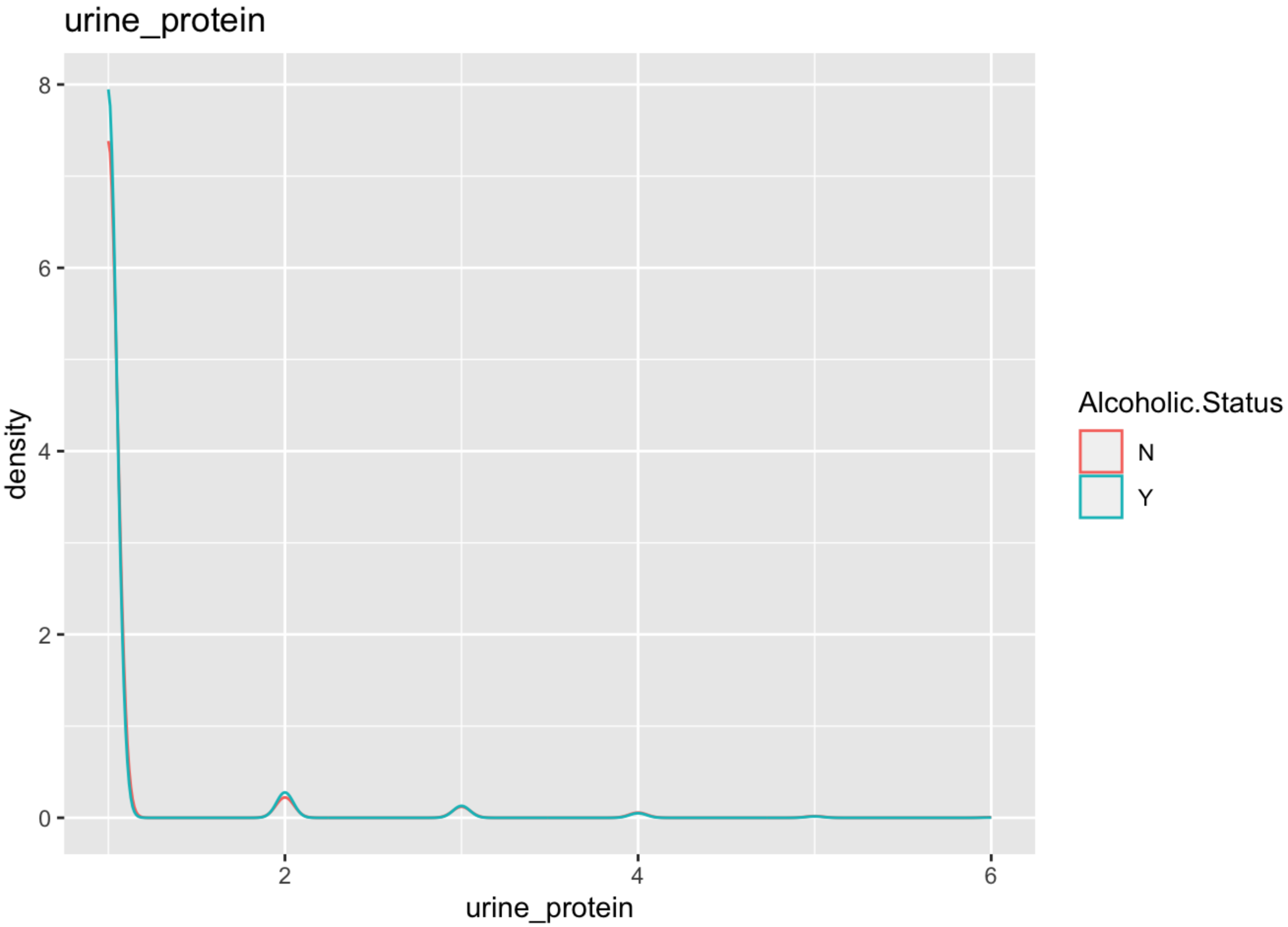
```
## Warning: Removed 4877 rows containing non-finite values (`stat_density()`).
```



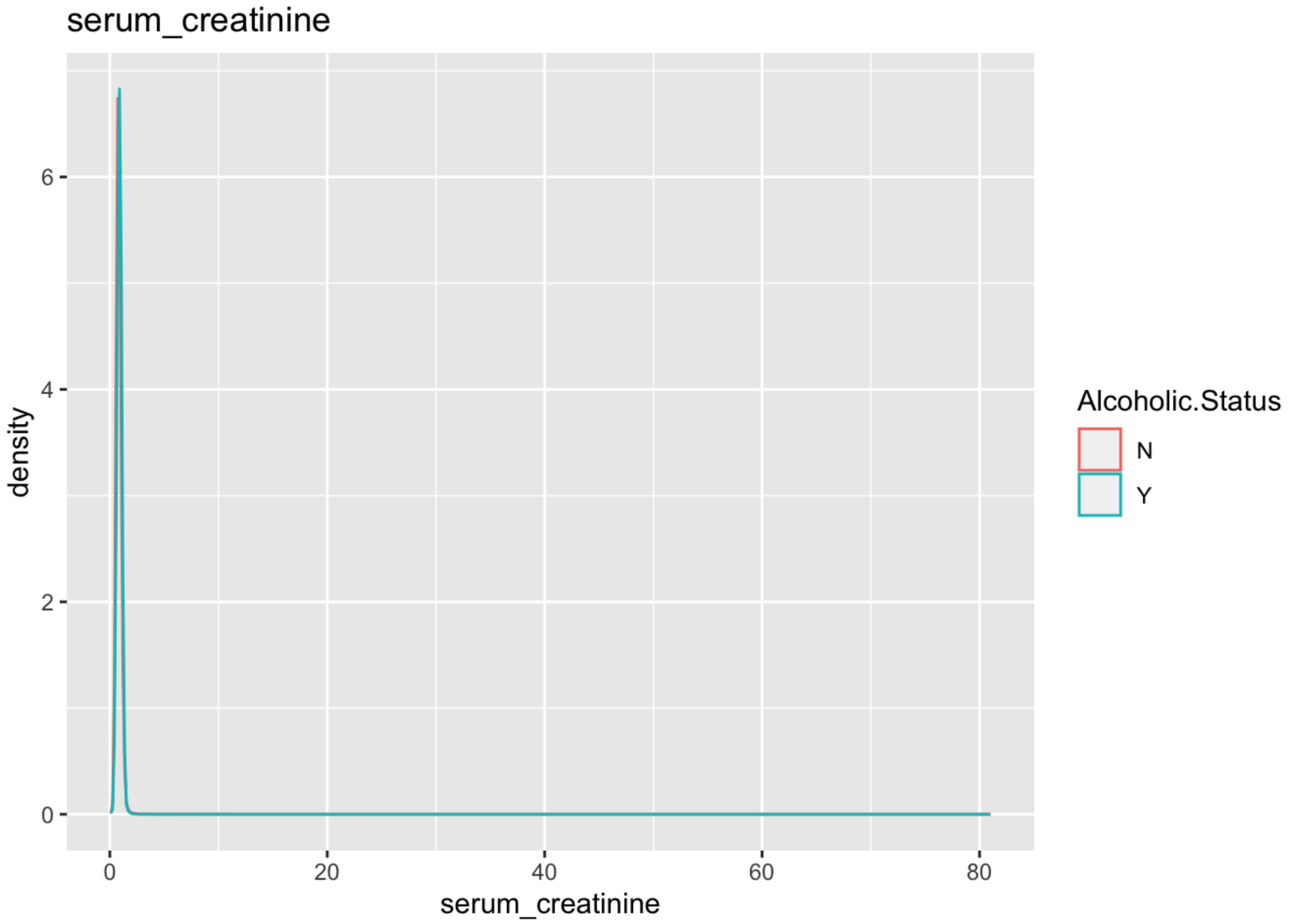
```
## Warning: Removed 4961 rows containing non-finite values (`stat_density()`).
```



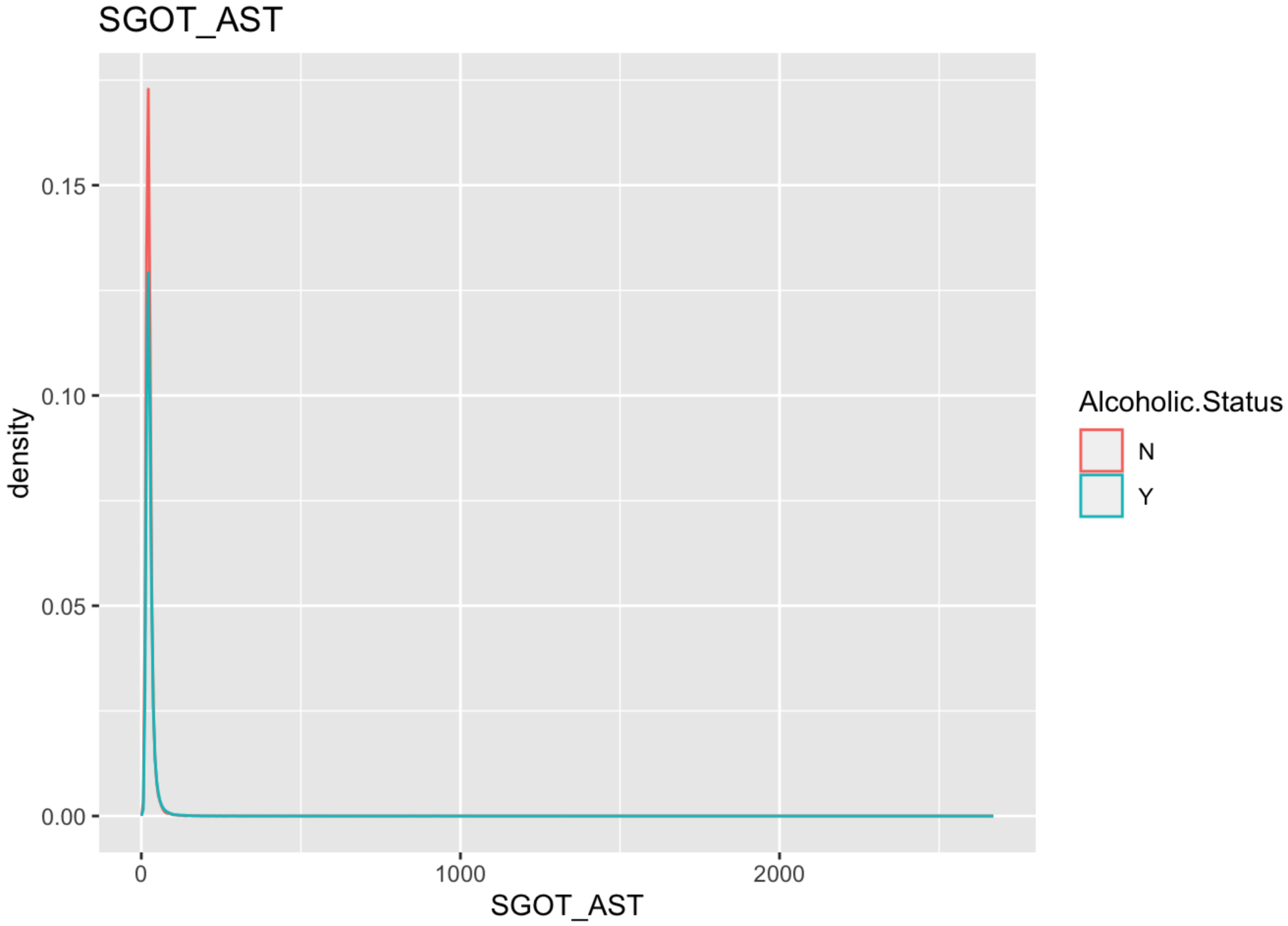
```
## Warning: Removed 4899 rows containing non-finite values (`stat_density()`).
```



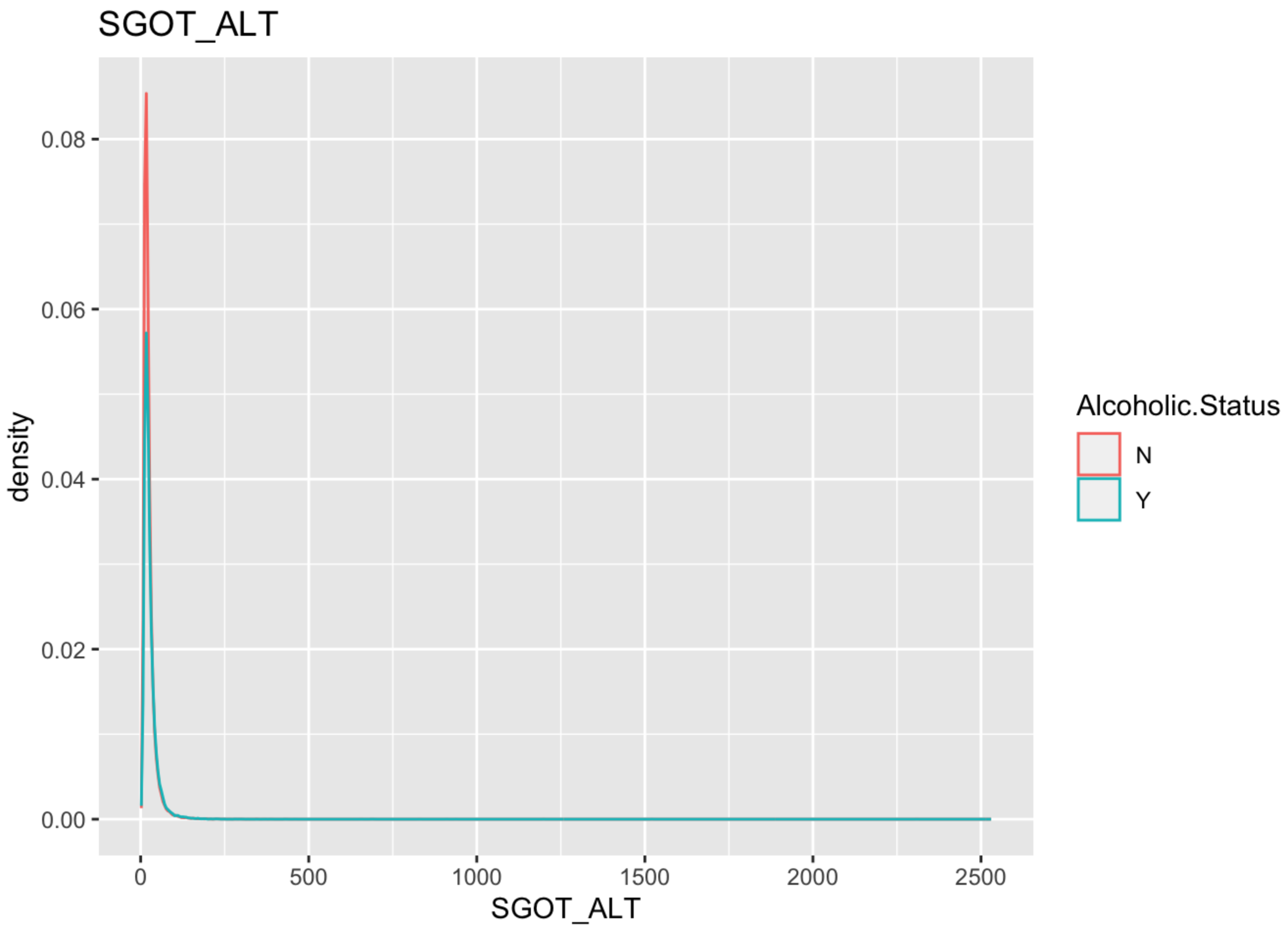
```
## Warning: Removed 4847 rows containing non-finite values (`stat_density()`).
```



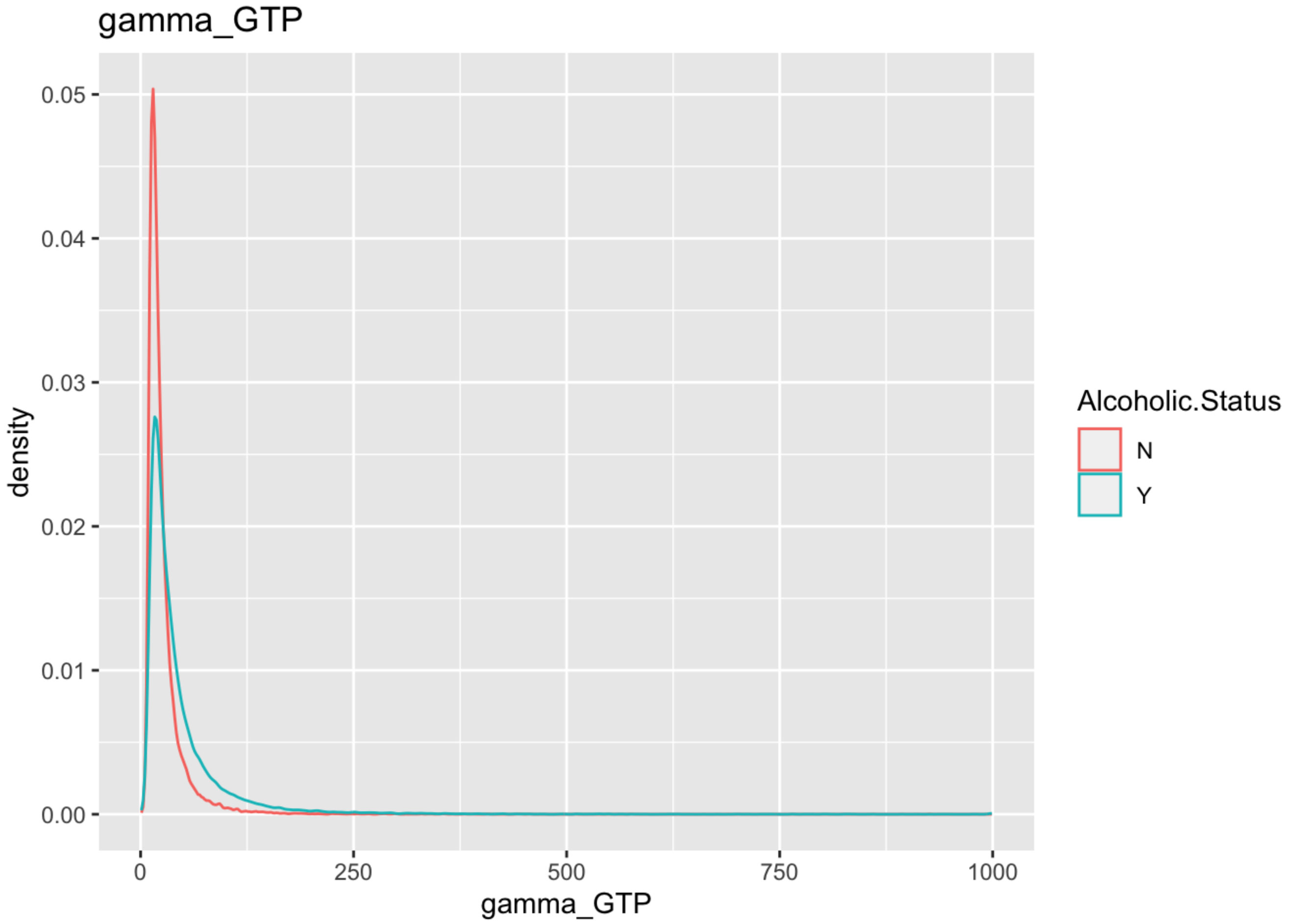
```
## Warning: Removed 4887 rows containing non-finite values (`stat_density()`).
```



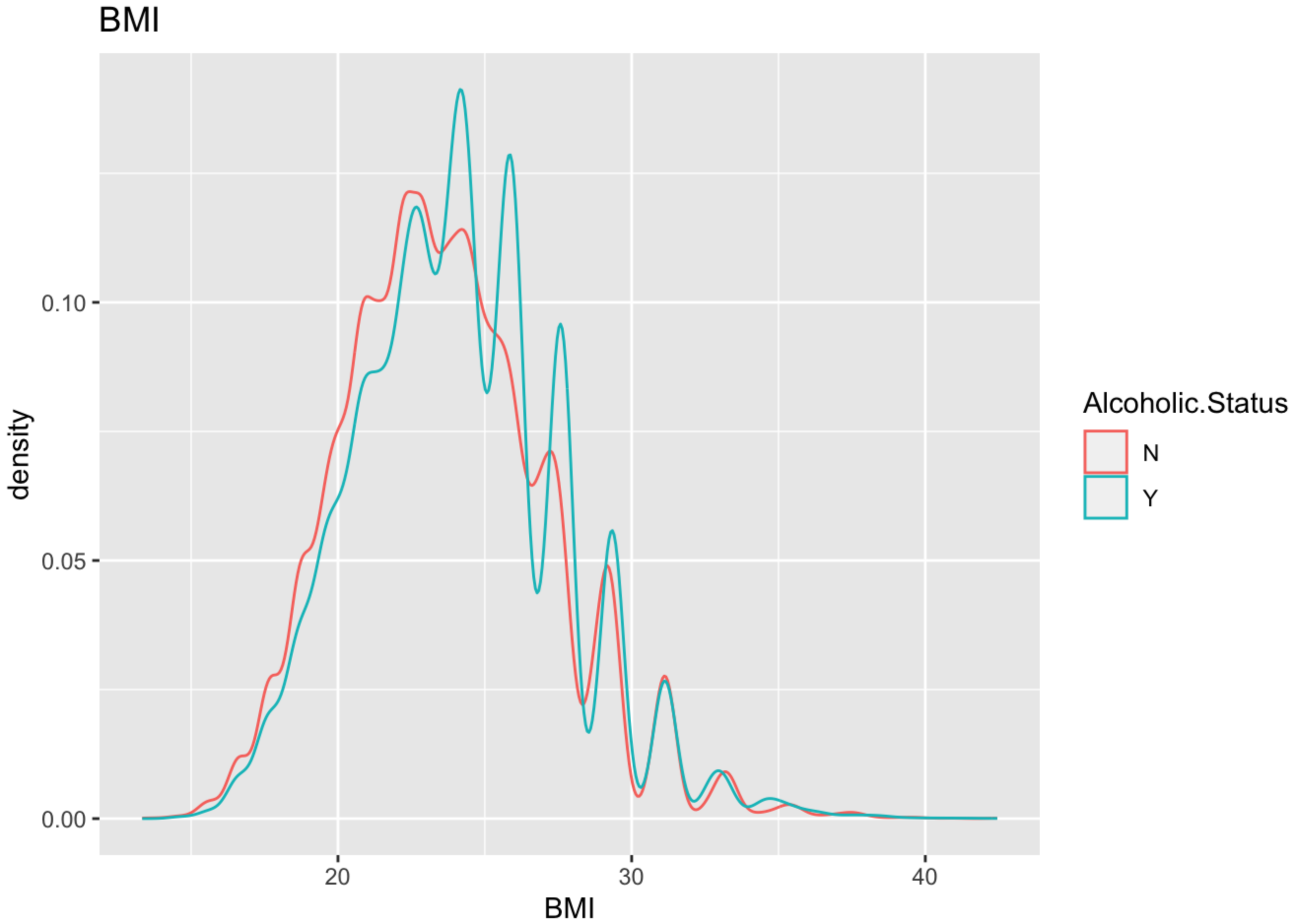
```
## Warning: Removed 4893 rows containing non-finite values (`stat_density()`).
```



```
## Warning: Removed 4961 rows containing non-finite values (`stat_density()`).
```



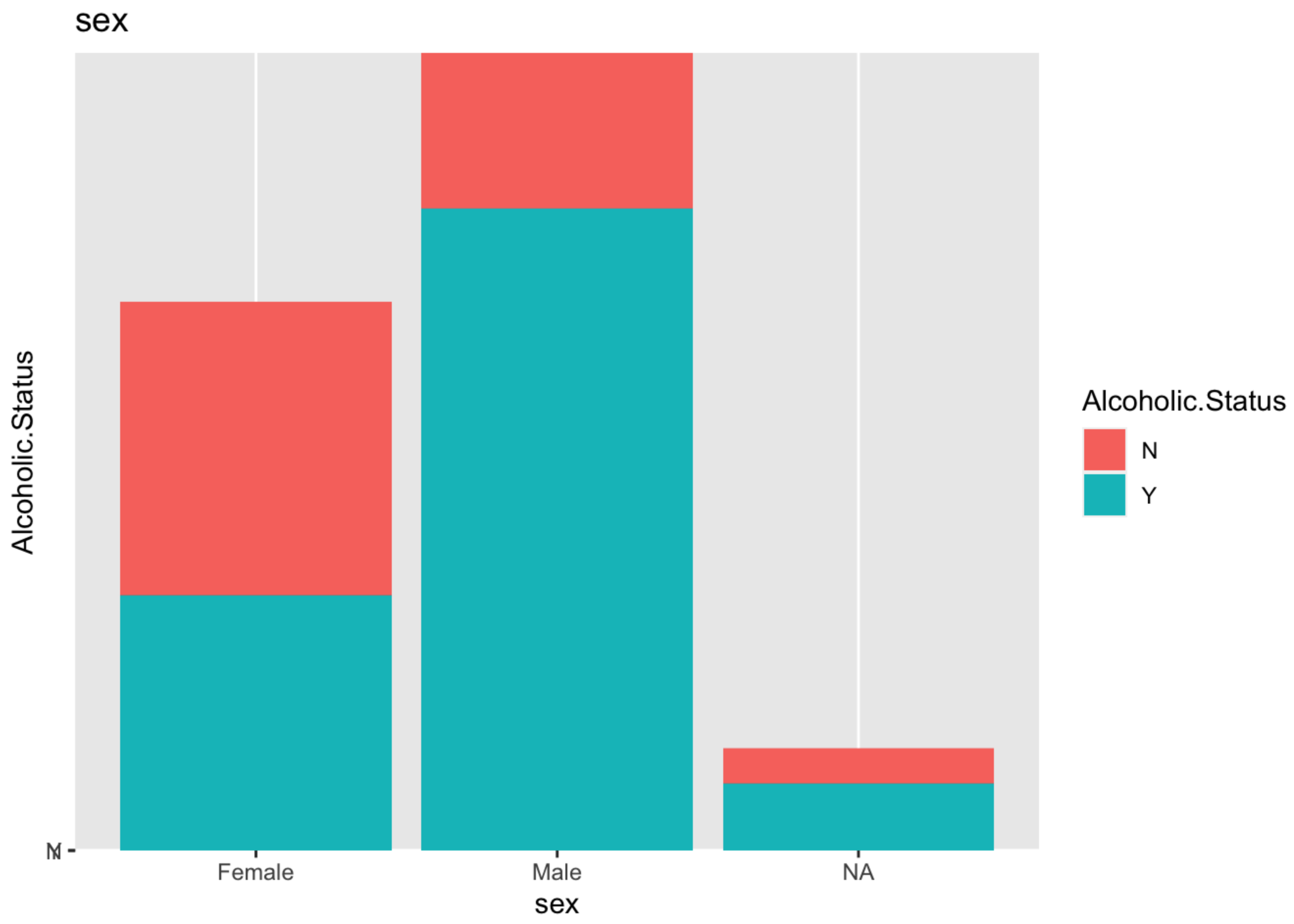
```
## Warning: Removed 4967 rows containing non-finite values (`stat_density()`).
```

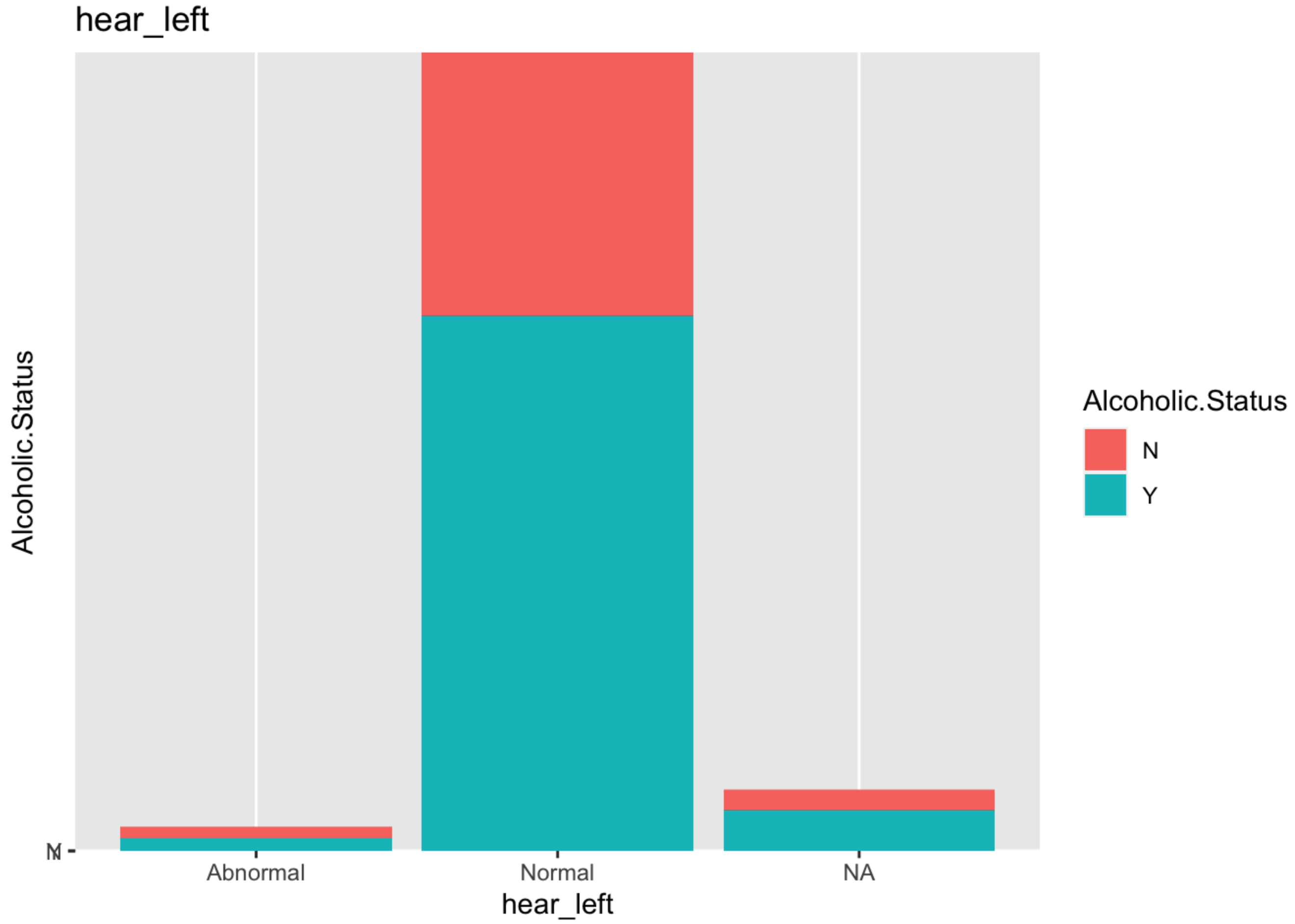


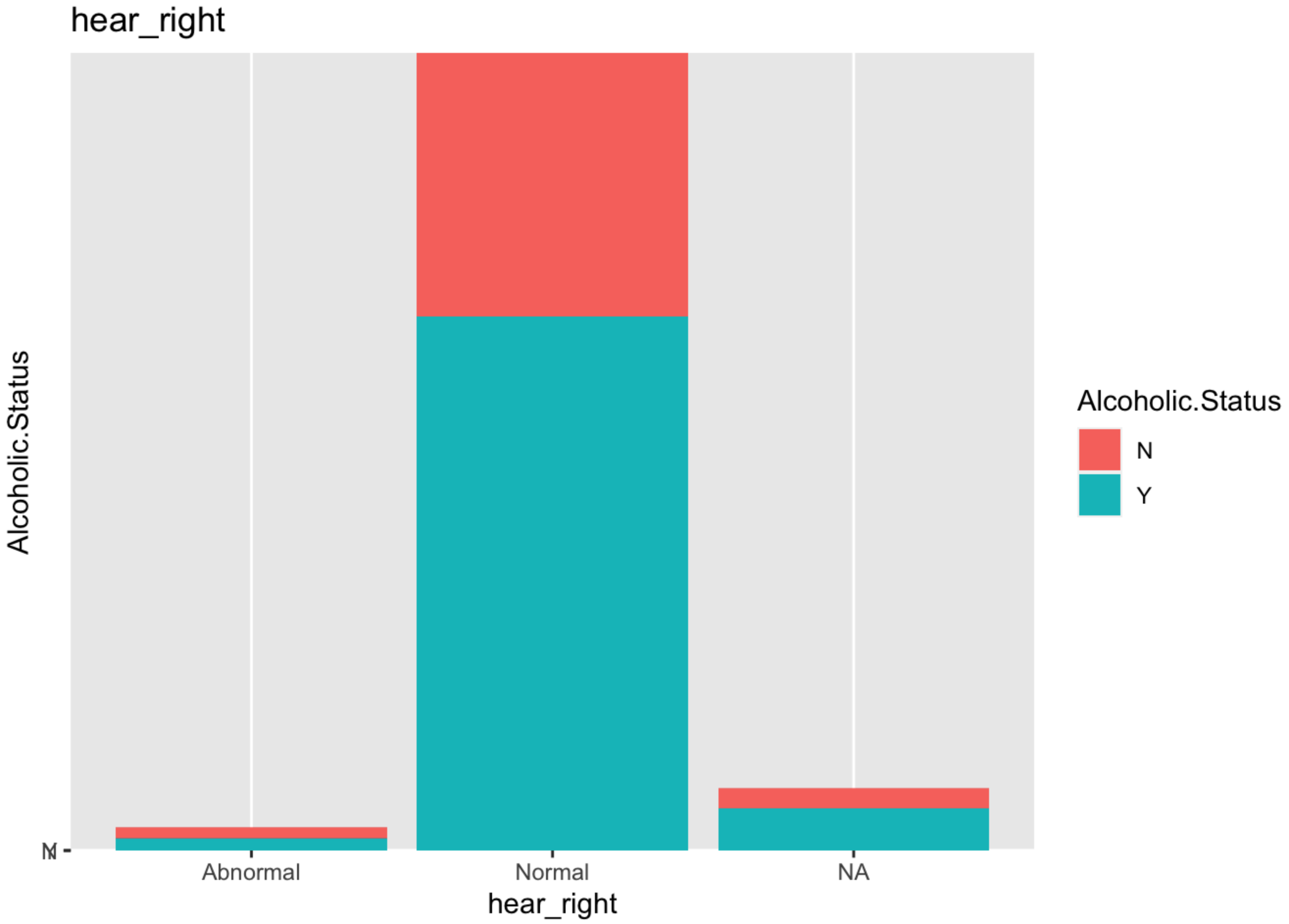
The best four numerical predictors are age, height, hemoglobin and BMI. We can infer this information from their density charts.

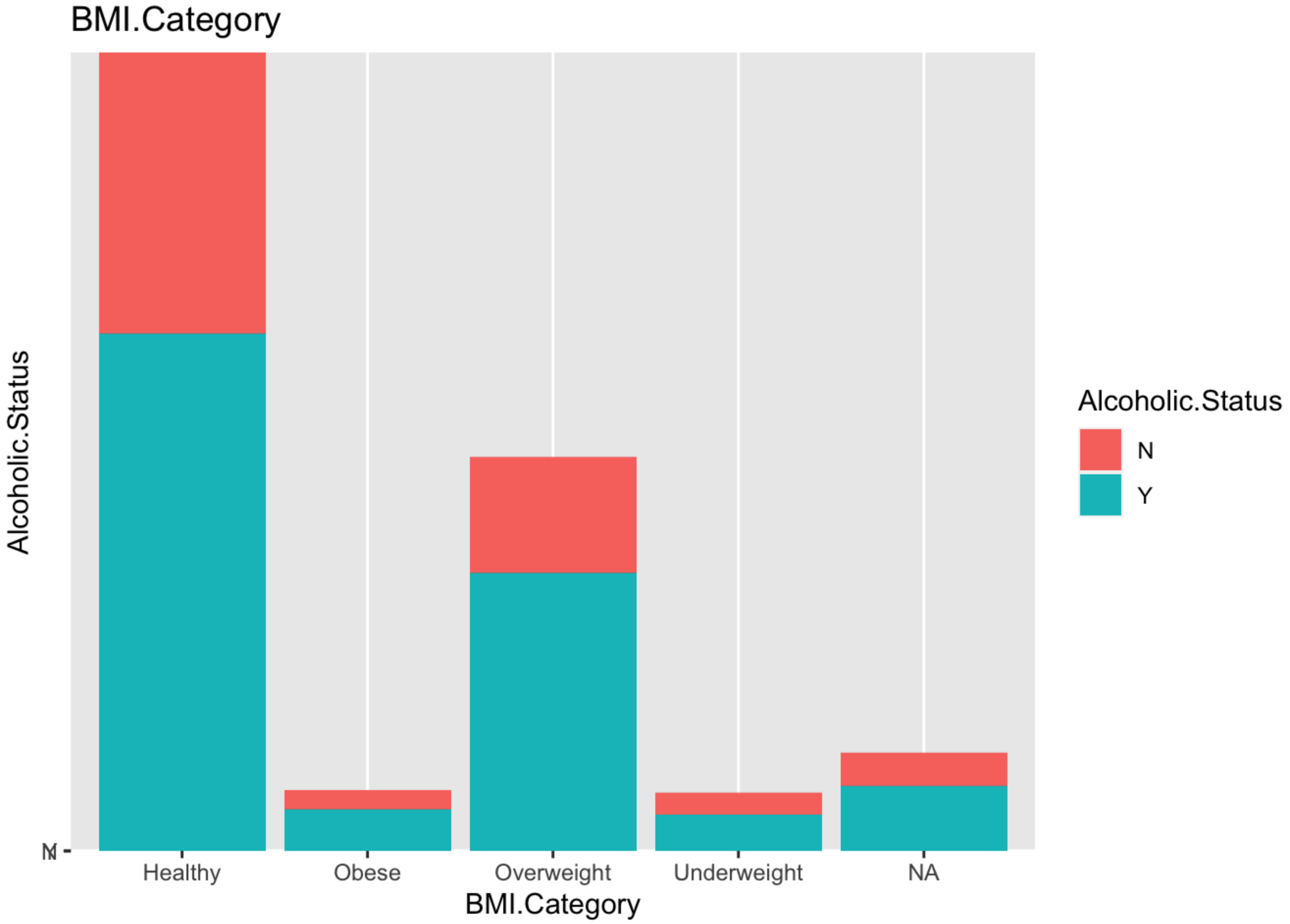
g.

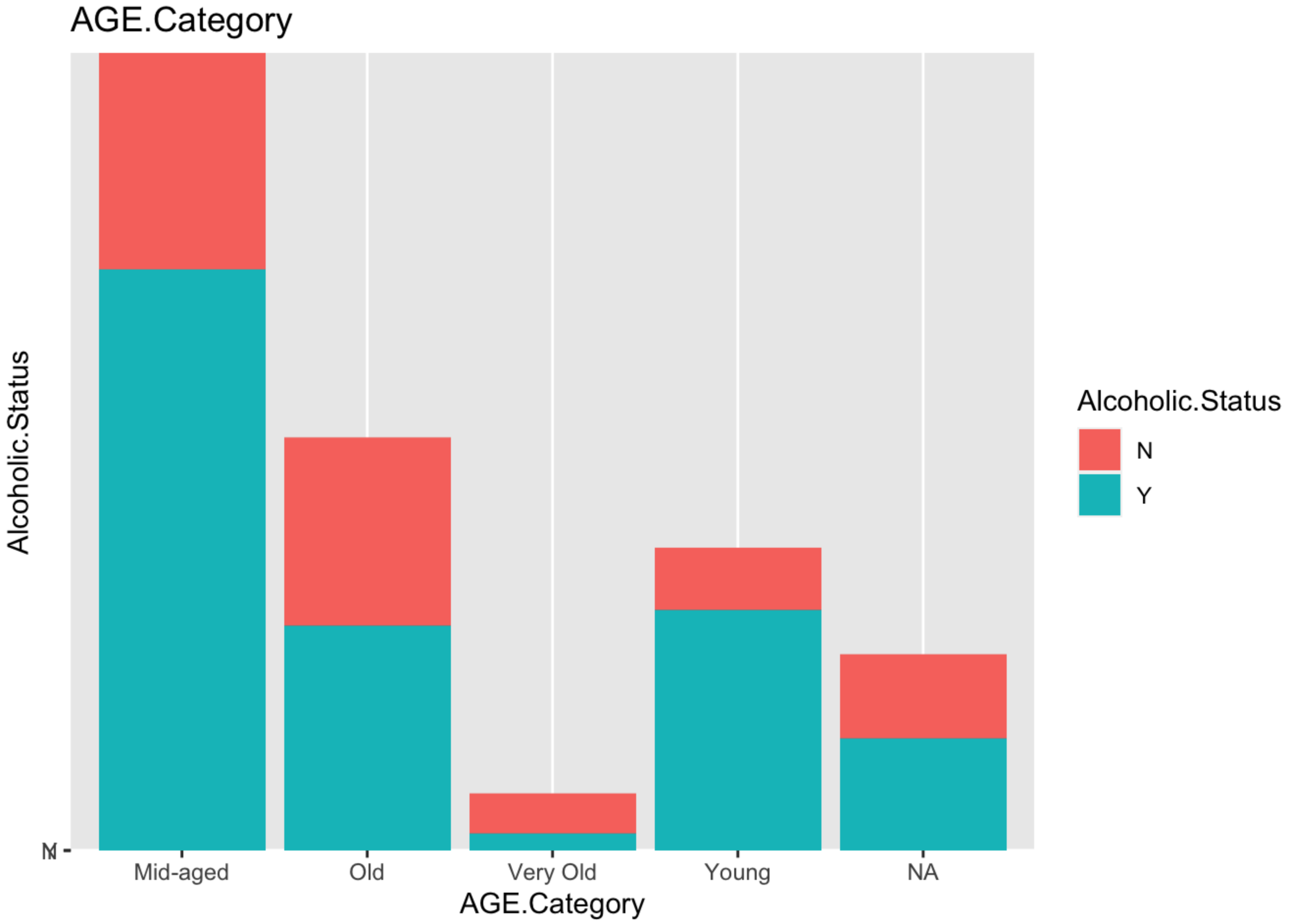
```
cat_names <- names(kagtrain[sapply(kagtrain, is.character)])
for(variable in cat_names){
  plot <- ggplot(kagtrain, aes_string(fill = "Alcoholic.Status", y = "Alcoholic.Status", 
x = variable)) + geom_bar(position = "stack", stat = "identity") + ggtitle(variable)
  print(plot)
}
```

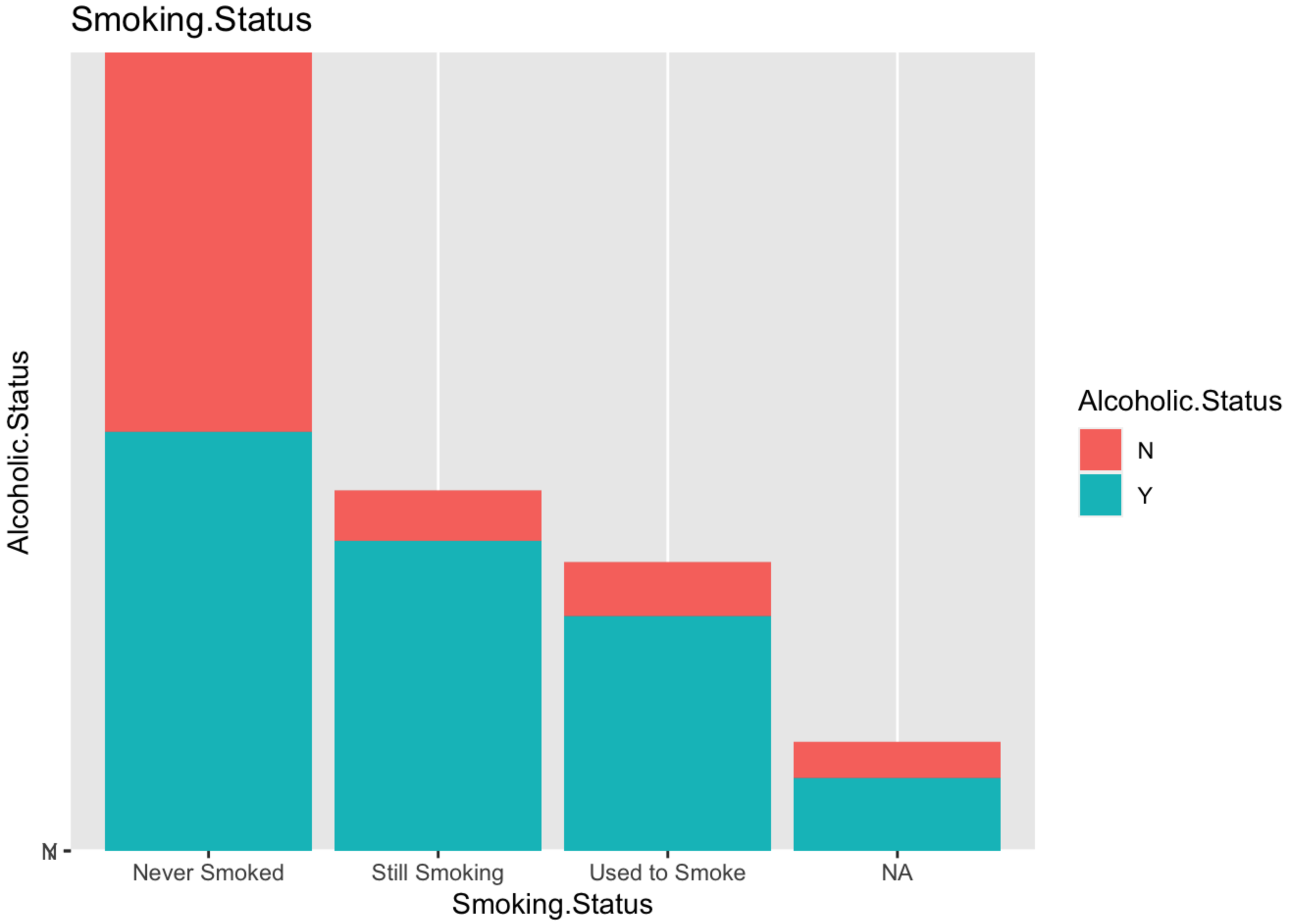

sex
Alcoholic.Status
N
Y
Female
Male
NA
sex
Alcoholic.Status
N
Y

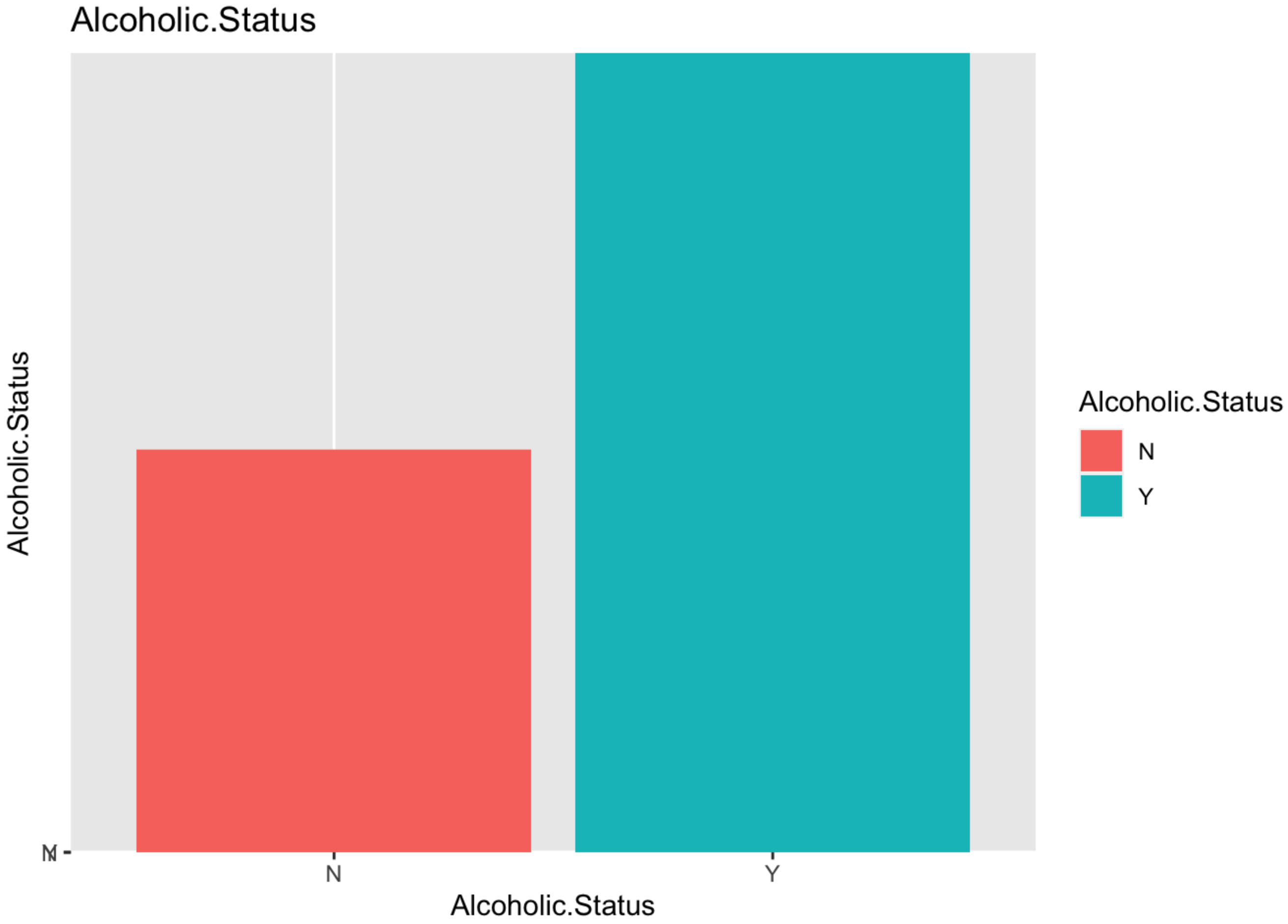

hear_left
Alcoholic.Status
N
Y
Abnormal
Normal
NA
hear_left
Alcoholic.Status
N
Y


hear_right
Alcoholic.Status
N
Y
Abnormal
Normal
NA
hear_right
Alcoholic.Status
🟥 N
🟦 Y


BMI.Category
Alcoholic.Status
N
Y
Healthy
Obese
Overweight
Underweight
NA
BMI.Category
Alcoholic.Status
🟥 N
🟦 Y


AGE.Category
Alcoholic.Status
N
Y
Mid-aged
Old
Very Old
Young
NA
AGE.Category
Alcoholic.Status
🟥 N
🟦 Y


Smoking.Status
Alcoholic.Status
N
Y
Never Smoked
Still Smoking
Used to Smoke
NA
Smoking.Status
Alcoholic.Status
🟥 N
🟦 Y



Our best two categorical predictor variables are Smoking.Status and AGE.Category.

Question 2

a.

```
head(kagtrain %>% mutate(across(where(is.numeric), ~replace_na(., median(., na.rm = TRUE)))))
```

```
##   ID    sex age height weight waistline sight_left sight_right hear_left
## 1  1   Male  75    160     60      81.0        1.0         0.7    Normal
## 2  2 Female  50    160     60      74.0        1.0         1.2    Normal
## 3  3   Male  65    170     80      95.0        1.0         1.5    Normal
## 4  4   <NA>  65    155     55      81.0        0.3         0.4  Abnormal
## 5  5   Male  35    160     60      85.0        1.0         1.0    Normal
## 6  6 Female  50    160     70      73.2        0.3         0.4    Normal
##   hear_right SBP DBP BLDS tot_chole HDL_chole LDL_chole triglyceride hemoglobin
## 1     Normal 120  76  136       215        33       143          193       15.0
## 2     Normal 118  70  125       207        85       111          110       13.3
## 3     Normal 149  83  130       115        48        33          170       16.4
## 4   Abnormal 118  67   97       171        65        67          195       13.9
## 5     Normal  96  62   78       114        42        58           72       16.0
## 6     Normal 119  79  220       178        61        80          181       10.5
##   urine_protein serum_creatinine SGOT_AST SGOT_ALT gamma_GTP      BMI
## 1             3              0.9       28       23        36 23.43750
## 2             1              0.6       28       19        22 23.43750
## 3             1              1.4       41       64        53 23.87511
## 4             1              0.8       26       25        23 22.89282
## 5             1              1.0       17       24        34 23.87511
## 6             1              0.5       36       20        20 27.34375
##   BMI.Category AGE.Category Smoking.Status Alcoholic.Status
## 1      Healthy     Very Old  Still Smoking                Y
## 2         <NA>     Mid-aged   Never Smoked                Y
## 3   Overweight          Old  Still Smoking                Y
## 4         <NA>          Old   Never Smoked                N
## 5      Healthy     Mid-aged  Still Smoking                N
## 6   Overweight     Mid-aged   Never Smoked                N
```

```
kagtrain$sex <- as.factor(kagtrain$sex)
kagtrain$hear_left <- as.factor(kagtrain$hear_left)
kagtrain$hear_right <- as.factor(kagtrain$hear_right)
kagtrain$BMI.Category <- as.factor(kagtrain$BMI.Category)
kagtrain$AGE.Category <- as.factor(kagtrain$AGE.Category)
kagtrain$Smoking.Status <- as.factor(kagtrain$Smoking.Status)
kagtrain$Alcoholic.Status <- as.factor(kagtrain$Alcoholic.Status)
cleankagtrain <- kagtrain[complete.cases(kagtrain), ]
cleankagtrain$Alcoholic.Status <- as.factor(cleankagtrain$Alcoholic.Status)
```

```
glmkag <- glm(Alcoholic.Status ~ . - ID - Alcoholic.Status, data = cleankagtrain, family
= binomial())
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
summary(glmkag)
```

```
## 
## Call:
## glm(formula = Alcoholic.Status ~ . - ID - Alcoholic.Status, family = binomial(), 
##     data = cleankagtrain)
## 
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)    
## (Intercept)                 -3.9771959  3.2391986  -1.228  0.21951    
## sexMale                      1.0663028  0.0945390  11.279  < 2e-16 ***
## age                         -0.0379901  0.0052914  -7.180 6.99e-13 ***
## height                       0.0108923  0.0197531   0.551  0.58135    
## weight                       0.0073973  0.0245745   0.301  0.76340    
## waistline                   -0.0005591  0.0020247  -0.276  0.78242    
## sight_left                   0.0134764  0.0485802   0.277  0.78147    
## sight_right                 -0.0247307  0.0453646  -0.545  0.58565    
## hear_leftNormal             -0.0928936  0.1769397  -0.525  0.59958    
## hear_rightNormal             0.0594782  0.1846674   0.322  0.74739    
## SBP                          0.0025443  0.0026671   0.954  0.34011    
## DBP                          0.0118107  0.0037365   3.161  0.00157 ** 
## BLDS                         0.0001888  0.0010225   0.185  0.85354    
## tot_chole                    0.0004400  0.0043060   0.102  0.91861    
## HDL_chole                    0.0230691  0.0044950   5.132 2.86e-07 ***
## LDL_chole                   -0.0019803  0.0043409  -0.456  0.64825    
## triglyceride                 0.0008135  0.0007352   1.107  0.26849    
## hemoglobin                  -0.0044983  0.0211150  -0.213  0.83130    
## urine_protein               -0.0437604  0.0548591  -0.798  0.42505    
## serum_creatinine            -0.3112565  0.1164993  -2.672  0.00755 ** 
## SGOT_AST                     0.0196459  0.0034722   5.658 1.53e-08 ***
## SGOT_ALT                    -0.0249463  0.0023168 -10.768  < 2e-16 ***
## gamma_GTP                    0.0134537  0.0010989  12.243  < 2e-16 ***
## BMI                          0.0154784  0.0660724   0.234  0.81478    
## BMI.CategoryObese           -0.5100170  0.1930533  -2.642  0.00825 ** 
## BMI.CategoryOverweight      -0.0727624  0.0886899  -0.820  0.41198    
## BMI.CategoryUnderweight     -0.0980623  0.1306307  -0.751  0.45284    
## AGE.CategoryOld             -0.1812045  0.0966219  -1.875  0.06074 .  
## AGE.CategoryVery Old        -0.4333644  0.2273759  -1.906  0.05666 .  
## AGE.CategoryYoung            0.0412159  0.1071919   0.385  0.70060    
## Smoking.StatusStill Smoking  0.8290526  0.0711244  11.656  < 2e-16 ***
## Smoking.StatusUsed to Smoke  0.8717824  0.0725326  12.019  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for binomial family taken to be 1)
## 
##     Null deviance: 13906  on 10032  degrees of freedom
## Residual deviance: 10852  on 10001  degrees of freedom
## AIC: 10916
## 
## Number of Fisher Scoring iterations: 5
```

b.

```
kagprob <- predict(glmkag, data = cleankagtrain, type = "response")
kagpredlog <- rep("Y", length(kagprob))
kagpredlog[kagprob <= 0.5] <- "N"
table(kagpredlog, cleankagtrain$Alcoholic.Status)
```

```
##
## kagpredlog    N    Y
##          N 3577 1371
##          Y 1364 3721
```

```
mean(kagpredlog != cleankagtrain$Alcoholic.Status)
```

```
## [1] 0.2726004
```

The misclassification rate is 27.26%.

c.

```
kptest <- predict(glmkag, data = cleankagtrain, newdata = kagtest, type = "response")
kgtestpl <- rep("Y", length(kptest))
kgtestpl[kptest <= 0.5] <- "N"
my_kaggle <- data.frame(ID = 1:nrow(kagtest), predictions = kgtestpl)
write.csv(my_kaggle, file = "kagglepredictions.csv", row.names = FALSE)
```

My kaggle public score is 0.52996.

d. My kaggle rank is 64th.

Question 3

```
winetrain <- read.csv("WineTrain copy.csv")
winetest <- read.csv("WineTest copy.csv")
winetrain$Class <- as.factor(winetrain$Class)
winetrain$Wine.Color <- as.factor(winetrain$Wine.Color)
winetest$Class <- as.factor(winetest$Class)
winetest$Wine.Color <- as.factor(winetest$Wine.Color)
winedat <- rbind(winetrain, winetest)
head(winedat)
```

```
##   X Wine.Color fixed.acidity volatile.acidity citric.acid residual.sugar
## 1 1          W           7.3             0.23        0.41           14.6
## 2 2          R          10.0             0.32        0.59            2.2
## 3 3          W           6.2             0.27        0.43            7.8
## 4 4          W           6.6             0.25        0.32            5.6
## 5 5          W           6.9             0.24        0.39            1.3
## 6 6          W           7.1             0.23        0.39            1.6
##   chlorides free.sulfur.dioxide total.sulfur.dioxide density   pH sulphates
## 1     0.048                  73                  223 0.99863 3.16      0.71
## 2     0.077                   3                   15 0.99940 3.20      0.78
## 3     0.056                  48                  244 0.99560 3.10      0.51
## 4     0.039                  15                   68 0.99163 2.96      0.52
## 5     0.063                  18                  136 0.99280 3.31      0.48
## 6     0.032                  12                   65 0.98980 3.25      0.40
##   alcohol Class
## 1     9.4   Bad
## 2     9.6   Bad
## 3     9.0   Bad
## 4    11.1  Good
## 5    10.4  Good
## 6    12.7  Good
```

```
dim(winedat)
```

```
## [1] 4000   14
```

```
library(crossval)
```

```
## 
## Attaching package: 'crossval'
```

```
## The following object is masked from 'package:caret':
## 
##     confusionMatrix
```

```
library(boot)
```

```
## 
## Attaching package: 'boot'
```

```
## The following object is masked from 'package:lattice':
## 
##     melanoma
```

a.

```
# logistic regression
wineglm <- glm(Class ~ . - X - Class, data = winedat, family = binomial())
wineprob <- predict(wineglm, data = winedat, type = "response")
winepredl <- rep("Good", length(wineprob))
winepredl[wineprob <= 0.5] <- "Bad"
table(winepredl, winedat$Class)
```

```
##
## winepredl  Bad Good
##      Bad  1374  755
##      Good  676 1195
```

```
mean(winepredl != winedat$Class)
```

```
## [1] 0.35775
```

We can see our confusion matrix in our output above. Our misclassification rate for this model is 35.775%.

b.

```
# lda model
winelda <- lda(Class ~ . - X - Class, data = winedat, CV = TRUE)
summary(winelda)
```

```
##           Length Class  Mode
## class     4000   factor numeric
## posterior 8000   -none- numeric
## terms        3   terms  call
## call         4   -none- call
## xlevels      1   -none- list
```

```
table(winelda$class, winedat$Class)
```

```
##
##         Bad Good
##   Bad  1374  771
##   Good  676 1179
```

```
mean(winelda$class != winedat$Class)
```

```
## [1] 0.36175
```

Our misclassification rate is 36.175%.

c.

```
# qda model
wineqda <- qda(Class ~ . - X - Class, data = winedat, CV = TRUE)
summary(wineqda)
```

```
##           Length Class  Mode   
## class     4000   factor numeric
## posterior 8000   -none- numeric
## terms        3   terms  call   
## call         4   -none- call   
## xlevels      1   -none- list   
```

```
table(wineqda$class, winedat$Class)
```

```
##       
##         Bad Good
##   Bad  1058  499
##   Good  992 1451
```

```
mean(wineqda$class != winedat$Class)
```

```
## [1] 0.37275
```

Our misclassification rate for our qda model of the wine data is 37.275%.

d.

```
# knn model with k = 25
wine_knn1 <- train(as.factor(Class) ~ . - X, data = winedat, method = "knn", trControl =
trainControl(method = "LOOCV", number = 10), tuneGrid = data.frame(k = 25))
```

e. Our model with the lowest misclassification rate is our glm model for our data. The highest misclassification rate is from our qda model.

Question 4

a.

```
# logistic regression with 10 fold method
wineglm10f <- cv.glm(winedat, wineglm, K = 10)
summary(wineglm10f)
```

```
##       Length Class  Mode   
## call    4    -none- call   
## K       1    -none- numeric
## delta   2    -none- numeric
## seed  626    -none- numeric
```

```
cv.err.10 <- wineglm10f$delta
cv.err.10
```

```
## [1] 0.2267839 0.2267017
```

The MSE for the glm of the wine data is 0.2266443 and the second error of 0.2265667 is for the LOOCV.

b.

```
wine_lda <- train(as.factor(Class) ~ . - X, data = winedat, method = "lda", trControl =
trainControl(method = "cv", number = 10))
caret::confusionMatrix(wine_lda)
```

```
## Cross-Validated (10 fold) Confusion Matrix
##
## (entries are percentual average cell counts across resamples)
##
##           Reference
## Prediction  Bad Good
##       Bad  34.5 19.1
##       Good 16.8 29.6
##
##  Accuracy (average) : 0.6408
```

The misclassification rate is 1 - 0.6413 = 0.3587.

c.

```
wine_qda <- train(as.factor(Class) ~ . - X, data = winedat, method = "qda", trControl =
trainControl(method = "cv", number = 10))
caret::confusionMatrix(wine_qda)
```

```
## Cross-Validated (10 fold) Confusion Matrix
##
## (entries are percentual average cell counts across resamples)
##
##           Reference
## Prediction  Bad Good
##       Bad  26.4 12.6
##       Good 24.9 36.2
##
##  Accuracy (average) : 0.6255
```

The misclassification rate is 1 - 0.623 = 0.377.

d.

```
wine_knn <- train(as.factor(Class) ~ . - X, data = winedat, method = "knn", trControl =
trainControl(method = "cv", number = 10), tuneGrid = data.frame(k = 25))
caret::confusionMatrix(wine_knn)
```

```
## Cross-Validated (10 fold) Confusion Matrix
##
## (entries are percentual average cell counts across resamples)
##
##           Reference
## Prediction  Bad Good
##       Bad  32.2 22.2
##       Good 19.0 26.6
##
##  Accuracy (average) : 0.5875
```

The misclassification rate is 1 - 0.5882 = 0.4118.

e. The cv glm model has the lowest misclassification rate amongst all of the cv models. Our highest misclassification rate is from our knn model.