Viper Mortality

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```
# Packages you definitely need
library(ggplot2)
library(dplyr)
library(ranger) # for looking up help on Conceptual Problem
library(MASS) # see Applied Problem 2
library(parsnip)
library(rsample)
# Please load any other packages you need either all in this chunk
# or in the chunk you need it for
library(keras)
library(tensorflow)
library(ISLR2)
library(esquisse)



# Data you need for applied problems
SoCalRent <- readr::read_csv("SoCalRent.csv")
viper_train <- readr::read_csv("viper_train.csv")
viper_test <- readr::read_csv("viper_test.csv")
```

Snakebite Mortality

Gopalakrishnan and colleagues (2022) attempted to build a model to predict mortality from snakebite based on predictors that could be measured within 48 hours of admission to a hospital or clinic.

The `viper_train` dataset on Canvas contains information about 239 patients from southern India who were diagnosed with having been poisoned by a viper bite. These patients were used to fit their model. The `viper_test` dataset on Canvas contains the same information about a separate set of 140 patients, who were used to validate the model. Please see the `viper_dictionary` file on Canvas for an explanation of each of the variables.

- Changing the `Outcome` variable appropriately, or creating a new response based on `Outcome`, to reflect that this is a classification problem

```
viper_test$Outcome <- factor(viper_test$Outcome)
viper_train$Outcome <- factor(viper_train$Outcome)


#viper_test$Sex <- factor(viper_test$Sex)
#viper_train$Sex <- factor(viper_train$Sex)
#viper_test$Outcome<-ifelse(viper_test$Outcome=="0",0,1)
```

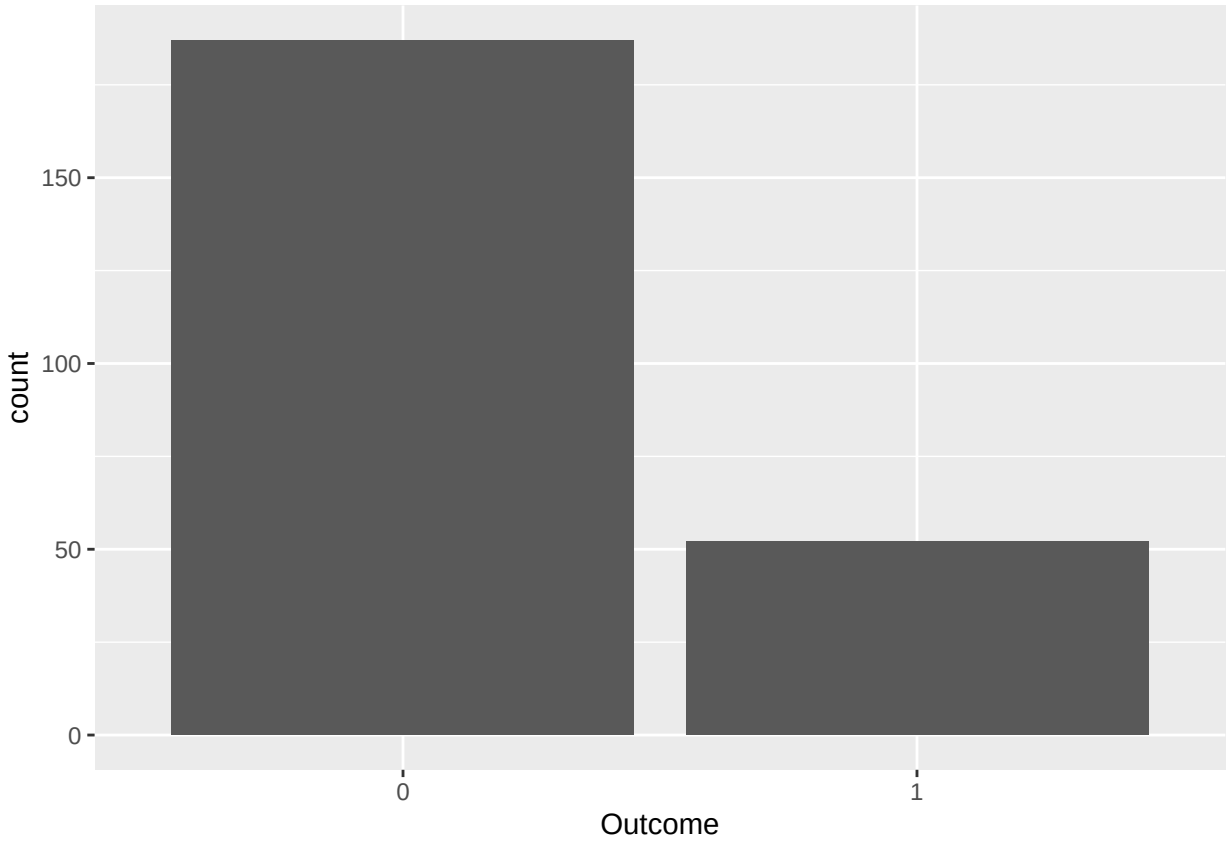
```
#viper_train$Outcome<-ifelse(viper_train$Outcome=="0",0,1)

viper_test$Sex<-ifelse(viper_test$Sex=="M",1,0)
viper_train$Sex<-ifelse(viper_train$Sex=="M",1,0)
```

- Performing exploratory data analysis on the training set and documenting your findings

```
#eda on response of interest: outcome
viper_train %>% group_by(Outcome)%>%count()
```

```
## # A tibble: 2 x 2
## # Groups:   Outcome [2]
##   Outcome     n
##   <fct>   <int>
## 1 0         187
## 2 1          52
```

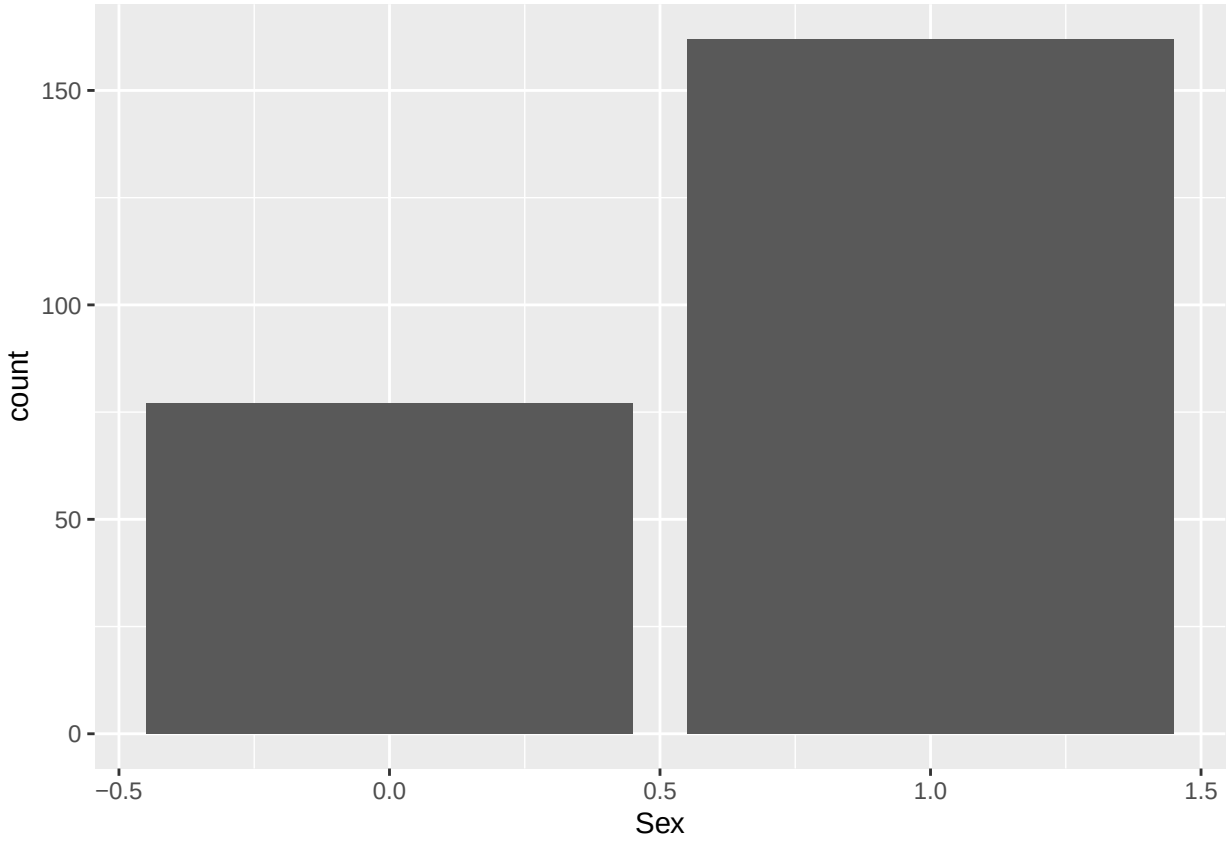
```
#we have 187 people who lived a snake bite and 52 who died in this training set
ggplot(viper_train, aes(x=Outcome)) + geom_bar()
```



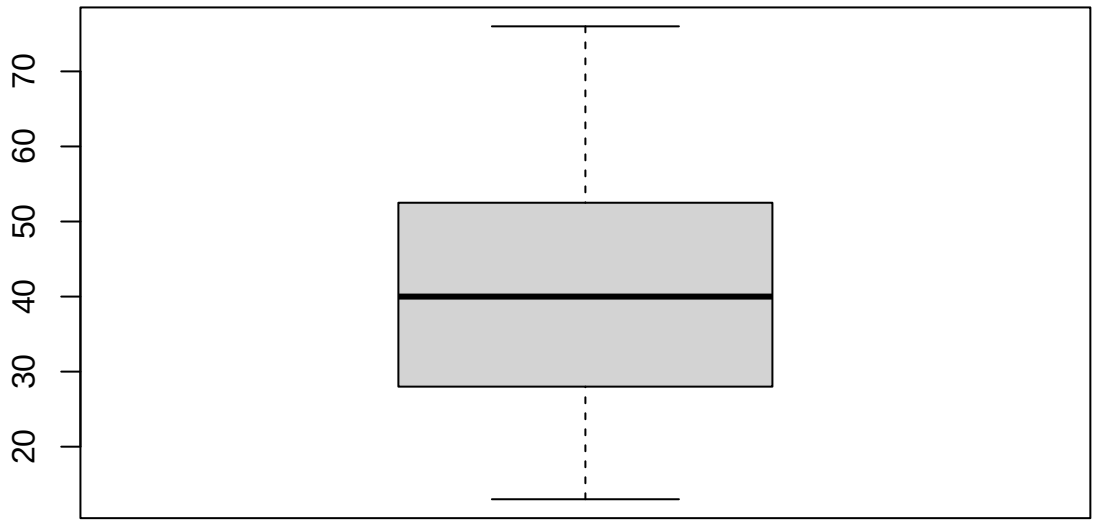

```
#eda on predictors
#77 females and 162 males in the training set
viper_train %>% group_by(Sex)%>%count()
```

```
## # A tibble: 2 x 2
## # Groups:   Sex [2]
##     Sex     n
##   <dbl> <int>
## 1     0    77
## 2     1   162
```

```
ggplot(viper_train, aes(x=Sex)) + geom_bar()
```




```
#age
age_boxplot <- boxplot(viper_train$Age)
```

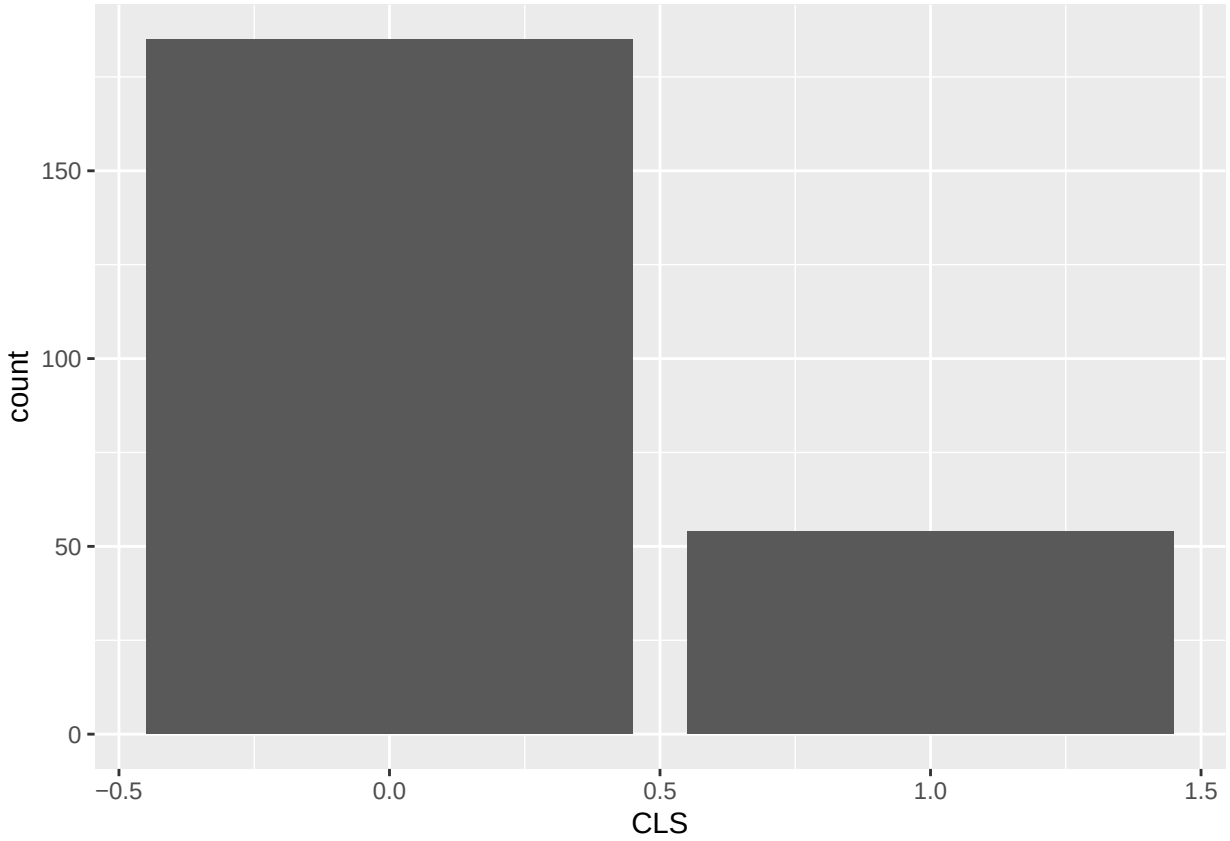



```
age_hist <- hist(viper_train$Age, xlab = 'patient age')
```


```
#CLS capillary leak syndrome
# no(0) = 185, yes(1) = 54
viper_train %>% group_by(CLS)%>%count()
```

```
## # A tibble: 2 x 2
## # Groups:   CLS [2]
##     CLS     n
##   <dbl> <int>
## 1     0   185
## 2     1    54
```

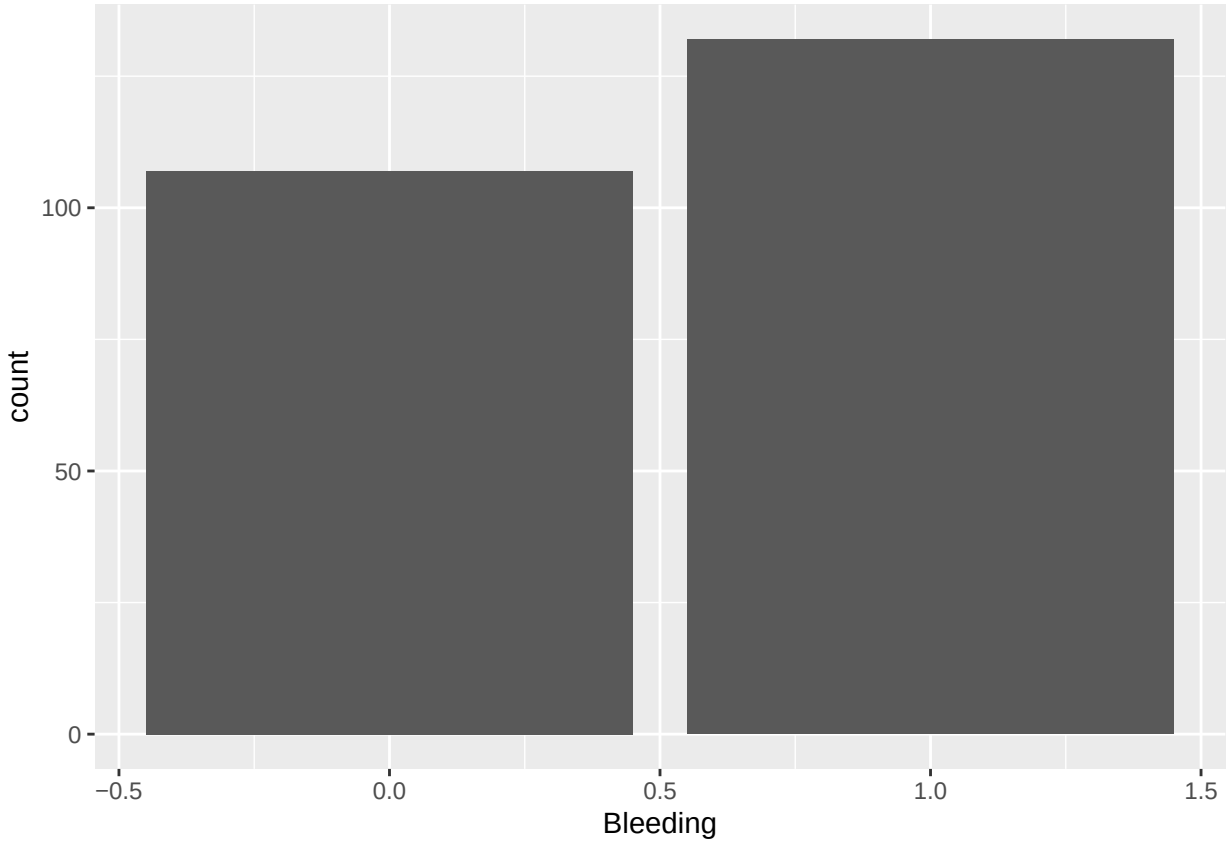
```
ggplot(viper_train, aes(x=CLS)) + geom_bar()
```



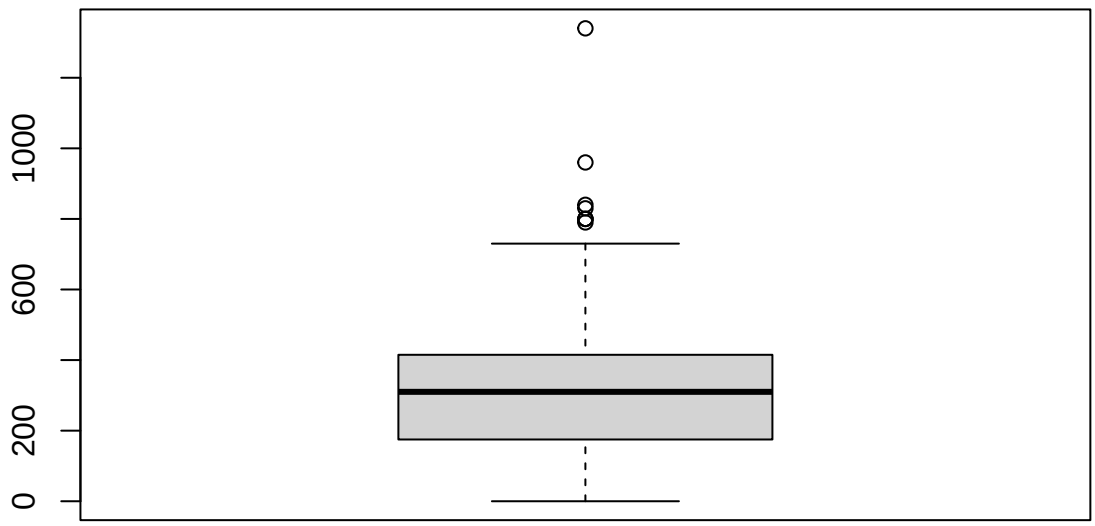

```
#Bleeding
# no bleeding = 107, yes bleeding = 132
viper_train %>% group_by(Bleeding)%>%count()
```

```
## # A tibble: 2 x 2
## # Groups:   Bleeding [2]
##   Bleeding     n
##      <dbl> <int>
## 1        0   107
## 2        1   132
```

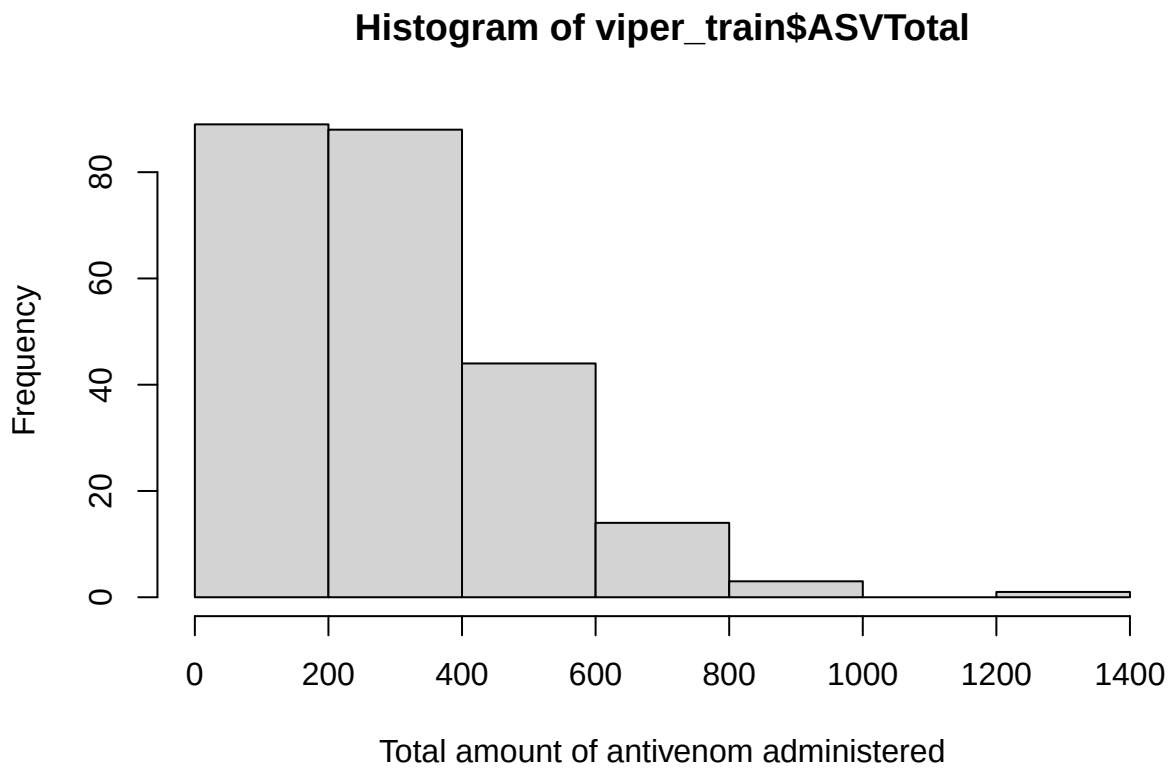
```
ggplot(viper_train, aes(x=Bleeding)) + geom_bar()
```



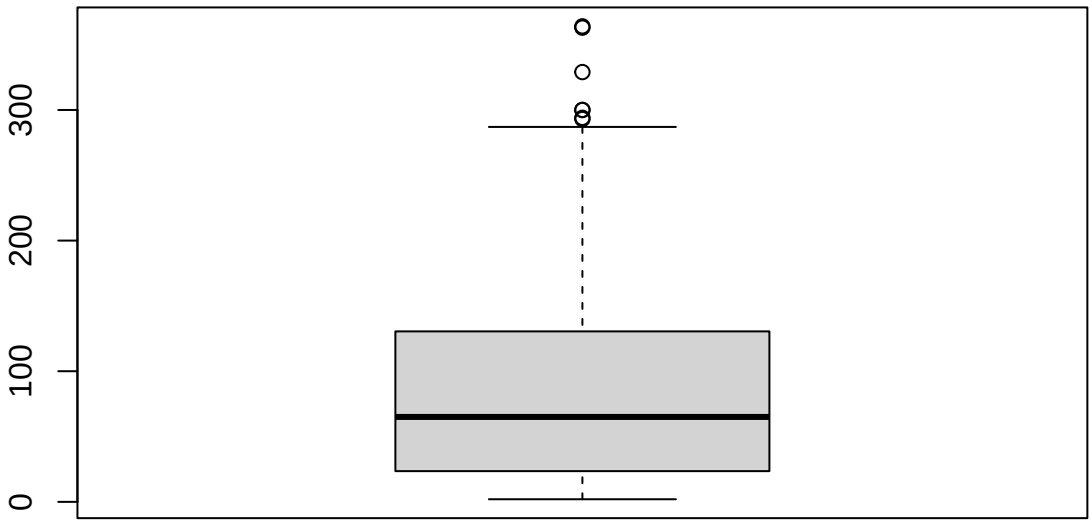

```
#ASVTotal
asv_boxplot <- boxplot(viper_train$ASVTotal)
```



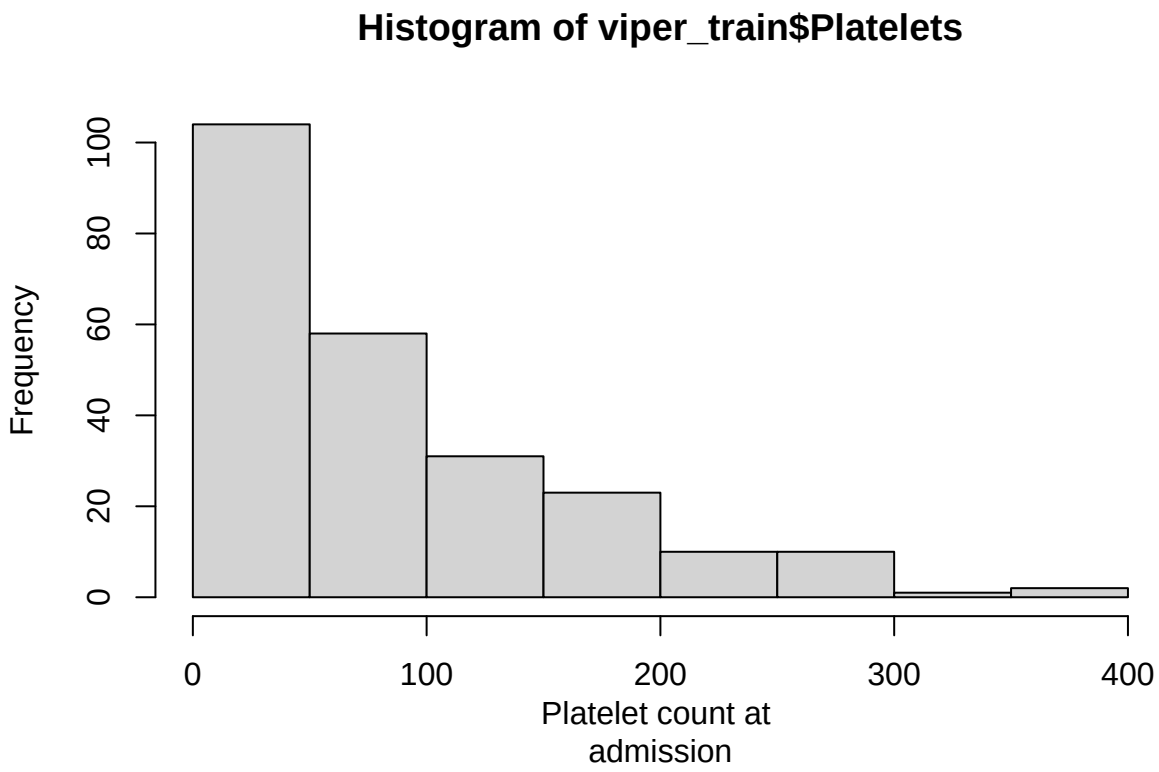

```
asv_hist <- hist(viper_train$ASVTotal, xlab = 'Total amount of antivenom administered')
```



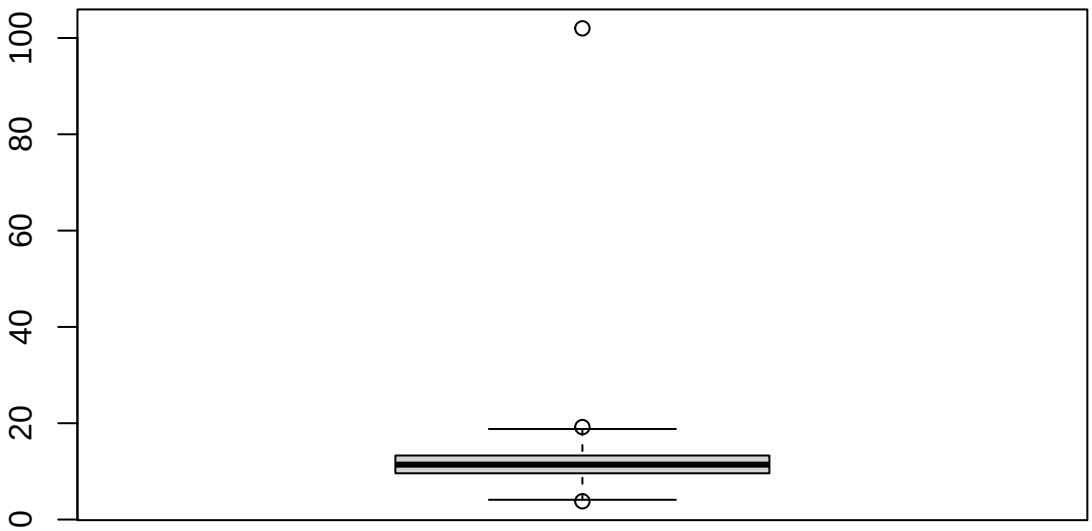

```
#platelets
plate_boxplot <- boxplot(viper_train$Platelets)
```



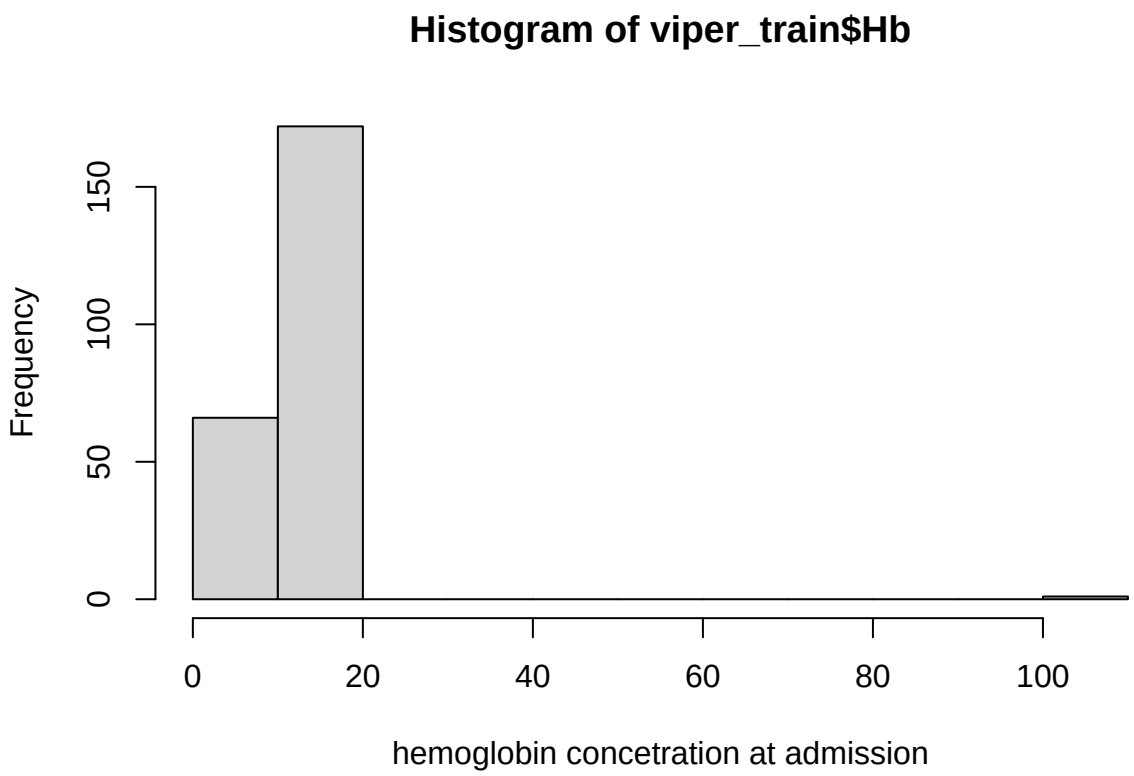

```
plate_hist <- hist(viper_train$Platelets, xlab = 'Platelet count at
admission')
```



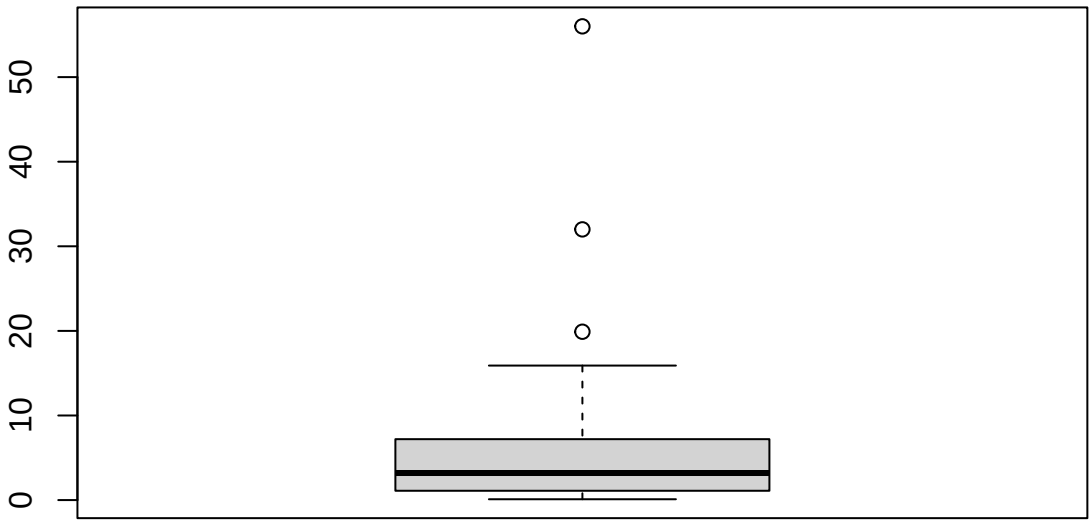

```
#Hb

hb_boxplot <- boxplot(viper_train$Hb)
```



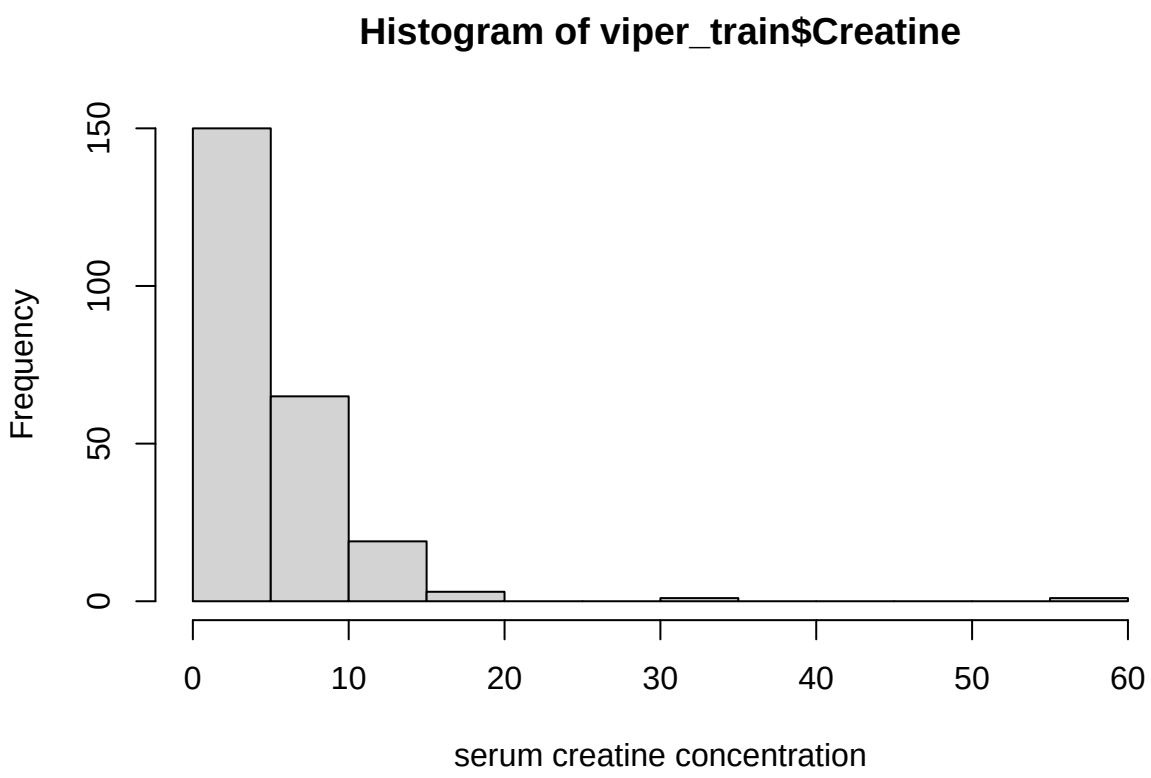

```
hb_hist <- hist(viper_train$Hb, xlab = 'hemoglobin concetration at admission')
```



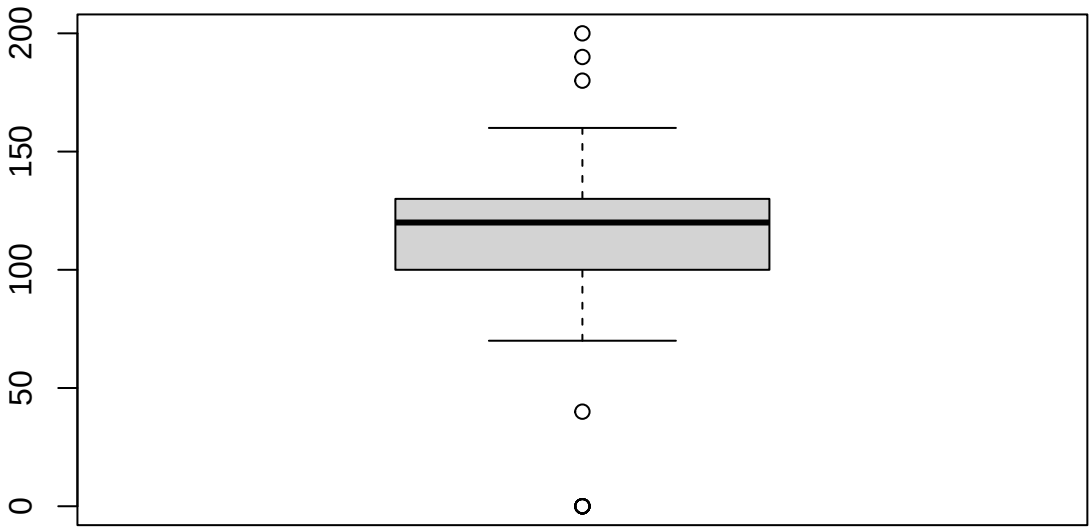

```
#creatine
creatine_boxplot <- boxplot(viper_train$Creatine)
```



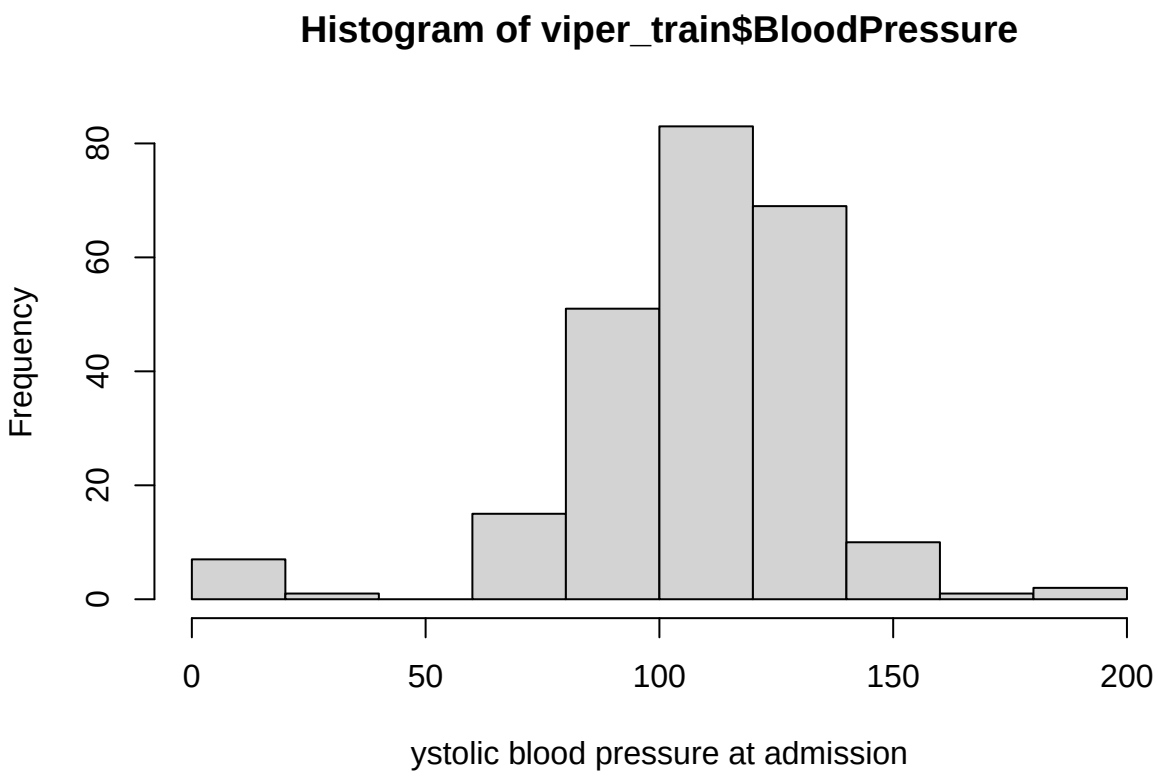

```
creatine_hist <- hist(viper_train$Creatine, xlab = 'serum creatine concentration')
```




```
#blood pressure
#is it possible to have 200bp?
#can dead people have more than 0 bp?
bp_boxplot <- boxplot(viper_train$BloodPressure)
```




```
bp_hist <- hist(viper_train$BloodPressure, xlab = 'ystolic blood pressure at admission')
```



- Performing backward stepwise selection using BIC as a selection criterion and obtaining an estimate of the test error rate on the selected logistic regression model (HINT: `regsubsets` will not work for logistic regression, but you can use the `stepAIC` function in the `MASS` package instead to do stepwise selection. The output of `stepAIC` will be a `glm` object, which means you can do prediction without the workarounds)

```
library(MASS)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v tibble  3.1.6     v purrr   0.3.4
## v tidyr   1.1.4     v stringr 1.4.0
## v readr   2.1.2     v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x MASS::select()  masks dplyr::select()
```

```
set.seed(10)


outcome_test <- viper_test$Outcome
```

```r
bglm <- glm(Outcome~.,data=viper_train, family = 'binomial')
backward <- stepAIC(bglm, data=viper_train,method='backward')
```

```
## Start:  AIC=114.95
## Outcome ~ Age + Sex + CLS + Bleeding + ASVTotal + Platelets +
##     Hb + Creatine + BloodPressure
##
##                 Df Deviance    AIC
## - Creatine       1   95.008 113.01
## - Age            1   95.263 113.26
## - Platelets      1   95.530 113.53
## - Sex            1   96.910 114.91
## <none>               94.951 114.95
## - Hb             1   98.794 116.79
## - ASVTotal       1  102.381 120.38
## - BloodPressure  1  117.582 135.58
## - CLS            1  119.912 137.91
## - Bleeding       1  122.572 140.57
##
## Step:  AIC=113.01
## Outcome ~ Age + Sex + CLS + Bleeding + ASVTotal + Platelets +
##     Hb + BloodPressure
##
##                 Df Deviance    AIC
## - Age            1   95.339 111.34
## - Platelets      1   95.904 111.90
## - Sex            1   96.982 112.98
## <none>               95.008 113.01
## - Hb             1   98.933 114.93
## - ASVTotal       1  102.650 118.65
## - BloodPressure  1  118.002 134.00
## - CLS            1  120.162 136.16
## - Bleeding       1  122.963 138.96
##
## Step:  AIC=111.34
## Outcome ~ Sex + CLS + Bleeding + ASVTotal + Platelets + Hb +
##     BloodPressure
##
##                 Df Deviance    AIC
## - Platelets      1   96.233 110.23
## <none>               95.339 111.34
## - Sex            1   97.724 111.72
## - Hb             1   99.717 113.72
## - ASVTotal       1  102.727 116.73
## - BloodPressure  1  118.310 132.31
## - CLS            1  120.870 134.87
## - Bleeding       1  124.021 138.02
##
## Step:  AIC=110.23
## Outcome ~ Sex + CLS + Bleeding + ASVTotal + Hb + BloodPressure
##
##                 Df Deviance    AIC
## <none>               96.233 110.23
```

```
## - Sex            1   98.405 110.41
## - Hb             1  101.192 113.19
## - ASVTotal       1  103.579 115.58
## - BloodPressure  1  121.528 133.53
## - CLS            1  125.266 137.27
## - Bleeding       1  127.859 139.86
```

```
back_pred <- predict(backward, viper_test)



#back_error <- sum((outcome_test/sum(backward$residuals))^2)
```

- Fitting at least two of the following four types of models and obtaining an estimate of the test error rate on each model: k-nearest neighbors, generative models (LDA/QDA/naive Bayes), tree-based methods (bagging/random forests/boosting), neural networks

```
set.seed(10)

#viper_test$Sex<-ifelse(viper_test$Sex=="M",1,0)
#viper_train$Sex<-ifelse(viper_train$Sex=="M",1,0)
#boosted tree



x_scale_test <- data.frame(
outcome = as.numeric(viper_test$Outcome),
sex = as.numeric(viper_test$Sex),
age = scale(viper_test$Age),
cls = scale(viper_test$CLS),
bleeding = scale(viper_test$Bleeding),
asvTotal = scale(viper_test$ASVTotal),
platelets = scale(viper_test$Platelets),
hb = scale(viper_test$Hb),
creatine = scale(viper_test$Creatine),
bp = scale(viper_test$BloodPressure)
) %>% as.matrix()


x_scale_train <- data.frame(
outcome = as.numeric(viper_train$Outcome),
sex = as.numeric(viper_train$Sex),
age = scale(viper_train$Age),
cls = scale(viper_train$CLS),
bleeding = scale(viper_train$Bleeding),
asvTotal = scale(viper_train$ASVTotal),
platelets = scale(viper_train$Platelets),
hb = scale(viper_train$Hb),
creatine = scale(viper_train$Creatine),
bp = scale(viper_train$BloodPressure)
) %>% as.matrix()
```

```r
#viper_test$Sex <- as.numeric(viper_test$Sex)

#1/2 (fast n dirty random forest)
library(ranger)
viper_rf<- ranger(Outcome~., data=viper_train, importance = "permutation", seed=758)
viper_rf
```

```
## Ranger result
##
## Call:
##  ranger(Outcome ~ ., data = viper_train, importance = "permutation",      seed = 758)
##
## Type:                             Classification
## Number of trees:                  500
## Sample size:                      239
## Number of independent variables:  9
## Mtry:                             3
## Target node size:                 1
## Variable importance mode:         permutation
## Splitrule:                        gini
## OOB prediction error:             10.88 %
```

```r
#estimate the test MSE :3333333
#(find the default test)
viper_class <- predict(viper_rf, data=viper_test)$predictions

#predict each tree and then avg the preds
viper_predictions <- predict(viper_rf, data = viper_test, predict.all = TRUE)

rf_probs <- apply(viper_predictions$predictions-1,1,mean)



#neural net
library(keras)


nn_1layer <- keras_model_sequential() %>%
layer_dense(units = 10, activation = "relu",
input_shape = ncol(x_scale_train)) %>%
layer_dropout(rate = 0.4) %>%
layer_dense(units = 1, activation = "sigmoid")
```

```
## Loaded Tensorflow version 2.9.0
```

```r
nn_1layer %>% compile(loss = "binary_crossentropy",
optimizer = optimizer_rmsprop(),
metrics = list("accuracy"))

outcome_train <- as.numeric(viper_train$Outcome)
```

```
nn_fit <- nn_1layer %>% fit(x = x_scale_train,
y = outcome_train)

nn_preds <- predict(nn_1layer,x=x_scale_test)
nn_class <- if_else(nn_preds >= 0.5, '0','1')

library(yardstick)
```

```
## Warning: package 'yardstick' was built under R version 4.1.3
```

```
## For binary classification, the first factor level is assumed to be the event.
## Use the argument `event_level = "second"` to alter this as needed.
```

```
##
## Attaching package: 'yardstick'
```

```
## The following object is masked from 'package:readr':
##
##     spec
```

```
## The following object is masked from 'package:keras':
##
##     get_weights
```

```
prediction_df <- data.frame(
  actual = viper_test$Outcome,
  rf = viper_class,
  nn = factor(nn_class, levels = c('0','1'))
)
```

- Further investigating the prediction accuracy of at least one model (e.g., by creating a confusion matrix or a ROC Curve, computing sensitivity/specificity, etc.)

```
#nnet
#nn
(nn_conf<- conf_mat(prediction_df, truth = actual, estimate = nn))
```

```
##            Truth
## Prediction   0   1
##          0 103  15
##          1  17   5
```

```
(rf_conf<- conf_mat(prediction_df, truth = actual, estimate = rf))
```

```
##            Truth
## Prediction   0   1
##          0 113  14
##          1   7   6
```

- Selecting a best model and justifying your choice; in particular, you should explain why your model is better than a very stupid model that predicts no one will die

My best model is accurate 85% of the time, but at least it is still better than predicting no one will die(?)

```
summary(nn_conf, event_level = "second")
```

```
## # A tibble: 13 x 3
##    .metric              .estimator .estimate
##    <chr>                <chr>          <dbl>
##  1 accuracy             binary         0.771
##  2 kap                  binary         0.104
##  3 sens                 binary         0.25
##  4 spec                 binary         0.858
##  5 ppv                  binary         0.227
##  6 npv                  binary         0.873
##  7 mcc                  binary         0.104
##  8 j_index              binary         0.108
##  9 bal_accuracy         binary         0.554
## 10 detection_prevalence binary         0.157
## 11 precision            binary         0.227
## 12 recall               binary         0.25
## 13 f_meas               binary         0.238
```

```
table(prediction_df$actual,prediction_df$nn)
```

```
##
##       0   1
##   0 103  17
##   1  15   5
```

```
summary(rf_conf,event_level = 'second')
```

```
## # A tibble: 13 x 3
##    .metric              .estimator .estimate
##    <chr>                <chr>          <dbl>
##  1 accuracy             binary        0.85
##  2 kap                  binary        0.283
##  3 sens                 binary        0.3
##  4 spec                 binary        0.942
##  5 ppv                  binary        0.462
##  6 npv                  binary        0.890
##  7 mcc                  binary        0.291
##  8 j_index              binary        0.242
##  9 bal_accuracy         binary        0.621
## 10 detection_prevalence binary        0.0929
## 11 precision            binary        0.462
## 12 recall               binary        0.3
## 13 f_meas               binary        0.364
```