EDA of the heartdisease dataset

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1.1 Dataset information

Kaggle direct link to dataset: https://www.kaggle.com/fedesoriano/heart-failure-prediction

1.1.1 Research question

Is it possible to create an accurate(F/P. <= 20% & F/N <= 10%) machine learning model that predicts the chance of developing heartdisease in a broad spectrum of patients?

Due to the potential damage false negatives (F/N) will cause, it is important to reduce the F/N. Altough there is a balance between F/N and false positive (F/P) A high F/P will cause unnesscary testing and will increase costs, while a high F/N will be potential dangerous as it misses true positive (T/P) patients.

1.2 Dataparsing

```
heartdata <- read.table("data/heart.csv", sep=",", header=TRUE)
heartdata$HeartDisease <- as.logical(heartdata$HeartDisease)
heartdata$FastingBS <- as.logical(heartdata$FastingBS)
```

```
flags = data.frame(Reduce(cbind,
     lapply(levels(heartdata$ChestPainType), function(x){(heartdata$ChestPainType == x)*1})
))
colnames(flags) <- c("ASY", "ATA", "NAP", "TA")
heartdata$ASY = as.logical(flags$ASY)
heartdata$ATA = as.logical(flags$ATA)
heartdata$NAP = as.logical(flags$NAP)
heartdata$TA = as.logical(flags$TA)

flags = data.frame(Reduce(cbind,
     lapply(levels(heartdata$ST_Slope), function(x){(heartdata$ST_Slope == x)*1})
))
colnames(flags) <- c("Flat", "Down", "Up")
heartdata$ST_Slope_Flat = as.logical(flags$Flat)
heartdata$ST_Slope_Down = as.logical(flags$Down)
heartdata$ST_Slope_Up = as.logical(flags$Up)


# Changes Y/N to Boolean
heartdata$ExerciseAngina = heartdata$ExerciseAngina == "Y"
heartdata$FastingBS = as.logical(heartdata$FastingBS)
```

```
s <- sapply(heartdata, typeof)
sr <- data.frame("attribute" = colnames(heartdata),
                 "type" = sapply(heartdata, typeof),
                 "class" = sapply(heartdata, class),
                 row.names = NULL)
codebook <- as_tibble(sr)
kable(codebook, caption = "Codebook") %>%
  kable_styling(latex_options = c("hold_position"))
```

Table 1: (#tab:get data types)Codebook

attribute	type	class
Age	integer	integer
Sex	integer	factor
ChestPainType	integer	factor
RestingBP	integer	integer
Cholesterol	integer	integer
FastingBS	logical	logical
RestingECG	integer	factor
MaxHR	integer	integer
ExerciseAngina	logical	logical
Oldpeak	double	numeric
ST_Slope	integer	factor
HeartDisease	logical	logical
ASY	logical	logical
ATA	logical	logical
NAP	logical	logical
TA	logical	logical
ST_Slope_Flat	logical	logical
ST_Slope_Down	logical	logical
ST_Slope_Up	logical	logical

1.3 Summary

```
summ <- summary(heartdata[c("Age", "RestingBP", "Cholesterol", "MaxHR", "Oldpeak")])
tab <- sub('.*:', '', summ)
rownames(tab) <- c("Min", "1st. Qu", "Median", "Mean", "3rd. Qu", "Max")
kable(tab, caption = "5 num of numerical valies") %>%
  kable_styling(latex_options="scale_down")
```

Table 2: 5 num of numerical valies

	Age	RestingBP	Cholesterol	MaxHR	Oldpeak
Min	28.00	0.0	0.0	60.0	-2.6000
1st. Qu	47.00	120.0	173.2	120.0	0.0000
Median	54.00	130.0	223.0	138.0	0.6000
Mean	53.51	132.4	198.8	136.8	0.8874
3rd. Qu	60.00	140.0	267.0	156.0	1.5000
Max	77.00	200.0	603.0	202.0	6.2000

1.4 Visualisations

1.4.1 Datapoints per sex

```
# counts (or sums of weights)
ggplot(heartdata) +
  geom_bar(aes(Sex, fill=HeartDisease)) +
  labs(title = "Datapoints per sex")  +
  ylab("Datapoints")
```

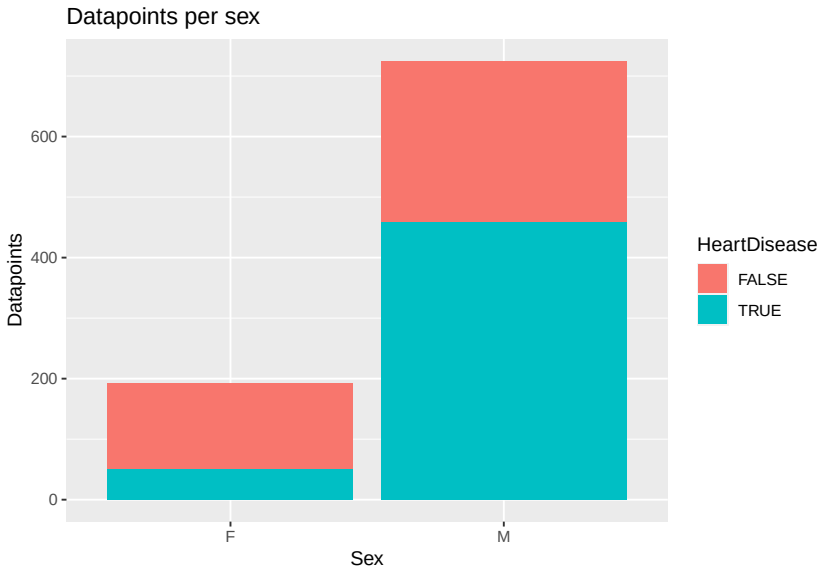


Figure 1: Ratio male to female

(#fig:Ratio male to female)

```
p <- prop.table(table(heartdata$Sex))
```

As visible in the barplot, the ratio of female(21.02%) to male(78.98%) is very skewed towards males. Females have a much lower proportion of positive heartdiseases, whereas males are more likely to have heartdisease in this dataset.

1.4.2 Histogram

```
ggplot(heartdata, aes(Age, fill=HeartDisease)) +
  geom_histogram(bins=12) +
  geom_vline(aes(xintercept=mean(Age[HeartDisease==F]), colour="Mean age without HD"),  size=1, linetyp
  geom_vline(aes(xintercept=mean(Age[HeartDisease==T]), colour="Mean age with HD"),  size=1, linetype="
  scale_color_manual(name="Means", values =c("dodgerblue1", "red")) +
    guides(col = guide_legend(override.aes = list(shape = 15, size=5))) +
  ggtitle("Histogram of age while also visualising HD")
```

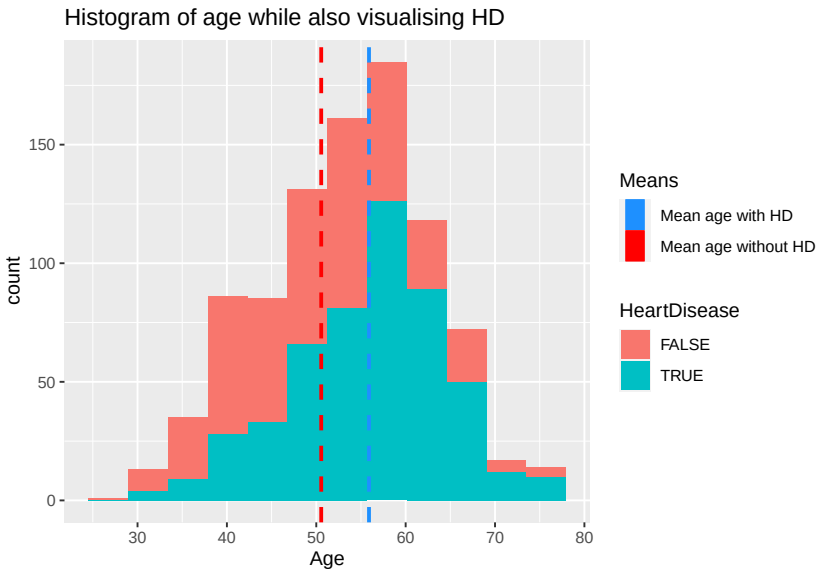


Figure 2: Histogram of age grouped by HD diagnoses

As seen in the above graph, we can discover that there seems to be a relation between age increase and an increase in heartdisease. We will explore this further in the underlying graph. When watching the age mean lines it is further seen that the average age of patients with HD is higher then the average patient without HD.

1.4.3 Heartdisease linked to age

```
ggplot(heartdata) +
  geom_smooth(aes(Age, HeartDisease * 100), method="loess", formula = "y ~ x", color=hue_pal()(1), fill
  ylab("Heart Disease (%)") +
  ggtitle("Percentage of patients affected by HD by age") +
  ylim(c(0, 100))
```

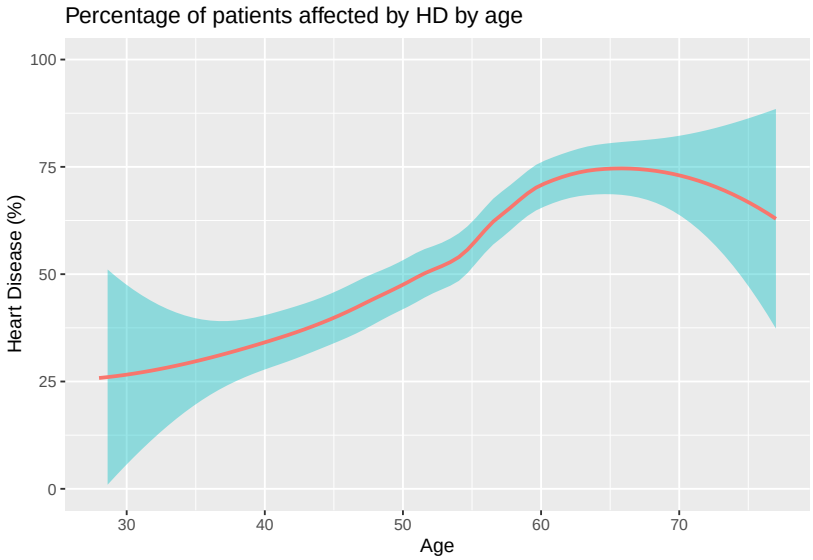


Figure 3: Percentage of patients affected by HD by age

Using a Smooth line we can see that the percentage of patients with HD increases with age and declines after 65. The reason for decline might be that patients who have HD above the age of 65 will die earlier then healthy individuals. A short internet search will also confirm that HD is the leading cause of death for people above the age of 65. Underlying image provides further insight. Source: ec.europa.eu

```
# Define variable containing url
url <- "https://ec.europa.eu/eurostat/statistics-explained/images/2/25/Major_causes_of_death%2C_EU-27%2
```

1.5 Plotting pain types with different variables

1.5.1 Pain types table

The graphs below use abreviasions. The meaning of these can be found in this table:

Pain type:

Code	Type	Explanation
TA	Typical Angina	Meets all three of the following characteristics: 1. Substernal chest discomfort of characteristic quality and duration 2. Provoked by extortion or emotional stress 3. Relieved by rest and/or nitrates within minutes.
ATA	Atypical Angina	Meets two of the above characteristics
NAP	Non-Anginal Pain	Lacks or meets only one or none of the characteristics
ASY	Asymptomatic Pain	

1.5.2 Chestpain and their outcome

```
ggplot(heartdata) +
  geom_bar(aes(ChestPainType, fill=HeartDisease)) + ggtitle("Chestpaintype outcome")
```

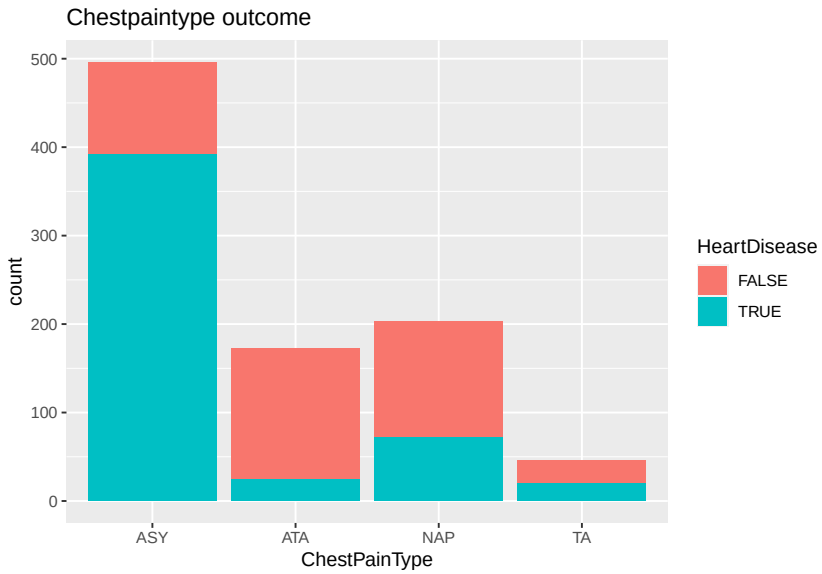


Figure 4: Ratio of diagnosis grouped by chestpain type

As visible in the above barplot, asymptomic pain (ASY) is the most frequently reported and has the highest propabilty of HD.

1.5.3 Resting blood pressure split by pain type

```
p <- ggplot(heartdata, aes(x=RestingBP, group=ChestPainType, colour=ChestPainType)) +
  geom_density() +
  xlab("Resting BP (mm Hg)") +
  ggtitle("Density plot of RestingBP split by ChestPainType")
p
```

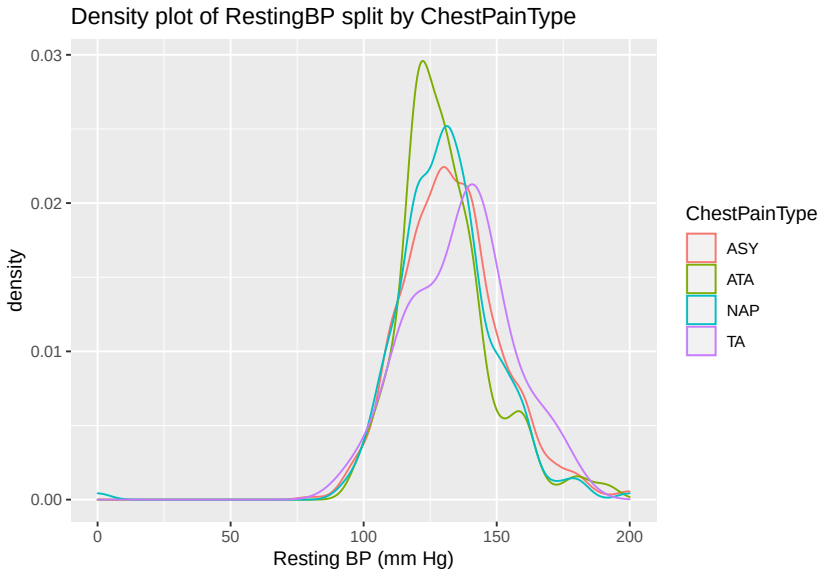


Figure 5: Density plot of Resting BP by pain type

The type of pain an individual experiences doesn't seem to change the blood pressure of the individual.

1.5.4 The effect of chestpain on cholesterol or vice versa

```
p <- ggplot(heartdata, aes(x=Cholesterol, group=ChestPainType, colour=ChestPainType)) +
  geom_density() +
  xlab("Cholesterol in serum (mm/dl)") +
  ggtitle("Density plot of cholesterol in serum split by ChestPainType")
p
```

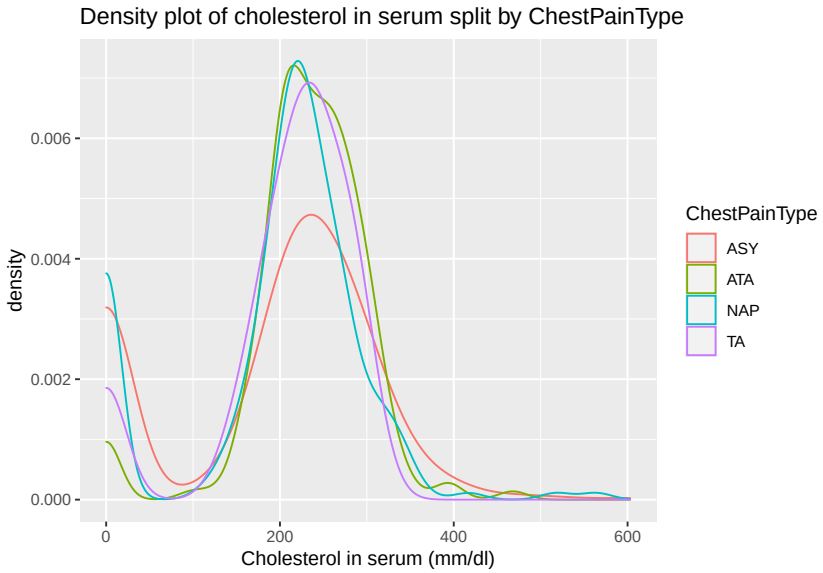


Figure 6: Density plot of cholesterol by pain type

As visible in the above plot. The type of chestpain doesn't seem to differ based on the concentration of cholesterol in blood.

1.5.5 Is the max heart rate affected by certain chestpain?

```
p <- ggplot(heartdata, aes(x=MaxHR, group=ChestPainType, colour=ChestPainType)) +
  geom_density() +
  xlab("Max heartrate") +
  ggtitle("Density plot of MaxHR split by ChestPainType")
p
```

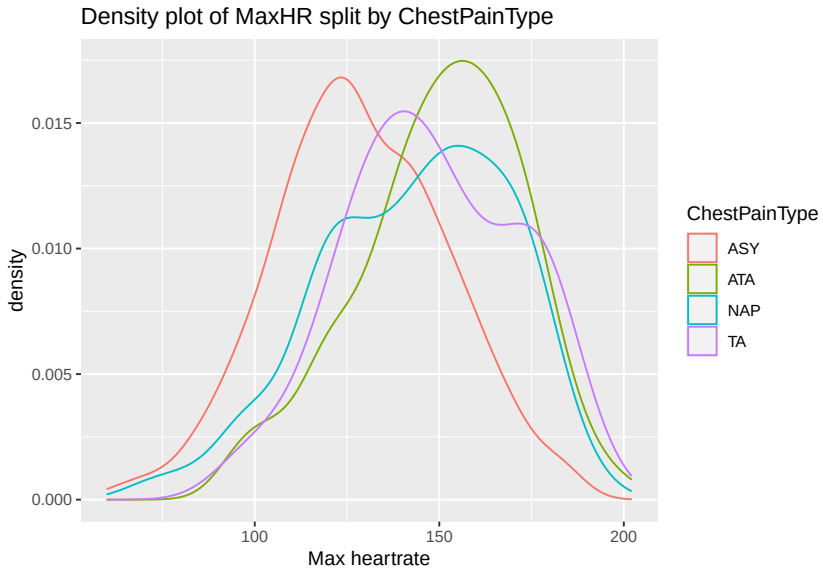


Figure 7: Density plot of maxHR by pain type

There seems to be a small gap in max heartrate with patients ASY (Asymptomatic) vs ATA (Atypical Angina).

Age vs MaxHR grouped by Sex

```
ggplot(heartdata, aes(Age, MaxHR, group=Sex, colour = Sex)) +
  geom_point(alpha=0.15) + geom_smooth(se=F) + ggtitle("Comparing MaxHR with age split by sex")
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

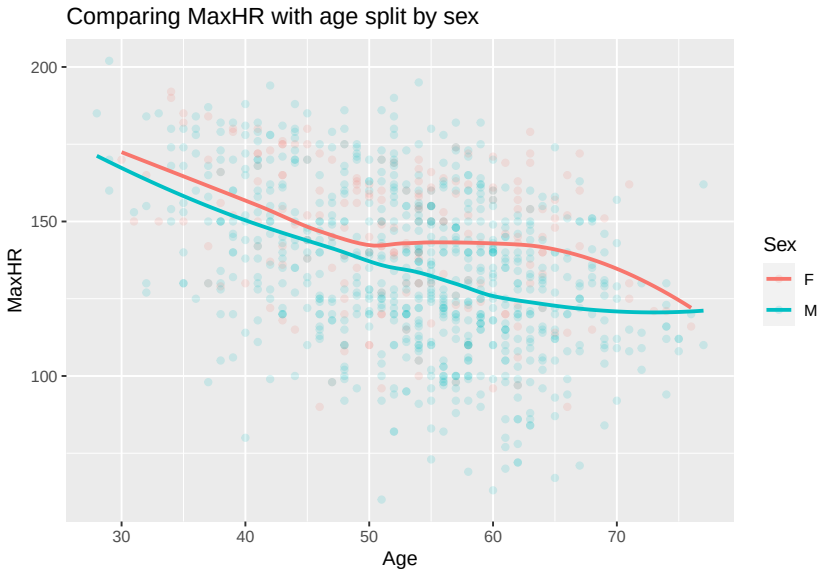


Figure 8: Max heartrate by sex and age

(#fig:Age-Sex vs MaxHR)

As expected MaxHR goes down with age. The female lines doesnt go down as expected, this might be due to the fact there is a smaller amount of data for older females(Age $> 55 = 71$) in comparison with males (Age $> 55 = 335$). To further analyse the difference in datapoints per sex, a density plot is made.

1.5.6 Density of ages split by sex

```
ggplot(heartdata) +
  geom_density(aes(Age, colour=Sex, fill=Sex), alpha=0.05) +
  ggtitle("Density plot comparing sexes")
```

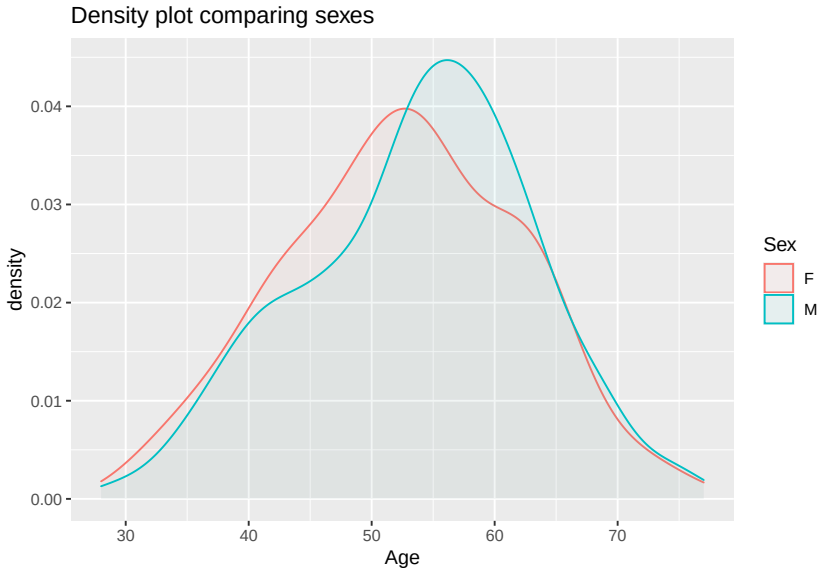


Figure 9: Amount of datapoints per age grouped by sex

The above graph shows that there is not much difference in age comparing male and female.

1.5.7 Finding correlation between MaxHR and HD

```
ggplot(heartdata[heartdata$Cholesterol > 0,], aes(x=Age, y=Cholesterol, colour=HeartDisease, shape=Ches
  geom_point() +
  ggtitle("Age vs Cholesterol") +
  geom_abline(color = "dodgerblue1")
```

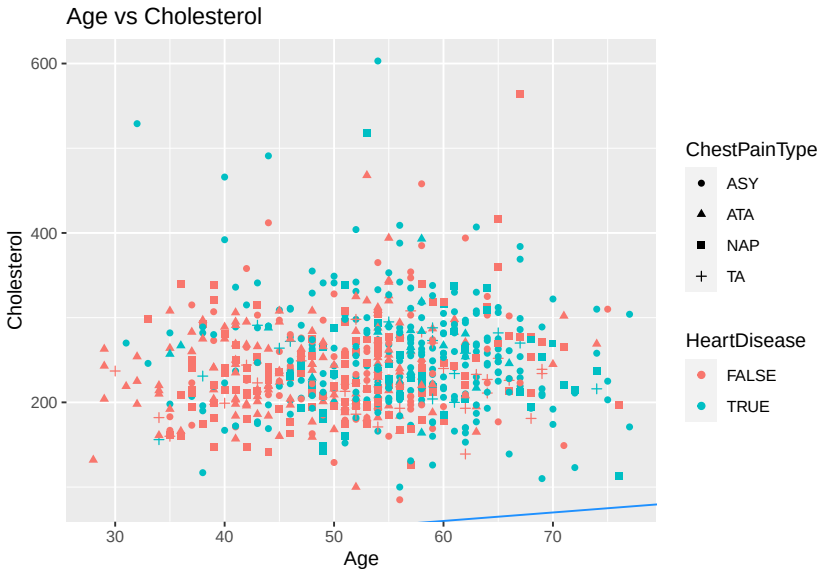


Figure 10: Correlation between age and cholesterol

The amount of cholesterol increases slightly with age.

1.6 PCA plotting

```
heartdata.active = heartdata[, c(1,4,5,6,8,13:16)]
res.pca <- prcomp(heartdata.active, scale = TRUE)

fviz_pca_var(res.pca,
             col.var = "contrib",
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
             repel = TRUE
             )
```

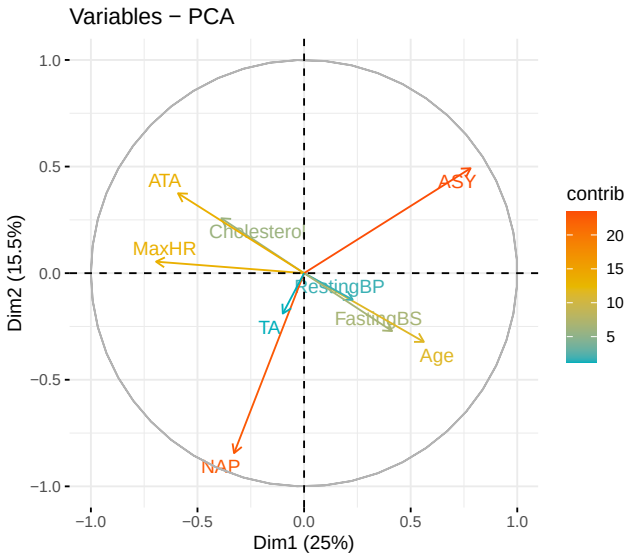


Figure 11: PCA Biplot of all non-categoral variables

```
fviz_pca_biplot(res.pca,
                col.var = "#2E9FDF", # Variables color
                col.ind = heartdata$HeartDisease,
                label = T,
                addEllipses = TRUE,
                geom.var = c("arrow", "text"),
                ellipse.type = "t",
                axes=c(1,2),
                legend.title = "Heartdisease")
```

Using the above lying PCA graphs it seems that asymptomic pain is the biggest contributor in the diagnosis of heartdisease in this dataset. This makes it hard to predict HD as asymptomic patients have no (visible) symptoms. The other pain categories do not seem to have a direct relation with the presence of HD. So far we can expect that age is the best variable in predicting HD as the percentage goes from around 25% at age ~30 to 75% at age ~65.

1.7 Algorithms

```
write.csv(heartdata, "data/heart_cleaned_report.csv", sep=",", row.names = FALSE)
heartdata$ChestPainType <- NULL
heartdata$ST_Slope <- NULL

heartdata$Cholesterol[heartdata$Cholesterol == 0] <- "?"
```

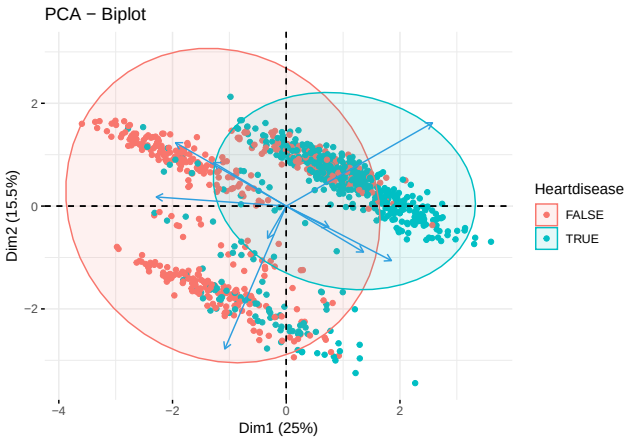


Figure 12: PCA Variable plot of all non-categoral variables

```
heartdata$RestingBP[heartdata$RestingBP == 0] <- "?"

heartdata$Cholesterol <- as.integer(heartdata$Cholesterol)
heartdata$RestingBP <- as.integer(heartdata$RestingBP)
## Set Heartdata as last column before exporting
disease <- heartdata$HeartDisease
heartdata$HeartDisease <- NULL
heartdata$HeartDisease <- disease
write.arff(heartdata, "data/heart_cleaned.arff")
write.csv(heartdata, "data/heart_cleaned.csv", sep=",", row.names = FALSE)
```

Autoparsing data from weka text files to csv so that it can be used in R.

```
import os
import pandas as pd

path = "data/weka_data"
output_path = "data/weka_parse.csv"

pdcons = []
for file in os.listdir(path):
    if "txt" not in file:
        continue
    fileinfo = {}
    with open(os.path.join(path, file), "r") as stream:
        fileinfo["name"] = file.split(".")[0]
        for line in stream:
            if line.startswith("Correctly Classified Instances  "):
                fileinfo["accuracy"] = line.split(" ")[-2]
            elif line.startswith("Incorrectly Classified Instances "):
                fileinfo["incorrect"] = line.split(" ")[-2]
            elif line.startswith("Scheme:       "):
                fileinfo["parameters"] = line.split("Scheme:       ")[1].replace("\n", "")
    pdcons.append(fileinfo)
dataframe = pd.DataFrame.from_dict(pdcons)
dataframe.to_csv(output_path, index=False)
```

```
mlresults <- read.table("data/weka_parse.csv", sep=",", header=T)

ggplot(mlresults, aes(x=reorder(name, -accuracy), y=accuracy)) +
  geom_bar(stat = "identity", fill="dodgerblue1") +
  coord_flip() + ylim(c(0,100)) + ggtitle("Accuracy of models") + xlab("Algorithm") + ylab("Accuracy (%
```

```
## Warning: Removed 1 rows containing missing values (position_stack).
```

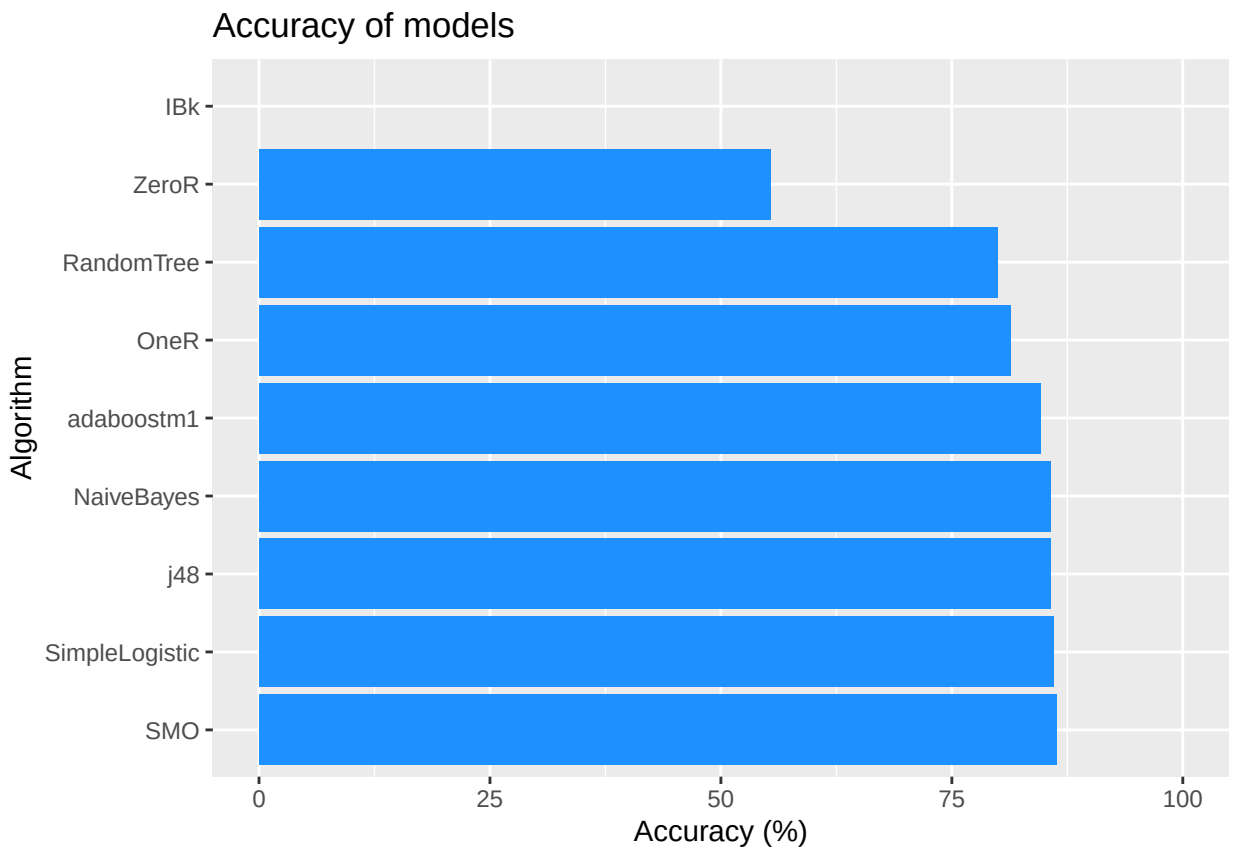


Figure 13: Accuracy by algorithm

```
kable(mlresults[order(mlresults$accuracy, decreasing = T), ], col.names = c("Algorithm", "Run Parameters
```

	Algorithm	Run Parameters
9	SMO	weka.classifiers.functions.SMO -C 1.0 -L 0.001 -P 1.0E-12 -N 0 -V -1 -W 1 -K "weka.classifiers.functio
7	SimpleLogistic	weka.classifiers.functions.SimpleLogistic -I 0 -M 500 -H 50 -W 0.0
1	NaiveBayes	weka.classifiers.bayes.NaiveBayes
6	j48	weka.classifiers.trees.J48 -C 0.25 -M 15
5	adaboostm1	weka.classifiers.meta.AdaBoostM1 -P 100 -S 1 -I 10 -W weka.classifiers.trees.DecisionStump
2	OneR	weka.classifiers.rules.OneR -B 6
8	RandomTree	weka.classifiers.trees.RandomTree -K 0 -M 1.0 -V 0.001 -S 1
3	ZeroR	weka.classifiers.rules.ZeroR
4	IBk	weka.classifiers.lazy.IBk -K 1 -W 0 -A "weka.core.neighboursearch.LinearNNSearch -A \"weka.core.Eu

1.8 Analysis of multiple ML algorithms first run

A fair amount of algorithms are significantly better then ZeroR, With al of them having an accuracy => 80%.

```
algorithms <- c("ZeroR", "OneR", "J48", "RandomTree", "AdaBoostM1", "SMO", "SimpleLogistic", "NaiveBayes
correct_p <- c(55.36, 81.37, 83.35, 79.89, 86.03, 86.00, 85.76, 85.33, 79.24)
sig_vs_zeror <- c(F, T, T, T, T, T, T, T, T)
sig_vs_ada <- c(T, T, T, T, F, F, F, F, T)
experimenter <- data.frame(algorithm = algorithms, accuracy = correct_p, significance_zeror = sig_vs_ze
experimenter <- tibble::rowid_to_column(experimenter, "Key")
```

```
ggplot(experimenter, aes(x=reorder(algorithm, accuracy), y=accuracy, fill=significance_ada)) +
  geom_bar(stat = "identity") +
  coord_flip() + ylim(c(0,100)) + ggtitle("Accuracy of models") + xlab("Algorithm") + ylab("Accuracy (%
```

Figure 14: Accuracy of various models. Coloured by significace

```
kable(experimenter[order(-correct_p),] , col.names = c("Key", "Algorithm", "Accuracy (%)", "Significant
  kable_styling(bootstrap_options = c("striped", "hover", "condensed"))
```

Key	Algorithm	Accuracy (%)	Significant different then ZeroR	Significant different then AdaBoostM1
5	AdaBoostM1	86.03	TRUE	FALSE
6	SMO	86.00	TRUE	FALSE
7	SimpleLogistic	85.76	TRUE	FALSE
8	NaiveBayes	85.33	TRUE	FALSE
3	J48	83.35	TRUE	TRUE
2	OneR	81.37	TRUE	TRUE
4	RandomTree	79.89	TRUE	TRUE
9	IBk	79.24	TRUE	TRUE
1	ZeroR	55.36	FALSE	TRUE

Key & Run parameters: (1) rules.ZeroR ” 48055541465867954
(2) rules.OneR ‘-B 6’ -3459427003147861443
(3) trees.J48 ‘-C 0.25 -M 2’ -217733168393644444
(4) trees.RandomTree ‘-K 0 -M 1.0 -V 0.001 -S 1’ -9051119597407396024
(5) meta.AdaBoostM1 ‘-P 100 -S 1 -I 10 -W trees.DecisionStump’ -1178107808933117974
(6) functions.SMO ‘-C 1.0 -L 0.001 -P 1.0E-12 -N 0 -V -1 -W 1 -K "functions.supportVector.PolyKernel -E 1.0 -C 250007" -calibrator "functions.Logistic -R 1.0E-8 -M -1 -num-decimal-places 4"’ -6585883636378691736
(7) functions.SimpleLogistic ‘-I 0 -M 500 -H 50 -W 0.0’ 7397710626304705059
(8) bayes.NaiveBayes ” 5995231201785697655
(9) lazy.IBk ‘-K 1 -W 0 -A "weka.core.neighboursearch.LinearNNSearch -A \"weka.core.EuclideanDistance -R first-last\""’ -3080186098777067172

As we can see in the above table (figure **??**) AdaBoostM1 scores, altough there is no significant difference with non-meta algorithms like SMO and SimpleLogistic. Other ensemble learners will be tested now.

1.9 Dataset (5) meta.Ada | (1) rules (2) meta. (3) meta. (4) meta. (6) funct (7) funct (8) bayes

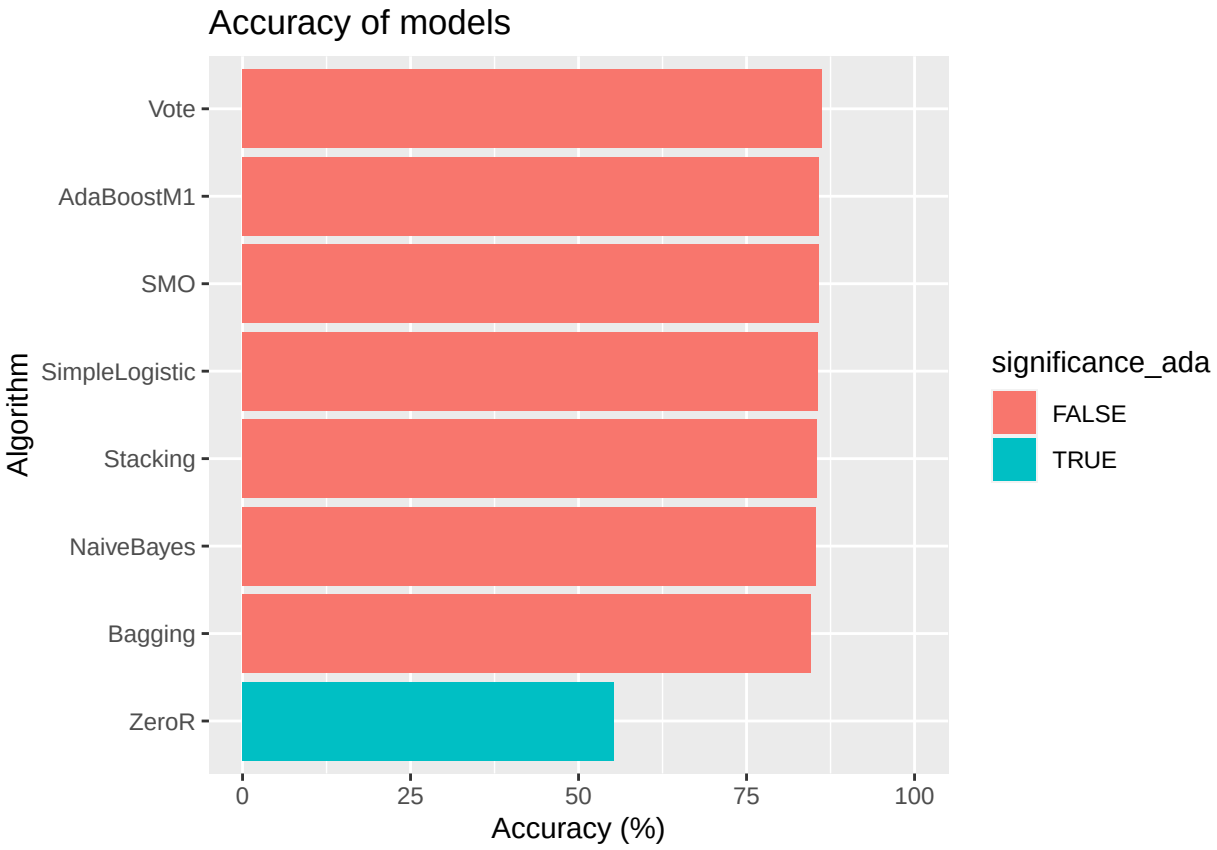
1.10 R_data_frame (100) 85.82 | 55.34 * 84.54 85.53 86.20 85.73 85.68 85.40

```
(v/ /*) |   (0/0/1)   (0/1/0)   (0/1/0)   (0/1/0)   (0/1/0)   (0/1/0)   (0/1/
```

Key: (1) rules.ZeroR ” 48055541465867954
(2) meta.Bagging ‘-P 100 -S 1 -num-slots 1 -I 10 -W trees.REPTree – -M 2 -V 0.001 -N 3 -S 1 -L -1 -I 0.0’ -115879962237199703
(3) meta.Stacking ‘-X 10 -M "trees.J48 -C 0.25 -M 2" -S 1 -num-slots 1 -B "functions.SMO -C 1.0 -L 0.001 -P 1.0E-12 -N 0 -V -1 -W 1 -K \"functions.supportVector.PolyKernel -E 1.0 -C 250007\" -calibrator \"functions.Logistic -R 1.0E-8 -M -1 -num-decimal-places 4\"" -B "functions.SimpleLogistic -I 0 -M 500 -H 50 -W 0.0" -B "bayes.NaiveBayes "’ 5134738557155845452
(4) meta.Vote ‘-S 1 -B "meta.AdaBoostM1 -P 100 -S 1 -I 10 -W trees.DecisionStump" -B "functions.SMO -C 1.0 -L 0.001 -P 1.0E-12 -N 0 -V -1 -W 1 -K \"functions.supportVector.PolyKernel -E 1.0 -C 250007\" -calibrator \"functions.Logistic -R 1.0E-8 -M -1 -num-decimal-places 4\"" -B "functions.SimpleLogistic -I 0 -M 500 -H 50 -W 0.0" -B "bayes.NaiveBayes " -R AVG’ -637891196294399624
(5) meta.AdaBoostM1 ‘-P 100 -S 1 -I 10 -W trees.DecisionStump’ -1178107808933117974
(6) functions.SMO ‘-C 1.0 -L 0.001 -P 1.0E-12 -N 0 -V -1 -W 1 -K "functions.supportVector.PolyKernel -E 1.0 -C 250007" -calibrator "functions.SimpleLogistic -I 0 -M 500 -H 50 -W 0.0"’ -6585883636378691736
(7) functions.SimpleLogistic ‘-I 0 -M 500 -H 50 -W 0.0’ 7397710626304705059
(8) bayes.NaiveBayes ” 5995231201785697655

```
algorithms <- c("ZeroR", "Bagging", "Stacking", "Vote", "AdaBoostM1", "SMO", "SimpleLogistic", "NaiveBa
accuracy <- c(55.34, 84.54, 85.53, 86.20, 85.82, 85.73, 85.68, 85.40)
stdeviation <- c(0.2, 3.61, 3.53, 3.37, 3.49, 3.46, 3.51, 3.32)
stat_dif_ada <- c(T, F, F, F, F, F, F, F)
```

```
ensemble <- data.frame(algorithm = algorithms, accuracy = accuracy, stdeviation = stdeviation, significa
ensemble <- tibble::rowid_to_column(ensemble, "Key")

ggplot(ensemble, aes(x=reorder(algorithms, accuracy), y=accuracy, fill=significance_ada)) +
  geom_bar(stat = "identity") +
  coord_flip() + ylim(c(0,100)) + ggtitle("Accuracy of models") + xlab("Algorithm") + ylab("Accuracy (%
```



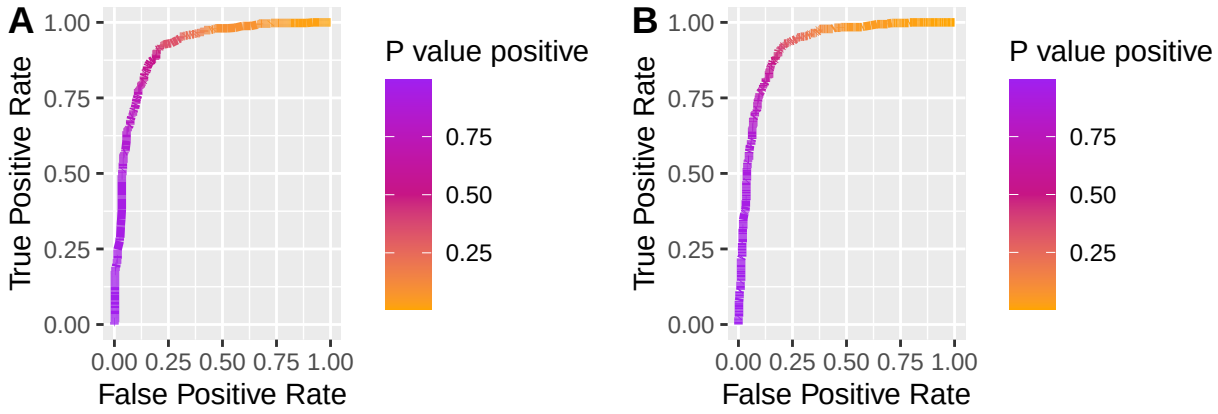

```
kable(ensemble[order(-accuracy),] , col.names = c("Key", "Algorithm", "Accuracy (%)", "Standard deviatio
  kable_styling(bootstrap_options = c("striped", "hover", "condensed"))
```

Key	Algorithm	Accuracy (%)	Standard deviation	Significant different then AdaBoostM1
4	Vote	86.20	3.37	FALSE
5	AdaBoostM1	85.82	3.49	FALSE
6	SMO	85.73	3.46	FALSE
7	SimpleLogistic	85.68	3.51	FALSE
3	Stacking	85.53	3.53	FALSE
8	NaiveBayes	85.40	3.32	FALSE
2	Bagging	84.54	3.61	FALSE
1	ZeroR	55.34	0.20	TRUE

Adaboost has a lower processing

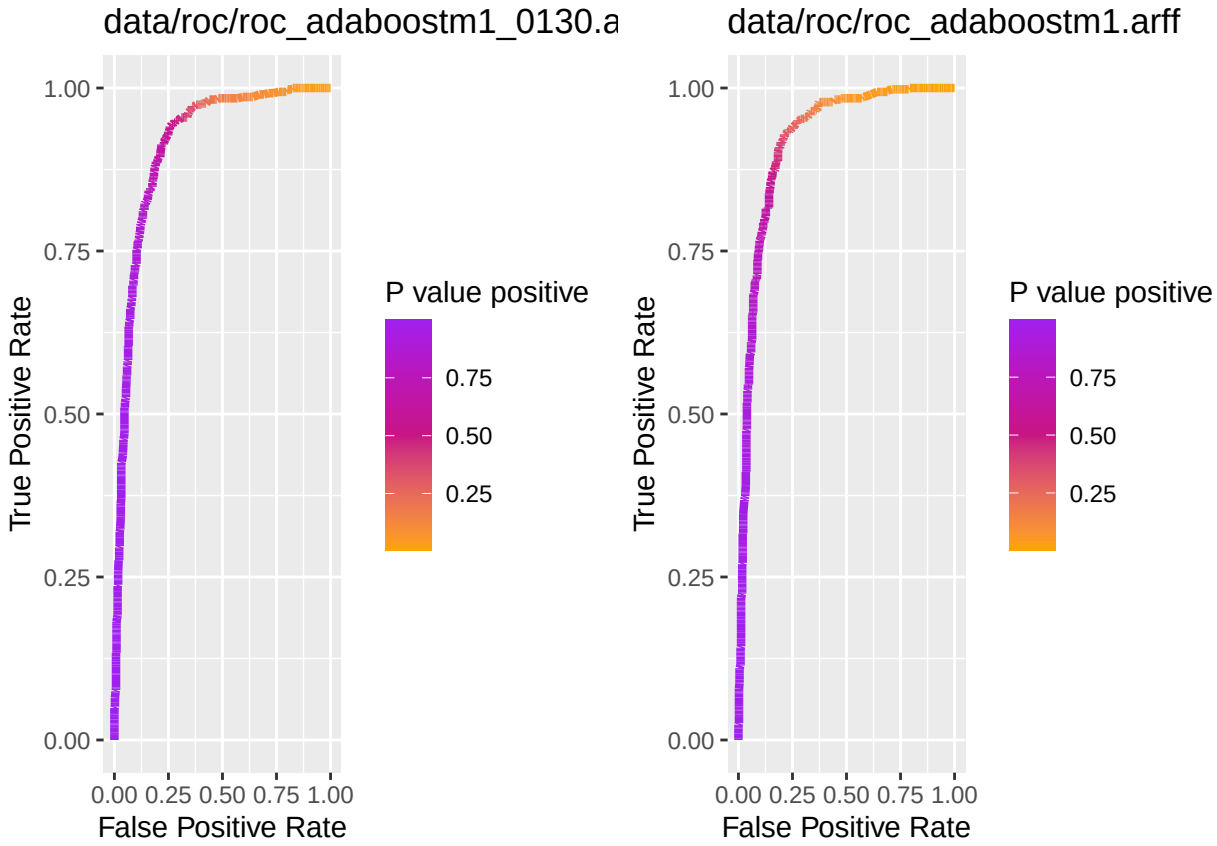
```
roc.smplog.stand <- read.arff("data/roc/roc_simplelog_stand.arff")
roc.smplog.cost <- read.arff("data/roc/roc_simplelog_0120.arff")

colourss <- hue_pal()(3)
```

```
stand <- ggplot(roc.smplog.stand) +
  geom_path(aes(x = `False Positive Rate`, y=`True Positive Rate`, color = Threshold), size=1.5) + scale

cost <- ggplot(roc.smplog.cost) +
  geom_path(aes(x = `False Positive Rate`, y=`True Positive Rate`, color = Threshold), size=1.5) + scale

ggarrange(stand,cost,
          ncol = 2, nrow = 2,
          labels = c("A", "B"))
```

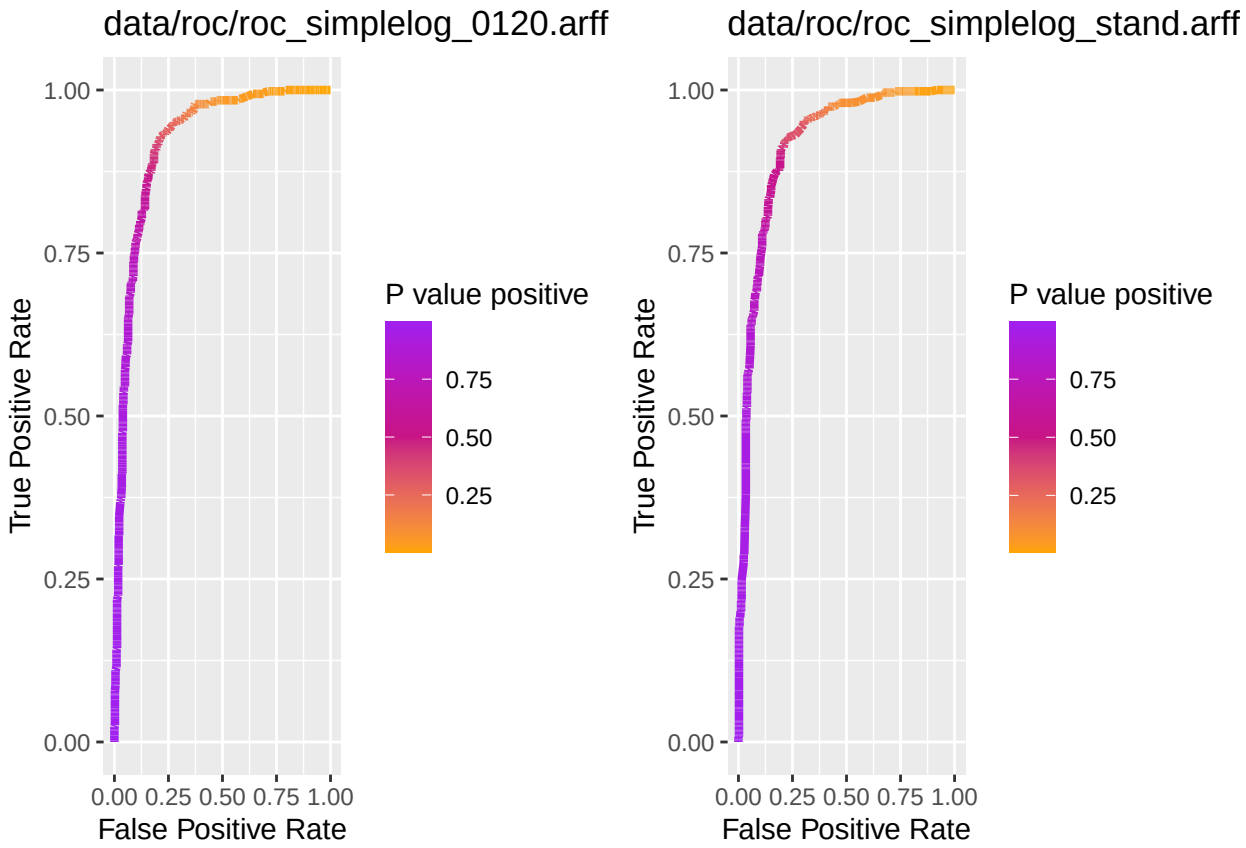



```
drawplots <- function(filepath) {
  files <- paste(filepath, list.files(filepath), sep = "/")
  plots = lapply(files, genplot)
  return(plots)
}

genplot <- function(x){
  roc.load = read.arff(x)
  pl <- ggplot(roc.load) +
   geom_path(aes(x = `False Positive Rate`, y=`True Positive Rate`, color = Threshold), size=1.5) + scal
  return(pl)
}

xs = drawplots("data/roc")
do.call(ggarrange, c(xs, ncol = 2))
```

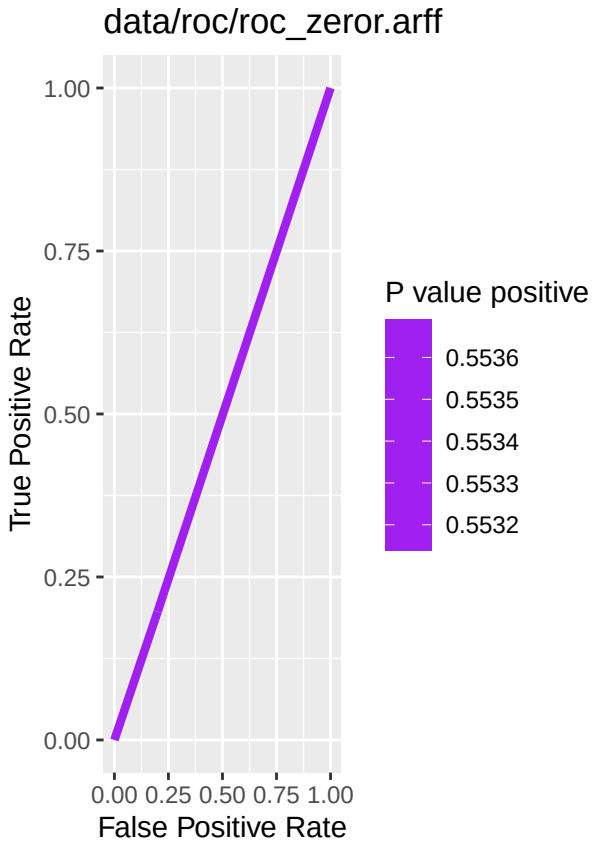
```
## $`1`
```


data/roc/roc_adaboostm1_0130.a
1.00
0.75
0.50
0.25
0.00
True Positive Rate
0.00 0.25 0.50 0.75 1.00
False Positive Rate
P value positive
0.75
0.50
0.25
data/roc/roc_adaboostm1.arff
1.00
0.75
0.50
0.25
0.00
True Positive Rate
0.00 0.25 0.50 0.75 1.00
False Positive Rate
P value positive
0.75
0.50
0.25

```
##
## $`2`
```


data/roc/roc_simplelog_0120.arff
True Positive Rate
False Positive Rate
P value positive
0.75
0.50
0.25
0.00
0.00 0.25 0.50 0.75 1.00
data/roc/roc_simplelog_stand.arff
True Positive Rate
False Positive Rate
P value positive
0.75
0.50
0.25
0.00
0.00 0.25 0.50 0.75 1.00

```
##
## $`3`
```




```
##
## attr(,"class")
## [1] "list"      "ggarrange"
```

Area under curve is not calculated as it is not a good metric because the ratio between FP and FN is not the same. False negatives weigh more as false negatives are patients who will not get any further diagnoses as they are deemed not having heart disease

Further experimenting teaches that using a cost matrix of [0 1 3 0] decreases the amount of false negatives heavily. Using a voting algorithm in combination with a cost sensitive classifier performes worse then a cost sensitive classifier in with adaboost m1, using the previously mentioned cost matrix. The resulting algorithm has an accuracy of 84.5% with the following confusion matrix: a b <– classified as
295 115 | a = FALSE
27 481 | b = TRUE

Using the same algorithm using the cost matrix of [0 1 1 0] will result in an accuracy of 85.7 and the following confusion matrix: a b <– classified as
345 65 | a = FALSE
66 442 | b = TRUE

Increasing the FN costs to 3 will result in approximatly halving the amount of false negative results doubling the amount of false postitives while reducing the overall accuracy by rougly 1.2%. Increasing the costs of false negatives any further will create a lot more false positives which will increase monitary costs while false negatives will not be reduced in the same rate as the increase of false positives.

The precise setting is no exact science so the resulting algorithm used will be a cost sensitive adaboostm1 model with cost matrix set to [0 1 3 0]. Weka Scheme: **weka.classifiers.meta.CostSensitiveClassifier -cost-matrix "[0.0 1.0; 3.0 0.0]" -S 1 -W weka.classifiers.meta.AdaBoostM1 – -P 100 -S 1 -I 10 -W weka.classifiers.trees.DecisionStump** This will result in an overall accuracy of 84.5%

Since Adaboost m1 is used the data needs to be checked for large outliers as Adaboost tries to correct outliers and tries to prevent missclassification. Reducing the amount of attributes does not increase model accuracy.