Explore the Heart disease data

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Install and load helpful library for analysis.

```
# Install required library, need not to re-install if you already have
# install.packages("dplyr")
# install.packages("Hmisc")
# install.packages("ggplot2")

# Load the require library
# library(dplyr)
# library(Hmisc)
# library(ggplot2)
```

1 Data Loading & Exploratory data analysis

1.1 Load the data in csv file and store to variable name `data`.

```
path <- "https://raw.githubusercontent.com/pnhuy/datasets/master/heart_uci/heart.csv"
data <- read.csv(path)
```

1.2 Show some rows of data to get some insight of data.

```
head(data)
```

```
##   X Age Sex    ChestPain RestBP Chol Fbs RestECG MaxHR ExAng Oldpeak Slope
## 1 1  63   1      typical    145  233   1       2   150     0     2.3     3
## 2 2  67   1 asymptomatic    160  286   0       2   108     1     1.5     2
## 3 3  67   1 asymptomatic    120  229   0       2   129     1     2.6     2
## 4 4  37   1   nonanginal    130  250   0       0   187     0     3.5     3
## 5 5  41   0   nontypical    130  204   0       2   172     0     1.4     1
## 6 6  56   1   nontypical    120  236   0       0   178     0     0.8     1
##   Ca       Thal AHD
## 1  0      fixed  No
## 2  3     normal Yes
## 3  2 reversable Yes
## 4  0     normal  No
## 5  0     normal  No
## 6  0     normal  No
```

1.3 Remove the first columns because it is not useful for analysis.

```
data_col <- colnames(data)
data <- data[data_col[2:length(data_col)]]
head(data)
```

```
##   Age Sex    ChestPain RestBP Chol Fbs RestECG MaxHR ExAng Oldpeak Slope
## 1  63   1      typical    145  233   1       2   150     0     2.3     3
## 2  67   1 asymptomatic    160  286   0       2   108     1     1.5     2
## 3  67   1 asymptomatic    120  229   0       2   129     1     2.6     2
```

```
## 4  37   1   nonanginal    130  250   0       0   187     0     3.5     3
## 5  41   0   nontypical    130  204   0       2   172     0     1.4     1
## 6  56   1   nontypical    120  236   0       0   178     0     0.8     1
##   Ca       Thal AHD
## 1  0      fixed  No
## 2  3     normal Yes
## 3  2 reversable Yes
## 4  0     normal  No
## 5  0     normal  No
## 6  0     normal  No
```

1.4 What was the average age?

```
mean(data$Age)
```

```
## [1] 54.43894
```

1.5 From sex column, create new variable gender which only have 'male', 'female'?

```
gender <- factor(data$Sex, levels=c(0,1), labels=c('female', 'male'))
```

1.6 How many percent of patient who was male were there in the data?

```
sum(data$Sex == 1)/length(data$Sex)*100
```

```
## [1] 67.9868
```

1.7 How many percent of male patient who suffered heart disease were there in the data? What about female?

```
print(sum(data[data$Sex == 1, 'AHD'] == 'Yes')/length(data[data$Sex == 1, 'AHD']))
```

```
## [1] 0.5533981
```

```
print(sum(data[data$Sex == 0, 'AHD'] == 'Yes')/length(data[data$Sex == 0, 'AHD']))
```

```
## [1] 0.257732
```

1.8 What was the range of RestBP?

```
print(c(min(data$RestBP), max(data$RestBP)))
```

```
## [1]  94 200
```

1.9 What was the distribution of AHD?

```
print(table(data$AHD))
```

```
##
##  No Yes
## 164 139
```

1.10 Calculate some basic desciptive statistics

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##     filter, lag
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
summary(data)
```

```
##       Age             Sex               ChestPain       RestBP
##  Min.   :29.00   Min.   :0.0000   asymptomatic:144   Min.   : 94.0
##  1st Qu.:48.00   1st Qu.:0.0000   nonanginal  : 86   1st Qu.:120.0
##  Median :56.00   Median :1.0000   nontypical  : 50   Median :130.0
##  Mean   :54.44   Mean   :0.6799   typical     : 23   Mean   :131.7
##  3rd Qu.:61.00   3rd Qu.:1.0000                      3rd Qu.:140.0
##  Max.   :77.00   Max.   :1.0000                      Max.   :200.0
##
##       Chol            Fbs            RestECG           MaxHR
##  Min.   :126.0   Min.   :0.0000   Min.   :0.0000   Min.   : 71.0
##  1st Qu.:211.0   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:133.5
##  Median :241.0   Median :0.0000   Median :1.0000   Median :153.0
##  Mean   :246.7   Mean   :0.1485   Mean   :0.9901   Mean   :149.6
##  3rd Qu.:275.0   3rd Qu.:0.0000   3rd Qu.:2.0000   3rd Qu.:166.0
##  Max.   :564.0   Max.   :1.0000   Max.   :2.0000   Max.   :202.0
##
##      ExAng           Oldpeak         Slope             Ca
##  Min.   :0.0000   Min.   :0.00   Min.   :1.000   Min.   :0.0000
##  1st Qu.:0.0000   1st Qu.:0.00   1st Qu.:1.000   1st Qu.:0.0000
##  Median :0.0000   Median :0.80   Median :2.000   Median :0.0000
##  Mean   :0.3267   Mean   :1.04   Mean   :1.601   Mean   :0.6722
##  3rd Qu.:1.0000   3rd Qu.:1.60   3rd Qu.:2.000   3rd Qu.:1.0000
##  Max.   :1.0000   Max.   :6.20   Max.   :3.000   Max.   :3.0000
##                                                  NA's   :4
##          Thal      AHD
##  fixed     : 18   No :164
##  normal    :166   Yes:139
##  reversable:117
##  NA's      :  2
##
##
##
```

```
library(Hmisc)
```

```
## Loading required package: lattice
## Loading required package: survival
## Loading required package: Formula
```

```
## Loading required package: ggplot2
##
## Attaching package: 'Hmisc'
## The following objects are masked from 'package:dplyr':
##
##     src, summarize
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
describe(data)
```

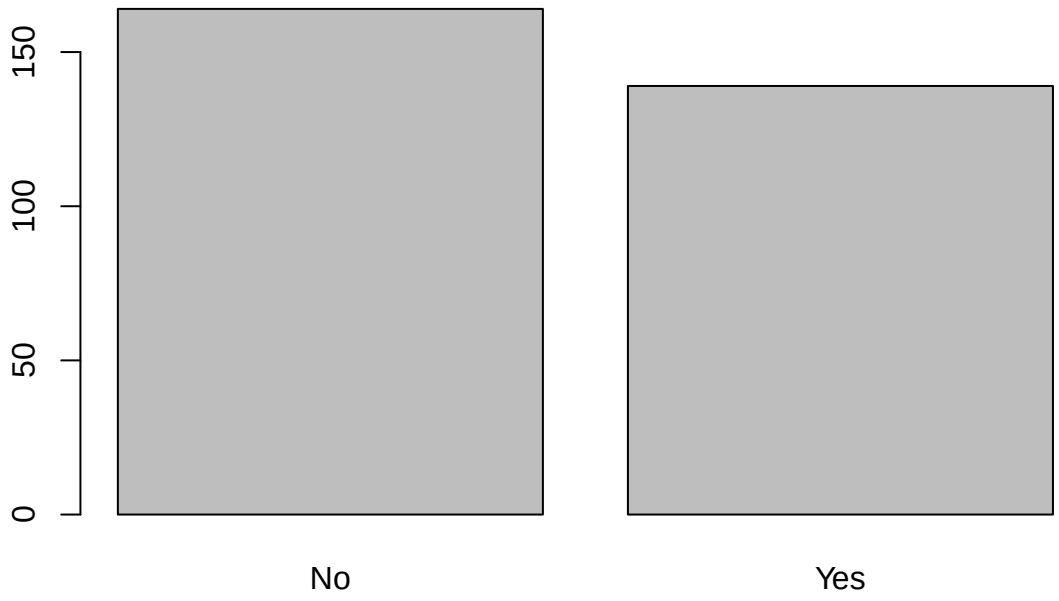
```
## data
##
##  14  Variables      303  Observations
## --------------------------------------------------------------------------------
## Age
##        n  missing distinct     Info     Mean      Gmd      .05      .10
##      303        0       41    0.999    54.44     10.3       40       42
##      .25      .50      .75      .90      .95
##       48       56       61       66       68
##
## lowest : 29 34 35 37 38, highest: 70 71 74 76 77
## --------------------------------------------------------------------------------
## Sex
##        n  missing distinct     Info      Sum     Mean      Gmd
##      303        0        2    0.653      206   0.6799   0.4367
##
## --------------------------------------------------------------------------------
## ChestPain
##        n  missing distinct
##      303        0        4
##
## Value      asymptomatic   nonanginal   nontypical      typical
## Frequency           144           86           50           23
## Proportion        0.475        0.284        0.165        0.076
## --------------------------------------------------------------------------------
## RestBP
##        n  missing distinct     Info     Mean      Gmd      .05      .10
##      303        0       50    0.995    131.7    19.41      108      110
##      .25      .50      .75      .90      .95
##      120      130      140      152      160
##
## lowest :  94 100 101 102 104, highest: 174 178 180 192 200
## --------------------------------------------------------------------------------
## Chol
##        n  missing distinct     Info     Mean      Gmd      .05      .10
##      303        0      152        1    246.7    55.91    175.1    188.8
##      .25      .50      .75      .90      .95
##    211.0    241.0    275.0    308.8    326.9
##
## lowest : 126 131 141 149 157, highest: 394 407 409 417 564
## --------------------------------------------------------------------------------
```

```
## Fbs
##        n  missing distinct     Info      Sum     Mean      Gmd
##      303        0        2    0.379       45   0.1485   0.2538
##
## ------------------------------------------------------------------------
## RestECG
##        n  missing distinct     Info     Mean      Gmd
##      303        0        3     0.76   0.9901    1.003
##
## Value          0     1     2
## Frequency    151     4   148
## Proportion 0.498 0.013 0.488
## ------------------------------------------------------------------------
## MaxHR
##        n  missing distinct     Info     Mean      Gmd      .05      .10
##      303        0       91        1    149.6    25.73    108.1    116.0
##      .25      .50      .75      .90      .95
##    133.5    153.0    166.0    176.6    181.9
##
## lowest :  71  88  90  95  96, highest: 190 192 194 195 202
## ------------------------------------------------------------------------
## ExAng
##        n  missing distinct     Info      Sum     Mean      Gmd
##      303        0        2     0.66       99   0.3267   0.4414
##
## ------------------------------------------------------------------------
## Oldpeak
##        n  missing distinct     Info     Mean      Gmd      .05      .10
##      303        0       40    0.964     1.04    1.225      0.0      0.0
##      .25      .50      .75      .90      .95
##      0.0      0.8      1.6      2.8      3.4
##
## lowest : 0.0 0.1 0.2 0.3 0.4, highest: 4.0 4.2 4.4 5.6 6.2
## ------------------------------------------------------------------------
## Slope
##        n  missing distinct     Info     Mean      Gmd
##      303        0        3    0.798    1.601   0.6291
##
## Value          1     2     3
## Frequency    142   140    21
## Proportion 0.469 0.462 0.069
## ------------------------------------------------------------------------
## Ca
##        n  missing distinct     Info     Mean      Gmd
##      299        4        4    0.783   0.6722   0.9249
##
## Value          0     1     2     3
## Frequency    176    65    38    20
## Proportion 0.589 0.217 0.127 0.067
## ------------------------------------------------------------------------
## Thal
##        n  missing distinct
##      301        2        3
##
```

```
## Value           fixed     normal reversable
## Frequency          18        166        117
## Proportion      0.060      0.551      0.389
## ---------------------------------------------------------------------------
## AHD
##        n  missing distinct
##      303        0        2
##
## Value         No   Yes
## Frequency    164   139
## Proportion 0.541 0.459
## ---------------------------------------------------------------------------
```

1.11 Plot the distribution of AHD?

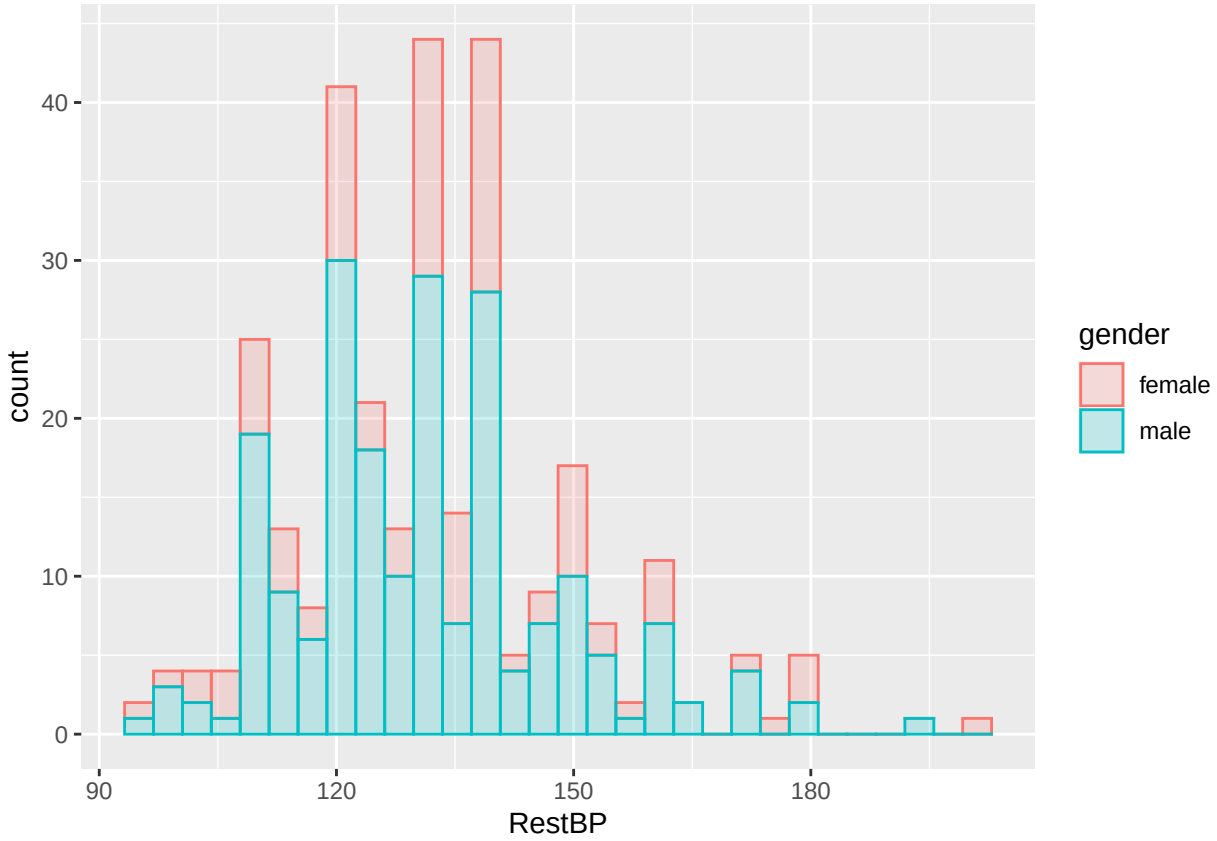
```
barplot(table(data$AHD))
```



1.12 Plot the distribution of RestBP per Sex?

```
# In this plot, the distribution need a Factor variable to split, so we input the `gender`
# instead of `Sex`
ggplot(data, aes(x=RestBP)) + geom_histogram(aes(color=gender, fill=gender), alpha=0.2)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



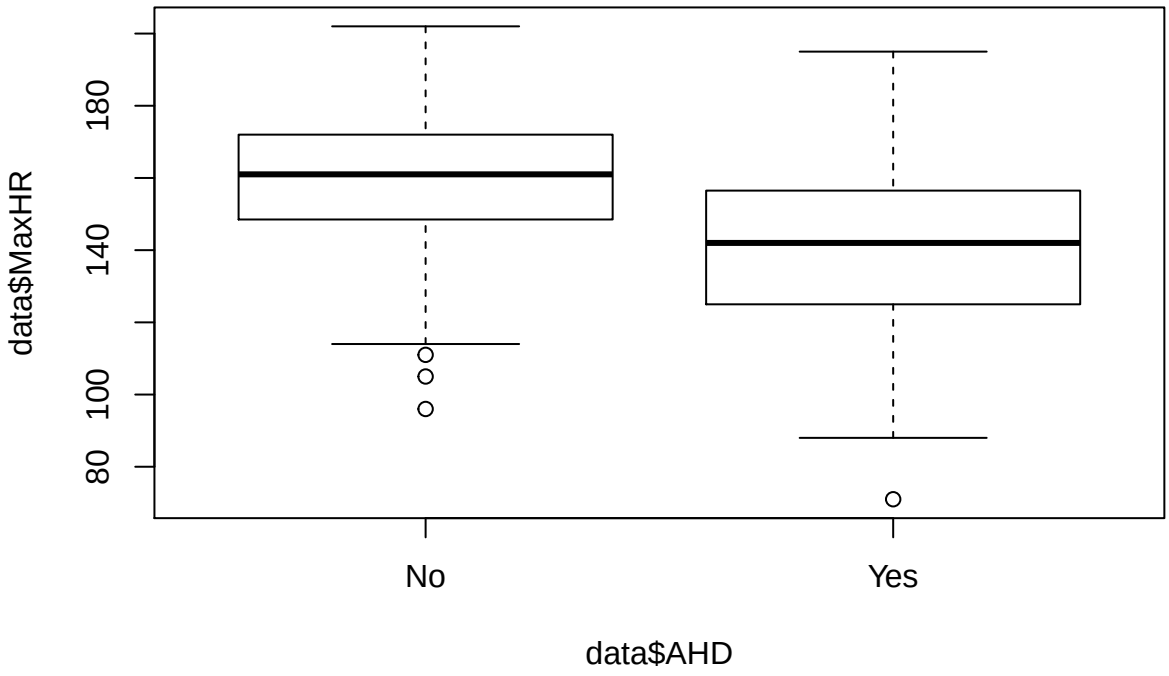
1.13 Illustrate the relationship between sex and AHD?

```
table(data$Sex, data$AHD)
```

```
##
##      No Yes
##   0  72  25
##   1  92 114
```

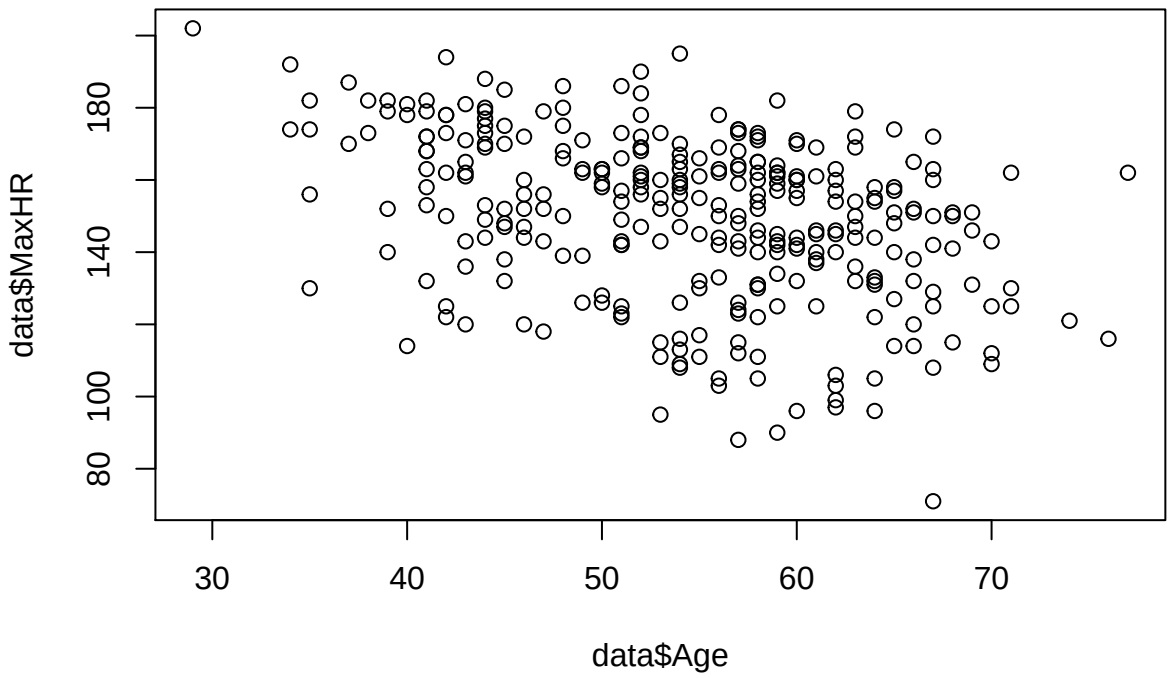
1.14 Illustrate the relationship between MaxHR and AHD?

```
boxplot(data$MaxHR ~ data$AHD)
```



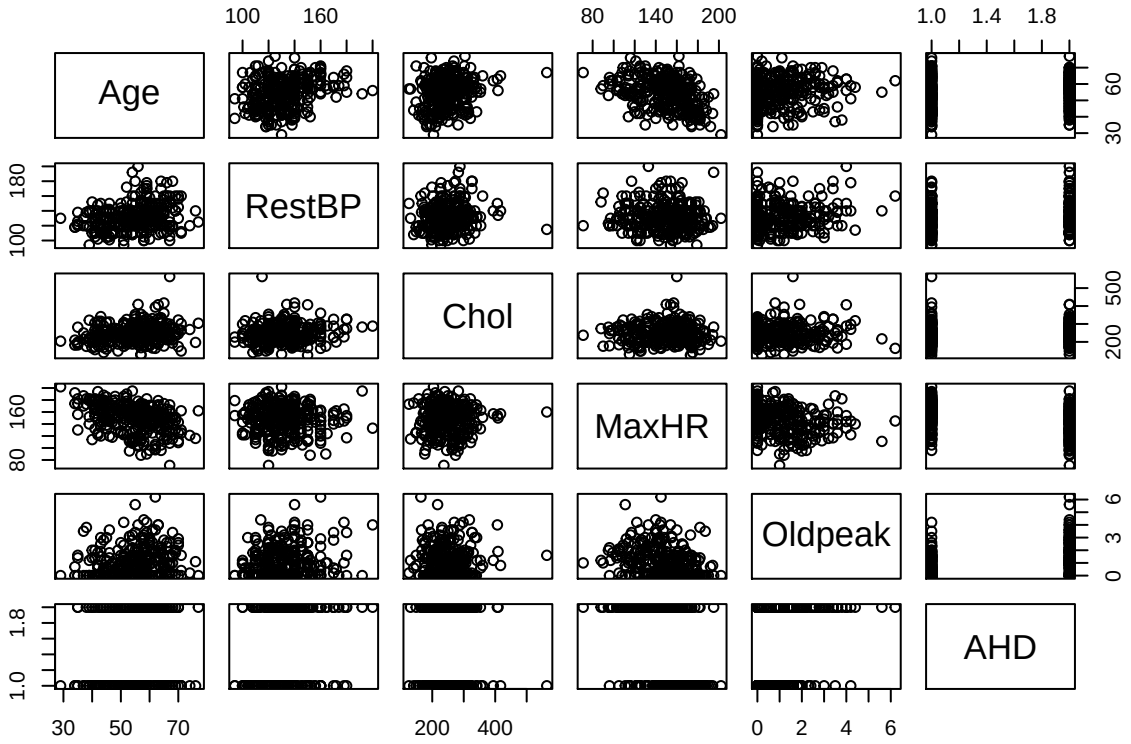
1.15 Illustrate the relationship between Age and MaxHR?

```
plot(data$Age, data$MaxHR)
```



1.16 Illustrate the relationship between the continuous variables and the target?

```
pairs(data[c('Age', 'RestBP', 'Chol', 'MaxHR', 'Oldpeak', 'AHD')])
```



2 Hypothesis testing

2.1 Compare the mean RestBP with normal BP (120)?

```
t.test(data$RestBP, mu=120)
```

```
##
##  One Sample t-test
##
## data:  data$RestBP
## t = 11.562, df = 302, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 120
## 95 percent confidence interval:
##  129.7001 133.6794
## sample estimates:
## mean of x
##  131.6898
```

2.2 Compare mean RestBP by AHD?

```
RestBP_Yes = data[data$AHD == "Yes", "RestBP"]
RestBP_No = data[data$AHD == "No", "RestBP"]
t.test(RestBP_Yes, RestBP_No)
```

```
##
```

```
##  Welch Two Sample t-test
##
## data:  RestBP_Yes and RestBP_No
## t = 2.6152, df = 274.64, p-value = 0.009409
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.314915 9.321775
## sample estimates:
## mean of x mean of y
##  134.5683  129.2500
```

2.3 Test the independence between AHD and Sex?

```
chisq.test(data$Sex, data$AHD)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  data$Sex and data$AHD
## X-squared = 22.043, df = 1, p-value = 2.667e-06
```

2.4 Compare mean MaxHR by Thal

2.4.1 ANOVA

```
anova <- aov(MaxHR ~ Thal, data=data)
summary(anova)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## Thal          2  14396    7198   15.06 5.86e-07 ***
## Residuals   298 142389     478
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 2 observations deleted due to missingness
```

2.4.2 Pairwise T-Test

```
pairwise.t.test(data$MaxHR, data$Thal)
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  data$MaxHR and data$Thal
##
##            fixed   normal
## normal     0.00036 -
## reversable 0.13359 1.5e-05
##
## P value adjustment method: holm
```

2.4.3 Tukey multiple pairwise-comparisons

```
TukeyHSD(anova)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = MaxHR ~ Thal, data = data)
##
## $Thal
##                          diff        lwr       upr     p adj
## normal-fixed       20.587684   7.810658 33.364710 0.0005225
## reversable-fixed    8.324786  -4.711349 21.360922 0.2903956
## reversable-normal -12.262898 -18.478131 -6.047665 0.0000150
```

3 Linear Regression

3.1 Build a model to predict MaxHR by Age?

```
model_1 <- lm(MaxHR ~ Age, data=data)
summary(model_1)
```

```
##
## Call:
## lm(formula = MaxHR ~ Age, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -66.088 -12.040   3.965  15.937  44.955
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 203.8634     7.3991  27.553  < 2e-16 ***
## Age          -0.9966     0.1341  -7.433 1.11e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 21.06 on 301 degrees of freedom
## Multiple R-squared:  0.1551, Adjusted R-squared:  0.1523
## F-statistic: 55.25 on 1 and 301 DF,  p-value: 1.109e-12
```

3.2 Build a model to predict MaxHR by Age & RestBP & Thal?

```
model_2 <- lm(MaxHR ~ Age + RestBP + Thal, data=data)
summary(model_2)
```

```
##
## Call:
## lm(formula = MaxHR ~ Age + RestBP + Thal, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -70.046 -12.269   3.579  14.086  52.824
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    172.57393   11.48221  15.030  < 2e-16 ***
```

```
## Age             -0.98287    0.13478  -7.292  2.8e-12 ***
## RestBP           0.13314    0.06932   1.921 0.055720 .
## Thalnormal      18.34722    5.04476   3.637 0.000325 ***
## Thalreversable   7.69466    5.11709   1.504 0.133721
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 20.19 on 296 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2301, Adjusted R-squared:  0.2197
## F-statistic: 22.12 on 4 and 296 DF,  p-value: 5.425e-16
```