Heart Rate Analysis

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Heart disease and potential risk factors

Millions of people develop some sort of heart disease every year and heart disease is the biggest killer of both men and women in the United States and around the world. Statistical analysis has identified many risk factors associated with heart disease such as age, blood pressure, total cholesterol, diabetes, hypertension, family history of heart disease, obesity, lack of physical exercise, etc. In this project, we're going to run statistical tests and regression models using the Cleveland heart disease dataset to assess one particular factor – maximum heart rate one can achieve during exercise and how it is associated with a higher likelihood of getting heart disease.

```r
# Read datasets Cleveland_hd.csv into hd_data
Cldata <- read.csv("C:/Users/O&1/OneDrive/Documents/Heart Rate/Cleveland_hd.csv")

# take a look at the first 5 rows of Cldata
head(Cldata,5)
```

```
##   age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
## 1  63   1  1      145  233   1       2     150     0     2.3     3  0    6
## 2  67   1  4      160  286   0       2     108     1     1.5     2  3    3
## 3  67   1  4      120  229   0       2     129     1     2.6     2  2    7
## 4  37   1  3      130  250   0       0     187     0     3.5     3  0    3
## 5  41   0  2      130  204   0       2     172     0     1.4     1  0    3
##   class
## 1     0
## 2     2
## 3     1
## 4     0
## 5     0
```

Converting diagnosis class into outcome variable

We noticed that the outcome variable class has more than two levels. According to the codebook, any non-zero values can be coded as an "event." We create a new variable called hd to represent a binary 1/0 outcome.

There are a few other categorical/discrete variables in the dataset. We also convert sex into a 'factor' for next step analysis. Otherwise, R will treat this as continuous by default.

```r
# load the tidyverse package
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```
# Use the 'mutate' function from dplyr to recode our data
Cldata %>% mutate(hd = ifelse(class > 0, 1, 0))-> Cldata

# recode sex using mutate function and save as hd_data
Cldata %>% mutate(sex = factor(sex, levels = 0:1, labels = c("Female", "Male")))-> Cldata
```

Identifying important clinical variables

Now, we use statistical tests to see which predictors are related to heart disease. We can explore the associations for each variable in the dataset. Depending on the type of the data (i.e., continuous or categorical), we use t-test or chi-squared test to calculate the p-values.

T-test is used to determine whether there is a significant difference between the means of two groups (e.g., is the mean age from group A different from the mean age from group B?). A chi-squared test for independence compares the equivalence of two proportions.

```
# Does sex have an effect?
# Sex is a binary variable in this dataset, so the appropriate test is chi-squared test
Cl_sex <- chisq.test(Cldata$hd, Cldata$sex)

# Does age have an effect? Age is continuous, so we use a t-test
Cl_age <- t.test(age~hd, Cldata)

# And Thalach is a continuous variable as well, so we use a t-test
Cl_heartrate <- t.test(thalach~hd, Cldata)

# Print the results to see if p<0.05.
print(Cl_sex)
```

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

```
print(Cl_age)
```

```
##
##  Welch Two Sample t-test
##
## data:  age by hd
## t = -4.0303, df = 300.93, p-value = 7.061e-05
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -6.013385 -2.067682
## sample estimates:
## mean in group 0 mean in group 1
##        52.58537        56.62590
```

```
print(Cl_heartrate)
```

```
##
##  Welch Two Sample t-test
##
## data:  thalach by hd
## t = 7.8579, df = 272.27, p-value = 9.106e-14
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  14.32900 23.90912
## sample estimates:
## mean in group 0 mean in group 1
##         158.378         139.259
```

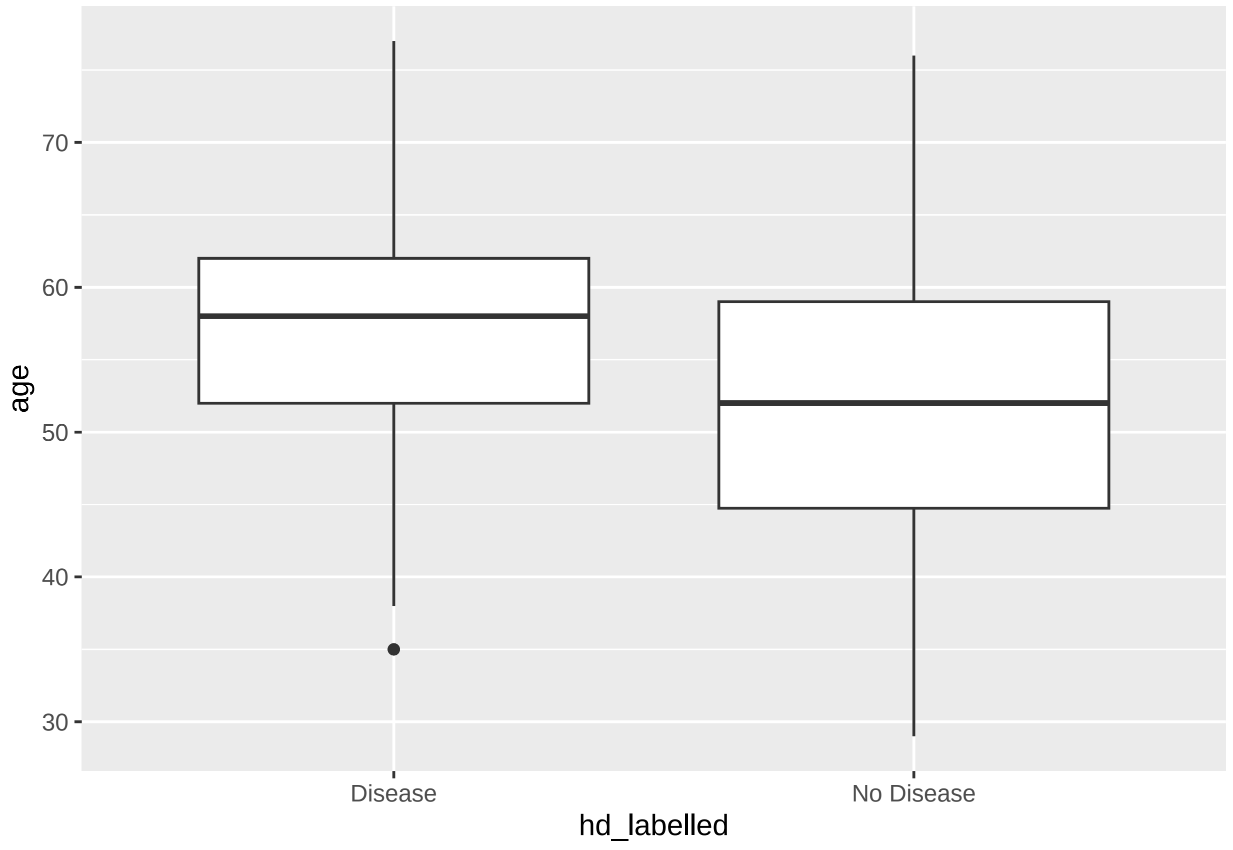
Exploring the data graphically

In addition to p-values from statistical tests, we can plot the age, sex, and maximum heart rate distributions with respect to our outcome variable. This will give us a sense of both the direction and magnitude of the relationship.

- First, we plot age using a boxplot since it is a continuous variable.

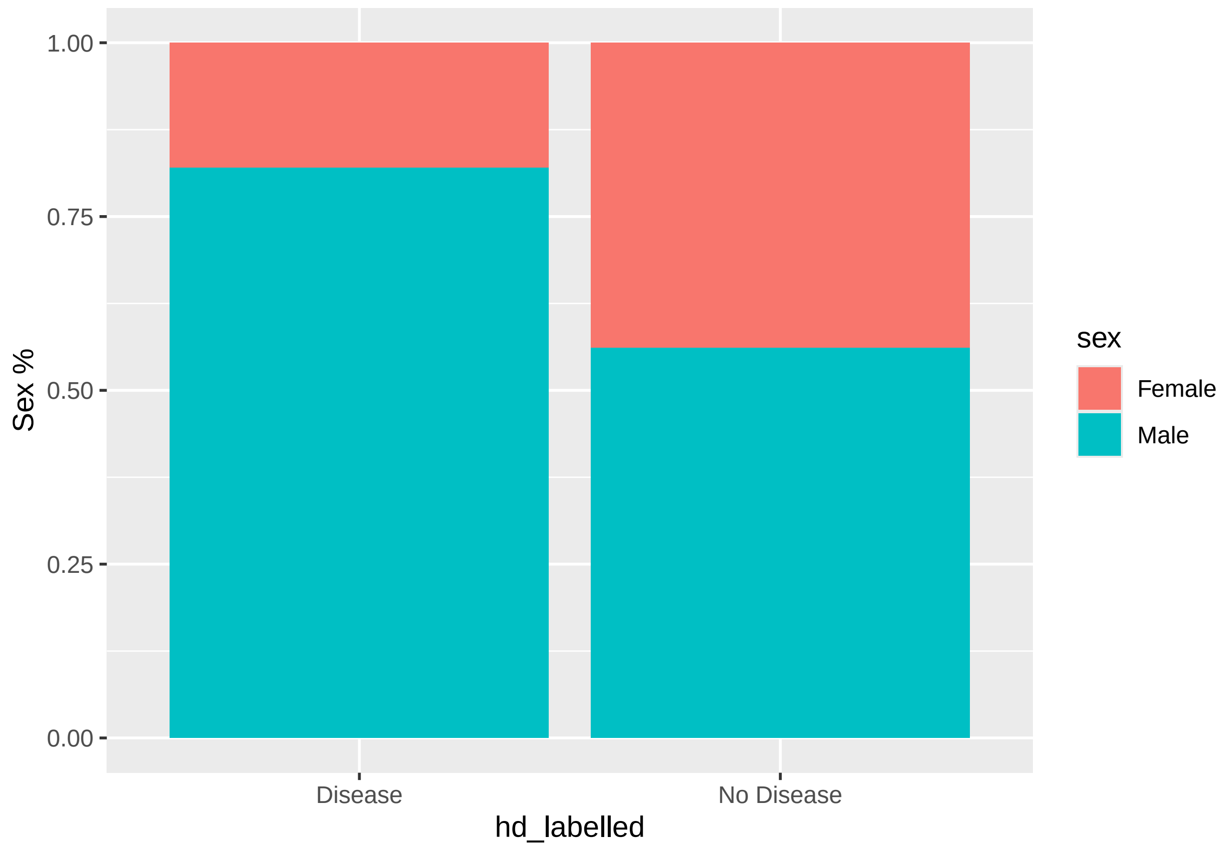
```r
# Recode hd to be labelled
Cldata%>%mutate(hd_labelled = ifelse(hd == 0, "No Disease", "Disease")) -> Cldata

# age vs hd
ggplot(data = Cldata, aes(x = hd_labelled,y = age)) + geom_boxplot()
```



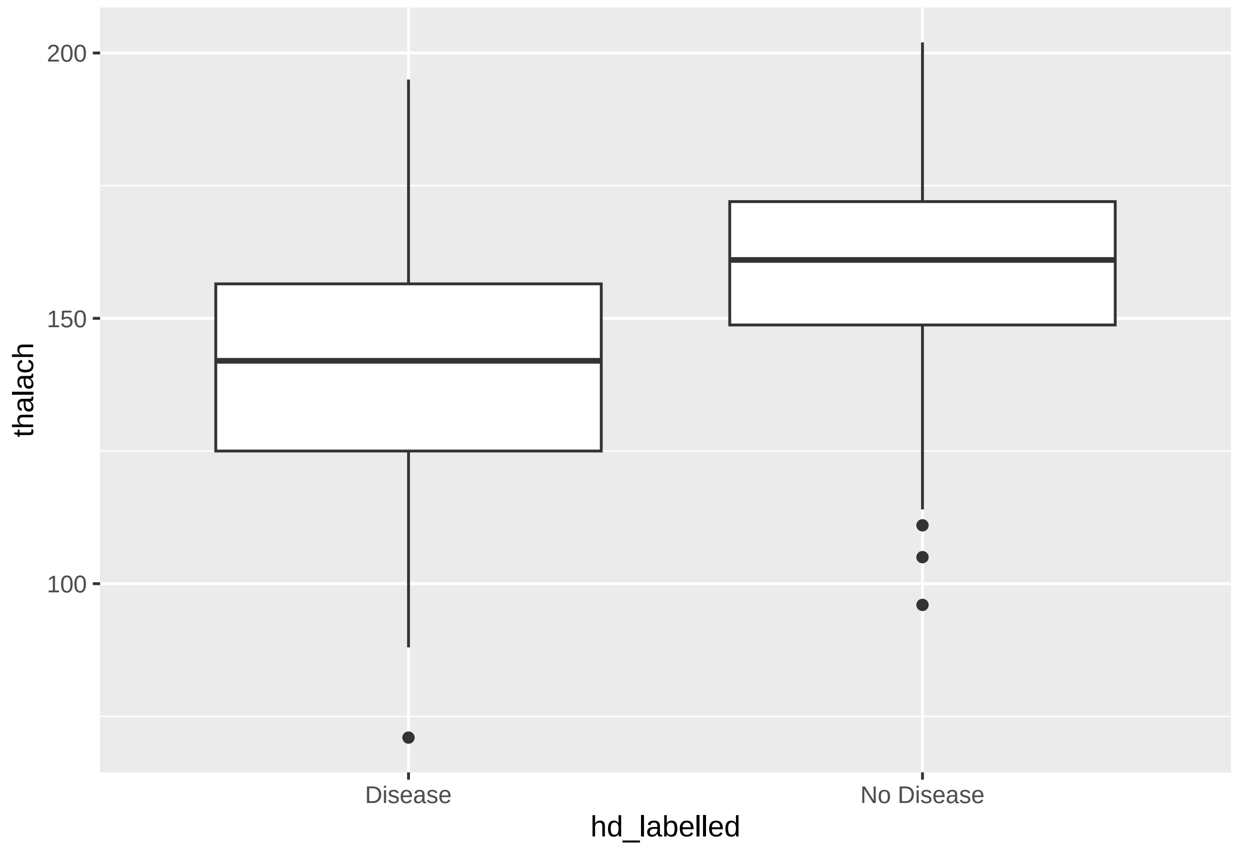
- Next, we plot sex using a barplot since it is a binary variable in this dataset.

```r
# sex vs hd
ggplot(data = Cldata,aes(x=hd_labelled,fill=sex)) + geom_bar(position="fill")+ ylab("Sex %")
```



- Finally, we plot thalach using a boxplot since it is a continuous variable.

```r
# max heart rate vs hd
ggplot(data = Cldata,aes(x=hd_labelled,y=thalach)) + geom_boxplot()
```



~~~
## Putting variables in one model
The plots and the statistical tests both confirmed that all the three variables are highly significantl

In general, we want to use multiple logistic regression when we have one binary outcome variable and tw

The glm() command is designed to perform generalized linear models (regressions) on binary outcome data

``` r
# use glm function from base R and specify the family argument as binomial
model <-glm(data = Cldata, hd~age+sex+thalach, family="binomial")

# extract the model summary
summary(model)
~~~

```
##
## Call:
## glm(formula = hd ~ age + sex + thalach, family = "binomial",
##     data = Cldata)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.111610   1.607466   1.936   0.0529 .
## age          0.031886   0.016440   1.940   0.0524 .
## sexMale      1.491902   0.307193   4.857 1.19e-06 ***
## thalach     -0.040541   0.007073  -5.732 9.93e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 417.98  on 302  degrees of freedom
## Residual deviance: 332.85  on 299  degrees of freedom
## AIC: 340.85
##
## Number of Fisher Scoring iterations: 4
```

Extracting useful information from the model output

It's common practice in medical research to report Odds Ratio (OR) to quantify how strongly the presence or absence of property A is associated with the presence or absence of the outcome. When the OR is greater than 1, we say A is positively associated with outcome B (increases the Odds of having B). Otherwise, we say A is negatively associated with B (decreases the Odds of having B).

The raw glm coefficient table (the 'estimate' column in the printed output) in R represents the log(Odds Ratios) of the outcome. Therefore, we need to convert the values to the original OR scale and calculate the corresponding 95% Confidence Interval (CI) of the estimated Odds Ratios when reporting results from a logistic regression.

```
# load the broom package
 library(broom)

# tidy up the coefficient table
tidy_m <- tidy(model)
tidy_m
```

```
## # A tibble: 4 x 5
##   term        estimate std.error statistic       p.value
##   <chr>          <dbl>     <dbl>     <dbl>         <dbl>
## 1 (Intercept)   3.11     1.61         1.94 0.0529
## 2 age           0.0319   0.0164       1.94 0.0524
## 3 sexMale       1.49     0.307        4.86 0.00000119
## 4 thalach      -0.0405   0.00707     -5.73 0.00000000993
```

```
# calculate OR
tidy_m$OR <- exp(tidy_m$estimate)

# calculate 95% CI and save as lower CI and upper CI
tidy_m$lower_CI <- exp(tidy_m$estimate - 1.96 * tidy_m$std.error)
tidy_m$upper_CI <- exp(tidy_m$estimate + 1.96 * tidy_m$std.error)

# display the updated coefficient table
tidy_m
```

```
## # A tibble: 4 x 8
##   term        estimate std.error statistic      p.value     OR lower_CI upper_CI
##   <chr>          <dbl>     <dbl>     <dbl>        <dbl>  <dbl>    <dbl>    <dbl>
## 1 (Intercept)   3.11     1.61         1.94      5.29e-2 22.5      0.962  524.
## 2 age           0.0319   0.0164       1.94      5.24e-2  1.03     1.00     1.07
## 3 sexMale       1.49     0.307        4.86      1.19e-6  4.45     2.43     8.12
## 4 thalach      -0.0405   0.00707     -5.73      9.93e-9  0.960    0.947    0.974
```

Predicted probabilities from our model

So far, we have built a logistic regression model and examined the model coefficients/ORs. We may wonder how can we use this model we developed to predict a person's likelihood of having heart disease given his/her age, sex, and maximum heart rate. Furthermore, we'd like to translate the predicted probability into a decision rule for clinical use by defining a cutoff value on the probability scale. In practice, when an individual comes in for a health check-up, the doctor would like to know the predicted probability of heart disease, for specific values of the predictors: a 45-year-old female with a max heart rate of 150. To do that, we create a data frame called newdata, in which we include the desired values for our prediction.

```r
# get the predicted probability in our dataset using the predict() function
pred_prob <- predict(model,Cldata, type = "response")

# create a decision rule using probability 0.5 as cutoff and save the predicted decision into the main
Cldata$pred_hd <- ifelse(pred_prob >= 0.5,1,0)

# create a newdata data frame to save a new case information
newdata <- data.frame(age = 45, sex = "Female", thalach = 150)

# predict probability for this new case and print out the predicted value
p_new <- predict(model,newdata, type = "response")
p_new
```

```
##         1
## 0.1773002
```

Model performance metrics

We are going to use some common metrics to evaluate the model performance. The most straightforward one is Accuracy, which is the proportion of the total number of predictions that were correct. On the other hand, we can calculate the classification error rate using 1- accuracy. However, accuracy can be misleading when the response is rare (i.e., imbalanced response). Another popular metric, Area Under the ROC curve (AUC), has the advantage that it's independent of the change in the proportion of responders. AUC ranges from 0 to 1. The closer it gets to 1 the better the model performance. Lastly, a confusion matrix is an N X N matrix, where N is the level of outcome. For the problem at hand, we have N=2, and hence we get a 2 X 2 matrix. It cross-tabulates the predicted outcome levels against the true outcome levels.

After these metrics are calculated, we'll see (from the logistic regression OR table) that older age, being male and having a lower max heart rate are all risk factors for heart disease. We can also apply our model to predict the probability of having heart disease. For a 45 years old female who has a max heart rate of 150, our model generated a heart disease probability of 0.177 indicating low risk of heart disease.

```r
# load Metrics package
library(Metrics)

# calculate auc, accuracy, clasification error
auc <- auc(Cldata$hd,Cldata$pred_hd)
accuracy <- accuracy(Cldata$hd,Cldata$pred_hd)
classification_error <- ce(Cldata$hd,Cldata$pred_hd)

# print out the metrics on to screen
print(paste("AUC=", auc))
```

```
## [1] "AUC= 0.706483593612915"
```

```r
print(paste("Accuracy=", accuracy))
```

```
## [1] "Accuracy= 0.70957095709571"
```

```
print(paste("Classification Error=", classification_error))
```

```
## [1] "Classification Error= 0.29042904290429"
```

```
# confusion matrix
 b_table <- table(Cldata$hd,Cldata$pred_hd, dnn=c('True Status','Predicted Status'))
 b_table
```

```
##            Predicted Status
## True Status   0   1
##           0 122  42
##           1  46  93
```

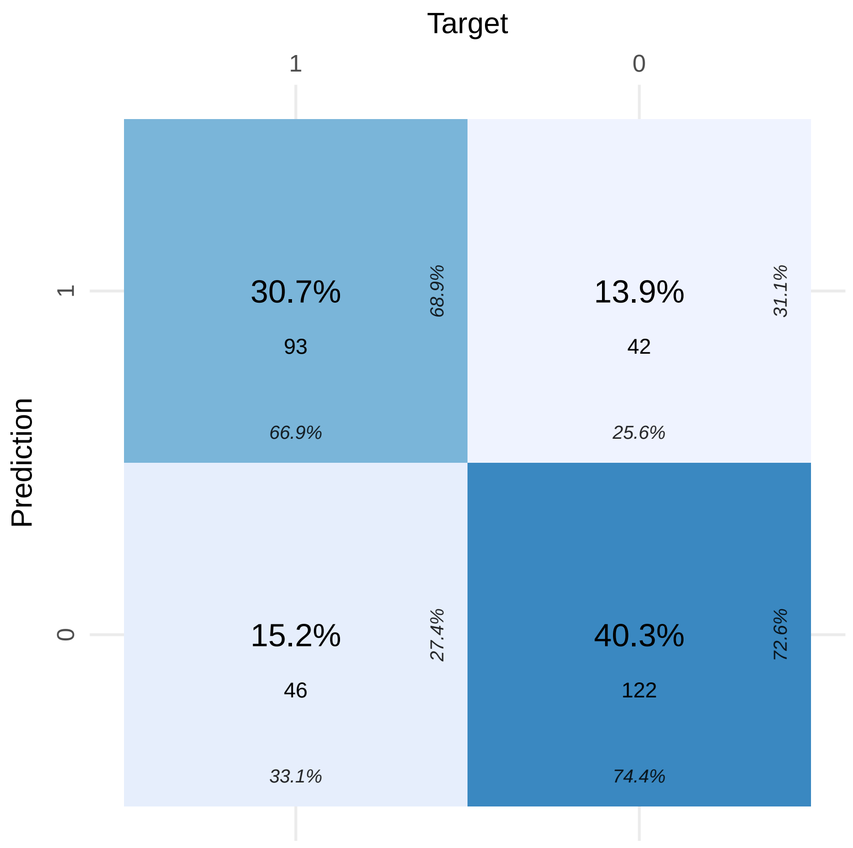
```
library(cvms)
library(tibble)   # tibble()
cm <- as_tibble(b_table)
cm
```

```
## # A tibble: 4 x 3
##   `True Status` `Predicted Status`     n
##   <chr>         <chr>              <int>
## 1 0             0                    122
## 2 1             0                     46
## 3 0             1                     42
## 4 1             1                     93
```

```
plot_confusion_matrix(cm,
                      target_col = "True Status",
                      prediction_col = "Predicted Status",
                      counts_col = "n")
```

```
## Warning in plot_confusion_matrix(cm, target_col = "True Status", prediction_col
## = "Predicted Status", : 'ggimage' is missing. Will not plot arrows and
## zero-shading.
```

```
## Warning in plot_confusion_matrix(cm, target_col = "True Status", prediction_col
## = "Predicted Status", : 'rsvg' is missing. Will not plot arrows and
## zero-shading.
```


Target
1
0
Prediction
1
0
30.7%
93
66.9%
68.9%
13.9%
42
25.6%
31.1%
15.2%
46
33.1%
27.4%
40.3%
122
74.4%
72.6%