Team 1:

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Setup

```
install.packages('readr', dependencies = TRUE, repos='http://cran.rstudio.com/')
## package 'readr' successfully unpacked and MD5 sums checked
## The downloaded binary packages are in
   C:\Users\wky\AppData\Local\Temp\Rtmp4KvxjM\downloaded_packages
library(readr)
library(data.table)
library(ggplot2)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:data.table':
##
##
       between, first, last
  The following objects are masked from 'package:stats':
##
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
CHD_raw <-read_csv("framingham.csv")</pre>
## Rows: 4238 Columns: 16
## -- Column specification -----
## Delimiter: ","
## dbl (16): male, age, education, currentSmoker, cigsPerDay, BPMeds, prevalent...
```

```
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Clean Data

```
CHD<-na.omit(CHD_raw)
colnames(CHD)[1] <- 'is_male'</pre>
```

EDA

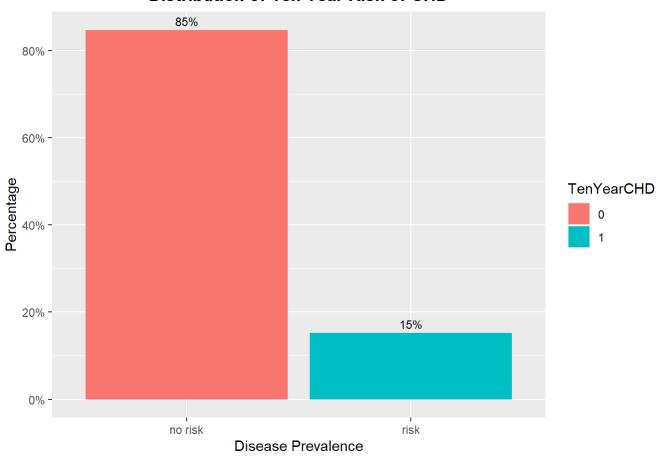
```
count1 <- length(which(CHD$TenYearCHD == 1))
count1</pre>
```

```
## [1] 557
```

```
count2 <- length(which(CHD$TenYearCHD == 0))
count2</pre>
```

```
## [1] 3099
```

Distribution of Ten Year Risk of CHD



```
#summary(CHD)
sapply(CHD, class)
```

```
##
           is_male
                                            education
                                                         currentSmoker
                                                                              cigsPerDay
                                 age
         "numeric"
                                            "numeric"
                                                                               "numeric"
                           "numeric"
                                                             "numeric"
##
##
             BPMeds prevalentStroke
                                         prevalentHyp
                                                              diabetes
                                                                                 totChol
##
          "numeric"
                           "numeric"
                                            "numeric"
                                                             "numeric"
                                                                               "numeric"
                               diaBP
                                                  BMI
                                                             heartRate
##
              sysBP
                                                                                 glucose
##
         "numeric"
                           "numeric"
                                            "numeric"
                                                             "numeric"
                                                                               "numeric"
        TenYearCHD
##
         "numeric"
##
```

```
CHD$agec <-
  cut(CHD$age, breaks = c(30,35,40,45,50,55,60,65,70),
      labels = c("30-35","35-40","40-45","45-50","50-55","55-60","60-65","65-70"))

d <- CHD %>% group_by(agec) %>% summarise(perc = mean(TenYearCHD=='1'))

d$perc_r <- round(d$perc,2)*100

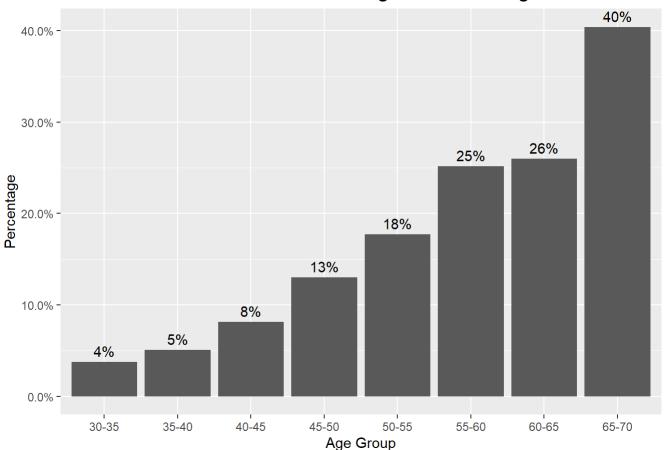
d$perc_r <- interaction(d$perc_r, "%", sep = "")

d</pre>
```

agec <fct></fct>	<pre>perc perc_r <dbl> <fct></fct></dbl></pre>
30-35	0.03773585 4%
35-40	0.05059022 5%
40-45	0.08126722 8%
45-50	0.13023952 13%
50-55	0.17704918 18%
55-60	0.25196850 25%
60-65	0.25990099 26%
65-70	0.40425532 40%
8 rows	

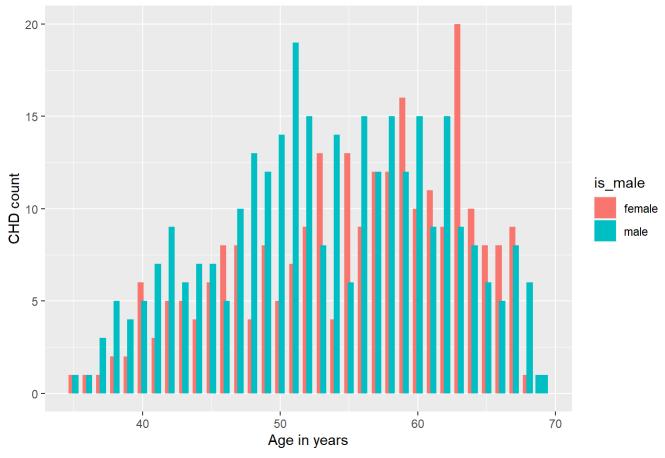
```
ggplot(d,aes(x=agec,y=perc)) +
geom_col()+
scale_y_continuous(labels=scales::percent)+
geom_text(aes(label = perc_r), vjust = -0.5)+
labs(x='Age Group',y='Percentage')+
ggtitle("Distribution of Percentage of CHD with Age")+
common_theme
```

Distribution of Percentage of CHD with Age



```
#cbPalette <- c("#999999", "#E69F00", "#56B4E9", "#009E73", #"#F0E442", "#0072B2", "#D55E00", "#
CC79A7")
CHD_1 <- CHD[ CHD$TenYearCHD=='1',]
CHD_1$is_male[CHD_1$is_male == 0] <- "female"
CHD_1$is_male[CHD_1$is_male == 1] <- "male"
ggplot(data=CHD_1,aes(age,fill=is_male))+
    geom_bar(position = position_dodge(width = 0.5))+
# scale_fill_brewer(palette=cbPalette)+
    labs(x = "Age in years",y = "CHD count")+
    ggtitle("Distribution of CHD with age and gender")+
    common_theme</pre>
```

Distribution of CHD with age and gender



d2 <- CHD %>% group_by(currentSmoker) %>% summarise(perc = mean(TenYearCHD=='1'))
d2

currentSmoker <dbl></dbl>	perc <dbl></dbl>
0	0.1456103
1	0.1593960
2 rows	

```
d3 <- CHD %>% group_by(agec,factor(is_male)) %>% summarise(perc = mean(TenYearCHD=='1'))
```

`summarise()` has grouped output by 'agec'. You can override using the `.groups` argument.

d3

agec <fct></fct>	factor(is_male) <fct></fct>	perc <dbl></dbl>
30-35	0	0.02941176
30-35	1	0.05263158
35-40	0	0.03833866
35-40	1	0.06428571
40-45	0	0.05958549
40-45	1	0.10588235
45-50	0	0.08571429
45-50	1	0.19081272
50-55	0	0.13142857
50-55	1	0.23846154
1-10 of 16 ro	WS	Previous 1 2 Next

```
ggplot() +
geom_line(data=d3,aes(agec, perc,group =`factor(is_male)`,color =`factor(is_male)` ))+
scale_y_continuous(labels=scales::percent)+
labs(x='Age Group',y='Percentage',color='Gender' )+
ggtitle("Distribution of Percentage of CHD with Age and Gender")+
common_theme
```

