WCGS data lab workbook

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this R Markdown file assumes you went through the Week 1 R Tutorial first

```r
library(ggplot2)
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
```

```r
library(readr)
library(epitools)
library(readr)
library(rmarkdown)
library(knitr)

data(wcgs)
```

```r
wcgs$dibpat0_fact <- factor(wcgs$dibpat0, ordered = TRUE, labels = c("A","B"))


wcgs$smoker0[wcgs$ncigs0 > 0] <- 1
wcgs$smoker0[wcgs$ncigs0 == 0] <- 0


wcgs$highsbp0[wcgs$sbp0 >= 140] <- 1
wcgs$highsbp0[wcgs$sbp0 < 140] <- 0


wcgs$heightcm0 <- round(wcgs$height0 * 2.54, digits = 2)
wcgs$weightkg0 <- round(wcgs$weight0/2.2, digits = 2)
wcgs$BMI0 <- round(wcgs$weightkg0/((wcgs$heightcm0/100)^2), digits = 1)
```

```
# Question 1 to turn in

# average cholesterol at baseline for smokers and non-smokers

wcgs %>% group_by(smoker0) %>% summarize(average = mean(sbp0))
```

```
## # A tibble: 2 x 2
##   smoker0 average
##     <dbl>   <dbl>
## 1       0    129.
## 2       1    129.
```

```
# create a factor variable out of the 4-level behavioral pattern variable, behpat0

wcgs$behpat0_fact <- factor(wcgs$behpat0,
                            ordered = TRUE,
                            labels = c("A", "some A", "mix A and B","B"))
```

```
# cut gives us a lot of flexibility
# in our specifications of the interval endpoints
# the intervals here are the commonly used ones

wcgs$bmi_cat <- cut(wcgs$BMI0,
                    breaks = c(0, 18.5, 25.0, 30.0, Inf),
                    include.lowest = TRUE,
                    right = FALSE,
                    ordered_results = TRUE,
                    labels = c("underweight", "normal", "overweight", "obese") )
```

```
wcgs$chd69 <- factor(wcgs$chd69, labels = c("No CHD", "CHD"))
```

```
# these are examples for additional tables

behpat_table <- table(wcgs$behpat0_fact)
addmargins(behpat_table)
```

```
##
##           A      some A mix A and B           B         Sum
##         264        1325        1216         349        3154
```

```
round(prop.table(behpat_table), digits = 3)
```

```
##
##           A      some A mix A and B           B
##       0.084       0.420       0.386       0.111
```

```
# table for behavioral pattern and chd

# the proportion option 1 asks for "row percents" in the two-way table
# this is Question 2 to turn in
```

```r
chd_behpat_table <- table(wcgs$behpat0_fact, wcgs$chd69)
addmargins(chd_behpat_table)
```

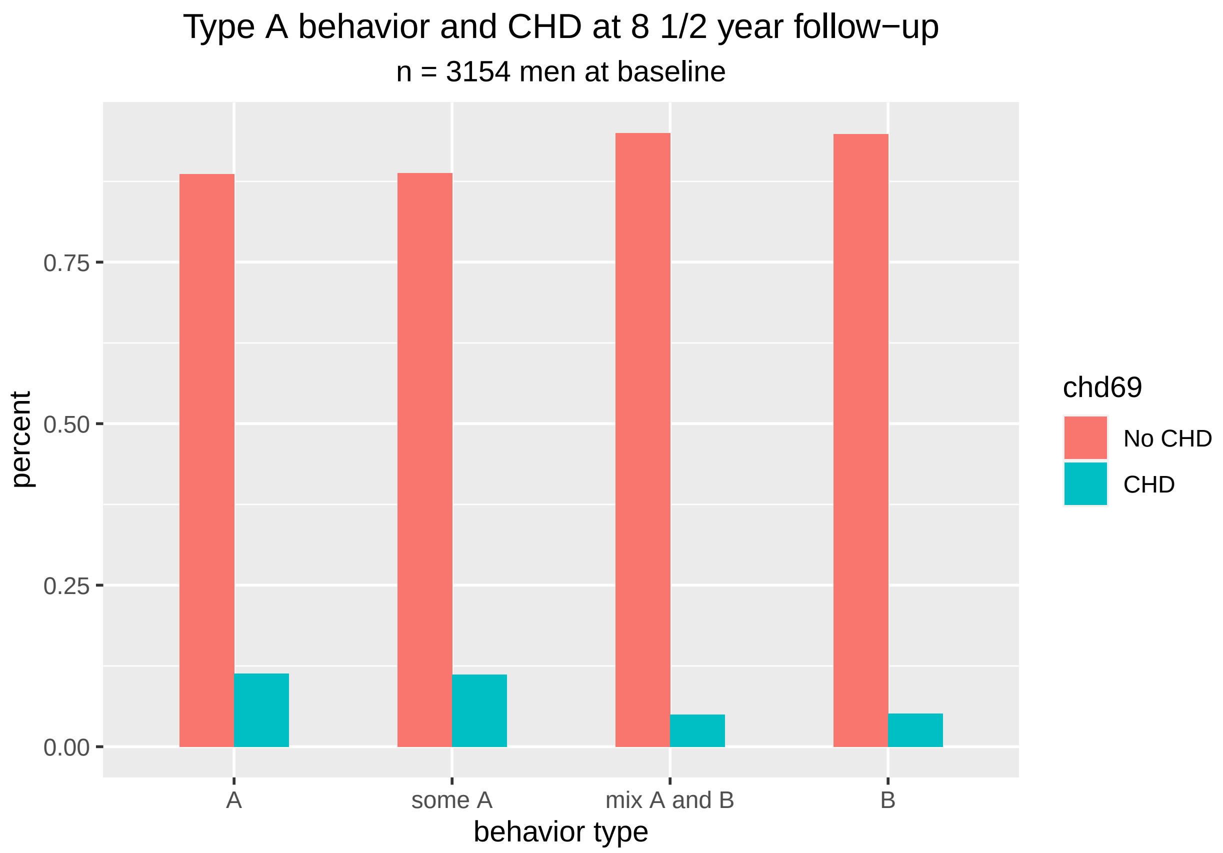
```
##
##                No CHD  CHD  Sum
##   A               234   30  264
##   some A         1177  148 1325
##   mix A and B    1155   61 1216
##   B               331   18  349
##   Sum            2897  257 3154
```

```r
round(prop.table(chd_behpat_table, 1), digits = 3)
```

```
##
##                No CHD   CHD
##   A             0.886 0.114
##   some A        0.888 0.112
##   mix A and B   0.950 0.050
##   B             0.948 0.052
```

```r
# this is Question 3 to turn in

wcgs %>% count(behpat0_fact, chd69) %>%
  group_by(behpat0_fact) %>%
  mutate(prop = n/sum(n))  %>%
  ggplot(aes(x = behpat0_fact, y = prop, fill = chd69)) +
  geom_bar(width = 0.5, stat = "identity", position = "dodge") +
  labs(y = "percent", x = "behavior type", title = "Type A behavior and CHD at 8 1/2 year follow-up",
       subtitle = "n = 3154 men at baseline") +
  theme(plot.title = element_text(hjust = 0.5), plot.subtitle = element_text(hjust = 0.5))
```



```r
# summary for BMI by CHD at 8 /12 yr follow-up

no_chd_summary <- summary(subset(wcgs, chd69 == "No CHD", select = BMI0))

chd_summary <- summary(subset(wcgs, chd69 == "CHD", select = BMI0))

no_chd_summary
```

```
##       BMI0
##  Min.   :11.20
##  1st Qu.:22.90
##  Median :24.40
##  Mean   :24.53
##  3rd Qu.:25.90
##  Max.   :37.70
```

```r
chd_summary
```

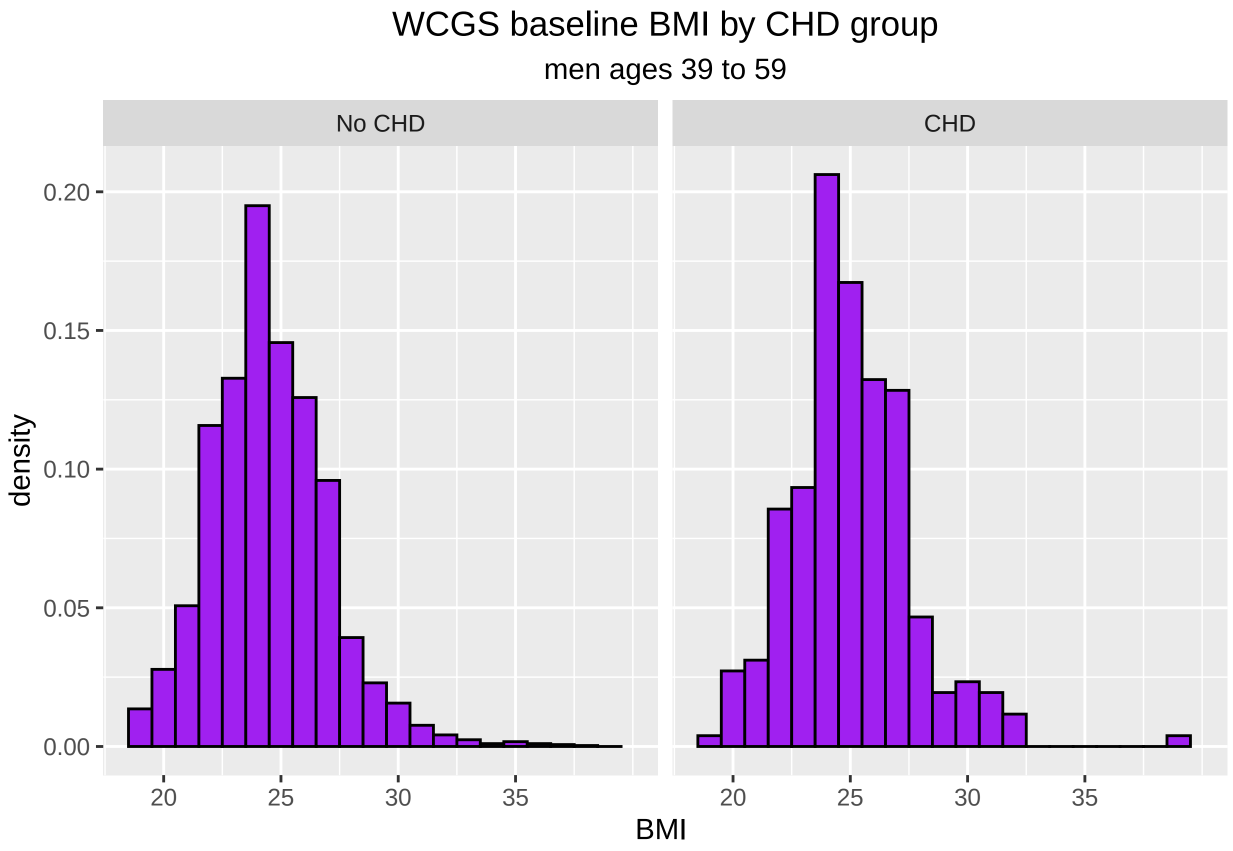
```
##       BMI0
##  Min.   :19.30
##  1st Qu.:23.70
##  Median :24.90
##  Mean   :25.11
##  3rd Qu.:26.60
##  Max.   :39.00
```

```
#use facet wrap to get side by side histgrams for baseline BMI by CHD

ggplot(wcgs, aes(x = BMI0, y = ..density..)) +
  geom_histogram(binwidth = 1, color = "black", fill = "purple") +
  facet_wrap(.~wcgs$chd69) +
  labs(title = "WCGS baseline BMI by CHD group",
       subtitle = "men ages 39 to 59",
       x = "BMI ",
       y = "density" ) +
  scale_x_continuous(limits = c(18.5, 40),
                     breaks = c(20, 25, 30, 35),
                     labels = c(20, 25, 30, 35)) +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```

```
## Warning: Removed 20 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```


WCGS baseline BMI by CHD group
men ages 39 to 59
No CHD
CHD
density
BMI