

Session 3: How can I perform univariate analysis?

A Slower Introduction to R

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Arguments

The NA mean

- from last week:

```
mean(nhanes$bpxodi1)
#|  [1] NA
class(nhanes$bpxodi1)
#|  [1] "integer"
head(nhanes$bpxodi1)
#|  [1] 98 84 79 NA NA 72
```

The help pages

- to access the help page for a function, use the `help()` function:

```
> help(sqrt)
```

- or, equivalently, use `?:`

```
> ?sqrt
```

Live demonstration

Function arguments in `sqrt()`

- you can optionally type `x=` when you use `sqrt()`:

```
sqrt(x=81)  
#| [1] 9
```

- or, you can continue to omit it:

```
sqrt(81)  
#| [1] 9
```

- `x` is known as an argument

What are function arguments?

- you may think of arguments as being like **options** or settings
- using another cooking analogy, suppose that **baking** is a function
 - we can think of the temperature setting on the oven as an argument to the function
 - **what's another possible argument to baking?**

What are function arguments?

```
sqrt(x=81)  
#| [1] 9
```

- 81 is the argument value
- x is the argument name

Function arguments in mean()

Usage

```
mean(x, ...)
```

```
## Default S3 method:
```

```
mean(x, trim = 0, na.rm = FALSE, ...)
```

Arguments

<code>x</code>	an R object. Currently there are methods for numeric objects. Complex vectors are allowed for <code>trim = 0</code>
<code>trim</code>	the fraction (0 to 0.5) of observations to be trimmed from each end of the sorted data. Values of <code>trim</code> outside that range are taken as the nearest value in the range.
<code>na.rm</code>	a logical evaluating to TRUE or FALSE indicating whether <code>NA</code> values should be removed before the computation proceeds.

- notice the **commas** and the **default values**

Function arguments in `mean()`

- the `na.rm` argument is:

a logical evaluating to TRUE or FALSE indicating whether NA values should be stripped before the computation proceeds.

- the Usage section (previous slide) shows that the default value for `na.rm` is `FALSE`, suggesting that NA values will not be “stripped”

The missing mean

```
mean(nhanes$bpxodi1, na.rm=TRUE)  
#|  [1] 74.97469
```



The missing mean

```
mean(nhanes$bpxodi1, na.rm=TRUE)
#|  [1] 74.97469
```

- notice that I've used a comma to separate the two arguments
- TRUE must be in all caps
- na.rm=TRUE does not delete missing values from your data
- all it does is make mean() ignore missing values

na.rm



The `na.rm` argument **does not** exist in every R function!

- most of the functions in the next section have an `na.rm` argument
- but, for example, the function for linear regression, `lm()`, **does not** have an `na.rm` argument

When should I include argument names?

```
sqrt(x=81)
#| [1] 9
sqrt(81)
#| [1] 9
```

- if there is just one argument, the argument name is optional

When should I include argument names?

```
mean(nhanes$bpxodi1, na.rm=TRUE)  
#| [1] 74.97469
```

- if there is more than one argument, you should include argument names if:
 - you skip an argument
 - or, write the arguments out of order

When should I include argument names?

```
sd(nhanes$bpxodi1, TRUE)
#| [1] 11.41659
sd(nhanes$bpxodi1, na.rm=TRUE)
#| [1] 11.41659
```

- regardless of the considerations on the prior slides, including argument names can **improve the readability of your code**

Writing across multiple lines

- when writing across multiple lines, type the comma before the line break:

```
mean(nhanes$bpxodi1,  
     na.rm=TRUE)
```

Exercise 1

Exercise 1

1. Open the help page for the `quantile()` function, which you'll use in Exercise 2 to find percentiles of continuous variables.
2. What is the name of the second argument?
3. Does the function support the `na.rm` argument?

Summarizing continuous variables

What is a continuous variable?

- continuous variable = a variable that has numeric values
- examples:
 - age
 - height
 - systolic blood pressure

Means, standard deviations, and variances

```
mean(nhanes$bpxodi1, na.rm=TRUE)
#|  [1] 74.97469
sd(nhanes$bpxodi1, na.rm=TRUE)
#|  [1] 11.41659
var(nhanes$bpxodi1, na.rm=TRUE)
#|  [1] 130.3386
```

Percentiles

```
median(nhanes$bpxodi1, na.rm=TRUE)
#|  [1] 74
quantile(nhanes$bpxodi1, probs=0.5, na.rm=TRUE)
#|  50%
#|   74
quantile(nhanes$bpxodi1, 0.5, na.rm=TRUE)
#|  50%
#|   74
```

Percentiles

```
quantile(nhanes$bpxodi1,0.25,na.rm=TRUE)
#| 25%
#| 67
quantile(nhanes$bpxodi1,0.75,na.rm=TRUE)
#| 75%
#| 82
```

Percentiles

```
> quantile(nhanes$bpxodi1,c(0.25,0.5,0.75),na.rm=TRUE)
25% 50% 75%
 67  74  82
```

- in the second argument, we've used the `c()` function to create a **vector** containing 3 values

Minimum and maximum values

```
min(nhanes$bpxodi1,na.rm=TRUE)
#|  [1] 36
max(nhanes$bpxodi1,na.rm=TRUE)
#|  [1] 142
range(nhanes$bpxodi1,na.rm=TRUE)
#|  [1] 36 142
```

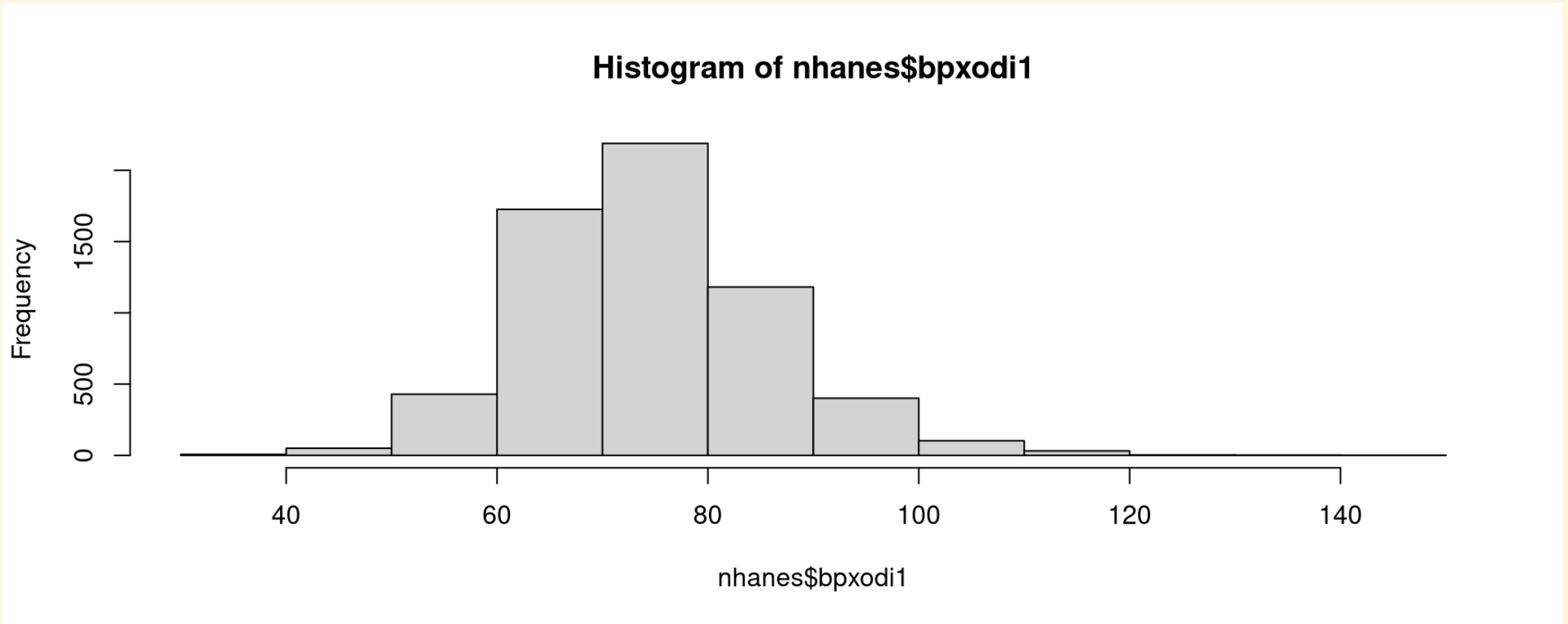
summary()

```
summary(nhanes$bpxodi1)
```

#	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
#	36.00	67.00	74.00	74.97	82.00	142.00	2030

Histograms

```
hist(nhanes$bpxodi1)
```

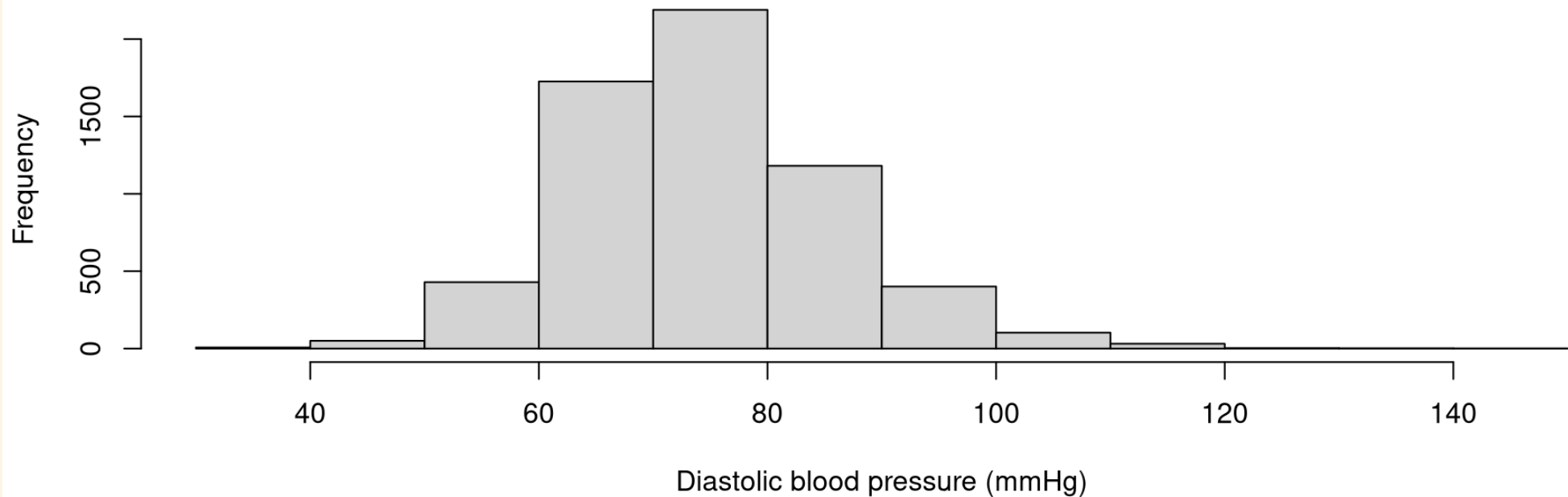


Histogram titles and labels

- `main`: the title at the top
- `xlab`: the label on the x axis

Histograms titles and labels

```
hist(nhanes$bpxodi1,main='',xlab='Diastolic blood pressure (mmHg)')
```



Histogram bars

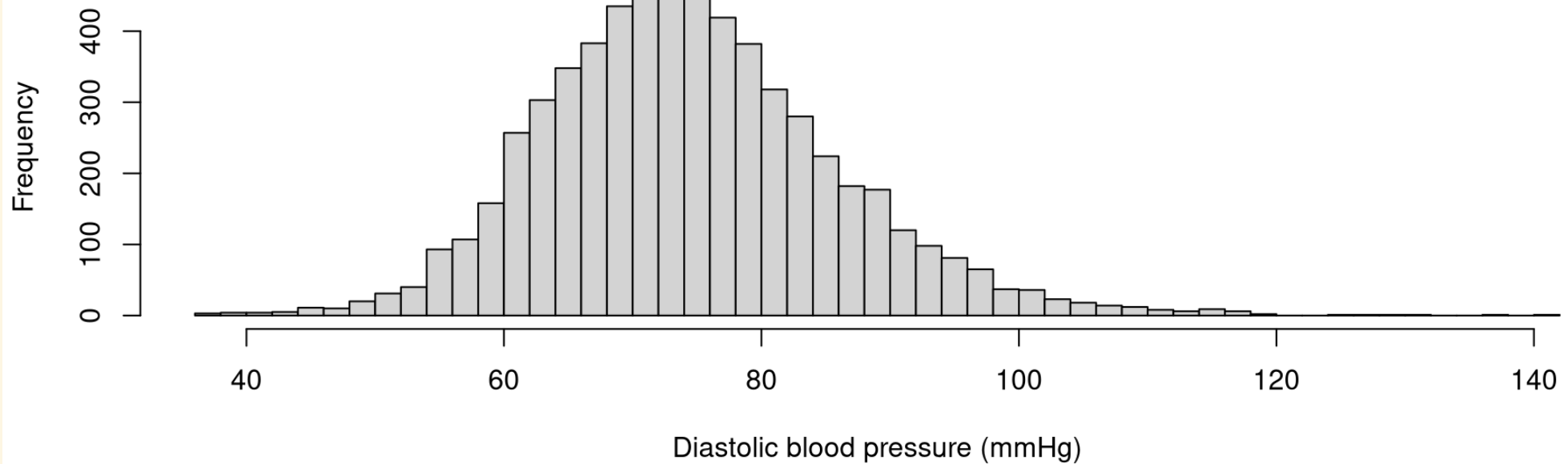
- to set the number of bars in the histogram, use the `breaks` argument

```
hist(nhanes$bpxodi1,main='',xlab='Diastolic blood pressure (mmHg)',breaks=50)
```

When you use `breaks` in this way, you won't always get exactly the number of bars you

Histograms bars

```
hist(nhanes$bpxodi1,main='',xlab='Diastolic blood pressure (mmHg)',breaks=50)
```



Quotes in function arguments



Tip

If a function argument needs to be in quotes, you can use single quotes or double quotes.

```
hist(nhanes$bpxodi1,main='',xlab="Diastolic blood pressure (mmHg)",breaks=50)
```

- if you start with a single quote, you must end with a single quote
- and, if you start with a double quote, you must end with a double quote

Exercise 2

Exercise 2

Across the exercises today, you'll build an R script that will import the NHANES data and perform some univariate analysis. You'll also practice going back and forth between the console and your script.

1. **At the top of a new script**, include code for importing the data. Hopefully, you already copied and pasted code for doing this from last week. If you didn't, re-obtain the code by using RStudio's import tool. Add a comment above that code. Run that code.

Exercise 2

2. In the console or the script, write code for displaying a histogram of fasting glucose (`lbg1u`). Now do this again, specifying that you want to use 60 bins. Feel free to try other numbers of bins.
3. A common threshold for a health level of fasting glucose is 100 mg/dL. In the console or the script, add a red vertical line to your histogram at that threshold:
`abline(v=100,col='red')`.

Exercise 2

4. In the script, type code for finding the mean level of fasting glucose. Add a comment above that code. Run that code.
5. In the script, type code for finding the 25th, 50th, and 75th percentiles of fasting glucose. Add a comment above that code. Run that code.

Confidence intervals for population means

Confidence interval for mean diastolic blood pressure

- what is a **95% confidence interval** for the mean diastolic blood pressure in the US adult population?

```
t.test(nhanes$bpxodi1)
#|
#|      One Sample t-test
#|
#| data:  nhanes$bpxodi1
#| t = 513.88, df = 6122, p-value < 2.2e-16
#| alternative hypothesis: true mean is not equal to 0
#| 95 percent confidence interval:
#|   74.68867 75.26070
#| sample estimates:
#| mean of x
#|   74.97469
```

Function values

- `t.test()` prints a summary report
- it is possible to extract specific values

Function values

Value

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the t-statistic.
<code>parameter</code>	the degrees of freedom for the t-statistic.
<code>p.value</code>	the p-value for the test.
<code>conf.int</code>	a confidence interval for the mean and standard deviation.
<code>estimate</code>	the estimated mean or difference in means for a one-sample test or a two-sample test.
<code>null.value</code>	the specified hypothesized value of the population mean (for a one-sample test) or the specified hypothesized value of the population difference in means (for a two-sample test).
<code>stderr</code>	the standard error of the mean (difference).

Function values

```
diastolic_ci<-t.test(nhanes$bpxodi1)
names(diastolic_ci)
#|    [1] "statistic"    "parameter"    "p.value"      "conf.int"     "estimate"
#|    [6] "null.value"   "stderr"       "alternative"  "method"       "data.name"
```

Extracting function values

```
diastolic_ci$estimate
#|  mean of x
#|  74.97469
diastolic_ci$conf.int
#|  [1] 74.68867 75.26070
#|  attr(,"conf.level")
#|  [1] 0.95
```

Summarizing categorical variables

What is a categorical variable?

- categorical variable = a variable that has groups
- examples:
 - age group
 - level of educational attainment
 - exposure (yes or no)
 - disease (yes or no)
- variables with two groups are known as dichotomous variables

Hypertension

```
class(nhanes$hypertension)
#|  [1] "character"
head(nhanes$hypertension)
#|  [1] "Stage 2" "Stage 1" "No"      NA      NA      "No"
```

Counts

```
table(nhanes$hypertension)
```

```
#|
```

```
#| Elevated      No  Stage 1  Stage 2
```

```
#|          841    2657      1409      1216
```

Missing values?

- what about the missing values?

The help page for `table()`

Arguments

<code>...</code>	one or more objects which can be factors (or character strings), or a <u>list</u> (such as a data frame) as <code>.table</code> , arguments passed to <code>summary</code> .
<code>exclude</code>	levels to remove for all factors in <code>.table</code> . If <code>exclude = "ifany"</code> , it implies <code>useNA = "ifany"</code> . See <code>summary</code> .
<code>useNA</code>	whether to include NA values in the output. If <code>useNA = "ifany"</code> , it implies <code>exclude = "ifany"</code> . See <code>summary</code> .
<code>dnn</code>	the names to be given to the dimensions of the array.
<code>deparse.level</code>	controls how the default <code>dnn</code> is constructed.

The help page for `table()`

- the `useNA` argument can be used to control:
 - | whether to include NA values in the table

Counts

```
table(nhanes$hypertension,useNA='always')
#|
#| Elevated      No  Stage 1  Stage 2    <NA>
#|      841     2657     1409     1216    2030
table(nhanes$hypertension,useNA='ifany')
#|
#| Elevated      No  Stage 1  Stage 2    <NA>
#|      841     2657     1409     1216    2030
```

Percents

```
prop.table(table(nhanes$hypertension,useNA='always'))  
#|  
#|    Elevated          No    Stage 1    Stage 2      <NA>  
#| 0.1031522 0.3258923 0.1728198 0.1491476 0.2489881
```

- notice that you must put `table()` inside of `prop.table()`

Percents

- without the NA included:

```
prop.table(table(nhanes$hypertension))  
#|  
#|      Elevated      No      Stage 1      Stage 2  
#| 0.1373510 0.4339376 0.2301160 0.1985955
```

Percents

- on a percent scale:

```
prop.table(table(nhanes$hypertension,useNA='always'))*100
#|
#| Elevated      No Stage 1 Stage 2      <NA>
#| 10.31522 32.58923 17.28198 14.91476 24.89881
```

Percents

```
prop.table(table(nhanes$hypertension))*100
```

```
#|
```

```
#| Elevated      No Stage 1 Stage 2
```

```
#| 13.73510 43.39376 23.01160 19.85955
```

Exercise 3

Exercise 3

1. In the script from Exercise 2, write code for obtaining the percent of adults who have a history of smoking (`smoking`). Add a comment above that code. Run that code.
2. In the script, write code for obtaining the percent of adults who have a history of asthma (`asthma`). Add a comment above that code. Run that code.

Exercise 3

3. Select all of the text and code in your script. You can optionally use a keyboard shortcut: **ctrl + A** on Windows machines or **cmd + A** on Mac machines. Run the code, and verify that your computer reproduced all of the work.