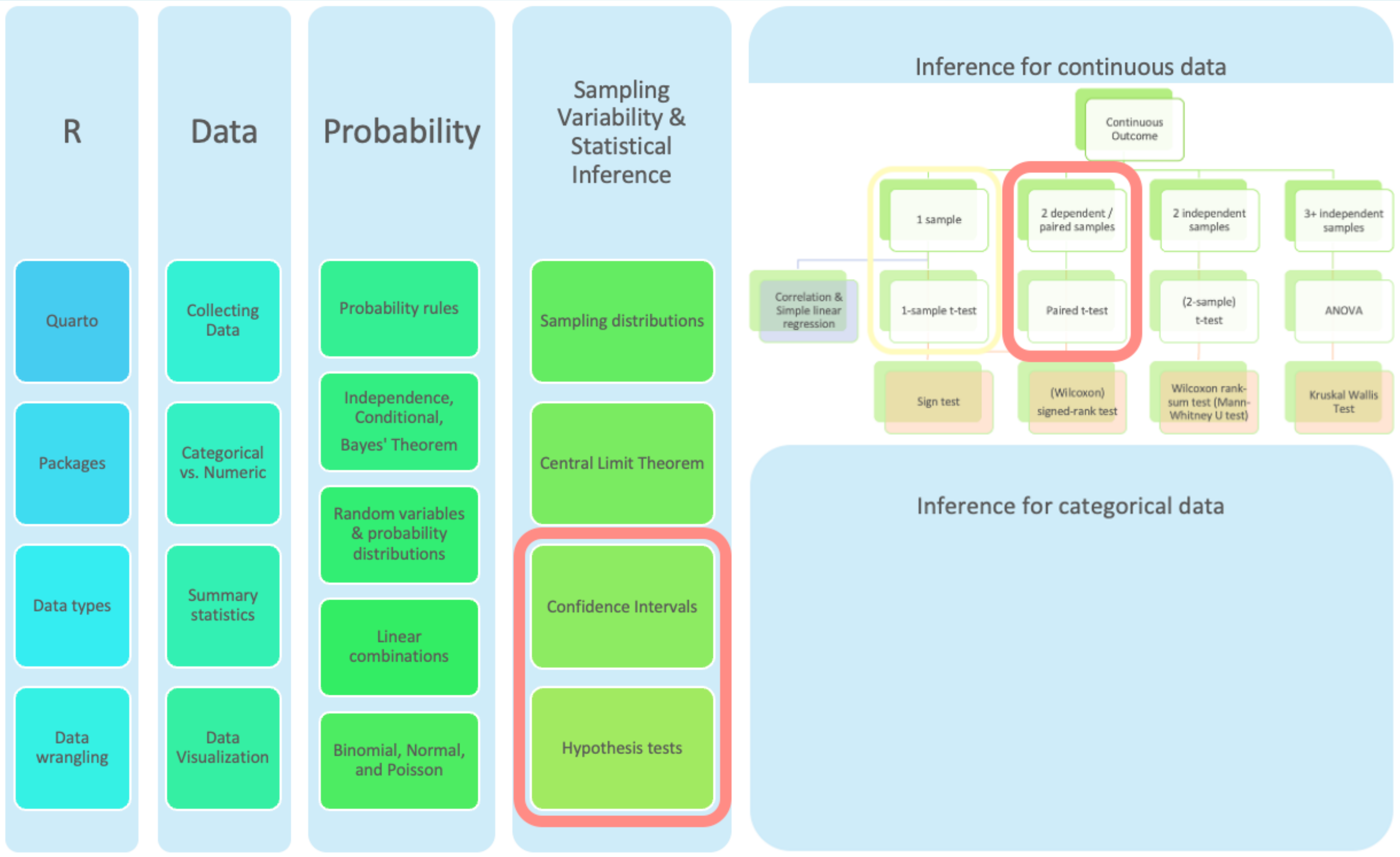
Day 10 Part 2: Inference for mean difference from two-sample dependent/paired data (Section 5.2)

BSTA 511/611

Meike Niederhausen, PhD
OHSU-PSU School of Public Health

2023-11-01

Where are we?



R

Quarto

Packages

Data types

Data wrangling

Data

Collecting Data

Categorical vs. Numeric

Summary statistics

Data Visualization

Probability

Probability rules

Independence, Conditional, Bayes' Theorem

Random variables & probability distributions

Linear combinations

Binomial, Normal, and Poisson

Sampling Variability & Statistical Inference

Sampling distributions

Central Limit Theorem

Confidence Intervals

Hypothesis tests

Inference for continuous data

Continuous Outcome

1 sample

2 dependent / paired samples

2 independent samples

3+ independent samples

Correlation & Simple linear regression

1-sample t-test

Paired t-test

(2-sample) t-test

ANOVA

Sign test

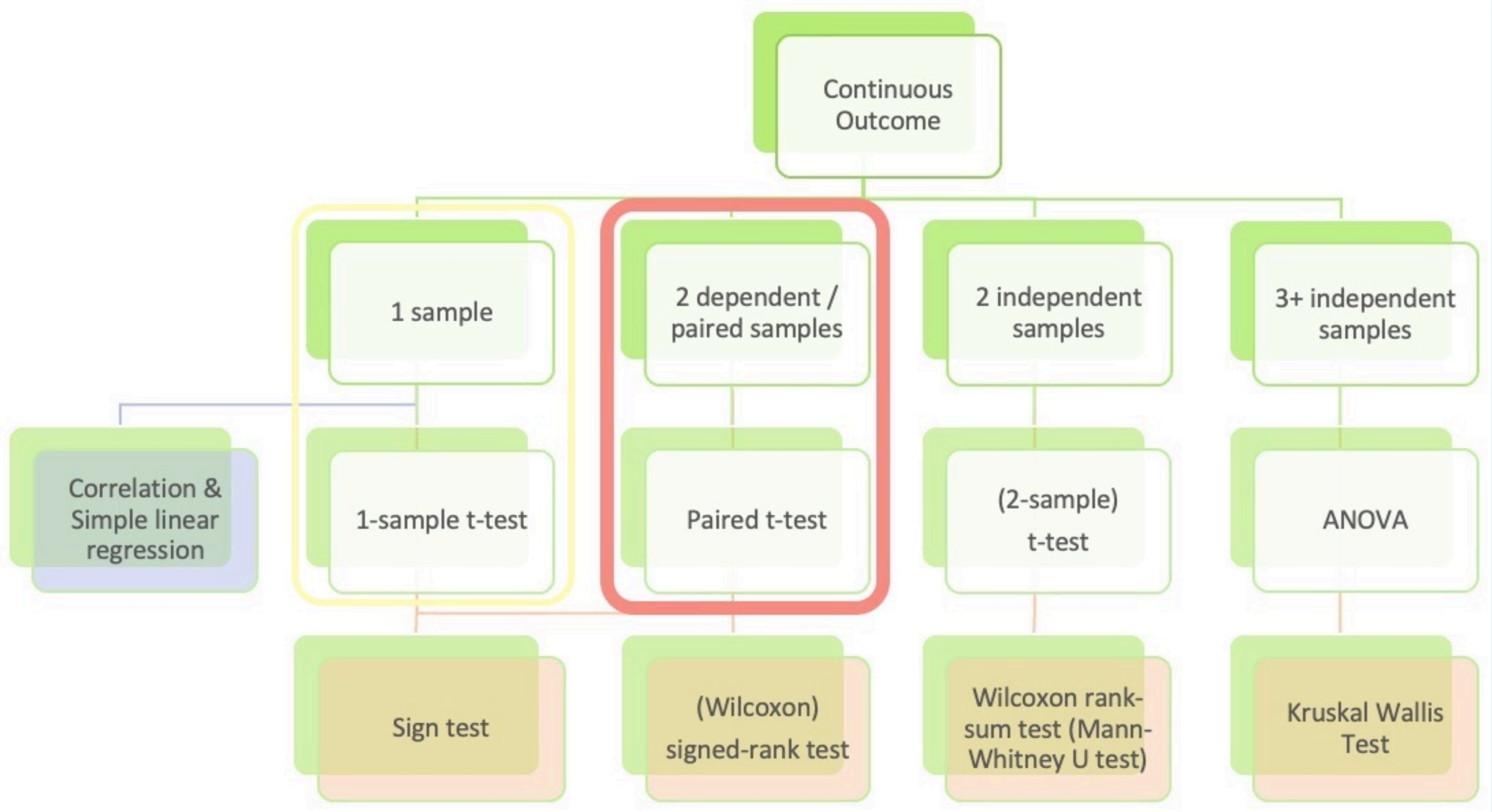
(Wilcoxon) signed-rank test

Wilcoxon rank-sum test (Mann-Whitney U test)

Kruskal Wallis Test

Inference for categorical data

Where are we? Continuous outcome zoomed in



What we covered in Day 10 Part 1

(4.3, 5.1) Hypothesis testing for mean from one sample

- Introduce hypothesis testing using the case of analyzing a mean from one sample (group)

- Steps of a hypothesis test:
  1. level of significance
  2. null (H_0) and alternative (H_A) hypotheses
  3. test statistic
  4. p-value
  5. conclusion

- Run a hypothesis test in R
  - Load a dataset - need to specify location of dataset
  - R projects
  - Run a t-test in R
  - `tidy()` the test output using `broom` package

(4.3.3) Confidence intervals (CIs) vs. hypothesis tests

Goals for today: Part 2 - Class discussion

(5.2) Inference for **mean difference** from dependent/paired 2 samples

- Inference: CIs and hypothesis testing
- Exploratory data analysis (EDA) to visualize data
- Run paired t-test in R

One-sided CIs

Class discussion

- Inference for the mean difference from dependent/paired data is a special case of the inference for the mean from just one sample, that was already covered.
- Thus this part will be used for class discussion to practice CIs and hypothesis testing for one mean and apply it in this new setting.
- In class I will briefly introduce this topic, explain how it is similar and different from what we already covered, and let you work through the slides and code.

CI's and hypothesis tests for different scenarios:

$$\text{point estimate} \pm z^*(or\ t^*) \cdot SE, \quad \text{test stat} = \frac{\text{point estimate} - \text{null value}}{SE}$$

Day	Book	Population parameter	Symbol	Point estimate	Symbol	SE
10	5.1	Pop mean	μ	Sample mean	$\bar{x}$	$\frac{s}{\sqrt{n}}$
10	5.2	Pop mean of paired diff	μ_d or δ	Sample mean of paired diff	$\bar{x}_d$	???
11	5.3	Diff in pop means	$\mu_1 - \mu_2$	Diff in sample means	$\bar{x}_1 - \bar{x}_2$	
12	8.1	Pop proportion	p	Sample prop	$\widehat{p}$	
12	8.2	Diff in pop proportions	$p_1 - p_2$	Diff in sample proportions	$\widehat{p}_1 - \widehat{p}_2$	

Steps in a Hypothesis Test

1. Set the **level of significance** α
2. Specify the **null** (H_0) and **alternative** (H_A) **hypotheses**
    1. In symbols
    2. In words
    3. Alternative: one- or two-sided?
3. Calculate the **test statistic**.
4. Calculate the **p-value** based on the observed test statistic and its sampling distribution
5. Write a **conclusion** to the hypothesis test
    1. Do we reject or fail to reject H_0?
    2. Write a conclusion in the context of the problem

Examples of paired designs (two samples)

- Enroll pairs of identical twins to study a disease
- Enroll father & son pairs to study cholesterol levels
- Studying pairs of eyes
- Enroll people and collect data before & after an intervention (longitudinal data)
- Textbook example: Compare maximal speed of competitive swimmers wearing a wetsuit vs. wearing a regular swimsuit
  - WIll use these data on homework

Come up with 2 more examples of paired study designs.

Can a vegetarian diet change cholesterol levels?

- **Scenario**:
  - 24 non-vegetarian people were enrolled in a study
  - They were instructed to adopt a vegetarian diet
  - Cholesterol levels were measured before and after the diet
- **Question**: Is there evidence to support that cholesterol levels changed after the vegetarian diet?
- How to answer the question?
  - First, calculate changes (differences) in cholesterol levels
    - We usually do after - before if the data are longitudinal

Calculate **CI for the mean difference** δ:

$$\bar{x}_d \pm t^* \cdot \frac{s_d}{\sqrt{n}}$$

Run a **hypothesis test**

Hypotheses

$$H_0 : \delta = \delta_0$$
$$H_A : \delta \neq \delta_0$$
$$(or \;\; <, >)$$

Test statistic

$$t_{\bar{x}_d} = \frac{\bar{x}_d - \delta_0}{\frac{s_d}{\sqrt{n}}}$$

EDA: Explore the cholesterol data

- Scenario:
    - 24 non-vegetarian people were enrolled in a study
    - They were instructed to adopt a vegetarian diet
    - Cholesterol levels were measured before and after the diet

```r
chol <- read_csv(here::here("data", "chol213.csv"))
glimpse(chol)
```

```
Rows: 24
Columns: 2
$ Before <dbl> 195, 145, 205, 159, 244, 166, 250, 236, 192, 224, 238, 197, 169…
$ After  <dbl> 146, 155, 178, 146, 208, 147, 202, 215, 184, 208, 206, 169, 182…
```

```r
chol %>%
  get_summary_stats(type = "common") %>%
  gt()
```

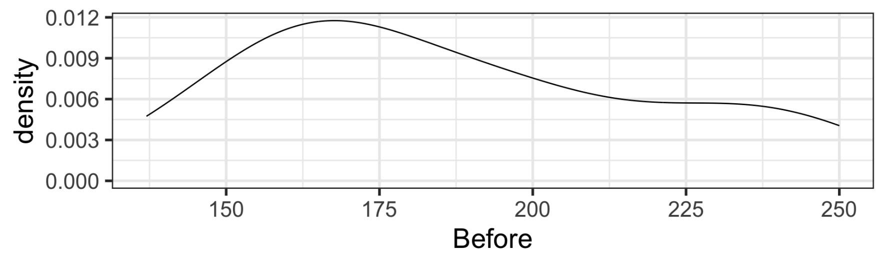
variable	n	min	max	median	iqr	mean	sd	se	ci
Before	24	137	250	179	44.5	187.792	33.160	6.769	14.002
After	24	125	215	165	38.0	168.250	26.796	5.470	11.315

Make sure you are able to load the data on your computer!

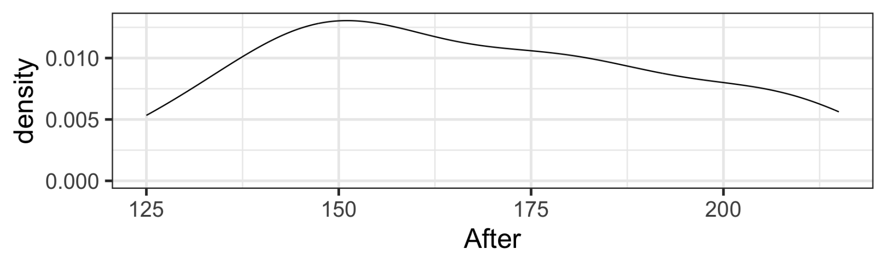
EDA: Cholesterol levels before and after vegetarian diet

Describe the distributions of the before & after data.

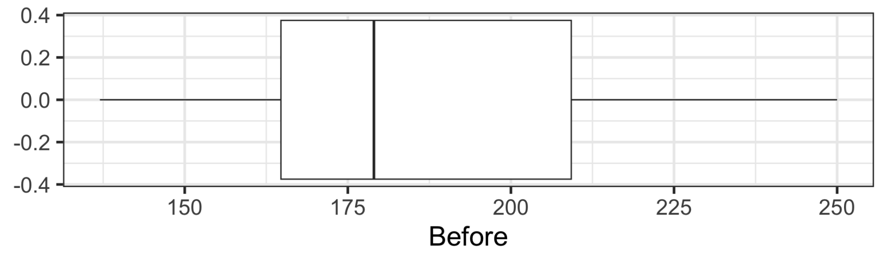
```r
ggplot(chol, aes(x=Before)) +
  geom_density()
```



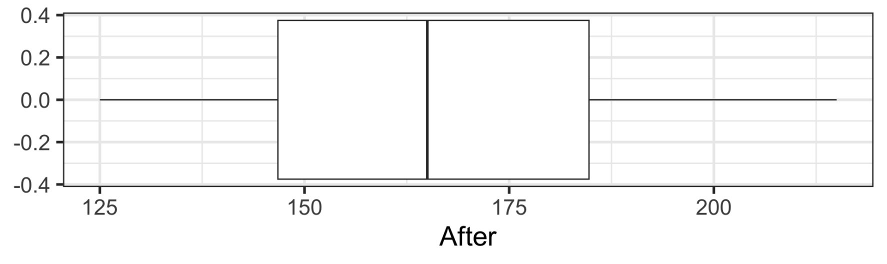
```r
ggplot(chol, aes(x=After)) +
  geom_density()
```



```r
ggplot(chol, aes(x=Before)) +
  geom_boxplot()
```



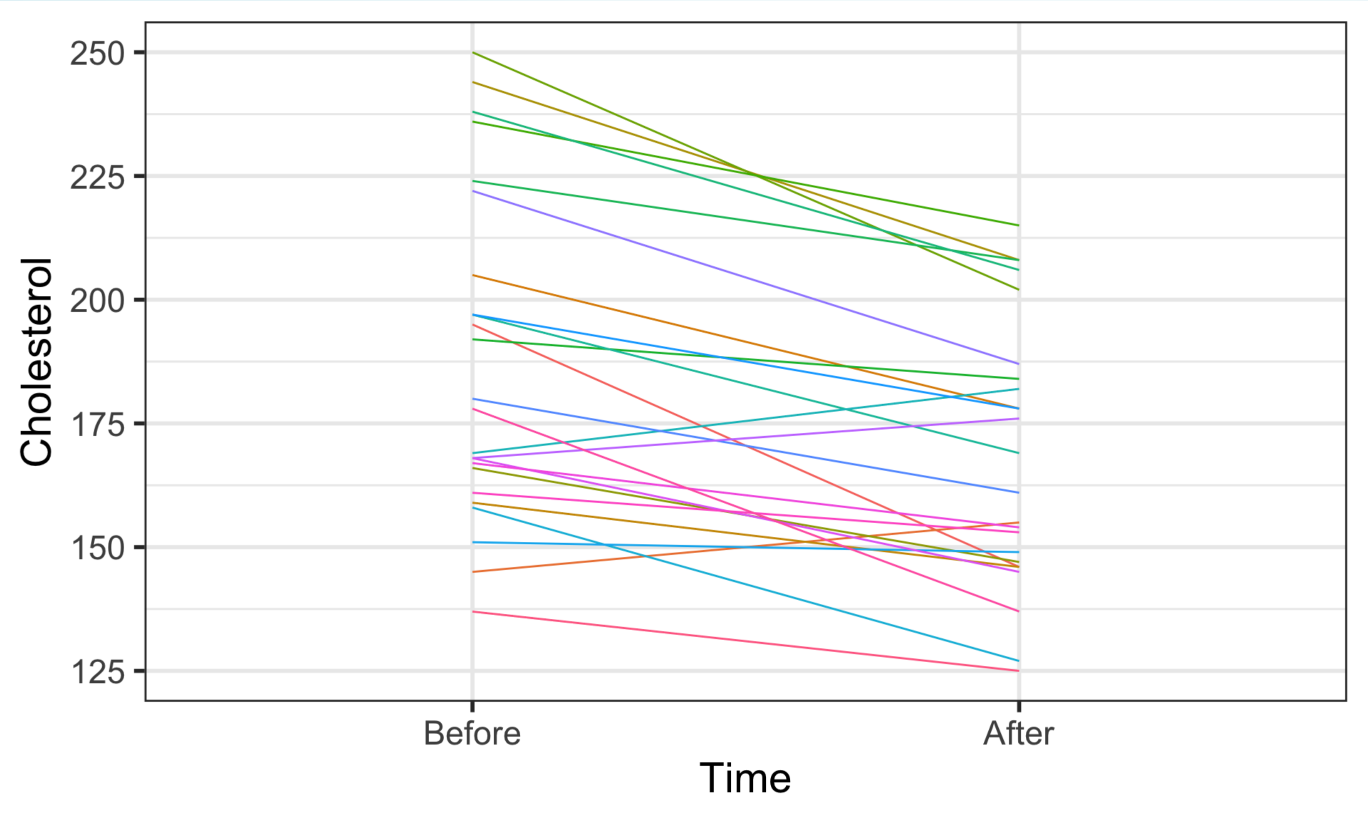
```r
ggplot(chol, aes(x=After)) +
  geom_boxplot()
```



EDA: Spaghetti plot of cholesterol levels before & after diet

- Visualize the individual before vs. after diet changes in cholesterol levels

What does this figure tell us?



- See code file for how to wrangle the data and create the figure - *you will not be expected to do this yourself*.

EDA: Differences in cholesterol levels: After - Before diet

What is this code doing?

```r
chol <- chol %>%
  mutate(DiffChol = After-Before)
head(chol, 8)
```

```
# A tibble: 8 × 3
  Before After DiffChol
   <dbl> <dbl>    <dbl>
1    195   146      -49
2    145   155       10
3    205   178      -27
4    159   146      -13
5    244   208      -36
6    166   147      -19
7    250   202      -48
8    236   215      -21
```

Is the mean of DiffChol the same as the difference in means of After - Before? Should it be? Why or why not?

```r
chol %>%
  get_summary_stats(type = "common") %>%
  gt()
```

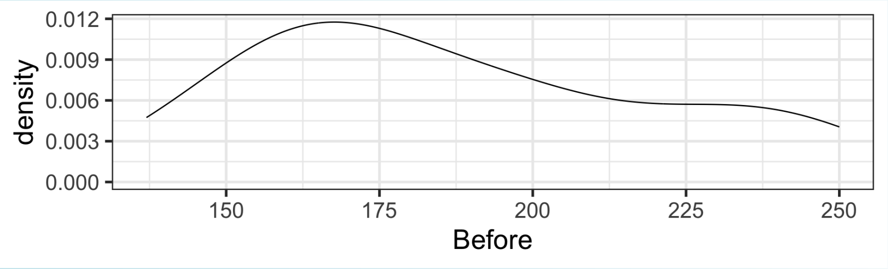
variable	n	min	max	median	iqr	mean	sd	se	ci
Before	24	137	250	179	44.50	187.792	33.160	6.769	14.002
After	24	125	215	165	38.00	168.250	26.796	5.470	11.315
DiffChol	24	-49	13	-19	20.25	-19.542	16.806	3.430	7.096

EDA: Differences in cholesterol levels: After - Before diet

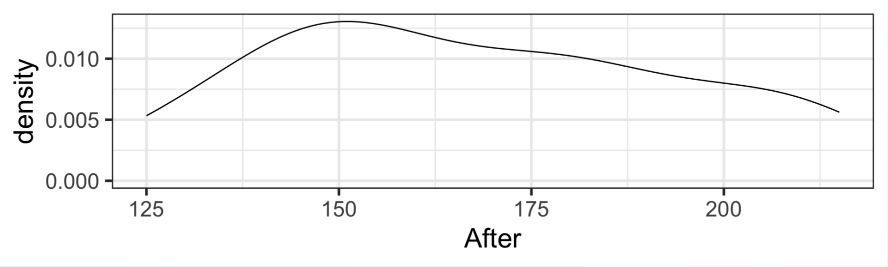
Compare and contrast the 3 distributions. Comment on shape, center, and spread.

Before & After

```
ggplot(chol, aes(x=Before)) +
  geom_density()
```

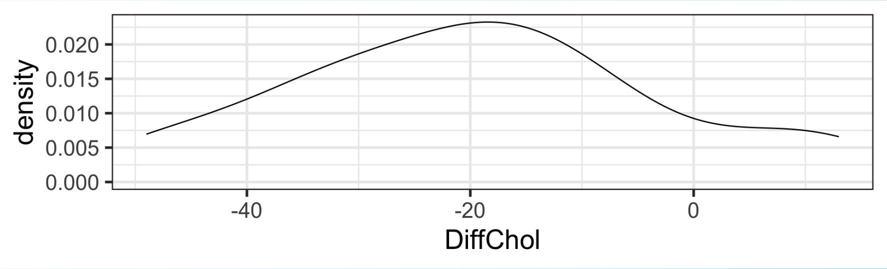


```
ggplot(chol, aes(x=After)) +
  geom_density()
```

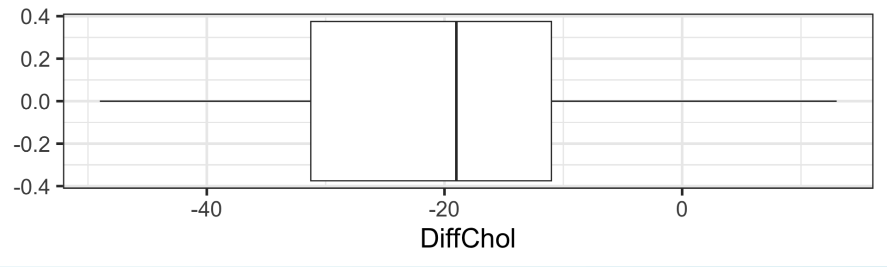


DiffChol

```
ggplot(chol, aes(x=DiffChol)) +
  geom_density()
```



```
ggplot(chol, aes(x=DiffChol)) +
  geom_boxplot()
```



Steps in a Hypothesis Test

1. Set the **level of significance** α
2. Specify the **null** (H_0) and **alternative** (H_A) **hypotheses**
    1. In symbols
    2. In words
    3. Alternative: one- or two-sided?
3. Calculate the **test statistic**.
4. Calculate the **p-value** based on the observed test statistic and its sampling distribution
5. Write a **conclusion** to the hypothesis test
    1. Do we reject or fail to reject H_0?
    2. Write a conclusion in the context of the problem

Step 2: Null & Alternative Hypotheses

- **Question**: Is there evidence to support that cholesterol levels changed after the vegetarian diet?

Null and alternative hypotheses in **words** Include as much context as possible

- H_0: The population mean difference in cholesterol levels after a vegetarian diet is *fill in*
- H_A: The population mean difference in cholesterol levels after a vegetarian diet is *fill in*

Null and alternative hypotheses in **symbols**

fill in the missing parts of the hypotheses.

$$H_0 : \delta =$$
$$H_A : \delta$$

Step 3: Test statistic

```r
chol %>% select(DiffChol) %>% get_summary_stats(type = "common") %>% gt()
```

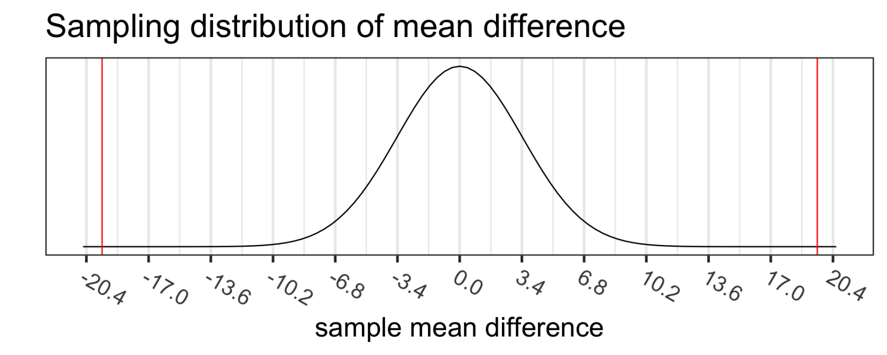
variable	n	min	max	median	iqr	mean	sd	se	ci
DiffChol	24	-49	13	-19	20.25	-19.542	16.806	3.43	7.096

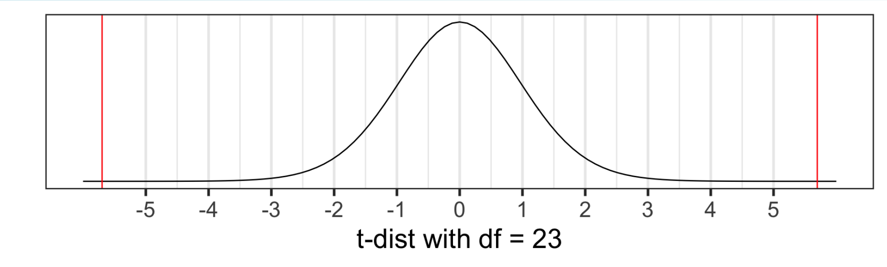
$$t_{\bar{x}_d} = \frac{\bar{x}_d - \delta_0}{\frac{s_d}{\sqrt{n}}}$$

- *Calculate the test statistic.*
- Based on the value of the test statistic, do you think we are going to reject or fail to reject H_0?
- What probability distribution does the test statistic have?
- Are the **assumptions** for a paired t-test satisfied so that we can use the probability distribution to calculate the p-value??

Step 4: p-value

The **p-value** is the **probability** of obtaining a test statistic *just as extreme or more extreme* than the observed test statistic assuming the null hypothesis H_0 is true.





Calculate the *p*-value and shade in the area representing the p-value:

Step 5: Conclusion to hypothesis test

$$H_0 : \delta = 0$$
$$H_A : \delta \neq 0$$

- Recall the p-value = $8.434775 \cdot 10^{-6}$
- Use α = 0.05.
- Do we reject or fail to reject H_0?

Conclusion statement:

- Stats class conclusion
  - There is sufficient evidence that the (population) mean difference in cholesterol levels after a vegetarian diet is different from 0 mg/dL (p-value < 0.001).
- More realistic manuscript conclusion:
  - After a vegetarian diet, cholesterol levels decreased by on average 19.54 mg/dL (SE = 3.43 mg/dL, 2-sided p-value < 0.001).

95% CI for the mean difference in cholesterol levels

```r
chol %>%
  select(DiffChol) %>%
  get_summary_stats(type = "common") %>%
  gt()
```

variable	n	min	max	median	iqr	mean	sd	se	ci
DiffChol	24	-49	13	-19	20.25	-19.542	16.806	3.43	7.096

CI for μ_d (or δ): *How was t^* calculated?*

$$\bar{x}_d \pm t^* \cdot \frac{s_d}{\sqrt{n}}$$

$$-19.542 \pm 2.069 \cdot \frac{16.806}{\sqrt{24}}$$

$$-19.542 \pm 2.069 \cdot 3.43$$

$$-19.542 \pm 7.096$$

$$(-26.638, -12.445)$$

Conclusion:
We are 95% that the (population) mean difference in cholesterol levels after a vegetarian diet is between -26.638 mg/dL and -12.445 mg/dL.

- *Based on the CI, is there evidence the diet made a difference in cholesterol levels? Why or why not?*

Running a paired t-test in R

R option 1: Run a 1-sample `t.test` using the paired differences

$H_A : \delta \neq 0$

```r
t.test(x = chol$DiffChol, mu = 0)
```

```

	One Sample t-test

data:  chol$DiffChol
t = -5.6965, df = 23, p-value = 8.435e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -26.63811 -12.44522
sample estimates:
mean of x 
-19.54167 
```

Run the code without `mu = 0`. Do the results change? Why or why not?

R option 2: Run a 2-sample `t.test` with `paired = TRUE` option

$H_A : \delta \neq 0$

- For a 2-sample t-test we specify both `x=` and `y=`
- Note: `mu = 0` is the default value and doesn't need to be specified

```r
t.test(x = chol$Before, y = chol$After, mu = 0, paired = TRUE)
```

```

	Paired t-test

data:  chol$Before and chol$After
t = 5.6965, df = 23, p-value = 8.435e-06
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 12.44522 26.63811
sample estimates:
mean difference 
       19.54167 
```

What is different in the output compared to option 1?

R option 3: Run a 2-sample `t.test` with `paired = TRUE` option, but using the long data and a "formula" (1/2)

- The data have to be in a `long` format for option 3, where each person has 2 rows: one for Before and one for After.
  - The long dataset `chol_long` was created for the slide "EDA: Spaghetti plot of cholesterol levels before & after diet".
  - See the code to create it there.
- *What information is being stored in each of the columns?*

```r
# first 16 rows of long data
head(chol_long, 16)
```

```
# A tibble: 16 × 3
   ID    Time   Cholesterol
   <fct> <fct>        <dbl>
 1 1     Before         195
 2 1     After          146
 3 2     Before         145
 4 2     After          155
 5 3     Before         205
 6 3     After          178
 7 4     Before         159
 8 4     After          146
 9 5     Before         244
10 5     After          208
11 6     Before         166
12 6     After          147
13 7     Before         250
14 7     After          202
15 8     Before         236
16 8     After          215
```

R option 3: Run a 2-sample `t.test` with `paired = TRUE` option, but using the long data and a “formula” (2/2)

- Use the usual `t.test`
- What’s different is that
  - instead of specifying the variables with `x=` and `y=`,
  - we give a **formula** of the form `y ~ x` using *just the variable names*,
  - and then specify the name of the dataset using `data =`
- This method is often used in practice, and more similar to the coding style of running a regression model (BSTA 512 & 513)

```r
# using long data
# with columns Cholesterol & Time
t.test(Cholesterol ~ Time,
       paired = TRUE,
       data = chol_long)
```

```

	Paired t-test

data:  Cholesterol by Time
t = 5.6965, df = 23, p-value = 8.435e-06
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 12.44522 26.63811
sample estimates:
mean difference 
       19.54167 
```

- *What is different in the output compared to option 1?*
- *Rerun the test using* `Time ~ Cholesterol` *(switch the variables). What do you get?*

Compare the 3 options

- *How is the code similar and different for the 3 options?*
- *Given a dataset, how would you choose which of the 3 options to use?*

```r
# option 1
t.test(x = chol$DiffChol, mu = 0) %>% tidy() %>% gt() # tidy from broom package
```

estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-19.54167	-5.696519	8.434775e-06	23	-26.63811	-12.44522	One Sample t-test	two.sided

```r
# option 2
t.test(x = chol$Before, y = chol$After, mu = 0, paired = TRUE) %>% tidy() %>% gt(
```

estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
19.54167	5.696519	8.434775e-06	23	12.44522	26.63811	Paired t-test	two.sided

```r
# option 3
t.test(Cholesterol ~ Time, paired = TRUE, data = chol_long) %>% tidy() %>% gt()
```

estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
19.54167	5.696519	8.434775e-06	23	12.44522	26.63811	Paired t-test	two.sided

What if we wanted to test whether the diet *decreased* cholesterol levels?

What changes in each of the steps?

1. Set the **level of significance** α
2. Specify the **hypotheses** H_0 and H_A
    - Alternative: one- or two-sided?
3. Calculate the **test statistic**.
4. Calculate the **p-value** based on the observed test statistic and its sampling distribution
5. Write a **conclusion** to the hypothesis test

R: What if we wanted to test whether the diet *decreased* cholesterol levels?

- *Which of the 3 options to run a paired t-test in R is being used below?*
- *How did the code change to account for testing a decrease in cholesterol levels?*
- *Which values in the output changed compared to testing for a change in cholesterol levels? How did they change?*

```r
# alternative = c("two.sided", "less", "greater")
t.test(x = chol$DiffChol, mu = 0, alternative = "less") %>%
  tidy() %>%
  gt()
```

estimate	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-19.54167	-5.696519	4.217387e-06	23	-Inf	-13.6623	One Sample t-test	less

One-sided confidence intervals

Formula for a **2-sided** (1- α)% **CI**:

$$\bar{x} \pm t^* \cdot \frac{s}{\sqrt{n}}$$

- t^* = `qt(1-alpha/2, df = n-1)`
- α is split over both tails of the distribution

A **one-sided** (1- α)% **CI** has all (1- α)% on just the left or the right tail of the distribution:

$$(\bar{x} - t^* \cdot \frac{s}{\sqrt{n}},\ \infty)$$

$$(\infty,\ \bar{x} + t^* \cdot \frac{s}{\sqrt{n}})$$

- t^* = `qt(1-alpha, df = n-1)` for a 1-sided lower (1- α)% CI
- t^* = `qt(alpha, df = n-1)` for a 1-sided upper (1- α)% CI
- A 1-sided CI gives estimates for a lower or upper bound of the population mean.
- See Section 4.2.3 of the V&H book for more

Today & what's next?

CI's and hypothesis tests for different scenarios:

$$\text{point estimate} \pm z^*(or\ t^*) \cdot SE, \quad \text{test stat} = \frac{\text{point estimate} - \text{null value}}{SE}$$

Day	Book	Population parameter	Symbol	Point estimate	Symbol	SE
10	5.1	Pop mean	μ	Sample mean	$\bar{x}$	$\frac{s}{\sqrt{n}}$
10	5.2	Pop mean of paired diff	μ_d or δ	Sample mean of paired diff	$\bar{x}_d$	$\frac{s_d}{\sqrt{n}}$
11	5.3	Diff in pop means	$\mu_1 - \mu_2$	Diff in sample means	$\bar{x}_1 - \bar{x}_2$	???
12	8.1	Pop proportion	p	Sample prop	$\widehat{p}$	
12	8.2	Diff in pop proportions	$p_1 - p_2$	Diff in sample proportions	$\widehat{p}_1 - \widehat{p}_2$	