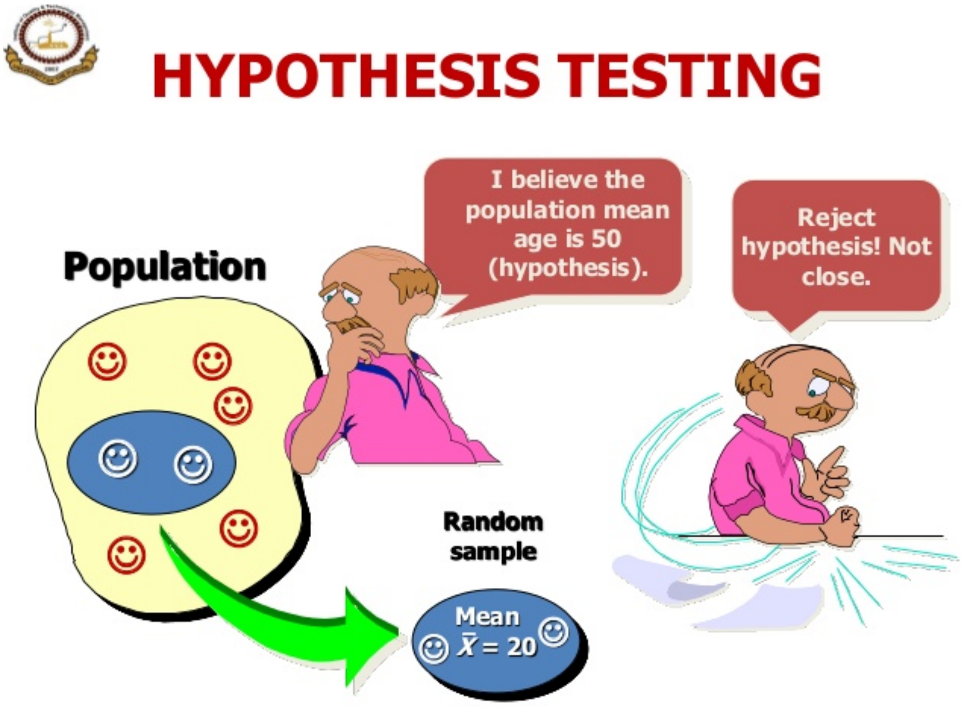
Practical: Statistics

BaselRBootcamp 2017



Source: https://www.slideshare.net/hakeemrehman/8-testing-of-hypothesis-for-variable-amp-attribute-data (https://www.slideshare.net/hakeemrehman/8-testing-of-hypothesis-for-variable-amp-attribute-data)

Slides

- Here are the introduction slides for this practical on statistics! ((https://therbootcamp.github.io/_sessions/D2S2_Statistics/Statistics.html))

Overview

In this practical you'll conduct hypothesis tests. By the end of this practical you will know how to:

1. Calculate basic descriptive statistics.
2. Conduct a hypothesis test on complete datasets.
3. Conduct a hypothesis test on subsets of datasets.

Glossary and Packages

Here are the main descriptive statistics functions we will be covering.

Function	Description
`table()`	Frequency table
`mean()`, `median()`, `mode()`	Measures of central tendency
`sd()`, `range()`, `iqr()`, `var()`	Measures of variability
`max()`, `min()`	Extreme values
`summary()`	Several summary statistics

Here are the main hypothesis test functions we will be covering.

Function	Hypothesis Test	Additional Help
`t.test()`	One and two sample t-test	https://bookdown.org/ndphillips/YaRrr/htests.html#t-test-t.test (https://bookdown.org/ndphillips/YaRrr/htests.html#t-test-t.test)
`cor.test()`	Correlation test	https://bookdown.org/ndphillips/YaRrr/htests.html#correlation-cor.test (https://bookdown.org/ndphillips/YaRrr/htests.html#correlation-cor.test)
`chisq.test()`	Chi-Square test	https://bookdown.org/ndphillips/YaRrr/htests.html#chi-square-chsq.test (https://bookdown.org/ndphillips/YaRrr/htests.html#chi-square-chsq.test)
`aov(), TukeyHSD()`	ANOVA and post-hoc test	https://bookdown.org/ndphillips/YaRrr/anova.html#full-factorial-between-subjects-anova (https://bookdown.org/ndphillips/YaRrr/anova.html#full-factorial-between-subjects-anova)

Examples

- The following examples will take you through the steps of doing basic hypothesis tests. Follow along and try to see how piece of code works!

```r
# ---------------------------------------------
# Examples of hypothesis tests on the ChickWeight data
# ---------------------------------------------
library(tidyverse)

chick <- as_tibble(ChickWeight)   # Save a copy of the ChickWeight data as a tibble c
alled chick

# -----
# Descriptive statistics
# -----

mean(chick$weight)   # What is the mean weight?
median(chick$Time)   # What is the median time?
max(chick$weight)    # What is the maximum weight?
table(chick$Diet)    # How many observations for each diet?

# -----
# 1-sample hypothesis test
# -----

# Q: Is the mean weight of chickens different from 110?

htest_A <- t.test(x = chick$weight,     # The data
                  alternative = "two.sided",  # Two-sided test
                  mu = 110)                   # The null hyopthesis

htest_A            # Print result
names(htest_A)     # See all attributes in object
htest_A$statistic  # Get just the test statistic
htest_A$p.value    # Get the p-value
htest_A$conf.int   # Get a confidence interval

# -----
# 2-sample hypothesis test
# -----

# Q: Is there a difference in weights from Diet 1 and Diet 2?

htest_B <- t.test(formula = weight ~ Diet,     # DV ~ IV
                  alternative = "two.sided",  # Two-sided test
                  data = chick,         # The data
                  subset = Diet %in% c(1, 2)) # Compare Diet 1 and Diet 2

htest_B  # Print result

# -----
# Correlation test
# ------

# Q: Is there a correlation between Time and weight?

htest_C <- cor.test(formula = ~ weight + Time,
                   data = chick)

htest_C
```

```
# A: Yes. r = 0.84, t(576) = 36.7, p < .001


# Q: Does the result hold when ONLY considering Diets 1 and 2?

htest_D <- cor.test(formula = ~ weight + Time,
                    data = chick,
                    subset = Diet %in% c(1, 2))     # Only take data where Diet is 1
 or 2

htest_D

# A: Yes. r = 0.81, t(339) = 25.08, p < .001


# -----
# Chi-Square test
# ------

# Q: Are there more observations from chicks on one diet versus another?

htest_E <- chisq.test(x = table(chick$Diet))  # Input is a table of values

htest_E

# A: Yes, some diets are observed more than others. X2(3) = 52.6, p < .001

# -----
# ANOVA
# -----

# Q: Is there an overall effect of diet on weight?

Diet_aov <- aov(formula = weight ~ factor(Diet),   # Run the anova
                data = chick)

summary(Diet_aov)       # Look at summary for overall test results
TukeyHSD(Diet_aov)      # Conduct post-hoc tests

# A: Yes, there is an overall effect of diet on weight, F(3, 574) = 10.81, p < .001
# Furthermore, we find significant differences between diets 1-3, and diets 1-4 at th
e 0.05 level.
```

Tasks

Gettting started

A. For this practical, we'll use the `ACTG175` dataframe from the `speff2trial` package, load the package with the `library()` function. Also load the `tidyverse` as always!

```
library(tidyverse)
library(speff2trial)
```

B. Convert the data to a tibble (Hint, use assignment and `as_tibble()`)

```
ACTG175 <- as_tibble(ACTG175)
```

C. First thing's first, take a look at the data by printing it. It should look like this

```
ACTG175
```

```
# A tibble: 2,139 x 27
   pidnum   age    wtkg  hemo  homo drugs karnof oprior   z30 zprior
    <int> <int>   <dbl> <int> <int> <int>  <int>  <int> <int>  <int>
 1  10056    48 89.8128     0     0     0    100      0     0      1
 2  10059    61 49.4424     0     0     0     90      0     1      1
 3  10089    45 88.4520     0     1     1     90      0     1      1
 4  10093    47 85.2768     0     1     0    100      0     1      1
 5  10124    43 66.6792     0     1     0    100      0     1      1
 6  10140    46 88.9056     0     1     1    100      0     1      1
 7  10165    31 73.0296     0     1     0    100      0     1      1
 8  10190    41 66.2256     0     1     1    100      0     1      1
 9  10198    40 82.5552     0     1     0     90      0     1      1
10  10229    35 78.0192     0     1     0    100      0     1      1
# ... with 2,129 more rows, and 17 more variables: preanti <int>,
#   race <int>, gender <int>, str2 <int>, strat <int>, symptom <int>,
#   treat <int>, offtrt <int>, cd40 <int>, cd420 <int>, cd496 <int>,
#   r <int>, cd80 <int>, cd820 <int>, cens <int>, days <int>, arms <int>
```

Descriptive statistics

D. What was the mean age of all patients?

```
mean(ACTG175$age)
```

```
[1] 35.24825
```

E. What was the median weight of all patients?

```
median(ACTG175$age)
```

```
[1] 34
```

F. What was the mean CD4 T cell count at baseline? What was it at 20 weeks?

```
mean(ACTG175$cd40)
```

```
[1] 350.5012
```

G. How many patients have a history of intraveneous drug use and how many do not? (Hint: use `table()`)

```
table(ACTG175$drugs)
```

```

   0    1 
1858  281 
```

T tests with t.test()

1. Conduct a one-sample t-test comparing the age of the patients versus a null hypothesis of 40 years. What is the test statistic? What is the p-value? Do you accept or reject the hull hypothesis?

```
t.test(x = ACTG175$age,
       alternative = "two.sided",
       mu = 40)
```

```

	One Sample t-test

data:  ACTG175$age
t = -25.234, df = 2138, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 40
95 percent confidence interval:
 34.87896 35.61753
sample estimates:
mean of x 
 35.24825 
```

2. Now, compare the mean age to a null hypothesis of 35 years. What has changed?

```
t.test(x = ACTG175$age,
       alternative = "two.sided",
       mu = 35)
```

```

	One Sample t-test

data:  ACTG175$age
t = 1.3183, df = 2138, p-value = 0.1875
alternative hypothesis: true mean is not equal to 35
95 percent confidence interval:
 34.87896 35.61753
sample estimates:
mean of x 
 35.24825 
```

3. A researcher wants to make sure that men and women in the clinical study are similar in terms of age. Conduct a two-sample t-test comparing the age of men versus women to test if they are indeed similar or not.

- Women are coded as 0 in `gender` , and men are coded as 1.
- Be sure to use the formula notation `formula = age ~ gender`

```
t.test(formula = age ~ gender,
       data = ACTG175,
       alternative = "two.sided")
```

```
	Welch Two Sample t-test

data:  age by gender
t = -2.3524, df = 554.82, p-value = 0.019
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -2.0618384 -0.1854089
sample estimates:
mean in group 0 mean in group 1 
       34.31793        35.44156 
```

4. Conduct a two-sample t-test comparing the number of days until the first occurrence of a major negative event (`days`) between those with a history of intravenous drug use (`drugs`) and those without a history of intravenous drug use

```
t.test(formula = days ~ drugs,
       data = ACTG175)
```

```
	Welch Two Sample t-test

data:  days by drugs
t = 1.0058, df = 368.61, p-value = 0.3152
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -18.05634  55.86764
sample estimates:
mean in group 0 mean in group 1 
       881.5818        862.6762 
```

Correlation test with cor.test()

5. Do older people tend to weigh more? Conduct a correlation test between weight (`wtkg`) and age (`age`). What is your conclusion?

```
cor.test(formula = ~ age + wtkg,
         data = ACTG175)
```

```
	Pearson's product-moment correlation

data:  age and wtkg
t = 6.1966, df = 2137, p-value = 6.901e-10
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.09098745 0.17425902
sample estimates:
      cor 
0.1328577 
```

6. We would expect a correlation between CD4 T cell count at baseline (`cd40`) and at 20 weeks (`cd420`). But how strong is the correlation? Answer this question by conducting a correlation test between CD4 T cell count at baseline (`cd40`) and CD4 T cell count at 20 weeks (`cd420`).

```
cor.test(formula = ~ cd40 + cd420,
         data = ACTG175)
```

```

    Pearson's product-moment correlation

data:  cd40 and cd420
t = 33.221, df = 2137, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.5549209 0.6108523
sample estimates:
      cor
0.5835783
```

7. Is there a relationship between CD4 T cell count at baseline (`cd40`) and the number of days until the first occurrence of major negative event (`days`)?

```
cor.test(formula = ~ cd40 + days,
         data = ACTG175)
```

```

    Pearson's product-moment correlation

data:  cd40 and days
t = 9.0164, df = 2137, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1502728 0.2319368
sample estimates:
      cor
0.1914361
```

8. Only considering men, is there a correlation between CD4 T cell count at baseline (`cd40`)and CD8 T cell count at baseline (`cd80`)?

- Include the argument `subset = gender == 0` to restrict the analysis to men

```
cor.test(formula = ~ cd40 + cd80,
         data = ACTG175,
         subset = gender == 0)
```

```

    Pearson's product-moment correlation

data:  cd40 and cd80
t = 5.3518, df = 366, p-value = 1.54e-07
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1719038 0.3616702
sample estimates:
      cor
0.2694002
```

9. Now, repeat the previous test, but only for women

```
cor.test(formula = ~ cd40 + cd80,
         data = ACTG175,
         subset = gender == 1)
```

```

    Pearson's product-moment correlation

data:  cd40 and cd80
t = 8.8997, df = 1769, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1619967 0.2511713
sample estimates:
      cor
0.2070139
```

Chi-square test with chisq.test()

10. Do men and women (`gender`) have different distributions of race (`race`)? That is, is the percentage of women who are white differ from the percentage of men who are white?

- Be sure to create a table of gender and race values with `table(ACTG175$gender, ACTG175$race)`

```
chisq.test(table(ACTG175$gender, ACTG175$race))
```

```

    Pearson's Chi-squared test with Yates' continuity correction

data:  table(ACTG175$gender, ACTG175$race)
X-squared = 180.86, df = 1, p-value < 2.2e-16
```

11. Is there a relationship between a history of intravenous drug use (`drugs`) and hemophilia (`hemo`)?

```
chisq.test(table(ACTG175$hemo, ACTG175$drugs))
```

```

    Pearson's Chi-squared test with Yates' continuity correction

data:  table(ACTG175$hemo, ACTG175$drugs)
X-squared = 17.505, df = 1, p-value = 2.866e-05
```

12. Is there a relationship between homosexual activity (`homo`) and gender (`gender`)

```
chisq.test(table(ACTG175$homo, ACTG175$gender))
```

```

    Pearson's Chi-squared test with Yates' continuity correction

data:  table(ACTG175$homo, ACTG175$gender)
X-squared = 786.84, df = 1, p-value < 2.2e-16
```

13. Only for patients older than 40, is there a relationship between antiretroviral history (`str2`) and race (`race`)?

- Create a new dataframe called `ACTG175.o40 <- subset(ACTG175, age > 40)` and then do your analysis on this new dataframe.

```
ACTG175.o40 <- subset(ACTG175, age > 40)

chisq.test(table(ACTG175.o40$str2, ACTG175.o40$race))
```

```

    Pearson's Chi-squared test with Yates' continuity correction

data:  table(ACTG175.o40$str2, ACTG175.o40$race)
X-squared = 0.20265, df = 1, p-value = 0.6526
```

14. Now repeat the previous analysis, but only for male patients

- Create a new dataframe called `ACTG175.male <- subset(ACTG175, gender == 0)` and then do your analysis on this new dataframe.

```
ACTG175.male <- subset(ACTG175, gender == 0)

chisq.test(table(ACTG175.male$str2, ACTG175.male$race))
```

```

    Pearson's Chi-squared test with Yates' continuity correction

data:  table(ACTG175.male$str2, ACTG175.male$race)
X-squared = 0.94379, df = 1, p-value = 0.3313
```

ANOVA with aov()

15. One of the main research hypotheses might be that there is an effect of treatment on CD8 T cell count at 20 weeks of treatment. Test this hypothesis to see if there an effect of treatment arms (`arms`) on CD8 T cell count at 20 weeks (`cd820`). If there is a significant effect, conduct post-hoc tests to see which treatment arms differed.

```
arms_cd820_aov <- aov(formula = cd820 ~ factor(arms),
                     data = ACTG175)

summary(arms_cd820_aov)
```

```
               Df    Sum Sq Mean Sq F value Pr(>F)
factor(arms)    3   1215009  405003   2.048  0.105
Residuals    2135 422116872  197713
```

```
TukeyHSD(arms_cd820_aov)
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = cd820 ~ factor(arms), data = ACTG175)

$`factor(arms)`
         diff        lwr        upr     p adj
1-0  39.76081  -30.66927 110.190890 0.4673285
2-0 -26.60169  -96.96390  43.760515 0.7654127
3-0  15.13331  -54.05007  84.316688 0.9431584
2-1 -66.36250 -137.05835   4.333344 0.0748390
3-1 -24.62750  -94.15018  44.895175 0.7991186
3-2  41.73500  -27.71892 111.188914 0.4107559
```

16. A researcher might be concerned that certain treatments might lead to substantial weight-loss or weight-gain. Answer this question by testing if there an effect of treatment arms (`arms`) on weight (`wtkg`). If the effect is significant, conduct post-hoc tests.

```
arms_weight_aov <- aov(formula = wtkg ~ factor(arms),
                     data = ACTG175)

summary(arms_weight_aov)
```

```
               Df Sum Sq Mean Sq F value Pr(>F)
factor(arms)    3    629   209.7   1.192  0.311
Residuals    2135 375470   175.9
```

```
TukeyHSD(arms_weight_aov)
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = wtkg ~ factor(arms), data = ACTG175)

$`factor(arms)`
           diff       lwr       upr     p adj
1-0 -1.19127351 -3.291805 0.9092584 0.4632230
2-0 -1.34766063 -3.446168 0.7508470 0.3501741
3-0 -1.20366756 -3.267017 0.8596824 0.4377330
2-1 -0.15638712 -2.264845 1.9520711 0.9975420
3-1 -0.01239405 -2.085863 2.0610752 0.9999987
3-2  0.14399307 -1.927425 2.2154116 0.9979732
```

17. The main variable of interest is if there is an effect of treatment arms (`arms`) on the number of days until the occurrence of a major negative event (`days`). Answer this by conducting the appropriate ANOVA (with post-hoc tests if necessary).

```
arms_days_aov <- aov(formula = days ~ factor(arms),
                     data = ACTG175)

summary(arms_days_aov)
```

```
              Df    Sum Sq Mean Sq F value   Pr(>F)
factor(arms)    3   4433564 1477855   17.71 2.37e-11 ***
Residuals    2135 178203547   83468
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(arms_days_aov)
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = days ~ factor(arms), data = ACTG175)

$`factor(arms)`
         diff       lwr       upr     p adj
1-0 115.00262  69.24115 160.76409 0.0000000
2-0 104.51507  58.79769 150.23244 0.0000000
3-0  92.24266  47.29122 137.19410 0.0000009
2-1 -10.48756 -56.42171  35.44660 0.9360273
3-1 -22.75996 -67.93186  22.41193 0.5659229
3-2 -12.27241 -57.39962  32.85481 0.8974078
```

18. Does the previous result hold if you only consider patients with a history of intravenous drug use (`drugs`)? Answer this by conducting the same ANOVA *only* on these patients.

- Create a new dataframe called `ACTG175_drugs = subset(ACTG175, drugs == 1)` and run your analysis on this dataframe

```
ACTG175_drugs <- subset(ACTG175, drugs == 1)

arms_days_drugs_aov <- aov(formula = days ~ factor(arms),
                           data = ACTG175_drugs)

summary(arms_days_drugs_aov)
```

```
             Df   Sum Sq Mean Sq F value  Pr(>F)
factor(arms)   3  1296577  432192    5.23 0.00159 **
Residuals    277 22890714   82638
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(arms_days_drugs_aov)
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = days ~ factor(arms), data = ACTG175_drugs)

$`factor(arms)`
          diff        lwr        upr     p adj
1-0  166.91476   39.14248 294.687049 0.0046345
2-0  138.35673   11.75803 264.955423 0.0259714
3-0   39.38647  -90.09006 168.863005 0.8606653
2-1  -28.55804 -150.32342  93.207338 0.9300538
3-1 -127.52829 -252.28305  -2.773536 0.0429768
3-2  -98.97025 -222.52276  24.582258 0.1654111
```

Extras and Challenges

Generating random samples from distributions

19. You can easily generate random samples from statistical distributions in R. To see all of them, run `?distributions`. For example, to generate samples from the well known Normal distribution, you can use `rnorm()`. Look at the help menu for `rnorm()` to see its arguments.

20. Using `rnorm()`, create a new object `samp_10` which is 10 samples from a Normal distribution with mean 10 and standard deviation 5. Print the object to see what the elements look like. What should the mean and standard deviation of this sample? be? Test it by evaluating its mean and standard deviation directly using the appropriate functions. Then, do a one-sample t-test on this sample against the null hypothesis that the true mean is 12. What are the results?

21. Evalaute your code for the previous question *exactly* as it is – that is, don't change *anything*. What are the new values in `samp_10` and the new mean, standard deviation, and t-test result. Why are the new results different?

22. Now, create a new object called `samp_1000` which is 1,000 samples from a Normal distribution (again with mean 12 and standard deviation 5). Print this object to see what it looks like. What should the mean and standard deviation of this sample be? Do the same hypothesis test as you did in the previous question. What is your new p-value?

2 - Way ANOVA

23. Conduct a two-way ANOVA testing the effects of *both* hemophilia (`hemo`) and drug use (`drugs`) on the number of days until a major negative event.

- To include multiple factors in an anova, just include both in the formula such as: `formula = dv ~ factor(x) + factor(y) + ...`. See https://bookdown.org/ndphillips/YaRrr/anova.html#ex-two-way-anova (https://bookdown.org/ndphillips/YaRrr/anova.html#ex-two-way-anova) for an example

```
hemo_drugs_days_aov <- aov(formula = days ~ factor(hemo) + factor(drugs),
                           data = ACTG175)

summary(hemo_drugs_days_aov)
```

```
               Df    Sum Sq Mean Sq F value Pr(>F)
factor(hemo)     1     55937   55937   0.655  0.419
factor(drugs)    1    101590  101590   1.189  0.276
Residuals     2136 182479584   85431
```

24. Repeat the previous ANOVA, but now test if there is an *interaction* between hemophilia and drugs on the number of days until a major negative event.

- To include interactions in an ANOVA, just include both in the formula using the `*` operator: `formula = dv ~ factor(x) * factor(y)`. See https://bookdown.org/ndphillips/YaRrr/anova.html#ex-two-way-anova (https://bookdown.org/ndphillips/YaRrr/anova.html#ex-two-way-anova) for an example

```
hemo_drugs_days_aov <- aov(formula = days ~ factor(hemo) * factor(drugs),
                           data = ACTG175)

summary(hemo_drugs_days_aov)
```

```
                            Df    Sum Sq Mean Sq F value Pr(>F)
factor(hemo)                 1     55937   55937   0.655  0.419
factor(drugs)                1    101590  101590   1.189  0.276
factor(hemo):factor(drugs)   1     26536   26536   0.311  0.577
Residuals                 2135 182453048   85458
```

You choose the test!

25. Is there a difference in the CD4 T cell count at baseline between whites and non-whites? Answer this by conducting the appropriate hypothesis test.

```
t.test(formula = cd40 ~ race,
       data = ACTG175,
       alternative = "two.sided")
```

```

    Welch Two Sample t-test

data:  cd40 by race
t = 0.060098, df = 1159.4, p-value = 0.9521
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -10.68451  11.35974
sample estimates:
mean in group 0 mean in group 1
       350.5986        350.2609
```

26. A researcher is particularly interested in whether or not there is a difference in the number of days until the first occurrence of a major negative event between patients taking zidovudine and those taking didanosine. Conduct the appropriate test to answer this question.

```
t.test(formula = days ~ arms,
       data = ACTG175,
       subset = arms %in% c(0, 3))
```

```
	Welch Two Sample t-test

data:  days by arms
t = -4.9596, df = 1053.8, p-value = 8.228e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -128.7374  -55.7479
sample estimates:
mean in group 0 mean in group 3 
       801.2368        893.4795 
```

27. A researcher wants to know if the relationship between CD4 T cell count at baseline and age is similar for whites and non-whites. Specifically, she wants to know if both correlations are significant (and in the same direction!) or not. Conduct the appropriate statistical test separately for both groups. Are the conclusions the same or different?

```
cor.test(formula = ~ cd40 + days,
         data = subset(ACTG175, race == 0))
```

```
	Pearson's product-moment correlation

data:  cd40 and days
t = 7.3822, df = 1520, p-value = 2.553e-13
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1370787 0.2341013
sample estimates:
      cor 
0.1860435 
```

```
cor.test(formula = ~ cd40 + days,
         data = subset(ACTG175, race == 1))
```

```
	Pearson's product-moment correlation

data:  cd40 and days
t = 5.2065, df = 615, p-value = 2.628e-07
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1286189 0.2798605
sample estimates:
      cor 
0.2054661 
```

28. A researcher is concerned that patients were not properly randomly assigned to the different treatment arms. Using the appropriate test(s), see if there is a significant imbalance between treatment arms in terms of gender, drug use, race, and homosexual activity. Do you find evidence for a significant imbalance in any of these domains?

```
chisq.test(table(ACTG175$gender, ACTG175$arms))
```

```
	Pearson's Chi-squared test

data:  table(ACTG175$gender, ACTG175$arms)
X-squared = 1.3898, df = 3, p-value = 0.7079
```

```
chisq.test(table(ACTG175$race, ACTG175$arms))
```

```
	Pearson's Chi-squared test

data:  table(ACTG175$race, ACTG175$arms)
X-squared = 2.632, df = 3, p-value = 0.4519
```

```
chisq.test(table(ACTG175$drugs, ACTG175$arms))
```

```
	Pearson's Chi-squared test

data:  table(ACTG175$drugs, ACTG175$arms)
X-squared = 2.3131, df = 3, p-value = 0.51
```

Additional reading

- For more details on hypothesis tests in R, check out the chapter on hypothesis tests in YaRrr! The Pirate's Guide to R YaRrr! Chapter Link (https://bookdown.org/ndphillips/YaRrr/htests.html)
- For more advanced mixed level ANOVAs with random effects, consult the `afex` and `lmer` packages.
- To do Bayesian versions of common hypothesis tests, try using the `BayesFactor` package. BayesFactor Guide Link (https://cran.r-project.org/web/packages/BayesFactor/vignettes/manual.html)