# Stat 140: Inference for a Difference in Means 

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## Jumping Frog Jubilee

## Introduction

Quote from Astley et al., 2013. Chasing maximal performance: a cautionary tale from the celebrated jumping frogs of Calaveras County. The Journal of Experimental Biology 216, 3947-3953.

We recorded video of 3124 bullfrog jumps over the course of the 4 -day contest at the Calaveras County Jumping Frog Jubilee, and determined jump distance from these images and a calibration of the jump arena. Frogs were divided into two groups: 'rental' frogs collected by fair organizers and jumped by the general public, and frogs collected and jumped by experienced, 'professional' teams.

Read in the data, and subset to non-professional frog-jumpers:

```
frogs <- read.csv("https://mhc-stat140-2017.github.io/data/misc/frogs/frogs.csv")
head(frogs)
```



Plot jump distance by jump number:

```
ggplot(frogs_amateur, aes(x = distance, color = factor(jump_n))) +
    geom_density()
```



Plot jump distance by frog type:


Example 1: Are mean frog jump distances the same for "rental" frogs and for frogs brought to the fair by amateur "individual"s?

State Null and Alternative Hypotheses

Check Assumptions for Two-Sample t test

1. Independence within each group
2. Independence across groups
3. Nearly normal distribution

To deal with the issue of independence within each group, let's look at just one of the jumps - how about the second. Here's a plot of jump distance by frog type for just the second jump:

```
frogs_amateur_jump_2 <- frogs_amateur %>% filter(jump_n == 2)
ggplot() +
    geom_density(mapping = aes(x = distance, color = frog_type),
        data = frogs_amateur_jump_2)
```



```
frog_type
```



```
ggplot() +
```

ggplot() +
geom_histogram(mapping = aes(x = distance, fill = frog_type),
geom_histogram(mapping = aes(x = distance, fill = frog_type),
bins = 8,
bins = 8,
data = frogs_amateur_jump_2) +
data = frogs_amateur_jump_2) +
facet_wrap(~ frog_type)

```
    facet_wrap(~ frog_type)
```


4. Sample size
table(frogs_amateur_jump_2\$frog_type)
\#\#

| \#\# individual | pro | rental | unknown |  |
| :--- | ---: | ---: | ---: | ---: |
| \#\# | 20 | 0 | 125 | 0 |

## Calculate a p-value

```
frogs_rental_jump_2 <- filter(frogs_amateur_jump_2, frog_type == "rental")
frogs_individual_jump_2 <- filter(frogs_amateur_jump_2, frog_type == "individual")
t.test(
    frogs_rental_jump_2$distance,
    frogs_individual_jump_2$distance,
    alternative = "two.sided",
    conf.level = 0.95)
##
## Welch Two Sample t-test
##
## data: frogs_rental_jump_2$distance and frogs_individual_jump_2$distance
## t = -2.6071, df = 25.33, p-value = 0.01509
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -41.264804 -4.855552
## sample estimates:
## mean of x mean of y
## 82.28787 105.34805
```

Draw a conclusion for the hypothesis test.

Find a $95 \%$ confidence interval for the difference in means and interpret it in context.

Example 2: Are mean jump distances the same for the first and second jumps, among frogs brought by individuals?

```
frogs_individual_jumps_1_2 <- frogs_amateur \%>\%
    filter (frog_type == "individual" \& jump_n >= 1 \& jump_n <= 2)
ggplot() +
    geom_density(mapping \(=\) aes( \(x=\) distance, color \(=\) factor(jump_n)), data = frogs_individual_jumps_1_2)
```



State Null and Alternative Hypotheses

## Check Assumptions for Two-Sample t test

1. Independence within each group
2. Independence across groups
3. Nearly normal distribution
4. Sample size

We can't do a regular two-sample $t$ test because assumptions of independence across groups are violated. Instead, we can do a "paired t test":

- Calculate differences between observed values for each pair
- Perform a t test of whether the average difference is equal to 0

```
frogs_individual_wide <- frogs_individual_jumps_1_2 \%>\%
    select(id, frog_type, distance, jump_n) \%>\%
    spread(key = jump_n, value = distance, sep = "_distance_") \%>\%
    mutate(distance_difference = jump_n_distance_2 - jump_n_distance_1)
head(frogs_individual_wide)
```



```
ggplot() +
    geom_density(mapping = aes(x = distance_difference), data = frogs_individual_wide)
\#\# Warning: Removed 2 rows containing non-finite values (stat_density).
```



## Check Assumptions for Paired t-test

1. Differences between paired observations are independent across different pairs
2. Differences between paired observations follow a nearly normal distribution
3. Sample size

## Calculate a p-value (shown two ways, you only have to do one)

```
t.test(
    frogs_individual_wide$jump_n_distance_2,
    frogs_individual_wide$jump_n_distance_1,
    mu = 0,
    alternative = "two.sided",
    paired = TRUE
)
##
## Paired t-test
##
## data: frogs_individual_wide$jump_n_distance_2 and frogs_individual_wide$jump_n_distance_1
## t = 2.2044, df = 19, p-value = 0.04002
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.5596879 21.5895121
## sample estimates:
## mean of the differences
## 11.0746
t.test(
    frogs_individual_wide$distance_difference,
    mu = 0,
    alternative = "two.sided"
)
##
## One Sample t-test
##
## data: frogs_individual_wide$distance_difference
## t = 2.2044, df = 19, p-value = 0.04002
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.5596879 21.5895121
## sample estimates:
## mean of x
## 11.0746
```

Draw a conclusion for the hypothesis test.

Find a $95 \%$ confidence interval for the difference in means and interpret it in context.

