S&DS 101 Intro Statistics: Life Sciences

Overview

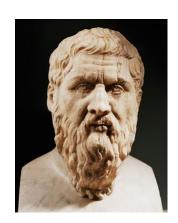
Parametric tests for comparing 2 means

The bootstrap

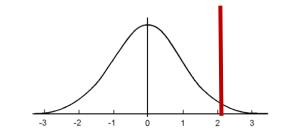
Five steps of hypothesis testing

- 1. State H₀ and H_A
 - Assume Gorgias (H₀) was right
- 2. Calculate the actual observed statistic





- 3. Create a distribution of what statistics would look like if Gorgias is right
 - Create the null distribution (that is consistent with H₀)
- 4. Get the probability we would get a statistic more than the observed statistic from the null distribution
 - p-value



- 5. Make a judgement
 - Assess whether the results are statistically significant

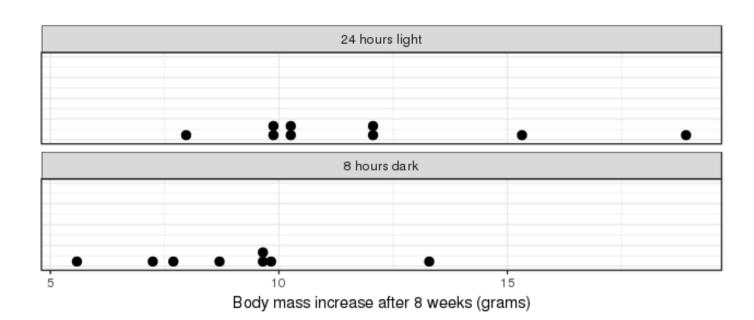


A study by Fonken et al, 2010, wanted to examine whether more weight was gained by mice who could eat late at night

Mice were randomly divided into 2 groups:

- <u>Dark condition</u>: 8 mice were given 8 hours of darkness at night (when they couldn't eat)
- <u>Light condition</u>: 9 were constantly exposed to light for 24 hours (so they could always eat)

What's a good first thing to do when analyzing data?



Hypothesis tests for differences in two group means

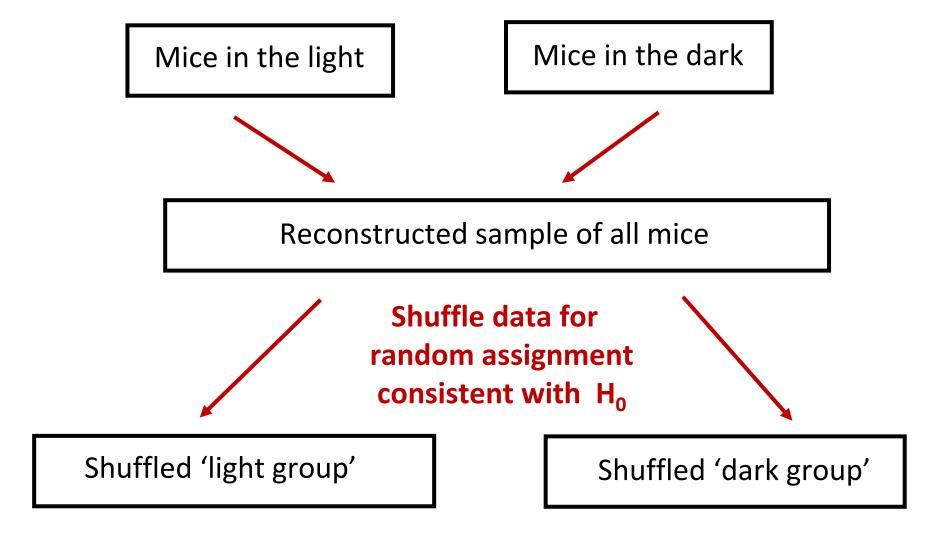
1. State the null and alternative hypothesis

- H_0 : $\mu_{Dark} = \mu_{Light}$ or $\mu_{Dark} \mu_{Light} = 0$ • H_A : $\mu_{Dark} > \mu_{Light}$ or $\mu_{Dark} - \mu_{Light} > 0$
- 2. Calculate statistic of interest
 - $\overline{X}_{effect} = \overline{X}_{Dark} \overline{X}_{Light}$

```
You can get the data using:
> download_class_data('mice.Rda')
> dark BM increase
                     # length(dark BM increase)
> light_BM_increase
                      # length(light_BM increase)
Can you calculate the observed statistic (step 2)?
   > obs_stat <- mean(light_BM_increase) - mean(dark_BM_increase)
```

What's next?

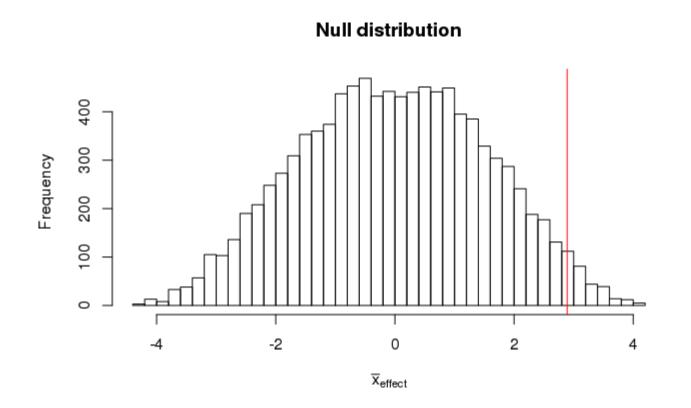
3. Create the null distribution!



One null distribution statistic: $\overline{x}_{Shuff_Dark} - \overline{x}_{Shuff_Light}$

```
What is the first thing we need to do for creating the null distribution?
       combo_data <- c(light_BM_increase, dark_BM_increase)</pre>
null dist <- NULL
for (i in 1:10000) {
        shuff data <- sample(combo_data)</pre>
        shuff light <- shuff data[1:9]
        shuff_dark <- shuff_data[10:17]</pre>
        null_dist[i] <- mean(shuff_light) - mean(shuff_dark)</pre>
```

Plot the null distribution: hist(null_dist, nclass = 50)



What do we do next?

Get the p-value

p_val <- sum(null_dist >= obs_stat)/10000

p-value = 0.02





Two-sided tests

If we did not have a belief about whether the light or the dark group would gain more weight, then we would state our hypotheses as follows:

State the null and alternative hypothesis

$$H_0: \ \mu_{Dark} = \mu_{Light} \qquad \qquad or \qquad \mu_{Dark} - \mu_{Light} = 0$$

$$H_A: \ \mu_{Dark} \neq \mu_{Light} \quad or \qquad \qquad \mu_{Dark} - \mu_{Light} \neq 0$$

Steps 1-3 of hypothesis testing would still be the same, but for step 4 we would need to calculate the p-values by examining extreme values in both tails

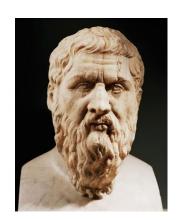
```
p_val <- sum(abs(null_distr) >= abs(obs_stat))/10000
```

Parametric methods for comparing 2 means

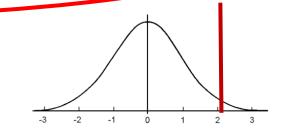
Five steps of hypothesis testing

- 1. State H₀ and H_A
 - Assume Gorgias (H₀) was right
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- 3. Create a distribution of what statistics would look like if Gorgias is right
 - Create the null distribution (that is consistent with H₀)
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- 5. Make a judgement
 - Assess whether the results are statistically significant



Parametric methods for comparing 2 means

If we are testing the hypothesis comparing two means

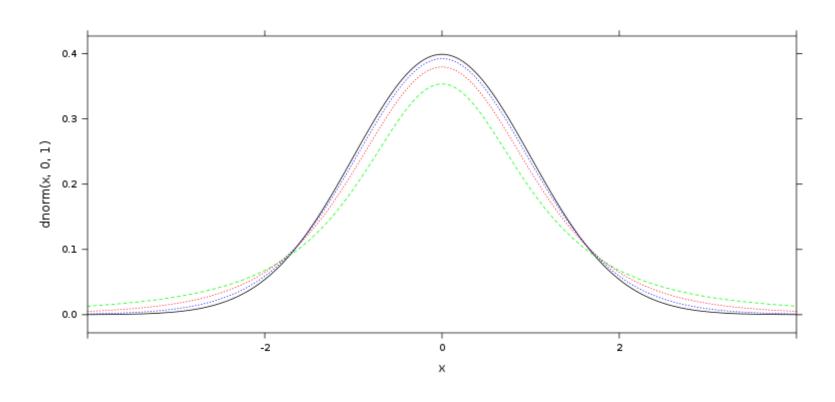
- H_0 : μ_{Dark} μ_{Light} = 0
- H_A : μ_{Dark} μ_{Light} > 0

And we have two samples of size n₁ and n₂

We can calculate a t-statistic
$$t = \frac{\overline{x}_1 - \overline{x}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

When H_0 is true, we can use a t-distribution, with degrees of freedom equal to the minimum of n_1 - 1 and n_2 - 1 as a null distribution

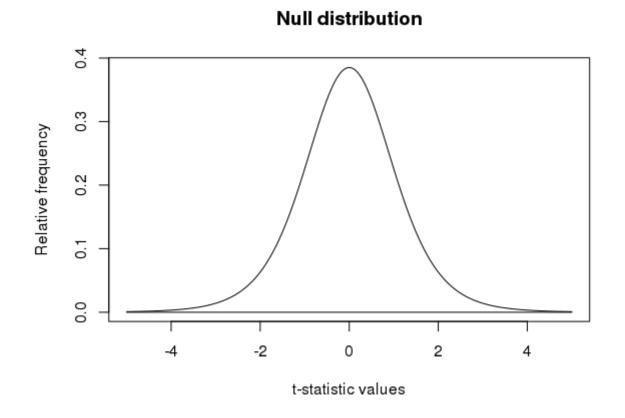
t-distributions



$$N(0, 1), df = 2, df = 5, df = 15$$

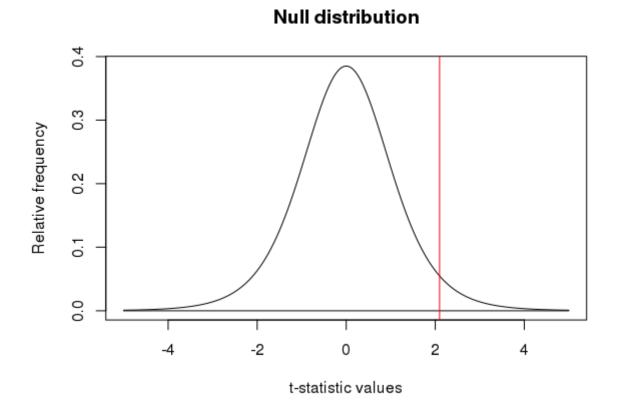
Null distribution

We can get the null density function using: dt(x_vals, df)



p-value

We can get the p-value using: pt(obs_stat, df, lower.tail = FALSE)



Get the p-value

p_val <- pt(obs_stat, df, lower.tail = FALSE)</pre>

p-value = 0.037





Two-sided tests

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Steps 1-3 of hypothesis testing would still be the same, but for step 4 we would need to calculate the p-values by examining extreme values in both tails

```
p_val <- 2 * pt(abs(obs_stat), df, lower.tail = FALSE)</pre>
```

Let's try it in R...