

ANOVA

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Conditions for using
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Example: Sleep and insight

Example: Cannabis to treat
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After a significant
ANOVA ...

Bonferroni

Tukey's HSD

3+ Sample testing with continuous outcomes: ANOVA

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Skipping around

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To stick with continuous outcomes, we are going to skip ahead to chapter 24 (ANOVA) and chapter 23(regression) and bring in some outside information about non-parametric testing.

Summary of Continuous outcomes so far - Z and the flavors of T

In R, the `t.test` function will allow you to conduct any of the t-tests we have covered so far

- ▶ One sample T test comparing a sample mean to a hypothesized null
(if we know σ and have a large sample we could also consider a Z test)
`t.test(data, mu=value)`
- ▶ Two sample T test comparing samples from independent populations
`t.test(continuousvar~categoricalvar)` or `t.test(data1, data2)`
- ▶ Two sample T test comparing paired (non-independent) groups of observations
`t.test(continuousvar~categoricalvar, paired=TRUE)` or
`t.test(data1, data2, paired=TRUE)`

Three sample testing

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Now that we have looked at how to compare one sample to a value and means between two samples, let's extend this to a case where we have 3 samples or 3 groups that we are interested in comparing.

Statistics is everywhere

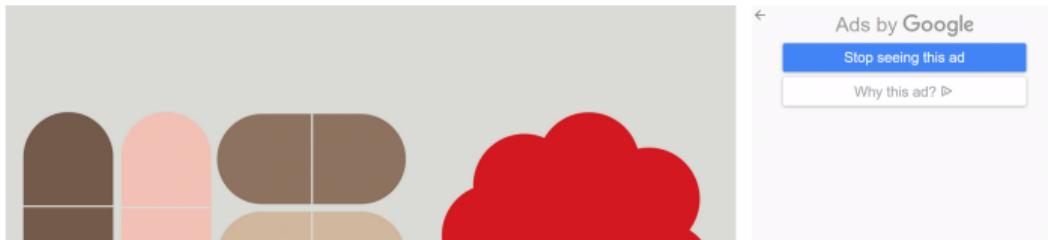
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PAGING DR. HAMBLIN

Paging Dr. Hamblin: Does Vitamin D Help Fight COVID-19?

Evidence is slowly mounting. Some researchers think that's enough to recommend it.

JAMES HAMBLIN JUNE 3, 2020



Atlantic article

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Statistics is everywhere

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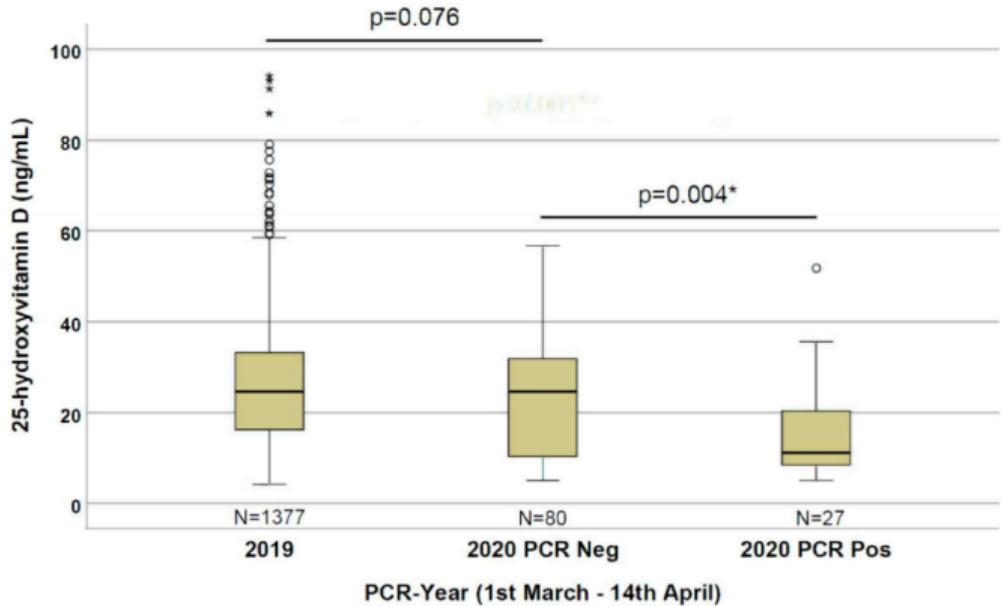


Figure 1. 25-hydroxyvitamin D concentrations in the three evaluated groups (patients from 1 March to 14 April of 2019 and 2020 with a negative PCR, and of 2020 with a positive PCR for SARS-CoV-2.
*: significant results.

from D'Avolio et al. Nutrients 2020, 12, 1359; doi:10.3390/nu12051359

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Today's lecture

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- ▶ Introducing ANOVA - what is the null hypothesis of this test?
- ▶ Visualizing 3 sample data
- ▶ Using ANOVA to test for a difference
- ▶ Example

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ANOVA or analysis of variance can be thought of as an extension of the two-sample t-test to three or more samples.

If we had 3 groups to compare, we could do this by using the two-sample t test multiple times. This would result in $\binom{3}{2}$ comparisons:

$$\mu_1 \neq \mu_2 \quad \mu_2 \neq \mu_3 \quad \mu_1 \neq \mu_3$$

The problem with that approach is that we would end up with 3 p-values, one for each test performed. That doesn't tell us how likely it is that three sample means are spread apart as far as they are. If we are comparing more than 3 groups, this problem is compounded by creating even more comparisons.

We need a method that allows us to have an overall measure of confidence in all our conclusions about comparisons. This is a common problem of multiple comparisons.

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Here we are testing a null hypothesis that all the means are the same, for 3 samples this would be

$$H_0: \mu_1 = \mu_2 = \mu_3$$

Our alternative hypothesis is that at least one of the means is not equal to the others

Even though your hypothesis involves means, the test compares the variability between groups to the variability within groups

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Analysis of variance (ANOVA) is also referred to as the F test.

The ANOVA is based on two kinds of variability:

- The variability among sample means or how much the individual group means vary around the overall mean
- The variability within groups, how much do individual observation values vary around the group mean

If the variability within the k different populations is small relative to the variability among their respective means, this suggests that the population means are in fact different.

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Loosely expressed:

$$F = \left(\frac{\text{variation among sample means}}{\text{variation among observations in the same sample}} \right)$$

Note: You will NOT need to know the full formula for the F-test, you will need to know how to do one in R

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What would the data look like in a data frame?

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What would the data look like in a data frame?

- ▶ One “grouping” variable (categorical)
- ▶ One continuous response variable

ANOVA asks if there is an association between the grouping variable and the response variable.

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Visualizing first

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What graphical strategies have we learned to look at variability within and between groups?

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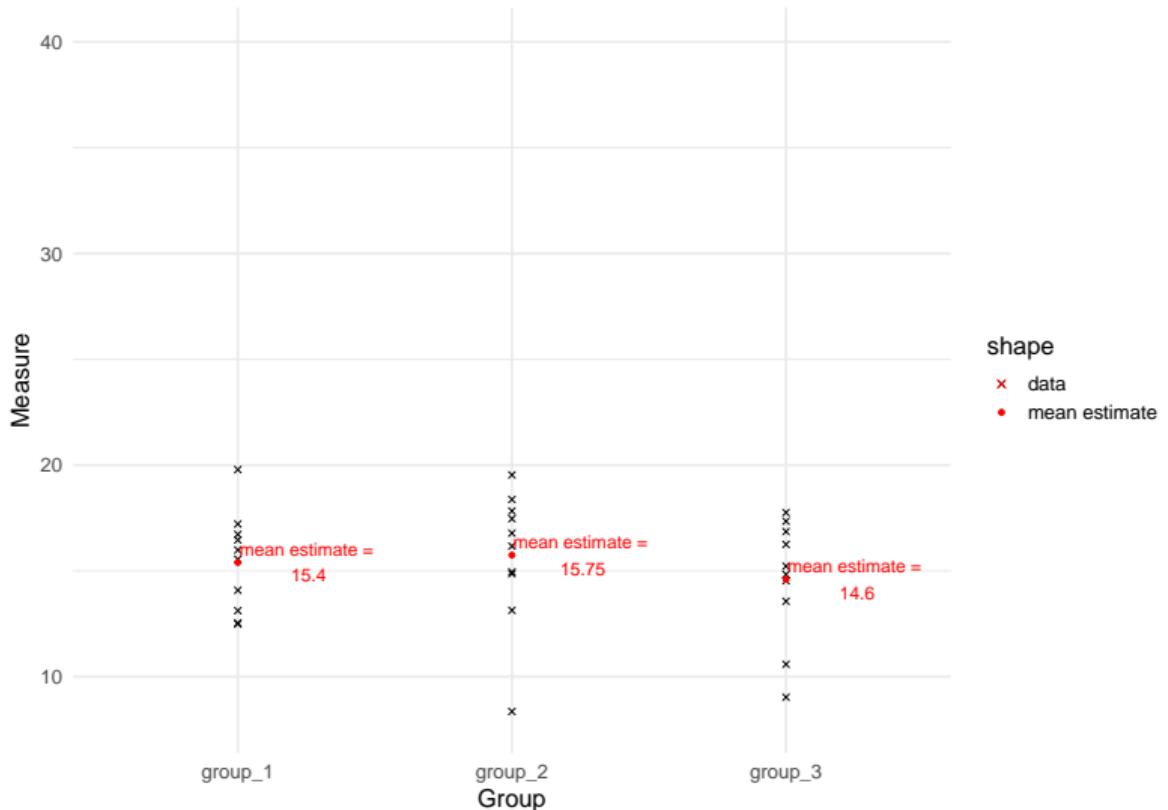
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A) Is there a difference between these means?

Describe why you do or do not think so.



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Summary of the plots

Plot (A)

- ▶ The means (red dots) were not very different across the groups. This means the variation **between** the group means was small.
- ▶ The distribution of the data (black Xs) was wide enough that the distribution of points for each group overlapped almost completely. This means that the variation **within** each group was relatively wide

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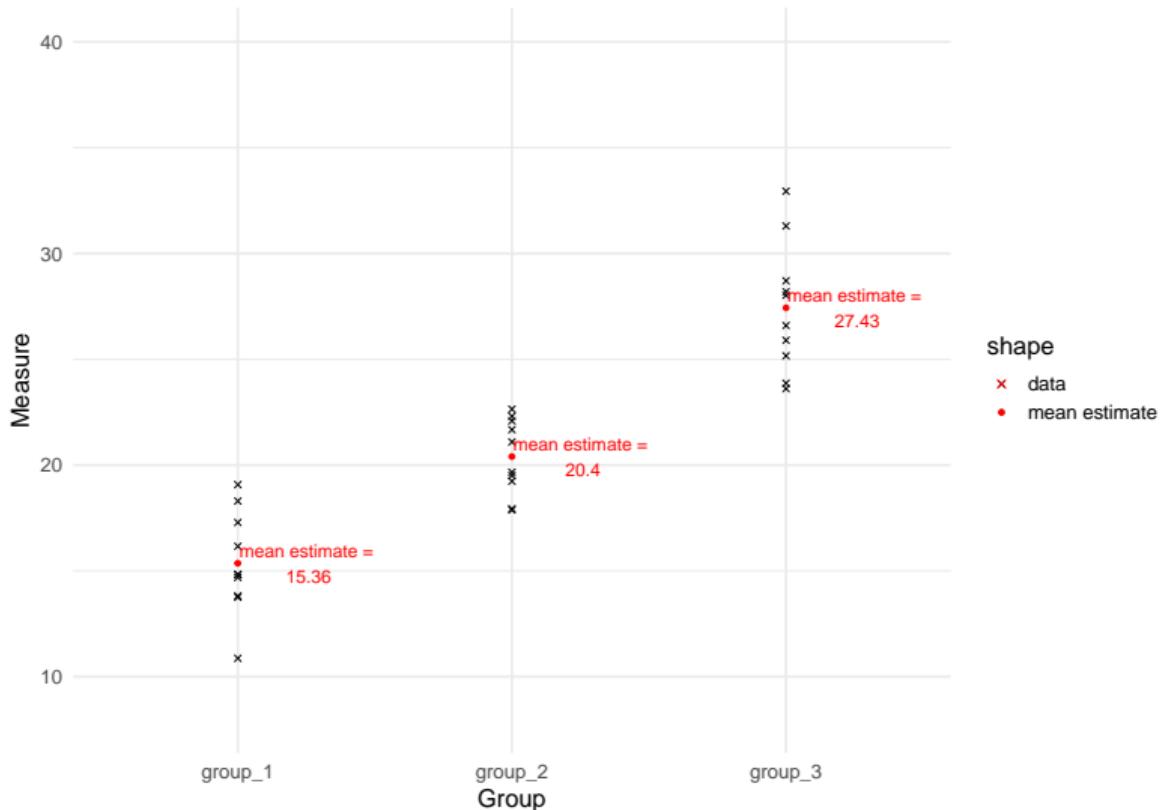
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B) Is there a difference between these means?

Describe why you do or do not think so.



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Summary of the plots

Plot (B)

- ▶ The means are quite different across the groups. The variation **between** the group means would be larger than in plot (A)
- ▶ The distribution of the data overlaps between groups 1 and 2 and 2 and 3, but not 1 and 3. The variation **within** each group is as wide as it was in Plot (A) but doesn't mask the mean differences, especially between group 1 and 3

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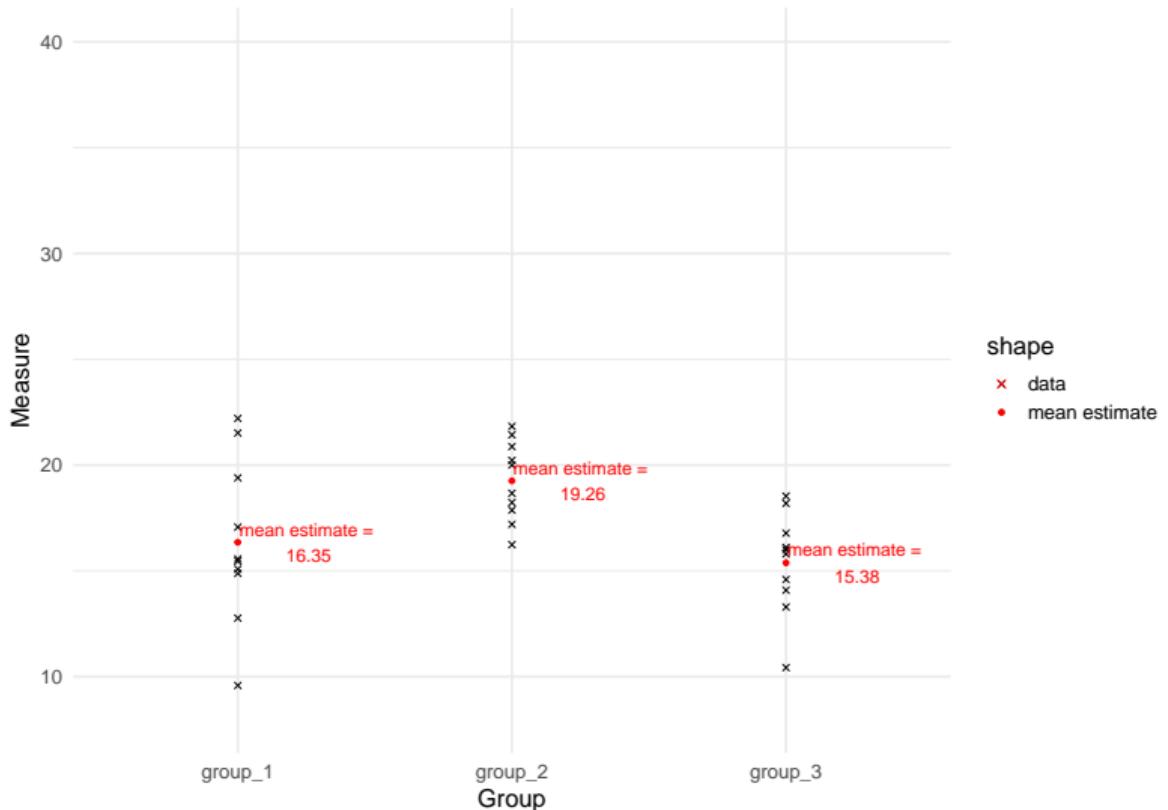
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C) Is there a difference between these means?

Describe why you do or do not think so.



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Plot (C)

- ▶ Here, the means for group 1 and 3 look similar, but the mean for group 2 appears a bit higher than the other two, though there is still overlap between the data from all the groups
- ▶ Is there evidence that at least one of the means is different?

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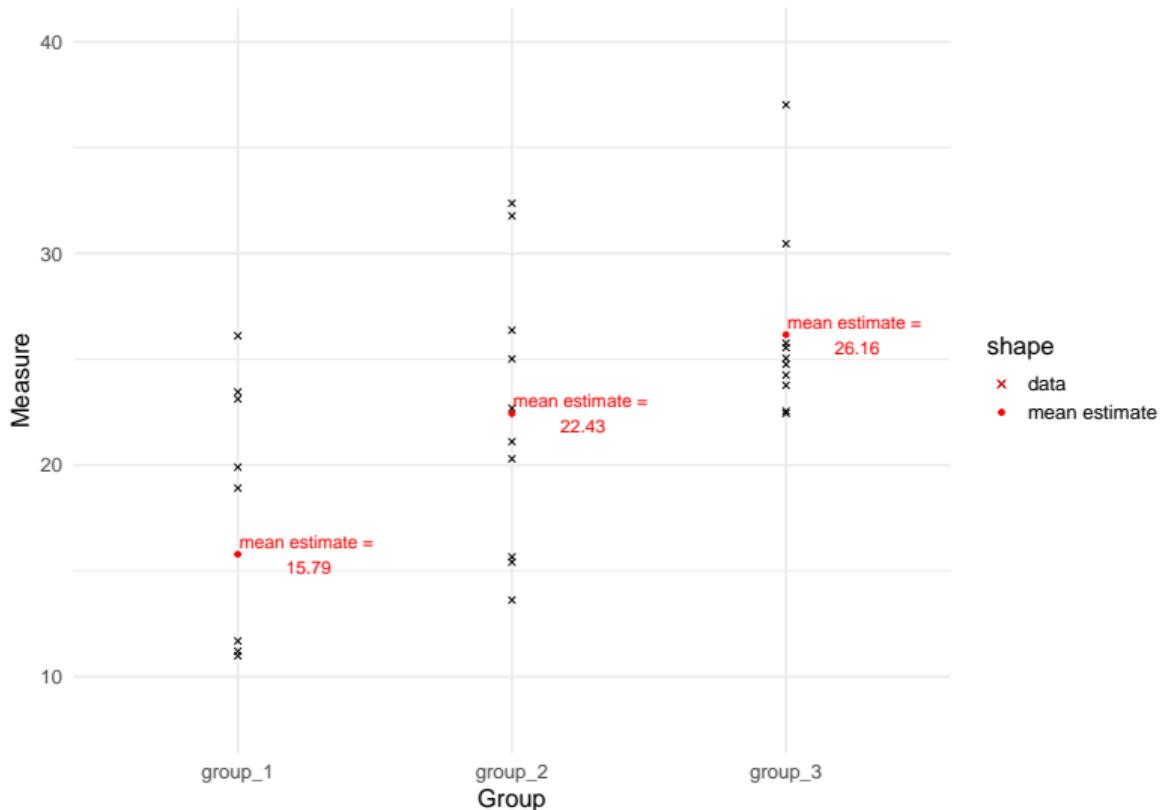
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D) Is there a difference between these means?

Describe why you do or do not think so.



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Plot (D)

- ▶ Plot (D) looked like Plot (B) but with more variation **within** groups
- ▶ This variation makes the difference between the means harder to detect

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Overall summary

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- ▶ What we informally did on the previous slides was compare the variation *between* group means to the variation *within* the groups
- ▶ This focus on variation is why this test is called ANOVA: an ANalysis Of VAriance
- ▶ When the ratio of between vs. within variation is large enough then we detect a difference between the groups
- ▶ When the ratio isn't large enough we don't detect the difference.
- ▶ This ratio is our test statistic, denoted by F

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What other ways to present the data visually have we learned that might be useful before we move on to testing?

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How would you want to plot these data before you conduct a test?

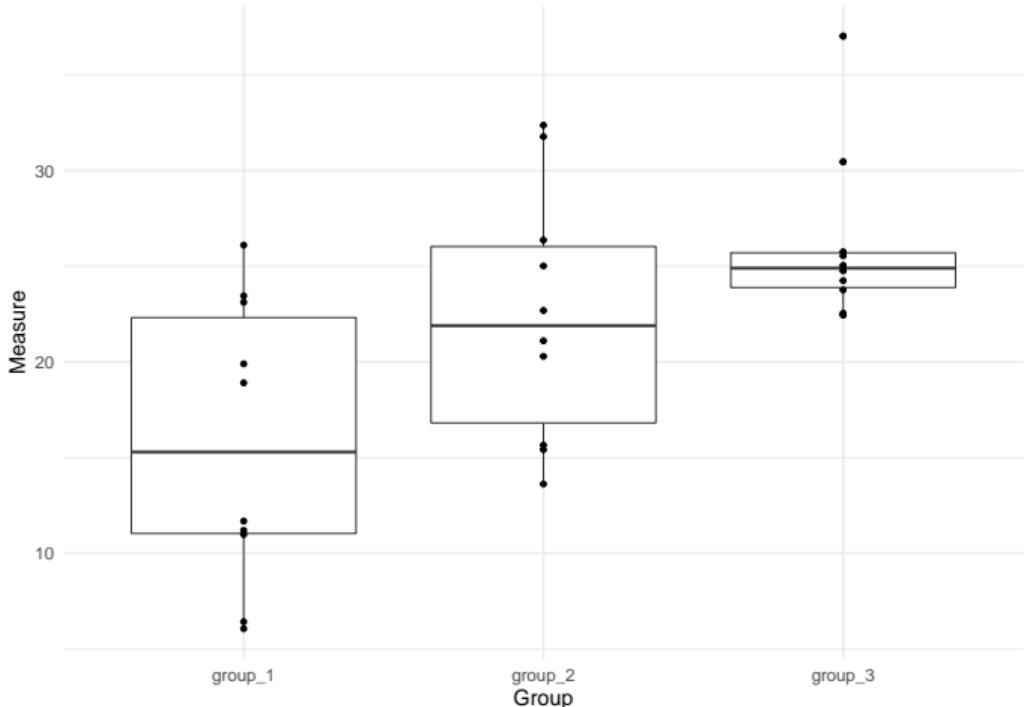
- ▶ Option 1: Box plot for each level of the grouping variable (with overlaid data points)

```
ggplot(diff_3_narrow, aes(x = Group, y = Measure)) +  
  geom_boxplot() +  
  geom_point() +  
  theme_minimal(base_size = 15)
```

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Box plot

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How would you want to plot these data before you conduct a test?

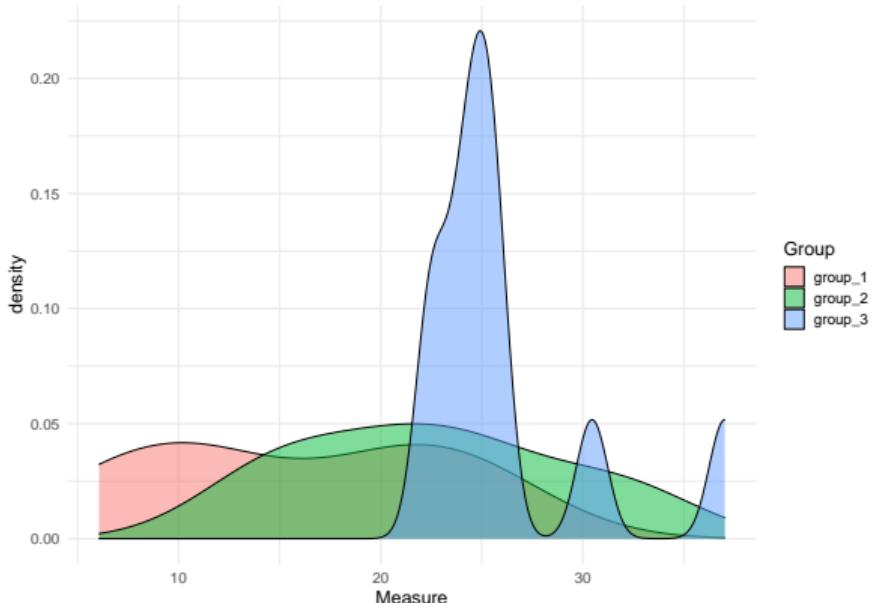
- ▶ Option 2: Density plot for each level of the grouping variable

```
ggplot(diff_3_narrow, aes(x = Measure)) +  
  geom_density(aes(fill = Group), alpha = 0.5) +  
  theme_minimal(base_size = 15)
```

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How would you want to plot these data before you conduct a test?

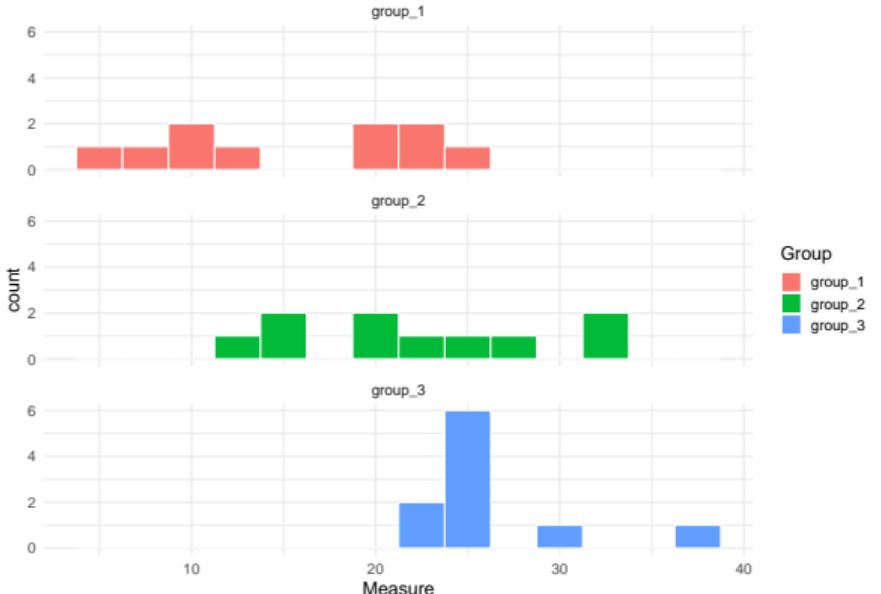
- ▶ Option 3: Histogram for each level of the grouping variable

```
ggplot(diff_3_narrow, aes(x = Measure)) +  
  geom_histogram(aes(fill = Group), col = "white", binwidth = 2.5) +  
  theme_minimal(base_size = 15) +  
  facet_wrap(~ Group, nrow = 3)
```

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Histograms with facet wrap

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The hypotheses

Null hypothesis

$H_0 : \mu_1 = \mu_2 = \dots = \mu_K$, where K is the number of levels of the grouping variable

- ▶ Can you also state the null hypothesis in words?

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The hypotheses

Alternative hypothesis

H_a : not all $\mu_1, \mu_2, \dots, \mu_K$ are equal

- ▶ In words: Not all means are the same. Or, at least one of the means differs from the others.



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The test statistic (ANOVA F Statistic)

$$F = \frac{\text{variation among group means}}{\text{variation among individuals in the same group}}$$

- ▶ Numerator is, fundamentally, the variance of the sample means
- ▶ Denominator is, fundamentally, an average of the group variances.
- ▶ The F statistic follows an F distribution
- ▶ Computation details are at the end of the book chapter (these computation details will not be tested)

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The F distribution

- ▶ Skewed right
- ▶ Take only positive values
- ▶ The F distribution depends on the number of means being compared and the sample size for each of the groups
- ▶ Let k be the number of groups being compared and $N_{Total} = n_1 + n_2 + \dots + n_k$ (the total sample size across all the groups)
- ▶ Then the F statistic follows an F distribution with $k - 1$ degrees of freedom in the numerator and $N_{Total} - k$ degrees of freedom in the denominator
- ▶ The p-value of the ANOVA F statistic is always the area to the right of the test statistic

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ANOVA in R: use `aov()`, then `tidy()` it up!

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- ▶ `aov()` stands for analysis of variance

The general syntax for the ANOVA is:

```
aov(outcomevariable ~ groupvariable, data=dataset)
```

We will save the output of this as an object and then use `tidy(object)` to get the output we want.

reference: https://broom.tidyverse.org/reference/anova_tidiers.html

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ANOVA in R: use `aov()`, then `tidy()` it up!

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We will focus on two parts of the output from this package:

- ▶ `statistic` is the F test statistic, the ratio of the variation between means vs. the variation within groups.
- ▶ `p.value` is the p-value for the test.

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p of an f statistic in R

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You can check that you can calculate the p-value from the F distribution.

Remember, that you need to specify a degrees of freedom for the numerator and for the denominator:

```
pf(value, df1=numerator degrees of freedom, df2= denominator degrees of  
freedom, lower.tail=F)
```

This general pattern of syntax should look familiar by now....

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Condition 1: k independent SRSs, one from each of k populations.

- ▶ The most important assumption, because this method, like the others in Part III of the course, depends on the premise of having taken a random sample.

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Condition 2: Each of the k populations has a Normal distribution with an unknown mean μ_i .

- ▶ This assumption is less necessary
- ▶ The ANOVA test is **robust** to non-Normality.
- ▶ Remember that the ANOVA is based on comparing the differences of sample means
- ▶ What did the CLT tell us about variability of sample means when the samples are not normally distributed?

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Conditions for ANOVA

Condition 3: All the populations have the same standard deviation σ , whose value is unknown.

- ▶ Hardest condition to satisfy and check
- ▶ If this condition is not satisfied ANOVA is often okay if the sample sizes are large enough and if they are similar across the groups
- ▶ Can use `group_by()` and `summarize()` to calculate the sample SDs to see if they're similar and indicative that the population parameters are too
- ▶ General rule: we want the largest sample standard deviation to be less than twice as large as the smallest one. I.e., $s_{max}/s_{min} < 2$

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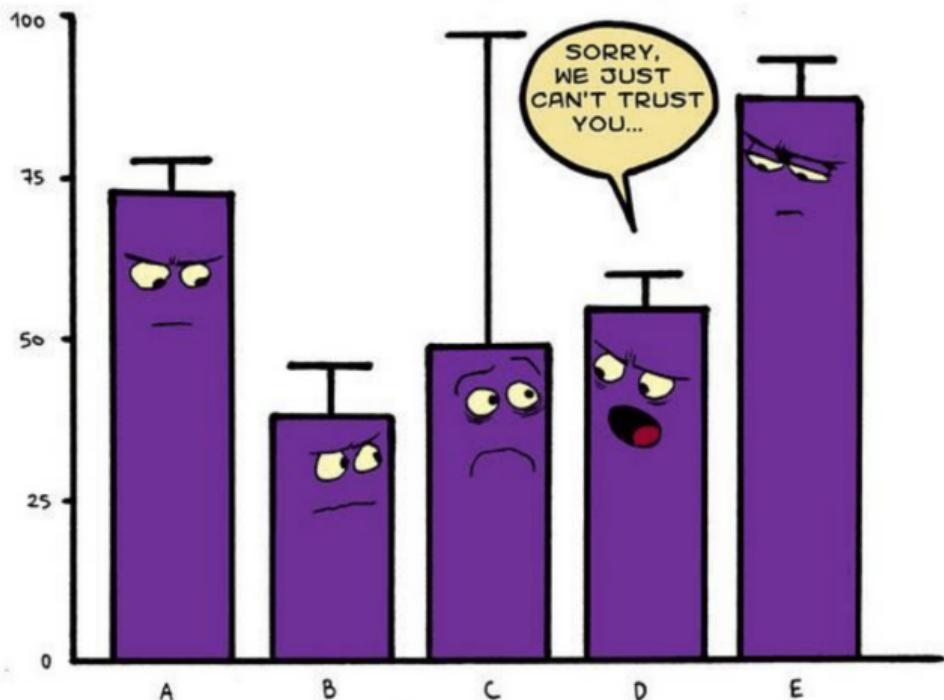
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Example: Sleep and insight

From a 2004 article in Nature

..... **Sleep inspires insight**

Ullrich Wagner¹, Steffen Gais¹, Hilde Haider², Rolf Verleger³ & Jan Born¹

¹*Department of Neuroendocrinology, University of Lübeck, Ratzeburger Allee 160,
23538 Lübeck, Germany*

²*Institute of Psychology, University of Cologne, Gronewaldstrasse 2,
50931 Cologne, Germany*

³*Department of Neurology, University of Lübeck, Ratzeburger Allee 160,
23538 Lübeck, Germany*

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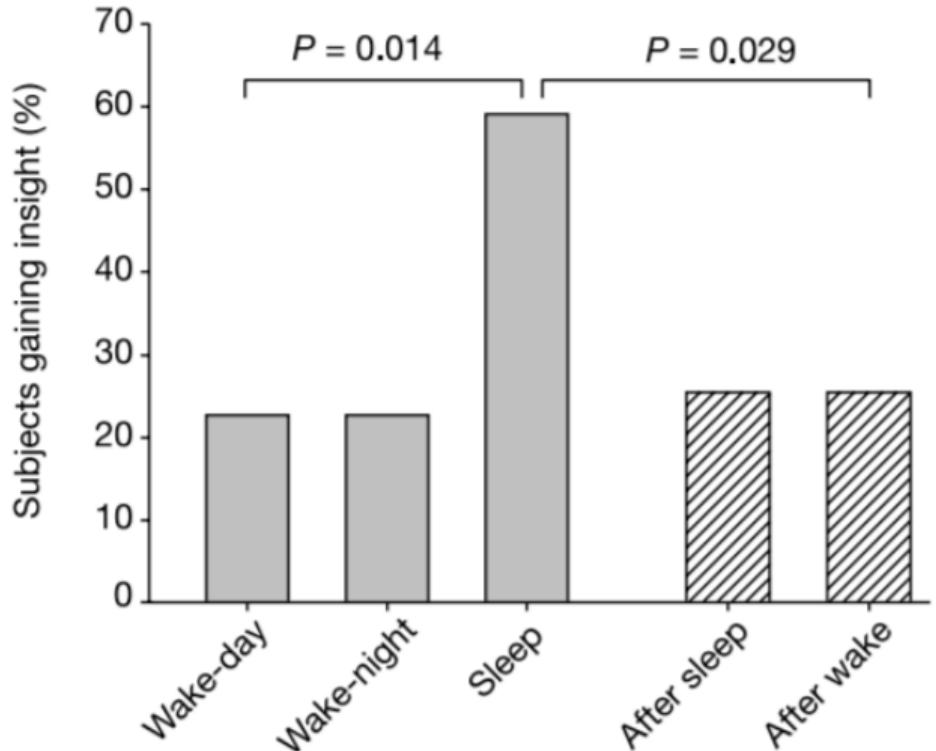
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Example: Cannabis to treat brain cancer (in mice)

High-grade glioma is an aggressive type of brain cancer with a low long-term survival rate. Cannabinoids, which are chemical compounds found in cannabis, are thought to inhibit glioma cell growth. Researchers transplanted glioma cells in otherwise-healthy mice, and then randomly assigned these mice to 4 cancer treatments: irradiation alone, cannabinoids, alone, irradiation combined with cannabinoids, or no cancer treatment. The treatments were administered for 21 days, after which the glioma tumor volume (in cubic millimeters) was assessed in each mouse using brain imaging.

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The data

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```
head(cancer_data)
```

```
##          treatment tumor_volume
## 1    Irradiation           30
## 2    Irradiation           46
## 3    Irradiation           46
## 4    Irradiation          95
## 5 Cannabinoids            12
## 6 Cannabinoids            14
```

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Organize the data

- ▶ Think about how you want the data to look.
- ▶ I want to plot the raw data points and display the mean for each treatment group
- ▶ I also want to specify the order that the treatment groups show up in the graph

```
# specify the order of the treatment groups for plotting
library(forcats)
cancer_data <- cancer_data %>%
  mutate(trt_order = fct_relevel(treatment, c("Neither", "Irradiation",
                                             "Cannabinoids", "Both")))
```

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Look at summary statistics

```
# calculate the means and SD for each group
summary_stats <- cancer_data %>%
  group_by(trt_order) %>%
  summarise(mean_vol = mean(tumor_volume),
            sd_vol = sd(tumor_volume),
            samp_size = n())
summary_stats
```

```
## # A tibble: 4 x 4
##   trt_order   mean_vol   sd_vol samp_size
##   <fct>       <dbl>     <dbl>     <int>
## 1 Neither      48.3     24.8       7
## 2 Irradiation  54.2     28.2       4
## 3 Cannabinoids 26.0     16.6       5
## 4 Both         6.0      2.76       6
```

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Graph the data

```
ggplot(cancer_data, aes(x = trt_order, y = tumor_volume)) +  
  geom_jitter(pch = 4, width = 0.1) +  
  geom_point(data = summary_stats, aes(y = mean_vol, col = "Mean"), pch =  
  19) +  
  labs(y = "Tumor volume (mm cubed)", x = "Treatment") +  
  theme_minimal(base_size = 15)
```

note: `geom_jitter()` with `width = 0.1` randomly “jitters” the location of the points along the x axis so that we can see each of them since some have the exact same values.

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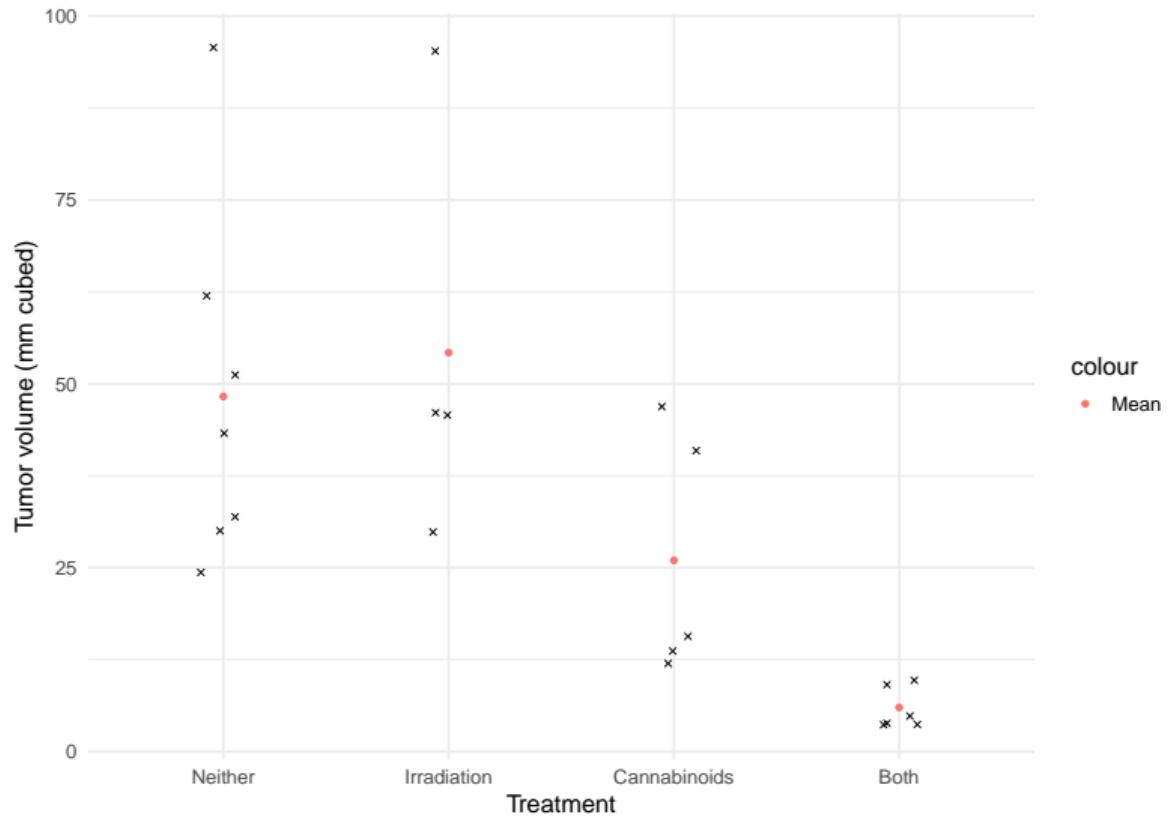
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ANOVA in R: use `aov()`, then `tidy()` it up!

```
library(broom)
cancer_anova <- aov(formula = tumor_volume ~ treatment, data = cancer_data)
tidy(cancer_anova)

## # A tibble: 2 x 6
##   term        df    sumsq   meansq statistic p.value
##   <chr>     <dbl> <dbl>    <dbl>     <dbl>    <dbl>
## 1 treatment     3 8060.  2687.      6.70  0.00313
## 2 Residuals    18 7218.   401.       NA      NA
```

This F says that the variation between the means is nearly 7 times as large as the variation within the groups.

This p-value is equal to 0.3%. There is a 0.3% chance of observing the F statistic we observed (or more extreme) under the null hypothesis that all the means are the same.

P value of the F test

Remember

- ▶ k is the number of groups being compared and $N_{Total} = n_1 + n_2 + \dots + n_k$ is the total sample size across all the groups.
- ▶ The F statistic follows an F distribution with $k - 1$ degrees of freedom in the numerator and $N_{Total} - k$ degrees of freedom in the denominator
- ▶ The p-value of the ANOVA F statistic is always the area to the right of the test statistic

```
pf(6.699489, df1 = 3, df2 = 22 - 4, lower.tail = F)
```

```
## [1] 0.003131703
```

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- The p-value equaled 0.003, indicating a difference. But what groups are actually different?

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- ▶ You could look at all pairwise differences (i.e., comparing each combination of treatments), but we have to be careful because we will find differences “just by chance” if we compare enough groups.

A key example of what not to do?

3+ Sample testing
with continuous
outcomes: ANOVA

FOOD FOR THOUGHT

Cornell Food Researcher's Downfall Raises Larger Questions For Science

September 26, 2018 - 3:07 PM ET

BRETT DAHLBERG

FROM **WXXI**



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A brief reminder about p-hacking

Remember, one of the issues with multiple comparisons is that when you repeatedly question the same dataset, you can end up finding “significant” results by chance alone.

We talked about this before as p-hacking or p-fishing or data dredging

This along with other issues that are sometimes unconscious can lead to bias in what is found and what is published.

Ioannidis, John P.A. (August 30, 2005). “Why Most Published Research Findings Are False”. PLoS Medicine. <https://journals.plos.org/plosmedicine/article?id=10.1371/journal.pmed.0020124>

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- ▶ Conduct multiple pairwise tests and adjust the critical value for significance using a Bonferroni correction
- ▶ Use a Tukey's HSD to generate the pairwise comparisons with adjusted p-values

Bonferroni

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Bonferroni Adjustment for multiple comparisons

We could do a series, comparing each combination of groups in pairs or $\binom{k}{2}$ comparisons.

To compensate for making multiple comparisons and set the overall probability of making a type I error at 0.05, we can adjust our α to α^* for each comparison by dividing by the number of comparisons we are making.

$$\alpha^* = \left(\frac{0.05}{\binom{k}{2}} \right)$$

We then use α^* as the significance level for each individual comparison. So for a comparison of 3 groups we would use an α of 0.0167 as the significance level for each comparison.

This modification is known as the Bonferroni correction. Bonferroni is fairly basic and can become unwieldy - what happens if you have a lot of groups?

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This would entail doing a series of two-sample t tests for each pairwise comparison or 4 choose 2 comparisons = 6 two-sample tests so the adjustment would be:

$$\alpha^* = \left(\frac{0.05}{\binom{4}{2}} \right) = \left(\frac{0.05}{6} \right) = 0.0083$$

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Bonferroni for our example

So we would conduct each pairwise test:

```
both<-cancer_data%>%filter(treatment=="Both")%>%select(tumor_volume)
neither<-cancer_data%>%filter(treatment=="Neither")%>%select(tumor_volume)
can<-cancer_data%>%filter(treatment=="Cannabinoids")%>%select(tumor_volume)
irr<-cancer_data%>%filter(treatment=="Irradiation")%>%select(tumor_volume)
n_b<-t.test(neither, both, alternative="two.sided")
c_b<-t.test(can,both, alternative="two.sided")
i_b<-t.test(irr, both, alternative="two.sided")
n_c<-t.test(neither, can, alternative="two.sided")
n_i<-t.test(neither, irr, alternative="two.sided")
c_i<-t.test(can, irr, alternative="two.sided")
```

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and compare the p-value of this test to an alpha of 0.0083

```
t_statistics<-c(n_b$statistic, c_b$statistic, i_b$statistic, n_c$p_value,
p_values<-c(n_b$p.value, c_b$p.value, i_b$p.value, n_c$p.value, n_i$p.value)
t_statistics
```

```
##          t          t          t          t          t          t          t
##  4.479504  2.659192  3.411826  1.862690 -0.352323 -1.772461
```

```
p_values
```

```
## [1] 0.003912559 0.053873393 0.041289736 0.092130403 0.737291103
```

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Tukey's honest significant differences (Tukey's HSD)



John Wilder Tukey

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- ▶ Tukey's test maintains a 5% experimentwise or “family” error rate.
- ▶ Even if you make many pairwise comparisons, the overall error rate is 5% (at most)
- ▶ Overcomes the issue of multiple testing. Recall: If you conducted 100 tests with a 5% error rate (i.e., $\alpha = 0.05$) AND the H_0 was always true, how many p-values would you expect to be < 0.05 ?
- ▶ The Tukey's error rate is 5% overall, no matter how many tests you do. Thus it overcomes the problem of multiple testing

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Tukey's HSD

TukeyHSD() to calculate the differences in R

You can think of the TukeyHSD() as a wrap-around for the anova, you can either nest the statements like this:

```
TukeyHSD(aov(outcome ~ group))
```

or save the ANOVA as an object and use that in the statement:

```
modelresult<-aov(outcome ~ group)
```

```
TukeyHSD(modelresult, overall_alpha)
```

TukeyHSD() to calculate the differences in R

Here is the R code and output for the cancer example:

```
diffs <- TukeyHSD(cancer_anova, conf.level = 0.05) %>% tidy()  
diffs%>%select(contrast, adj.p.value)
```

```
## # A tibble: 6 x 2  
##   contrast           adj.p.value  
##   <chr>                 <dbl>  
## 1 Cannabinoids-Both     0.378  
## 2 Irradiation-Both      0.00756  
## 3 Neither-Both          0.00661  
## 4 Irradiation-Cannabinoids 0.190  
## 5 Neither-Cannabinoids  0.263  
## 6 Neither-Irradiation   0.964
```

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TukeyHSD() to calculate the differences in R

Each row in the table corresponds to a pairwise test. So the first row is looking at the difference between Cannabinoids vs. Both treatments. The estimated difference in means is 20 and the 95% CI is 13.54 to 26.45. The adjusted p-value is 0.38.

- ▶ “Adjusted” means that it is adjusted for conducting multiple tests. The unadjusted p-value would be smaller. You can tell the unadjusted p-value would be < 0.05 because the 95% CI doesn’t include 0.
- ▶ Thus, when you have an adjusted test you can’t use the CI to infer the value of the p-value!

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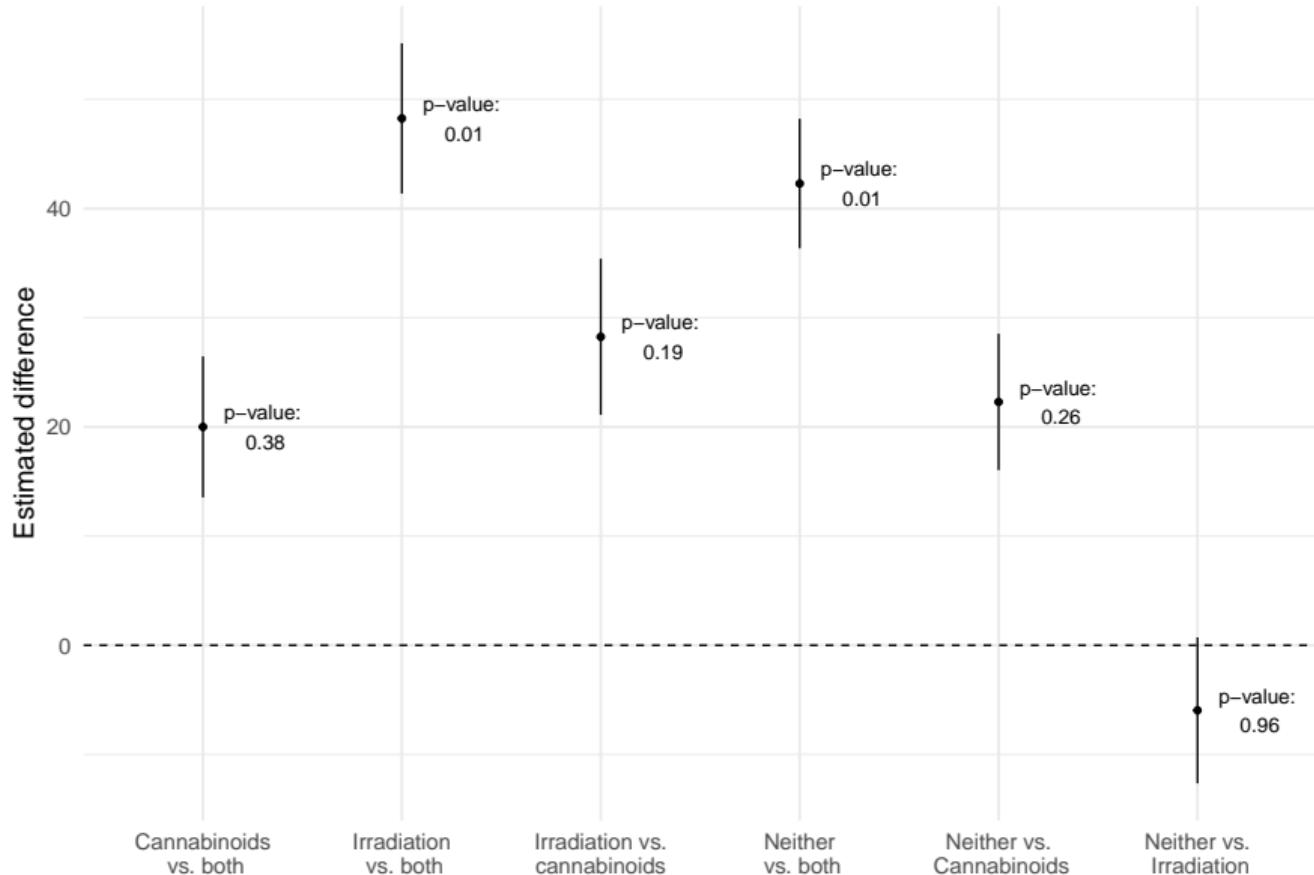
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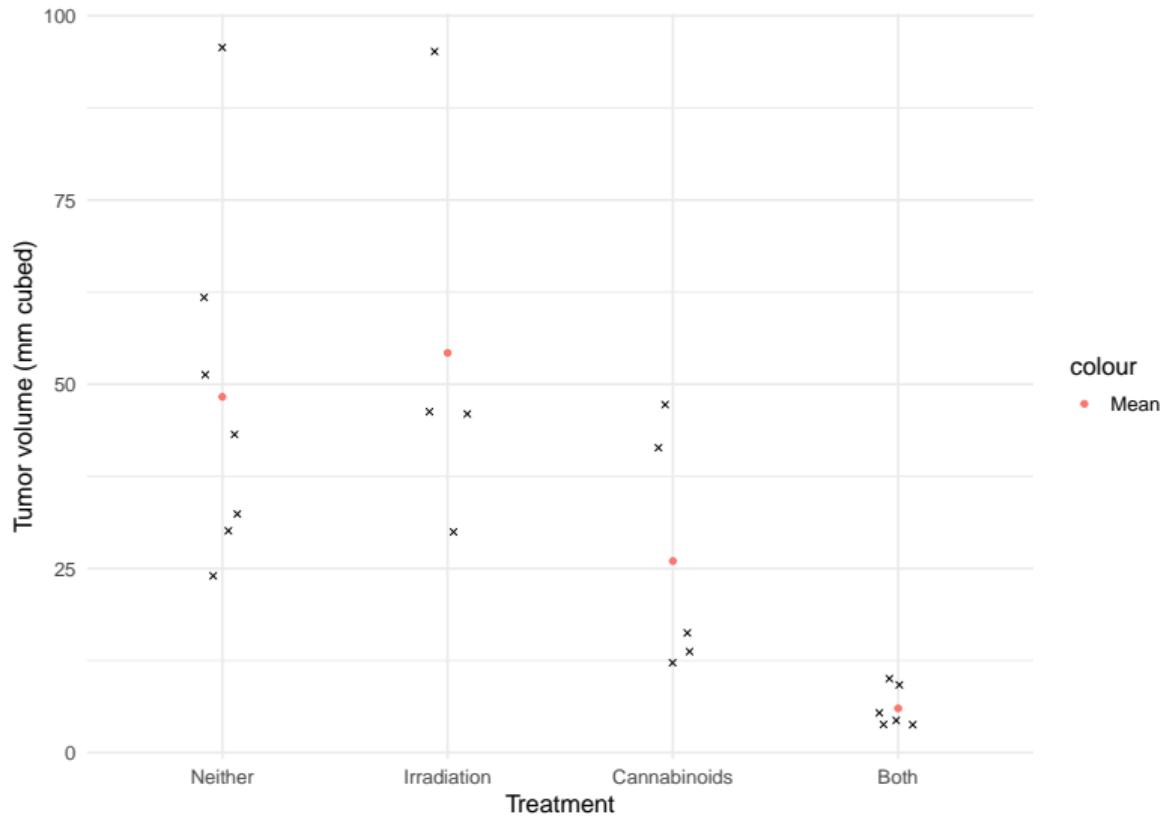
Tukey’s HSD

Visualize the pairwise differences



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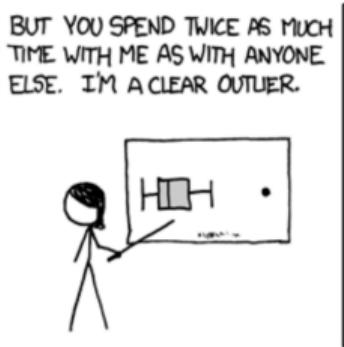
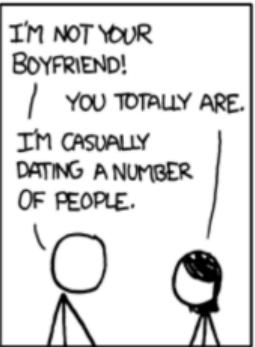
Review raw data for comparison



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Parting humor XKCD.com

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