ME 488: Design of Experiments

Lecture 2: ANalysis Of VAriance

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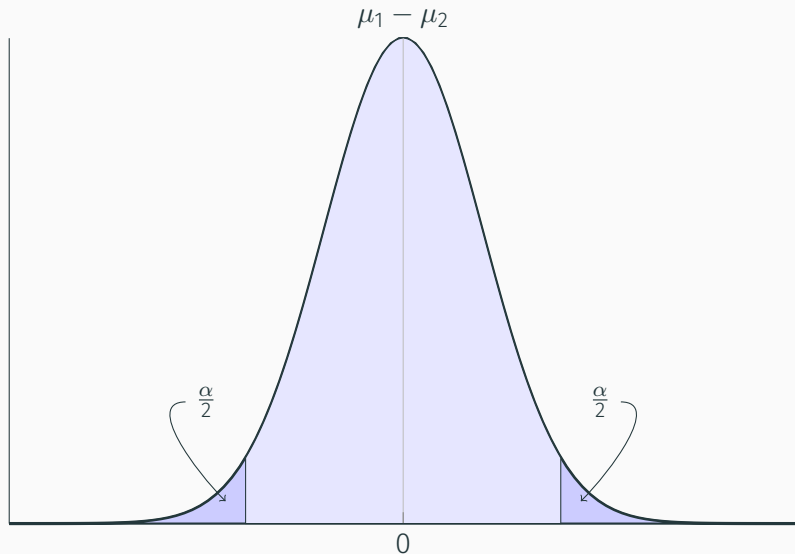Portland, Oregon 97223

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Two Sample Means Test

- If you are comparing two means with a t-test,
- significance level $\alpha = 0.05$

You want to find out

- What is the possible chance you will make a mistake if you claim they are different, but they really are not?
- What type of error is that?

$$\mu_1 - \mu_2$$

$$\frac{\alpha}{2}$$

$$\frac{\alpha}{2}$$

$$0$$

Comparison

Simple T-tests [z-scores and t-scores] and even F-tests work great when we are ==comparing between two items==, but what happens when....

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Simple T-tests [z-scores and t-scores] and even F-tests work great when we are <mark>comparing between two items</mark>, but what happens when....

More than 2 Comparisons

The issue is now, if we have more than two samples to compare, or in our case more than two experimental options, with no other tools in our tool box we are stuck doing pair-wise comparisons. So how many do we need to do?

Number of 2-Sample Tests

Let's visualize for k pairs:

	1	2	$\cdots$	k
1				
2	X			
$\cdots$	X	X		
k	X	X	X	

More than 2 Comparisons

Number of 2-Sample Tests

- Total Number of Pairs $= k^2$
- Number of Self-Pairs $= k$
- Number of Non-Self Pairs $= k^2 - k$
- But each pair is duplicated [i.e. 1x2 is same as 2x1]
- Number of Pairs to Compare $= \frac{k^2 - k}{2} = \frac{k(k-1)}{2} = \binom{k}{2}$

Examples

- $k = 2$: Number of Tests $= \binom{k}{2} = \binom{2}{2} = \frac{2(2-1)}{2} = 1$
- $k = 5$: Number of Tests $= \binom{k}{2} = \binom{5}{2} = \frac{5(5-1)}{2} = 10$
- $k = 20$: Number of Tests $= \binom{k}{2} = \binom{20}{2} = \frac{20(20-1)}{2} = 190$
- $k = 100$: Number of Tests $= \binom{k}{2} = \binom{100}{2} = \frac{100(100-1)}{2} = 4950$

More than 2 Comparisons - Errors

Each one of those tests carries a α chance of making a Type I mistake. What then is the overall chance of making even one error in all your pair-wise comparisons?

Total Error

- Total Number of Treatments [or scenarios] to test $= k$
- Type I Error chance of each one $= \alpha$
- Number of Non-Self Pairs $= \binom{k}{2}$
- Chance you will get any one correct $= 1 - \alpha_i$
- Chance you will get ALL of them correct $= \prod\limits_{i=1}^{\binom{k}{2}} (1 - \alpha_i)$
- If all the α are the same then $= (1-\alpha)^{\binom{k}{2}}$
- $\therefore$ chance you make even one error is $\alpha_{total} = 1 - (1-\alpha)^{\binom{k}{2}}$

Example of Total Error Calculation

Given 18 different types of struts to pair-wise test in an automotive design experiment, and each test has a 1% chance of an Type I error. What is the over all chance of making an error in analyzing the experiment?

- Total Number of Treatments [or scenarios] to test $= k = 18$
- Type I Error chance of each one $= \alpha = 0.01$
- Number of Non-Self Pairs $= \binom{k}{2} = \binom{18}{2} = \frac{18(18-1)}{2} = 153$
- Chance you will get any one correct
  $= 1 - \alpha_i = 1 - 0.01 = 0.99$
- $\alpha_{total} = 1 - (1 - \alpha)^{\binom{k}{2}} = 1 - (0.99)^{153} = 0.785$

This is unacceptable!

Obviously, this method isn't going to work. We need a way to do better.

What can we do?

- Do more experiments, why?
- Test less options, why?
- Do better experiments, why?

This is unacceptable!

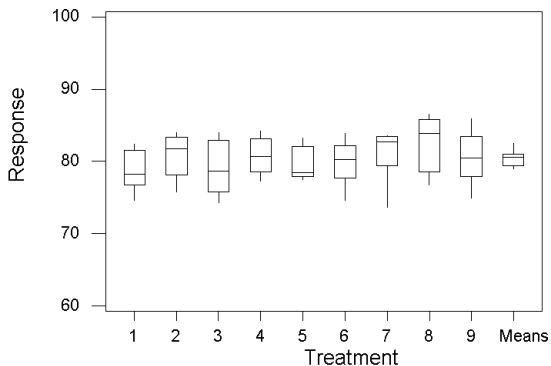Obviously, this method isn't going to work. We need a way to do better.

What can we do?

- Do more experiments, why?
- Test less options, why?
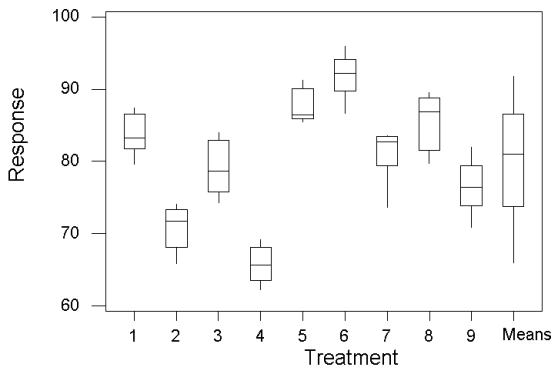- Do better experiments, why?

What else can we do?

- Get a different tool in the 'toolbox'
- Use one that isn't effected by combinatorial explosions
- Use one that we can use a reasonable significance value
- In other words, use ANOVA [ANalysis Of VAriance]

ANOVA: A Graphical Conception

ANOVA
Analysis of variation in an experimental outcome and especially of a statistical variance in order to determine the contributions of given factors or variables to the variance. *Pragmatically, a single statistical test to simultaneously compare all possible pairs of means to see if there are differences between them*

You have done this since you were 3 years old, its just time to put some formality behind it...

ANOVA Hypotheses

- H_0: $\forall i, j | i \neq j \qquad \mu_i = \mu_j$
- H_A: $\exists i, j \qquad \mu_i \neq \mu_j$

The idea is the bOring result is ALL the pairs are the same. The amAzing result is AT LEAST ONE pair is different.

Cloud in the Silver Lining...

The problem is it can only tell you one exists, it can't tell you WHICH pair is different. You can use POST HOC analysis afterwards once you have confirmed one of the pairs IS different.

ANOVA Measures Two Sources of Variation

- Variation BETWEEN groups
  - For each TREATMENT, look at the difference between the treatment mean $\bar{y}_i$ and the OVERALL mean $\bar{\bar{y}}$
  - Remember, we want to 'make the pain hurt'...so we measure $(\bar{y}_i - \bar{\bar{y}})^2$

- Variation WITHIN groups
  - For each DATA POINT, look at the difference between the data point value y_{ij} and it's TREATMENT mean $\bar{y}_i$
  - Remember, we want to 'make the pain hurt'...so we measure $(y_{ij} - \bar{y}_i)^2$

Basically, if these variations are statistically the same, then it is highly unlikely that a pair of means are different.

ANOVA Notation to Remember

- i: $i = 1, 2, \ldots, k$ treatments
- n_i: size of the sample in each treatment (for most of this class, n is the same for each treatment)
- y_{ij}: The jth sample data point value for the ith treatment
- $\bar{y}_i$: the mean of the ith treatment's data
- $\bar{\bar{y}}$: the grand mean, or the mean of the means.

  Careful! $\bar{\bar{y}}$ is NOT (always) the mean of ALL the data!

$$\bar{\bar{y}} = \tfrac{1}{k} \sum_{i=1}^{k} \bar{y}_i$$

Variation WITHIN treatments

- $s_\varepsilon^2 = \frac{1}{k} \sum\limits_{i=1}^{k} s_i^2$

- $s_\varepsilon^2 = \frac{1}{k} \sum\limits_{i=1}^{k} \left(\frac{1}{n-1} \sum\limits_{j=1}^{n} (y_{ij} - \bar{y}_i)^2 \right)$

- $s_\varepsilon^2 = \frac{1}{k(n-1)} \sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{y}_i)^2$

Variation WITHIN treatments

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- $s_\varepsilon^2 = \frac{1}{k(n-1)} \sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{y}_i)^2$

Variation BETWEEN treatments

- $s_{\bar{y}}^2 = \dfrac{\sum\limits_{i=1}^{k} (\bar{y}_i - \bar{\bar{y}})^2}{k-1}$

These Variances can be used as estimates of population variances $\hat{\sigma_y}^2$

- $\hat{\sigma}^2_{y_{within}} \approx s^2_\varepsilon = \frac{1}{k(n-1)} \sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{y}_i)^2$

- $\hat{\sigma}^2_{y_{between}} \approx n s^2_{\bar{y}} = \frac{\sum\limits_{i=1}^{k} (\bar{y}_i - \bar{\bar{y}})^2}{k-1}$

And we can use our two variances test, with the F-statistic

- $F = \dfrac{\hat{\sigma}^2_{y_{between}}}{\hat{\sigma}^2_{y_{within}}} \approx \dfrac{ns^2_{\bar{y}}}{s^2_{\varepsilon}}$

- $df_{between} = k - 1$

- $df_{within} = k(n - 1)$

- If $F \cong 1$, accept H_0, bOring result is probably occurring

- If $F \gg 1$, reject H_0, amAzing result is probably occurring

There is a lot of math and calculations to do in the traditional method. So there is a trick that takes advantage of the relationship between the values you are calculating that makes it much easier to do and more importantly, to analyze.

Sum of Squares Method

- Total variance: $s_{total}^2 = \frac{1}{k(n-1)} \sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{\bar{y}})^2$

- $\sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{\bar{y}})^2 = \sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{y}_i)^2 + n \sum\limits_{i=1}^{k} (\bar{y}_i - \bar{\bar{y}})^2$

- $SS_{total} = SS_{error} + SS_{treatment}$

Sum of Squares Method: Degrees of Freedom

- $df_{total} = kn - 1$
- $df_{error} = k(n - 1)$
- $df_{treatment} = k - 1$
- $df_{total} = df_{error} + df_{treatment}$

ANOVA: Sum of Squares Method

Sum of Squares Method: Degrees of Freedom

- $df_{total} = kn - 1$
- $df_{error} = k(n - 1)$
- $df_{treatment} = k - 1$
- $df_{total} = df_{error} + df_{treatment}$

And conveniently...

- MS: Mean Square
- $s_{total}^2 = \frac{SS_{total}}{df_{total}}$
- $s_{\varepsilon}^2 = \frac{SS_{error}}{df_{error}} = MS_{error}$
- $ns_{\bar{y}}^2 = \frac{SS_{treatment}}{df_{treatment}} = MS_{treatment}$

ANOVA Table

The Table

Source	df	SS	MS	F
Treatment	$df_{treatment}$	$SS_{treatment}$	$MS_{treatment}$	F
Error	df_{error}	SS_{error}	MS_{error}	
Total	df_{total}	SS_{total}		

$$F = \frac{MS_{treatment}}{MS_{error}}$$

- $SS_{total} = \sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{\bar{y}})^2; \ df_{total} = kn - 1$

- $SS_{error} = \sum\limits_{i=1}^{k} \sum\limits_{j=1}^{n} (y_{ij} - \bar{y}_i)^2; \ df_{error} = k(n - 1)$

- $SS_{treatment} = n \sum\limits_{i=1}^{k} (\bar{y}_i - \bar{\bar{y}})^2; \ df_{treatment} = k - 1$

Steps to Do ANOVA

1. Calculate *SS* between the treatments
2. Calculate *SS* within the treatments
3. Determine degrees of freedom for each
4. Use Steps 1-3 to tabulate and calculate the *MS*s
5. Use those to estimate *F*
6. Make a Decision based on the significance of *F*

ANOVA: An Example

Let's do an example by hand

As part of the investigation of the collapse of the roof of a building, a testing laboratory is given all the available bolts that connected the steel structures at 3 different positions on the roof. The forces required to shear each of these bolts (coded values) are as follows:

Position 1	90	82	79	98	83
Position 2	105	89	93	104	89
Position 3	83	89	80	94	91

Given $\alpha = 0.05$, find out whether the differences among the sample means at the 3 positions are significant.

Step 1: Calculate SS between the treatments

Position(i)	y_{i1}	y_{i2}	y_{i3}	y_{i4}	y_{i5}	$\bar{y}_i$
Position 1	90	82	79	98	83	$\frac{436}{5} = 86.4$
Position 2	105	89	93	104	89	$\frac{480}{5} = 96.0$
Position 3	83	89	80	94	91	$\frac{437}{5} = 87.4$

- $n = 5; k = 3$
- Grand Mean: $\bar{\bar{y}} = \frac{86.4+96.0+87.4}{3} = 89.9$
- $SS_{treatment} = n \sum\limits_{i=1}^{k} (\bar{y}_i - \bar{\bar{y}})^2 = 5 \sum\limits_{i=1}^{3} (\bar{y}_i - \bar{\bar{y}})^2$
- $SS_{treatment} = 5 \left[(86.4 - 89.9)^2 + (96.0 - 89.9)^2 + (87.4 - 89.9)^2 \right]$
- $SS_{treatment} = 278.6$

Step 2: Calculate *SS* within the treatments

Pos (i)	$y_{i1} - \bar{y}_i$	$y_{i2} - \bar{y}_i$	$y_{i3} - \bar{y}_i$	$y_{i4} - \bar{y}_i$	$y_{i5} - \bar{y}_i$	$\sum_{j=1}^{5}(y_{ij} - \bar{y}_i)^2$
Pos 1	90-86.4	82-86.4	79-86.4	98-86.4	83-86.4	233.2
Pos 2	105-96.0	89-96.0	93-96.0	104-96.0	89-96.0	252.0
Pos 3	83-87.4	89-87.4	80-87.4	94-87.4	91-87.4	133.2

- $SS_{error} = \sum_{i=1}^{k}\sum_{j=1}^{n}(y_{ij} - \bar{y}_i)^2 = \sum_{i=1}^{3}\sum_{j=1}^{5}(y_{ij} - \bar{y}_i)^2$

- $SS_{error} = 233.2 + 252.0 + 133.2 = 618.4$

Step 3: Determine degrees of freedom for each

- $n = 5; k = 3$
- $df_{error} = k(n-1) = 3(5-1) = 12$
- $df_{treatment} = k - 1 = 3 - 1 = 2$
- $df_{total} = ?$

ANOVA: An Example

Step 4: Use Steps 1-3 to tabulate and calculate the *MS*s

Source	df	SS	MS	F
Treatment	$df_{treatment}$	$SS_{treatment}$	$MS_{treatment}$	F
Error	df_{error}	SS_{error}	MS_{error}	
Total	df_{total}	SS_{total}		

$$F = \frac{MS_{treatment}}{MS_{error}}$$

Step 4: Use Steps 1-3 to tabulate and calculate the MSs

Source	df	SS	MS	F
Treatment	$df_{treatment}$	$SS_{treatment}$	$MS_{treatment}$	F
Error	df_{error}	SS_{error}	MS_{error}	
Total	df_{total}	SS_{total}		

$$F = \frac{MS_{treatment}}{MS_{error}}$$

Step 4a: Tabulate the example data

Source	df	SS	MS	F
Treatment	2	278.6	$MS_{treatment}$	F
Error	12	618.4	MS_{error}	
Total	14	SS_{total}		

ANOVA: An Example

Step 4b: Calculate the example data

Source	df	SS	MS	F
Treatment	2	278.6	$\frac{278.6}{2} = 139.3$	F
Error	12	618.4	$\frac{618.4}{12} = 51.5$	
Total	14	897.0		

- $MS_{error} = \frac{SS_{error}}{df_{error}}$
- $MS_{treatment} = \frac{SS_{treatment}}{df_{treatment}}$

Step 5: Use those to estimate F

Source	df	SS	MS	F
Treatment	2	278.6	139.3	$F = \frac{139.3}{51.5} = 2.70$
Error	12	618.4	51.5	
Total	14	897.0		

- $F = \frac{MS_{treatment}}{MS_{error}}$

Step 6: Make Decisions

- Use a F Hypothesis test
- H_0: $F = 1$; The bOring result : claim basically the same
- H_A: $F > 1$; The amAzing result : claim significantly different
- $\alpha = 0.05$
- Acceptance interval: $P(0 < F \leq F_\alpha) = 1 - \alpha$
- $F_{\alpha, df_{treatment}, df_{error}} = F_{0.05, 2, 12} = 3.89$
- Acceptance interval: $P(0 < F \leq 3.89) = 0.95$
- Our $F = 2.70$ so conclusion is?

Step 6: Make Decisions

- Use a F Hypothesis test
- H_0: $F = 1$; The bOring result : claim basically the same
- H_A: $F > 1$; The amAzing result : claim significantly different
- $\alpha = 0.05$
- Acceptance interval: $P(0 < F \le F_\alpha) = 1 - \alpha$
- $F_{\alpha, df_{treatment}, df_{error}} = F_{0.05, 2, 12} = 3.89$
- Acceptance interval: $P(0 < F \le 3.89) = 0.95$
- Our $F = 2.70$ so conclusion is?
- Not enough evidence to reject H_0, so can not say there is a difference. If we did, we would be wrong how many times out of 100?

Let's do the same example using R

As part of the investigation of the collapse of the roof of a building, a testing laboratory is given all the available bolts that connected the steel structures at 3 different positions on the roof. The forces required to shear each of these bolts (coded values) are as follows:

Position 1	90	82	79	98	83
Position 2	105	89	93	104	89
Position 3	83	89	80	94	91

Given $\alpha = 0.05$, find out whether the differences among the sample means at the 3 positions are significant.

Steps to Do ANOVA in R

1. Load or Enter Data into R
2. Set Factors
3. Run ANOVA function
4. Interpret Results

Step 1: Load or Enter Data into R

- Create the data set as a CSV file (Text Editor or Excel)
- Text file Example is located on website
- To load it into a dataframe (think Excel or Access Table) in R
- Confirm data is loaded

Input

```
1 > setwd("~/Desktop") # This is the location of the file
2 > myData <- read.csv("ME488_Week2_Lecture_ANOVA_Example_DATA.
     csv")
3 > myData # Confirm data is loaded, myData is the dataframe
     name
```

Output

```
    Position Force
1         1    90
2         1    82
3         1    79
4         1    98
5         1    83
6         2   105
7         2    89
8         2    93
9         2   104
10        2    89
11        3    83
12        3    89
13        3    80
14        3    94
15        3    91
```

Step 2: Set Factors

- By default R treats numbers as numbers
- But Position is nominal and should be used as a category, or what R calls a factor
- We need to covert the data we want to be factors to factors
- This is not needed when the data is already categorical text
- This ↑ ↑ ↑ ↑ ↑ is the most common project FUBAR error that students make

STEP 2: SET FACTORS

Input

```
1  > myData$Position <- factor(myData$Position)
```

Note there is no real output for this function.

Dataframes and Variables

- In the example the dataframe is called 'myData'
- There are two variables in the dataframe, Position and Force
- To refer to just one column follow the 'dataframe$variable' format
- In the example, we used 'myData$Position'

Step 3/4: Run the ANOVA and Interpret

- It really is just a wrapper for 'lm';
- Does all the nasty work you did with the calculator
- Need to 'store' the results and call them later

Input

```
1  > m <- aov(Force~Position, data=myData)
2  > anova(m) # Displays an ANOVA Table 'summary(m)' does the
        same thing
```

Output

```
1  Analysis of Variance Table
2
3  Response: Force
4            Df Sum Sq Mean Sq F value Pr(>F)
5  Position   2 278.53 139.267  2.7025 0.1074
6  Residuals 12 618.40  51.533
```

Compare to your by-hand version! R gives you the p_{value}

ANOVA
- Can not tell you WHICH pair is different
- Can not be used for multiple response at one time
- Need to use other tests to do those

Assumptions
- Data is normally distributed - Flexible if N is high
- Homoscedastic: Variances are approximately equal between groups
- Observations are independent

Model for One Factor (One Way ANOVA)

$y_{ij} = \mu + A_i + \varepsilon_{ij}$

- μ: Constant Term Common to All Observations
- A_i: i^{th} treatment's deviation from μ
- ε_{ij}: Random/error term

Model for One Factor (One Way ANOVA)

$y_{ij} = \mu + A_i + \varepsilon_{ij}$

- μ: Constant Term Common to All Observations
- A_i: i^{th} treatment's deviation from μ
- ε_{ij}: Random/error term

Model for Two Factor (Two Way ANOVA)

$y_{ij} = \mu + A_i + B_i + \varepsilon_{ij}$

- μ: Constant Term Common to All Observations
- A_i: i^{th} treatment's deviation from μ due to *A* effect
- B_i: i^{th} treatment's deviation from μ due to *B* effect
- ε_{ij}: Random/error term

ANOVA FOR MORE THAN ONE FACTOR

Sum of Squares Method Still Works!

- $SS_{total} = SS_{error} + SS_A + SS_B$
- $df_{total} = df_{error} + df_A + df_B$
- $df_{total} = kn - 1$ $df_{error} = k(n-1)$ $df_{treatment} = k - 1$

Degrees of Freedom are bit different

- $df_A = (K_a - 1)$
- $df_B = (K_b - 1)$
- $df_{total} = (K_a K_b - 1)$
- $df_{error} = df_{total} - df_A - df_B$
    - $= (K_a K_b - 1) - (K_a - 1) - (K_b - 1)$
    - $= (K_a K_b - K_a) - (K_b - 1) = K_a(K_b - 1) - (K_b - 1)$
    - $= (K_a - 1)(K_b - 1)$

The Table is similar

Source	df	SS	MS	F
A	df_A	SS_A	MS_A	F_A
B	df_B	SS_B	MS_B	F_B
Error	df_{error}	SS_{error}	MS_{error}	
Total	df_{total}	SS_{total}		

$$F_{factor} = \frac{MS_{factor}}{MS_{error}}$$

Assuming your data set had another column of values 'Angle'
[Download the file to get it]

Input

```
1  > myData <- read.csv("ME488_Week2_Lecture_2W_ANOVA_Example_
       DATA.csv")
2  > myData$Position <- factor(myData$Position)
3  > myData$Angle <- factor(myData$Angle)
4  > library(car) # built in function in R does odd way of
       multivariable ANOVA
5  > m <- lm(Force~Position+Angle, data=myData)
6  > Anova(m, type='III') # We want the Type III kind
```

Output

```
1   Anova Table (Type III tests)
2
3   Response: Force
4               Sum Sq Df  F value    Pr(>F)
5   (Intercept) 17024.5  1 636.0324 6.543e-09 ***
6   Position      278.5  2   5.2030   0.03569 *
7   Angle         404.3  4   3.7758   0.05197 .
8   Residuals     214.1  8
9   ---
10  Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Now we have some evidence that the factors matter! Why do I
say that?

Just forget about even bothering to do this by hand! But know
how to 'fill in the blanks' in a table.

Recall...

ANOVA is limited in that it can only tell you that at least one pair is different [in effect the factor/treatment matters] but it can't tell you WHICH pair is different.

Post Hoc

We need a different method to check for which one. There are many of these **Post Hoc** tests, we are going to only cover the **Tukey HSD** test.

POST HOC

Let's look at our example again

[Note: Data is **different** this time around]
As part of the investigation of the collapse of the roof of a
building, a testing laboratory is given all the available bolts
that connected the steel structures at 3 different positions on
the roof. The forces required to shear each of these bolts
(coded values) are as follows :

Position 1	90	82	79	78	83
Position 2	105	99	93	104	98
Position 3	83	89	80	74	71

Given $\alpha = 0.05$, find out whether the differences among the
sample means at the 3 positions are significant.

ANOVA in R for our new example

The output from R is:

```
1  Analysis of Variance Table
2
3  Response: Force
4            Df Sum Sq Mean Sq F value    Pr(>F)
5  Position   2 1213.2  606.60  18.703 0.0002053 ***
6  Residuals 12  389.2   32.43
```

This time there is a 0.02% chance of making a Type I error if we reject the H_0, so we claim there IS a difference in at least one pair comparison, so Position does matter.
But we don't know which one...

Tukey HSD Test

Tukey's Honest Significant Difference Test is a method to pair-wise compare multiple sets in a single step. The basic idea is compare means against each other and look for any difference that is more than expected standard error.

Notes:

- In effect, a t-test, corrected for overall α to reduce Type I.
- Use it **after** an ANOVA to have more confidence that a detected difference is meaningful.
- Order of comparison matters, starts by comparing largest and smallest ones, if there is no significant difference there then stops.

Comparison Concept Example

If you had factor with 4 levels($k = 4$) A,B,C,D,
with means $\overline{x_A}$, $\overline{x_B}$, $\overline{x_C}$, and $\overline{x_D}$,
such that $\overline{x_B} > \overline{x_D} > \overline{x_A} > \overline{x_C}$
The the order of comparisons would be:

- B vs C
- B vs A
- B vs D
- D vs C
- D vs A
- A vs C

Tukey Test in R

Assuming the ANOVA model is in 'm', run a Tukey test as follows

```
> TukeyHSD(m, ordered=TRUE, conf.level=0.95)
```

Note: the default options are 95% and NOT to order the list]

Tukey Test in R

Output

```
1    Tukey multiple comparisons of means
2      95% family-wise confidence level
3      factor levels have been ordered
4
5  Fit: aov(formula = Force ~ Position, data = myData)
6
7  $Position
8      diff       lwr      upr      p adj
9  1-3  3.0 -6.609248 12.60925 0.6905922
10 2-3 20.4 10.790752 30.00925 0.0002860
11 2-1 17.4  7.790752 27.00925 0.0011059
```
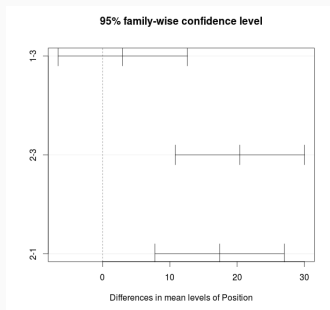
To interpret, look at the p_{values} or look at the confidence ranges
[i.e. see if 0 is in there]. In this case, which one is obviously the
different one?

Plotting Tukey Test in R

You can also plot the differences to visually see them

```
1  > plot(TukeyHSD(m,ordered=TRUE))
```

Homework

- Homework is less this week. But there are practice ANOVA tables posted online with solutions
- HIGHLY recommended that you try them to get familiar with them, especially the last one in the second group.
- Homework #002 is posted. See online for format.