STAT1201 - Summer Semester, 2022

Live Lectures 9 & 10 - Analysis of Variance (ANOVA-Module 9)

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Learning Objectives

We use the concept of variance to compare population means

- ► ONE WAY ANOVA (also called completely randomised designs)
- One quantitative response (or dependent) varaible
- One independent categorical variable
 - TWO WAY ANOVA
- One quantitative response (or dependent) variable
- Two independent categorical variables

ONE WAY ANOVA

- We used two sample t-test to compare two population means (e.g. to compare average breath holding times for young adult males and females).
- ► However, there are cases that we need to compare more than two populations (or groups).
- Many scientific applications involve experiments that consider more than two groups or populations pertaining to one factor of interest. We use One-way ANOVA to compare more than two groups or populations.
- Examples
 - Age groups (1 (20-29), 2-(30-39), 3-(40-49), 4-(50-59))
 - Type of fertiliser (1, 2, 3)
 - Social media usage (Low, Medium, High)

ONE WAY ANOVA

Following example is used to discuss the concept of ONE WAY ANOVA.

A researcher is interested to analyse the birth weights of new borns on a particular day in a New York hospital.

The data file "M9BirthWeight.csv" includes data for the following variables.

BirthWeight (g) - Birth weights of new borns

Age (years) - Mother's age

Race - Mother's race (White, Black, Other)

Smoking (Yes/No) - Mother's smoking status

Question

Is there a difference in the mean birth weights of the new borns in three race groups?

We can perform an One Way ANOVA test to answer this question.

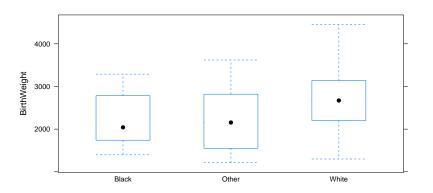
First we campute sample means using R.

```
bw = read.csv("M9BirthWeight.csv")
aggregate(BirthWeight ~ Race, data = bw, mean)
```

```
Race BirthWeight
1 Black 2240.111
2 Other 2288.833
3 White 2644.867
```

Sample means are different. We are interested to see whether these differences are by chance (or due to sampling variability) or whether differences are statistially significant. That is whether population mean birth weights are different for three race groups.

```
library(lattice)
bwplot(BirthWeight ~ Race, data=bw)
```



Define μ as the population mean birth weight

 H_0 : $\mu_B = \mu_O = \mu_W$ (population means are equal)

 H_1 : Not all population means are equal (or at least one population mean is different from others)

To perform an ANOVA test of equality of population means, we subdivide the total variation in the values into two parts.

- 1) Variation between the groups
- 2) Variation within the groups

Total variation (SST) = Between Group Variation (SSB or SSG) + Within Group Variation (SSW or SSR)

```
Define
```

 $\mathsf{SST} = \mathsf{Total} \; \mathsf{sum} \; \mathsf{of} \; \mathsf{squares}$

.

SSG = Sum of squares between groups

.

 $\mathsf{SSR} = \mathsf{Sum}$ of squares within group or residual sum of squares

.

 $\mathsf{SST} = \mathsf{SSG} + \mathsf{SSR}$

Statistical software usually summarises an analysis of variance in the form of an ANOVA table.

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Group (categorical Variable Name)	k-1	SSG	MSG = SSG/(k-1)	MSG/MSR	P(F>=F*)
Residuals	n-k	SSR	MSR = SSR/(n-k)		
Total	n - 1	SST	MST = SST/(n-1)		
k = number of groups			n = sample size		

 $F_{stat} = \frac{MSG}{MSR}$

Use R to obtain the ANOVA table

summary(aov(BirthWeight ~ Race, data=bw))

```
Df Sum Sq Mean Sq F value Pr(>F)
Race 2 3002792 1501396 2.899 0.0604 .
Residuals 87 45060356 517935
---
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 '
Note: R does not provide total column. We can calculate using SST
= SSG + SSR
```

This F statistic has a F distribution with numerator degrees of freedom equals 2 (=k-1) and numerator degrees of freedom equals 87 (=n-k).

Find the p-value Using R.

p-value = 1 - pf(2.899, df1 = 2, df2 = 87)

p-value = 0.064

Poll Question 1

Based on the p-value there is

- a) weak evidence to conclude that there is a difference in the population mean birth weights of new borns between three race groups.
- b) moderate evidence to conclude that there is a difference in the population mean birth weights of new borns between three race groups.
- strong evidence to conclude that there is a difference in the population mean birth weights of new borns between three race groups.
- d) no evidence to conclude that there is a difference in the population mean birth weights of new borns between three race groups.

ONE WAY ANOVA - Coefficient of Determination

Similar to linear regression models, we can calculate coefficient of Determination \mathbb{R}^2 .

$$R^{2} = \frac{SSG}{SST}$$

$$R^{2} = \frac{SSG}{SSG + SSR}$$

$$R^{2} = \frac{3,002,792}{3,002,792 + 45,060,356}$$

$$R^{2} = \frac{3,002,792}{48,063,148}$$

$$R^{2} = 0.0625$$

6.25% of variability in the birth weight is explained by the race of the mother.

ONE WAY ANOVA - Assumptions

To use ONE WAY ANOVA, certain assumptions need to be satisfied.

- 1) Observations are random and independent.
- 2) Observations in each sample group are drawn from approximately normally distributed populations.

One-way ANOVA test is quite robust to violations of normality assumption. That is, the assumption can be a little violated and still provide valid results.

 Population variances of the groups are equal (homogeneity of variances).

This assumption can be tested using Levene's test. However we do not discuss it in STAT1201.

If you are doing ONE-WAY ANOVA for your research project, testing only normality assumption is sufficient.

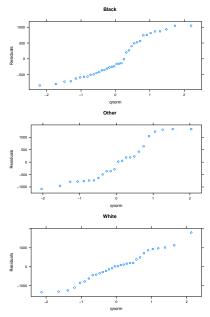
ONE WAY ANOVA - Residuals

Residuals from ONE-WAY ANOVA is different from residuals from linear regression models. Residuals are the differences between the observed responses and the sample mean of their group.

We can use residuals to chack normality assumption. We can draw Quantile-Quantile plots (Normal probability plots) for the residuals for each race group. If the points in each group form an approximate straight line, the respective population is approximately normally distributed.

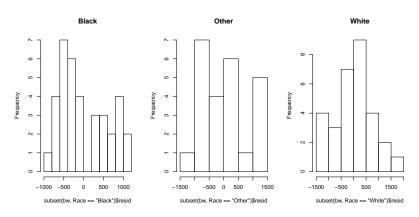
In addition we can use histograms or boxplots for residuals for each race group and see the shape of the distributions.

ONE WAY ANOVA - Normal Probability plots for Residuals



ONE WAY ANOVA - Histograms for Residuals

```
par(mfrow=c(1,3))
hist(subset(bw, Race=="Black")$resid, main="Black")
hist(subset(bw, Race=="Other")$resid, main="Other")
hist(subset(bw, Race=="White")$resid, main="White")
```



ONE WAY ANOVA - Multiple comparisons

The null and alternative hypothesis in ONE WAY ANOVA is such that:

$$H_0: \mu_1 = \mu_2 = \ldots = \mu_k \text{ (k = no. of groups)}$$

 H_1 : Not all μ_j 's are the same

If H_0 is rejected then the obvious question is to ask which population means are different.

That is whether:

$$\mu_1 \neq \mu_2$$
 or

$$\mu_1 \neq \mu_3$$
 or

$$\mu_2 \neq \mu_4$$
 and so on.

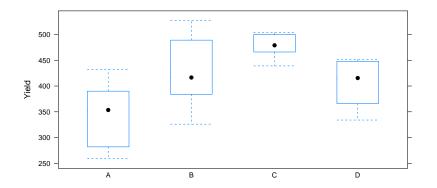
Suppose a completely randomised design is carried out to see the response of potato yield for a four treatment groups (treatment group: A, B, C, D)

$$H_0: \mu_A = \mu_B = \ldots = \mu_D$$

 H_1 : Not all population mean potato yields are the same

We can use data saved in "M9Potato.csv" file to obtain the results in R.

```
potato = read.csv("M9Potato.csv")
library(lattice)
bwplot(Yield ~ Treatment, data=potato)
```



```
summary(aov(Yield ~ Treatment, data = potato))
```

```
Treatment 3 54416 18139 5.773 0.00517 **

Residuals 20 62837 3142
---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '
```

Df Sum Sq Mean Sq F value Pr(>F)

Poll Question 2 Based on the ANOVA table, what are the numerator and denominator degrees of freedom of the F distribution to find the p-value?

- a) (20, 3)
- b) (3, 20)
- c) (2, 19)
- d) (4, 21)

```
summary(aov(Yield ~ Treatment, data = potato))
```

```
Treatment 3 54416 18139 5.773 0.00517 **

Residuals 20 62837 3142
---

Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 '
```

Df Sum Sq Mean Sq F value Pr(>F)

From the results table, $F_{stat} = 5.773$ and p-value = 0.00517

Thus, there is strong evidence to conclude that means are not all equal.

Then the obvious question is mean yields of the which treatment pairs are different?

ONE WAY ANOVA - Multiple comparisons

To answer the question that mean yields of the which treatment pairs are different, we can use two approaches.

- Use two sample t-test to compare differences between each pair of treatments (can use pooled two sample t - test). However, when there are a large number of pairs, this method will be tedious.
- 2) Tukey's Honestly Significant Difference (Tukey's HSD)

There are 4 treatment groups in "Potato" example. That is, k=4.

Number of pairs to be compared is $\binom{k}{2}$.

Number of pairs to be compared is $\frac{k!}{2!(k-2)!}$

Number of pairs to be compared is $\frac{4!}{2!(4-2)!}$

Number of pairs to be compared is 4*(4-1)/2 = 6

Pairwise comparisons using t tests with pooled SD

data: potato\$Yield and potato\$Treatment

```
A B C
B 0.02041 - - -
C 0.00055 0.12837 -
D 0.07778 0.51728 0.03620
```

P value adjustment method: none

If we use the 5% level of significance (i.e. $\alpha=0.05$) for the pairwise *t*-tests, reject individual null hypothesis if each p-value in the matrix is less than 0.05. That is $\mu_A \neq \mu_B$, $\mu_A \neq \mu_C$ and $\mu_C \neq \mu_D$

ONE WAY ANOVA - Multiple comparisons - Bonferroni correction

Bonferroni correction is used to counteract the problem of multiple comparisons. We use a smaller level of significance than in the two-sample t-test.

The new level of significance $=\frac{0.05}{q}$, where q is the number of pairs.

Thus for Bonferroni correction, new $\alpha = \frac{0.05}{6} = 0.0083$

ONE WAY ANOVA - Multiple comparisons Example - Bonferroni correction

Pairwise comparisons using t tests with pooled SD

data: potato\$Yield and potato\$Treatment

```
A B C
B 0.1225 - - -
C 0.0033 0.7702 -
D 0.4667 1.0000 0.2172
```

P value adjustment method: bonferroni

Now reject individual null hypothesis if each adjusted p-value in the matrix is less than 0.0083.

ONE WAY ANOVA - Multiple comparisons Example - Bonferroni correction

Poll Question 3

Using Bonferroni correction, population mean potato yields are different for treatment pairs

- a) A and B only
- b) A and D only
- c) A and C only
- d) B and C only

Tukey's HSD

- Bonferroni method is a little too conservative, reducing the overall power
- Deatailed information about Tukey's HSD will not be discussed here
- ► We can use R

ONE WAY ANOVA - Multiple comparisons Example - Tukey's HSD

```
TukeyHSD(aov(potato$Yield ~ potato$Treatment))
  Tukey multiple comparisons of means
    95% family-wise confidence level
Fit: aov(formula = potato$Yield ~ potato$Treatment)
$`potato$Treatment`
         diff
                     lwr
                               upr padj
B-A 81.50000 -9.078612 172.07861 0.0873484
C-A 132.83333 42.254721 223.41195 0.0028498
D-A 60.16667 -30.411946 150.74528 0.2765269
C-B 51.33333 -39.245279 141.91195 0.4084051
D-B -21.33333 -111.911946 69.24528 0.9110515
D-C -72.66667 -163.245279 17.91195 0.1451915
```

Overall we can conclude that the population mean potato yields are different for treatment pair A and C.

There is inconclusive evidence of differences between the other five pairs of treatments.

TWO WAY ANOVA

- One response (or dependent) numerical variable
- Two independent categorical variables

		Treatment 1 (Categorical Variable 1)					
		1	2	3	4		
Treatment 2	1						
(Categorical	2						
Variable 2)	3						

Allows to examine the interaction effect of the two treatments (categorical variables). In this class we focus the case where the number of items in each cell is equal.

TWO WAY ANOVA - An example

Based on the study of Oxytocin and Emotions (Inspired by the work of Turner et al (1999)). 24 women (12 single, 12- in a relationship) participated in an study and plasma oxytocin level was measured before and after receiving an stimulus event. The following variables are considered in the data file M9Oxytocin.csv

Before - Plasma oxytocin level (pg/ml) before receiving stimulus event

After - Plasma oxytocin level (pg/ml) after receiving stimulus event

Relationship - Whether partcipant is in a relationship or not (Yes, No)

Stimulus - Stimulus event received (Happy, sad, Massage)

TWO WAY ANOVA - An example

- ▶ 24 women The sample size (n=24)
- Response variable Change in Oxytocin level (pg/ml).
 Calculate as (After Basal)
- Two independent categorical variables
 - Stimulus Stimulus event (Happy, Sad, Massage) -> k=3
 - Relationship relationship status (Yes, No) -> c=2

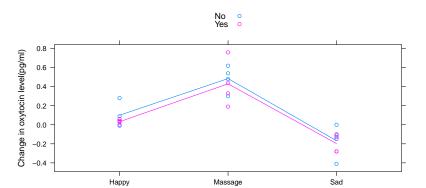
```
oxy = read.csv("M90xytocin.csv", as.is=FALSE)
table(oxy$Relationship, oxy$Stimulus)
```

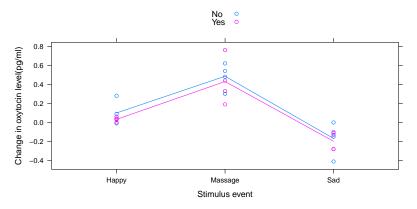
```
Happy Massage Sad
No 4 4 4
Yes 4 4
```

The table shows the number of observations in each cell.

Draw a plot and compare the changes in Oxytocin level by relationship status and stimulus event.

```
oxy$change = oxy$After - oxy$Before
library(lattice)
xyplot(change ~ Stimulus, data=oxy, group=Relationship,
type=c("p", "a"), auto.key = TRUE, ylab="Change in oxytocinxlab="Stimulus event")
```





The lines connecting the means of each row (relationship status here) do not cross each other. This indicates that interaction of stimulus event and relationship status on change in Oxytocin is unlikely. However, we include interaction term in our TWO WAY ANOVA here to statistically test this.

We can first see the mean change in Oxytocin level for each combination of stimulus event and relationship status.

```
aggregate(change ~ Stimulus*Relationship, data=oxy, mean)
```

```
Stimulus Relationship change
                    No
                        0.1000
    Happy
2
  Massage
                  No 0.4850
3
      Sad
                    No -0.1675
4
    Happy
                  Yes 0.0325
5
  Massage
                  Yes 0.4300
6
      Sad
                   Yes -0.1975
```

To test whether the observed differences are significant, we need to perform a TWO WAY ANOVA.

is related to the stimulus event.

```
summary(aov(change ~ Stimulus*Relationship, data=oxy))
```

```
Df Sum Sq Mean Sq F value Pr(>F)
Stimulus 2 1.6655 0.8327 37.443 3.85e-07 **
Relationship 1 0.0155 0.0155 0.697 0.415
Stimulus:Relationship 2 0.0015 0.0007 0.033 0.968
Residuals 18 0.4003 0.0222
---
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 '
```

p - value <0.001 for the effect of stimulus event. We have strong evidence to conclude that population mean change in Oxytocin level

p - value =0.415 for the effect of relationship status. There is no evidence to conclude that population mean change in Oxytocin level is related to the relationship status.

```
Df Sum Sq Mean Sq F value Pr(>F)
Stimulus 2 1.6655 0.8327 37.443 3.85e-07 **
Relationship 1 0.0155 0.0155 0.697 0.415
Stimulus:Relationship 2 0.0015 0.0007 0.033 0.968
Residuals 18 0.4003 0.0222
```

Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 '

summary(aov(change ~ Stimulus*Relationship, data=oxy))

Poll Question 4

Based on the Two-way ANOVA results there is

- a) moderate evidence to conclude that population mean change in Oxytocin level is affected by relationship status and stimulus event (p=0.032).
- b) no evidence to conclude that population mean change in Oxytocin level is affected by relationship status and stimulus event (p=0.968).
- c) weak evidence to conclude that population mean change in Oxytocin level is affected by relationship status and stimulus event (p=0.064).
- d) no evidence to conclude that population mean change in Oxytocin level is affected by relationship status and stimulus event (p=0.484).

TWO WAY ANOVA - Assumptions

- Observations are independent. There should be no relationship between the observations in each group or between the groups themselves. That is, there must be different participants (or subjects) in each cell.
- The populations from which samples are obtained for each combination of the groups of the two independent variables should be approximately normally distributed.

two-way ANOVA test is quite robust to violations of noramality assumption. That is, the assumption can be a little violated and still provide valid results.

 Population variances of the each combination of the groups of the two independent variables are equal (homogeneity of variances).

Next

Reminders

Next week

Quiz 6 will be closed on Monday, 9 Jan, 2023 at 3:00 pm

Module 10 - Experimental Design, Presenting Data, Tuesday 10 Jan

by Dr. Masato Yamamichi(Zoom: 818 1453 7986)

Module 11 - Categorical Data, Thursday 12 Jan

by Dr. Wasanthi Thenuwara (Zoom: 818 1453 7986)