Chapter 11

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Stat 205: Elementary Statistics for the Biological and Life Sciences

Comparing more than two means

- In Chapter 7 we had two groups and tested $H_0 : \mu_1 = \mu_2$.
- In Chapter 11 we will have I groups and test $H_0 : \mu_1 = \mu_2 = \cdots = \mu_I$.
- We are still interested in whether the population means are the same across groups, there's just more than two.
- The alternative hypothesis is H_A : one or more of $\mu_1, \mu_2, \ldots, \mu_I$ are different.
- Let's look at an example where $I = 5$.

Example 11.1.1: Organic farming of corn

When growing sweet corn, can organic methods be used successfully to control harmful insects and limit their effect on the corn? In a study researchers compared the weights of ears of corn under five organic conditions: (a) using a beneficial soil nematode, (b) parasitic wasp, (c) both the nematode and the wasp, (d) a bacterium, and (e) a control with no treatment. In summary, the treatments are

- Treatment 1: Nematodes
- Treatment 2: Wasps
- Treatment 3: Nematodes and wasps
- Treatment 4: Bacteria
- Treatment 5: Control

Corn data

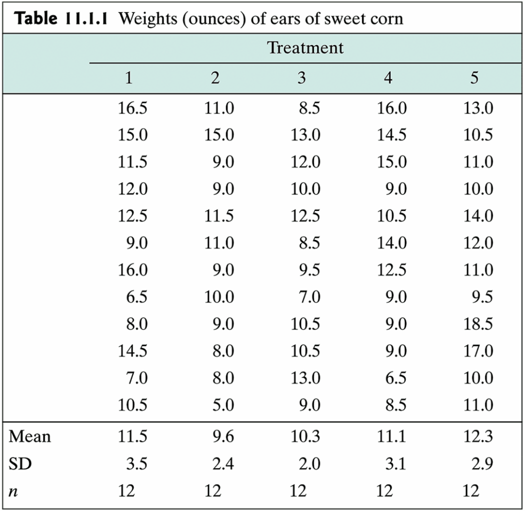
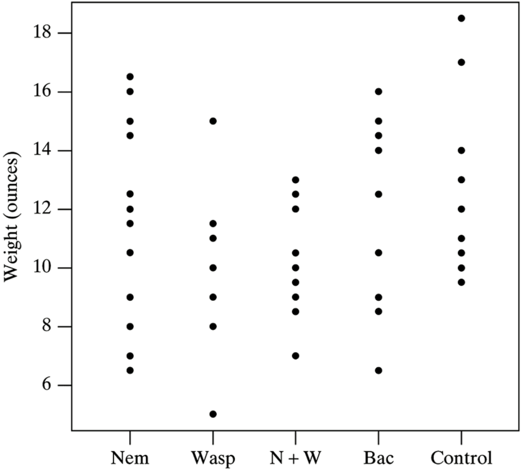


Table 11.1.1 Weights (ounces) of ears of sweet corn

	Treatment				
	1	2	3	4	5
	16.5	11.0	8.5	16.0	13.0
	15.0	15.0	13.0	14.5	10.5
	11.5	9.0	12.0	15.0	11.0
	12.0	9.0	10.0	9.0	10.0
	12.5	11.5	12.5	10.5	14.0
	9.0	11.0	8.5	14.0	12.0
	16.0	9.0	9.5	12.5	11.0
	6.5	10.0	7.0	9.0	9.5
	8.0	9.0	10.5	9.0	18.5
	14.5	8.0	10.5	9.0	17.0
	7.0	8.0	13.0	6.5	10.0
	10.5	5.0	9.0	8.5	11.0
Mean	11.5	9.6	10.3	11.1	12.3
SD	3.5	2.4	2.0	3.1	2.9
n	12	12	12	12	12

Side-by-side dotplots of corn data

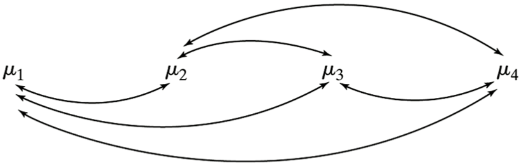


Comparing more than two means at the same time

- It's natural to ask: why not now just compare all possible pairs $\mu_1 - \mu_2, \mu_1 - \mu_3, \mu_2 - \mu_3$, etc., with a bunch of pairwise t-tests?
- This results in *multiple comparisons*: the same data set is used to make multiple inferences on $I > 2$ associated parameters.
- The overall Type I error is then larger (perhaps much larger) than α.
- ANOVA keeps α fixed, even with lots of comparisons all at once.

Comparing four population means requires six comparisons

$$\begin{array}{lll} H_0\colon \mu_1 = \mu_2 & H_0\colon \mu_1 = \mu_3 & H_0\colon \mu_1 = \mu_4 \\ H_0\colon \mu_2 = \mu_3 & H_0\colon \mu_2 = \mu_4 & H_0\colon \mu_3 = \mu_4 \end{array}$$



Comparing 3 means requires 3 comparisons, 4 means requires 6 comparisons, 5 means requires, 10 comparisons, etc. In general, there's $I(I-1)/2$ pairwise comparisons to make.

Type I error

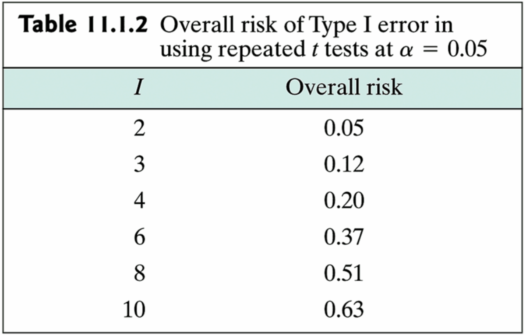


Table 11.1.2 Overall risk of Type I error in using repeated t tests at $\alpha = 0.05$

I	Overall risk
2	0.05
3	0.12
4	0.20
6	0.37
8	0.51
10	0.63

This is an example of what the true Type I error might be if we didn't use ANOVA, but rather used $I(I-1)/2$ t-tests.

Building the test

- We will test $H_0 : \mu_1 = \mu_2 = \cdots = \mu_I$ via *analysis of variance* (ANOVA).
- ANOVA compares how variable the sample means $\bar{y}_1, \bar{y}_2, \ldots, \bar{y}_I$ are to how variable observations are *around each mean*.
- Assumptions: Observations in each group are indepedently normally distributed with the same variance σ^2.
- The data in different groups are also independent.

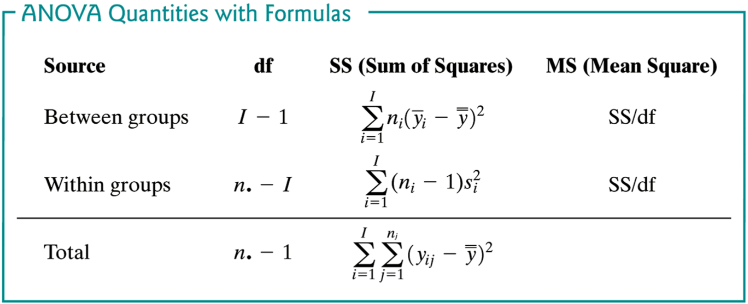
Sums of Squares

- SS(between)$= \sum_{i=1}^{I} n_i(\bar{y}_i - \bar{\bar{y}})^2$ measures the variability *explained by letting each group have its own mean*.
- SS(within)$= \sum_{i=1}^{I}(n_i - 1)s_i^2$ measures the variability *that is left over*, also called "pure error."
- SS(total)$= \sum_{i=1}^{I}\sum_{j=1}^{n_i}(y_{ij} - \bar{y})^2$ measures *the total variability in the data ignoring groups*.
- SS(total)$=$SS(between)$+$SS(within).
- The variability in the data is equal to the variability explained by the model plus the slop that's left over.

ANOVA table

- A mean square is the average of the squared deviations from a central value. It is a sum of squares divided by the number of informative values in the sum of squares, called the "degrees of freedom", or df.
- The df for between is $df_b = I - 1$; the df for within is $df_w = n - I$ where $n = n_1 + n_2 + \cdots + n_I$.
- MS(between)=SS(between)$/(I-1)$, MS(within)=SS(within)$/(n-I)$.
- We collect the sums of squares, mean squares, df, in a table called an ANOVA table.

ANOVA formulae



ANOVA Quantities with Formulas

Source	**df**	**SS (Sum of Squares)**	**MS (Mean Square)**
Between groups	$I - 1$	$\sum_{i=1}^{I} n_i(\bar{y}_i - \bar{\bar{y}})^2$	SS/df
Within groups	$n_{\cdot} - I$	$\sum_{i=1}^{I} (n_i - 1)s_i^2$	SS/df
Total	$n_{\cdot} - 1$	$\sum_{i=1}^{I} \sum_{j=1}^{n_i} (y_{ij} - \bar{\bar{y}})^2$	

Lamb weights

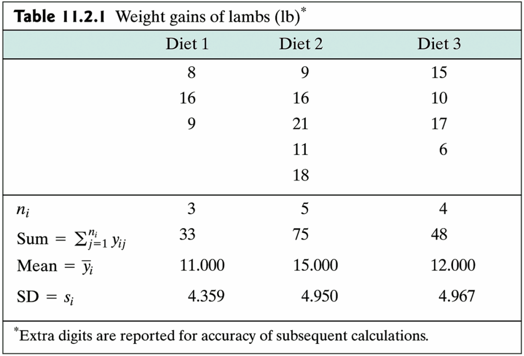


Table 11.2.1 Weight gains of lambs (lb)*

	Diet 1	Diet 2	Diet 3
	8	9	15
	16	16	10
	9	21	17
		11	6
		18	
n_i	3	5	4
Sum $= \sum_{j=1}^{n_i} y_{ij}$	33	75	48
Mean $= \overline{y}_i$	11.000	15.000	12.000
SD $= s_i$	4.359	4.950	4.967

*Extra digits are reported for accuracy of subsequent calculations.

ANOVA table

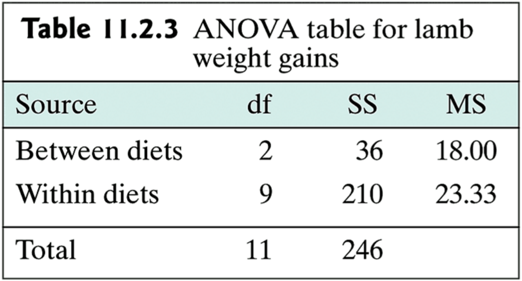


Table 11.2.3 ANOVA table for lamb weight gains

Source	df	SS	MS
Between diets	2	36	18.00
Within diets	9	210	23.33
Total	11	246	

Estimate of common $\sigma^2 = \text{MS(within)}$.

F test

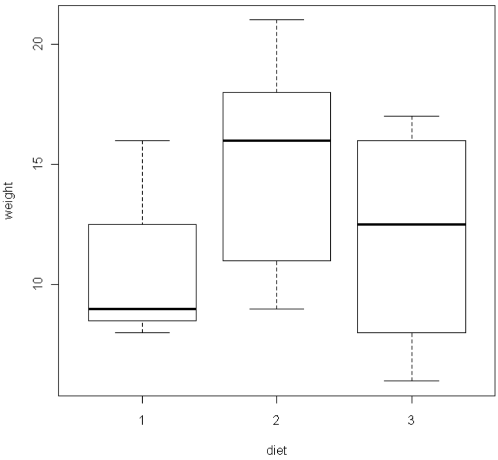
- Want to reject $H_0 : \mu_1 = \mu_2 = \cdots = \mu_I$.
- Test statistic is $F = MS(Between)/MS(Within)$, which has an $F(df_b, df_w)$ distribution if H_0 is true.
- R uses this F-distribution to get the P-value. Read your text if you are interested in more details.
- In R, need to define two lists. One list has the response measurement of interest, the other has which group each response is from. The grouping list needs to be a 'factor' – the sample code shows how to do this.
- In R, SS(within) is called 'Residuals Sum Sq' and SS(between) takes the same name as the group list name.
- Obtain P-value from R. Reject H_0 if P-value is less than α as usual.

R code for lamb diet data

```
weight=c( 8,16, 9, 9,16,21,11,18,15,10,17, 6)
diet  =c( 1, 1, 1, 2, 2, 2, 2, 2, 3, 3, 3, 3)
diet=factor(diet)
boxplot(weight˜diet)
fit=aov(weight˜diet)
summary(fit)
            Df Sum Sq Mean Sq F value Pr(>F)
diet         2     36  18.000  0.7714 0.4907
Residuals    9    210  23.333
```

We accept $H_0 : \mu_1 = \mu_2 = \mu_3$ at the $\alpha = 0.05$ level. There is no significant difference in weight across diet.

Lamb data

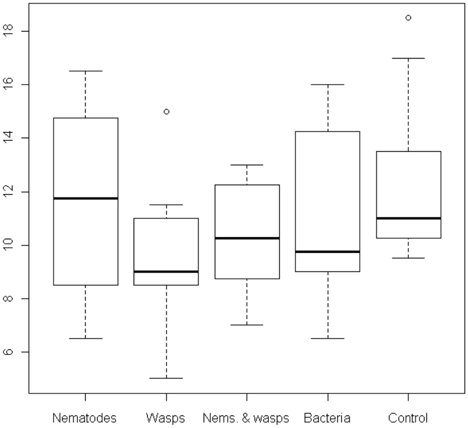


R code for corn growth data

```
weight=c(16.5,11.0, 8.5,16.0,13.0,15.0,15.0,13.0,14.5,10.5,
         11.5, 9.0,12.0,15.0,11.0,12.0, 9.0,10.0, 9.0,10.0,
         12.5,11.5,12.5,10.5,14.0, 9.0,11.0, 8.5,14.0,12.0,
         16.0, 9.0, 9.5,12.5,11.0, 6.5,10.0, 7.0, 9.0, 9.5,
          8.0, 9.0,10.5, 9.0,18.5,14.5, 8.0,10.5, 9.0,17.0,
          7.0, 8.0,13.0, 6.5,10.0,10.5, 5.0, 9.0, 8.5,11.0)
treat= c(1,2,3,4,5,1,2,3,4,5,1,2,3,4,5,1,2,3,4,5,1,2,3,4,5,
         1,2,3,4,5,1,2,3,4,5,1,2,3,4,5,1,2,3,4,5,1,2,3,4,5,
         1,2,3,4,5,1,2,3,4,5)
treat=factor(treat)
boxplot(weight~treat,names=c("Nematodes","Wasps","Nems. & wasps","Bacteria","Control"))
fit=aov(weight~treat)
summary(fit)
            Df Sum Sq Mean Sq F value Pr(>F)
treat        4  52.31 13.0771  1.6461 0.1758
Residuals   55 436.94  7.9443
```

We accept $H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5$ at the $\alpha = 0.05$ level. There is no significant difference in weight across treatment.

Organic sweet corn boxplots



Example 1.1.4: MOA and schizophrenia

- Monoamine oxidase (MOA) enzyme thought to regulate behavior.
- Blood from $n = 42$ schizophrenia patients collected, *stratified* by diagnosis (I, II, III).
- Is there an association between MOA and diagnosis?

Example 1.1.4: MOA and schizophrenia

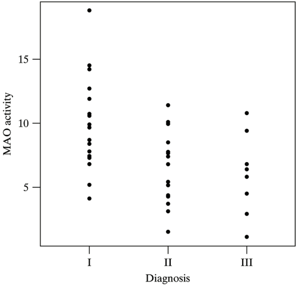


Figure 1.1.2 MAO activity in schizophrenic patients

- What happens to MOA as severity of diagnosis increases? Is the relationship perfect?
- Let's test $H_0 : \mu_1 = \mu_2 = \mu_3$ in R.

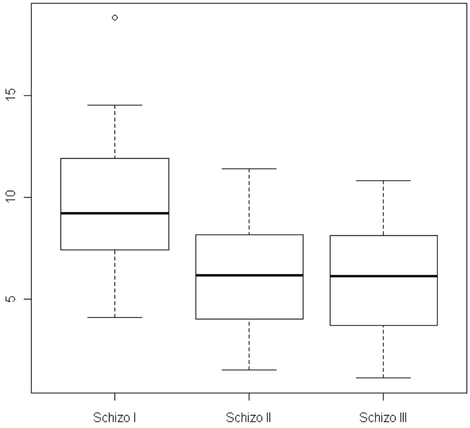
MAO activity (Fig. 1.1.2)

```
moa=c(6.8,4.1,7.3,14.2,18.8,9.9,7.4,11.9,5.2,7.8,7.8,8.7,12.7,14.5,10.7,8.4,9.7,
      10.6,7.8,4.4,11.4,3.1,4.3,10.1,1.5,7.4,5.2,10.0,3.7,5.5,8.5,7.7,6.8,3.1,
      6.4,10.8,1.1,2.9,4.5,5.8,9.4,6.8)
group=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,3,3,3,3,3,3,3,3)
group=factor(group)
boxplot(moa~group,names=c("Schizo I","Schizo II","Schizo III"))

            Df Sum Sq Mean Sq F value   Pr(>F)
group        2 136.12  68.059  6.3461 0.004111 **
Residuals   39 418.25  10.724
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

Reject $H_0 : \mu_1 = \mu_2 = \mu_3$ at $\alpha = 0.05$ because $0.004 < 0.05$. There is a significant difference in mean MOA activity across the three diagnoses.

MAO activity in schizophrenia



Side-by-side boxplots from R code.