

STA221

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the t - F connection - I

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For example, consider the two-sample t test (equal variance version using pooled variance s_p^2 - section 21.3 of the text).

Q21.20 “Hard Water” Mortality rates per county in 61 counties in England and Wales classified as “North” and “South” of Derby. Is there a difference in mean mortality rate? Here's the R output:

```
##  
## Two Sample t-test  
##  
## data: Mortality by Derby  
## t = 6.5312, df = 59, p-value = 0.00000001673  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:
```

mortality data via F test

From above:

$t = 6.5312$, $df = 59$, $p\text{-value} = 0.00000001673$

The R ANOVA output:

##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## Derby	1	886712	886712	42.66	0.0000000167
## Residuals	59	1226462	20787		

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Also, $6.5312^2 = 42.6565734$.

the t - F connection - II

Recall from the Bodyfat example from regression:

```
##  
## Coefficients:  
##           Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 25.58078   14.15400   1.807   0.0719  
## Height      -0.09316    0.20119  -0.463   0.6438  
##  
## Residual standard error: 8.307 on 248 degrees of freedom  
## Multiple R-squared:  0.0008637, Adjusted R-squared:  -0.003165  
## F-statistic: 0.2144 on 1 and 248 DF,  p-value: 0.6438
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Again, $t^2 = F$ and the p-values are identical.

The practical downside of using F is that you lose information about the sign.

ANOVA model and calculations requirement

Look at the model again:

$$y_{ij} = \mu_i + \varepsilon_{ij}, \quad \varepsilon_{ij} \sim N(0, \sigma)$$

First, the errors are supposed to be independent, which would exclude experiments such as giving the same person different treatments over time, etc.

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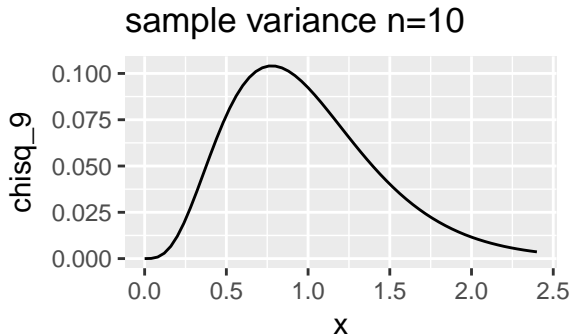
The main things to verify:

1. Do the groups come from a distribution with the same variance? (fatal if no)
2. Do the groups come from normal distributions? (OK if sample size is large enough)

Formal test for equality of variances

For the equal variance assumptions, the book says to look at plots. Other books gives a variety of heuristics. These suggestions tend to be wildly conservative.

The problem is twofold. Within-group sample sizes tend to be small. And the sample variance itself has a very large variance.



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$$H_0 : \sigma_1^2 = \cdots = \sigma_k^2$$

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The form of the test is exactly an ANOVA, but not on the original y_{ij} . Instead, it is on the *absolute differences from the group medians*:

$$Z_{ij} = |y_{ij} - \tilde{y}_i|$$

where \tilde{y}_i is the sample median of the i^{th} group.

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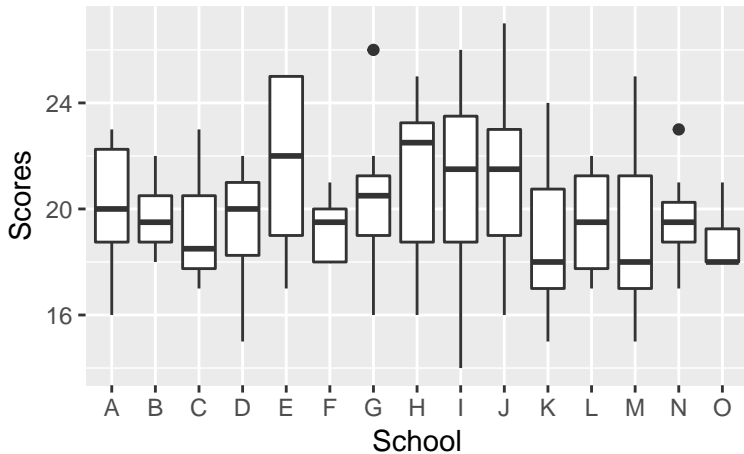
Plugging the Z_{ij} into the ANOVA formulae gives an approximate $F_{k-1, N-k}$ distribution.

Levene's test example - yeast

```
## # A tibble: 2 × 3
##       Df `F value`  `Pr(>F)`
## * <int>      <dbl>      <dbl>
## 1       3  0.291724  0.8306011
## 2      12          NA          NA
```

tougher example

From textbook question 25.18 “School System”. 15 schools selected. 8 students per school.



tougher example - Levene

```
## # A tibble: 2 × 3
##       Df `F value`  `Pr(>F)`
## * <int>      <dbl>    <dbl>
## 1     14  1.264175  0.2422268
## 2    105          NA          NA
```

normality assumption

Technically, all the groups have to be normal. But the samples sizes are usually too small.

normality assumption

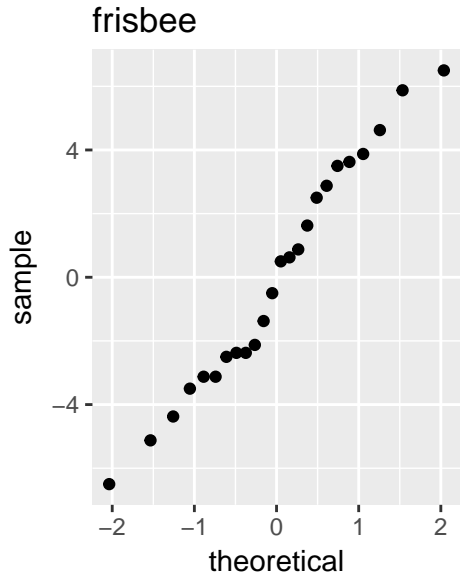
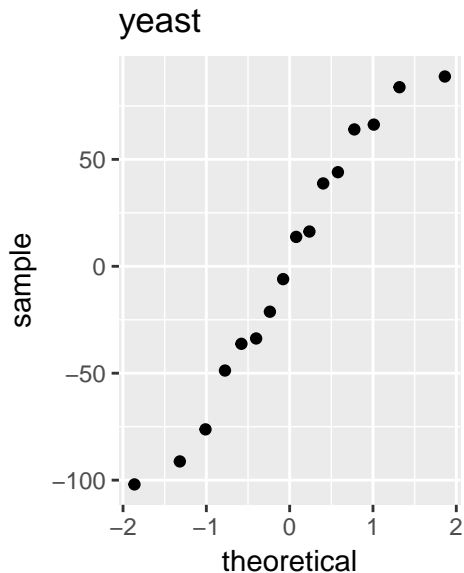
Technically, all the groups have to be normal. But the samples sizes are usually too small.

If the equal variance assumption has been satisfied (do that first), then the method is to pool all the *residuals* together:

$$y_{ij} - \bar{y}_i$$

and look at a normal quantile plot.

normal assumption verification examples



pairwise comparisons

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Or, there may be some differences between groups that are noticed after collecting data, which is gets us into dangerous territory!

The approach in any case will be to perform multiple pooled two-sample t procedures, using the overall MSE in place of the usual pooled variance:

$$\frac{\bar{y}_i - \bar{y}_j}{\sqrt{MSE} \sqrt{\frac{1}{n_i} + \frac{1}{n_j}}} \sim t_{N-k}$$

The usual technique is to produce confidence intervals for each desired pair. But at what confidence level? The usual 95% level leads to a problem. . .

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Recall: a lower α gives a *wider* confidence interval. In the t case the full formula is:

$$(\bar{y}_i - \bar{y}_j) \pm t_{N-k, \alpha/2} \sqrt{MSE} \sqrt{\frac{1}{n_i} + \frac{1}{n_j}}$$

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From “classical” hypothesis testing there was the notion of a “Type I Error”, which is *rejecting H_0 when it is true*, aka “false positive”.

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Definition: the *experimentwise error rate* is the probability of *any* Type I Errors among all tests done on the dataset from one experiment.

bounding the experimentwise error rate - I

Suppose we're going to do m hypothesis tests on a dataset.

Denote by A_1, A_2, \dots, A_m the events where A_i means “a Type I Error occurred when hypothesis test i took place”, and $P(A_i) = \alpha$.

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You might recall the expression $P(A \cup B) = P(A) + P(B) - P(A \cap B)$.

This implies $P(A \cup B) \leq P(A) + P(B)$. You can extend this to any number of events, i.e.:

$$P(A_1 \cup A_2 \cup \dots \cup A_m) \leq P(A_1) + P(A_2) + \dots + P(A_m)$$

bounding the experimentwise error rate - II

How could the individual tests all be adjusted so that α^* remains small?

An easy method uses:

$$\alpha^* = P(\text{any Type I Errors})$$

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So can achieve $\alpha^* = \alpha$ simply by dividing each of these α by m .

This is called a “Bonferroni correction”.

It's not a bad idea to apply a Bonferroni correct to any situation in which you are subjecting a dataset to lots of hypothesis tests.

full example, including some pairwise comparisons

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Suppose List4 was some sort of “default list”, and the other three lists were new word lists being evaluated. So it will be particularly interesting to investigate these three pairwise differences:

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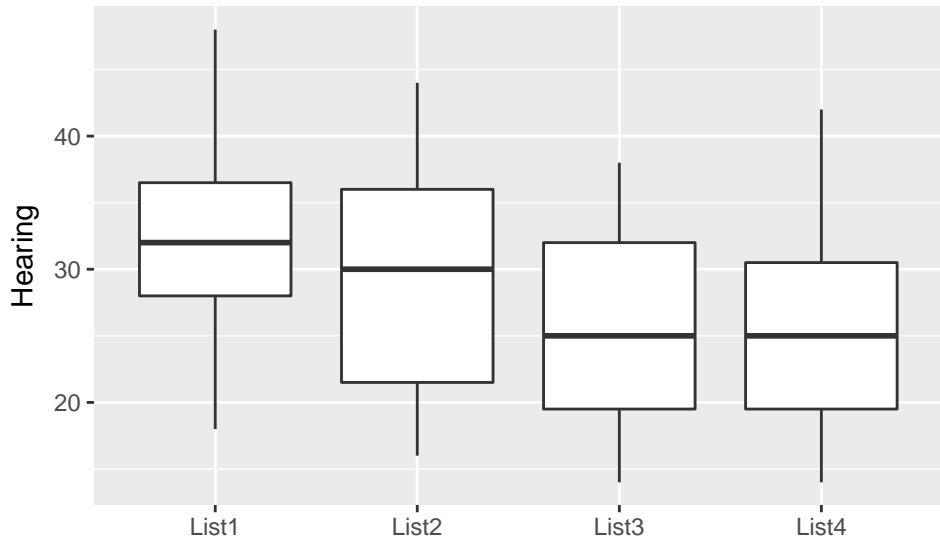
$$\mu_2 - \mu_4$$

$$\mu_3 - \mu_4$$

We will fix the experimentwise error rate at $\alpha^* = 0.05$ for the multiple comparisons.

hearing full example - I

First, look at a plot:



hearing full example - II

Next, verify the model assumptions starting with Levene's test:

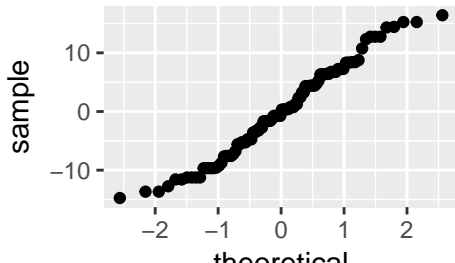
```
## # A tibble: 2 × 3
##       Df `F value`  `Pr(>F)`
## * <int>      <dbl>    <dbl>
## 1       3 0.5701226 0.6360853
## 2      92          NA          NA
```

hearing full example - II

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## 2      92          NA          NA
```

...followed by the normal quantile plot of the residuals:



hearing full example - III

Next we do the overall ANOVA F test:

##		Df	Sum Sq	Mean Sq	F value	Pr(>F)
##	ListID	3	920	306.82	4.919	0.00325
##	Residuals	92	5738	62.37		

hearing full example - III

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##		Df	Sum Sq	Mean Sq	F value	Pr(>F)
##	ListID	3	920	306.82	4.919	0.00325
##	Residuals	92	5738	62.37		

And since the p-value is low **we may proceed with the pairwise comparisons.**

hearing full example - IV

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To make the three confidence intervals we need the estimated mean differences and the group sample sizes:

```
## # A tibble: 4 × 3
##   ListID      n    mean
##   <fctr> <int>   <dbl>
## 1 List1     24 32.75000
## 2 List2     24 29.66667
## 3 List3     24 25.25000
## 4 List4     24 25.58333
```

We are doing three comparisons at an experimentwise error rate of 0.05, so we'll produce the $(1 - 0.05/3) \cdot 100\% = 98.33\%$ confidence intervals.

hearing full example - IV

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##   <fctr> <int>   <dbl>
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## 2 List2     24 29.66667
## 3 List3     24 25.25000
## 4 List4     24 25.58333
```

We are doing three comparisons at an experimentwise error rate of 0.05, so we'll produce the $(1 - 0.05/3) \cdot 100\% = 98.33\%$ confidence intervals.

The value of $t_{92,0.0167}$ is 2.4385416.

hearing full example - V

The three pairwise comparisons of interest can be made using these confidence intervals:

Comparison	Estimate	Margin of Error	Lower	Upper
$\mu_1 - \mu_4$	7.167	5.559	1.607	12.726
$\mu_2 - \mu_4$	4.083	5.559	-1.476	9.643
$\mu_3 - \mu_4$	-0.333	5.559	-5.893	5.226

post-hoc comparison trick

Dangerous territory: perform a comparison *after looking at the data*.

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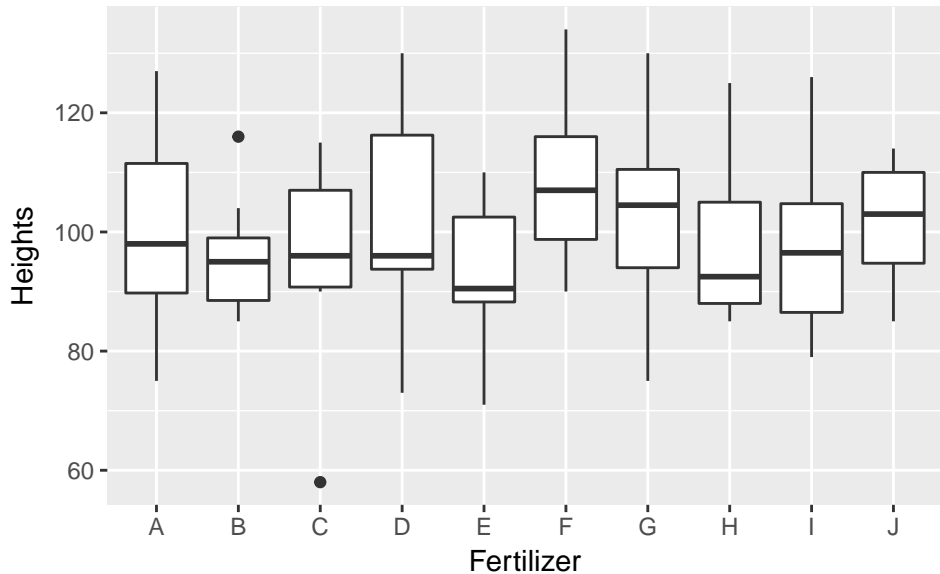
Dangerous territory: perform a comparison *after looking at the data*.

Trick: use Bonferroni's correction *assuming you were going to look at all the comparisons in advance*.

With k groups there will be $k(k - 1)/2$ such comparisons.

Example using question 25.19 “Fertilizers”. There are $k = 10$ fertilizers being compared with $n = 10$ mung bean sprouts each. After a week, the bean heights are measured.

“Fertilizers” example



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E and F look interesting. I think I'll test that pairwise difference at the end.

“Fertilizers” example

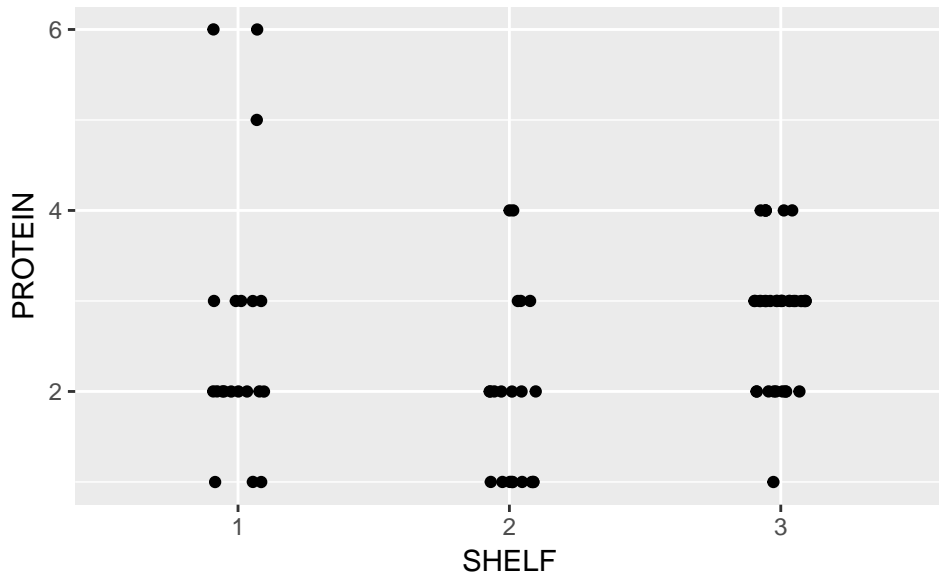
E and F look interesting. I think I'll test that pairwise difference at the end.

I need to run the ANOVA and verify the assumptions:

```
## # A tibble: 2 × 5
##       Df `Sum Sq` `Mean Sq` `F value` `Pr(>F)`
## * <int>     <dbl>     <dbl>     <dbl>     <dbl>
## 1       9      2074       230       1.19      0.31
## 2     110     21331      194        NA        NA
```

```
## # A tibble: 2 × 3
##       Df `F value` `Pr(>F)`
## * <int>     <dbl>     <dbl>
## 1       9      0.742      0.67
## 2     110        NA        NA
```

OK, so then let's look at the "Cereals" data from Q25.21



“Cereals redux”

I'd also like to see if there is a difference between shelves 2 and 3.

“Cereals redux”

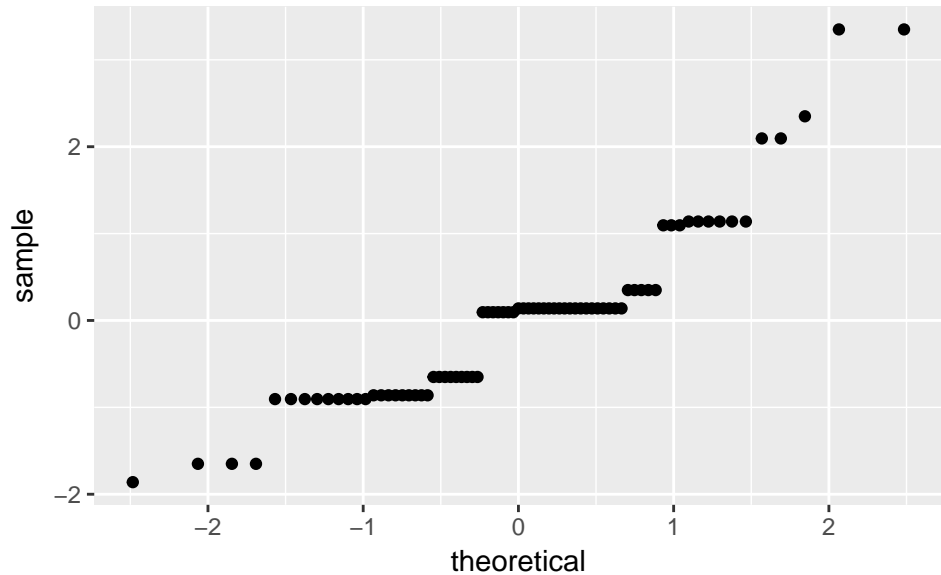
I'd also like to see if there is a difference between shelves 2 and 3.

Start with the analysis and assumption verification:

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## SHELF      2   12.4    6.21    5.84 0.0044
## Residuals  74   78.7    1.06
```

```
## # A tibble: 2 × 3
##       Df `F value` `Pr(>F)`
## * <int>     <dbl>     <dbl>
## 1      2      2.34      0.103
## 2     74      NA        NA
```

“Cereals redux”



comparing shelves 2 and 3

There are 3 *possible* comparisons, so a Bonferroni correction with $m = 3$ will be needed, even though I'm only actually doing one comparison.

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Computer says: $t_{74,0.05/6} = 2.45$

##		Df	Sum Sq	Mean Sq	F	value	Pr(>F)
##	SHELF	2	12.4	6.21	5.84	0.0044	
##	Residuals	74	78.7	1.06			

```
## # A tibble: 3 × 3
##   SHELF      n mean
##   <fctr> <int> <dbl>
## 1     1     20  2.65
## 2     2     21  1.90
## 3     3     36  2.86
```


“All pairwise comparisons”

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Here is an efficient algorithm for performing this task for cases when the group sample sizes are all the same (equal to some n). Let's look at the Yeast example again.

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Recipe      3 638968   212989    44.7 0.00000086
## Residuals   12  57128     4761
```

```
## # A tibble: 4 × 3
##   Recipe      n mean
##   <fctr> <int> <dbl>
## 1      D      4   184
## 2      B      4   196
## 3      A      4   486
## 4      C      4   656
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The “margin of error” is 153.82.