Chapter 10: Comparing multiple independent populations

(Ott & Longnecker Sections: 14.2 and 14.5)

https://dzwang91.github.io/stat324/

Outline

What we have learnt...

- One sample tests: test population mean/median/proportion
- Two independent sample tests: compare two independent populations
- Two paired sample tests: compare two dependent populations

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A natural extension: How do we compare multiple independent populations?

Example

- Four new formulations of rat poison are being tested, call them 1, 2, 3 and 4. All of the poisons work by thinning the blood, so the response of interest is the time it takes for the blood to coagulate. A longer blood coagulation time indicates a more effective poison.
- 24 rats were randomly selected, and then randomized to the four poisons. They were fed the poison, and then after a specified length of time, their blood was drawn and the time to blood coagulation was measured. The data is below:

Treatment								Sample Mean
1	62	60	63	59				61
2	63	67	71	64	65	66		66
3	68	66	71	67	68	68		68
4	56	62	60	61	63	64	63	59	61

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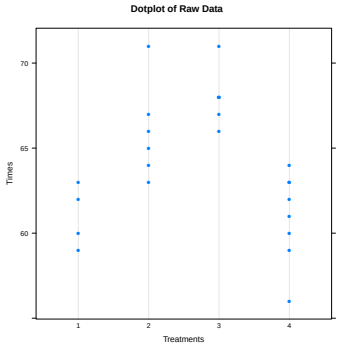
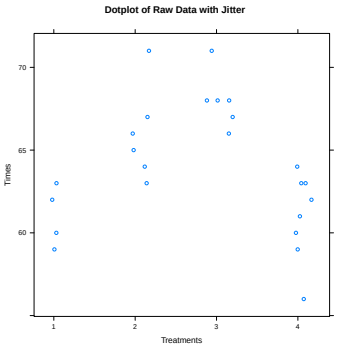
H_A: At least one mean differs from one other mean.

- Question: how can we do hypothesis testing in this setting? What is the test statistic?

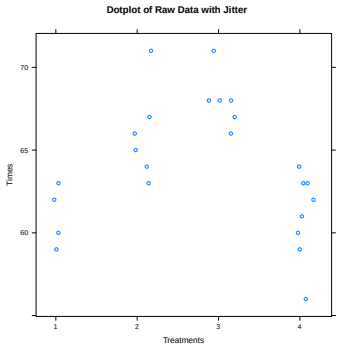
Example continued



Example continued

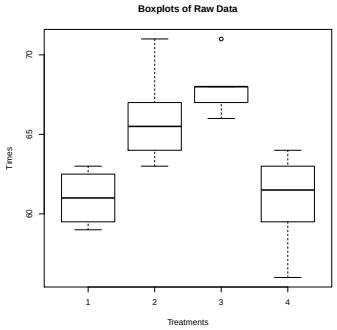


Example continued



The treatments seem to differ somewhat. Treatments 2 and 3 seem to have generally higher means than 1 and 4.

Example continued



It is clear that treatment 3 might be slightly higher than treatment 2.

Example continued

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A new approach: analysis of variance (ANOVA)

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A new approach: analysis of variance (ANOVA)

- By the end of this lecture, think about why we call it analysis of variance.

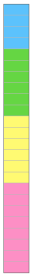
Outline

Notations

- Let t be the number of treatments.
- Let i index the treatments.
- Let n_i be the number of observations in treatment i.
- Let $N = \sum_{i=1}^{t} n_i$ be the total sample size.
- Let y_{ij} be observation j from treatment i.
- Let $\bar{y}_{i\cdot} = \frac{\sum_{j=1}^{n_i} y_{ij}}{n_i}$ be the sample mean for treatment i.
- Let $\bar{y}_{\cdot\cdot} = \frac{\sum_{i=1}^{t} \sum_{j=1}^{n_i} y_{ij}}{N}$ be the sample grand mean.

Sample mean for each treatment

Grand mean



$\bar{y}_{\cdot\cdot}$

Key idea of ANOVA

Where does the variability come from?

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- The key decomposition:

  Observation = Grand Mean + Deviation of Treatment Mean from Grand Mean + Deviation of Observation from Treatment Mean
- In notation,

$$y_{ij} = \bar{y}_{..} + (\bar{y}_{i.} - \bar{y}_{..}) + (y_{ij} - \bar{y}_{i.})$$

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- In notation,

$$y_{ij} = \bar{y}_{..} + (\bar{y}_{i.} - \bar{y}_{..}) + (y_{ij} - \bar{y}_{i.})$$

- Thus,

$$(y_{ij} - \bar{y}_{..}) = (\bar{y}_{i.} - \bar{y}_{..}) + (y_{ij} - \bar{y}_{i.})$$

Ingredient 1: Sum of squares

- Variability decomposition:

$$\sum_{i=1}^{t}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_{..})^2 = \sum_{i=1}^{t}\sum_{j=1}^{n_i}(\bar{y}_{i.} - \bar{y}_{..})^2 + \sum_{i=1}^{t}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_{i.})^2$$

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  - $\sum_{i=1}^{t}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_{..})^2$: sum of squares total
  - $\sum_{i=1}^{t}\sum_{j=1}^{n_i}(\bar{y}_{i.} - \bar{y}_{..})^2$: sum of squares treatment (SS between)
  - $\sum_{i=1}^{t}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_{i.})^2$: sum of squares error (SS within)
- In words,

  SSTot = SSTrt (SS between) + SSE (SS within)
- Proof in next chapter

Ingredient 2: Degrees of freedom

- For SSTot, degrees of freedom is $N - 1$
- For SSTrt, degrees of freedom is $t - 1$
- For SSE, degrees of freedom is $N - t$.

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- For SSE, degrees of freedom is $N - t$.

What do you find?

$$df_{Tot} = df_{Trt} + df_E$$

Ingredient 3: Mean squares and test staistic

- Mean squares:
  - $MSTrt = \frac{SSTrt}{df_{Trt}}$
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- Mean squares:
  - $MSTrt = \frac{SSTrt}{df_{Trt}}$
  - $MSE = \frac{SSE}{df_E}$
- Test statistic:
  - $F = \frac{MSTrt}{MSE}$
  - It is the ratio of the between variability to the within variability

Summarizing in a table

Source	SS	df	MS	F	p-value
Treat	SSTrt	$t-1$	MSTrt$=\frac{SSTrt}{df_{Trt}}$	F $=\frac{MSTrt}{MSE}$	?
Error	SSE	$N-t$	MSE $=\frac{SSE}{df_E}$		
Total	SSTot	$N-1$			

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- How do we calculate the p-value?
- What is the distribution of the test statistic given the null hypothesis is true?
- What are assumptions we need to assume?

F distribution

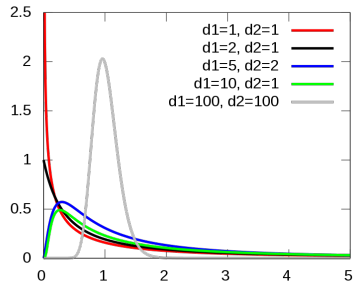
If we assume

- The data are independent within and between treatments
- The variances are the same for all treatments
- Each treatment has a normal distribution

then

- the distribution of the test statistic F is called an F distribution
- it has two parameters, called the numerator df and denominator df.
- The numerator df is df_{Trt}, and the denominator df is df_E.

Pdf of F distribution



Here $d1$ is the numerator df, $d2$ is the denominator df.

ANOVA table

If we are willing to assume:

- The data are independent within and between treatments
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then

Source	SS	df	MS	F	p-value
Treat	SSTrt	$t-1$	MSTrt$=\frac{SSTrt}{df_{Trt}}$	$F=\frac{MSTrt}{MSE}$	$P(F_{df_{Trt},df_E} > F)$
Error	SSE	$N-t$	MSE $=\frac{SSE}{df_E}$		
Total	SSTot	$N-1$			

- Use F table to calculate the p-value

Example

For our blood coagulation data, the ANOVA table is:

Source	SS	df	MS	F	p-value
Treat (between)	228	3	76	13.57	
Error (within)	112	20	5.6		
Total	340	23			

F table

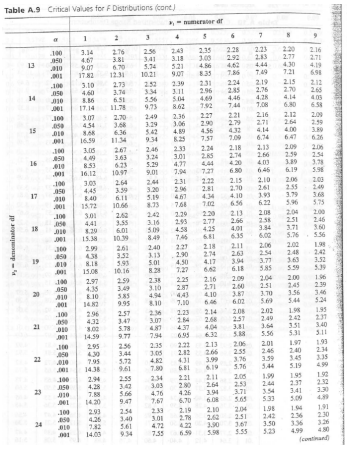
Table A.9 Critical Values for F Distributions (cont.)

Back to example

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Total	340	23			

Since the p-value is quite small, we would reject the null, and conclude that at least one poison has a different mean coagulation time than another.

Outline

Assumptions of ANOVA

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How do we check equal variance?

Approach 1: Use residuals vs. fitted values plot

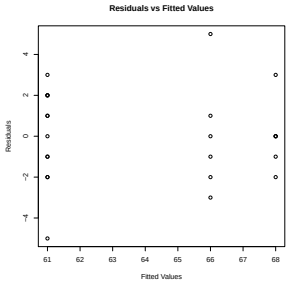
Approach 2: Ratio of SDs

Fitted values, residuals

- The fitted values are the treatment means $\bar{y}_{i\cdot}$.
- The residuals are the differences between the observed data(y_{ij}) and the treatment means $y_{ij} - \bar{y}_{i\cdot}$.
- In fact, the sum of squares error (SSE) is the sum of squares of the residuals.
- **Key idea:** If the spreads of residuals are about the same for each treatment, then we are safe to assume equal variance.

Residuals vs Fitted values plot

Assume there are 3 treatments. The y-axis is called 'Residuals' and the x-axis is called 'Fitted Values'.



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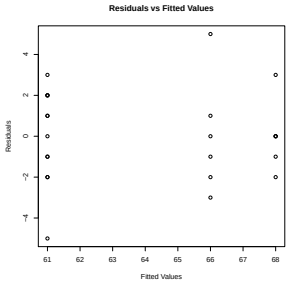

There might be slightly less spread in the last group, but they're close enough.

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The SD of weights of 5 elephants will tend to be larger than the SD of weights of 5 hamsters.

Equal variance does not always hold

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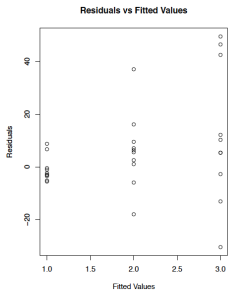
- It is often the case that variability will increase with increasing fitted values.
- An example: we see the classic funnel pattern where the variability increases with the fitted value.



Ratio of SDs

- Another option for checking equal variance is to use the ratio of SDs guideline first mentioned when comparing two populations.
- Since there are now more than two groups, it is typical to take the ratio of the largest and smallest sample SDs - if this ratio passes the test, then every other pair will as well.
- For our example, the sample SDs for the four groups are 1.83, 2.83, 1.67, and 2.62. The ratio of the smallest to the largest is $1.67/2.83 = 0.59$, which falls between 0.5 and 2.0, so assuming the variances equal should be safe.

Outline

Multiple comparisons following significant ANOVA

- Consequence of ANOVA:
  - if we do not reject the null, we're done.
  - if we reject, we only know that at least one mean differs from at least one other mean, but not how many means differ, or which ones, or by how much.

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- Two sample t test for i-th treatment and j-th treatment:
  - $H_0 : \mu_i = \mu_j$ vs. $H_A : \mu_i \neq \mu_j$
  - use $t = \frac{\bar{y}_{i\cdot} - \bar{y}_{j\cdot}}{S_p\sqrt{(1/n_i + 1/n_j)}}$ (t distribution with df=$n_i + n_j - 2$ given H_0 is true)
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  - compute rejection region or p-value to make a conclusion
  - $100(1-\alpha)\%$ CI on $\mu_i - \mu_j$:
    $$(\bar{y}_{i\cdot} - \bar{y}_{j\cdot}) \pm t_{n_i+n_j-2,\alpha/2} S_p \sqrt{(1/n_i + 1/n_j)}$$
    If the CI contains 0, then we don't reject the null hypothesis.

Why does CI approach work for two-sided tests?

If 0 is in $100(1-\alpha)\%$ CI, then

$$(\bar{y}_{i\cdot} - \bar{y}_{j\cdot}) - t_{n_i+n_j-2,\alpha/2} S_p \sqrt{\frac{1}{n_i} + \frac{1}{n_j}} \leq 0 \leq (\bar{y}_{i\cdot} - \bar{y}_{j\cdot}) + t_{n_i+n_j-2,\alpha/2} S_p \sqrt{\frac{1}{n_i} + \frac{1}{n_j}}$$

$$\downarrow$$

$$t_{obs} = \frac{\bar{y}_{i\cdot} - \bar{y}_{j\cdot}}{S_p\sqrt{(1/n_i + 1/n_j)}} \leq t_{n_i+n_j-2,\alpha/2} \qquad t_{obs} = \frac{\bar{y}_{i\cdot} - \bar{y}_{j\cdot}}{S_p\sqrt{(1/n_i + 1/n_j)}} \geq -t_{n_i+n_j-2,\alpha/2}$$

$$\downarrow$$

$$|t_{obs}| \leq t_{n_i+n_j-2,\alpha/2}$$

Therefore, we do not reject H_0 at significance level α.

Back to example

- Suppose we want 95% CIs, $t_{20,0.025} = 2.086$, and MSE $= 5.6$, so
  - Trt 1 vs Trt 2:
    $61 - 66 \pm 2.086\sqrt{5.6(1/4 + 1/6)} = -5 \pm 3.19 = (-8.19, -1.81)$
  - Trt 1 vs Trt 3:
    $61 - 68 \pm 2.086\sqrt{5.6(1/4 + 1/6)} = -7 \pm 3.19 = (-10.19, -3.81)$
  - Trt 1 vs Trt 4:
    $61 - 61 \pm 2.086\sqrt{5.6(1/4 + 1/8)} = 0 \pm 3.02 = (-3.02, 3.02)$
  - Trt 2 vs Trt 3:
    $66 - 68 \pm 2.086\sqrt{5.6(1/6 + 1/6)} = -2 \pm 2.85 = (-4.85, 0.85)$
  - Trt 2 vs Trt 4:
    $66 - 61 \pm 2.086\sqrt{5.6(1/6 + 1/8)} = 5 \pm 2.67 = (2.33, 7.67)$
  - Trt 3 vs Trt 4:
    $68 - 61 \pm 2.086\sqrt{5.6(1/6 + 1/8)} = 7 \pm 2.67 = (4.33, 9.67)$

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  - Trt 3 vs Trt 4:
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- The conclusion is that treatments 2 and 3 are the same, and 1 and 4 are the same, but 2 and 3 differ from 1 and 4.

Letter code

- The information is summarized by sorting the treatment means from largest to smallest, and then adding letter codes. Two treatments share a letter if they do not differ significantly:

Treatment	Sample Mean	Letter Code
3	68	A
2	66	A
1	61	B
4	61	B

Summary

If we end up doing a bunch of pairwise tests, why do we use ANOVA?

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If we end up doing a bunch of pairwise tests, why do we use ANOVA?

- Practically, if there are a lot of treatments, if there are really no differences between the treatments, doing one ANOVA could save time over doing many pairwise tests.
- Theoretically, the F-test is the most powerful test for the hypotheses we specified, provided all of our assumptions are met.

Outline

ANOVA in R

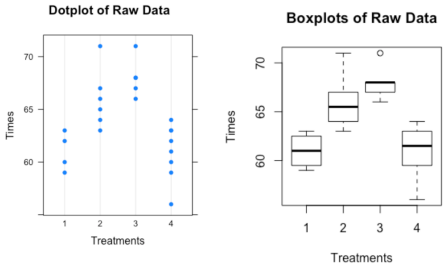
```
> #enter data
> times <- c(62, 60, 63, 59, 63, 67, 71, 64, 65, 66, 68,
+            66, 71, 67, 68, 68, 56, 62, 60, 61, 63, 64,
63, 59)
> diets <- c(rep(1, 4), rep(2, 6), rep(3, 6), rep(4, 8))
>
> #make diets an explicit factor
> dietsf <- factor(diets)
```


ANOVA in R

```
> #Run ANOVA: use aov
> mod <- aov(times ~ dietsf)
> summary(mod)
            Df Sum Sq Mean Sq F value   Pr(>F)
dietsf       3    228    76.0   13.57 4.66e-05 ***
Residuals   20    112     5.6
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

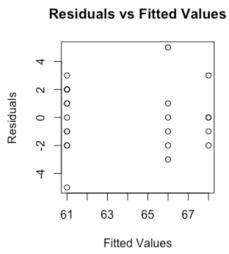

ANOVA in R

```
> #dotplot and boxplot
> library(lattice)
> dotplot(times ~ dietsf, ylab = "Times", xlab = "Treatme
nts", main = "Dotplot of Raw Data")
> boxplot(times ~ diets, ylab = "Times", xlab = "Treatmen
ts", main = "Boxplots of Raw Data")
```



ANOVA in R

```
> #residuals vs fitted plot
> plot(residuals(mod) ~ fitted(mod), ylab = "Residuals",
xlab = "Fitted Values", main = "Residuals vs Fitted Value
s")
```



What's the next?

We'll introduce linear regression in next lecture.