

Lecture 8 - ANOVA

part 2

Andrew Stewart

Andrew.Stewart@manchester.ac.uk



@ajstewart_lang

Session	Topic	Lecturer
1	Introduction, Open Science, and Power	Andrew Stewart
2	Introduction to R	Andrew Stewart
3	Data Wrangling and Visualisation	Andrew Stewart
4	General Linear Model - Regression	Andrew Stewart
5	General Linear Model - Regression	Andrew Stewart
6	Consolidation Lab	Bo Yao
7	General Linear Model - ANOVA	Andrew Stewart
8	General Linear Model - ANOVA	Andrew Stewart
9	Signal Detection Theory	Ellen Poliakoff
10	Signal Detection Theory	Ellen Poliakoff
11	Revision Session	Andrew Stewart

Semester 1 Assignments

ANOVA – Due start
December

Signal Detection Analysis –
Due around mid-January

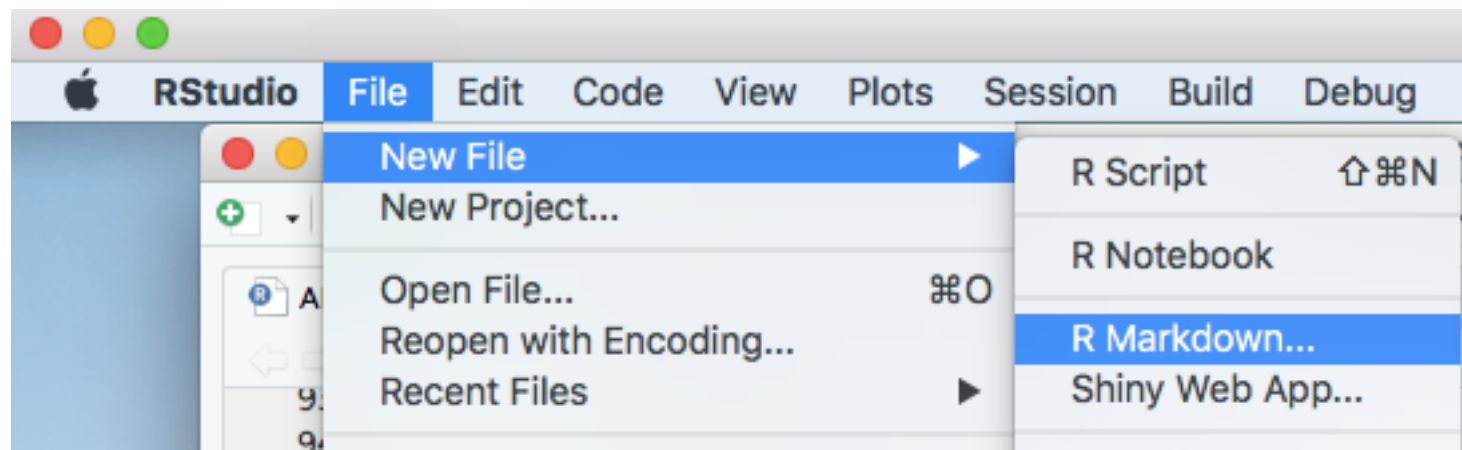
Assignment

- The data for the assignment were all generated by random sampling from the normal (and multivariate normal) distributions. Assume the assumptions of ANOVA have been met for the purposes of this assignment (i.e., you don't have to test/report them). We'll cover how to test these assumptions in Semester 2.

R Markdown

- R Markdown is a language in and of itself that allows you to produce documents in many formats (e.g., .html, .pdf, .doc) that contain your R code, the output of that code, and narrative that you write describing what you are doing (and why).
- R Markdown documents can be produced from within RStudio.
- R Markdown cheat sheet is in the R documentation folder on Blackboard.

- First we need to create a new R Markdown file:



Type the title of your document here.

New R Markdown

Document
Presentation
Shiny
From Template

Title: ANOVA example

Author: Andrew Stewart

Default Output Format:

☒ HTML
Recommended format for authoring (you can switch to PDF or Word output anytime).

☐ PDF
PDF output requires TeX (MiKTeX on Windows, MacTeX 2013+ on OS X, TeX Live 2013+ on Linux).

☐ Word
Previewing Word documents requires an installation of MS Word (or Libre/Open Office on Linux).


OK Cancel

Important - replace your name here with your student ID number.

Select the kind of file you want to be generated by your Markdown - you can change this later btw.

```
1 ---
2 title: "ANOVA example"
3 author: "Andrew Stewart"
4 date: "18/09/2018"
5 output: html_document
6 ---
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ```
11
12 ## R Markdown
13
14 This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word
15 documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.
16
17 When you click the Knit button a document will be generated that includes both content as well as the
18 output of any embedded R code chunks within the document. You can embed an R code chunk like this:
19
20 ```{r cars}
21 summary(cars)
22 ```
23
24 ## Including Plots
```

2:1 # ANOVA example R Markdown

You will now see a document like the above - it contains lots of example narrative (with a white background) and R code (with a grey background). We could actually 'knit' this document by clicking on  Knit to see what is produced...

What you will get is an html file (because that's the type of document we asked to be produced) that contains the R code, the associated output, plus the narrative. Notice how the ## symbols increasing the font size to allow us to generate headings in our narrative.

ANOVA example

Andrew Stewart

18/09/2018

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

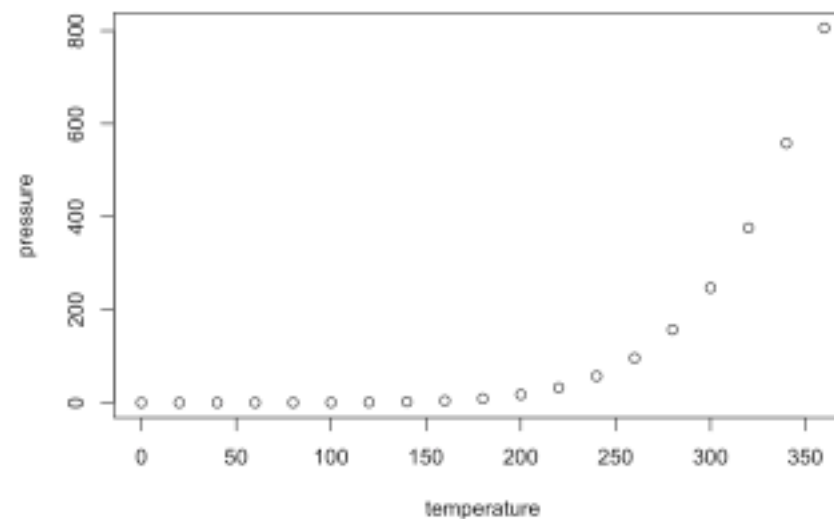
When you click the Knit button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0    Min.   : 2.00
##  1st Qu.:12.0    1st Qu.: 26.00
##  Median :15.0    Median : 36.00
##  Mean   :15.4    Mean   : 42.98
##  3rd Qu.:19.0    3rd Qu.: 56.00
##  Max.   :25.0    Max.   :120.00
```

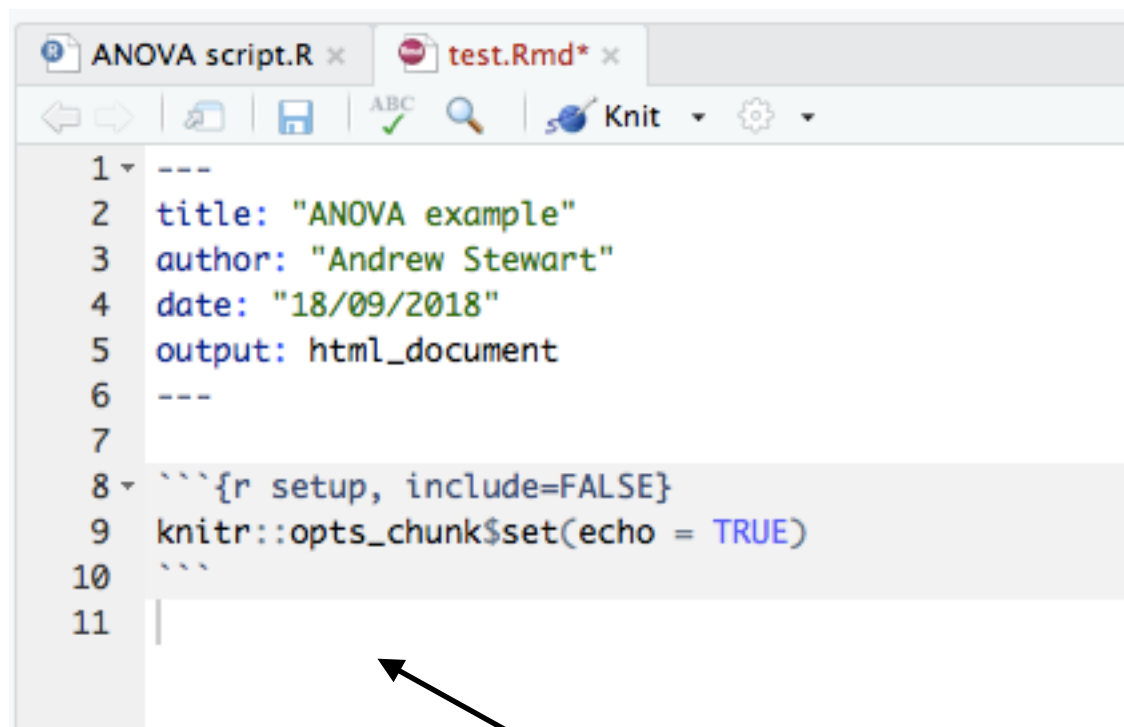
Including Plots

You can also embed plots, for example:



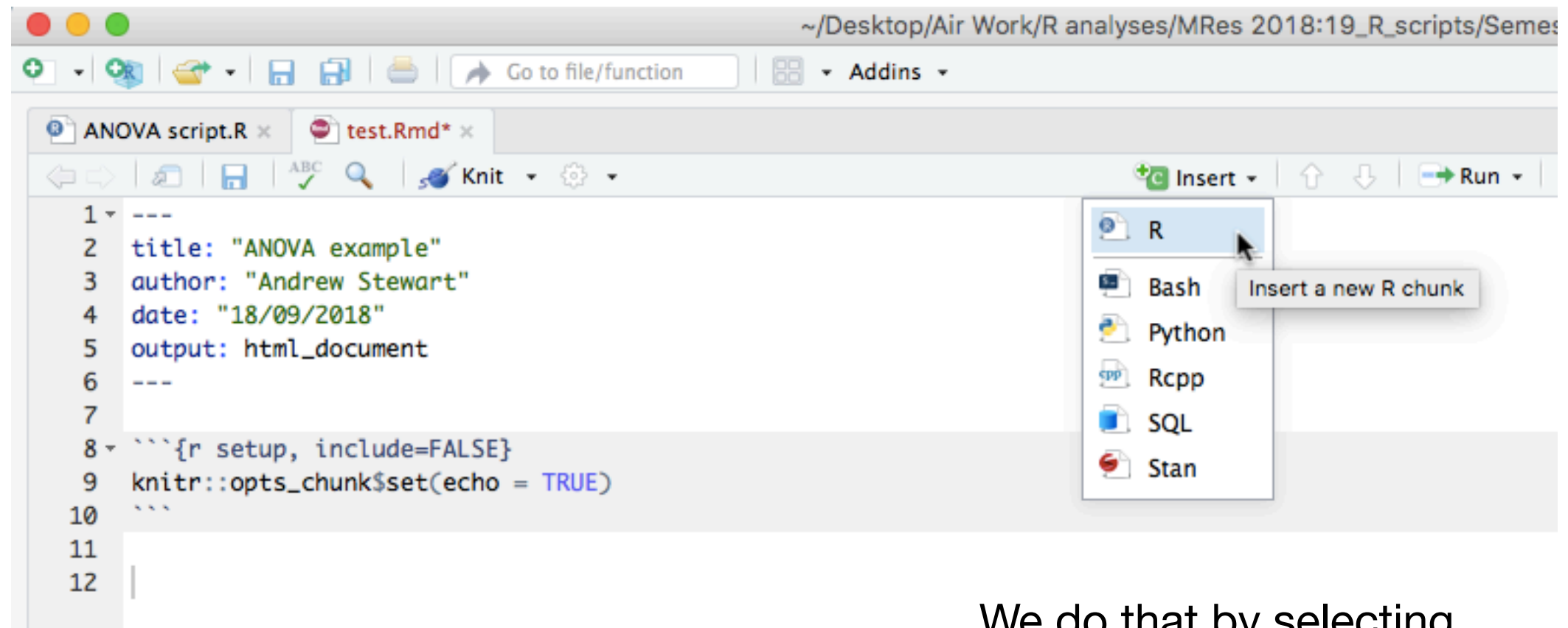
Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

When you come to create a document using R Markdown, you'll first want to delete a lot of the example code that appears when you first start a new Markdown file:



```
1 ---
2 title: "ANOVA example"
3 author: "Andrew Stewart"
4 date: "18/09/2018"
5 output: html_document
6 ---
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ```
11
```

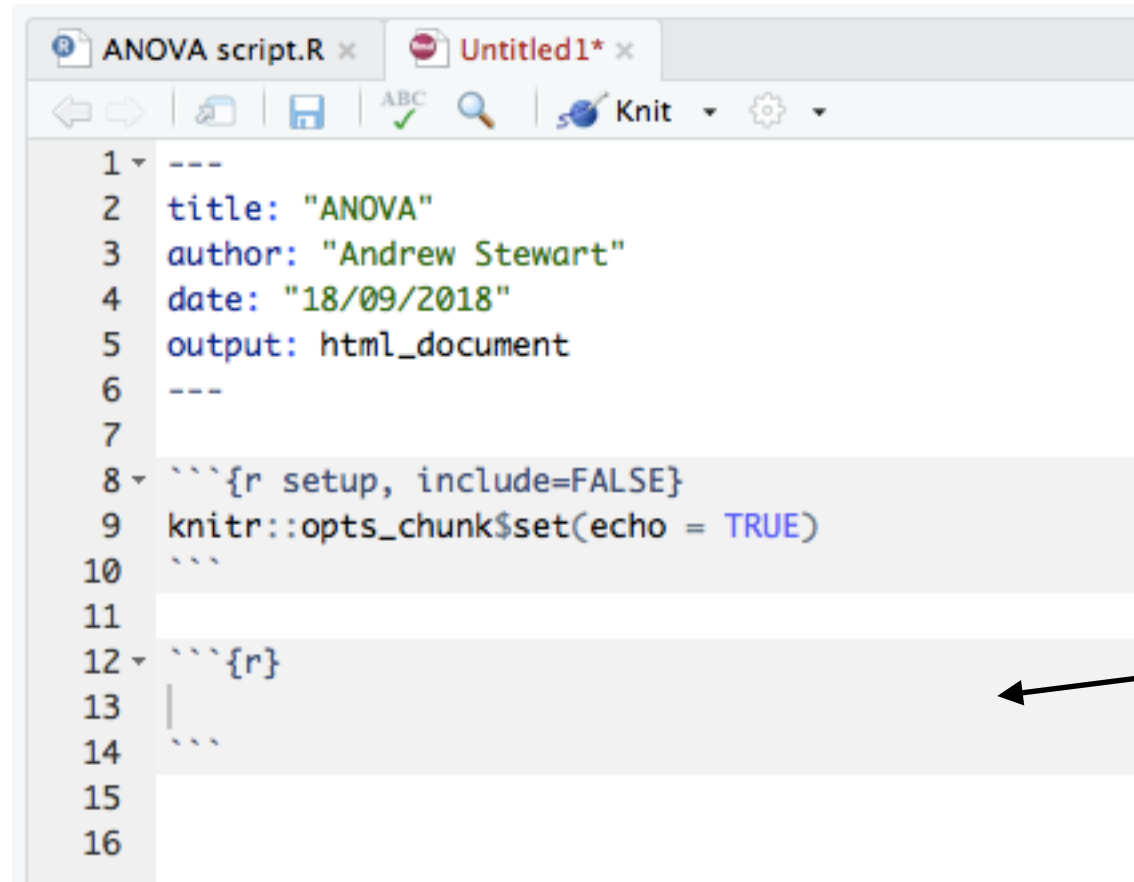
We now want to paste in chunks of our R code here



The screenshot shows the RStudio interface with a file named 'test.Rmd*' open. The editor contains a YAML header and an R chunk setup. The 'Insert' menu is open, showing options for R, Bash, Python, Rcpp, SQL, and Stan. The 'R' option is highlighted, and a tooltip says 'Insert a new R chunk'.

```
1 ---
2 title: "ANOVA example"
3 author: "Andrew Stewart"
4 date: "18/09/2018"
5 output: html_document
6 ---
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ```
11
12 |
```

We do that by selecting “Insert” and then “R” - this will allow us to add some new R code.



The screenshot shows the RStudio interface with a file named 'Untitled1*' open. The editor contains the same YAML header as the previous screenshot, but now with a new R chunk inserted at line 12. An arrow points to the new R chunk.

```
1 ---
2 title: "ANOVA"
3 author: "Andrew Stewart"
4 date: "18/09/2018"
5 output: html_document
6 ---
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ```
11
12 ```{r}
13 |
14 ```
15
16
```

We can now insert our new R code here.

```
1 ---
2 title: "ANOVA"
3 author: "Andrew Stewart"
4 date: "18/09/2018"
5 output: html_document
6 ---
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ```
11
12 ```{r}
13 library(tidyverse)
14 ```
15
16 |
```

We load the tidyverse packages first.

But maybe we should precede that with some narrative (and a heading) explaining what we're doing.

```
1 ---
2 title: "ANOVA"
3 author: "Andrew Stewart"
4 date: "18/09/2018"
5 output: html_document
6 ---
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ```
11
12 ## This is my first R Markdown document
13
14 First we load the tidyverse.
15 ```{r}
16 library(tidyverse)
17 ```
18
```

What happens if we now knit this short document?

ANOVA

Andrew Stewart

18/09/2018

This is my first R Markdown document

First we load the tidyverse.

```
library(tidyverse)
```


```
## -- Attaching packages ---- tidyverse 1.2.1 --  
--
```

```
## ✓ ggplot2 3.0.0      ✓ purrr  0.2.5  
## ✓ tibble  1.4.2      ✓ dplyr  0.7.6  
## ✓ tidyr   0.8.1      ✓ stringr 1.3.1  
## ✓ readr   1.1.1      ✓ forcats 0.3.0
```

```
## -- Conflicts ---- tidyverse_conflicts() --  
--  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::lag()     masks stats::lag()
```

Hmm, so we get some messages and warnings in our document - how can we get rid of these?

```
14 First we load the tidyverse.  
15 ```{r, message=FALSE}  
16 library(tidyverse)  
17 ```  
18
```



We can set the option for this chunk of R code not to display any messages by setting `message=FALSE` within the first curly bracket. There are lots of other options available to use (e.g., `warnings=FALSE`).

Everything you need (and probably lots you don't) can be found in this cheatsheet here:

<http://www.rstudio.com/wp-content/uploads/2016/03/rmarkdown-cheatsheet-2.0.pdf>

and here is the 'R Markdown: The Definitive Guide':

<https://bookdown.org/yihui/rmarkdown/>

I've even put together a video tutorial talking you through how to make an R Markdown document in the BB folder...

<https://youtu.be/cWGqWhfVkuw>

The ANOVA Assessment

- The ANOVA assessment this semester and the mixed models one next semester both need to be produced using R Markdown.
- Top tips:

Have lots of narrative explaining what you're doing (and why).

Use small chunks of code bookended by narrative - the ideal code chunk length is where you can have one comment that describes what that bit of code does.

If you find you're commenting about two things that one chunk of R code does, that chunk should probably be split into two...

Now onto ANOVA part 2

- Last week we looked at 1-way between participants ANOVA, 1-way repeated measures ANOVA, and 2-way repeated measures ANOVA.
- We used the `afex` package for building our models as it uses Type III Sums of Squares with effect coding of contrasts (allowing us to more easily interpret our results when we have interactions).

A slightly more complex study

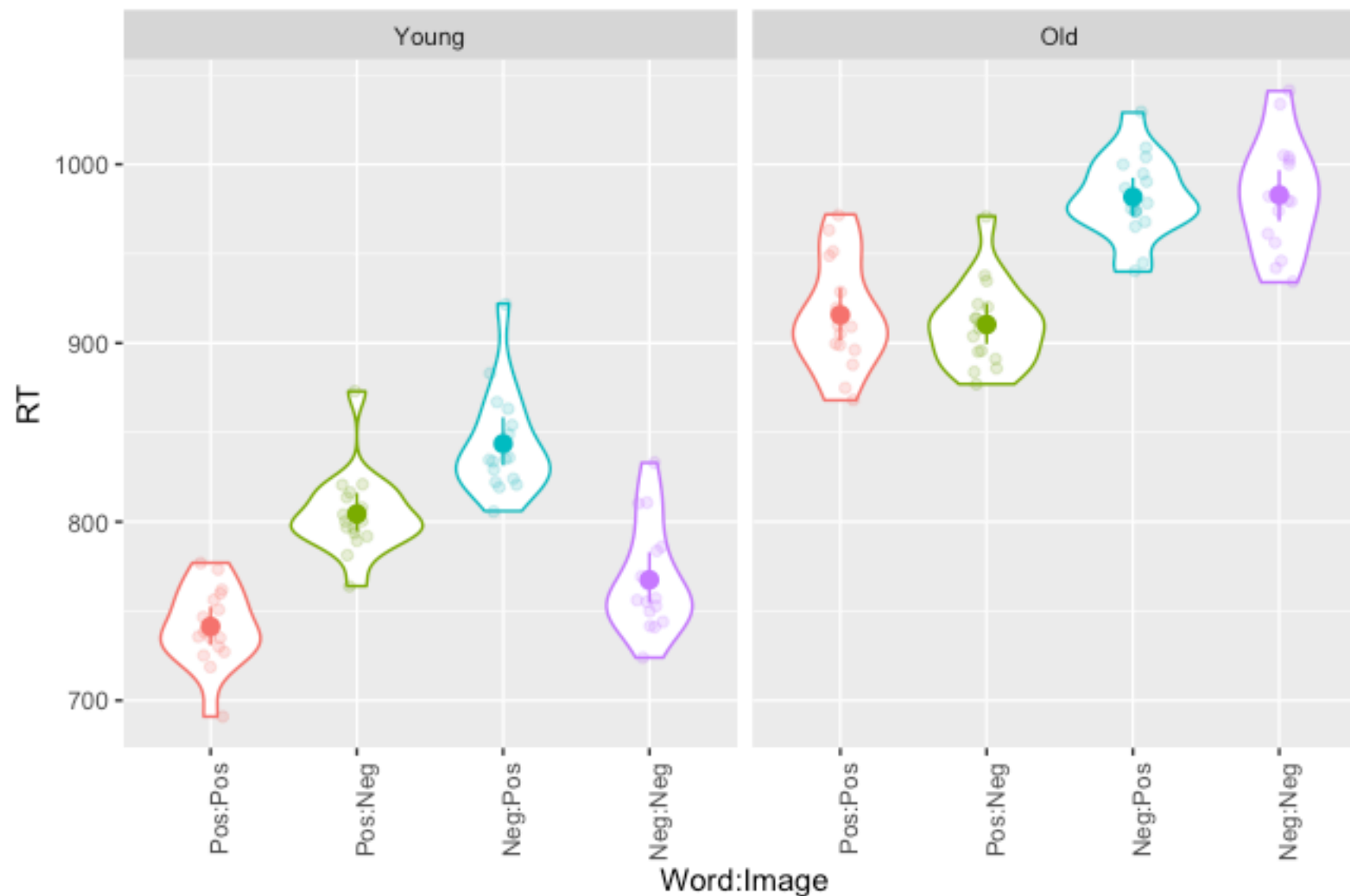
- Similar to our 2 x 2 ANOVA from last time, but let's say we now have Age as an additional factor. It's a between subjects factor. We might think that priming effects might be different for young vs old people.
- So we need to run a 2 x 2 x 2 ANOVA. The first two factors are still within subjects (i.e., repeated measures), but our new one (age) is between subjects and has two levels.

	Participant	Image	Word	Age	RT
1	1	Pos	Pos	Young	719
2	2	Pos	Pos	Young	756
3	3	Pos	Pos	Young	777
4	4	Pos	Pos	Young	691
5	5	Pos	Pos	Young	760
6	6	Pos	Pos	Young	762
7	7	Pos	Pos	Young	735
8	8	Pos	Pos	Young	736
9	9	Pos	Pos	Young	735
10	10	Pos	Pos	Young	727
11	11	Pos	Pos	Young	738
12	12	Pos	Pos	Young	725
13	13	Pos	Pos	Young	730
14	14	Pos	Pos	Young	751
15	15	Pos	Pos	Young	773
16	16	Pos	Pos	Young	747
17	1	Pos	Neg	Young	834
18	2	Pos	Neg	Young	822

Showing 1 to 18 of 128 entries

Remember, for the `aov_4` function we need each factor to be in its own column and for each row to be one observation - this is long or tidy format data.

```
ggplot(data, aes(x = Word:Image, y = RT, colour = Word:Image)) +
  geom_violin() + geom_jitter(width = .1, alpha = .2) +
  stat_summary(fun.data = "mean_cl_boot") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  facet_wrap(~ Age) + guides(colour = FALSE)
```



We can see it looks like the Young and Old groups are behaving a little differently.

We need to build our model with two repeated and one between participants factor...

```
model <- aov_4(RT ~ Word * Image * Age + (1 + Word * Image |  
Participant), data)
```

We are asking for the anova to be run on the three factors
- this will give us three possible main effects, 3 possible 2-way interactions, and a possible 3-way interaction...

The `aov_4` function doesn't need to be told which factors are repeated, and which are between - it can work this out itself from the data structure - note that between participant factors shouldn't appear in the random effects term - if you have only between factors then the term should be something like `(1 | Participant)`...

```

> anova(model)
Anova Table (Type 3 tests)

Response: RT

```

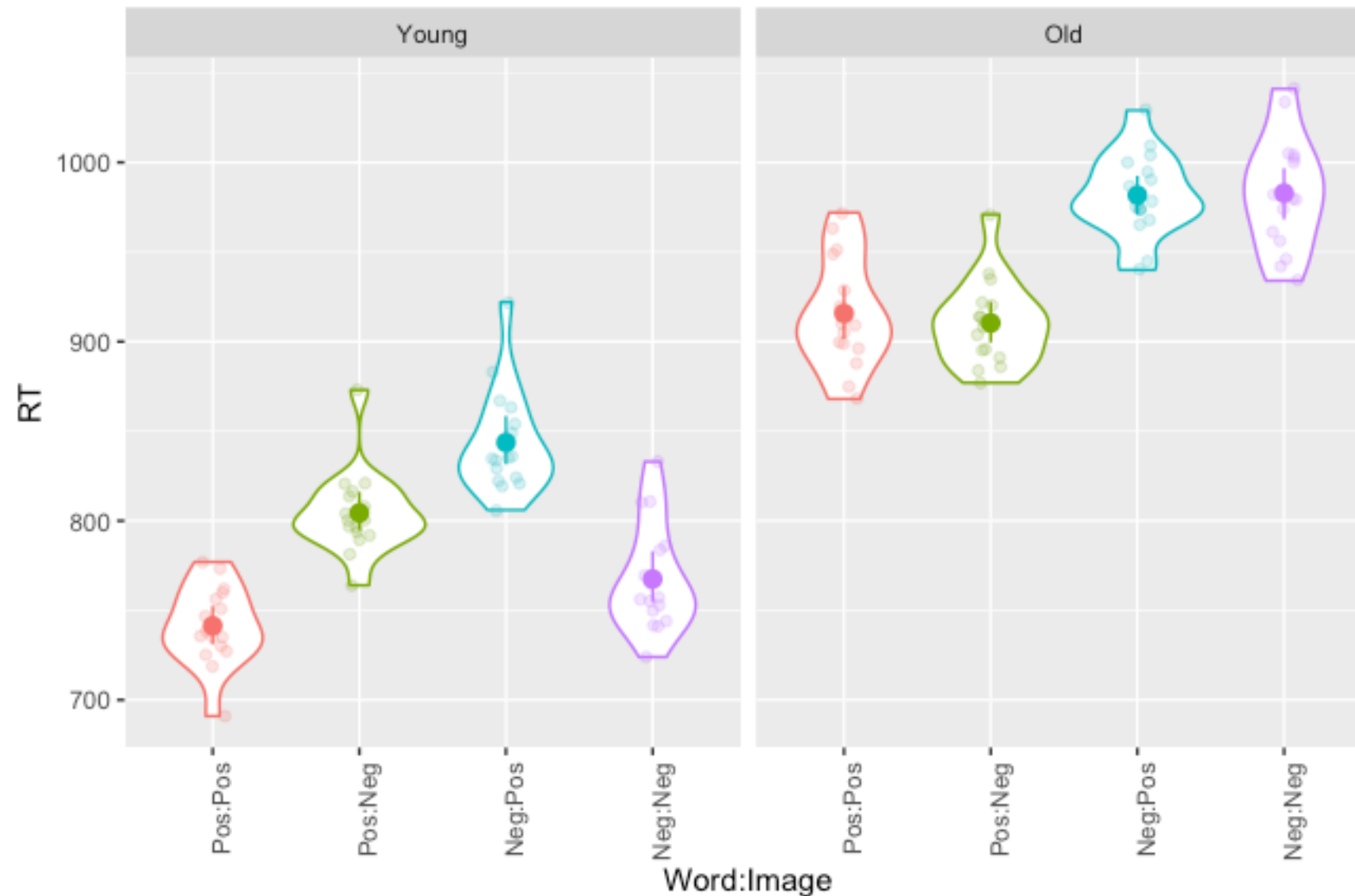
	num	Df	den	Df	MSE	F	ges	Pr(>F)	
Age		1		30	788.86	1017.8790	0.90328	< 2.2e-16	***
Word		1		30	750.85	110.7147	0.49157	1.380e-11	***
Age:Word		1		30	750.85	14.1946	0.11029	0.0007202	***
Image		1		30	752.62	0.8022	0.00697	0.3775568	
Age:Image		1		30	752.62	0.2152	0.00188	0.6460346	
Word:Image		1		30	573.74	61.4309	0.29074	9.553e-09	***
Age:Word:Image		1		30	573.74	73.9247	0.33033	1.363e-09	***

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

From this we can see we have main effects of Age and Word, no main effect of Image, significant 2-way interactions of Age x Word, and of Word x Image and, crucially, a 3-way interaction between all three factors - Age x Word x Image...



The 3-way interaction suggests that the Word x Image interaction is different for Young vs. Old people (which is supported by what we see in the graph...)

To interpret this 3-way, we should examine the Word x Image interaction separately for Young and Old people...

We can do this by filtering our dataset:

```
> young_filter <- filter(data, Age == "Young")
> model_young <- aov_4(RT ~ Word * Image + (1 + Word * Image | Participant),
  young_filter)
> anova(model_young)
Anova Table (Type 3 tests)
```

Response: RT

	num	Df	den	Df	MSE	F	ges	Pr(>F)	
Word		1		15	681.87	25.1197	0.29236	0.0001547	***
Image		1		15	918.44	0.7574	0.01650	0.3978527	
Word:Image		1		15	560.77	138.1887	0.65146	5.725e-09	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

**Significant
interaction**

We need to follow this up with pairwise comparisons.

```
> emmeans(model_young, pairwise ~ Word * Image, adjust = "Bonferroni")
```

```
$emmeans
```

Word	Image	emmean	SE	df	lower.CL	upper.CL
Pos	Pos	741.3750	6.571636	57.69	728.2189	754.5311
Neg	Pos	843.6875	6.571636	57.69	830.5314	856.8436
Pos	Neg	804.3750	6.571636	57.69	791.2189	817.5311
Neg	Neg	767.5000	6.571636	57.69	754.3439	780.6561

Confidence level used: 0.95

```
$contrasts
```

contrast	estimate	SE	df	t.ratio	p.value
Pos, Pos - Neg, Pos	-102.3125	8.812773	29.72	-11.610	<.0001
Pos, Pos - Pos, Neg	-63.0000	9.615140	28.34	-6.552	<.0001
Pos, Pos - Neg, Neg	-26.1250	10.000957	29.36	-2.612	0.0842
Neg, Pos - Pos, Neg	39.3125	10.000957	29.36	3.931	0.0028
Neg, Pos - Neg, Neg	76.1875	9.615140	28.34	7.924	<.0001
Pos, Neg - Neg, Neg	36.8750	8.812773	29.72	4.184	0.0014

P value adjustment: bonferroni method for 6 tests

Key pairwise comparisons are significant


But what about the Old group?

```
> old_filter <- filter(data, Age == "Old")
> model_old <- aov_4(RT ~ Word * Image + (1 + Word * Image | Participant),
old_filter)
> anova (model_old)
Anova Table (Type 3 tests)
```

Response: RT

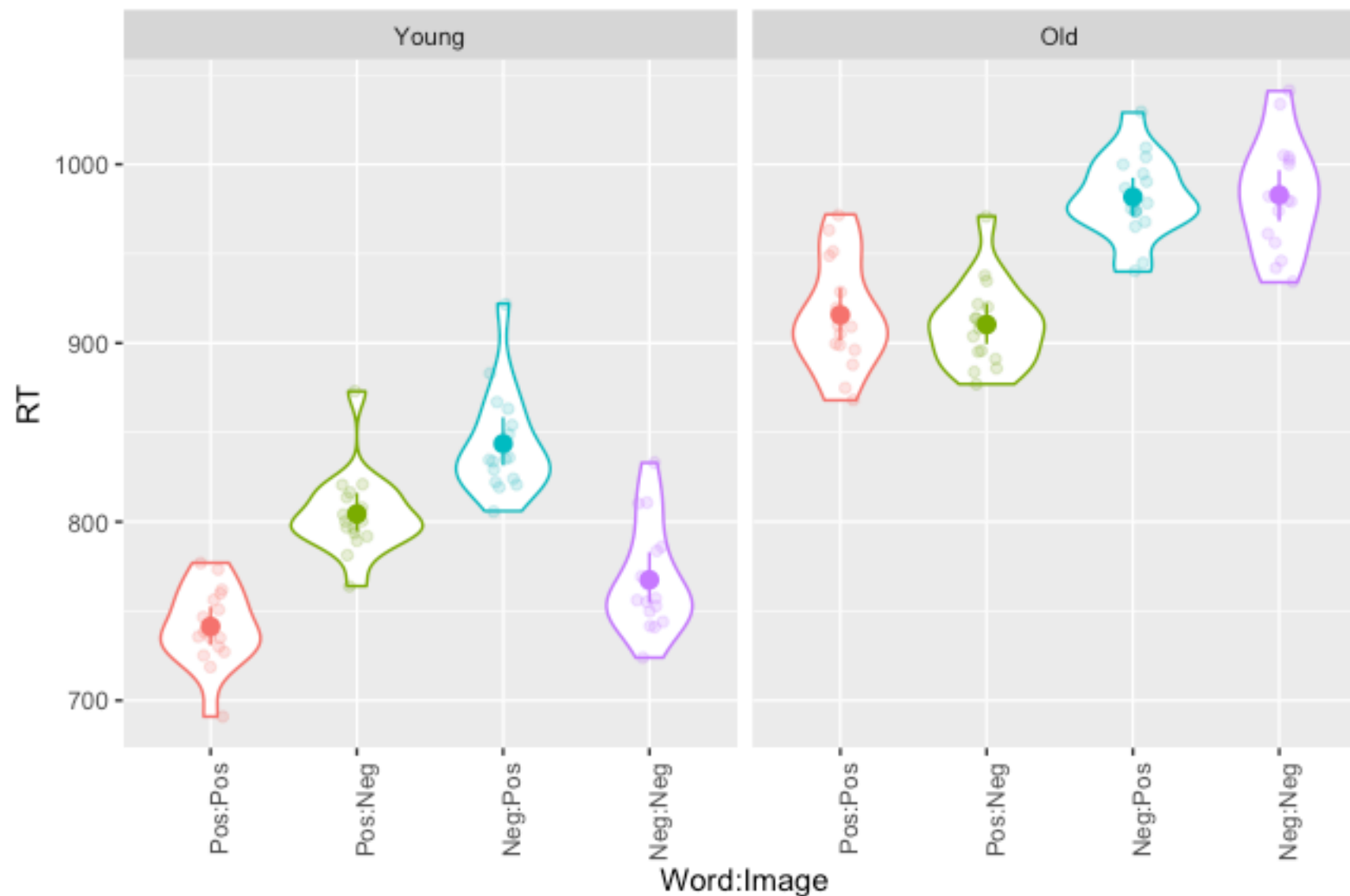
	num	Df	den	Df	MSE	F	ges	Pr(>F)	
Word		1		15	819.83	93.5066	0.63260	7.757e-08	***
Image		1		15	586.81	0.1195	0.00157	0.7343	
Word:Image		1		15	586.70	0.2825	0.00371	0.6028	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1



**Interaction
not significant**

So we have found a 2-way interaction of Word x Image that **differs** between our two groups. The 2-way interaction is significant for our Young group, but not significant for our Old group. For our Old group, we simply have a main effect of Word...

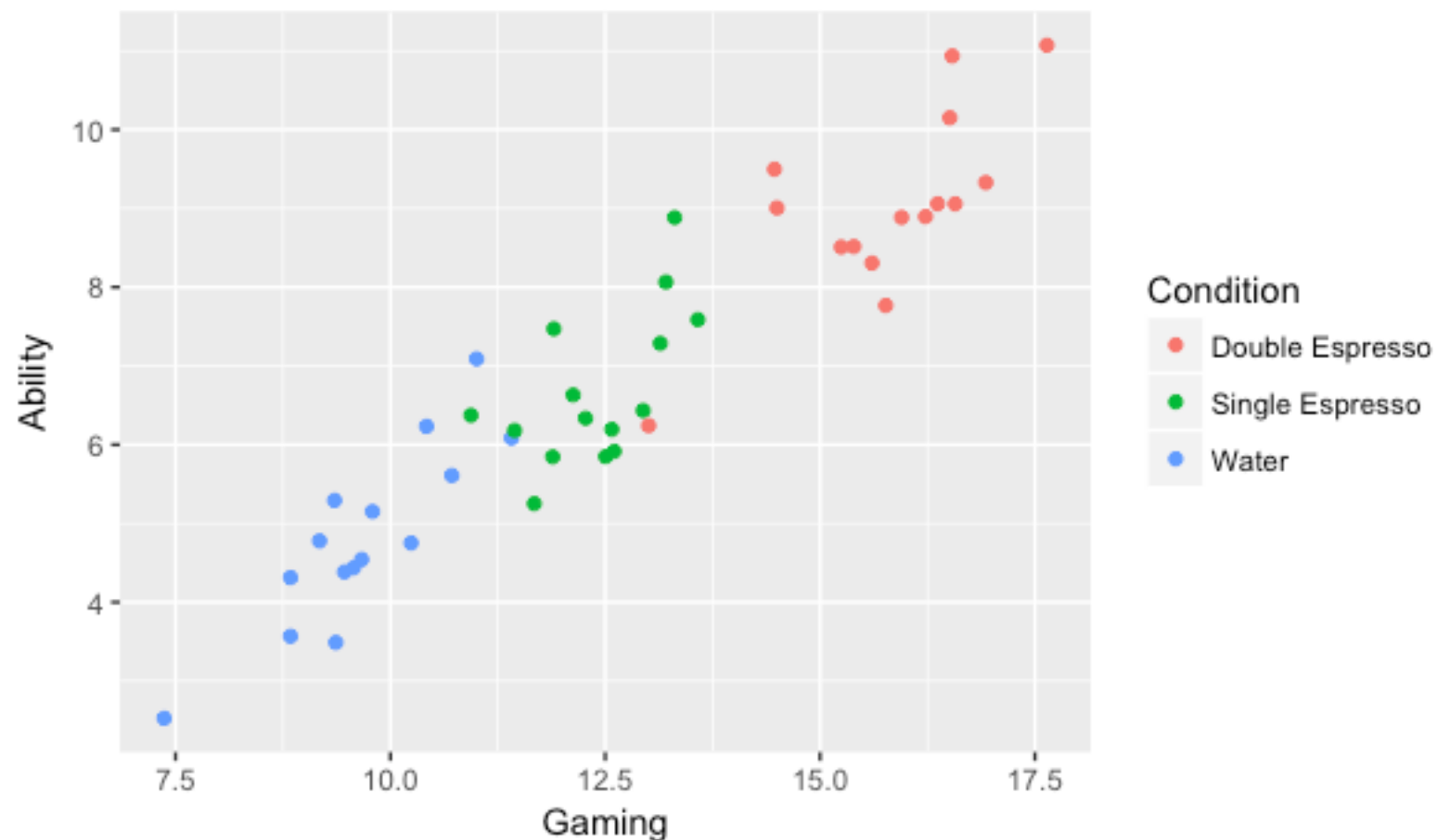


ANCOVA

- One of our examples from last week looked at how double espresso vs. single espresso vs. water drinking (our IV) might influence motor performance (our DV).
- Imagine we sampled from a new group of participants - and we think other factors that we are not manipulating might also influence the DV – e.g., practice with computer games.
- What we want is to be able to see the effect on our DV of our IV after we have removed the effects of other things (computer gaming frequency in this case).

- Now, imagine we have a measure of computer games frequency - perhaps hours per week people play computer games...
- So, in addition to manipulating the type of beverage we're giving people (i.e., double espresso vs. single espresso vs. water) we also measure how often they play computer games...
- Let's do a plot first with our DV (Ability) on the y-axis, and our covariate (Gaming Frequency) on the x-axis...

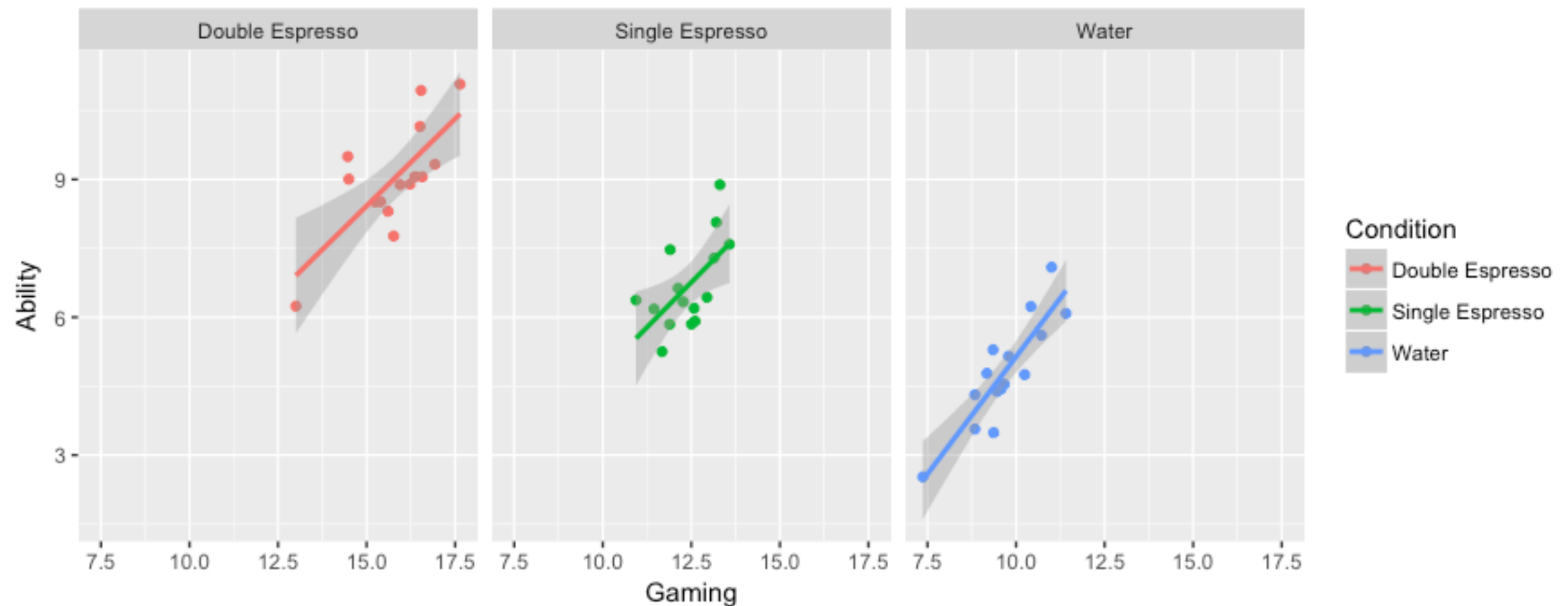
```
> ggplot(cond, aes(x = Gaming, y = Ability, colour = Condition)) + geom_point()
```



- So we can see there's a relationship between our DV (Ability) and our covariate (Gaming Frequency)...
- We can also see our Gaming Ability groups appear to be clustering in our data by Condition...

We can look at the data separately by condition using the *facet_wrap()* function:

```
> ggplot(cond, aes(x = Gaming, y = Ability, colour =  
Condition)) + geom_point() + facet_wrap(~ Condition) +  
geom_smooth(method = 'lm')
```



Running a 1-way between participants ANOVA (and ignoring the covariate)...

```
> model1 <- aov_4(Ability ~ Condition + (1 | Participant), data = cond)
Contrasts set to contr.sum for the following variables: Condition
> anova(model1)
Anova Table (Type 3 tests)
```

Response: Ability

	num	Df	den	Df	MSE	F	ges	Pr(>F)
Condition	2		42		1.2422	53.432	0.71786	2.882e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The factor Condition is significant with an $F = 53.432$. We would erroneously conclude that our manipulation has had an effect...

But now let's control for the effect of our co-variate (which we first need to scale and centre)...

```
> cond$Gaming <- scale(cond$Gaming)
> model_ancova <- aov_4(Ability ~ Gaming + Condition + (1 | Participant),
data = cond, factorize = FALSE)
Contrasts set to contr.sum for the following variables: Condition
> anova(model_ancova)
Anova Table (Type 3 tests)
```

Response: Ability

	num	Df	den	Df	MSE	F	ges	Pr(>F)	
Gaming		1		41	0.55171	53.5636	0.56643	5.87e-09	***
Condition		2		41	0.55171	0.8771	0.04103	0.4236	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The factor Condition is now not significant with an $F < 1$. However, our covariate *Gaming Frequency* is significant. Adding it means a lot of the variance we previously attributed to our experimental factor is actually explained by our covariate. Note, the F values are calculated using Type III Sum of Squares by the `aov_4()` function - more on that in a bit...

Rather than calculating over the raw means which are:

Water Group = 4.82

Double Espresso Group = 9.02

Single Espresso Group = 6.69

```
> describeBy(cond$Ability, group = cond$Condition)
```

```
Descriptive statistics by group
```

```
group: Double Espresso
```

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
X1	1	15	9.02	1.19	9.01	9.07	0.73	6.24	11.07	4.83	-0.26	0.16	0.31

```
group: Single Espresso
```

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
X1	1	15	6.69	0.98	6.37	6.63	0.78	5.25	8.88	3.63	0.69	-0.53	0.25

```
group: Water
```

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
X1	1	15	4.82	1.16	4.75	4.82	0.8	2.53	7.09	4.56	0.03	-0.57	0.3

The calculation is performed over the *adjusted* means (which take into consideration the influence of the covariate):

Water Group = 7.33

Double Espresso Group = 6.32

Single Espresso Group = 6.87

```
> emmeans(model_ancova, pairwise ~ Condition, adjust = "none")
```

```
$emmeans
```

Condition	emmean	SE	df	lower.CL	upper.CL
Double Espresso	6.319464	0.4152816	41	5.480786	7.158142
Single Espresso	6.871614	0.1934303	41	6.480974	7.262255
Water	7.327960	0.3931110	41	6.534056	8.121864

```
Confidence level used: 0.95
```

If our experimental factor in the ANCOVA *had* been significant, we could have looked at the pairwise comparisons reported by *emmeans* to determine what condition was different from what other condition...

```
$contrasts
contrast
Double Espresso - Single Espresso -0.5521505 0.4779448 41 -1.155 0.2547
Double Espresso - Water -1.0084959 0.7614421 41 -1.324 0.1927
Single Espresso - Water -0.4563454 0.4179276 41 -1.092 0.2812
```

But once we take account of the influence of our covariate we found no effect of Condition...

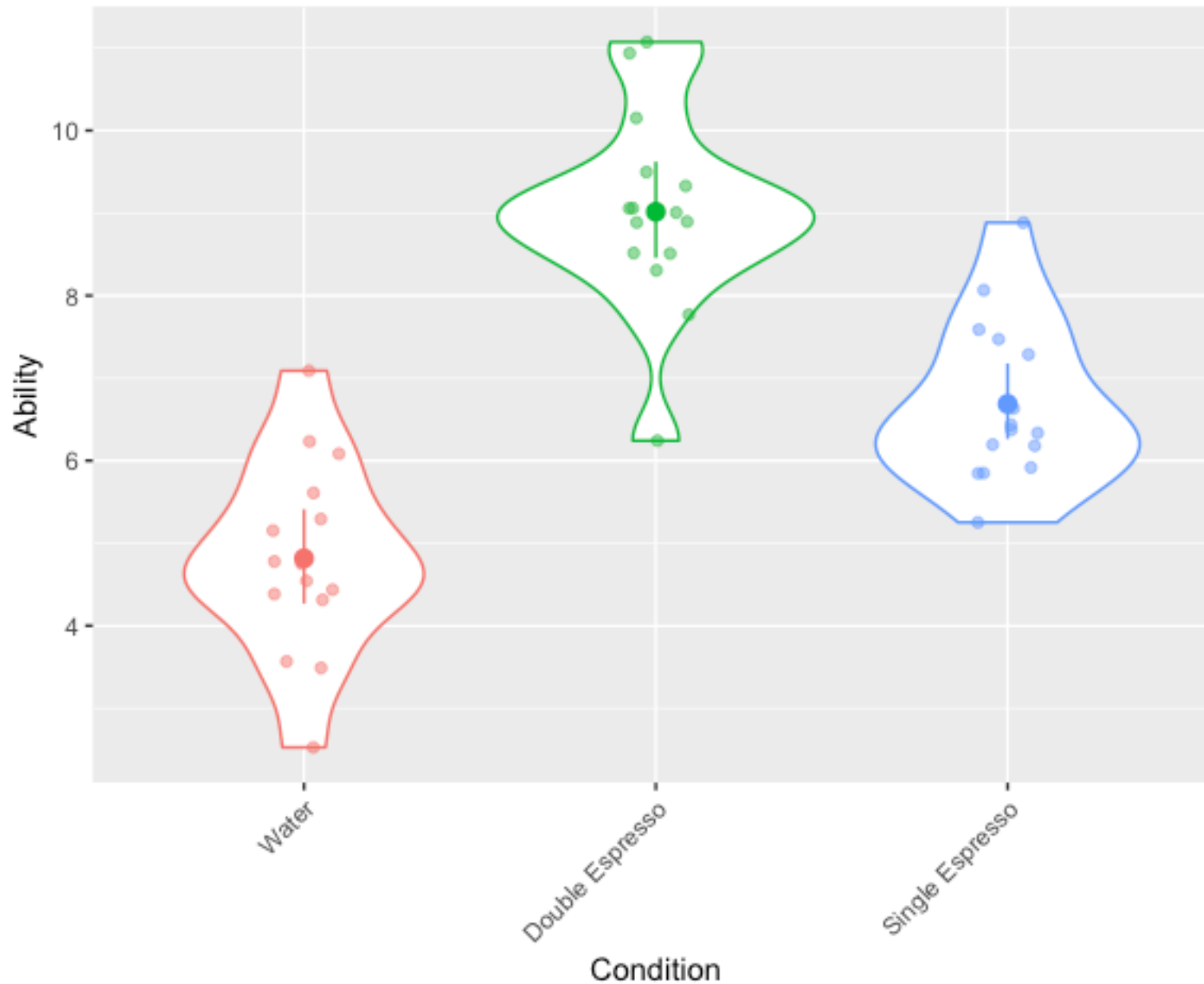
Note, if we had used the `aov()` function the F-tests would have been conducted using Type I (sequential) Sums of Squares. For Type III, we need to use the `aov_4()` function.

Type I vs. II vs. III Sums of Squares

- Type I Sum of Squares is calculated sequentially - e.g., first for Factor A main effect, then for Factor B main effect, then for the interaction. The order in which they are calculated matters and can be misleading for unbalanced design or cases where predictors are correlated. Total SS is the sum of the individual effect SS.
- Type II Sum of Squares assumes no interaction(s) when testing main effects or higher order interaction(s) when testing lower order interaction(s).
- Type III Sum of Squares tests for effects adjusted for the presence of the other effects (so does not depend on the order of terms).
- Much debate about which one is 'correct' - each has their own purpose - for factorial designs where you're interested in testing an interaction (or when your predictors correlate), Type III is most commonly used.

AN(C)OVA as a special case of regression...

- Let's return to the example we looked at for ANCOVA - and let's forget the co-variate for a moment...
- We looked at how double espresso vs. single espresso vs. water drinking (our IV) might influence people's gaming ability (our DV).



Water mean = 4.82

Double Espresso mean = 9.02

Single Espresso mean = 6.69

- First we need to use dummy coding of the levels of our experimental factor - which is the default coding in R for factors...

```
> # Set up the Water level as the reference level and check the contrasts
> cond$Condition <- relevel(cond$Condition, ref = 3)
> contrasts(cond$Condition)
```

	Double Espresso	Single Espresso
Water	0	0
Double Espresso	1	0
Single Espresso	0	1

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

The Intercept is our reference category (Water) with coding (0, 0), while the dummy coding for Double Espresso is (1, 0) and for Single Espresso (0, 1)

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

We want to calculate β_1 and β_2

```
> lm1 <- lm(Ability ~ Condition, data = cond)
> lm1
```

Call:

```
lm(formula = Ability ~ Condition, data = cond)
```

Coefficients:

(Intercept)	ConditionDouble Espresso	ConditionSingle Espresso
4.817	4.199	1.871

The intercept is 4.817 (which is the mean of our Water group), β_1 is 4.2, and β_2 is 1.87

To work out the mean Ability of our Double Espresso Group:

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

$$\text{Ability} = 4.82 + 4.2(1) + 1.87(0) + \varepsilon$$

$$\text{Ability} = 4.82 + 4.2 + \varepsilon$$

$$\text{Ability} = 9.02 + \varepsilon$$

To work out the mean Ability of our Single Espresso Group:

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

$$\text{Ability} = 4.82 + 4.2(0) + 1.87(1) + \varepsilon$$

$$\text{Ability} = 4.82 + 1.87 + \varepsilon$$

$$\text{Ability} = 6.69 + \varepsilon$$

Which are the exact same means generated by the ANOVA...

Water mean = 4.82

Double Espresso mean = 9.02

Single Espresso mean = 6.69



We can do ANCOVA like this too - let's consider our co-variate of Gaming frequency...

The *adjusted* means from the ANCOVA (which take into consideration the influence of the covariate) were:

Water Group = 7.33

Double Espresso Group = 6.32

Single Espresso Group = 6.87

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Gaming}) + \beta_2(\text{Double Espresso}) + \beta_3(\text{Single Espresso}) + \varepsilon$$

Add the covariate to our model *before* the experimental factor:

```
> lm2 <- lm(Ability ~ Gaming + Condition, data = cond)
> lm2
```

```
Call:
lm(formula = Ability ~ Gaming + Condition, data = cond)
```

```
Coefficients:
            (Intercept)              Gaming  ConditionDouble Espresso  ConditionSingle Espresso
                -3.4498                0.8538                -1.0085                -0.4563
```

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Gaming}) + \beta_2(\text{Double Espresso}) + \beta_3(\text{Single Espresso}) + \varepsilon$$

The β_2 and β_3 coefficients tell us the difference between each group mean (i.e., the adjusted mean) compared to the reference Group (Water) when taking into account the covariate of Gaming frequency:

β_2 is the difference between the Double Espresso and Water group adjusted means (= -1.01) while β_3 is the difference between the Double Espresso and Water group adjusted means (= -0.46)...

Let's check - the following are the adjusted means output by the ANCOVA model:

Water Group = 7.33

Double Espresso Group = 6.32

Single Espresso Group = 6.87

Difference between the Water and Double Espresso Group is 1.01 and the difference between the Water and Single Espresso Group is 0.46...

We can work out the mean of our reference group (Water) by plugging in the values to our equation - note that Gaming is not a factor and we need to enter the mean of this variable (which is 12.62296). So,...

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Gaming}) + \beta_2(\text{Double Espresso}) + \beta_3(\text{Single Espresso}) + \varepsilon$$

$$\text{Ability} = -3.4498 + 0.8538(12.62296) + (-1.0085)(0) + (-0.4563)(0) + \varepsilon$$

$$\text{Ability} = -3.4498 + 10.777 + \varepsilon$$

$$\text{Ability} = 7.33 + \varepsilon$$

7.33 is the adjusted mean for the Water group...which is what we had from calling the `emmeans` function following the ANCOVA...

You can now build ANOVA models in R for different kinds of designs, add between participant co-variates, factor out the influence of these co-variates, and you also know why AN(C)OVA is a special case of regression (with dummy coding of variables)...



To the computer lab...