

17C

Laboratory & Professional Skills:  
Data Analysis

# Emma Rand

## Data Analysis in R

More than one explanatory variable:  
Two-way ANOVA

# Last week

- Extended our ability to test for differences between two or more groups with the one-way ANOVA and its non-parametric equivalent Kruskal-Wallis
  - Rationale for ANOVA rather than multiple  $t$ -tests
  - ANOVA terminology and concepts:  $SS$ ,  $MS$ ,  $F$
  - Post-hoc tests
- In RStudio
  - Importing data from csv files
  - One way ANOVA and Kruskal-Wallis and their post-hoc tests
  - Summarising and reporting
  - Figure annotations

# Summary of this week

Extend of our understanding to testing with two explanatory variables using the two-way ANOVA

- Comparison with one-way ANOVA
- The three null hypotheses
- Running, interpreting and reporting a two-way ANOVA
- Investigating the assumptions
- Understanding the interaction
- Post-hoc analysis (after a significant two-way ANOVA)

# Learning objectives for the week

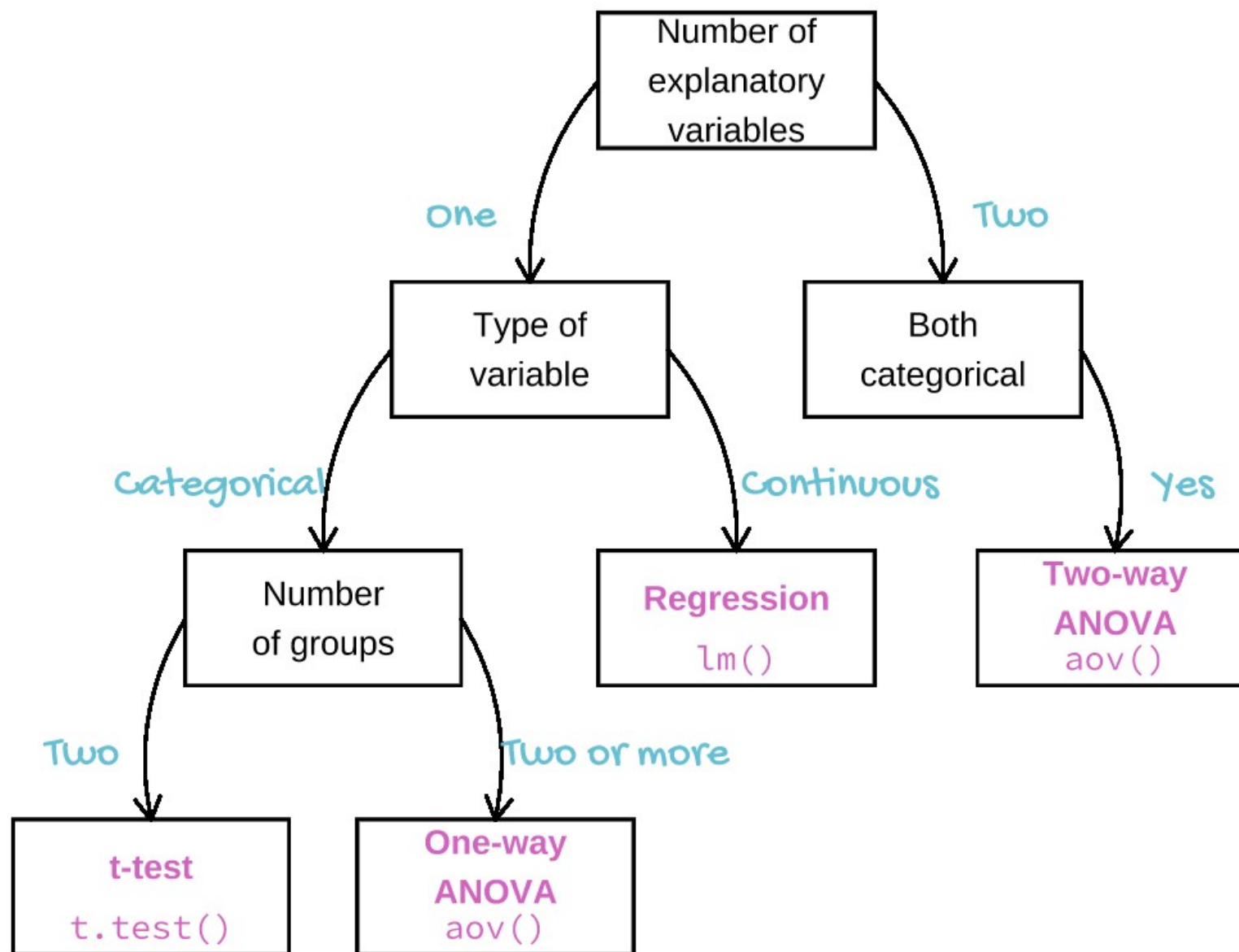
By the end of this week the successful student should be able to:

- List the sheets in, and read data from, Excel files (MLO 3)
- Combine dataframes of the same structure (MLO 3)
- Select, appropriately two-way ANOVA (MLO 2)
- Understand the meaning of the interaction term (MLO 2)
- Apply and interpret the two-way ANOVA (including the interaction), and post-hoc tests in R (MLO 3 and 4)
- Evaluate whether the assumptions of the test are met (MLO 2)
- Summarise and illustrate with appropriate R figures test results scientifically (MLO 3 and 4)

# Review and rationale

# Choosing tests: 3 steps

1. What is a one sentence description of what you want to know?
2. What are your explanatory variables?
  - **Categories:** *t*-tests, ANOVA, Wilcoxon, Mann-Whitney
  - Continuous: Regression, correlation
3. What is your response variable?
  - **Normally distributed:** *t*-tests, ANOVA, regression
  - Counts: Chi-squared or stage 2 😊



Choosing tests

# Choosing between one-way and two-way ANOVA?

Response:  
wing lengths



The screenshot shows a data table with two columns: 'winglen' and 'spp'. The 'winglen' column contains numerical values representing wing lengths, and the 'spp' column contains categorical values representing species. The table is displayed in a software interface with a toolbar at the top and a status bar at the bottom.

	winglen	spp
1	23.6	F.flappa
2	23.3	F.flappa
3	18.2	F.flappa
4	22.6	F.flappa
5	29.3	F.flappa
6	22.2	F.flappa
7	24.5	F.flappa
8	26.3	F.flappa
9	20.6	F.flappa
10	23.9	F.flappa
11	26.5	F.flappa
12	24.7	F.flappa
13	28.3	F.flappa
14	22.3	F.flappa
15	21.8	F.flappa
16	30.0	F.flappa
17	21.5	F.flappa
18	20.1	F.flappa
19	24.3	F.flappa
20	27.2	F.flappa
21	28.6	F.concocti
22	17.2	F.concocti
23	20.4	F.concocti
24	21.9	F.concocti
25	26.3	F.concocti
26	27.8	F.concocti

Showing 1 to 26 of 40 entries

Explanatory:  
species



Choosing tests

# Choosing between one-way and two-way ANOVA?

What if we have two explanatory variables?

- Two one-way ANOVAs?? **NO**
- A Two-way ANOVA **YES**
- Note: tidy data format



lect 080 two-way ANOVA.R x butter x

Filter

	winglen	spp	region
1	23.6	F.flappa	south
2	23.3	F.flappa	south
3	18.2	F.flappa	south
4	22.6	F.flappa	south
5	29.3	F.flappa	south
6	22.2		
7	24.5		
8	26.3		
9	20.6		
10	23.9		
11	26.5		
12	24.7	F.flappa	north
13	28.3	F.flappa	north
14	22.3	F.flappa	north
15	21.8	F.flappa	north
16	30.0	F.flappa	north
17	21.5	F.flappa	north
18	20.1	F.flappa	north
19	24.3	F.flappa	north
20	27.2	F.flappa	north
21	28.6	F.concocti	south
22	17.2	F.concocti	south
23	20.4	F.concocti	south
24	21.9	F.concocti	south

Showing 1 to 24 of 40 entries, 3 total columns

Explanatory:  
species  
region

## Two-way ANOVA

# Assumptions

- Same as for one-way ANOVA
- Normality and homogeneity of variance in residuals
  - Common sense
  - **Check after ANOVA** using the \$residuals variable and diagnostic plots (as we did after one-way ANOVA)

# The two-way ANOVA

A parametric test

## Two-way ANOVA Example

Response: wing lengths

Explanatory variables:

region: two levels

spp: two levels

lect 080 two-way ANOVA.R × butter ×			
Filter			
	winglen	spp	region
1	23.6	F.flappa	south
2	23.3	F.flappa	south
3	18.2	F.flappa	south
4	22.6	F.flappa	south
5	29.3	F.flappa	south
6	22.2	F.flappa	south
7	24.5	F.flappa	south
8	26.3	F.flappa	south
9	20.6	F.flappa	south
10	23.9	F.flappa	south
11	26.5	F.flappa	north
12	24.7	F.flappa	north
13	28.3	F.flappa	north
14	22.3	F.flappa	north
15	21.8	F.flappa	north
16	30.0	F.flappa	north
17	21.5	F.flappa	north
18	20.1	F.flappa	north
19	24.3	F.flappa	north
20	27.2	F.flappa	north
21	28.6	F.concocti	south
22	17.2	F.concocti	south
23	20.4	F.concocti	south
24	21.9	F.concocti	south

Showing 1 to 24 of 40 entries, 3 total columns

Two-way ANOVA example

## What does it test?

The null hypotheses here are:

1. mean of *F.flappa* (averaged over the regions) = mean of *F.concocti* (averaged over the regions),
2. mean of north (averaged over the spp) = mean of south (averaged over the spp) and
3. the effects of the two factors are independent.

## Two-way ANOVA example

# What does it test?

The null hypotheses here are:

1. mean of *F.flappa* (averaged over the regions) = mean of *F.concocti* (averaged over the regions),
2. mean of north (averaged over the spp) = mean of south (averaged over the spp) and
3. the effects of the two factors are independent.

## Two-way ANOVA example

# Reading in and examining the structure of the data

```
butter <- read_table2("../data/butterf.txt")
glimpse(butter)
Observations: 40
Variables: 3
$ winglen <dbl> 23.6, 23.3, 18.2, 22.6, 29.3, 22.2, 24.5, 26.3, 20.6, 23.9...
$ spp      <fct> F.flappa, F.flappa, F.flappa, F.flappa, F.flappa, F.flappa...
$ region   <fct> south, south, south, south, south, south, south, south, so...
```

## Assumptions

Common sense

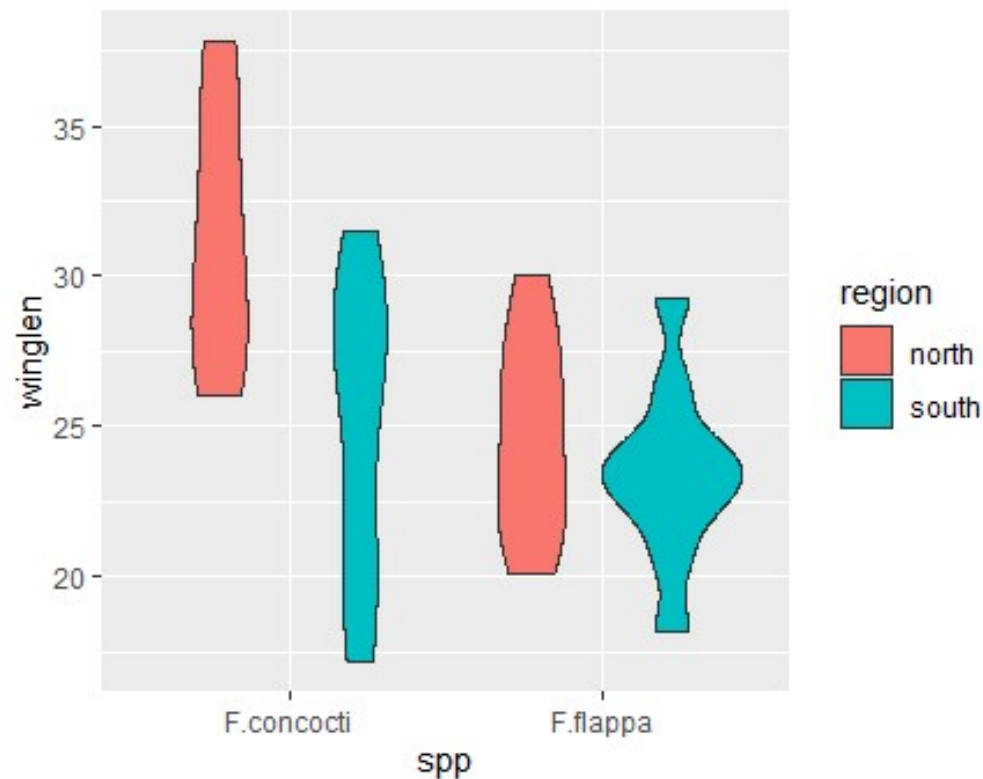
Can be checked after analysis

Two-way ANOVA example

# Plot your data

Plot your data: roughly – perhaps..

```
ggplot(data = butter,  
       aes(x = spp, y = winglen, fill = region)) +  
  geom_violin()
```





## Two-way ANOVA example

# Example

## Summarise

```
buttersum <- butter %>%  
  group_by(region, spp) %>%  
  summarise(mean = mean(winglen),  
            median = median(winglen),  
            sd = sd(winglen),  
            n = length(winglen),  
            se = sd/sqrt(n))
```

```
buttersum  
# A tibble: 4 x 7  
# Groups:   region [2]  
  region spp      mean median    sd     n    se  
  <fct> <fct>    <dbl>  <dbl> <dbl> <int> <dbl>  
1 north F.concocti 31.4   31.0  4.28   10  1.35  
2 north F.flappa   24.7   24.5  3.27   10  1.03  
3 south F.concocti 25.0   27.0  4.96   10  1.57  
4 south F.flappa   23.4   23.5  3.01   10  0.953
```

## Two-way ANOVA example

# Example

Run the ANOVA

```
mod <- aov(data = butter,  
           winglen ~ region * spp)
```


Assign result because we will be able to access residuals from this object later

## Two-way ANOVA example

# Example

Run the anova

```
mod <- aov(data = butter,  
           winglen ~ region * spp)
```



The model: explain winglen by region, spp and the interaction between them

## Two-way ANOVA example

# Understanding the test output

```
mod <- aov(data = butter, winglen ~ region * spp)
summary(mod)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
region	1	145.16	145.161	9.2717	0.004334	**
spp	1	168.92	168.921	10.7893	0.002280	**
region:spp	1	67.08	67.081	4.2846	0.045692	*
Residuals	36	563.63	15.656			

---

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

Three tests  
Three p values

## Two-way ANOVA example

# Understanding the test output

```
mod <- aov(data = butter, winglen ~ region * spp)
summary(mod)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
region	1	145.16	145.161	9.2717	0.004334	**
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Residuals	36	563.63	15.656			

---

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

1. There is an effect of region (difference between regions)
2. There is an effect of species (difference between species)
3. There is an interaction between region and species.....

## Two-way ANOVA example

# Understanding the test output

```
mod <- aov(data = butter, winglen ~ region * spp)
summary(mod)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
region	1	145.16	145.161	9.2717	0.004334	**
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---

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

Total d.f. is no. of values – 1:

$$40 - 1 = 39$$

region d.f. is no. regions – 1:

$$2 - 1 = 1$$

spp d.f. is no. spp – 1:

$$2 - 1 = 1$$

Interaction d.f. is region d.f. \* spp d.f. :

$$1 * 1 = 1$$

Residual d.f. is total d.f. – all other d.f.:

$$39 - 1 - 1 - 1 = 36$$

## Two-way ANOVA example

# Understanding the test output

```
mod <- aov(data = butter, winglen ~ region * spp)
summary(mod)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
region	1	145.16	145.161	9.2717	0.004334	**
spp	1	168.92	168.921	10.7893	0.002280	**
region:spp	1	67.08	67.081	4.2846	0.045692	*
Residuals	36	563.63	15.656			
---						
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1						

'Error term' for all 3 tests

## Two-way ANOVA example

# Checking Assumptions

- Common sense
  - response should be continuous
  - No/few repeats
- Plot the residuals
- Using a test in R



## Two-way ANOVA

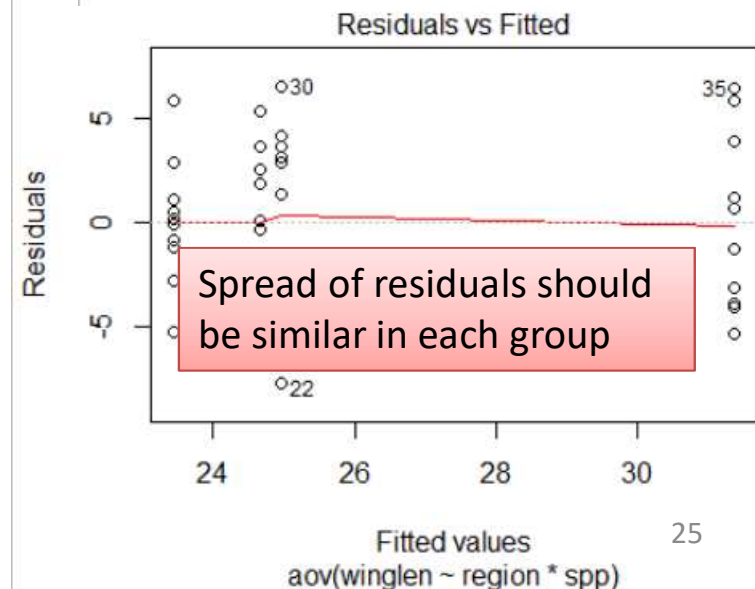
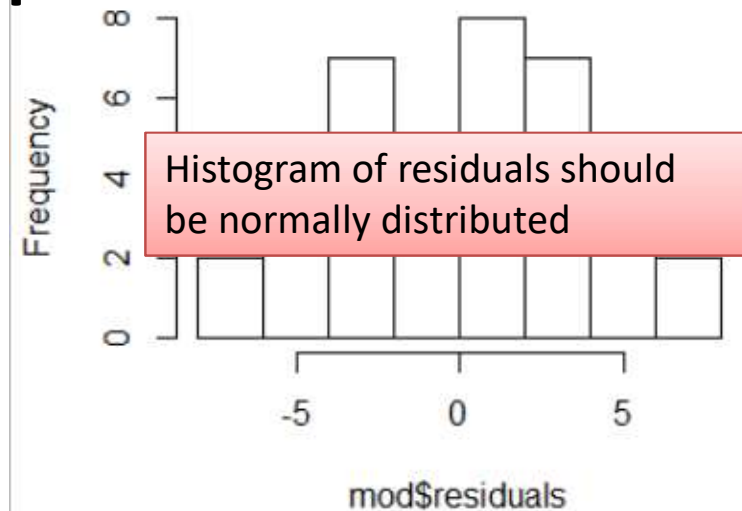
# Checking Assumptions

Residuals are calculated for you already!

```
hist(mod$residuals)  
shapiro.test(mod$residuals)
```

Shapiro-wilk normality test

```
data: mod$residuals  
W = 0.97306, p-value = 0.4474  
plot(mod, which=1)
```



Two-way ANOVA example

## Reporting the result

Reporting the result: “significance, direction, magnitude”

There was a significant difference between the species (ANOVA:  $F = 10.79$ ;  $d.f. = 1,36$ ;  $p = 0.002$ ) and between the regions ( $F = 9.27$ ;  $d.f. = 1,36$ ;  $p = 0.004$ ). However, there was also a significant interaction between region and species ( $F = 4.28$ ;  $d.f. = 1,36$ ;  $p = 0.046$ )

What about direction and magnitude??

Two-way ANOVA example

# Reporting the result: Post-hoc?

Post-hoc test e.g., Tukey



John Wilder Tukey



Wild Turkey



Wild Turkey

## Two-way ANOVA example

# Reporting the result

Which means differ? Post-hoc test needed e.g., Tukey

3 parts to the output. First two parts for region and spp

### TukeyHSD(mod)

Tukey multiple comparisons of means  
95% family-wise confidence level

Fit: aov(formula = winglen ~ region \* spp, data = butter)

#### \$region

	diff	lwr	upr	p adj
south-north	-3.81	-6.347658	-1.272342	0.004334

#### \$spp

	diff	lwr	upr	p adj
F.flappa-F.concocti	-4.11	-6.647658	-1.572342	0.0022796

## Two-way ANOVA example

# Reporting the result

Which means differ? Post-hoc test needed e.g., Tukey

3 parts to the output. Third part for the interaction

```
$`region:spp`  
              diff      lwr      upr      p adj  
south:F.concocti-north:F.concocti -6.40 -11.165769 -1.634231 0.0048102  
north:F.flappa-north:F.concocti   -6.70 -11.465769 -1.934231 0.0030099  
south:F.flappa-north:F.concocti   -7.92 -12.685769 -3.154231 0.0004123  
north:F.flappa-south:F.concocti   -0.30  -5.065769  4.465769 0.9982343  
south:F.flappa-south:F.concocti   -1.52  -6.285769  3.245769 0.8257284  
south:F.flappa-north:F.flappa     -1.22  -5.985769  3.545769 0.9004525
```

## Two-way ANOVA example

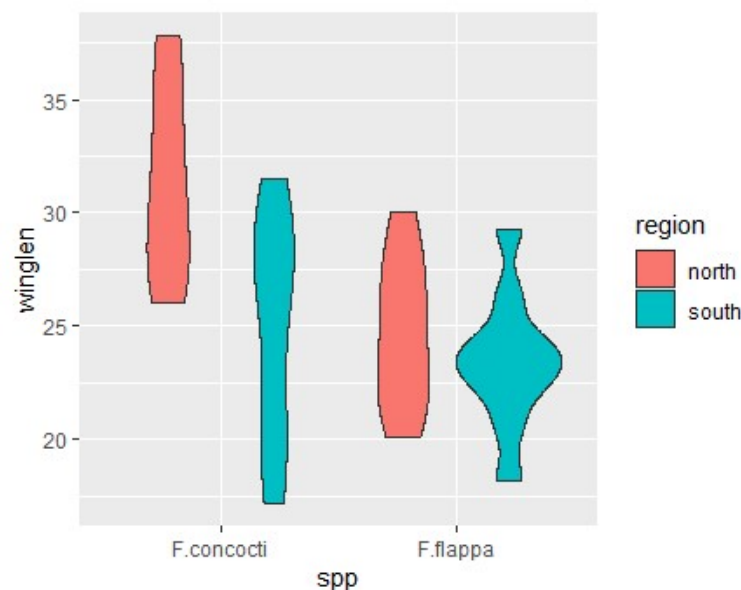
# Reporting the result: direction and magnitude

```
$`region:spp`
```

	diff	lwr	upr	p adj
south:F.concocti-north:F.concocti	-6.40	-11.165769	-1.634231	0.0048102
north:F.flappa-north:F.concocti	-6.70	-11.465769	-1.934231	0.0030099
south:F.flappa-north:F.concocti	-7.92	-12.685769	-3.154231	0.0004123
north:F.flappa-south:F.concocti	-0.30	-5.065769	4.465769	0.9982343
south:F.flappa-south:F.concocti	-1.52	-6.285769	3.245769	0.8257284
south:F.flappa-north:F.flappa	-1.22	-5.985769	3.545769	0.9004525

```
buttersum
```

```
# A tibble: 4 x 7
# Groups:   region [2]
  region spp      mean
  <fct> <fct>    <dbl>
1 north F.concocti 31.4
2 north F.flappa   24.7
3 south F.concocti 25.0
4 south F.flappa   23.4
```



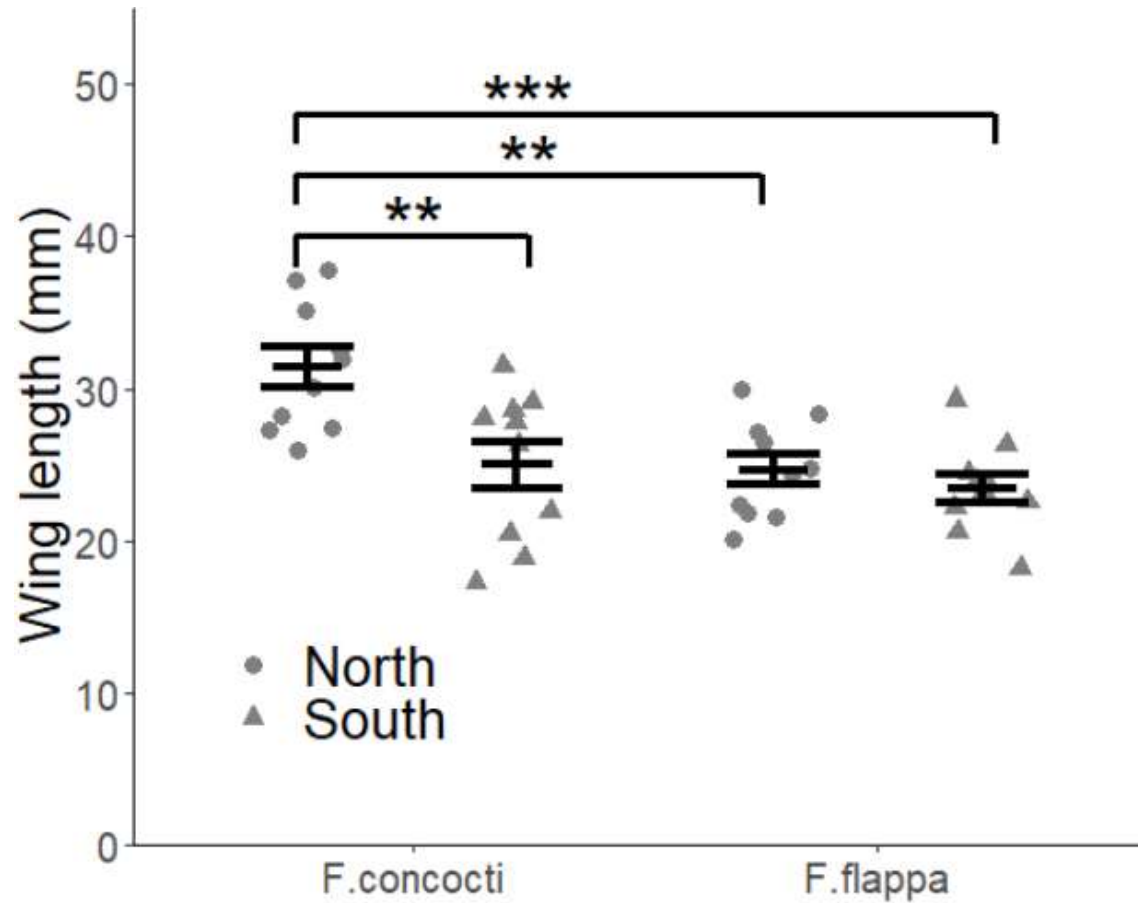
Two-way ANOVA example

## Reporting the result: direction and magnitude

*F.concocti* had significantly longer wings on average than *F.flappa* (ANOVA:  $F = 10.79$ ;  $d.f. = 1,36$ ;  $p = 0.002$ ) and individuals were significantly bigger in the North than the South ( $F = 9.27$ ;  $d.f. = 1,36$ ;  $p = 0.004$ ). However, this was primarily because northern *F.concocti* were significantly larger than the other three groups (Tukey Honest Significant difference: southern *F.concocti*  $p = 0.0048$ , southern *F.flappa*  $p = 0.0004$ , northern *F.flappa*  $p = 0.003$ , ). See Figure 1.

## Two-way ANOVA example

# Reporting the result: figure





# Two-way ANOVA summary

- Parametric
- Two explanatory categorical variables
- Three null hypotheses: main effects and interaction
- Function in R:  

```
mod <- aov(data = df, response ~ explanatory1 *  
  explanatory2)  
summary(mod)
```
- assumptions: normally and homogenously distributed residuals

continued

*t*-tests

## Two-way ANOVA summary

- ANOVA tells at least two means differ and a post-hoc test is needed to determine which means differ
- Tukey Honest Significant Difference is the post-hoc we used
- Function in R:  
`TukeyHSD(mod)`
- Interpret the interaction
- Significance, direction, magnitude
- Figure: data and 'model'

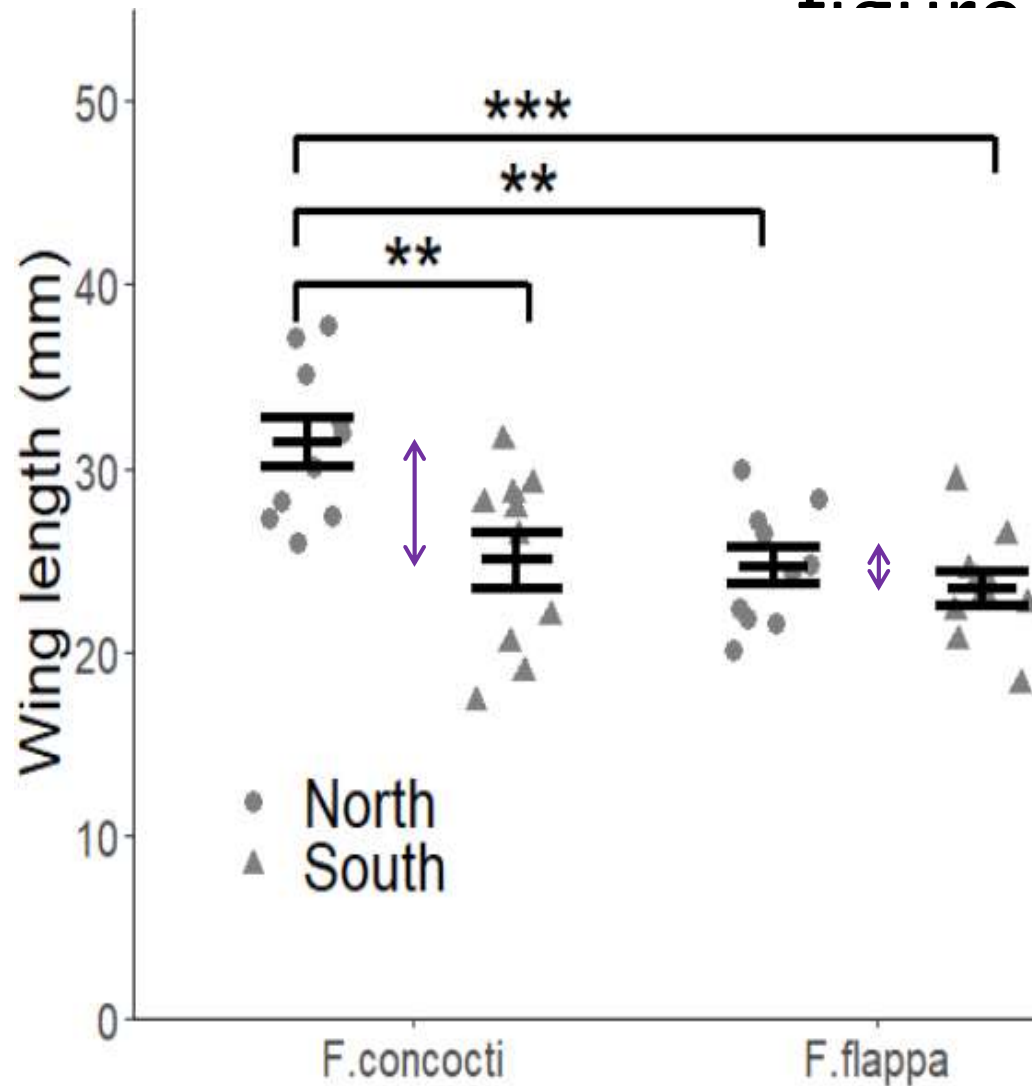
# Understanding the interaction

in two-way ANOVA

Two-way ANOVA example

# Understanding the interaction from the

figure



region – Sig

Spp – Sig

Int – Sig

Effect of region is greater in *F.concocti* (i.e., the gap between regions is bigger)

‘effect of one factor depends on the level of another’

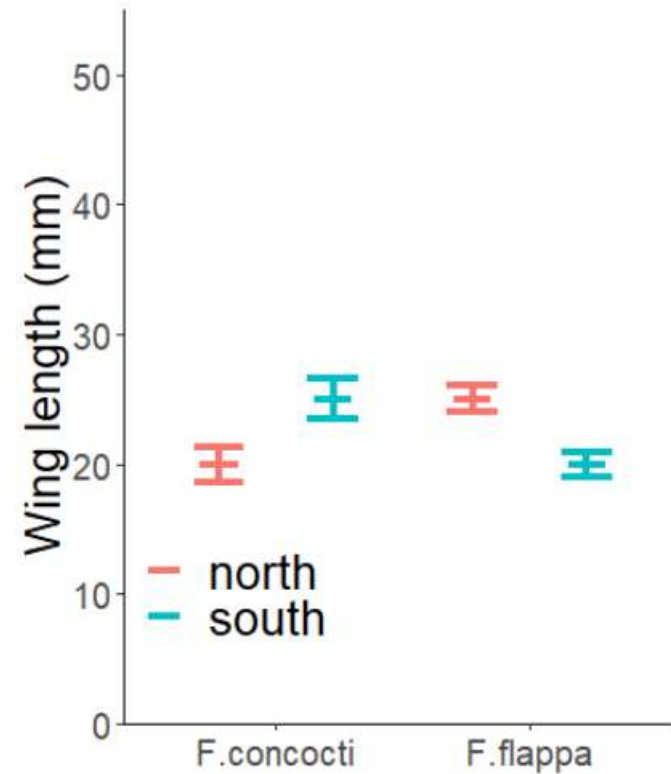
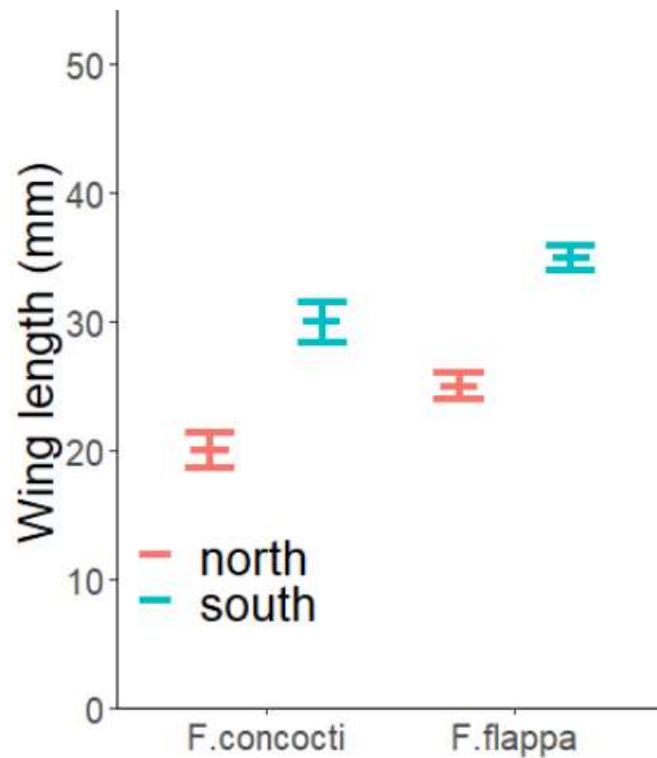
Two-way ANOVA example

# Understanding the interaction from the figure

Some other possible results

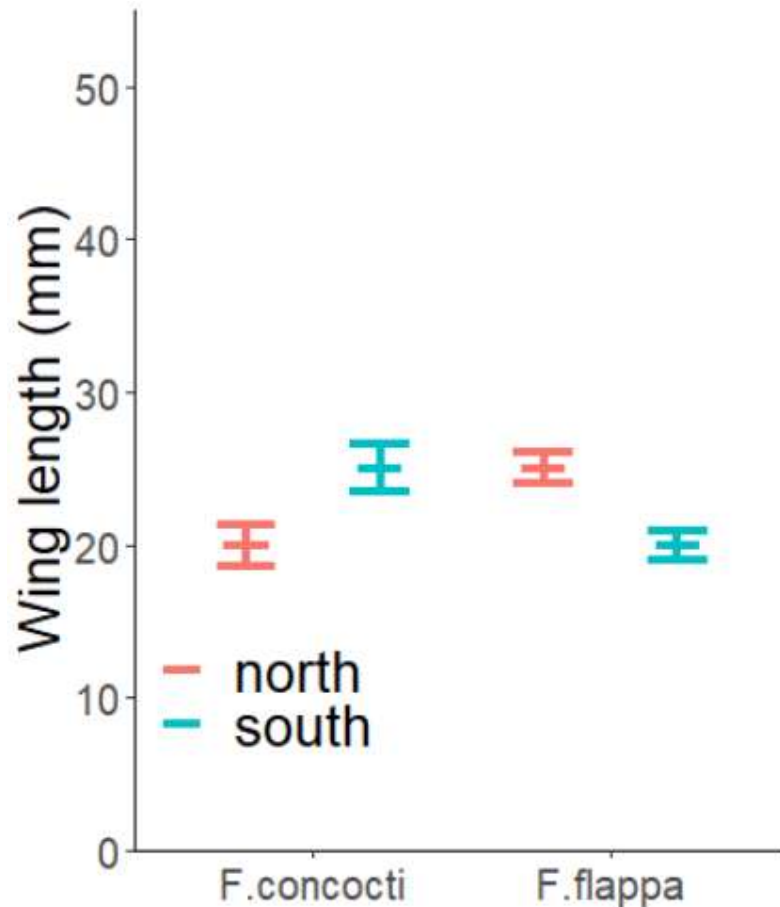
No interaction: Gap the same

Interaction: Gap the reversed



## Two-way ANOVA example

# Understanding the interaction from the figure



Region – NS

Spp – NS

Int – Sig

But region does have an effect!

It is just reversed!

If you have a significant interaction, interpret main effects with care. Look at the Post-hoc test