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

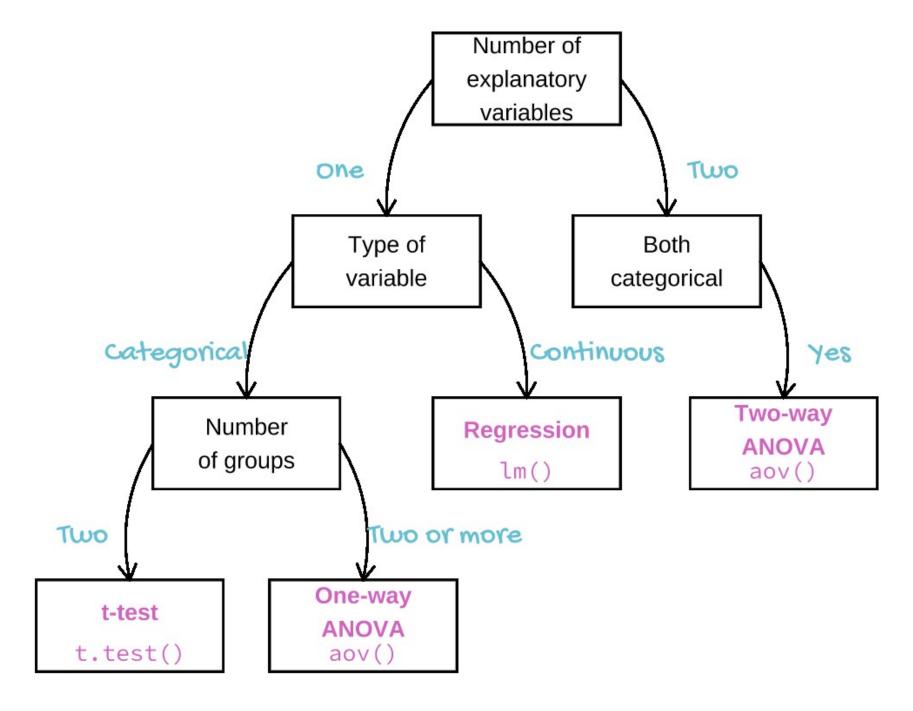
By the end of this week the successful student should be able to:

- 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

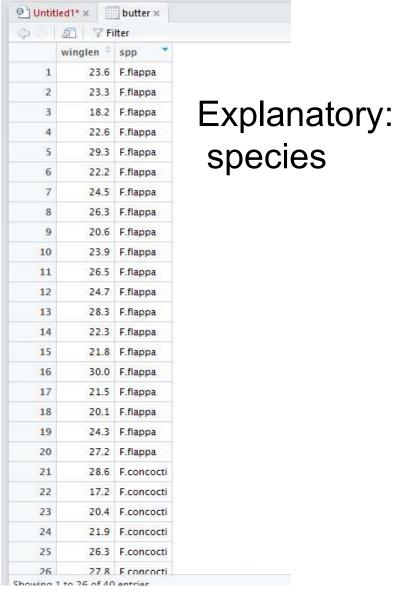
- 1. What is a one sentence description of what you want to know?
- 2. What are your explanatory variables?
 - Categories: *t*-tests, ANOVA, Wilcoxon, Mann-Whitney
 - Continuous: Regression, correlation
- 3. What is your response variable?
 - Normally distributed: *t*-tests, ANOVA, regression
 - Counts: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



Choosing tests

Choosing between one-way and two-way ANOVA?

Response: wing lengths



Choosing tests

What if we have two explanatory variables?

- Two one-way ANOVAs?? NO
- A Two-way ANOVA YES

Note: tidy data format



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

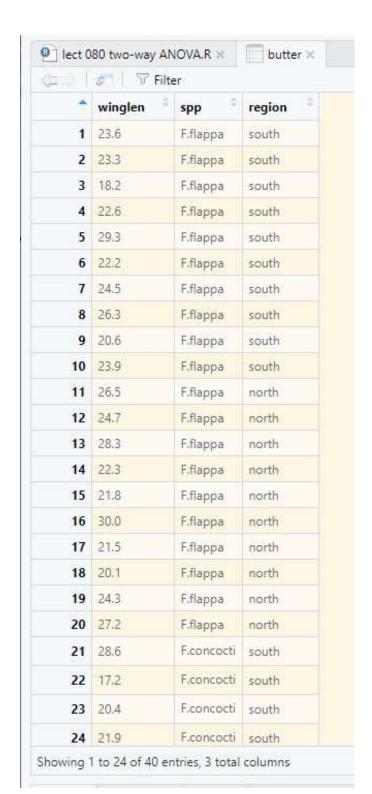
Example

Response: wing lengths

Explanatory variables:

region: two levels

spp: two levels



What does it test?

The null hypotheses here are:

- 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.

What does it test?

The null hypotheses here are:

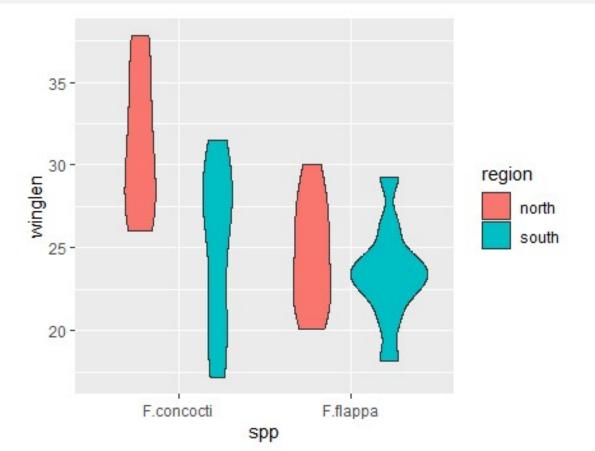
- mean of *F.flappa* (averaged over the regions)
 mean of *F.concocti* (averaged over the regions),
- 2. mean of north (averaged over the spp) = mean of south (averaged over the spp) and
- 3. the effects of the two factors are independent.

Reading in and examining the structure of the data

Assumptions
Common sense
Can be checked after analysis

Plot your data

Plot your data: roughly – perhaps..



Example

Sumarise

```
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
                                     10 0.953
4 south F.flappa
                  23.4
                         23.5 3.01
```

Run the ANOVA Example

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

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

Example

Run the anova

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

Understanding the test output

Three tests
Three p values

Understanding the test output

- 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.....

Understanding the test output

```
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=36
```

Understanding the test output

```
mod <- aov(data = butter, winglen ~ region * spp)</pre>
summary(mod)
           Df Sum Sq Mean Sq F value Pr(>F)
            1 145.16 145.161 9.2717 0.004334 **
region
        1 168.92 168.921 10.7893 0.002280 **
spp
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

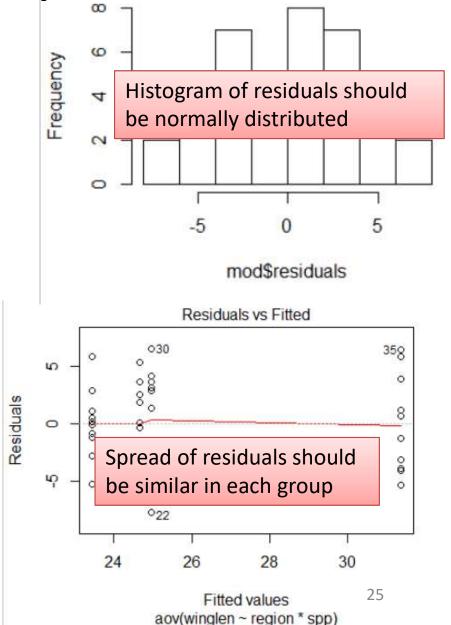
Checking Assumptions

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)



Reporting the result

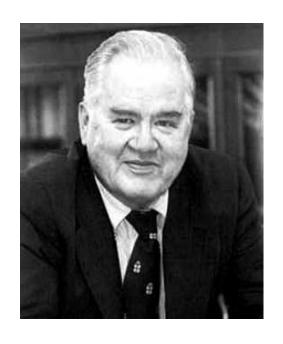
Reporting the result: "significance, direction, magnitude"

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??

Reporting the result: Post-hoc?

Post-hoc test e.g., Tukey







John Wilder Tukey

Wild Turkey

Wild Turkey

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 adi
south-north -3.81 -6.347658 -1.272342 0.004334
$spp
                   diff
                              lwr
                                       upr
                                               p adi
F.flappa-F.concocti -4.11 -6.647658 -1.572342 0.0022796
```

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

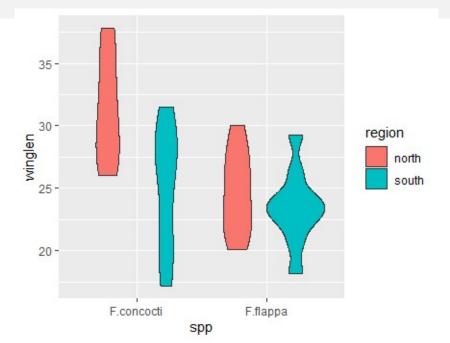
south:F.flappa-north:F.flappa -1.22 -5.985769 3.545769 0.9004525
```

Reporting the result: direction and magnitude

```
$`region:spp`
                                     diff
                                                 lwr
                                                                     p adi
                                                            upr
south: F. concocti - north: F. concocti - 6.40 - 11.165769 - 1.634231 0.0048102
                                    -6.70 -11.465769 -1.934231 0.0030099
north: F. flappa-north: F. concocti
south:F.flappa-north:F.concocti
                                   -7.92 -12.685769 -3.154231 0.0004123
                                  -0.30 -5.065769 4.465769 0.9982343
north: F. flappa-south: F. concocti
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 = bbl

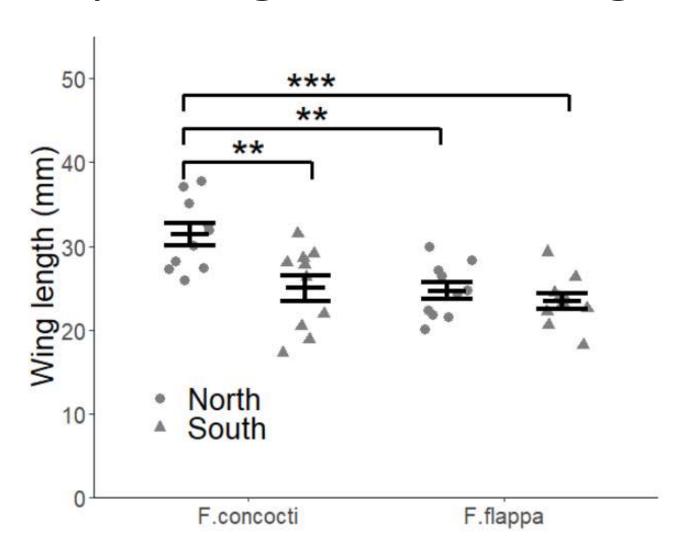
```
# A tibble: 4 \times 7
# Groups:
            region [2]
  region spp
                     mean
  <fct> <fct>
                    <fdb>>
1 north F.concocti
                     31.4
                     24.7
2 north F.flappa
3 south F.concocti
                     25.0
4 south
         F.flappa
 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



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.

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)</pre>
- assumptions: normally and homogenously distributed residuals

continued

t-tests

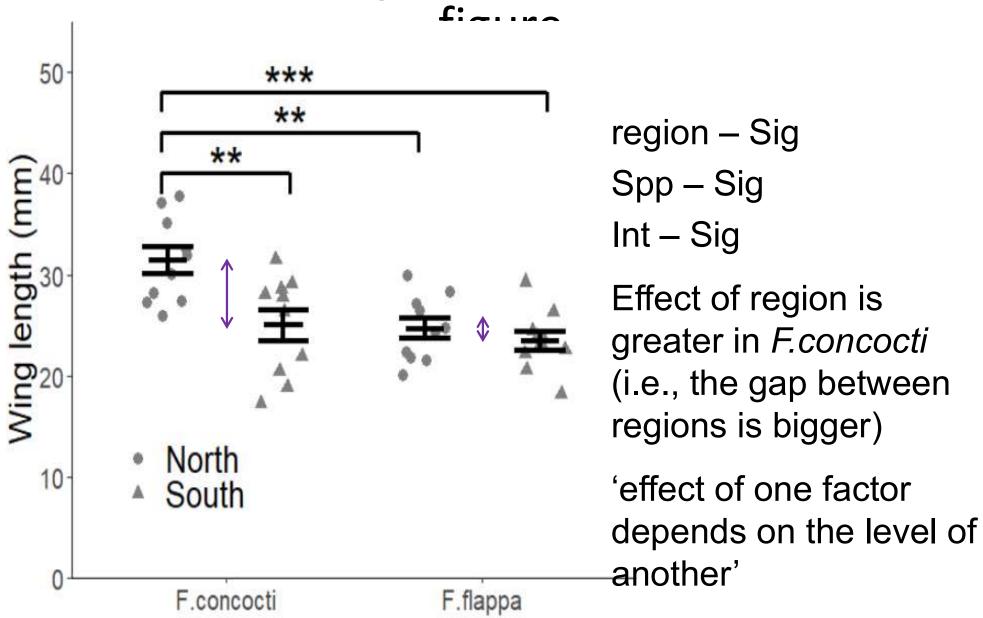
Two-way ANOVA summary

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

Understanding the interaction

in two-way ANOVA

Understanding the interaction from the

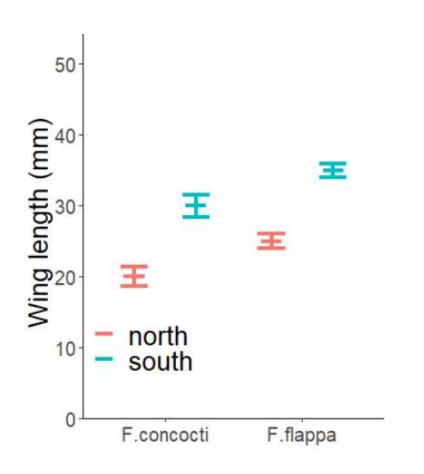


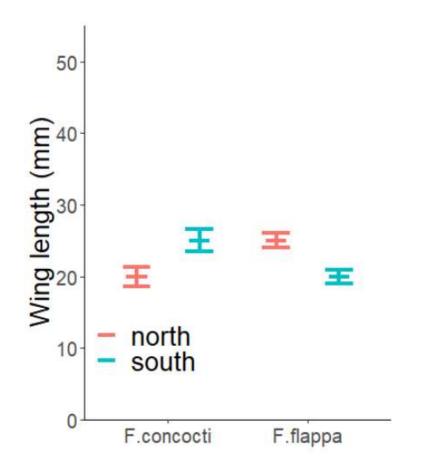
Understanding the interaction from the figure

Some other possible results

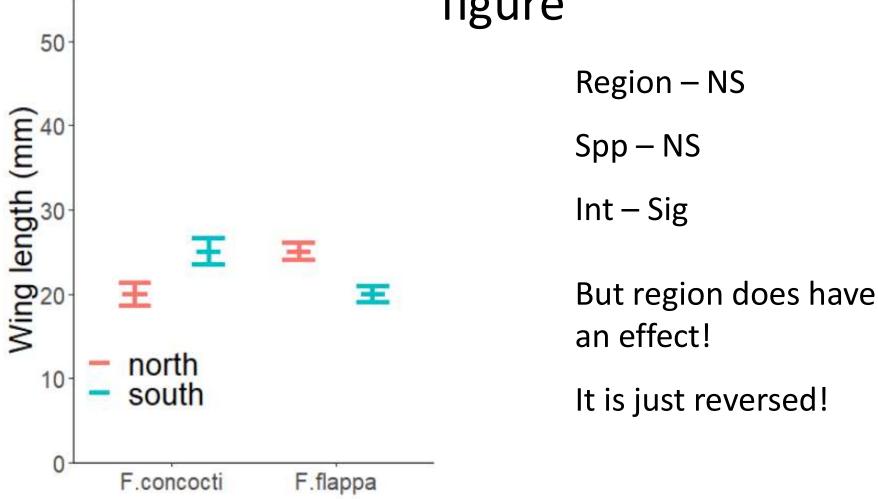
No interaction: Gap the same

Interaction: Gap the reversed





Understanding the interaction from the figure



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