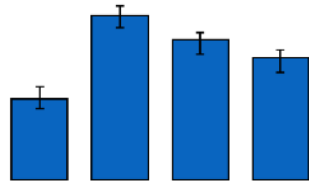


1

ANOVA: for comparing multiple means
numeric outcome, 3 or more groups

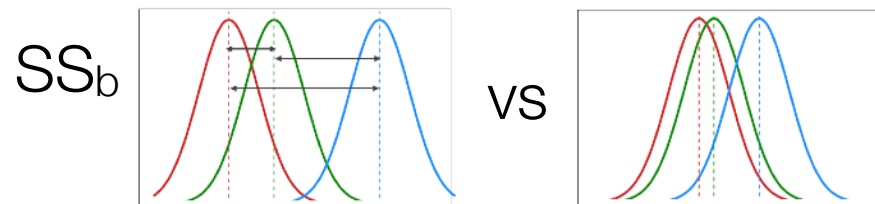


2

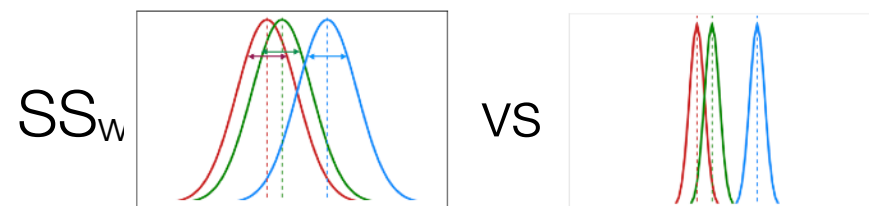
test statistic reflects the total variability SS_{tot}

$$SS_{tot} = SS_b + SS_w$$

between-
groups



within-
groups



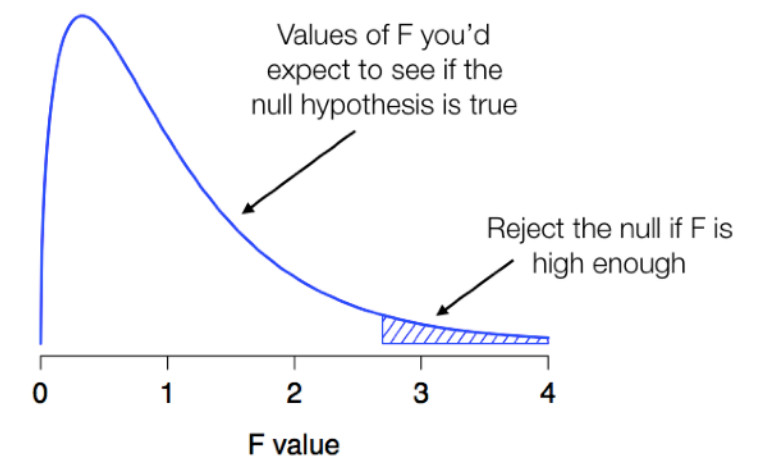
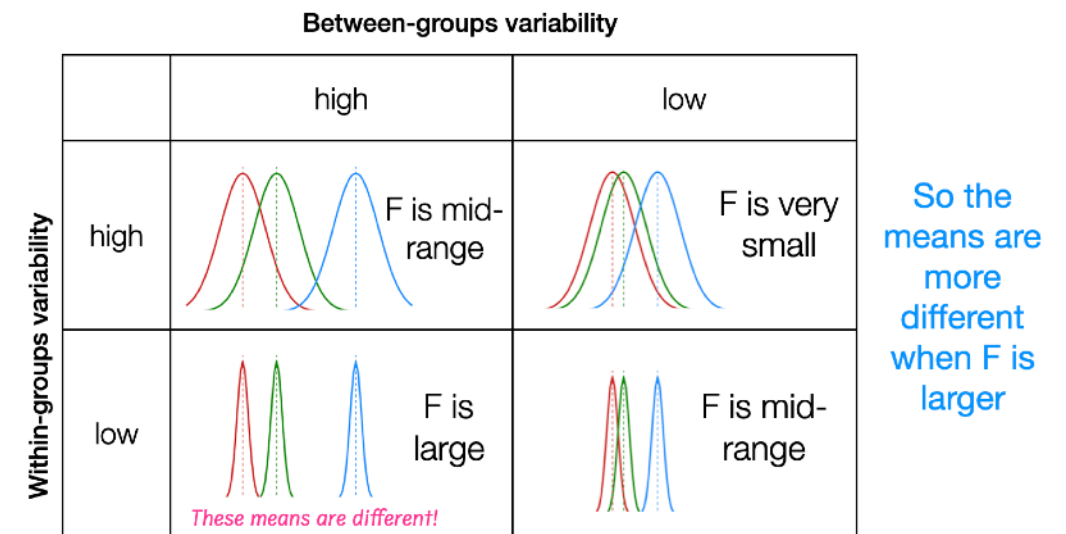
correct for **degrees of freedom**

between-groups MS_b : divide by $G-1$ where G =# of groups

within-groups MS_w : divide by $N-G$ where N =total sample size

F-statistic is ratio of these: MS_b/MS_w

3



4

ANOVA in R requires two commands

aov creates an aov object with all the info
summary runs the actual hypothesis test on that info

```
modelName <- aov( outcome ~ predictor, dataset )
summary(modelName)
```

5

ANOVA table

Each row corresponds to one source of variation: "type" = between groups (i.e., between land types); "residuals" = within groups

F-statistic is ratio of MS values

R also calculates the p-values

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
type	2	68.8	34.4	1.495	0.233
Residuals	57	1311.2	23.0		

Degrees of freedom... G=3 groups means that we have G-1 = 2 between-groups, N=60 observations means that we have N-G = 57 within groups

Sum of squares (SS_b and SS_w)

Divide SS by corresponding df to get MS

of stars gives different levels of significance

6

effect size eta-squared is proportion of the variance attributable to the grouping variable

$$\eta^2 = \frac{SS_b}{SS_{tot}}$$

```
etaSquared(modelName)
```

1

problem of multiple comparisons

ANOVA only tells you *that* there is a difference, not *which* groups are different

running many t-tests inflates Type 1 error

solve with Bonferroni or Holm corrections

Bonferroni: simple, but way conservative.

$$p' = m \times p$$

adjusted p-value number of tests you're doing original p-value

Holm: better, more complicated

```
library(lsr)
posthocPairwiseT(x=modelName)
```

default: Holm

Bonferroni: `p.adjust.method = "bonferroni"`

2

posthoc test: ran after ANOVA, don't have particular hypothesis. need a correction.

planned comparison one of only a few tests you planned in advance. no correction needed but *be honest and careful!*

3

Assumption: residuals are normal

- check with Shapiro-Wilk on the residuals
- if violated, run Kruskal-Wallis

get residuals: `model <- aov(blahblah)`
`model$residuals`

Shapiro-Wilk: `shapiro.test(model$residuals)`

Kruskal-Wallis:

```
kruskal.test(outcome ~ predictor, data=d)
```

```
library(rstatix)
```

```
kruskal_effsize(outcome ~ predictor, data=d)
```

4

Assumption: variance homogeneous

Use Levene Test to check

If violated, do Welch one-way ANOVA

Levene Test:

```
library(car)
```

```
LeveneTest(outcome ~ predictor, data=d)
```

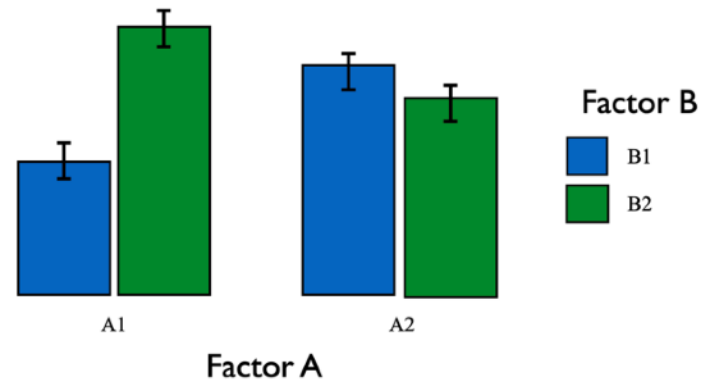
Welch one-way ANOVA

```
oneway.test(outcome ~ predictor, data=d)
```

5

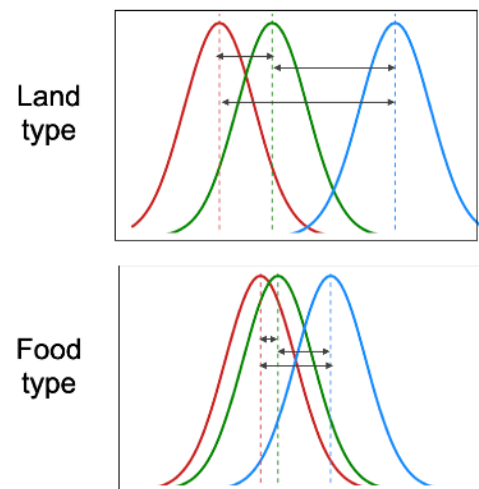
Two-way ANOVA

Has two factors instead of one, with a continuous outcome (comparing means)

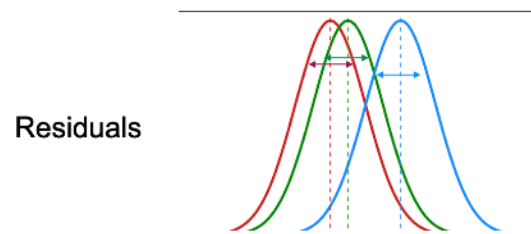


Data must be in long form!

Between groups SS (SS_A, SS_B): for each factor A and B, how different are the group means from one another?



Residual SS (SS_R): how much variation in the outcome is there after taking into account the variation associated with *both* factors?



$$MS_b = SS_b / (G - 1)$$

$$MS_R = SS_R / (N - R - C + 1)$$

$$F = MS_b / MS_R$$

6

Running in R

add + to formula to indicate multiple factors

`aov(outcome ~ pred1 + pred2, data=d)`

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
type	2	201	100	0.887	0.414
food	2	63852	31926	282.422	<2e-16 ***
Residuals	175	19783	113		

Each group has an F-statistic and can be significant or not.

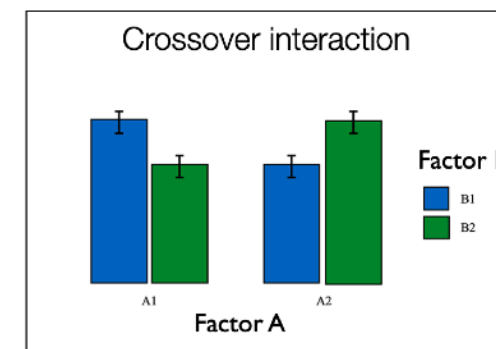
If a group is significant, that's a **main effect**

Different from testing each factor separately because the residuals are different!

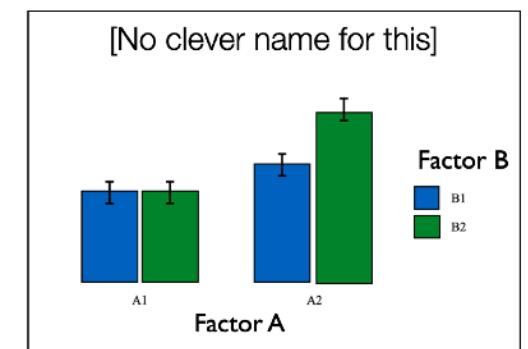
7

Interactions

Occur when the effect of one factor is different depending on the level of the other



Direction of effect of a factor depends on the level of the other factor



Magnitude of effect of a factor depends on the level of the other factor

Same idea, just get an interaction sum of squares as well as for each group

8

Running interactions in R

Indicate with a : in between the two variables

```
aov(outcome ~ pred1 + pred2 + pred1:pred2, data=d)
```

Or can use shorthand to tell R to do all three:

```
aov(outcome ~ pred1*pred2, data=d)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
type	2	201	100	1.205	0.302
food	2	63852	31926	383.612	< 2e-16 ***
type:food	4	5551	1388	16.675	1.47e-11 ***
Residuals	171	14231	83		

Each factor *and* the interaction have an F-statistic and can be significant or not

9

Effect size for ANOVA

Same as one-way: eta-squared

But partial eta squared needs to be interpreted

```
etaSquared(model)
```

η^2 : proportion of total variance due to each factor

Partial η^2 : proportion of variance due to each factor assuming you pretend the effect size of all of the others is zero