### **R Stats Bootcamp**

2.12 - ANOVA

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HARUG R Stats Bootcamp by Ed Harris

### R stats bootcamp - Module 2

#### Schedule:

- Session 7: Explore data
- Session 8: Distributions
- Session 9: Correlation
- Session 10: Regression
- Session 11: T-test
- Session 12: ANOVA



### R Stats Bootcamp

Arrange the arithmetic to compare more than two groups



### Session 12 objectives:

- The question of 1-way ANOVA
- Data and assumptions
- Graphing
- Tests and alternatives
- Practice exercises

### ANalysis Of VAriance

"The analysis of variance is not a mathematical theorem, but rather a convenient method of arranging the arithmetic." - R. A. Fisher (via Wishart 1934. Sppl. J. Roy. Soc. 1(1):26-61.)



### ANalysis Of VAriance

- Revolutionizing the idea of objectivity in using data to produce evidence
- Invented by R. A. Fisher while ar Rothamsted
- Intention that ANOVA would be useful tool for analysis of agricultural experiments
- Remains foundation of best practice of statistics



- Several reasons to use ANOVA
- Usual scenario:
  - one numeric continuous dependent variable
  - a factor with two or more levels (often with a control)
    - When only two levels, the 1-way ANOVA is conceptually equiv. to the t-test

- Example:
  - Classic field trial
    - Crop pest damage measured (numeric continuous variable)
    - $\circ\,$  Factor with three levels:
      - Control (No pesticide)
      - Organic pesticide
      - Chemical pesticide

- Basic question:
  - Is there an overall difference in numeric independent variable (pest damage) amongst the factor levels (treatment)

- Several kinds of question are also possible to answer:
  - Overall difference test of means between factor levels
  - Comparision of difference of each factor level with control or other reference factor level
  - posthoc tests of difference between specific factor levels (i.e., pairwise tests)
  - Examination of the "sources of variation" obsevred in dependent variable (i.e., what prop. of total var can be accounted for by the factor)

- The test statistic for ANOVA = F-ratio
  - Proportion of variance in the dependent variable between groups, relative to that within the categories

### **Data and Assumptions**

- R demo:
  - Explore these in R
  - Experiment in animal genetics
    - Weight of male chickens (8-week old weight in grams)
    - Factor variable = Sire identity
      - Five levels: A, B, C, D, E

### Wide Data vs. Long Data

- Data in wide or long format
  - Wide format: storing data in five vectors (one per factor level)
    - Not the usual way to store data nowadays
  - Long format: numeric data in single vector with sire vector
    - More preferred layout, conforms more to "Tidy Data" principles

## Off to R!

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### **ANOVA** assumptions

- Similar to assumptions for regression
  - Both are a specific kind of linear model
- Most important to consider are:
  - Gaussian residuals
  - Homoscedastcity
  - Equality of variance
  - Independent observations

# Off to R!

- Checking assumptions in R
  - Gaussian residuals: Test graphically and using NHST
  - Homoscedastcity: Test graphically with residuals vs fitted plot
  - Equality of variance: Test graphically with plot of residual vs factor and NHST for equal variance
  - Independent observations: Not testing formally, will assume with example data
    - Would likely know based off of your experimental design

### Graphing

- Classic graphing: Boxplot
  - Including display of central tendency of data separately for each factor level
  - For continuous variables, boxplots show this perfectly
  - With count variables, barplots are sometimes used
    - Height set to mean
    - $\circ$  Error bar included

## Off to R!

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### ANOVA : F test statistic and alternatives

- Basic application on ANOVA in R uses the aov() fucntion
  - BUT there are a lot of alternative ways to perform the EXACT same test in R
- ANOVA is essentially a subset of the Gaussian linear model
  - Which is a subset o the General Linear Model ...

### Performing the ANOVA

- Perform a one-way ANOVA
  - Look at basic output for *overall effect of sire*
  - Look at how to examine *contrasts* (i.e., diff between control or reference level)
  - Look at *post hoc* testing (i.e., pairwise comparisons)
  - Examine what happens in ANOVA in a little more detail...

## Off to R!

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aov(formula = Weight ~ factor(Sire), data = new.long)



Contrasts ... aov() versus lm()

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##

aov(formula = Weight ~ factor(Sire), data = new.long)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
factor(Sire)	4	17426	4356	1.872	0.137
Residuals	35	81442	2327		



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aov(formula = Weight ~ factor(Sire), data = new.long)

#### factor(Sire) Residuals

Df 4 = number of factor levels (5) minus 1 35 = total number of observations (40)

minus number of factor levels (5)

Call: lm(formula = Weight ~ Sire, data = new.long) Residuals: Median Min 1Q 30 Мах -93.625 -29.312 -2.875 33.906 104.750 Coefficients: Estimate Std. Error t value Pr(>|t|) 40.846 <2e-16 \*\*\* (Intercept) 696.63 17.05 SireA 18.38 24.12 0.762 0.451 SireB -31.50 24.12 -1.3060.200 -39.13 SireD 24.12 -1.622 0.114SireE -13.38 24.12 -0.555 0.583 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 Residual standard error: 48.24 on 35 degrees of freedom Multiple R-squared: 0.1763, Adjusted R-squared: 0.08211 F-statistic: 1.872 on 4 and 35 DF, p-value: 0.1373

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		Estimate	Std. Error	t value	Pr(> t )
_	(Intercept)	696.63	17.05	40.846	<2e-16 ***
5	SireA	18.38	24.12	0.762	0.451
rows	SireB	-31.50	24.12	-1.306	0.200
10003	SireD	-39.13	24.12	-1.622	0.114
	SireE	-13.38	24.12	-0.555	0.583

#### Reference

factor level:

SireC

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	696.63	17.05	40.846	<2e-16 ***
SireA	18.38	24.12	0.762	0.451
SireB	-31.50	24.12	-1.306	0.200
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SireE	-13.38	24.12	-0.555	0.583









One row for each other factor level

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#### **Post Hocs**

- Overall question of "is there a difference?" can be enhanced by asking whether there are specific differences
- The phrase **post hoc** implies these questions are an 'afterthought'
  - Thus, consideration should be given to whether these specific questions NEED to be asked

## Type I errors

- The alpha (α) value which we compare our P-value can be interpreted as the (maximum) probability we are willing to accept of being wrong if we conclude there is significance in our data
  - i.e., We are are happy to accept the *chance* of our significant finding being wrong 5% of the time when alpha = 0.05.

## Type I errors

- When multiple tests are made on the same data, it increases the chance of discovering a false positive, purely by chance alone, to above 5%
- As such there are methods used to avoid this by adjusting the p-value o keep the overall likelihood of a false positive error at 5%
- Examples:
  - The Bonferroni adjustment
  - Tukey HSD test

## **Bonferroni Adjustment**

- Baseline, conservative adjustment to the alpha value to avoid false positive errors
- Typically applied in one-way ANOVA situation where specific, pairwise comparisons between means are required and aren't covered by the overall tests or contrasts
- E.g., In our chicken data, we know there is no difference between offspring weights between Sire C and all other Sires
   - C:A, C:B, C:D, C:E
  - But don't know about other comparisons i.e. A:B, A:D, A:E etc...

## Tukey HSD

- Ideal for one-way ANOVA
- Less conservative than Bonferroni

#### Off to R!

#### Alternatives to one-way ANOVA

- When assumptions can not be met, some options:
  - Attempt to transform data (e.g., sqrt(), log()) to 'coerce' data to conform to assumptions
  - Use an alternative test for which assumptions are not violated
    - i.e., a non-parametric test like Kruskall Wallis

# Off to R!

#### Non-parametric tests

- Advantages:
  - Very easy to use
  - Very easy to interpret
- Disadvantages
  - Less statistical power
  - i.e., less likely than parametric cousins to detect a significant effect even when one exists

# ANOVA calculation details

#### **ANOVA** equations

$$(1) \ Grand \ Mean = GM = \sum_{i=1}^k \sum_{j=1}^n Y_{ij} imes rac{1}{n_{total}}$$

$$(2) \ Sum \ of \ Squares \ Between = SS_{between} = \sum_{i=1}^\kappa n_i (ar{Y_i} - GM)^2$$

$$(3) \ Sum \ of \ Squares \ Within = SS_{within} = \sum_{i=1}^k \sum_{j=1}^n (Y_{ij} - ar{Y}_i)^2$$

(4) Sum of Squares Total =  $SS_{between} + S\overline{S_{within}}$ 

#### **ANOVA** variables

- k = Number of factor levels
- $n_i$  = number of samples for group i
- $n_{total}$  = total number of samples for all groups
- Yij = observation j in group i
- $\bar{Y}_i$  = mean of group i

#### **ANOVA sources of variation**

Source of Variation	df	Sum Sq	Mean Sq	F
Between groups	k-1	Eq~(2)	$\frac{Eq\left(2\right)}{k{-}1}$	$rac{MeanSq_{between}}{MeanSq_{within}}$
Within groups	$n_{total}-k$	Eq~(3)	$rac{Eq\left(3 ight)}{n_{total}\!-\!k}$	
Total	$n_{total}-1$	EQ(4)		

# ANOVA 'by hand' in R

#### Practice excercise data

For these exercises, run the code below to recreate the data object pest. There are 40 rows and 2 variables with 2 variables: damage and treatment.

See bootcamp page

Think of this data as the result of an experiment looking at the effectiveness of pesticide treatment on leaf damage. Let us imagine that this experiment measured leaf damage (variable "damage" measured in mm squared) and that the plants were treated with one of 4 treatment levels: - Control - x.half - x.full - organic

#### Practice excercise data

The experiment is of course designed to look at an overall effect the various treatments may have to reduce leaf damage relative to the control. In addition, it is of interest to examine the effect of the organic treatment compared to that of the x.half to the x.full.

The experiment ran using 40 potted plants spaced 1m from each other in a greenhouse setting. Each treatment was randomly assigned to 10 plants. Onto each plant was placed 5 red lily beetle (Lilioceris lilii) pairs.

- Make a good, appropriate graph representing the overall experiment.
- Show your code.
- Describe any trends in the data that are apparent from the graph, as well as an initial assessment of principle assumptions of 1-way ANOVA based only on your single graph.

- Test the assumption of Gaussian residuals for 1-way ANOVA using any graphs or NHST approach that you deem appropriate.
- Show your code and briefly describe your EDA findings and conclusion as to whether these data adhere to the Gaussian assumption.

- Test the assumption of homoscedasticity of residuals for 1way ANOVA using any graphs or NHST approach that you deem appropriate.
- Show your code and briefly describe your EDA findings and conclusion as to whether these data adhere to the homoscedasticity assumption.

- Perform either a 1-way ANOVA or an appropriate alternative based on your findings in the previous answers.
- Show your code, state your results in the technical style and briefly interpret your findings.

- Perform an appropriate set of post hoc tests to compare pairwise mean differences in these data.
- Focus on the post hoc questions of interest:
  - Is the organic pesticide effective?
  - Does dose matter in the non-organic treatments?

 Write a plausible practice question involving any aspect of data handling, graphing or analysis for the 1-way ANOVA framework for the iris data (data(iris); help(iris)).