Lecture 15: ANOVA

Criminology 1200

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The basic ANOVA question

- Two variables: One quantitative (y) and one categorical (x).
- For example, y: birth weight, and x: race (white, Black, other).
- Main question: Are the values of y different for the groups? e.g., do people of different races have different birth weights?
- Note this is not a causal question necessarily.
- If categorical variable only has 2 values: use a 2-sample t-test.
- ANOVA allows for 3 or more groups.

Analysis of variance

- We saw how to use a t-test to see whether two groups have equal means.
- If you have more groups, you can't just look at differences in the means.
- We can build a hypothesis test to check whether the variation in the means is bigger than we'd expect it to be just from random fluctuations.
- We'll need a new sampling model, called the F-model.

Note: Regression vs. table

- You can think of ANOVA (analysis of variance) as a more general version of the t-test, or a special case of linear regression in which all covariates are factors (i.e. categorical variables).

We will see that you can write the results from an ANOVA test in a table. But they are no different than what we have already seen in linear regression.

History

- The ANOVA test was designed by R.A. Fisher.
- But it had been used since the 1800s by Laplace, with some foundations from Gauss.
- RA Fisher was a mathematician and a eugenist, which was common at the time. Eugenics were later used by Nazis, but at the time this was not clearly a racist endeavor.
- RA Fisher did not think race determined psychological attributes. He thought it was "common historical and social background".
- From "The Race Concept: Results of an Inquiry" (PDF). UNESCO. 1952.
- Famous for many things, but DVB says Fisher's F-distribution estimation was the development of the century.

Are the means of these four groups equal?

First, an informal graphical investigation (EDA): side-by-side boxplots, or multiple histograms.

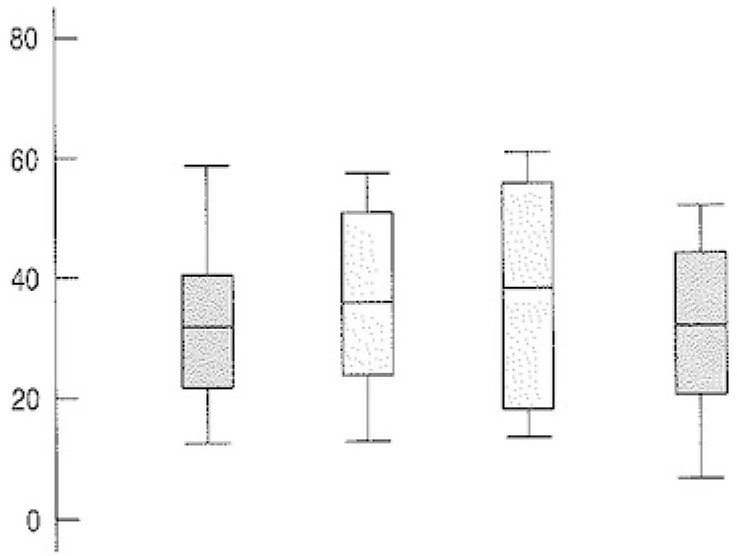


Figure 26.2

It's hard to see the difference in the means in these boxplots because the spreads are large relative to the differences in the means.

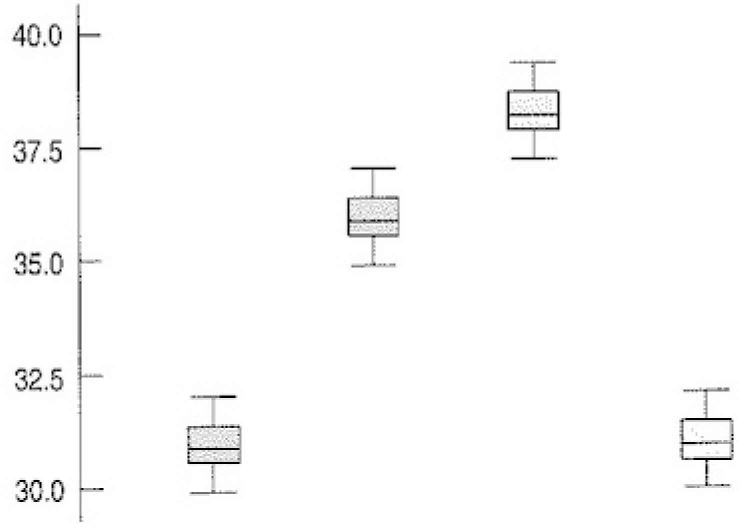


Figure 26.3

In contrast with Figure 26.2, the smaller variation makes it much easier to see the differences among the group means. (Notice also that the scale of the *y*-axis is considerably different from the plot on the left.)

Whether the differences between groups are signficant depends on: 1) the differences in the means, 2) the

Four groups

- Actually, the sets of means in both figures (left and right) are the same! (they're: 31, 36, 38, 31).
- Right: The variation *within* each group is so small that the differences *between* the means stand out.
- Left: The variation *within* each group is large, so that the differences *between* the means seems small.
- This is the central idea of the F-test: We compare the differences *between* the means of the groups with the variation *within* the groups.
- When the differences between means are large compared with the variation within the groups, we reject the null hypothesis and conclude that the means are not equal.

F-test

Let the null hypothesis be:

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu.$$

And let the alternative hypothesis be:

$$H_A : \text{Not all the means are equal.}$$

The alternative hypothesis does not say how or which ones differ. To answer more specific questions, we can follow up with multiple comparisons.

The F-statistic

The F-statistic is a ratio of the between-group variation and the within-group variation:

$$F = \frac{\text{Between}}{\text{Within}} = \frac{MSG}{MSE}.$$

A large value of F indicates relatively more difference between groups than within groups (evidence against the null hypothesis).

To get the p-value, we compute the F distribution based on certain numbers of degrees of freedom:

- I-1 df in numerator (# groups - 1)
- n-I df in denominator (rest of df)

Multiple comparisons

- Once ANOVA indicates that the groups do not all have the same means, we can compare them two by two by using 2-sample t-test.
- But we need to adjust our p-value threshold because we are doing multiple tests with the same data: the Bonferroni correction (can do this in R with p.adjust from the stats package).
- If we really just want to test the difference between one pair of treatments, then *just use the t-test*.
- We can use the Tukey HSD test.

Assumptions of ANOVA

- Each group is approximately normal.
    - Check this by looking at histograms and normal quantile plots.
    - Can handle some non-normality, but no severe outliers.
- The standard deviations of each group are approximately equal.
    - Rule of thumb: ratio of the largest to smallest sample standard deviation must be less than 2:1.

Example: Birth weight vs. race

- Question: Is there a significant association between race and birth weight?

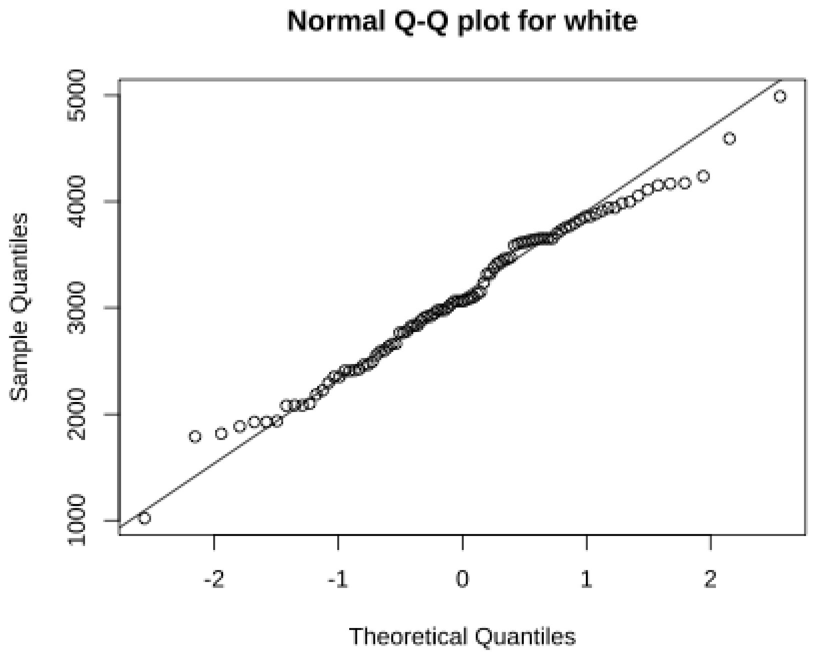
```
## # A tibble: 3 × 3
##   race  mean.bwt se.bwt
##   <fct>    <dbl>  <dbl>
## 1 white     3103     74
## 2 Black     2720    125
## 3 other     2805     88
```

- It looks like there's some association, but we don't yet know if it's statistically significant.

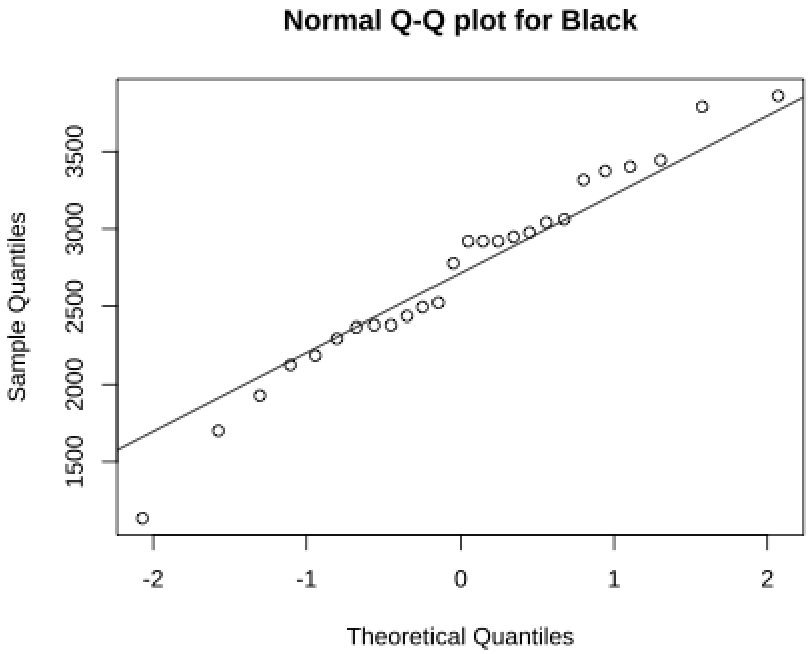
- Note that if we had just two racial categories in our data, we could run a t-test. Since we have more than 2, we need to run a 1-way analysis of variance (ANOVA).

Test assumptions in birthwt example: Normality

QQ plot for the individuals who are white

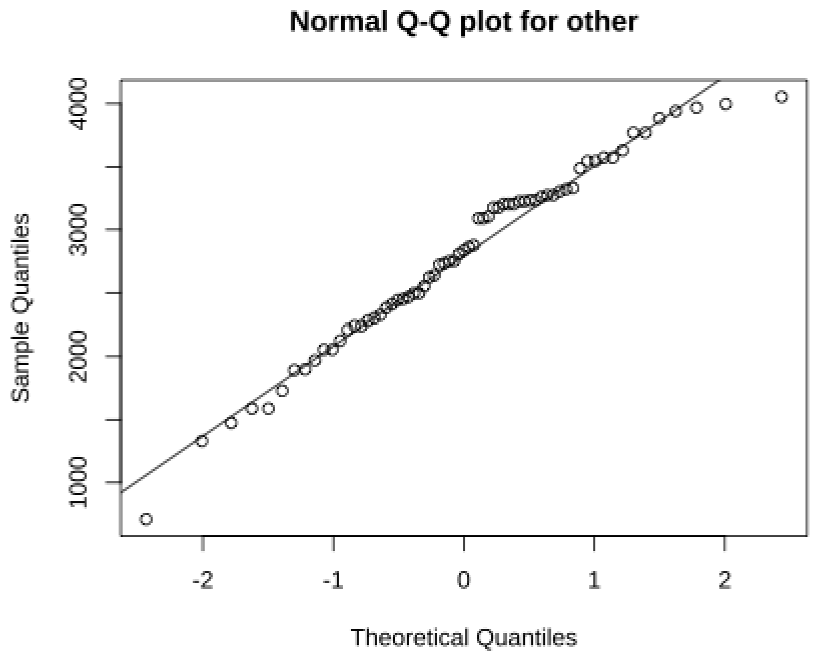


QQ plot for the individuals who are Black



Test assumptions in birthwt example: Normality

QQ plot for the individuals who are of another race



Testing assumptions in birthwt example: Standard deviations are approx equal

Compare the largest and smallest standard deviations:

- Largest: 125
- Smallest: 74
- Ratio: 125/74: 1.69. (Check, it's less than 2).

Brief interlude to discuss how to use factors in R

It is worth noting that your categorical variable in the ANOVA analysis in R, aov(), needs to be a factor.

This website gives a nice overview of how to use factors in R:

https://www.gormanalysis.com/blog/r-introduction-to-factors-tutorial/

ANOVA: Running this test in R

Actually, you can do this by using the same lm command we've been using!

```
##
## Call:
## lm(formula = birthwt.grams ~ race, data = birthwt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2096.28  -502.72   -12.72   526.28  1887.28
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3102.72      72.92  42.548  < 2e-16 ***
## raceBlack    -383.03     157.96  -2.425  0.01627 *
## raceother    -297.44     113.74  -2.615  0.00965 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 714.5 on 186 degrees of freedom
## Multiple R-squared:  0.05017,    Adjusted R-squared:  0.03996
## F-statistic: 4.913 on 2 and 186 DF,  p-value: 0.008336
```

ANOVA: Running this test in R

Can do this two ways: Using an lm model:

```
reg.output <- lm(birthwt.grams ~ race, data = birthwt)
anova.output <- aov(reg.output)
summary(anova.output)
```

```
##              Df   Sum Sq Mean Sq F value  Pr(>F)   
## race          2  5015725 2507863   4.913 0.00834 **
## Residuals   186 94953931  510505                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

or just doing aov directly:

```
anova.output1 <- aov(birthwt.grams ~ race, data = birthwt)
summary(anova.output1)
```

```
##              Df   Sum Sq Mean Sq F value  Pr(>F)   
## race          2  5015725 2507863   4.913 0.00834 **
## Residuals   186 94953931  510505                   
```

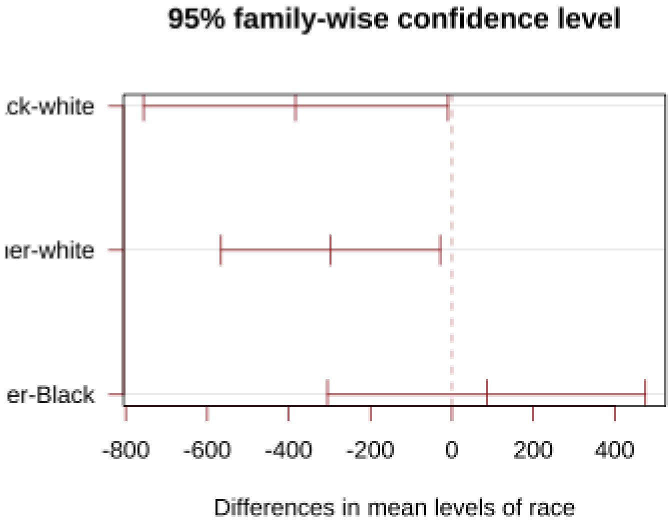
How to read ANOVA table in R

Coefficients are the same as in lm: anova.output$coefficients.

- Df (race): The degrees of freedom for the variable race. This is calculated as # groups - 1. In this case, there were 3 groups, so this value is 3-1=2.
- Df (Residuals): The degrees of freedom for the residuals. This is calculated as # total observations - # groups. In this case there were 189 observations and 3 groups: 189-3=186.
- Sum Sq.: The sum of squares associated with the variables race and the residuals.
- Mean Sq.: This is calculated as Sum Sq. / Df, for each of the two variables, race and residuals. For race, this is calculated as: 5015725 / 2 = 2507863.
- F value: The overall F-statistic of the ANOVA model. This is calculated as Mean Sq. race / Mean sq. Residuals. In this case it's 2507863/510505 = 4.913.
- Pr(>F): The p-value associated with the F-statistic with numerator df = 2 and denominator df = 186. In this case, the p-value is 0.00834, which is statistically significant at the 0.05 level.
- Signif. codes: The same as in the lm model.

Tukey Honest Significant Differences (HSD) test

The Tukey HSD procedure will run a pairwise comparison of all possible combinations of groups and test these pairs for significant differences between their means, all while adjusting the p-value to a higher threshold for significance in order to compensate for the fact that many statistical tests are being performed and the chance for a false positive increases with increasing numbers of tests.


95% family-wise confidence level
ck-white
ıer-white
er-Black
Differences in mean levels of race