Analysis of variance

Packages

```
library(tidyverse)
library(smmr)
library(PMCMRplus)
```

Jumping rats

- Link between exercise and healthy bones (many studies).
- Exercise stresses bones and causes them to get stronger.
- Study (Purdue): effect of jumping on bone density of growing rats.
- 30 rats, randomly assigned to 1 of 3 treatments:
  - No jumping (control)
  - Low-jump treatment (30 cm)
  - High-jump treatment (60 cm)
- 8 weeks, 10 jumps/day, 5 days/week.
- Bone density of rats (mg/cm^3) measured at end.

Jumping rats 2/2

- See whether larger amount of exercise (jumping) went with higher bone density.
- Random assignment: rats in each group similar in all important ways.
- So entitled to draw conclusions about cause and effect.

Reading the data

Values separated by spaces:

```r
my_url <- "http://ritsokiguess.site/datafiles/jumping.txt"
rats <- read_delim(my_url," ")
```

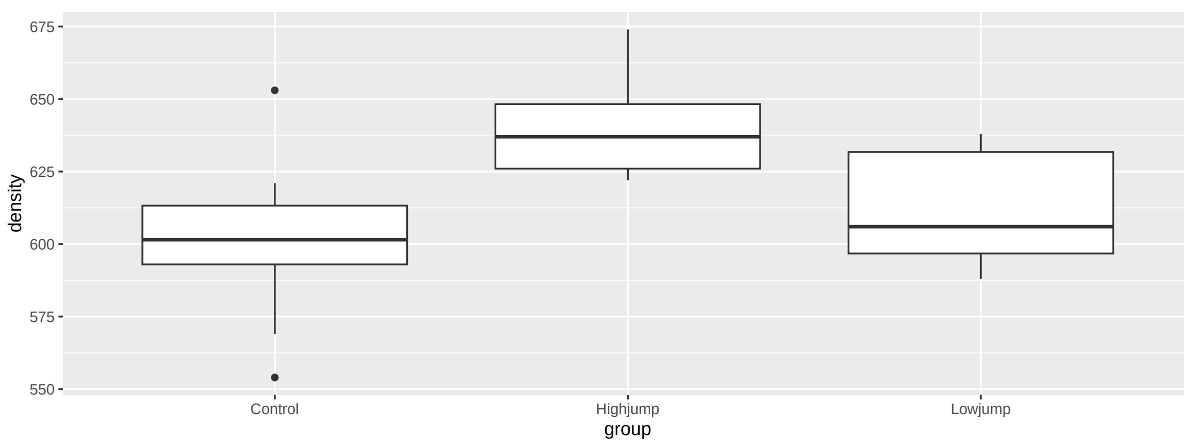
The data (some random rows)

```r
rats %>% slice_sample(n=12)
```

```
# A tibble: 12 x 2
   group    density
   <chr>      <dbl>
 1 Highjump     674
 2 Control      593
 3 Highjump     631
 4 Control      653
 5 Lowjump      635
 6 Lowjump      607
 7 Control      600
 8 Lowjump      588
 9 Control      593
10 Control      569
11 Highjump     643
12 Lowjump      594
```

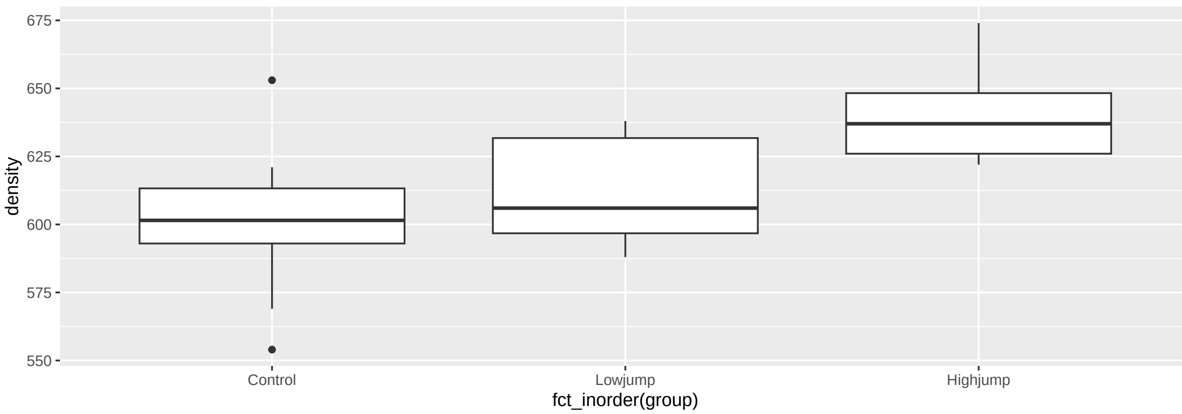
Boxplots

```r
ggplot(rats, aes(y=density, x=group)) + geom_boxplot()
```



Or, arranging groups in data (logical) order

```
ggplot(rats, aes(y=density, x=fct_inorder(group))) +
  geom_boxplot()
```



Analysis of Variance

- Comparing > 2 groups of independent observations (each rat only does one amount of jumping).
- Standard procedure: analysis of variance (ANOVA).
- Null hypothesis: all groups have same mean.
- Alternative: "not all means the same", at least one is different from others.

Testing: ANOVA in R

```
rats.aov <- aov(density~group,data=rats)
summary(rats.aov)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
group        2   7434    3717   7.978 0.0019 **
Residuals   27  12579     466
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Usual ANOVA table, small P-value: significant result.
- Conclude that the mean bone densities are not all equal.
- Reject null, but not very useful finding.

Which groups are different from which?

- ANOVA really only answers half our questions: it says "there are differences", but doesn't tell us which groups different.
- One possibility (not the best): compare all possible pairs of groups, via two-sample t.
- First pick out each group:

```
rats %>% filter(group=="Control") -> controls
rats %>% filter(group=="Lowjump") -> lows
rats %>% filter(group=="Highjump") -> highs
```

Control vs. low

```
t.test(controls$density, lows$density)
```

```

    Welch Two Sample t-test

data:  controls$density and lows$density
t = -1.0761, df = 16.191, p-value = 0.2977
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -33.83725  11.03725
sample estimates:
mean of x mean of y
    601.1     612.5
```

No sig. difference here.

Control vs. high

```
t.test(controls$density, highs$density)
```

```

    Welch Two Sample t-test

data:  controls$density and highs$density
t = -3.7155, df = 14.831, p-value = 0.002109
```

```
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -59.19139 -16.00861
sample estimates:
mean of x mean of y 
    601.1     638.7 
```

These are different.

Low vs. high

```
t.test(lows$density, highs$density)
```

```

	Welch Two Sample t-test

data:  lows$density and highs$density
t = -3.2523, df = 17.597, p-value = 0.004525
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -43.15242  -9.24758
sample estimates:
mean of x mean of y 
    612.5     638.7 
```

These are different too.

But…

- We just did 3 tests instead of 1.
- So we have given ourselves 3 chances to reject H_0 : all means equal, instead of 1.
- Thus α for this combined test is not 0.05.

John W. Tukey

- American statistician, 1915–2000
- Big fan of exploratory data analysis
- Popularized boxplot
- Invented "honestly significant differences"
- Invented jackknife estimation
- Coined computing term "bit"
- Co-inventor of Fast Fourier Transform

Honestly Significant Differences

- Compare several groups with one test, telling you which groups differ from which.

- Idea: if all population means equal, find distribution of highest sample mean minus lowest sample mean.
- Any means unusually different compared to that declared significantly different.

Tukey on rat data

```
rats.aov <- aov(density~group, data = rats)
TukeyHSD(rats.aov)
```

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

Fit: aov(formula = density ~ group, data = rats)

$group
                  diff       lwr       upr     p adj
Highjump-Control  37.6  13.66604 61.533957 0.0016388
Lowjump-Control   11.4 -12.53396 35.333957 0.4744032
Lowjump-Highjump -26.2 -50.13396 -2.266043 0.0297843
```

- Again conclude that bone density for highjump group significantly higher than for other two groups.

Why Tukey's procedure better than all t-tests

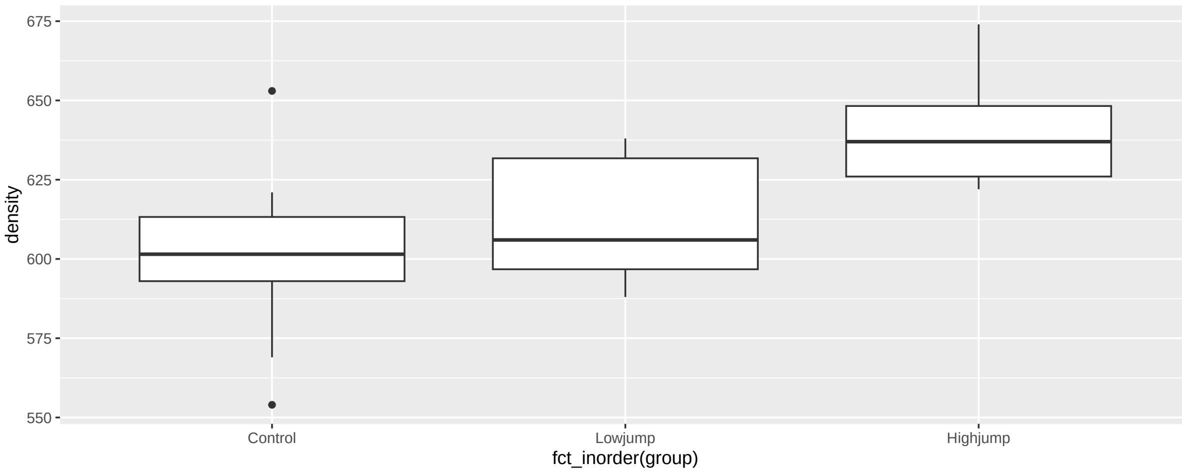
Look at P-values for the two tests:

```
Comparison        Tukey    t-tests
----------------------------------
Highjump-Control 0.0016     0.0021
Lowjump-Control  0.4744     0.2977
Lowjump-Highjump 0.0298     0.0045
```

- Tukey P-values (mostly) higher.
- Proper adjustment for doing three t-tests at once, not just one in isolation.

Checking assumptions

```
ggplot(rats,aes(y = density, x = fct_inorder(group)))+
  geom_boxplot()
```

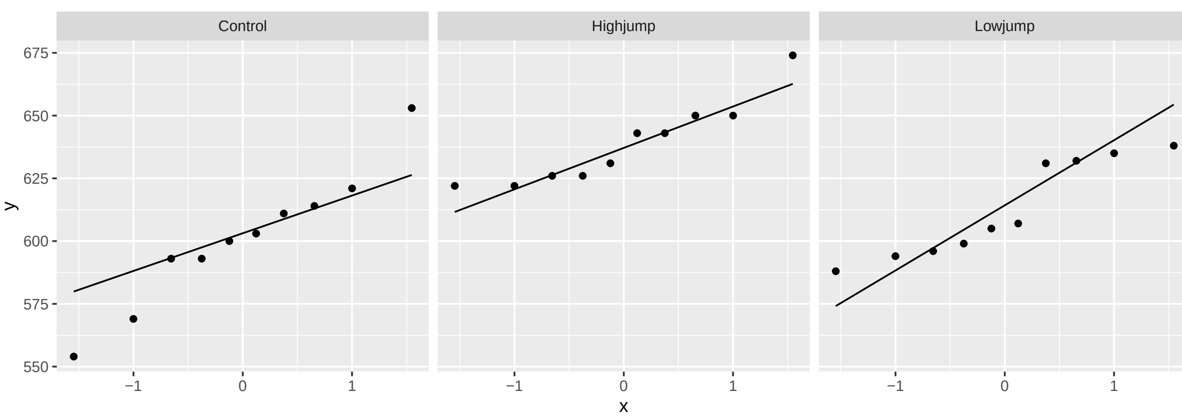


Assumptions:

- Normally distributed data within each group
- with equal group SDs.

Normal quantile plots by group

```
ggplot(rats, aes(sample = density)) + stat_qq() +
  stat_qq_line() + facet_wrap( ~ group)
```



The assumptions

- Normally-distributed data within each group
- Equal group SDs.
- These are shaky here because:
  - control group has outliers
  - highjump group appears to have less spread than others.
- Possible remedies (in general):
  - Transformation of response (usually works best when SD increases with mean)
  - If normality OK but equal spreads not, can use Welch ANOVA. (Regular ANOVA like pooled t-test; Welch ANOVA like Welch-Satterthwaite t-test.)
  - Can also use Mood's Median Test (see over). This works for any number of groups.

Mood's median test here

- Find median of all bone densities, regardless of group
- Count up how many observations in each group above or below overall median
- Test association between group and being above/below overall median, using chi-squared test.
- Actually do this using `median_test`:

```
median_test(rats, density, group)
```

```
$table
          above
group      above below
  Control      1     9
  Highjump    10     0
  Lowjump      4     6

$test
       what        value
1 statistic 1.680000e+01
2        df 2.000000e+00
3   P-value 2.248673e-04
```

Comments

- No doubt that medians differ between groups (not all same).
- This test is equivalent of F-test, not of Tukey.
- To determine which groups differ from which, can compare all possible pairs of groups via (2-sample) Mood's median tests, then adjust P-values by multiplying by number of 2-sample Mood tests done (Bonferroni):

```
pairwise_median_test(rats, density, group)
```

```
# A tibble: 3 x 4
  g1      g2        p_value adj_p_value
  <chr>   <chr>       <dbl>       <dbl>
1 Control Highjump 0.000148    0.000443
2 Control Lowjump  0.371       1
3 Highjump Lowjump 0.371       1
```

- Now, lowjump-highjump difference no longer significant.

Welch ANOVA

- For these data, Mood's median test probably best because we doubt both normality and equal spreads.
- When normality OK but spreads differ, Welch ANOVA way to go.
- Welch ANOVA done by `oneway.test` as shown (for illustration):

```
oneway.test(density~group, data=rats)
```

```

	One-way analysis of means (not assuming equal variances)

data:  density and group
F = 8.8164, num df = 2.000, denom df = 17.405, p-value = 0.002268
```

- P-value very similar, as expected.
- Appropriate Tukey-equivalent here called Games-Howell.

Games-Howell

- Lives in package `PMCMRplus`. Install first.

```
gamesHowellTest(density~factor(group),data=rats)
```

```
         Control Highjump
Highjump 0.0056  -
Lowjump  0.5417  0.0120
```

Deciding which test to do

For two or more samples: