Factorial ANOVA in R

Notation:

`DV ~ IV`$_1$` * IV2` is the same as **`DV ~ IV`$_1$` + IV`$_2$` + IV`$_1$` : IV`$_2$

"`:`" means 'interaction between'

1. **Examine IVs and DV.**

```
> attach(ToothGrowth)
```

   a. **Scale? Number of levels?**
   b. **Are IVs in the right format for R?**
      b.i. **E.g. IV – dose, 3-levels, 0.5, 1, 2 – make sure it's not treating the factor as numerical data:**

```
> str(ToothGrowth)
'data.frame':   60 obs. of  3 variables:
 $ len : num  4.2 11.5 7.3 5.8 6.4 10 11.2 11.2 5.2 7 ...
 $ supp: Factor w/ 2 levels "OJ","VC": 2 2 2 2 2 2 2 2 2 2 ...
 $ dose: num  0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
```

      b.ii. **Change it: (following long command should be entered in two parts)**

```
> ToothGrowth$dose = factor(ToothGrowth$dose, levels=c(0.5,1.0,2.0),
+
labels=c("low","med","high"))
> str(ToothGrowth)
'data.frame':   60 obs. of  3 variables:
 $ len : num  4.2 11.5 7.3 5.8 6.4 10 11.2 11.2 5.2 7 ...
 $ supp: Factor w/ 2 levels "OJ","VC": 2 2 2 2 2 2 2 2 2 2 ...
 $ dose: Factor w/ 3 levels "low","med","high": 1 1 1 1 1 1 1 1 1 1 ...
```

      b.iii. **Examine some of the data frame to make sure**

Look at every 5th observation between 1 and 60

```
> ToothGrowth[seq(1,60,5),]
    len supp dose
1   4.2   VC  low
6  10.0   VC  low
11 16.5   VC  med
16 17.3   VC  med
21 23.6   VC high
26 32.5   VC high
31 15.2   OJ  low
36 10.0   OJ  low
41 19.7   OJ  med
46 25.2   OJ  med
51 25.5   OJ high
56 30.9   OJ high
```

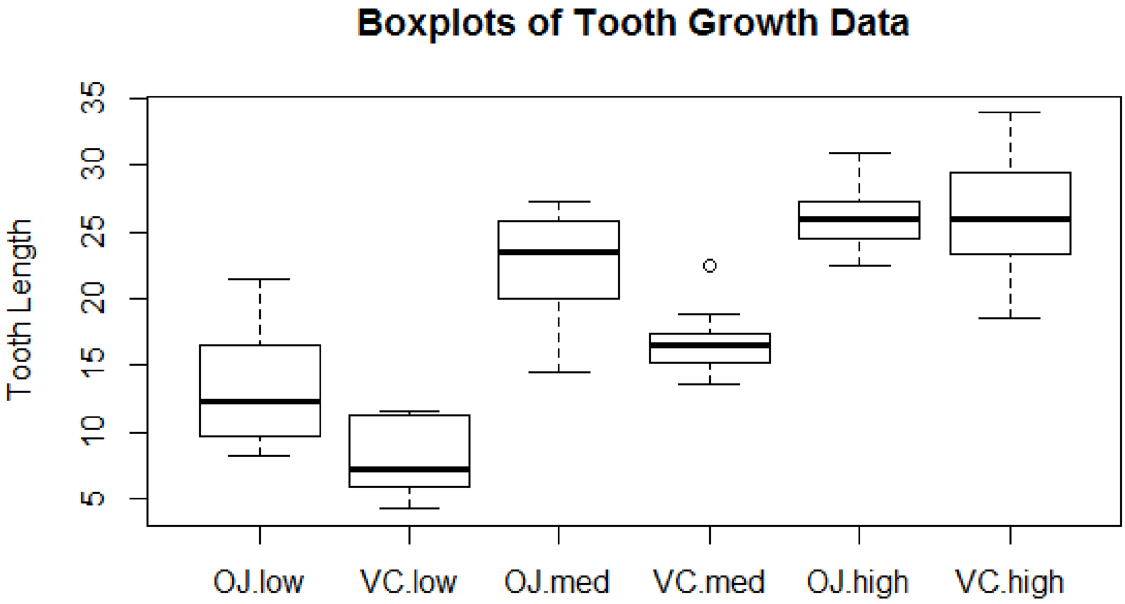
   c. **Check cell sizes are equal (ish) using** `replications()`

```
> replications(len ~ supp * dose, data=ToothGrowth)
     supp      dose supp:dose
       30        20        10
> replications(len ~ supp * dose, data=ToothGrowth[1:58,])
$supp
supp
OJ VC
28 30

$dose
dose
 low  med high
  20   20   18

$supp:dose
```

```
      dose
supp  low  med  high
  OJ   10   10     8
  VC   10   10    10
```

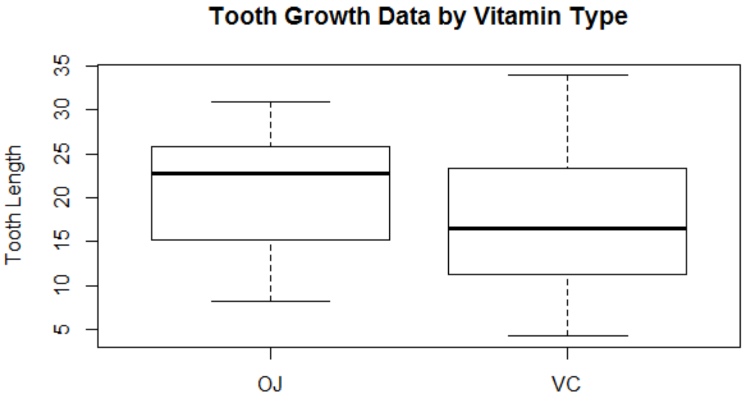
d. Graphical representation – visualise the data

```
> boxplot(len ~ supp * dose, data=ToothGrowth,
+ ylab="Tooth Length", main="Boxplots of Tooth Growth Data")
>
```

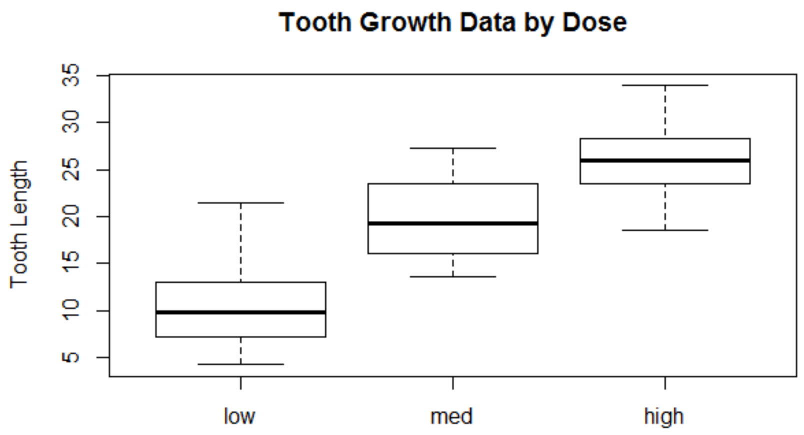


- There appear to be differences between the means.
- Variances don't seem to be very similar, which could be an issue.
    - See Bartlett's test for Homogeneity of Variance below.

Main effect of Vitamin Type



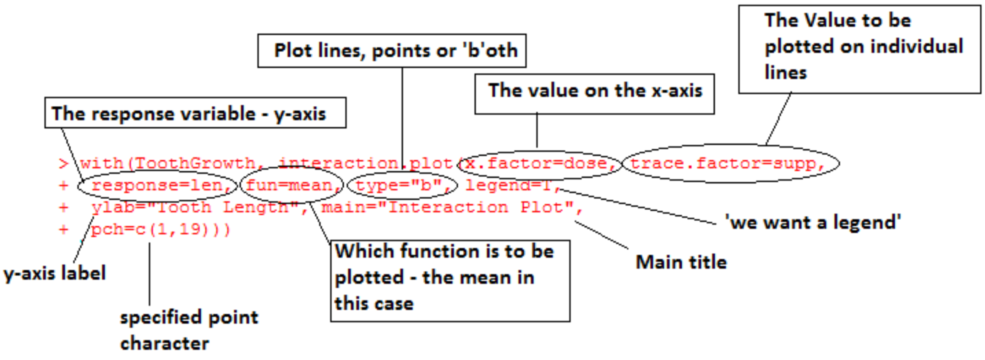
- Means don't look significantly different, but similar spread in each group



- Similar spread within each group; means of low/ medium and low/high seem to be different. But there is overlap between med and high.

Look at the interaction.

How to make an interaction plot in R



```
> with(ToothGrowth, interaction.plot(x.factor=dose, trace.factor=supp,
+   response=len, fun=mean, type="b", legend=T,
+   ylab="Tooth Length", main="Interaction Plot",
+   pch=c(1,19)))
```

Plot lines, points or 'b'oth

The Value to be plotted on individual lines

The value on the x-axis

The response variable - y-axis

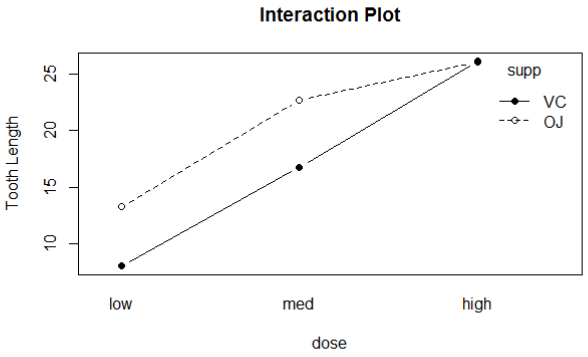
'we want a legend'

Main title

Which function is to be plotted - the mean in this case

y-axis label

specified point character



- There seems to be no difference between supp at high dose
- There seems to be a main effect of dose – higher dose results in higher tooth length
- There doesn’t seem to be much of a main effect of supp – there is little difference between the 2 groups overall.

e. Numerical summary of the data?

Means of simple main effects – i.e. each level of dose at each level of vitamin type (this is essentially a numerical summary of the interaction plot):

```
> with(ToothGrowth, tapply(len, list(supp,dose), mean))
     low   med  high
OJ 13.23 22.70 26.06
VC  7.98 16.77 26.14
```

Variance:

```
> with(ToothGrowth, tapply(len, list(supp,dose), var))
      low       med      high
OJ 19.889 15.295556  7.049333
VC  7.544  6.326778 23.018222
```

OR – perform the ANOVA, save the output into a model output and ask for this data:

```
> aov.out = aov(len ~ supp * dose, data=ToothGrowth)
```

"We want to look at length as a function of supplement and dose with all possible interactions between the factors"

```
> model.tables(aov.out, type="means", se=T)
```

"I want the means and standard errors of the data"

```
Tables of means
Grand mean

18.81333

 supp
supp
    OJ     VC
20.663 16.963

 dose
dose
   low    med   high
10.605 19.735 26.100

 supp:dose
    dose
supp low   med   high
  OJ 13.23 22.70 26.06
  VC  7.98 16.77 26.14

Standard errors for differences of means
          supp   dose supp:dose
        0.9376 1.1484    1.6240
replic.     30     20        10

> bartlett.test(len ~ supp * dose, data=ToothGrowth)

        Bartlett test of homogeneity of variances

data:  len by supp by dose
Bartlett's K-squared = 1.4217, df = 1, p-value = 0.2331
```

- Non-significant, therefore there is no difference between the variances – despite appearances to the contrary in the plot above – we can assume the variances to be homogenous.

2. Run a factorial ANOVA

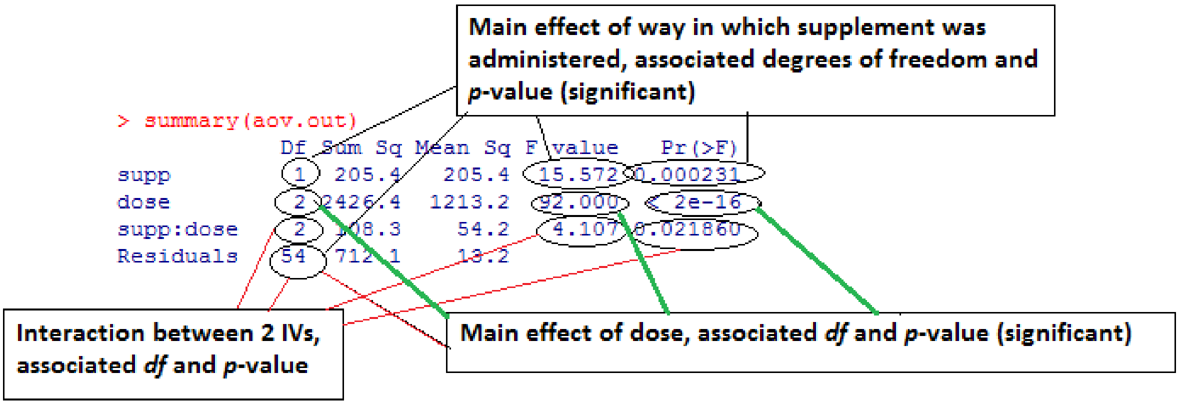
- Although we've already done this to get descriptives, previously, we do:

```
> aov.out = aov(len ~ supp * dose, data=ToothGrowth)
```

NB: For more factors, list all the factors after the tilde separated by asterisks. This gives a model with all possible main effects and interactions. To leave out interactions, separate the factor names with plus signs rather than asterisks.

- Turn off stars showing significance values if you want?

```
> options(show.signif.stars=F)
> summary(aov.out)
```



```
> summary(aov.out)
            Df Sum Sq Mean Sq F value   Pr(>F)
supp         1  205.4   205.4  15.572 0.000231
dose         2 2426.4  1213.2  92.000  < 2e-16
supp:dose    2  108.3    54.2   4.107 0.021860
Residuals   54  712.1    13.2
```

Main effect of way in which supplement was administered, associated degrees of freedom and *p*-value (significant)

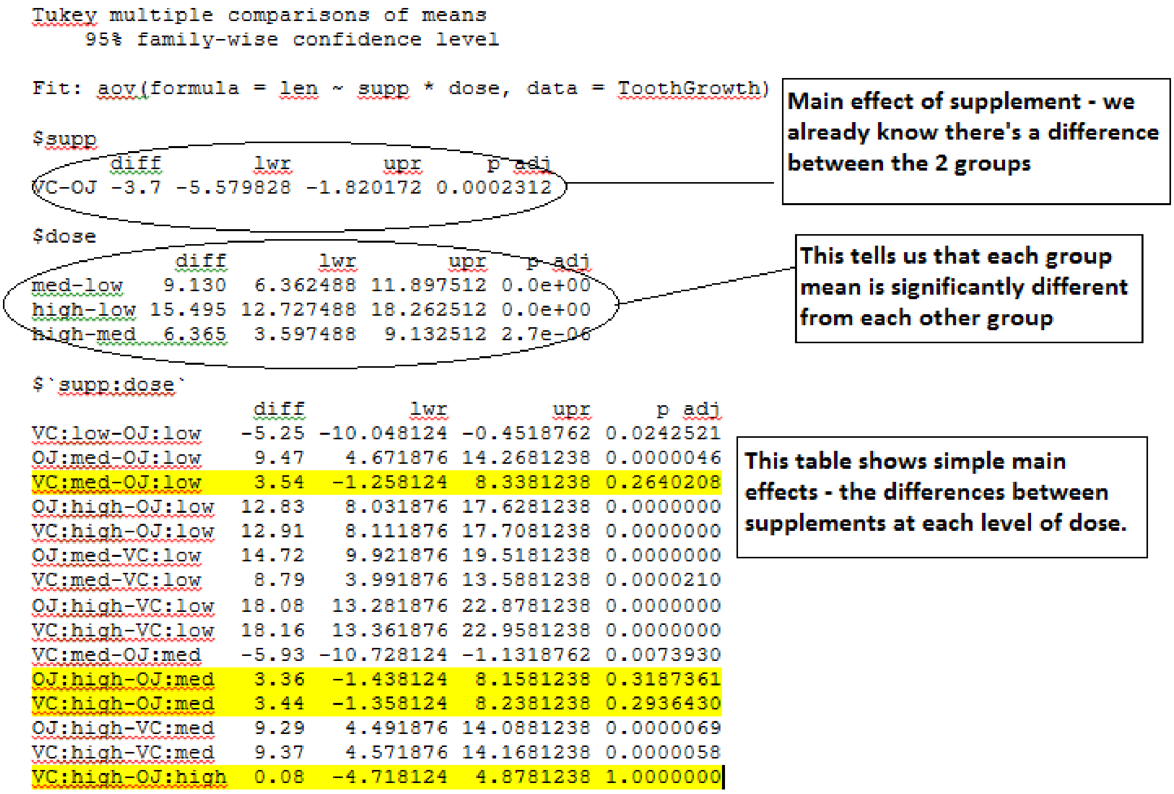
Interaction between 2 IVs, associated *df* and *p*-value

Main effect of dose, associated *df* and *p*-value (significant)

There's a main effect of supplement ($F(1,54)=15.572$; $p<.01$) and dose ($F(2,54)=92.0$; $p<.01$) (i.e. a difference between at least 2 of the means), as well as an interaction between them($F(2,54)=4.107$; $p<.05$).
Where do these differences lie – i.e. between which group means?

3. Run post hoc tests – Tukey HSD, Bonferroni …

```
> TukeyHSD(aov.out)
```



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

Fit: aov(formula = len ~ supp * dose, data = ToothGrowth)

$supp
      diff       lwr       upr     p adj
VC-OJ -3.7 -5.579828 -1.820172 0.0002312

$dose
           diff       lwr       upr   p adj
med-low   9.130  6.362488 11.897512 0.0e+00
high-low 15.495 12.727488 18.262512 0.0e+00
high-med  6.365  3.597488  9.132512 2.7e-06

$`supp:dose`
                 diff        lwr        upr     p adj
VC:low-OJ:low   -5.25 -10.048124 -0.4518762 0.0242521
OJ:med-OJ:low    9.47   4.671876 14.2681238 0.0000046
VC:med-OJ:low    3.54  -1.258124  8.3381238 0.2640208
OJ:high-OJ:low  12.83   8.031876 17.6281238 0.0000000
VC:high-OJ:low  12.91   8.111876 17.7081238 0.0000000
OJ:med-VC:low   14.72   9.921876 19.5181238 0.0000000
VC:med-VC:low    8.79   3.991876 13.5881238 0.0000210
OJ:high-VC:low  18.08  13.281876 22.8781238 0.0000000
VC:high-VC:low  18.16  13.361876 22.9581238 0.0000000
VC:med-OJ:med   -5.93 -10.728124 -1.1318762 0.0073930
OJ:high-OJ:med   3.36  -1.438124  8.1581238 0.3187361
VC:high-OJ:med   3.44  -1.358124  8.2381238 0.2936430
OJ:high-VC:med   9.29   4.491876 14.0881238 0.0000069
VC:high-VC:med   9.37   4.571876 14.1681238 0.0000058
VC:high-OJ:high  0.08  -4.718124  4.8781238 1.0000000
```

Main effect of supplement - we already know there's a difference between the 2 groups

This tells us that each group mean is significantly different from each other group

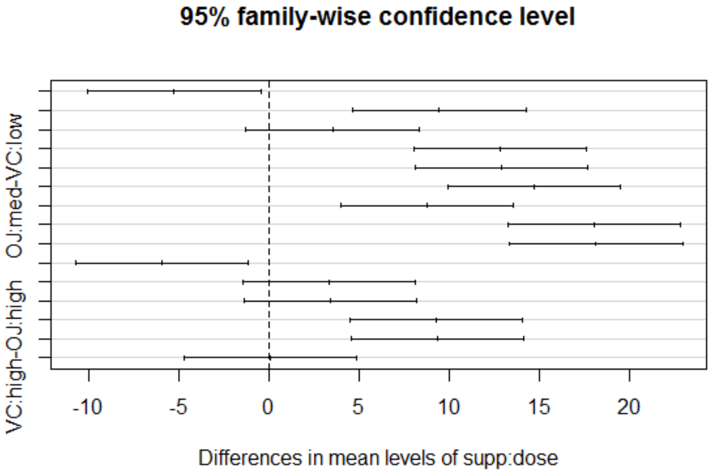
This table shows simple main effects - the differences between supplements at each level of dose.

- All significant simple main effects, except highlighted ones.
- Significant main effect of dose and way supplement was administered

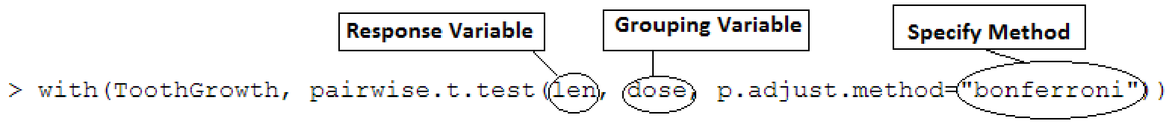
`conf.level=` `changes the confidence level`
 `"which="` option specifies which comparisons we want
`e.g. TukeyHSD(aov.out, which=c("dose"), conf.level=.99)` compares main effect of dose at a .99 probability level.

Graphical display – to plot CIs from Tukey:

```
> plot(TukeyHSD(aov.out))
```



Multiple t-tests with Bonferroni Adjustments



Response Variable

Grouping Variable

Specify Method

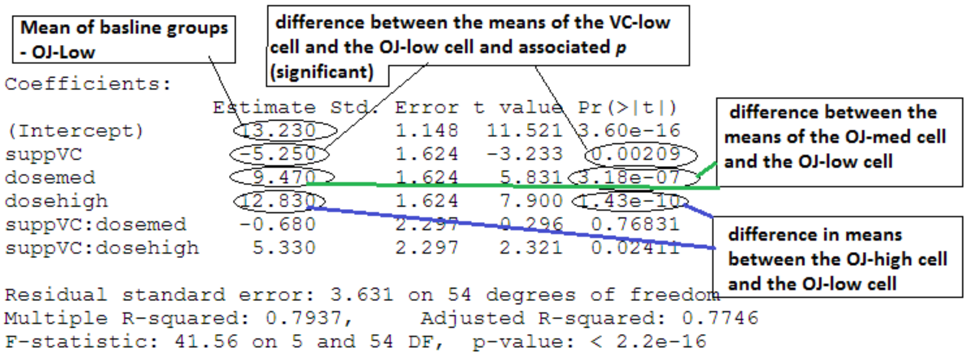
```
> with(ToothGrowth, pairwise.t.test(len, dose, p.adjust.method="bonferroni"))
```

```
Pairwise comparisons using t tests with pooled SD

data:  len and dose

     low     med    
med  2.0e-08 -      
high 4.4e-16 4.3e-05

P value adjustment method: bonferroni
```

Contrasts

- Analysis of treatment contrasts assumes a balanced design, homogeneity of variance, and additive effects (the effect of a treatment is to add a constant amount to each subject's score, plus or minus a bit of random error).

```
> options("contrasts")
```



Mean of basline groups - OJ-Low

difference between the means of the VC-low cell and the OJ-low cell and associated *p* (significant)

difference between the means of the OJ-med cell and the OJ-low cell

difference in means between the OJ-high cell and the OJ-low cell

```
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)        13.230      1.148  11.521 3.60e-16
suppVC             -5.250      1.624  -3.233  0.00209
dosemed             9.470      1.624   5.831 3.18e-07
dosehigh           12.830      1.624   7.900 1.43e-10
suppVC:dosemed     -0.680      2.297  -0.296  0.76831
suppVC:dosehigh     5.330      2.297   2.321  0.02411

Residual standard error: 3.631 on 54 degrees of freedom
Multiple R-squared: 0.7937,     Adjusted R-squared: 0.7746
F-statistic: 41.56 on 5 and 54 DF,  p-value: < 2.2e-16
```

Standard Errors are for the differences betweeen the means

BUT – nothing you can’t find in Tukey

4. **Plot Assumptions**
    a. **Look at regression for interpretation**

```
> plot(aov.out)
```