Analysis of Variance

The ASTA team

Contents

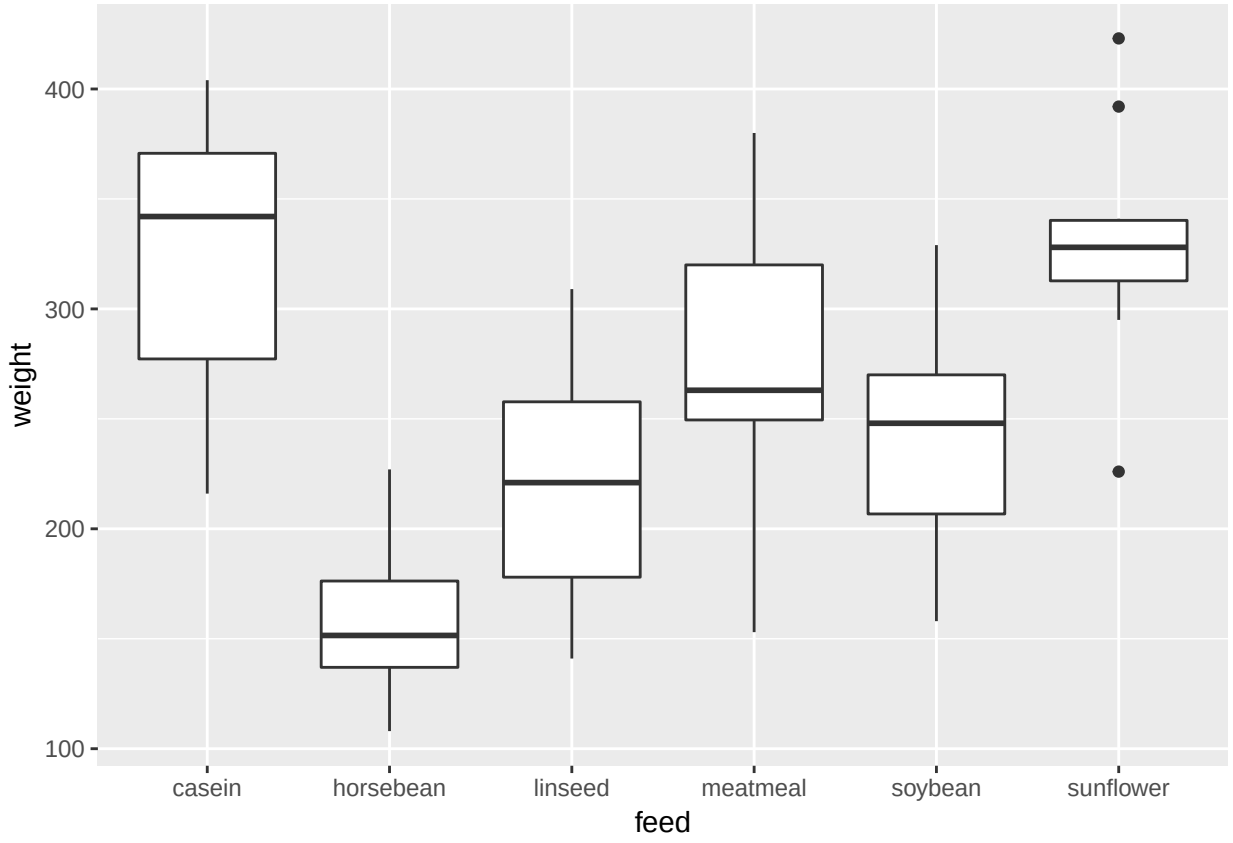
1 One way analysis of variance

1.1 Example

- The data set `chickwts` is available in `R`, and on the course webpage.
- Newly hatched chicks were randomly allocated into six groups, and each group was given a different feed supplement.

- Their weights in grams after six weeks are given along with feed types, i.e. we have a sample with corresponding measurements of 2 variables:
  - `weight`: a numeric variable giving the chick weight.
  - `feed`: a factor giving the feed type.
- Always start with some graphics:

```
library(mosaic)
gf_boxplot(weight ~ feed, data = chickwts)
```



1.2 The ANOVA Model

- We measure the response y which in this case is `weight`.
- We want to study the effect of the factor x on y. In this case $x =$`feed` and divides the sample in $g = 6$ groups.
- The mean responses within the groups are denoted $\mu_1, \mu_2, \ldots, \mu_g$.
- We will assume that
  - $y = \mu_x + \epsilon$, when y is a response in group x
  - ϵ are a sample from a population with mean zero and standard deviation σ.
  - The standard deviation for the population in each group is the same and equals σ
  - The response variable, y, is normal distributed within each group.
- The ANOVA test is a *test of independence* between the quantitative response variable and the qualitative explanatory variables.

2 Estimation of mean values

2.1 Estimates

- Least squares estimates for population means $\widehat{\mu}_x$ is given by the average of the response measurements in group x.
- For a given measured response y we let $\widehat{y}$ denote the model's prediction of y, i.e.

$$\widehat{y} = \widehat{\mu}_x$$

  if y is a response for an observation in group x.
- We use `mean` to find the mean, for each group:

```
mean(weight ~ feed, data = chickwts)
```

```
##    casein horsebean   linseed  meatmeal   soybean sunflower
##  323.5833  160.2000  218.7500  276.9091  246.4286  328.9167
```

- We can e.g. see that $\widehat{y} = 323.6$, when `feed=casein` but $\widehat{y} = 160.2$, when `feed=horsebean`.
- Is it a significant difference?

2.2 Contrast coding

- In many cases there is a group corresponding to "no treatment" and we are interested in the effect of different treatments.
- In this example we only have different `feeds`, which are sorted in lexicographical order by `R`, so `casein` is the reference.
- We can specify the model via:
  - `Intercept` corresponding to the mean response for the reference (`casein`).
  - For each of the other groups we have a **contrast**, which measures **the difference** between the mean value for that group and the reference group.
- For a given contrast we can calculate standard error, t-score and p-value, and thereby investigate whether there is a difference between this group and the reference group.
- In Agresti this is referred to as using **dummy variables**.

2.3 Example

```
model <- lm(weight ~ feed, data = chickwts)
summary(model)
```

```
##
## Call:
## lm(formula = weight ~ feed, data = chickwts)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -123.909  -34.413    1.571   38.170  103.091
##
## Coefficients:
```

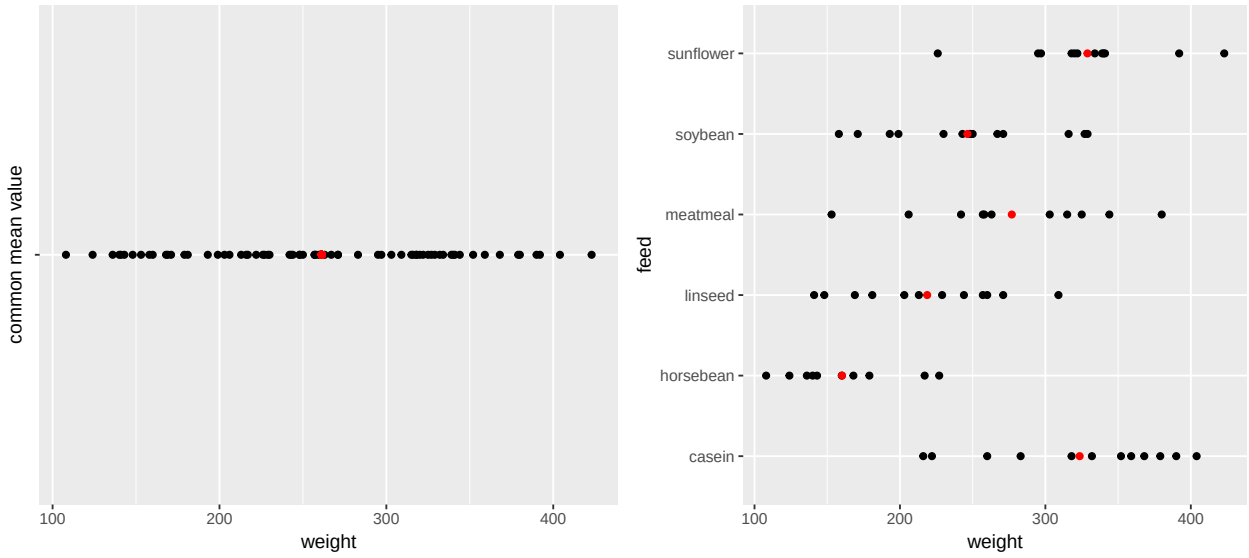
```
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     323.583     15.834  20.436  < 2e-16 ***
## feedhorsebean -163.383     23.485  -6.957 2.07e-09 ***
## feedlinseed   -104.833     22.393  -4.682 1.49e-05 ***
## feedmeatmeal   -46.674     22.896  -2.039 0.045567 *
## feedsoybean    -77.155     21.578  -3.576 0.000665 ***
## feedsunflower    5.333     22.393   0.238 0.812495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 54.85 on 65 degrees of freedom
## Multiple R-squared:  0.5417, Adjusted R-squared:  0.5064
## F-statistic: 15.36 on 5 and 65 DF,  p-value: 5.936e-10
```

- We get information about contrasts and their significance:
- `Intercept` corresponding to `casein` has `weight` different from zero ($p < 2 \times 10^{-16}$).
- Weight difference between `casein` and `horsebean` is extremely significant (p=2×10^{-9}).
- There is no significant weight difference between `casein` and `sunflower` (p=81%).

3 Overall test for effect

3.1 Graphical representation of models

- We have two alternative explanations of the data.
- Simple model with one parameter (mean): "The feed type doesn't matter. The weight is just random around a common mean value".
- Complex model with six parameters (means): "The feed type is important. For each feed type we get a different mean value and the weights are random around these values."



3.2 Hypotheses and test statistic

- Is the complex model significantly better (i.e. is there any effect of the explanatory grouping variable)? We can write the corresponding hypotheses in two different ways

$$H_0 : \mu_1 = \mu_2 = \ldots = \mu_g \quad \text{against} \quad H_a : \text{ At least 2 of the population means are different}$$

- Alternatively

$$H_0 : \text{ All contrasts are equal to zero.} \qquad H_a : \text{ At least one contrast is non-zero.}$$

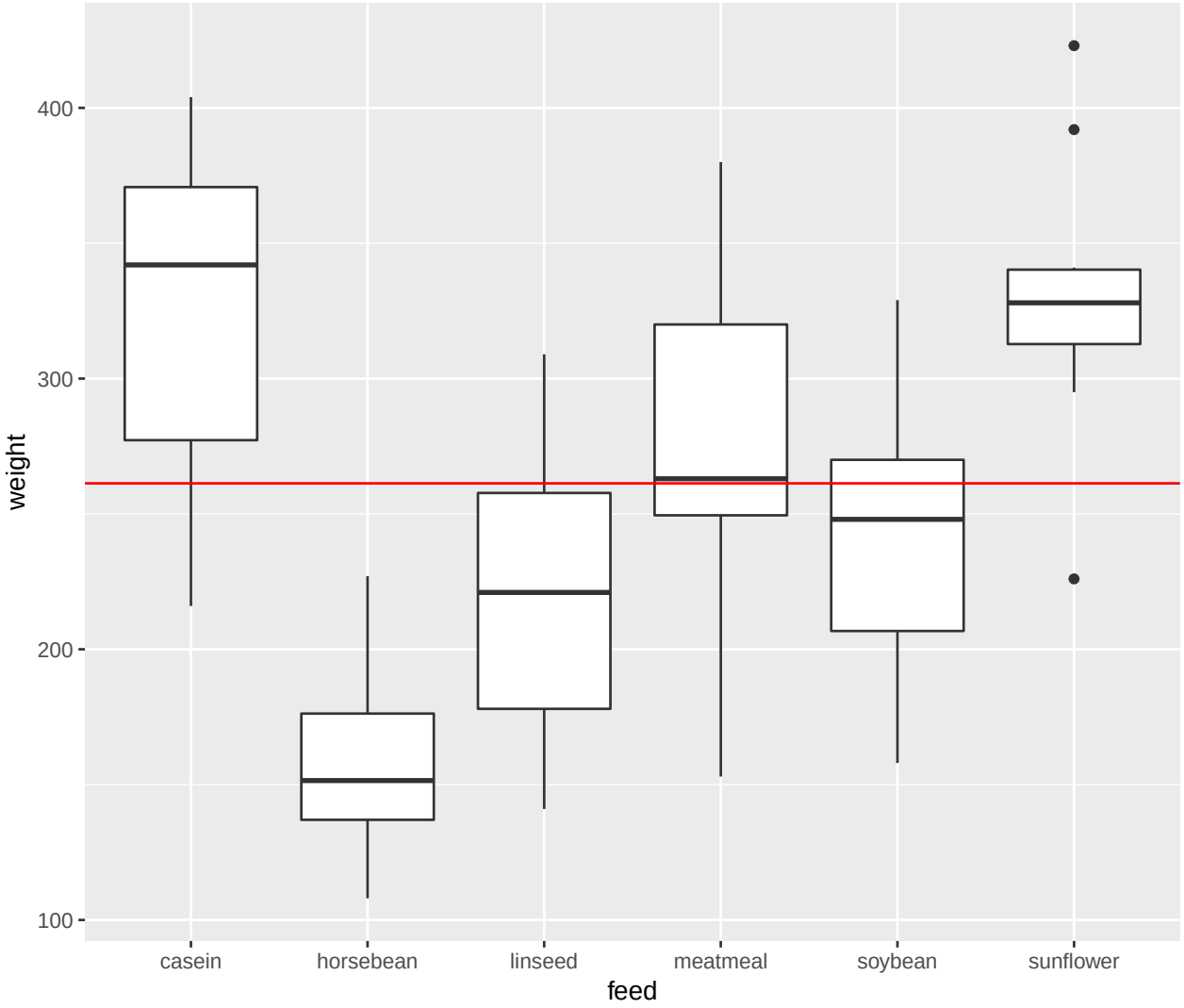
- We will (indirectly) use R^2 to do the test. If it is large, the complex model has good predictive power compared to the simple model. To judge significance we use

$$F_{obs} = \frac{(n-g)R^2}{(g-1)(1-R^2)} = \frac{(TSS - SSE)/(g-1)}{SSE/(n-g)}.$$

- Large values of R^2 implies large values of F_{obs}, which points to the alternative hypothesis.
- I.e. when we have calculated the observed value F_{obs}, then we have to find the probability that a new experiment would result in a larger value.

3.3 Interpretation of F statistic - Variance between/within groups

- It can be shown that the numerator of F_{obs} is a measure of **the variance between the groups**, i.e. how much "boxes" vary around the total average (the red line).
- Likewise it can be shown the denominator of F_{obs} is a measure for **the variance within groups**, i.e. how "tall" the boxes in the boxplot are.



- If the boxes' deviations from the red line are to be explained by randomness, then the two types of variances should be of same magnitude. This is measured by the F-test statistic, which can be stated as

$$F_{obs} = \frac{\text{variance between groups}}{\text{variance within groups}}$$

3.4 Example

```
model <- lm(weight ~ feed, data = chickwts)
summary(model)
```

```
##
## Call:
## lm(formula = weight ~ feed, data = chickwts)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -123.909  -34.413    1.571   38.170  103.091
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    323.583     15.834  20.436  < 2e-16 ***
## feedhorsebean -163.383     23.485  -6.957 2.07e-09 ***
## feedlinseed   -104.833     22.393  -4.682 1.49e-05 ***
## feedmeatmeal   -46.674     22.896  -2.039 0.045567 *
## feedsoybean    -77.155     21.578  -3.576 0.000665 ***
## feedsunflower    5.333     22.393   0.238 0.812495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 54.85 on 65 degrees of freedom
## Multiple R-squared:  0.5417, Adjusted R-squared:  0.5064
## F-statistic: 15.36 on 5 and 65 DF,  p-value: 5.936e-10
```

- The last line gives us the value of $F_{obs} = 15.36$ and the corresponding p-value (5.9×10^{-10}). Clearly there is a significant difference between the types of `feed`.

4 Two way analysis of variance

4.1 Additive effects

- The data set `ToothGrowth` is available in **R** and on the webpage. For more info about this data, use `?ToothGrowth`.
- The data describes the tooth length in guinea pigs where some recvieve vitamin C treatment and others are given orange juice in different dosage.
- A total of 60 observations on 3 variables.
  - `[,1] len` The tooth length
  - `[,2] supp` The type of the supplement (`OJ` or `VC`)
  - `[,3] dose` The dosage (`LO`, `ME`, `HI`)
- We will study the response `len` with the predictors `supp` and `dose`.
- At first we look at the model with additive effects
  - `len`=μ + `"effect of supp"`+ `"effect of dose"` + `error`
- This is also called the main effects model since it does not contain interaction terms.
- The parameter μ corresponds to the `Intercept` and is the mean tooth length in the reference group (supp `OJ`, dose `LO`).
- The effect of `supp` is the difference in mean when changing from `OJ` to `VC`.
- The effect of `dose` is the difference in mean when changing from `LO` to either`ME` or `HI`.

4.2 Dummy coding

- Let us introduce dummy variables:
  - $s_C = 1$ if supp `VC` and zero otherwise.
  - $d_M = 1$ if dose is `ME` and zero otherwise.
  - $d_H = 1$ if dose is `HI` and zero otherwise.
- Then we state the model

$$\text{length} = \mu + \beta_1 s_C + \beta_2 d_M + \beta_3 d_H + \text{error}.$$

- Interpretation:
  - μ is the expected tooth length when supp is `OJ` and `dose` is `LO` ($s_C = d_M = d_H = 0$)).
  - β_1 is the effect of supplement `OJ` to `VC` ($s_C = 1$).
  - β_2 is the effect of increasing dosage from `LO` to `ME` ($d_M = 1$).
  - β_3 is the effect of increasing dosage from `LO` to `HI` ($d_H = 1$).

4.3 Main effect model in R

- The main effects model is fitted by

```
MainEff <- lm(len ~ supp + dose, data = ToothGrowth)
summary(MainEff)
```

```
##
## Call:
## lm(formula = len ~ supp + dose, data = ToothGrowth)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -7.085 -2.751 -0.800  2.446  9.650
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  12.4550     0.9883  12.603  < 2e-16 ***
## suppVC       -3.7000     0.9883  -3.744 0.000429 ***
## doseME        9.1300     1.2104   7.543 4.38e-10 ***
## doseHI       15.4950     1.2104  12.802  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.828 on 56 degrees of freedom
## Multiple R-squared:  0.7623, Adjusted R-squared:  0.7496
## F-statistic: 59.88 on 3 and 56 DF,  p-value: < 2.2e-16
```

- The model has 4 parameters.
- The F test at the end compares with the (null) model with only one overall mean parameter. Does it seem like `supp` and `dose` has an additive effect?

4.4 Testing effect of supp

- Alternative model without effect of supp:

```
doseEff <- lm(len ~ dose, data = ToothGrowth)
```

- We can compare R^2 to see if `doseEff` (Model 1) is sufficent to explain the data compared to `MainEff` (Model 2). This is done by converting to F-statistic:

$$F_{obs} = \frac{(R_2^2 - R_1^2)/(df_1 - df_2)}{(1 - R_2^2)/df_2} = \frac{(SSE_1 - SSE_2)/(df_1 - df_2)}{(SSE_2)/df_2}.$$

- In **R** the calculations are done using `anova`:

```
anova(doseEff, MainEff)
```

```
## Analysis of Variance Table
##
## Model 1: len ~ dose
## Model 2: len ~ supp + dose
##   Res.Df     RSS Df Sum of Sq      F    Pr(>F)
## 1     57 1025.78
## 2     56  820.43  1    205.35 14.017 0.0004293 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.5 Testing effect of dose

- Alternative model without effect of dose:

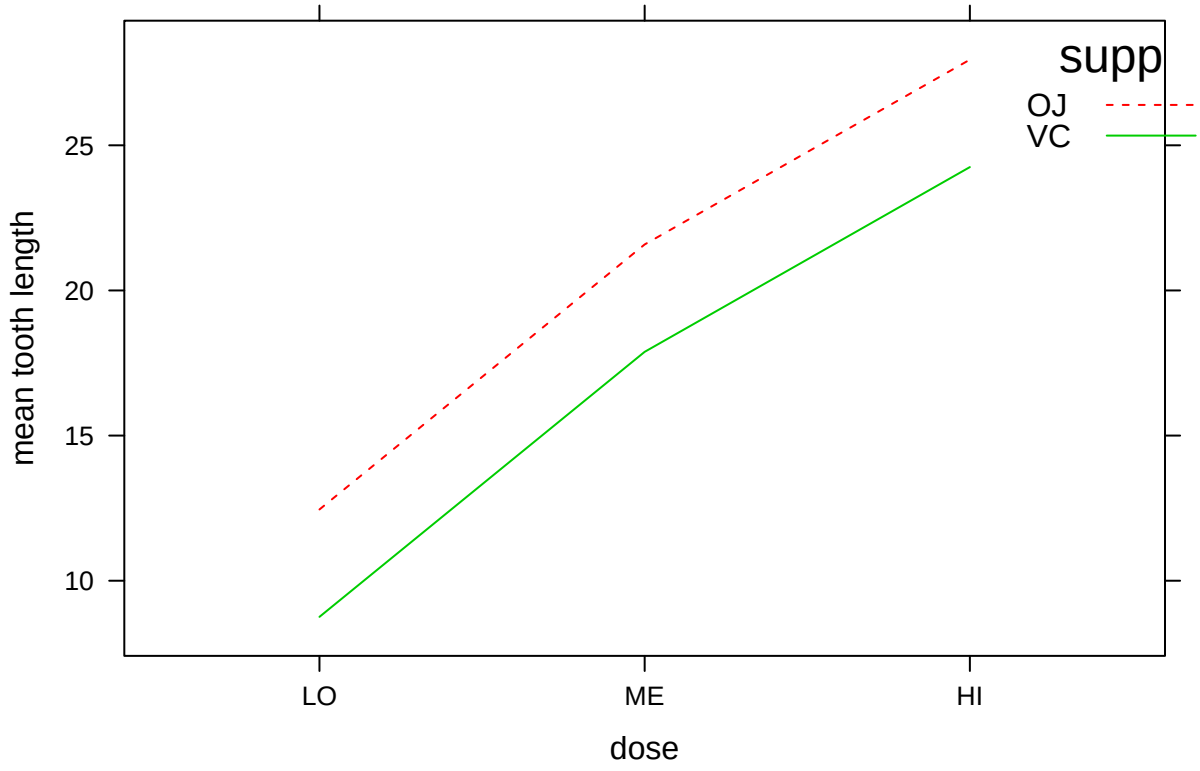
```
suppEff <- lm(len ~ supp, data = ToothGrowth)
anova(suppEff, MainEff)
```

```
## Analysis of Variance Table
##
## Model 1: len ~ supp
## Model 2: len ~ supp + dose
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1     58 3246.9
## 2     56  820.4  2    2426.4 82.811 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5 Interaction

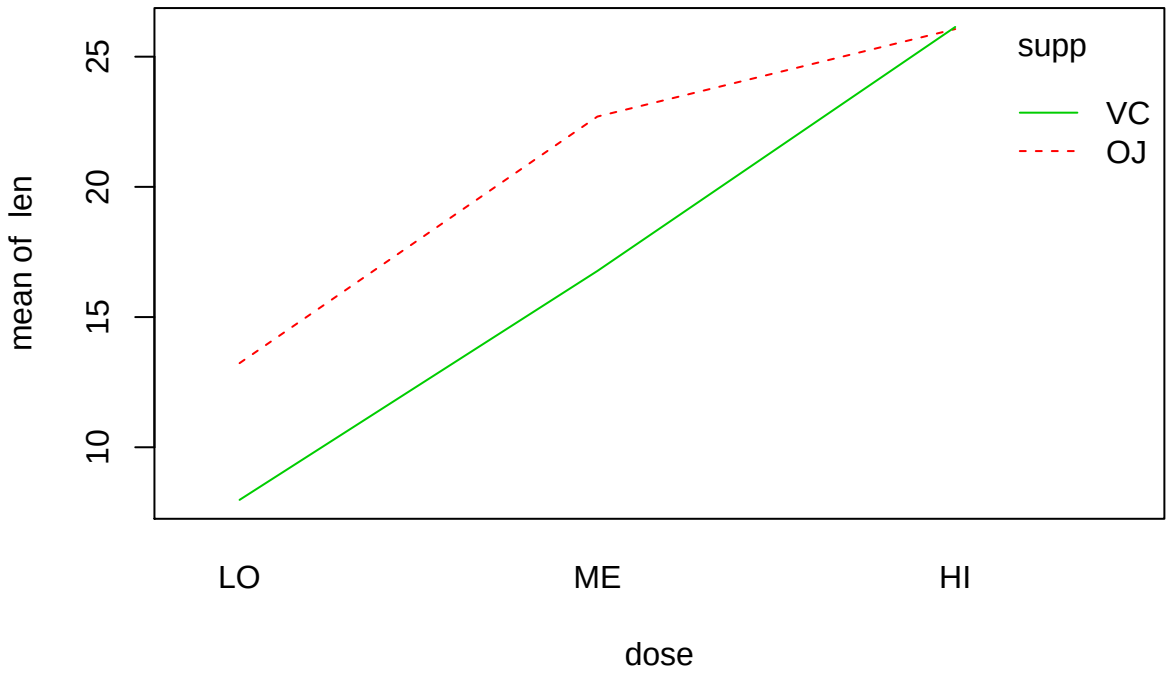
5.1 Example

- We will extend the model by introducing an interaction between `supp` and `dose`.
- A graphical check for no interaction in the main effects model:



- Interaction plot:

```
with(ToothGrowth, interaction.plot(dose, supp, len, col = 2:3))
```



- For each of the supplement types we plot the average number of tooth length as a function of dosage.
- If the main effects model is correct then the difference between supplements is the same for all levels of dosage, i.e. the curves should be parallel - except for noise.

- This does not seem to be the case.

5.2 Dummy coding

- The extended model can be formulated as

$$\texttt{length} = \mu + \beta_1 s_C + \beta_2 d_M + \beta_3 d_H + \beta_4 s_C d_M + \beta_5 s_C d_H + \texttt{error}$$

- Interpretation:
  - μ is the expected tooth length for `supp OJ` and `dose LO` ($s_C = d_M = d_H = 0$).
  - β_1 is the effect of changing from `supp OJ` to `VC`, `dose` is `LO` ($s_C = 1, d_M = d_H = 0$).
  - β_2 is the effect of increasing `dose` from `LO` to `ME`, when `supp` is `OJ` ($s_C = 0, d_M = 1$).
  - β_3 is the effect of increasing `dose` from `LO` to `HI`, when `supp` is `OJ` ($s_C = 0, d_H = 1$).
  - β_4 is an additional effect of both changing from `supp OJ` to `VC` and increasing `dose` from `LO` to `ME` ($s_C = 1, d_M = 1$)
  - β_5 is an additional effect of both changing from `supp OJ` to `VC` and increasing `dose` from `LO` to `HI` ($s_C = 1, d_H = 1$)

5.3 Example

- We fit the interaction model by changing plus to multiply in the model expression from before:

```
Interaction <- lm(len ~ supp*dose, data = ToothGrowth)
```

- Now we can think of an experiment with 6 groups corresponding to each combination of the predictors.
- Looking at the group averages it looks like, the supplement types behave quite differently depending on `dose`:

```
mean(len ~ supp + dose, data = ToothGrowth)
```

```
## OJ.LO VC.LO OJ.ME VC.ME OJ.HI VC.HI
## 13.23  7.98 22.70 16.77 26.06 26.14
```

- But is that significant?

```
anova(MainEff, Interaction)
```

```
## Analysis of Variance Table
##
## Model 1: len ~ supp + dose
## Model 2: len ~ supp * dose
##   Res.Df    RSS Df Sum of Sq     F  Pr(>F)
## 1     56 820.43
## 2     54 712.11  2    108.32 4.107 0.02186 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- With a p-value of 2.1860269% there is a significant interaction `supp:dose`, i.e. the lack of parallel curves in the interaction plot is significant.

```r
summary(Interaction)
```

```
##
## Call:
## lm(formula = len ~ supp * dose, data = ToothGrowth)
##
## Residuals:
##    Min     1Q Median     3Q    Max
##  -8.20  -2.72  -0.27   2.65   8.27
##
## 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 **
## doseME           9.470      1.624   5.831 3.18e-07 ***
## doseHI          12.830      1.624   7.900 1.43e-10 ***
## suppVC:doseME   -0.680      2.297  -0.296  0.76831
## suppVC:doseHI    5.330      2.297   2.321  0.02411 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## 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
```

- The additional effect of both changing from `supp OJ` to `VC` and increasing `dose` from `LO` to `HI` (β_5=`suppVC:doseHI`) is highly significant.