

Analysis of Variance

The ASTA team

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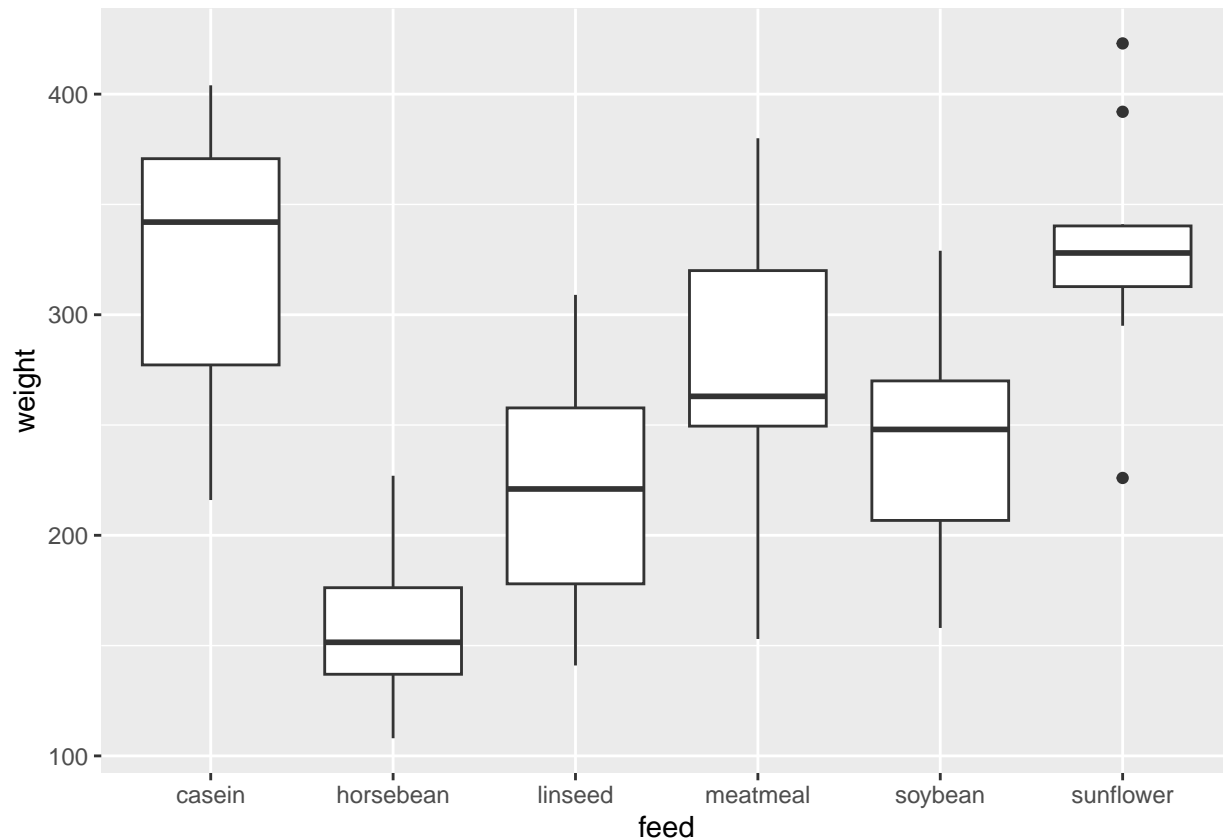
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1 One way analysis of variance

1.1 Example

- The data set `chickwts` is available in **R**, and on the course webpage.
- 71 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 $x = \text{feed}$ and divides the sample in $g = 6$ groups.
- The mean responses within the groups are denoted $\mu_1, \mu_2, \dots, \mu_g$.
- 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 equal means* for the different groups.

2 Estimation of mean values

2.1 Estimates

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

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

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 $\hat{y} = 323.6$, when `feed=casein` but $\hat{y} = 160.2$, 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 ($p < 2 \times 10^{-16}$) (of course, chickens grow a lot over 6 weeks)
- Weight difference between `casein` and `horsebean` is extremely significant ($p = 2 \times 10^{-9}$).

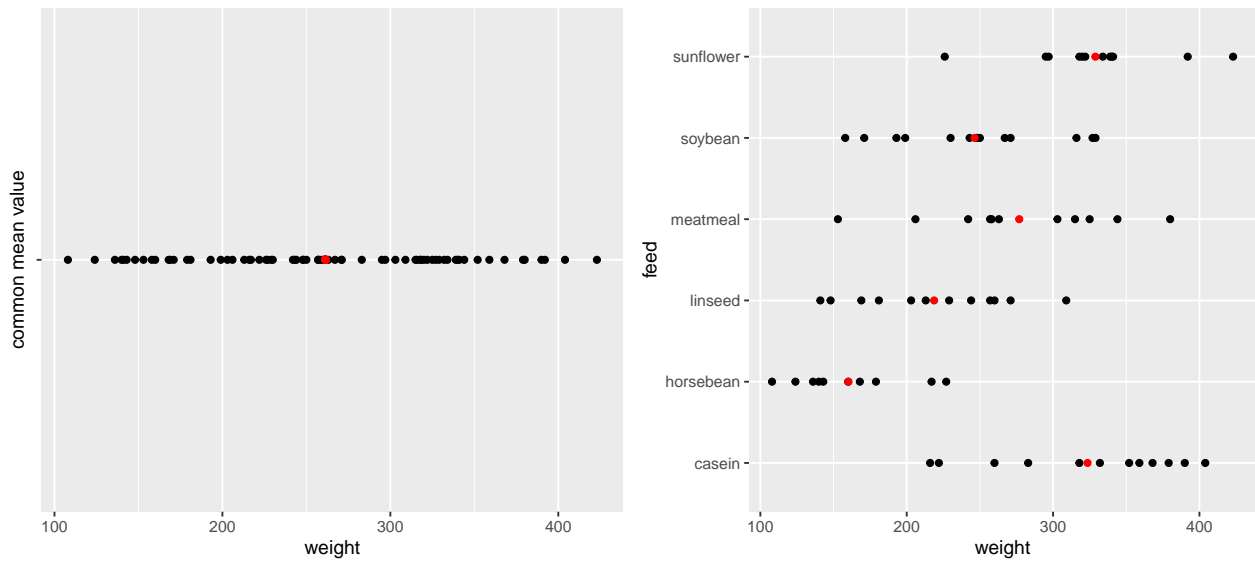
- There is no significant weight difference between `casein` and `sunflower` (p=81%).

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.”

```
## Warning in geom_point(aes(x = red_dot), color = "red"): All aesthetics have length 1, but the data has
## length 6
## i Please consider using `annotate()` or provide this layer with data containing
## a single row.
```



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

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

- Alternatively

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

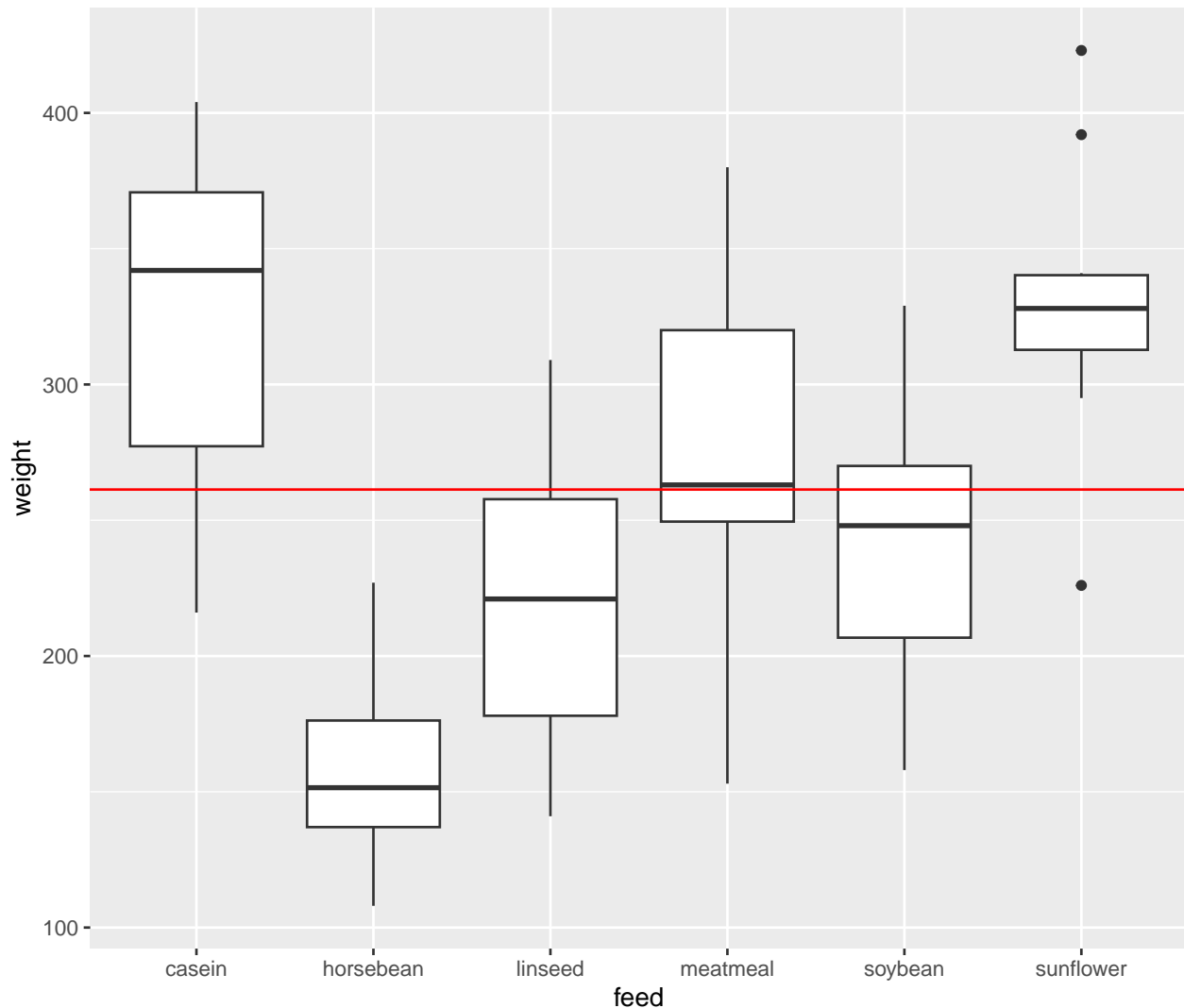
- We will (indirectly) use R^2 to do the test. If it is large, the complex model has good predictive power compared to the simple model. To judge significance we use

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

- 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.
- TSS: error sum of squares if common mean. SSE: error sum of squares if different means.
- TSS-SSE: how much does error sum of squares increase if means are restricted to be equal.

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.



- The bigger deviations between the red line and the box means relative to the variation within boxes, the less we trust H_0 . 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 receive 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 (L0, ME, HI)
- We will study the response `len` with the predictors `supp` and `dose`.
- At first we look at the model with additive effects
 - $\text{len} = \mu + \text{"effect of supp"} + \text{"effect of dose"} + \text{error}$
- 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 L0).
- 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 L0 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 ($d_H = 1$).
- As a two-way table:

	<i>LO</i>	<i>ME</i>	<i>HI</i>
<i>OJ</i>	μ	$\mu + \beta_2$	$\mu + \beta_3$
<i>VC</i>	$\mu + \beta_1$	$\mu + \beta_1 + \beta_2$	$\mu + \beta_1 + \beta_3$

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.

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 sufficient to explain the data compared to `MainEff` (Model 2). This is done by converting to F -statistic:

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

- $SSE_1 - SSE_2$: increase in error sum of square when using Model 1 instead of Model 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
```

- p -value is 0.004 hence we reject that `supp` does not have an effect. Thus we prefer Model 2.

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
```

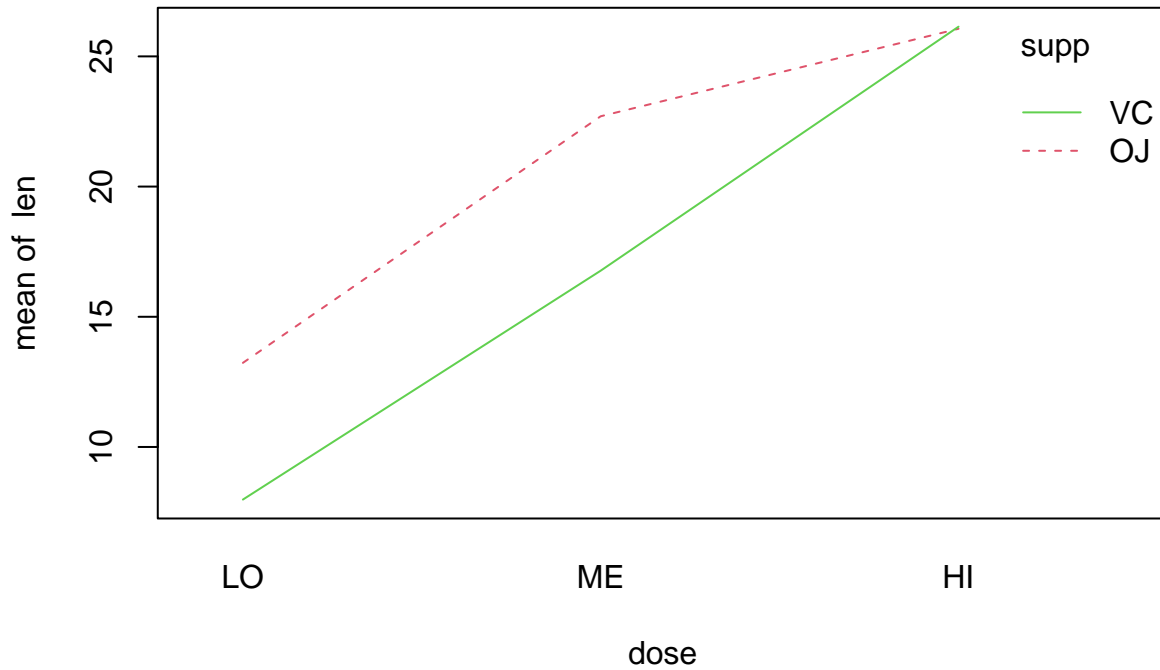
- p -value is ≈ 0 hence we reject that `dose` does not have an effect. Thus we prefer Model 2.

5 Interaction

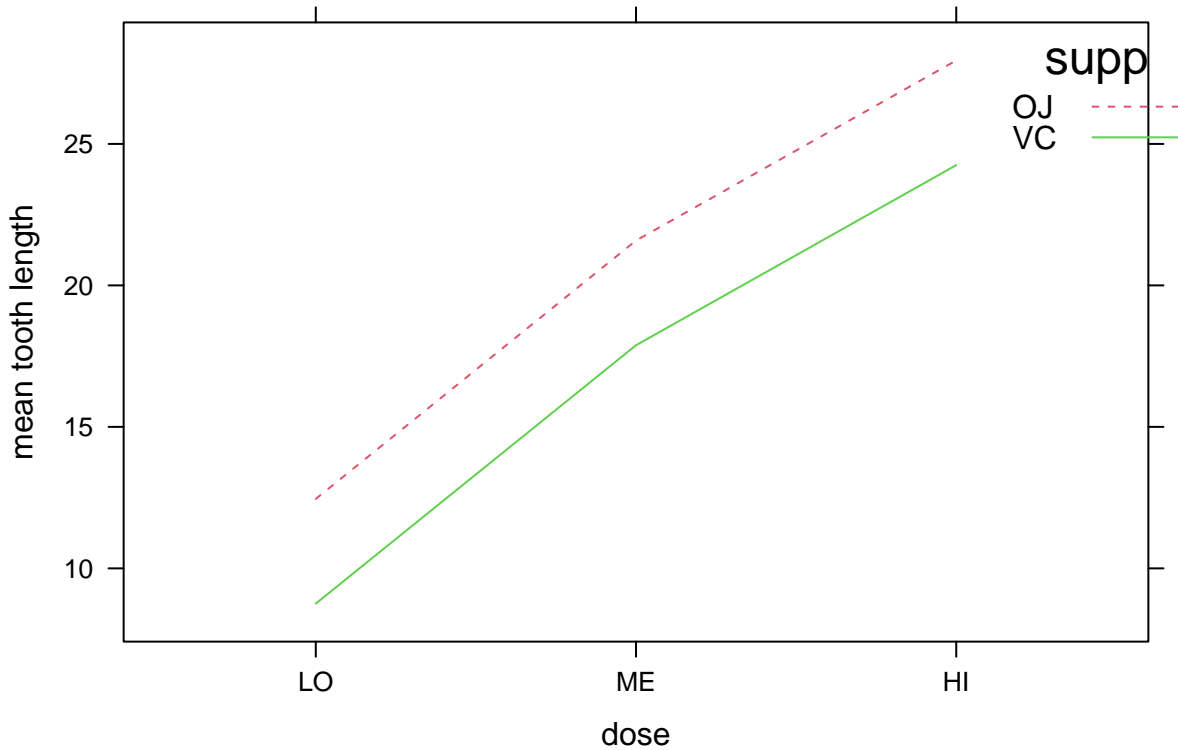
5.1 Example

- We will extend the model by introducing an interaction between `supp` and `dose`.
- Interaction plot:

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

- For each of the supplement types we plot the average 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.
- This is how the plot *should* look *if* the main effects model (no interaction) is correct:



- Parallel lines mean that effect of supplement does not depend on dose !

5.2 Dummy coding

- The extended model can be formulated as

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

- 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 ($s_C = 1, d_H = 1$)
- As a two-way table:

	<i>LO</i>	<i>ME</i>	<i>HI</i>
<i>OJ</i>	μ	$\mu + \beta_2$	$\mu + \beta_3$
<i>VC</i>	$\mu + \beta_1$	$\mu + \beta_1 + \beta_2 + \beta_4$	$\mu + \beta_1 + \beta_3 + \beta_5$

- Further examples:
 - effect of changing from **supp** OJ to VC if **dose** is LO is $\mu + \beta_1 - \mu = \beta_1$
 - effect of changing from **supp** OJ to VC if **dose** is ME is $\mu + \beta_1 + \beta_2 + \beta_4 - \mu - \beta_2 = \beta_1 + \beta_4$
 - effect of changing from **supp** OJ to VC if **dose** is HI is $\mu + \beta_1 + \beta_3 + \beta_5 - \mu - \beta_3 = \beta_1 + \beta_5$
 - if $\beta_4 = 0$ and $\beta_5 = 0$ the effect of changing from OJ to VC does not depend on **dose**

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.
- Is added interaction significant? - we compare main effects model and more complex interaction model using anova:

```
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.

```
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

```

- Note the negative effect of changing from OJ to VC when dose is low is cancelled by the positive interaction parameter $\beta_5 = \text{suppVC:doseHI}$ meaning almost no difference between OJ and VC when dose is high (compare with interaction plot)

5.4 Hierarchical principle

- In presence of interaction effect it does not make sense to make tests for absence of main effects ! Indeed each factor has an effect that just happens to vary depending on the other factor
- Hence start by investigating whether there is an interaction effect
- If yes: no further tests !
- If no: you may test main effects if relevant for your study