Transcript of Mick Crawley's R course 2010 Imperial College London, Silwood Park

Emanuel G Heitlinger

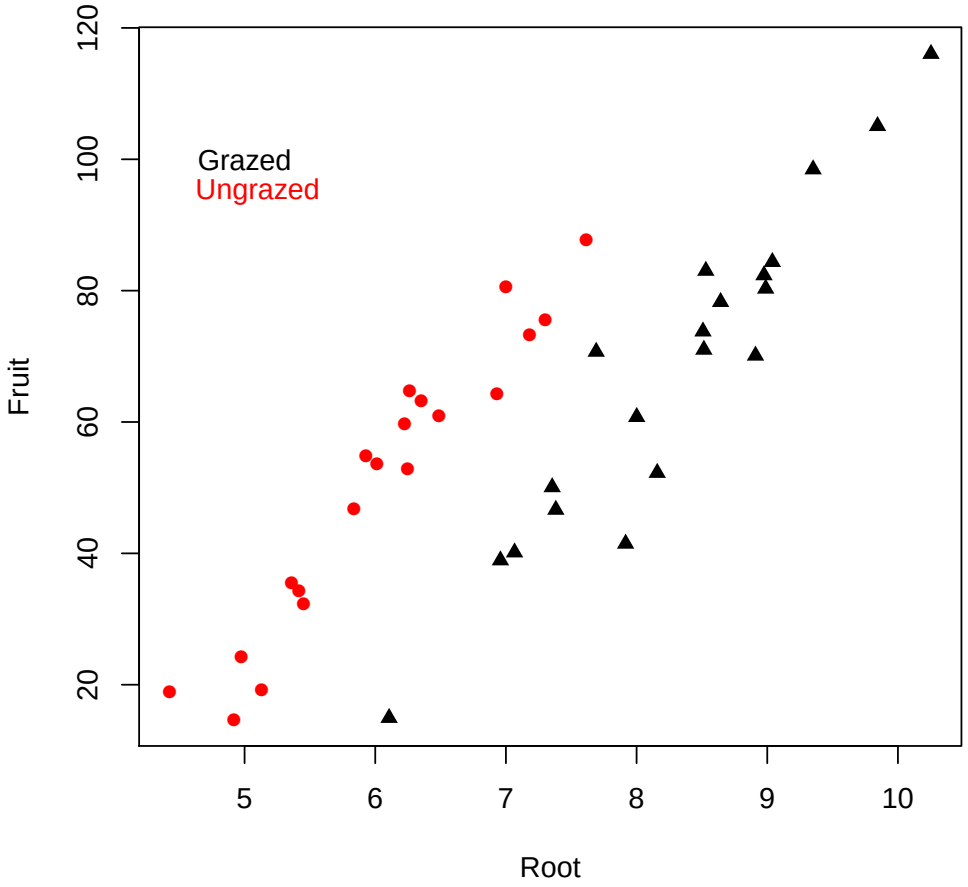
Day 6: Analysis of Covariance (ANCOVA) Part 2

ANCOVA with different values of the covariates

```
> ipo <- read.table("ipomopsis.txt", header = TRUE)
> attach(ipo)
```

Plot making clever use of logic arithmetic

```
> plot(Fruit ~ Root, pch = 16 + (Grazing == "Grazed"), col = as.numeric(Grazing
> text(5, 100, label = "Grazed")
> text(5.1, 95, label = "Ungrazed", col = 2)
```



Suprisingly the Grazed Plants seem to produce more fruits, but let's take a closer look.

To calculate the sum of squares manually we will use versions of our funcitions from berfore (Ancova-Anova writeup). A little general function for correction factors one that can be used to supply factor levels, and the function for the sum of products.

```
> CF <- function(x) sum(x)^2/length(x)
> Q.aov <- function(x, fac) {
+     sum(as.vector((tapply(x, fac, sum)^2)/tapply(x, fac, length)))
+ }
> SSXY <- function(x, y) sum(x * y) - (sum(x) * sum(y))/length(c(y))
```

Based on this we do the calculations for a model with interaction effects (differences in slope) and one without.

Note that we can **not** calculate a slope from the the simple regression sum of squares and the simple square of products, as the cavariates (Roots) have different values in the treatments (unlike photoperiode in the example in anova-ancova).

```
> sst <- sum(Fruit^2) - CF(Fruit)
> ssx <- sum(Root^2) - CF(Root)
> ssa <- Q.aov(Fruit, Grazing) - CF(Fruit)
> ssxy <- SSXY(Fruit, Root)
> b.wrong <- ssxy/ssx
> ssr <- b.wrong * ssxy
> sse <- sst - ssr
> multi.sst <- tapply(Fruit, Grazing, function(x) sum(x^2) - CF(x))
> multi.ssxy <- c(by(ipo, Grazing, function(d) SSXY(d$Fruit, d$Root)))
> multi.ssx <- tapply(Root, Grazing, function(x) sum(x^2) - CF(x))
> multi.b <- multi.ssxy/multi.ssx
> multi.ssr <- multi.b * multi.ssxy
> multi.sse <- multi.sst - multi.ssr
> combi.sst <- sum(multi.sst)
> combi.ssxy <- sum(multi.ssxy)
> combi.ssx <- sum(multi.ssx)
> combi.b <- sum(multi.b)
> combi.ssr <- sum(multi.ssr)
> combi.sse <- sum(multi.sse)
```

Now we can calculate the value of a single common slope and SSR_{diff} a measure for the difference of the two different slopes. Finaly we can calculate the error sum of squares for the modell without differernt slopes.

```
> ssr <- combi.ssxy^2/combi.ssx
> single.b <- combi.ssxy/combi.ssx
> ssr.diff <- combi.ssr - ssr
> sse.inter <- sst - ssa - ssr - ssr.diff
> sse.common <- sst - ssa - ssr
```

We can look at our models, first the complicated one with different slopes, then the less complicated without the non-significant interaction term:

Source	SS	df	MS (var)	F	p
Grazing	2910.436	1	2910.436	62.38	0.08
Root	19148.939	1	19148.939	410.42	0.031
Different slopes	4.812	1	4.812	0.103	0.75
Error	1679.649	36	46.657		
Total	23743.837	39			

Source	SS	df	MS (var)	F	p
Grazing	2910.436	1	2910.436	63.929	0.079
Root	19148.939	1	19148.939	420.616	0.031
Error	1684.461	36	45.526		
Total	23743.837	39			

Compare this with R's ancova. The step function finds the right minimal adequate model.

```
> model <- lm(Fruit ~ Grazing * Root)
> summary.aov(model)

             Df  Sum Sq Mean Sq  F value    Pr(>F)
Grazing       1  2910.4  2910.4  62.3795 2.262e-09 ***
Root          1 19148.9 19148.9 410.4201 < 2.2e-16 ***
Grazing:Root  1     4.8     4.8   0.1031      0.75
Residuals    36  1679.6    46.7
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ

> model2 <- step(model)

Start:  AIC=157.5
Fruit ~ Grazing * Root

               Df Sum of Sq    RSS    AIC
- Grazing:Root  1    4.8122 1684.5 155.61
<none>                      1679.7 157.50

Step:  AIC=155.61
```

```
Fruit ~ Grazing + Root

          Df Sum of Sq     RSS    AIC
<none>                  1684.5 155.61
- Grazing  1    5264.4  6948.8 210.30
- Root     1   19148.9 20833.4 254.22
```

```
> summary.aov(model2)

            Df  Sum Sq Mean Sq F value    Pr(>F)
Grazing      1  2910.4  2910.4  63.929 1.397e-09 ***
Root         1 19148.9 19148.9 420.616 < 2.2e-16 ***
Residuals   37  1684.5    45.5
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ
```

Surprisingly the **probabilities** seem to be wrong. But this is because R calculates not the simple p-values but **exclusion p-values**. To explain this a little excurse:

From what we got so far we can calculate the two different intercepts:

$a_1 = \bar{Y_1} - b\bar{X}_1$

$a_2 = \bar{Y_2} - b\bar{X}_2$

```
> multi.a <- by(ipo, Grazing, function(d) mean(d$Fruit) - single.b *
+     mean(d$Root))
> c(multi.a[1], multi.a[2])

    Grazed   Ungrazed
-127.82936  -91.72611
```

```
> a.diff <- multi.a[[2]] - multi.a[[1]]
> a.diff

[1] 36.10325
```

This demonstrates, that the ungrazed plants produce more fruits than the grazed plants, which is the opposite to what is obtained by looking at the means.

```
> tapply(Fruit, Grazing, mean)
```

```
  Grazed Ungrazed
 67.9405  50.8805
```

The **standard error of the intercept**. Standard errors for one common intercepts can be obtained as follows:

$$SE_a = \sqrt{s^2[\frac{1}{n} + \frac{(0-\bar{x})^2}{SSX}]}$$

```
> SE.a <- sqrt(sse.common/37 * (1/length(Root[Grazing == "Grazed"]) +
+     (0 - mean(Root[Grazing == "Grazed"]))^2/combi.ssx))
```

And the **standard error of the difference of the two intercepts** (which is equivalent to the inclusion of grazing).

$$SE_{\hat{y_1}-\hat{y_2}} = \sqrt{s^2[\frac{2}{n} + \frac{(\bar{x_1}-\bar{x_2})^2}{SSX}]}$$

```
> SE.yy <- sqrt(sse.common/37 * (2/length(Root[Grazing == "Grazed"]) +
+     (mean(Root[Grazing == "Grazed"]) - mean(Root[Grazing == "Ungrazed"]))^2/c
```

And finally the **standard error of the slope** (the common slope)

$$SE_b = \sqrt{\frac{s^2}{SSX}}$$

```
> SE.b <- sqrt((sse.common/37)/combi.ssx)
> SE.b

[1] 1.148771
```

These Standard errors can be found in the table generated by summary.lm and we can also genreate the t-values.

```
> summary.lm(model2)

Call:
lm(formula = Fruit ~ Grazing + Root)

Residuals:
     Min       1Q   Median       3Q      Max
-17.1920  -2.8224   0.3223   3.9144  17.3290
```

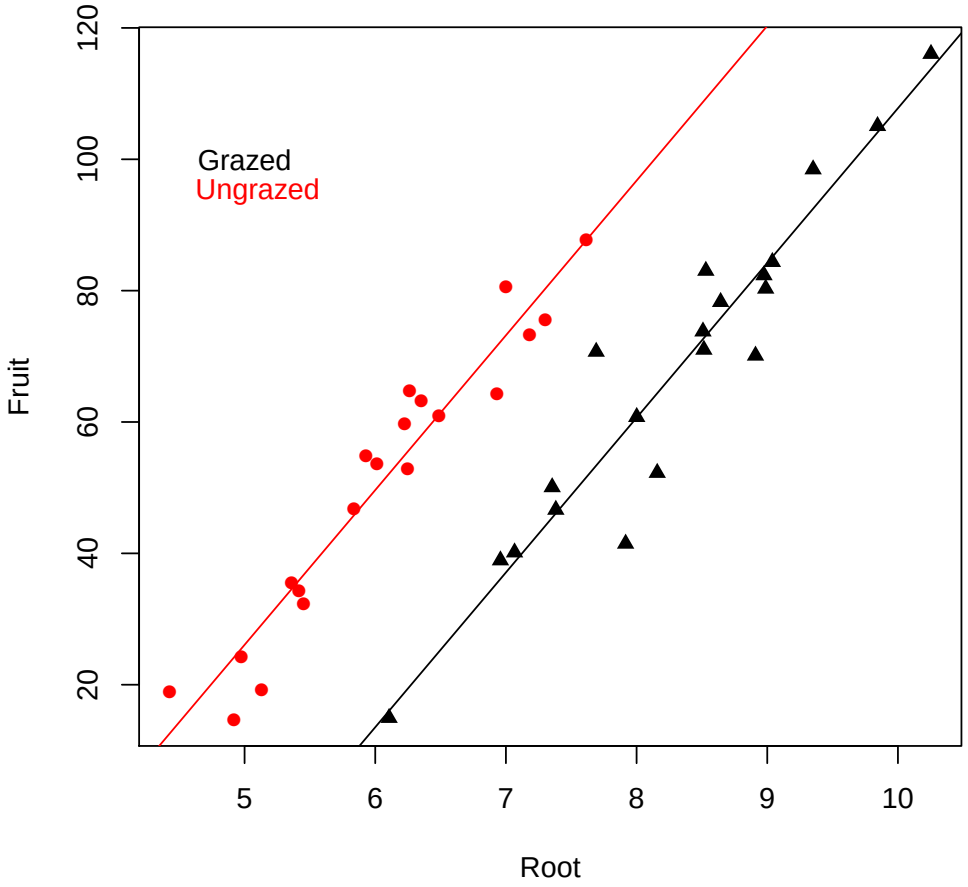
```
Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     -127.829      9.664  -13.23 1.35e-15 ***
GrazingUngrazed   36.103      3.357   10.75 6.11e-13 ***
Root              23.560      1.149   20.51  < 2e-16 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ

Residual standard error: 6.747 on 37 degrees of freedom
Multiple R-squared: 0.9291,         Adjusted R-squared: 0.9252
F-statistic: 242.3 on 2 and 37 DF,  p-value: < 2.2e-16
```

```
> c(SE.a = SE.a, SE.yy = SE.yy, SE.b = SE.b)

    SE.a    SE.yy     SE.b
9.664095 3.357396 1.148771
```

```
> tvals <- c(tval.Grazed = multi.a[[1]]/SE.a, tval.Ungrazed = a.diff/SE.yy,
+     tval.root = single.b/SE.b)
> tvals

  tval.Grazed tval.Ungrazed     tval.root
    -13.22725      10.75335      20.50892
```

The beauty of the summary output of these models is, that these p-values are presented, wich are more important in modeling. So finally after we understood all the output, we can draw two lines in our plot.

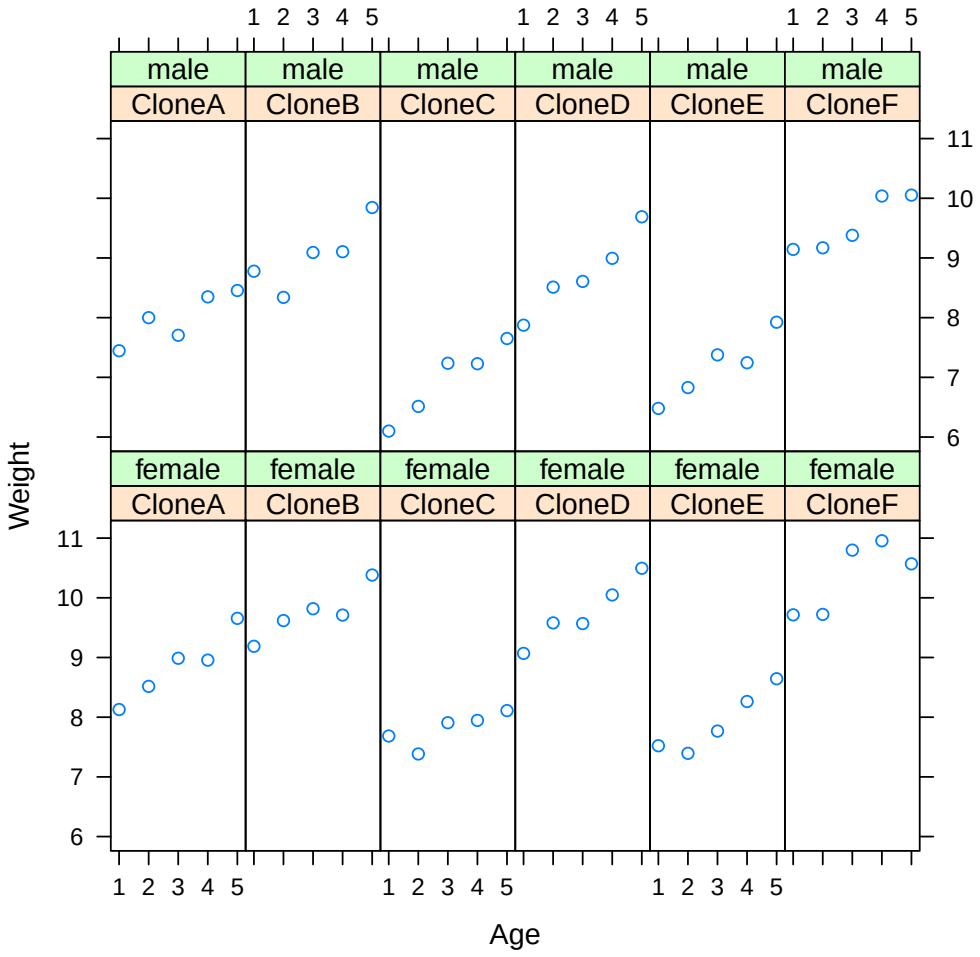
```
> plot(Fruit ~ Root, pch = 16 + (Grazing == "Grazed"), col = as.numeric(Grazing
> abline(multi.a[[1]], single.b)
> abline(multi.a[[2]], single.b, col = 2)
> text(5, 100, label = "Grazed")
> text(5.1, 95, label = "Ungrazed", col = 2)
```



A more complex example

We read in a more complex dataset and finally we use lattice for what it is good instead of learning how to build graphics from first principles in base.

```
> gain <- read.table("Gain.txt", header = TRUE)
> attach(gain)
> library(lattice)
> pl <- xyplot(Weight ~ Age | Genotype + Sex)

> print(pl)
```



After a first already allows some conclusions about differences in intercepts and slopes and we start modeling with this in mind.

```
> m1 <- lm(Weight ~ Sex * Age * Genotype)
> summary(m1)

Call:
lm(formula = Weight ~ Sex * Age * Genotype)

Residuals:
     Min       1Q   Median       3Q      Max
-0.40218 -0.12043 -0.01065  0.12592  0.44687

Coefficients:
```

```
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)                7.80053    0.24941  31.276  < 2e-16 ***
Sexmale                   -0.51966    0.35272  -1.473  0.14936
Age                        0.34950    0.07520   4.648 4.39e-05 ***
GenotypeCloneB             1.19870    0.35272   3.398  0.00167 **
GenotypeCloneC            -0.41751    0.35272  -1.184  0.24429
GenotypeCloneD             0.95600    0.35272   2.710  0.01023 *
GenotypeCloneE            -0.81604    0.35272  -2.314  0.02651 *
GenotypeCloneF             1.66851    0.35272   4.730 3.41e-05 ***
Sexmale:Age               -0.11283    0.10635  -1.061  0.29579
Sexmale:GenotypeCloneB    -0.31716    0.49882  -0.636  0.52891
Sexmale:GenotypeCloneC    -1.06234    0.49882  -2.130  0.04010 *
Sexmale:GenotypeCloneD    -0.73547    0.49882  -1.474  0.14906
Sexmale:GenotypeCloneE    -0.28533    0.49882  -0.572  0.57087
Sexmale:GenotypeCloneF    -0.19839    0.49882  -0.398  0.69319
Age:GenotypeCloneB        -0.10146    0.10635  -0.954  0.34643
Age:GenotypeCloneC        -0.20825    0.10635  -1.958  0.05799 .
Age:GenotypeCloneD        -0.01757    0.10635  -0.165  0.86970
Age:GenotypeCloneE        -0.03825    0.10635  -0.360  0.72123
Age:GenotypeCloneF        -0.05512    0.10635  -0.518  0.60743
Sexmale:Age:GenotypeCloneB 0.15469    0.15040   1.029  0.31055
Sexmale:Age:GenotypeCloneC 0.35322    0.15040   2.349  0.02446 *
Sexmale:Age:GenotypeCloneD 0.19227    0.15040   1.278  0.20929
Sexmale:Age:GenotypeCloneE 0.13203    0.15040   0.878  0.38585
Sexmale:Age:GenotypeCloneF 0.08709    0.15040   0.579  0.56616
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ

Residual standard error: 0.2378 on 36 degrees of freedom
Multiple R-squared: 0.9742,        Adjusted R-squared: 0.9577
F-statistic: 59.06 on 23 and 36 DF,  p-value: < 2.2e-16
```

> summary.aov(m1)

```
                Df Sum Sq Mean Sq  F value    Pr(>F)
Sex              1 10.374 10.3735 183.4398 1.065e-15 ***
Age              1 10.770 10.7700 190.4503 6.028e-16 ***
Genotype         5 54.958 10.9917 194.3710 < 2.2e-16 ***
Sex:Age          1  0.049  0.0489   0.8654    0.3584
Sex:Genotype     5  0.147  0.0294   0.5195    0.7598
Age:Genotype     5  0.168  0.0336   0.5946    0.7041
```

```
Sex:Age:Genotype  5  0.349  0.0698   1.2347    0.3132
Residuals        36  2.036  0.0566
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ
```

On the first few only the main effects seem significant all the interaction terms seem to cancel out. We start simplification and trust R's step function.

```
> m2 <- step(m1)

Start:  AIC=-155.01
Weight ~ Sex * Age * Genotype

                   Df Sum of Sq    RSS     AIC
- Sex:Age:Genotype  5   0.34912 2.3849 -155.51
<none>                          2.0358 -155.01

Step:  AIC=-155.51
Weight ~ Sex + Age + Genotype + Sex:Age + Sex:Genotype + Age:Genotype

               Df Sum of Sq    RSS     AIC
- Sex:Genotype  5  0.146901 2.5318 -161.92
- Age:Genotype  5  0.168136 2.5531 -161.42
- Sex:Age       1  0.048937 2.4339 -156.29
<none>                      2.3849 -155.51

Step:  AIC=-161.92
Weight ~ Sex + Age + Genotype + Sex:Age + Age:Genotype

               Df Sum of Sq    RSS     AIC
- Age:Genotype  5  0.168136 2.7000 -168.07
- Sex:Age       1  0.048937 2.5808 -162.78
<none>                      2.5318 -161.92

Step:  AIC=-168.07
Weight ~ Sex + Age + Genotype + Sex:Age

           Df Sum of Sq    RSS      AIC
- Sex:Age   1     0.049  2.749 -168.989
<none>                   2.700 -168.066
- Genotype  5    54.958 57.658    5.612
```

```
Step:  AIC=-168.99
Weight ~ Sex + Age + Genotype

           Df Sum of Sq    RSS      AIC
<none>                   2.749 -168.989
- Sex       1    10.374 13.122  -77.201
- Age       1    10.770 13.519  -75.415
- Genotype  5    54.958 57.707    3.662
```

> summary(m2)

```
Call:
lm(formula = Weight ~ Sex + Age + Genotype)

Residuals:
     Min       1Q   Median       3Q      Max
-0.40005 -0.15120 -0.01668  0.16953  0.49227

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     7.93701    0.10066  78.851  < 2e-16 ***
Sexmale        -0.83161    0.05937 -14.008  < 2e-16 ***
Age             0.29958    0.02099  14.273  < 2e-16 ***
GenotypeCloneB  0.96778    0.10282   9.412 8.07e-13 ***
GenotypeCloneC -1.04361    0.10282 -10.149 6.21e-14 ***
GenotypeCloneD  0.82396    0.10282   8.013 1.21e-10 ***
GenotypeCloneE -0.87540    0.10282  -8.514 1.98e-11 ***
GenotypeCloneF  1.53460    0.10282  14.925  < 2e-16 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ

Residual standard error: 0.2299 on 52 degrees of freedom
Multiple R-squared: 0.9651,        Adjusted R-squared: 0.9604
F-statistic: 205.7 on 7 and 52 DF,  p-value: < 2.2e-16
```

> summary.aov(m2)

```
            Df Sum Sq Mean Sq F value    Pr(>F)
Sex          1 10.374 10.3735  196.23 < 2.2e-16 ***
Age          1 10.770 10.7700  203.73 < 2.2e-16 ***
Genotype     5 54.958 10.9917  207.93 < 2.2e-16 ***
```

```
Residuals   52  2.749  0.0529
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ
```

We arrived at a model only containing main effects. It means that the slopes do not vary, but the intercepts do. This is reasonable if you remember our plot.

But what about factor levels? Don't some of the levels have the same intercept? We will come back to this when we talk about contrasts. For the moment we just look at the output of summary.lm:

Genotyp B and D seem to have a comparable intercept, so do C and E. We create a factor with 3 new levels accordingly.

I prefere nested ifelsestatment over logic arithmetic.

```
> ngen <- factor(ifelse(Genotype == "CloneB" | Genotype == "CloneD",
+     "BD", ifelse(Genotype == "CloneC" | Genotype == "CloneE",
+         "CE", ifelse(Genotype == "CloneA", "A", "F"))))
> ngen

 [1] A  A  A  A  A  BD BD BD BD BD CE CE CE CE CE BD BD BD BD BD CE CE CE CE CE
[26] F  F  F  F  F  A  A  A  A  A  BD BD BD BD BD CE CE CE CE CE BD BD BD BD BD
[51] CE CE CE CE CE F  F  F  F  F
Levels: A BD CE F
```

We use this in a third model.

```
> m3 <- lm(Weight ~ Sex + Age + ngen)
> summary(m3)

Call:
lm(formula = Weight ~ Sex + Age + ngen)

Residuals:
     Min       1Q   Median       3Q      Max
-0.42651 -0.16687  0.01211  0.18776  0.47736

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.93701    0.10308  76.996  < 2e-16 ***
Sexmale     -0.83161    0.06080 -13.679  < 2e-16 ***
Age          0.29958    0.02149  13.938  < 2e-16 ***
ngenBD       0.89587    0.09119   9.824 1.28e-13 ***
```

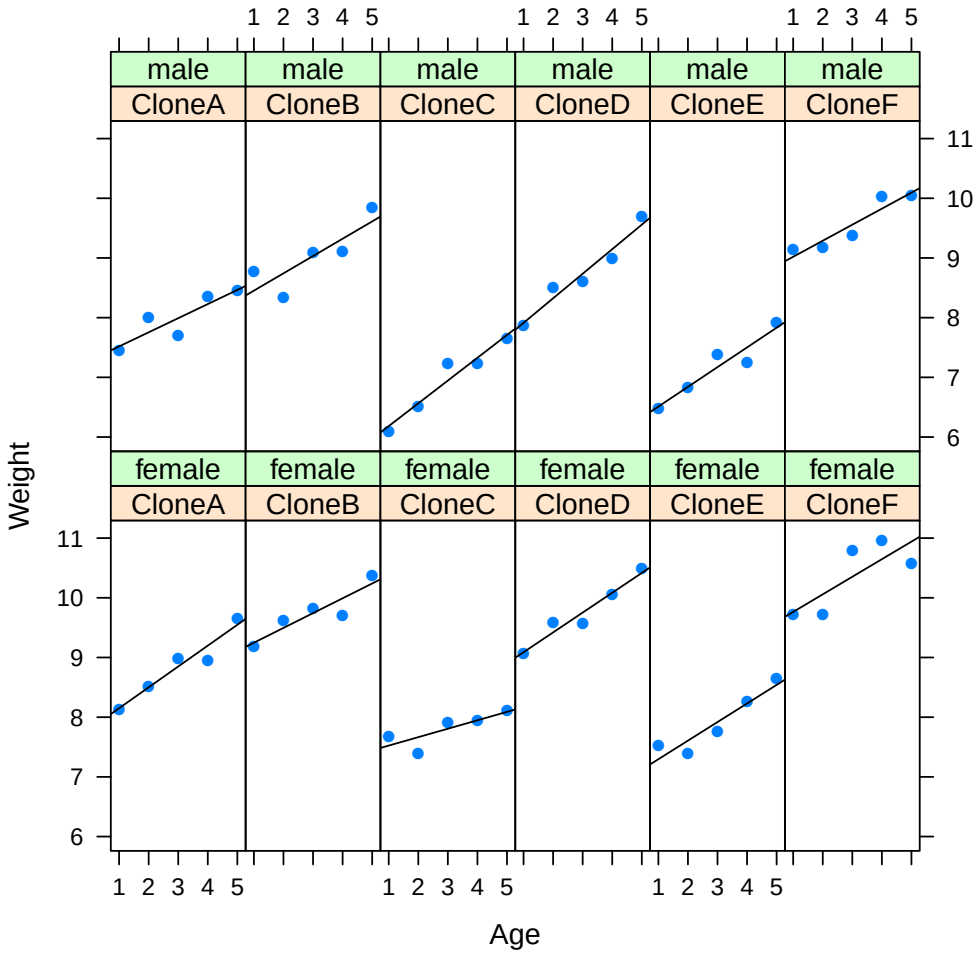
```
ngenCE      -0.95950    0.09119 -10.522 1.10e-14 ***
ngenF        1.53460    0.10530  14.574  < 2e-16 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ

Residual standard error: 0.2355 on 54 degrees of freedom
Multiple R-squared: 0.962,        Adjusted R-squared: 0.9585
F-statistic: 273.7 on 5 and 54 DF,  p-value: < 2.2e-16
```

And compare it to model two.

```
> anova(m2, m3)

Analysis of Variance Table

Model 1: Weight ~ Sex + Age + Genotype
Model 2: Weight ~ Sex + Age + ngen
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1     52 2.7489
2     54 2.9938 -2  -0.24489 2.3163 0.1087
```

Model 2 is not significantly better than model 2 and we prefere parsimony.
Finally we can plot the model:

```
> pl1 <- update(pl, panel = function(x, y) {
+     panel.xyplot(x, y, pch = 16)
+     panel.abline(lm(y ~ x))
+ })

> print(pl1)
```

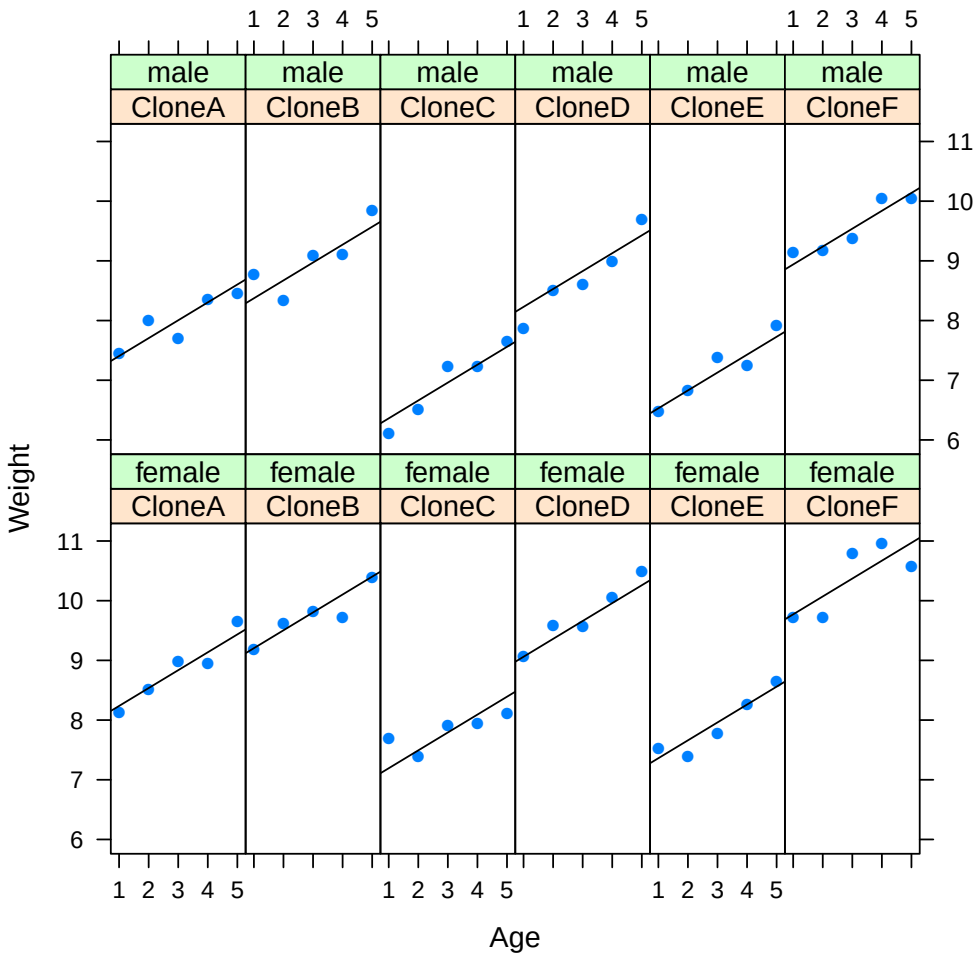


produces single linear models all with their own slope and intercept. **We want to plot our minimal adequate model!**

First we need to get the "raw value for the intercepts". Remember, how R presents them as differences from the first level! Extract them in the order needed in lattice. So here the proceedure for model 2.

```
> interc <- c(m2$coefficients[[1]], sapply(4:8, function(i) m2$coefficients[[1]
+     m2$coefficients[[i]]), m2$coefficients[[1]] + m2$coefficients["Sexmale"]
+     sapply(4:8, function(i) m2$coefficients[[1]] + m2$coefficients[[i]] +
+         m2$coefficients["Sexmale"]]))
> pl3 <- update(pl, panel = function(x, y, ...) {
+     panel.xyplot(x, y, pch = 16)
+     for (i in 1:12) {
+         if (panel.number() == i) {
```

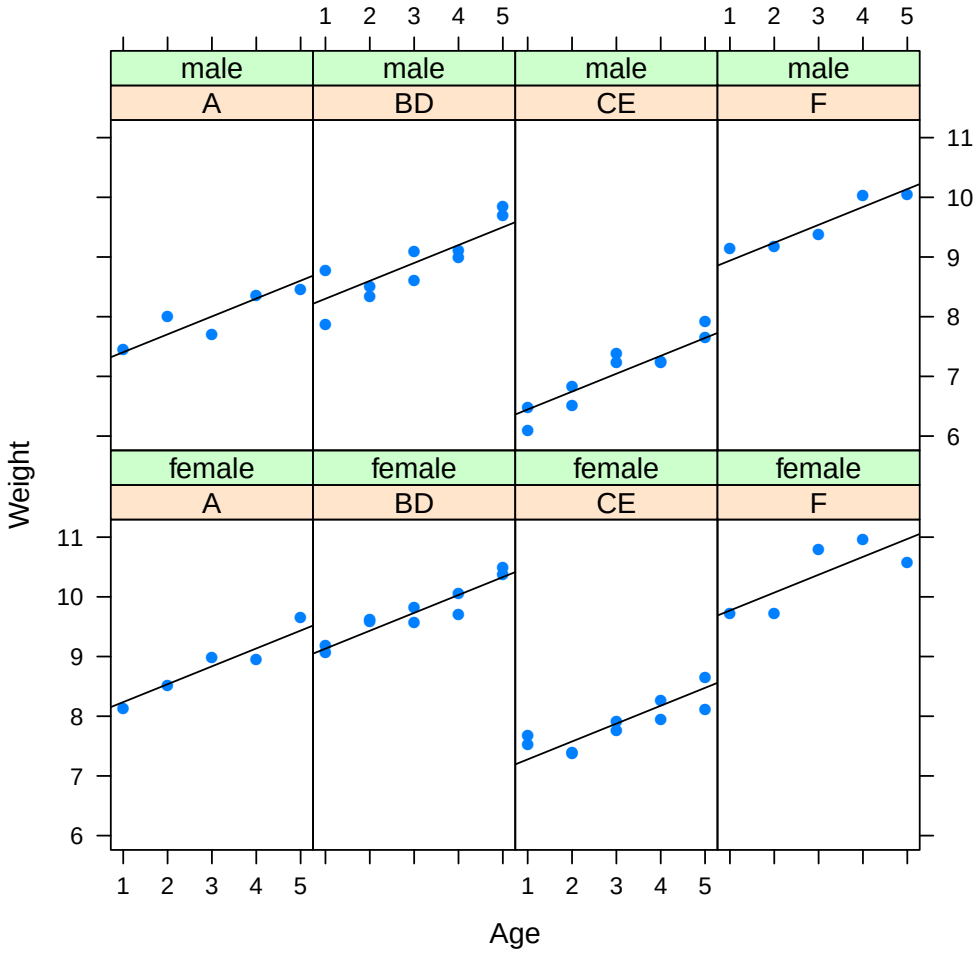
```
+                panel.abline(a = interc[i], b = m2$coefficients[["Age"]])
+            }
+        }
+ })

> print(pl3)
```



For model 3 with the reduced factor levels a new plot is needed

```
> pl4 <- xyplot(Weight ~ Age | ngen + Sex)
> interc2 <- c(m3$coefficients[[1]], sapply(4:6, function(i) m3$coefficients[[1
+     m3$coefficients[[i]]), m3$coefficients[[1]] + m3$coefficients[["Sexmale"]
+     sapply(4:6, function(i) m3$coefficients[[1]] + m3$coefficients[[i]] +
+         m3$coefficients[["Sexmale"]]))
```

```
> pl4 <- update(pl4, panel = function(x, y, ...) {
+     panel.xyplot(x, y, pch = 16)
+     for (i in 1:8) {
+         if (panel.number() == i) {
+             panel.abline(a = interc2[i], b = m3$coefficients[["Age"]])
+         }
+     }
+ })

> print(pl4)
```



The result looks good. It was quite hard to archieve, even with lattice. Or have I just used a stupid approach?