

# ANCOVA

## Analysis of covariance

The analysis of **covariance** is a hybrid of regression and ANOVA and measures the variance within each treatment level attributed to a continuous variable.

If a simple ANOVA can be expressed as  $Y_i = \alpha + \beta_{ji} * A + \epsilon_i$ , where  $j$  is each level of the treatment A and  $i$  is the replicate, then an ANCOVA can be expressed in two different ways:

- In each group, only the mean of the covariate differs, but the slope is the same across group:  $Y_{ij} = \alpha + \beta_{ji} * A + \delta_i * cov + \epsilon_i$
- In each group, the mean as well as the slope of the covariate differ:

$$Y_{ij} = \alpha + \beta_{ji} * A + \delta_i * cov + \gamma_{ji} * cov + \epsilon_i$$

## Let's look at a concrete example

I got this simulation example from Kery (2010) [Introduction to WinBUGS for Ecologists](#)

Here, we consider the relationship between body mass and body length of the asp viper (*Vipera aspis*) in three populations: Pyrenees, Massif Central, Jura Mountains. We simulate the data including an interaction effect and fit two different models to the simulated data:

```
n.groups <- 3
n.sample <- 10
n <- n.groups * n.sample          # Total number of data points
x <- rep(1:n.groups, rep(n.sample, n.groups)) # Indicator for population
pop <- factor(x, labels = c("Pyrenees", "Massif Central", "Jura"))
length <- runif(n, 45, 70)         # Obs. body length (cm) is rarely less than 45
```

```
Xmat <- model.matrix(~ pop*length)
print(Xmat, dig = 2)
```

	(Intercept)	popMassif Central	popJura	length	popMassif Central:length
1	1	0	0	49	0
2	1	0	0	46	0
3	1	0	0	60	0
4	1	0	0	68	0
5	1	0	0	66	0
6	1	0	0	64	0
7	1	0	0	47	0
8	1	0	0	63	0
9	1	0	0	59	0
10	1	0	0	53	0
11	1	1	0	69	69
12	1	1	0	46	46
13	1	1	0	70	70
14	1	1	0	55	55

15	1	1	0	47	47
16	1	1	0	69	69
17	1	1	0	55	55
18	1	1	0	54	54
19	1	1	0	51	51
20	1	1	0	59	59
21	1	0	1	65	0
22	1	0	1	69	0
23	1	0	1	57	0
24	1	0	1	54	0
25	1	0	1	60	0
26	1	0	1	65	0
27	1	0	1	63	0
28	1	0	1	46	0
29	1	0	1	47	0
30	1	0	1	53	0

popJura:length

1	0
2	0
3	0
4	0
5	0
6	0
7	0
8	0
9	0
10	0
11	0
12	0
13	0
14	0
15	0
16	0
17	0
18	0
19	0
20	0
21	65
22	69
23	57
24	54
25	60
26	65
27	63
28	46
29	47
30	53

attr("assign")

[1] 0 1 1 2 3 3

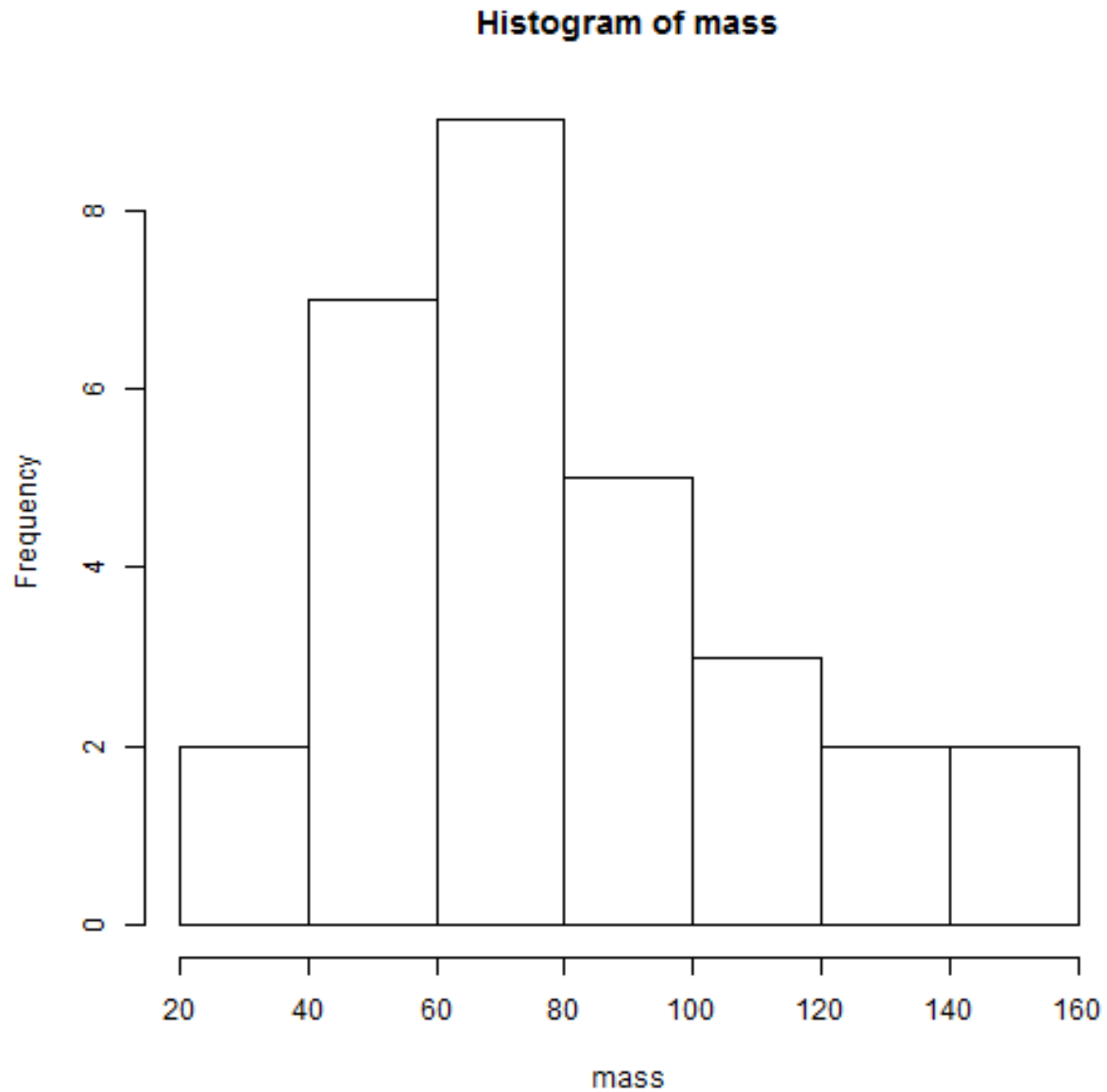
attr("contrasts")

attr("contrasts")\$pop

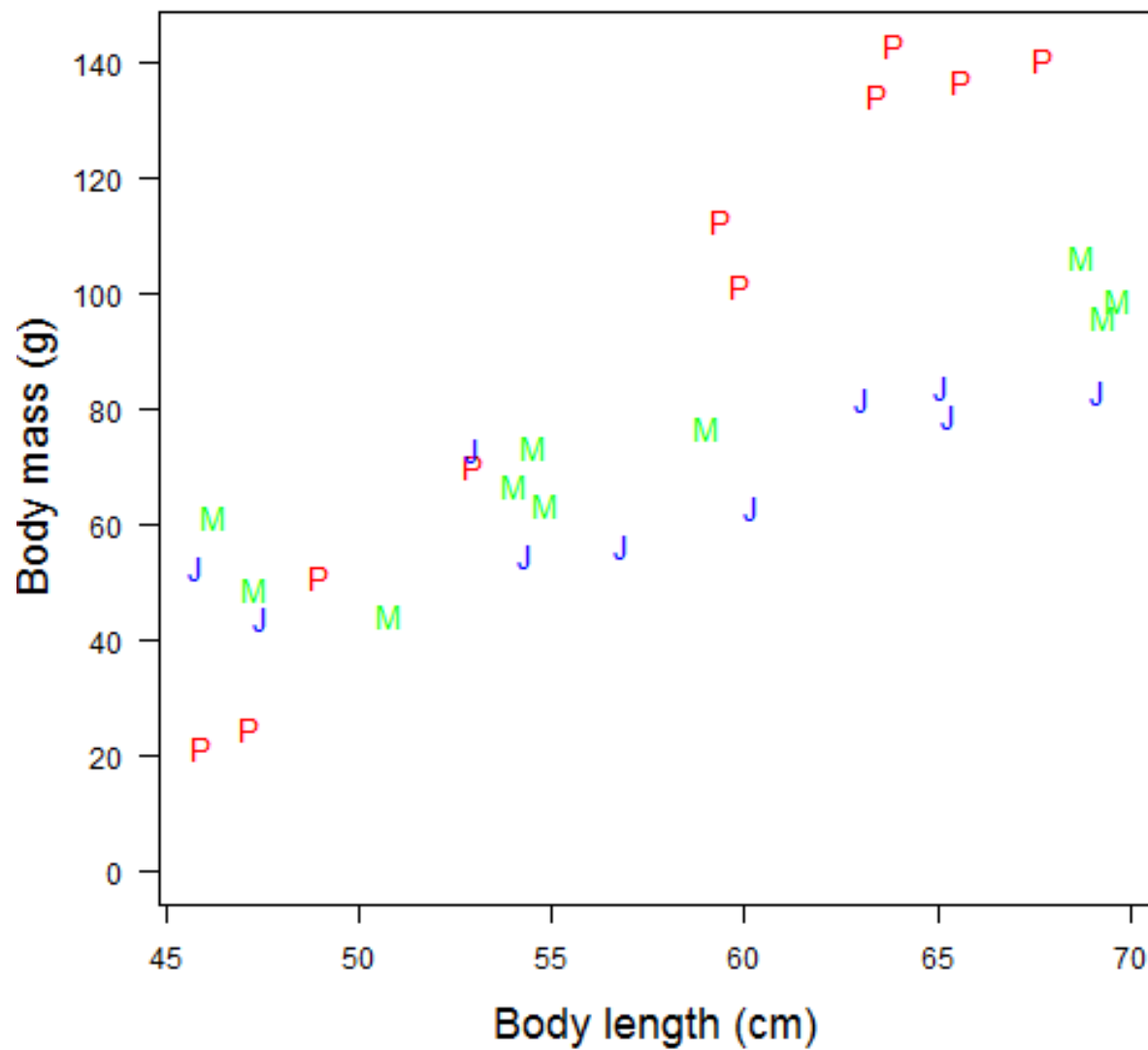
[1] "contr.treatment"

```
beta.vec <- c(-250, 150, 200, 6, -3, -4)
```

```
lin.pred <- Xmat[,] %*% beta.vec    # Value of lin.predictor
eps <- rnorm(n = n, mean = 0, sd = 10) # residuals
mass <- lin.pred + eps              # response = lin.pred + residual
hist(mass)                          # Inspect what we've created
```



```
matplot(cbind(length[1:10], length[11:20], length[21:30]), cbind(mass[1:10], mass[11:20],
mass[21:30]), ylim = c(0, max(mass)), ylab = "Body mass (g)", xlab = "Body length (cm)",
col = c("Red", "Green", "Blue"), pch = c("P", "M", "J"), las = 1, cex = 1.2, cex.lab = 1.5)
```



Common slope - different intercepts model

```
mod.csl=lm(mass ~ pop + length)
```

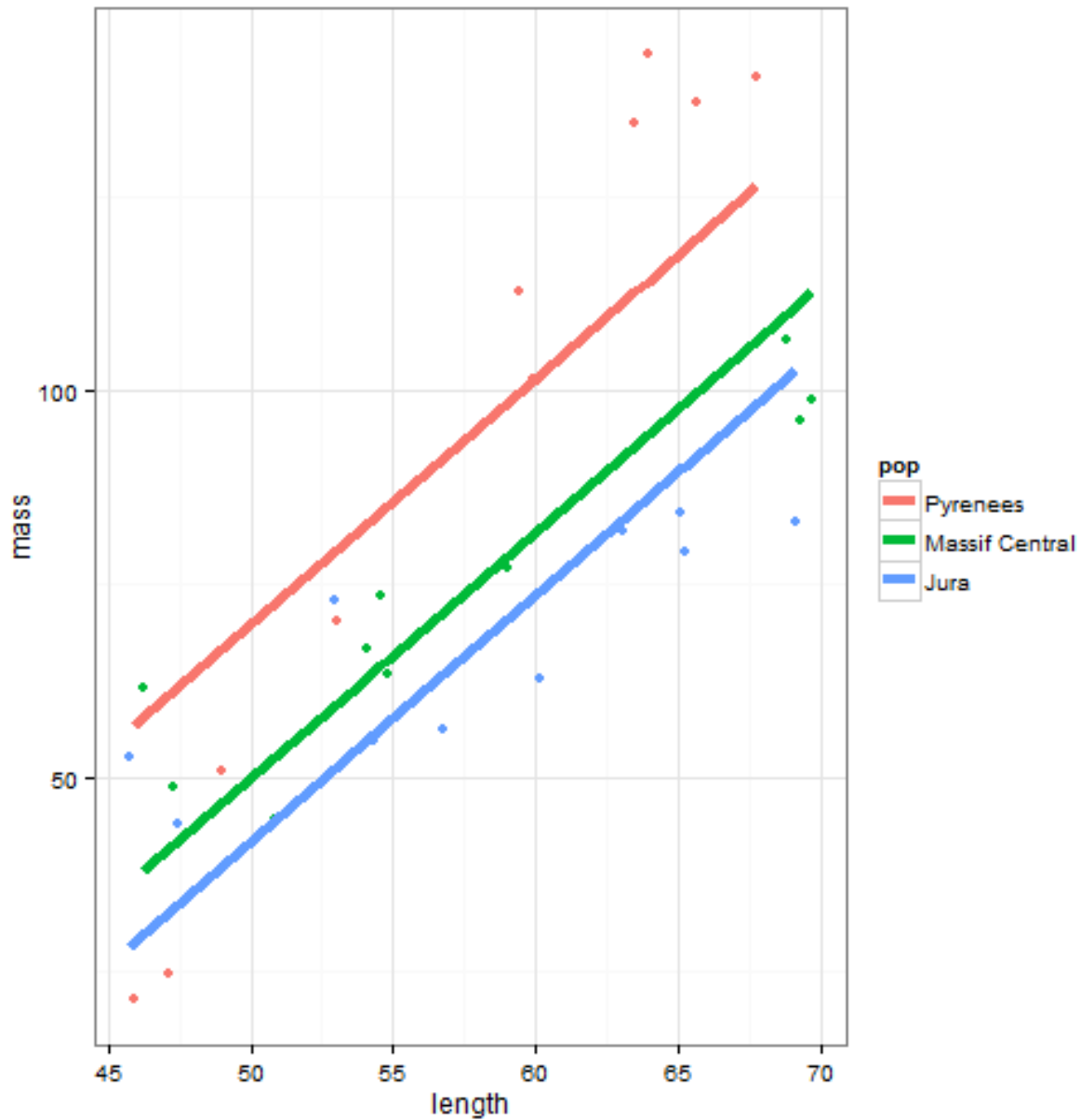
Visually, it would look like:

```
library(ggplot2)
```

```
data=data.frame(mass=mass,length=length,pop=pop,
               pred=predict(mod.csl))
```

```
plot.csl = ggplot(data, aes(x=length, y=mass,col=pop)) + geom_point() +
  geom_line(aes(x=length, y=pred),size=1.5)+
  theme_bw()
```

plot.csl



## Different slopes - different intercepts model

```
mod.dsl=lm(mass ~ pop * length)
```

Visually, it would look like:

```
library(ggplot2)

data=data.frame(mass=mass,length=length,pop=pop,
                pred=predict(mod.dsl))

plot.dsl = ggplot(data, aes(x=length, y=mass,col=pop)) + geom_point() +
  geom_line(aes(x=length, y=pred),size=1.5)+
  theme_bw()
```

```
plot.dsl
```

