

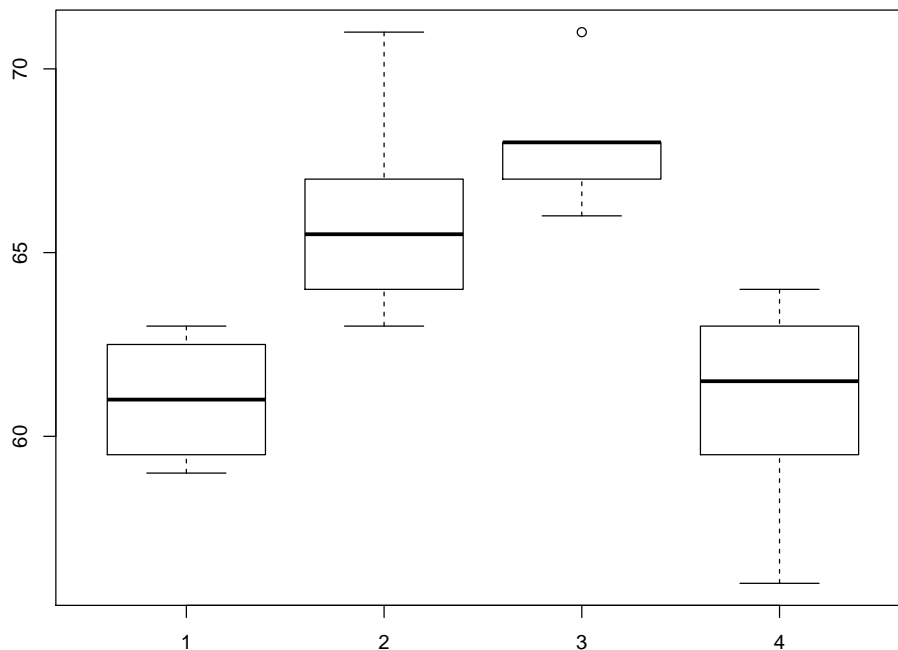
Solution to Series 1

1. Read in the data:

```
> blood <-c(62,60,63,59,63,67,71,64,65,66,68,66,71,67,68,68,56,62,60,61,63,64,63,59)
> tr <- c(1,1,1,1,2,2,2,2,2,2,3,3,3,3,3,3,4,4,4,4,4,4,4,4)
> b.data <- data.frame(cbind(blood,tr))
> b.data$tr <- as.factor(b.data$tr)
```

a) Plot the data and compute overall mean and group means.

```
> plot(b.data$tr,b.data$blood)
```



We see that the coagulation times vary a lot between different diets whereas the variation within a diet group is quite small.

In addition compute the overall mean and the group means. Do this by hand using a calculator.

overall mean = 64

treatment	group means
A	61
B	66
C	68
D	61

b) Compute the group sample variances s_i^2 and the pooled estimate of variance MS_{res} . Do this also by hand. For MS_{res} compute first SS_{res} .

$SS_{res}=112$ $MS_{res}=5.6$

treatment	s_i^2
A	3.333
B	8
C	2.8
D	6.85

- c) Compute MS_{treat} and compare it with MS_{res} (without formal test). Compute MS_{treat} by hand. First compute SS_{treat} and with it MS_{treat} .

$$SS_{treat}=228 \quad MS_{treat}=76$$

We see that the estimated variance between groups is substantially bigger than the estimated variance within groups. This could indicate an effect of diet on blood coagulation time.

- d) Construct an analysis of variance table. Use the R-function `aov(...)`.

```
> summary(fit.blood)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
b.data\$str	3	228	76.0	13.57	4.66e-05 ***
Residuals	20	112	5.6		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Compare your by hand computed SS_{res} , SS_{treat} , MS_{res} and MS_{treat} with the output of `summary(fit.blood)`.

- e) Does the diet have a significant effect on coagulation time? From the output above we see that the diet has a significant effect on blood coagulation time.

F-value = 13.57

P-value = 4.65847098469477e-05

2. a) Identify the parameters in a one-way analysis of variance model. The parameters in the one-way analysis of variance model $Y_{ij} = \mu + A_i + \epsilon_{ij}$ with $\sum A_i = 0$ are:
 $\mu = 7.2$, $A_1 = -2.1$, $A_2 = -0.9$, $A_3 = 0.7$, $A_4 = 2.3$ and $\sigma^2 = 2.8^2$.
- b) There are 25 randomly selected staff members for each group. What are $E(MS_{res})$ and $E(MS_{treat})$?
 What do you conclude? $E(MS_{res}) = \sigma^2 = 7.84$
 $E(MS_{treat}) = \sigma^2 + 25 \cdot \frac{\sum_{i=1}^4 A_i^2}{3} = 7.84 + 25 \cdot 3.666 = 99.5066$

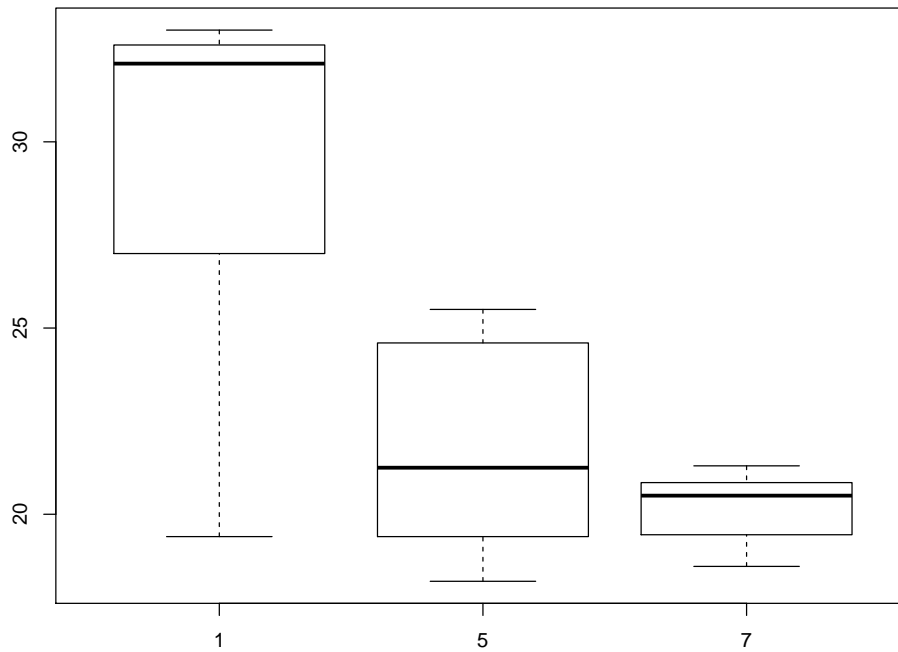
Therefore we can conclude that the duration of employment has an effect on the job satisfaction. Because $E(MS_{treat})$ is way larger than $E(MS_{res})$.

3. Read in the data:

```
> N2 <- c(19.4,32.6,27,32.1,33,18.2,24.6,25.5,19.4,21.7,20.8,20.7,
         21,20.5,18.8,18.6,20.1,21.3)
> strain <- c(1,1,1,1,1,5,5,5,5,5,5,7,7,7,7,7,7)
> r.data <- data.frame(cbind(N2,strain))
> r.data$strain <- as.factor(r.data$strain)
```

- a) Plot the data.

```
> plot(r.data$strain,r.data$N2)
```



The variance between strains looks larger than the variance within strains. This could be an indicator for a significant difference of nitrogen contents for different Rhizobium strains.

b) Carry out an analysis of variance.

```
> fit.n2 <- aov(r.data$N2 ~ r.data$strain)
> summary(fit.n2)
```

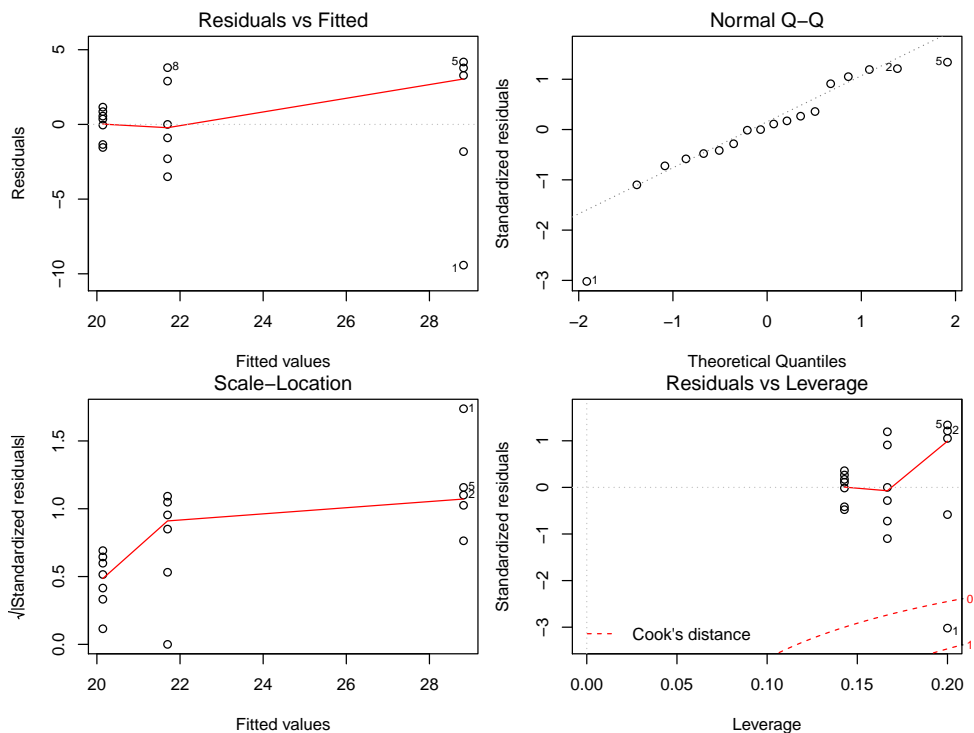
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
r.data\$strain	2	236.6	118.28	9.723	0.00196 **
Residuals	15	182.5	12.16		

Signif. codes:
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The F-value equals 9.72. By looking at the P-value we see that there are significant differences in nitrogen contents for different strains of Rhizobium.

c) Check the model assumptions.

```
> par(mfrow=c(2,2))
> plot(fit.n2)
```



From the diagnostic plots we see that there exists an outlier. On the basis of the plots, observation number 1 can be clearly identified as an outlier. After removing the outlier we repeat the analysis.

```
> rr.data <- r.data[-1,]
> fit.n2mod <- aov(rr.data$N2~rr.data$strain)
> summary(fit.n2mod)
```

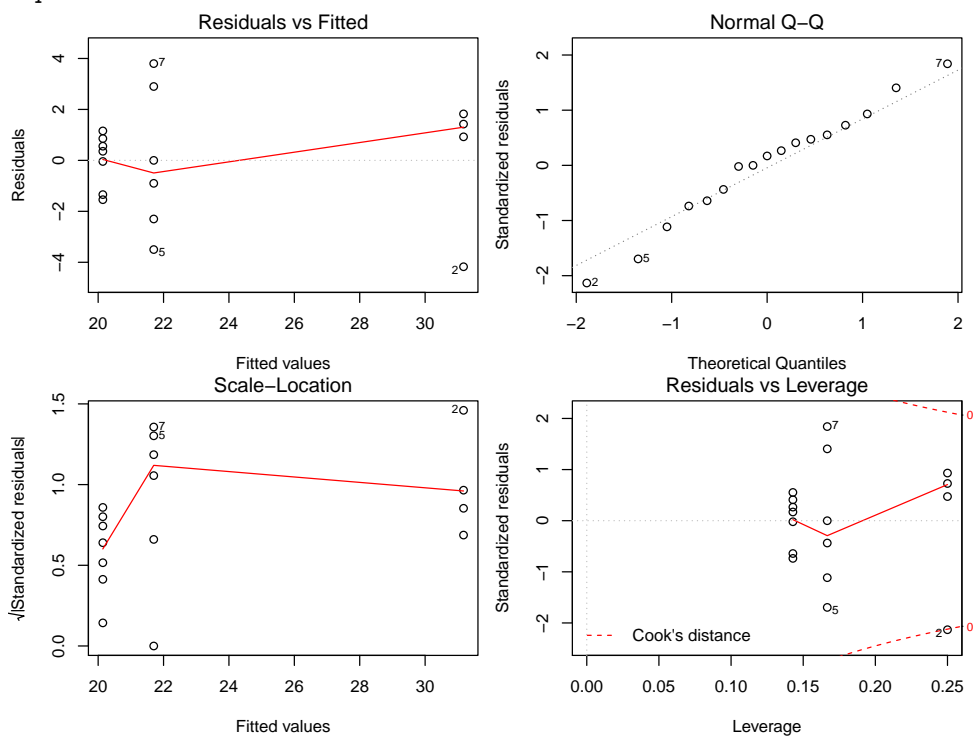
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
rr.data\$strain	2	333.2	166.60	32.6	5.39e-06 ***
Residuals	14	71.5	5.11		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> par(mfrow=c(2,2))
```

```
> plot(fit.n2mod)
```



We see that now the model assumptions are fulfilled.