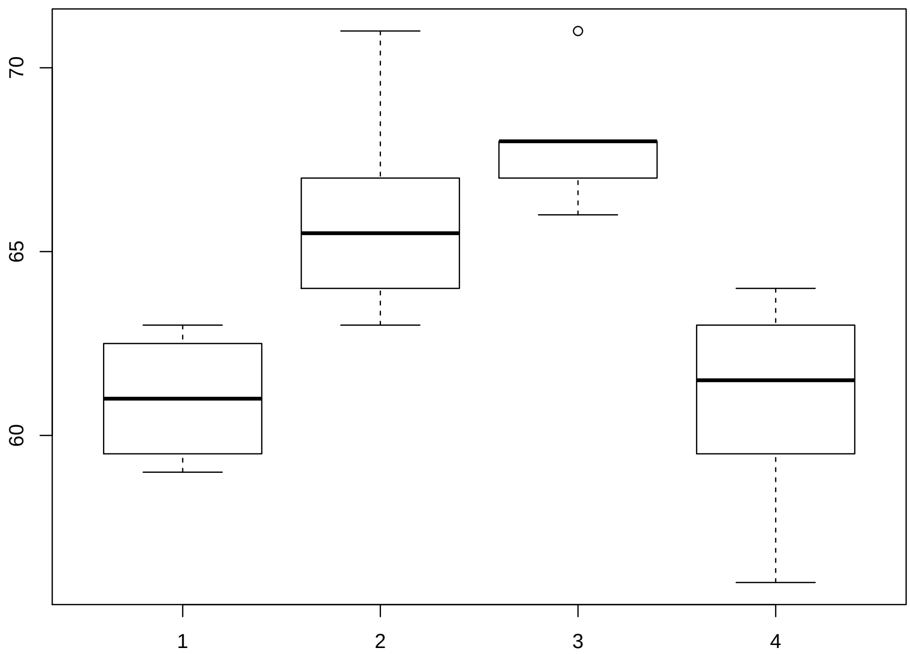
Solution to Series 1

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 MS_{treat}=76

We see that the estimated variance between groups is substantially bigger then 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$tr    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 an 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? $E(MS_{res}) = \sigma^2 = 7.84$
$E(MS_{treat}) = \sigma^2 + 25 \cdot \frac{\sum_{i=1}^{4} A_i^2}{3} = 7.84 + 25 \cdot 3.666 = 99.5066$

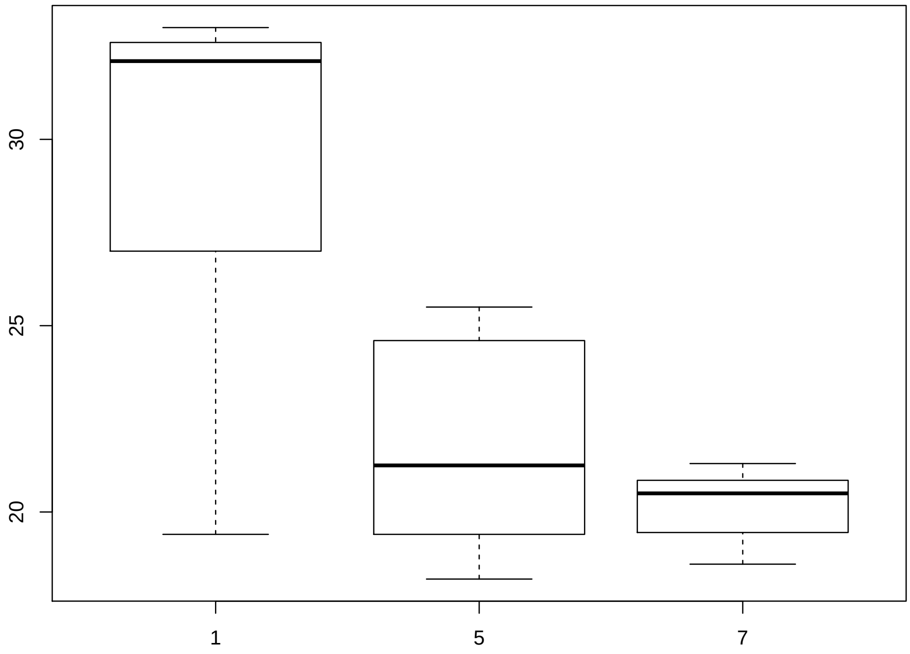
Therefore we can conclude that the duration of employment has an effect on the job satisfaction. Because $E(MS_{treat})$ is way larger then $E(MS_{res})$.

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(1,1,1,1,1,5,5,5,5,5,5,5,7,7,7,7,7,7,7)
> 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 then 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.

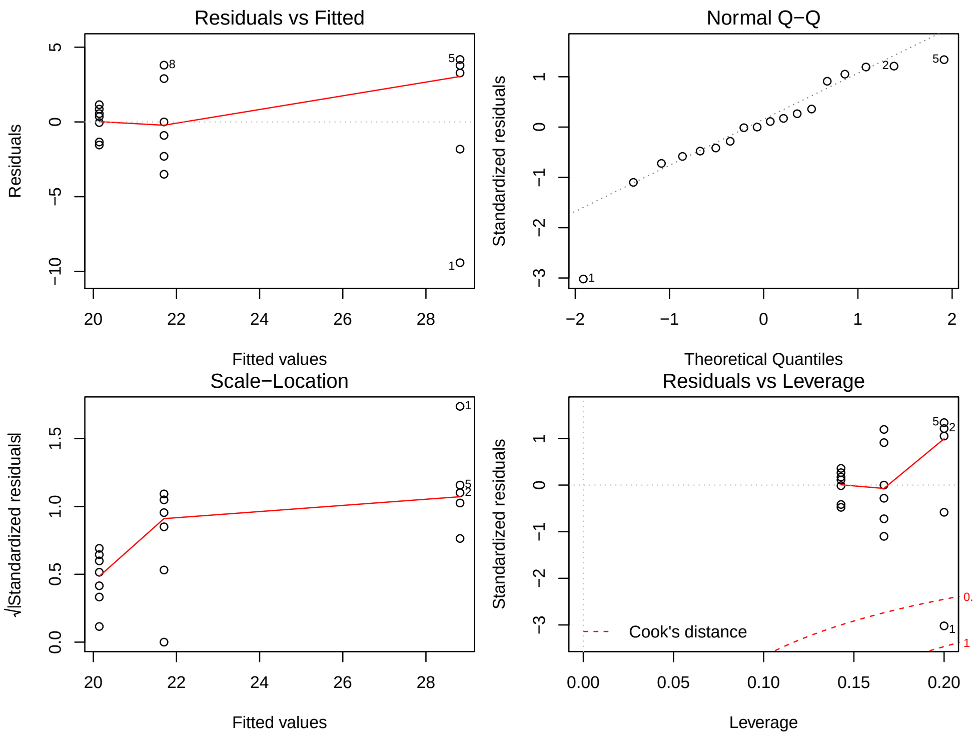
```
> fit.n2 <- aov(r.data$N2 ~ r.data$strain)
> summary(fit.n2)
```

```
              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:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

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)
```

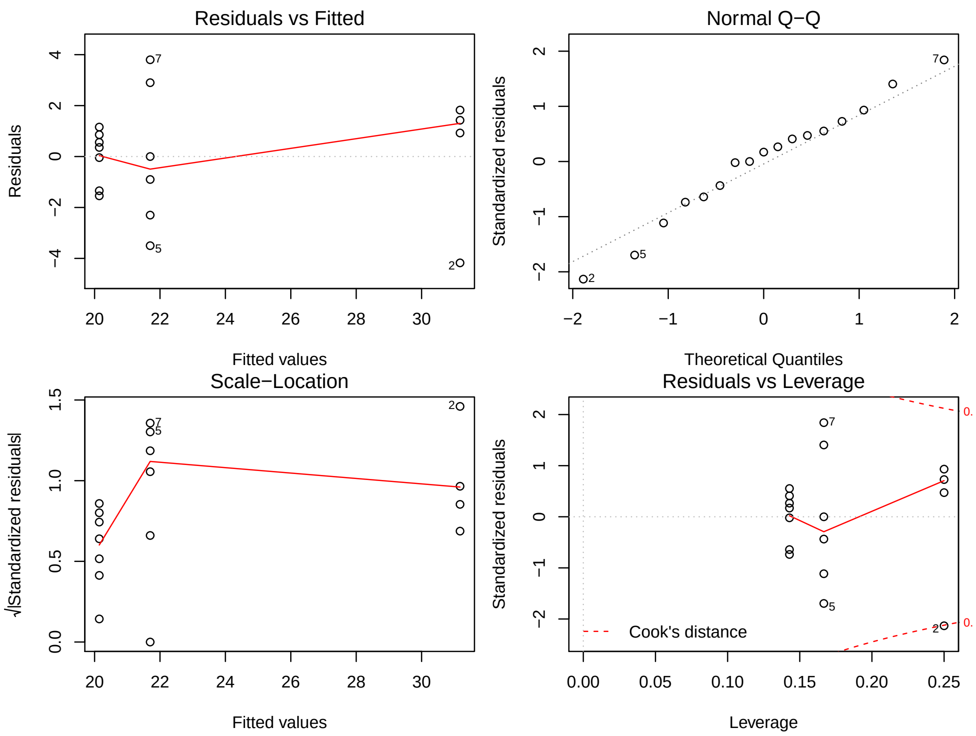


From the diagnostic plots we see that there exists an outlier. On the basis of the plots, observation number 1 can be clearly identified as an outlier. After removing the outlier we repeat the analysis.

```
> 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.