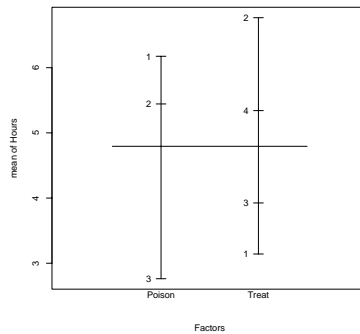


Linear Models: Two-way analysis of variance

The survival data set records survival times for 48 animals, 4 subjected to each combination of one of 3 poisons and one of 4 treatments (antidotes).

```
> survival
      Hours Poison Treat
1       3.1      1     1
2       4.5      1     1
3       4.6      1     1
...
47      3.1      3     4
48      3.3      3     4
```

A simple display of the mean response for each level of each factor is obtained by `plot(survival)`:



We fit a factorial model with interactions:

```
> fit<-lm(Hours~Poison*Treat,survival)
> anova(fit)
Analysis of Variance Table
Response: Hours
          Df Sum Sq Mean Sq F value    Pr(>F)
Poison      2  103.301   51.651  23.2217 3.331e-07 ***
Treat       3   92.121   30.707  13.8056 3.777e-06 ***
Poison:Treat 6   25.014    4.169   1.8743  0.1123
Residuals   36   80.072    2.224
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This is an example of the ANOVA table on slide 58, except that the Cells and Total rows are omitted from the **R** output.

There is no significant evidence of any interaction. Thus we might repeat the analysis, omitting the interaction altogether:

```
> fit2<-lm(Hours~Poison+Treat,survival)
```

```
> anova(fit2)
Analysis of Variance Table
Response: Hours

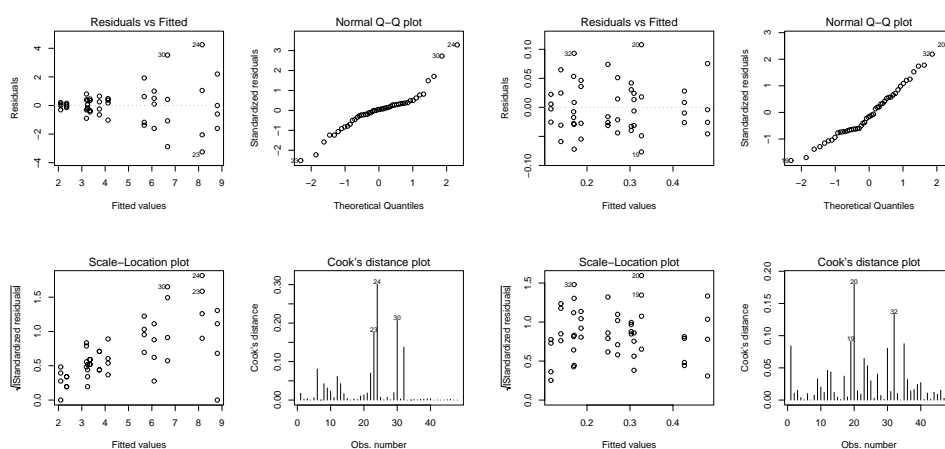
      Df Sum Sq Mean Sq F value    Pr(>F)
Poison   2 103.301   51.651  20.643 5.704e-07 ***
Treat    3  92.121   30.707  12.273 6.697e-06 ***
Residuals 42 105.086    2.502
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

and there is little change.

We should make a diagnostic plot to check all is well:

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



and see (on the left) a very pronounced pattern – the sizes of the residuals increase with fitted value. We might try transforming the response: taking reciprocals changes times into rates:

```
> fit3<-lm(1/Hours~Poison*Treat,survival)
> anova(fit3)
Analysis of Variance Table
Response: 1/Hours

      Df Sum Sq Mean Sq F value    Pr(>F)
Poison   2  0.34877   0.17439  72.6347 2.310e-13 ***
Treat    3  0.20414   0.06805  28.3431 1.376e-09 ***
Poison:Treat  6  0.01571   0.00262   1.0904  0.3867
Residuals  36  0.08643   0.00240
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> plot(fit3)
```

There is still no evidence of interaction, and this time the plot (on the right, above) seems fine.