19 Two-way ANOVA test

19.1 Two way layout: the Randomized Block design (P.629-649)

An experiment is designed to compare the effects of three different diets (B_1, B_2, B_3, say) to dog's weight. Assume that 12 dogs are available for this experiment.

Method 1. 12 dogs are randomly divided into three groups. In group i ($i = 1, 2, 3$), 4 dogs are given the same diet B_i ($i = 1, 2, 3$). After a period of time, the gain y_{ij} for $i = 1, 2, 3$, and $j = 1, 2, 3, 4$, in weight is collected. Then the one-way ANOVA test can be used to compare the different diets.

Method 1 involves a single *factor*, namely diet, which has three *levels* B_1, B_2, B_3 and is known as *one-way layout*. As all dogs are randomized assigned to diet groups, the experiment has called a *completely randomized* (CR) design.

Alternatively, the experiment may also consider the effects of other factors (like initial weight, age, etc).

Method 2. 12 dogs are divided into 4 groups (A_1, A_2, A_3, A_4, say) (of 3 dogs each), according to their weight at the beginning of the experiment, and then 3 dogs in each group A_i are randomly given 3 different diets B_1, B_2, B_3, respectively. After a period of time, the gain y_{ij} for $i = 1, 2, 3, 4$ and $j = 1, 2, 3$, in weight is collected.

Method 2 considers two factors: diet and dog's initial weight in a *two-way layout*. As only dogs within each block are randomized assigned to diet groups, the experiment has a *randomized block* (RB) design.

For $c = 2$ treatments with single replicate, we have *two-independent* samples and *matched-pair* (block of 2; Proof in Tutorial 8 Q3(c)) sample design generalized from one- and two-way ANOVA respectively.

Example: Twelve dogs are used to compare the effects of three different diets to dog's weight. An example of two-way design is given as follow:

	y_ij	Diet B_1	B_2	B_3
weight	A_1(2kg)	7.0	14.0	8.5
	A_2(4kg)	16.0	14.5	16.5
	A_3(6kg)	10.5	15.0	9.5
	A_4(8kg)	13.5	21.0	13.5

Note that there are 4 dogs for same diet. We may consider the effect of the initial weight to the gain in weight in the design.

In the two-way ANOVA, the categories along the top of the table are "*treatments*" and the categories along the side are "*blocks*". Next is a general case of a single replicate two-way data.

	Tr 1	Tr 2	...	Tr c
Block 1	y_11	y_12	...	y_1c
Block 2	y_21	y_22	...	y_2c
.	.	.		.
.	.	.		.
.	.	.		.
Block r	y_r1	y_r2	...	y_rc

Note: there are only rc observations in a c treatments and r blocks design, which means that in each block there are only one observation for each treatment.

In practice, to make statistical tests more accurate, we may give m observations for each treatment in each block, and then we get the multi-

replicates two-way data as follows:

Multi-replicates two-way data

```
              Tr 1    Tr 2     ... Tr c

              y_111   y_121    ... y_1c1
 Block 1      y_112   y_122    ... y_2c2
               .       .          .
               .       .          .
               .       .          .
              y_11m   y_12m    ... y_1cm

Block 2, ...., Block r-1

              Tr 1    Tr 2     ... Tr c

              y_r11   y_r21    ... y_rc1
 Block r      y_r12   y_r22    ... y_rc2
               .       .          .
               .       .          .
               .       .          .
              y_r1m   y_r2m    ... y_rcm
```

Now there are rcm observations for this design. We sometimes write this as

$$\{y_{ijk} : i = 1, ..., r; j = 1, ..., c; k = 1, ..., m\},$$

or just $\{y_{ijk}\}_{r\times c\times m}$ for short.

We first discuss the single replicate ($m = 1$) two-way data. Multi-replicates two-way data will be discussed later.

19.2 Additive decomposition

An *additive decomposition* of a two-way data $\{y_{ij}\}$ is given by

$$y_{ij} = \underbrace{\mu + \alpha_i + \beta_j}_{\mu_{ij}} + \epsilon_{ij}, \tag{1}$$

where

y_{ij} : the observation on treatment j in Block i;

μ: the overall effect;

α_i: the block effect (row effect);

β_j: the treatment effect (column effect);

ϵ_{ij}: the residual.

As compare to one-way data, $y_{ij} = \mu_j + \epsilon_{ij} \Rightarrow \mu_j = \mu + \beta_j;\ \alpha_i = 0.$

As well-known. the additive model:

$$E(Y_{ij}) = \mu_{ij} = \mu + \alpha_i + \beta_j, \quad \sum_{i=1}^{r} \alpha_i = \sum_{j=1}^{c} \beta_j = 0, \tag{2}$$

is appropriate if the residuals $\{\epsilon_{ij}\}$ in (1) have "no apparent patten". We call $\hat{y}_{ij} = \mu_{ij}$ the fitted value.

The model implies that $Y_{ij} \sim \mathcal{N}(\mu_{ij}, \sigma^2)$ and $Y_{ij} \sim \mathcal{N}(\mu, \sigma^2)$ under H_0 of no treatment and block effects, i.e. $\alpha_i = \beta_j = 0$.

We can either use *means or median* to find appropriate values for the effects (and hence fitted values).

The mean is appropriate for data in which there are no outliers. However, the median may be used to ensure that the analysis is "robust", that is, that single errors in recording any particular value will not result in markedly different fitted values.

19.3 Fitting using means

Write $\bar{y}_{i.}$ for the average of all observations in Block i:

$$\bar{y}_{i.} = \frac{1}{c}\sum_{j=1}^{c} y_{ij}, \ \ i = 1, \ldots, r;$$

$\bar{y}_{.j}$ for the average of all observations in treatment j:

$$\bar{y}_{.j} = \frac{1}{r}\sum_{i=1}^{r} y_{ij}, \ \ j = 1, \ldots, c;$$

$\bar{y}$ for the mean of all rs observations,

$$\hat{\mu} = \bar{y} = \frac{1}{rc}\sum_{i=1}^{r}\sum_{j=1}^{c} y_{ij} = \frac{1}{r}\sum_{i=1}^{r}\bar{y}_{i.} = \frac{1}{c}\sum_{j=1}^{c}\bar{y}_{.j}.$$

The common effect is obtained as $\bar{y}$, which is the mean of $\bar{y}_{i.}$ or $\bar{y}_{.j}$.

The row and column effects are obtained by subtracting the common effect from the row means ($\bar{y}_{i.}$) and the column means ($\bar{y}_{j}$), respectively. That is,

1. the block (row) effect: $\hat{\alpha}_i = \bar{y}_{i.} - \bar{y}$;
2. the treatment (column) effect: $\hat{\beta}_j = \bar{y}_{.j} - \bar{y}$.

Note that α_i and β_j measure relative (to mean) effects. Hence

$$\sum_{i=1}^{r}(\bar{y}_{i.} - \bar{y}) = \sum_{j=1}^{c}(\bar{y}_{.j} - \bar{y}) = 0 \Rightarrow \sum_{i=1}^{r}\alpha_i = \sum_{j=1}^{c}\beta_j = 0.$$

The residuals are:

$$\begin{aligned}\epsilon_{ij} &= y_{ij} - \hat{y}_{ij} = y_{ij} - \hat{\mu} - \hat{\alpha}_i - \hat{\beta}_j = y_{ij} - \bar{y} - (\bar{y}_{i.} - \bar{y}) - (\bar{y}_{.j} - \bar{y}) \\ &= y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}.\end{aligned}$$

as compare to $\epsilon_{ij} = y_{ij} - \hat{y}_{ij} = y_{ij} - \bar{y}_{j}$ in one-way data.

Example: (`penicillin` data) The data give the yields of penicillin using five different blends and four different methods in an experiment designed to primarily compare the methods.

	Method A	Method B	Method C	Method D	Row mean
	y_{i1}	y_{i2}	y_{i3}	y_{i4}	$\bar{y}_{i.}$
Blend 1	89	88	97	94	92
Blend 2	84	77	92	79	83
Blend 3	81	87	87	85	85
Blend 4	87	92	89	84	88
Blend 5	79	81	80	88	82
Col mean					
$\bar{y}_{.j}$	84	85	89	86	$\bar{y} =$ 86

Effects:

	Method A	Method B	Method C	Method D	Row effect
	ϵ_{i1}	ϵ_{i2}	ϵ_{i3}	ϵ_{i4}	$\alpha_i = \bar{y}_{i.} - \bar{y}$
Blend 1	-1	-3	2	2	6
Blend 2	3	-5	6	-4	-3
Blend 3	-2	3	-1	0	-1
Blend 4	1	5	-2	-4	2
Blend 5	-1	0	-5	6	-4
Col effect					
$\beta_j = \bar{y}_{.j} - \bar{y}$	-2	-1	3	0	$\mu =$ 86

Check $y_{ij} = \mu + \alpha_i + \beta_j + \epsilon_{ij}$. The additive decomposition by R is:

```
> pen=read.csv("data/penicillin.csv")
> attach(pen)
> pen
  Method.A Method.B Method.C Method.D
1       89       88       97       94
2       84       77       92       79
3       81       87       87       85
4       87       92       89       84
5       79       81       80       88
> r=5
```

```
> c=4
> penv=as.matrix(pen) #for matrix format; create vector
> penv=as.vector(penv) #for matrix format; create vector
> penv
 [1] 89 84 81 87 79 88 77 87 92 81 97 92 87 89 80 94 79 85 84 88
> pen=matrix(penv,r,c,byrow=F) #for vector format; create matrix
> mean=mean(penv)   #calculate overall mean
> mean
[1] 86
> mean.tr=apply(pen,2,mean)  #calculate col. mean
> mean.tr
Method.A Method.B Method.C Method.D
      84       85       89       86
> mean.bl=apply(pen,1,mean)   #calculate row mean
> mean.bl
 1  2  3  4  5
92 83 85 88 82
> mean.m=matrix(mean,r,c)  #overall mean, mu=bar y
> mean.m
     [,1] [,2] [,3] [,4]
[1,]   86   86   86   86
[2,]   86   86   86   86
[3,]   86   86   86   86
[4,]   86   86   86   86
[5,]   86   86   86   86
> mean.trm=matrix(mean.tr,r,c,byrow=T)  #col. mean, bar y_.j
> mean.trm
     [,1] [,2] [,3] [,4]
[1,]   84   85   89   86
[2,]   84   85   89   86
[3,]   84   85   89   86
[4,]   84   85   89   86
[5,]   84   85   89   86
> mean.blm=matrix(mean.bl,r,c,byrow=F)  #row mean, bar y_i.
> mean.blm
     [,1] [,2] [,3] [,4]
```

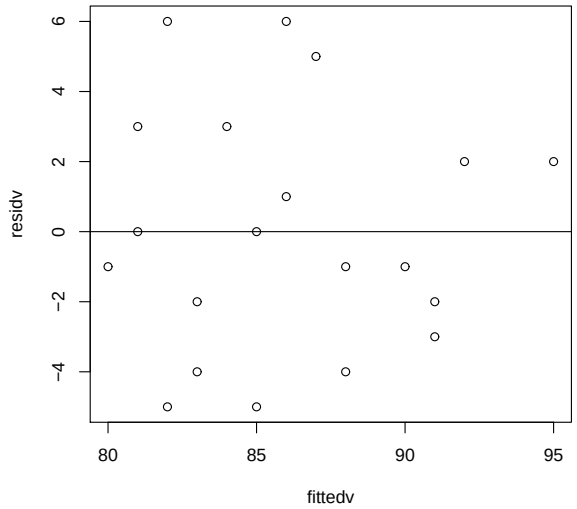
```
[1,]   92   92   92   92
[2,]   83   83   83   83
[3,]   85   85   85   85
[4,]   88   88   88   88
[5,]   82   82   82   82
> tr.effect=mean.trm-mean.m  #treat eff., beta_j=bar y_.j-bar y
> tr.effect
     [,1] [,2] [,3] [,4]
[1,]   -2   -1    3    0
[2,]   -2   -1    3    0
[3,]   -2   -1    3    0
[4,]   -2   -1    3    0
[5,]   -2   -1    3    0
> bl.effect=mean.blm-mean.m  #block eff., alpha_i=bar y_i.-bar y
> bl.effect
     [,1] [,2] [,3] [,4]
[1,]    6    6    6    6
[2,]   -3   -3   -3   -3
[3,]   -1   -1   -1   -1
[4,]    2    2    2    2
[5,]   -4   -4   -4   -4
> fitted=mean.m+tr.effect+bl.effect  #hat y_ij=mu+alpha_i+beta_j
> fitted
  Method.A Method.B Method.C Method.D
1       90       91       95       92
2       81       82       86       83
3       83       84       88       85
4       86       87       91       88
5       80       81       85       82
> resid=pen-fitted  #resid., e_ij=y_ij-hat y_ij
> resid
  Method.A Method.B Method.C Method.D
1       -1       -3        2        2
2        3       -5        6       -4
3       -2        3       -1        0
4        1        5       -2       -4
```

```
5       -1        0       -5        6
> fittedv=as.matrix(fitted)  #change fitted from matrix to vector
> fittedv=as.vector(fittedv)
> residv=as.matrix(resid)  #change resid. from matrix to vector
> residv=as.vector(residv)
> plot(fittedv,residv)
> abline(h=0)
```

The (i, j)-th fitted values is given by

$$\hat{y}_{ij} = \mu + \alpha_i + \beta_j = y_{ij} - \epsilon_{ij}.$$

We plot the residuals against the fitted values, to check for any pattern, same as regression model.



As the plot shows no particular pattern, the model is adequate.

20 Two-way ANOVA test II

Suppose we have two-way data:

	Tr 1	Tr 2	...	Tr c
Block 1	y_11	y_12	...	y_1c
Block 2	y_21	y_22	...	y_2c
.	.	.		.
.	.	.		.
.	.	.		.
Block r	y_r1	y_r2	...	y_rc

We want to test if

there are no differences between treatments ($\beta_j = 0$), and if
there are no differences between blocks ($\alpha_i = 0$).

It is equivalent to say that we want to test all

$$y_{ij} = \mu + \epsilon_{ij}$$

are from the *same* population with the same mean μ and variance σ^2.

20.1 ANOVA for two-way data

Let Y_{ij} denote the random variables that generate the observed value y_{ij} for $i = 1, 2, .., r$ and $j = 1, 2, ..., c$. The model for the two-way data is given by

$$y_{ij} = \mu + \alpha_i + \beta_j + \epsilon_{ij}, \tag{1}$$

and $\epsilon_{ij} = y_{ij} - \hat{y}_{ij} = y_{ij} - \mu - \alpha_i - \beta_j = y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}$.

The *analysis of variance* for a two-way data proceeds by partitioning an observation as

$$\begin{aligned} y_{ij} - \bar{y} &= (\bar{y}_{i.} - \bar{y}) + (\bar{y}_{.j} - \bar{y}) + (y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}) \\ &= \text{Block effect+Treatment effect+ Residual.} \end{aligned}$$

Some calculations show that

$$\underbrace{\sum_{i=1}^{r}\sum_{j=1}^{c}(y_{ij} - \bar{y})^2}_{SST_o} = \underbrace{c\sum_{i=1}^{r}(\bar{y}_{i.} - \bar{y})^2}_{SSB} + \underbrace{r\sum_{j=1}^{c}(\bar{y}_{.j} - \bar{y})^2}_{SST} + \underbrace{\sum_{i=1}^{r}\sum_{j=1}^{c}\epsilon_{ij}^2}_{SSR}$$

$$\underbrace{\sum_{i=1}^{r}\sum_{j=1}^{c}y_{ij}^2 - rc\,\bar{y}^2}_{SST_o} = \underbrace{c\sum_{i=1}^{r}\bar{y}_{i.}^2 - rc\,\bar{y}^2}_{SSB} + \underbrace{r\sum_{j=1}^{c}\bar{y}_{.j}^2 - rc\,\bar{y}^2}_{SST} + \underbrace{\sum_{i=1}^{r}\sum_{j=1}^{c}\epsilon_{ij}^2}_{SSR}$$

where the *correction for the mean* is

$$CM = rc(\bar{y})^2 = \frac{1}{rc}(\sum_{i=1}^{r}\sum_{j=1}^{c}y_{ij})^2.$$

Note that as it is difficult to calculate ϵ_{ij}, SSR is calculated using

$$SSR = SST_o - SSB - SST$$

with df=$rc - r - c + 1 = (r-1)(c-1)$ since $\epsilon_{ij} = y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}$.

As in ANOVA for one-way,

the larger the SST, the stronger will be the evidence to indicate a difference between treatments.

the larger the SSB, the stronger will be the evidence to indicate a difference between blocks.

The calculations are usually displayed in a *two-way ANOVA table*.

Two way ANOVA table for randomized block design

Source	**df**	**SS**	**MS**	**F**
Treatments	$c-1$	$SST = r\sum_{j=1}^{c}\overline{y}_{\cdot j}^2 - n\overline{y}^2$	$MST = \frac{SST}{c-1}$	$F_{t0} = \frac{MST}{MSR}$
Blocks	$r-1$	$SSB = c\sum_{i=1}^{r}\overline{y}_{i\cdot}^2 - n\overline{y}^2$	$MSB = \frac{SSB}{r-1}$	$F_{b0} = \frac{MSB}{MSR}$
Residuals	$(r-1)(c-1)$	$SSR = SST_o - SST - SSB$	$MSR = \frac{SSR}{(r-1)(c-1)}$	
Total	$n-1$	$SST_o = \sum_{i=1}^{r}\sum_{j=1}^{c} y_{ij}^2 - n\overline{y}^2$		

$\overline{y}_{i\cdot} = \frac{1}{c}\sum_{j=1}^{c} y_{ij}$, $\overline{y}_{\cdot j} = \frac{1}{r}\sum_{i=1}^{r} y_{ij}$, $n = rc$ and $\overline{y} = \frac{1}{n}\sum_{i=1}^{r}\sum_{j=1}^{c} y_{ij}$.

Note: Now SSR may be smaller than the $SSR = SST_0 - SST$ in one-way ANOVA if the blocking is effective. As a result, part of the SSR can be explained by the block effect giving a smaller SSR and hence a sharper detected treatment effect.

20.2 Two-way ANOVA test

The two-way ANOVA tests for treatment and/or block effects in five-steps are as follow:

1. **Hypothesis:** We test if all y_{ij} are from the same population. Equivalently, we test two hypotheses:

   For treatment effects:

   $$\begin{aligned} H_0: &\quad \beta_1 = \beta_2 = ... = \beta_c = 0 \quad \text{vs} \\ H_1: &\quad \text{Not all } \beta_j \text{ equal;} \end{aligned}$$

   For block effects:

   $$\begin{aligned} H_0: &\quad \alpha_1 = \alpha_2 = ... = \alpha_r = 0 \quad \text{vs} \\ H_1: &\quad \text{Not all } \alpha_i \text{ equal.} \end{aligned}$$

2. **Test statistic:** For treatment and block effects respectively:

   $$\begin{aligned} f_{t0} &= \frac{SST/(c-1)}{SSR/(r-1)(c-1)} \sim F_{c-1,(r-1)(c-1)}; \\ f_{b0} &= \frac{SSB/(r-1)}{SSR/(r-1)(c-1)} \sim F_{r-1,(r-1)(c-1)}. \end{aligned}$$

3. **Assumption:** $Y_{ij} \sim \mathcal{N}(\mu_{ij}, \sigma^2)$ and Y_{ij} are independent.

4. ***P*-value:** For treatment and block effects respectively:

   $$\begin{aligned} p\text{-value} &= \Pr(F_{c-1,(r-1)(c-1)} \geq f_{t0}); \\ p\text{-value} &= \Pr(F_{r-1,(r-1)(c-1)} \geq f_{b0}). \end{aligned}$$

5. **Decision:** reject H_0 if p-value $< \alpha$.

Example: (`penicillin` data)

	Method A	Method B	Method C	Method D	Total
Blend 1	89	88	97	94	368
Blend 2	84	77	92	79	332
Blend 3	81	87	87	85	340
Blend 4	87	92	89	84	352
Blend 5	79	81	80	88	328
Total	420	425	445	430	1720

$$\sum_{i=1}^{r}\sum_{j=1}^{c} y_{ij}^2 = 148480.$$

Is there evidence of differences in the yields of penicillin among the four methods?

Solution: The two-way ANOVA test for treatment effects is

1. **Hypothesis:**

$$\begin{aligned} H_0: &\quad \beta_1 = \beta_2 = \beta_3 = \beta_4 = 0 \quad \text{vs} \\ H_1: &\quad \text{Not all } \beta_j \text{ equal;} \end{aligned}$$

2. **Test statistic:**

$$\begin{aligned} CM &= rc\bar{y}^2 = \frac{1}{rc}\Big(\sum_{i=1}^{r}\sum_{j=1}^{c} y_{ij}\Big)^2 = \frac{1720^2}{4(5)} = 147920 \\ SST_o &= \sum_{i=1}^{r}\sum_{j=1}^{c} y_{ij}^2 - rc\bar{y}^2 = 148480 - 147920 = 560 \\ SSB &= c\sum_{i=1}^{r}(\bar{y}_{i.})^2 - rc\bar{y}^2 \\ &= \frac{4}{4^2}(368^2 + \cdots + 328^2) - 147920 = 264 \end{aligned}$$

$$\begin{aligned} SST &= r\sum_{j=1}^{c}(\bar{y}_{.j})^2 - N\bar{y}^2 \\ &= \frac{5}{5^2}(420^2 + \cdots + 430^2) - 147920 = 70 \\ SSR &= SST_o - SSB - SST = 560 - 264 - 70 = 226 \\ f_{t0} &= \frac{SST/(c-1)}{SSR/(r-1)(c-1)} = \frac{70/3}{226/12} = 1.24 \\ f_{b0} &= \frac{SSB/(r-1)}{SSR/(r-1)(c-1)} = \frac{264/4}{226/12} = 3.5 \end{aligned}$$

3. **Assumption:** $Y_{ij} \sim \mathcal{N}(\mu_{ij}, \sigma^2)$ and Y_{ij} are independent.

4. ***P*-value:** For treatment effect:

   p-value $= \Pr(F_{3,12} \geq 1.24) > 0.1$ (from table, 0.3383147 from R).

   Note that the p-value for block effect is

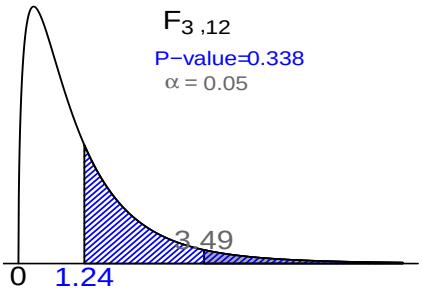
   p-value $= \Pr(F_{4,12} \geq 3.5) \in (0.025, 0.5)$ (from table, 0.04089467 from R).

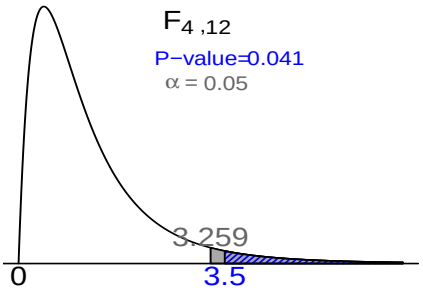
5. **Decision:** Since the p-value for treatment effects > 0.05. The data is consistent with H_0 for treatment effects, that is, there are no evidence of differences in the yields of penicillin among the four methods.

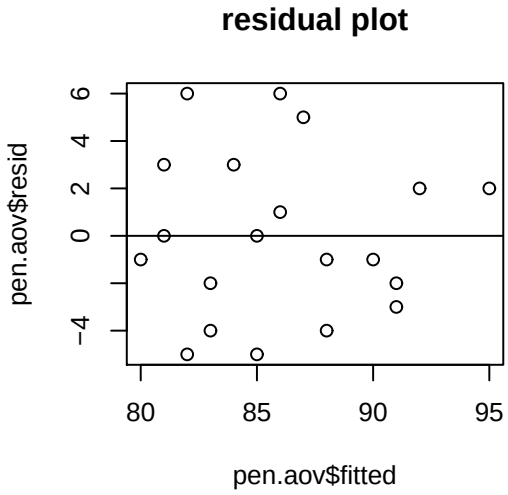
   Moreover, the data shows reasonably strong evidence against H_0 for block effects, that is, there are reasonably strong evidence of differences in the yields of penicillin among the five blends.

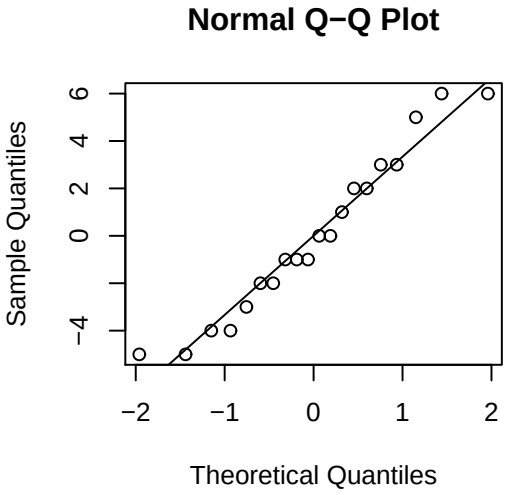
ANOVA table

Source	df	SS	MS	F	p-value
Treatments (Methods)	3	70	$\frac{70}{3} = 23.3$	$\frac{23.3}{18.8} = 1.24$	0.3383
Blocks (Blends)	4	264	$\frac{264}{4} = 66$	$\frac{66}{18.8} = 3.5$	0.0409
Residuals	12	226	$\frac{226}{12} = 18.8$		
Total	19	560			









Remark:

1. Individual comparisons, the Bonferroni methods of multiple comparisons are just as for a one-way data.

2. We use residual plots of residuals against fitted values to examine equality of variance assumption and qq-plot of residuals to examine normality assumption.

In R,

```
> factor.bl=factor(rep(letters[1:5],4))  #for matrix format
> factor.bl
 [1] a b c d e a b c d e a b c d e a b c d e
Levels: a b c d e
> factor.tr=factor(rep(letters[1:4],c(5,5,5,5))) #for matrix format
> factor.tr
 [1] a a a a a b b b b b c c c c c d d d d d
Levels: a b c d
> pen.aov=aov(penv~factor.bl+factor.tr)
> summary(pen.aov)
            Df  Sum Sq Mean Sq F value  Pr(>F)
factor.bl    4 264.000  66.000  3.5044 0.04075 *
factor.tr    3  70.000  23.333  1.2389 0.33866
Residuals   12 226.000  18.833
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> par(mfrow=c(2,1))  #check model assumptions
> plot(pen.aov$fitted,pen.aov$resid) #check equality of var of residuals
> abline(h=0)
> title("residual plot")
> qqnorm(pen.aov$resid)  #check normality of residuals
> qqline(pen.aov$resid)
>
> cm=(sum(penv))^2/(r*c)  #for checking
> SSTo=sum(penv^2)-cm
> SSB=c*sum(mean.bl^2)-cm
> SST=r*sum(mean.tr^2)-cm
> SSR=SSTo-SSB-SST
> MST=SST/(c-1)
> MSB=SSB/(r-1)
```

```
> MSR=SSR/((r-1)*(c-1))
> F.tr=MST/MSR
> F.bl=MSB/MSR
> p.tr=1-pf(F.tr,c-1,(c-1)*(r-1))
> p.bl=1-pf(F.bl,r-1,(c-1)*(r-1))
> c(cm,SSTo,SSB,SST,SSR)
[1] 147920 560 264 70 226
> c(MST,MSB,MSR,F.tr,F.bl,p.tr,p.bl)
[1] 23.33333 66.00000 18.83333 1.238938 3.504425
    0.3386581 0.04074617
```

Note:

1. Since the spread of residuals around $h = 0$ is similar across the fitted value in the *residual plot* with no particular pattern, the *equality of variance* and *independence* assumptions are approximately satisfied.

2. Moreover since the points lie close to the straight line in the *qq-plot*, the *normality* assumption is satisfied.

3. We do NOT check equality of variance assumption using boxplots because there is only one observation after allowing for treatment and block effects. So we can't do boxplots based on only one observation for each box.

To show that two-way ANOVA test is a generalization of paired sample t test when $g = 2$, we consider the first two groups in `pen`:

```
> pen1=pen[,1]  #paried sample t-test
> pen2=pen[,2]
> d=pen1-pen2
> dm=mean(d)
> dv=var(d)
> n=length(pen1)
```

```
> Nr=2*n
> t0=dm/sqrt(dv/n)
> pvt=2*(1-pt(abs(t0),n-1))
> c(t0^2,pvt)
[1] 0.1818182  0.6917613
>
> pen.12=c(pen1,pen2)  #2-way ANOVA test
> fb.12=factor(rep(letters[1:5],2))
> ft.12=factor(rep(letters[1:2],c(5,5)))
> aov.12=aov(pen.12~fb.12+ft.12)
> summary(aov.12)
            Df Sum Sq Mean Sq F value Pr(>F)
fb.12        4  155.0   38.75   2.818  0.170
ft.12        1    2.5    2.50   0.182  0.692
Residuals    4   55.0   13.75
```

Hence $t_0^2 = f_0$ and the 2-sided p-value for t-test and the upper-sided p-value for F-test also agree for treatment effect. The proof is given in T8 Q3(c).

21 Friedman test (P.682-684,689-693)

If the data are not well approximated by a normal model and transformations cannot correct this problem then a nonparametric test may be needed. The Friedman test as a *nonparametric* test, developed by the Nobel prize winning economist Milton Friedman, is a generalization of the *sign* test.

Assume we have a two-way data:

	Tr 1	Tr 2	...	Tr c
Block 1	y_11	y_12	...	y_1c
Block 2	y_21	y_22	...	y_2c
.	.	.		.
.	.	.		.
.	.	.		.
Block r	y_r1	y_r2	...	y_rc

To test no differences across the treatments (the equality of distributions for treatments), *within each of the r-blocks*, the observations are ranked. Then instead of the two-way data above, we get the following ranked data:

	Tr 1	Tr 2	...	Tr c
Block 1	r_11	r_12	...	r_1c
Block 2	r_21	r_22	...	r_2c
.	.	.		.
.	.	.		.
.	.	.		.
Block r	r_r1	r_r2	...	r_rc

Here r_{ij} denotes the rank of y_{ij} in the i-th Block. Midranks are used in the case of ties. The rank mean in the j-th treatment and the overall rank mean are respectively:

$$\bar{r}_{\cdot j} = \frac{1}{r}\sum_{i=1}^{r} r_{ij}, \text{ and } \bar{r} = \frac{1}{rc}\sum_{i=1}^{r}\sum_{j=1}^{c} r_{ij} = \frac{1+c}{2}.$$

The five steps of the Friedman test on the treatment effects are:

1. **Hypothesis:**

$$H_0 : \beta_1 = \cdots = \beta_c \text{ vs } H_1 : \text{ at least one } \beta_j \text{ does not equal}$$

2. **Test statistic:**

$$q_0 = \frac{SST}{MST_o'} = \frac{r\sum_{j=1}^{c}\bar{r}_{\cdot j}^2 - rc(\bar{r})^2}{\left[\sum_{i=1}^{r}\sum_{j=1}^{c} r_{ij}^2 - rc(\bar{r})^2\right]/[r(c-1)]}$$

$$\overset{\text{no ties}}{=} \frac{12r}{c(c+1)}\sum_{j=1}^{c}(\bar{r}_{\cdot j})^2 - 3r(c+1) \text{ (Proof in T8 Q3(a))}$$

where $q_0 \approx \sum_{j=1}^{c}\left(\frac{\bar{r}_{\cdot j} - \bar{r}}{\hat{\sigma}/\sqrt{r}}\right)^2 \sim \chi_{c-1}$, $\hat{\sigma}^2 = \sum_{i=1}^{r}\sum_{j=1}^{c}(r_{ij} - \bar{r})^2/[r(c-1)]$,

$$SST = r\sum_{j=1}^{c}(\bar{r}_{\cdot j} - \bar{r})^2 = r\sum_{j=1}^{c}\bar{r}_{\cdot j}^2 - rc(\bar{r})^2,$$

$$MST_o' = \frac{1}{r(c-1)}\sum_{i=1}^{r}\sum_{j=1}^{c}(r_{ij} - \bar{r})^2 = \frac{1}{r(c-1)}\sum_{i=1}^{r}\sum_{j=1}^{c}[r_{ij}^2 - rc(\bar{r})^2]$$

3. **Assumption:** No particular assumption for Y_{ij}. We have $q_0 \sim \chi^2_{c-1}$ under H_0.
4. ***P*-value:** $\Pr(\chi^2_{c-1} \geq q_0)$.
5. **Decision:** reject H_0 if p-value $< \alpha$.

Note:

1. The degree of freedom (d.f.) for MST_0' is $r(c-1)$ NOT $rc-1 = N-1$ in KW test. This is due to the way of ranking, related to d.f.

   In KW test, the ranking applies to all obs. Hence there are only $N-1$ free ranks because the last rank is fixed. E.g. when $N=3$, $r_1=2$, $r_2=3$ implies $r_3=1$.

   In Friedman test, the ranking is applied across block and there are $c-1$ free ranks for each block. Hence the total number of free ranks for all r blocks is $r(c-1)$.

2. For $c=2$ treatments, the rank for each block is 1, 2. One less these ranks are 0,1 which are just *signs* and $q_0 = z_0^2$ where $z_0 = \frac{X-\frac{n}{2}}{\sqrt{\frac{n}{4}}}$ is the standardized test statistic for the count of positive signs X. The proof is as well given in T8 Q3(b).

Example: (`penicillin` data) The ranks of the i-th block are given in the brackets.

	Method A	Method B	Method C	Method D
Blend 1	89 ( )	88 ( )	97 ( )	94 ( )
Blend 2	84 (3)	77 (1)	92 (4)	79 (2)
Blend 3	81 (1)	87 (3.5)	87 (3.5)	85 (2)
Blend 4	87 (2)	92 (4)	89 (3)	84 (1)
Blend 5	79 (1)	81 (3)	80 (2)	88 (4)
sum	9	12.5	16.5	12
sum square	19	39.25	57.25	34

The Friedman test of the treatment effects is

1. **Hypothesis:**

$$H_0: \beta_1 = \cdots = \beta_c \text{ vs } H_1: \text{ at least one } \beta_j \text{ does not equal}$$

2. **Test statistic:**

$$q_0 = \frac{SST}{MST'_o} = \frac{5.7}{1.633} = 3.49$$

where

$$SST = r\sum_{j=1}^{c} \bar{r}_{\cdot j}^2 - rc(\bar{r})^2$$

$$= \frac{1}{5}(9^2 + 12.5^2 + 16.5^2 + 12^2) - 5(4)2.5^2 = 5.7$$

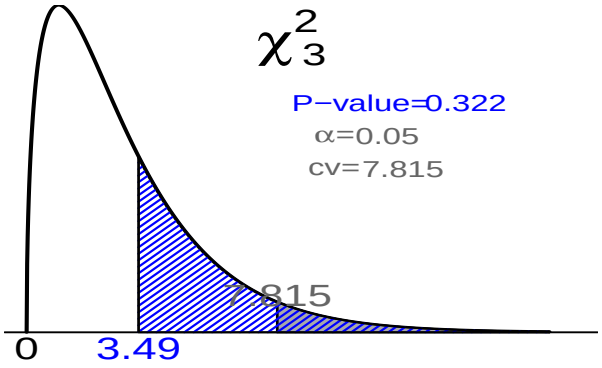
$$MST'_o = \frac{1}{r(c-1)}\Big[\sum_{i=1}^{r}\sum_{j=1}^{c} r_{ij}^2 - rc(\bar{r})^2\Big]$$

$$= \frac{1}{5(4-1)}[19 + 39.25 + 57.25 + 34 - 5(4)2.5^2] = 1.633$$

3. **Assumption:** No particular assumption for Y_{ij}. We have $q_0 \sim \chi^2_{c-1}$ under H_0.

4. ***P*-value:** p-value $= \Pr(\chi^2_3 \geq 3.49) = 0.3221$.

5. **Decision:** Since the p-value > 0.05, we accept H_0. The data is consistent with H_0 that there is no treatment effects across the 4 methods.



To perform a Friedman test to test for *treatment* effects with unreplicated blocked data, the R code is

```
friedman.test(y, treatment, block).
```

Similarly, to test for *block* effects, the R code is

```
friedman.test(y, block, treatment).
```

The following R codes perform the test and check its p-value.

```
> pen=read.csv("penicillin.csv")
> attach(pen)
> pen
  Method.A Method.B Method.C Method.D
1       89       88       97       94
2       84       77       92       79
3       81       87       87       85
4       87       92       89       84
5       79       81       80       88
```

```
> penv=as.matrix(pen) #for matrix format only; create vector
> penv=as.vector(penv)
> penv
 [1] 89 84 81 87 79 88 77 87 92 81 97 92 87 89 80 94 79 85 84 88
> factor.bl=factor(rep(letters[1:5],4)) #for matrix format
> factor.bl
 [1] a b c d e a b c d e a b c d e a b c d e
Levels: a b c d e
> factor.tr=factor(rep(letters[1:4],c(5,5,5,5))) #for matrix format
> factor.tr
 [1] a a a a a b b b b b c c c c c d d d d d
Levels: a b c d
> friedman.test(penv,factor.tr,factor.bl)

        Friedman rank sum test

data:  penv, factor.tr and factor.bl
Friedman chi-squared = 3.4898, df = 3, p-value = 0.3221

> rank.pen=apply(pen, 1, rank)
> rank.pen
         1 2   3 4 5
Method.A 2 3 1.0 2 1
Method.B 1 1 3.5 4 3
Method.C 4 4 3.5 3 2
Method.D 3 2 2.0 1 4
> rank.pen=t(rank.pen) # transpose
> dimnames(rank.pen)=list(paste("Blend", 1:5),
+                         paste("Method", 1:4))
> rank.pen
        Method 1 Method 2 Method 3 Method 4
Blend 1        2      1.0      4.0        3
Blend 2        3      1.0      4.0        2
Blend 3        1      3.5      3.5        2
Blend 4        2      4.0      3.0        1
```

```
Blend 5        1      3.0      2.0        4

> r=length(rank.pen[,1])  #for checking
> c=length(rank.pen[1,])
> c(r,c)
[1] 5 4
> bar.r=mean(rank.pen)
> bar.rj=apply(rank.pen,2,mean)
> bar.rj
Method 1 Method 2 Method 3 Method 4
     1.8      2.5      3.3      2.4
> SST=r*sum(bar.rj^2)-r*c*(bar.r^2)
> c(bar.r,SST)
[1] 2.5 5.7
> MSTo=(sum(rank.pen^2)-r*c*(bar.r^2))/(r*(c-1))
> q0=SST/MSTo
> p.value=1-pchisq(q0,c-1)
> c(MSTo,q0,p.value)
[1] 1.633333 3.489796 0.322088
```

To show that Friedman test is a generalization of sign test when $g = 2$, we consider again the first two columns in **pen**:

```
> x=length(d[d>0])  #sign test with normal approximation
> n=length(d[d!=0])
> z0=(x-n/2)/sqrt(n/4)  #z-test
> pvz=2*(1-pnorm(abs(z0)))  #two-sided
> c(z0^2,pvz)
[1] 0.2000000 0.6547208
>
> friedman.test(pen.12,ft.12,fb.12)  #Friedman test

        Friedman rank sum test
```

```
data:  pen.12, ft.12 and fb.12
Friedman chi-squared = 0.2, df = 1, p-value = 0.6547
```

Hence $z_0^2 = q_0$ and the 2-sided p-value for sign test and the upper-sided p-value for Friedman test also agree for treatment effect.

Summary of test for equaltiy of *means* with blocks or pairs,

No. of gps	**Parametric** Assume same *Normal* dist. across groups under H_0	**Non-parametric** Assume same dist. across groups under H_0
$g = 2$	matched pair t test $t_0 \sim t_{n-1}$	Sign test x or $z_0 = \dfrac{x - n/2}{\sqrt{n/4}} \sim \mathcal{N}(0,1)$
$g \geq 3$	two-way ANOVA test $f_{0t} \sim F_{c-1,(r-1)(c-1)}$ $(= t_0^2$ when $g = 2)$	Friedman test $q_0 \sim \chi^2_{c-1}$ $(= z_0^2$ when $g = 2)$

Note: The proofs for the generalization of the matched pair t test and sign test are given in Q3(b) & (c), Tutorial 8.

22 Two way ANOVA with replicates

22.1 Factorial design

We have discussed a *randomized block* design with a single replicate, that is, only one observation for each treatment in each block.

Now, we discuss two-way data with m replicates, that is, with m observations for each treatment in each block.

In general, we have the following data:

$$\{y_{ijk} : i = 1, ..., r; j = 1, ..., c; k = 1, ..., m\}, \tag{1}$$

where r, c, and m correspond to blocks, treatments and replicates, respectively.

Example: (Survival times) The data in the following table displays the survival times, in hours, of animals in a factorial design. In this experiment, animals were given one of three drugs, labelled I, II, and III and one of four treatments labelled a, b, c, and d. Four animals were used in each combination of drugs and treatments.

Poison	**Treatments**			
	a	b	c	d
I	3.23	1.22	2.33	2.22
	2.22	0.91	2.22	1.41
	2.17	1.14	1.59	1.52
	2.33	1.39	1.32	1.61
II	2.78	1.09	2.27	1.79
	3.45	1.64	2.86	0.98
	2.50	2.04	3.23	1.41
	4.35	0.81	2.25	2.63
III	4.55	3.33	4.35	3.33
	4.76	2.27	4.00	2.78
	5.56	2.63	4.17	3.23
	4.35	3.45	4.55	3.03

22.2 Additive decomposition

Let Y_{ijk} denote the random variables that generate the observed value y_{ijk} for $i = 1, 2, .., r$, $j = 1, 2, ..., c$ and $k = 1, 2, ..., m$. The statistical model for the two-way data with replicates is

$$y_{ijk} = \underbrace{\mu + \alpha_i + \beta_j + \delta_{ij}}_{\mu_{ij}} + \epsilon_{ijk},$$

where

y_{ijk}: the k-th observation on treatment j in Block i;

μ: the overall effect;

α_i: the block effect, where $\sum_{i=1}^{r} \alpha_i = 0$;

β_j: the treatment effect, where $\sum_{j=1}^{c} \beta_j = 0$;

δ_{ij}: the interaction effect, where $\sum_{i=1}^{r} \delta_{ij} = \sum_{j=1}^{c} \delta_{ij} = 0$;

ϵ_{ijk}: random error term such that ϵ_{ijk} are independent normally distributed with $E(\epsilon_{ijk}) = 0$ and $Var(\epsilon_{ijk}) = \sigma^2$.

For 2-way ANOVA model without replicates, the model is

$$y_{ij} = \underbrace{\mu + \alpha_i + \beta_j}_{\mu_{ij}} + \epsilon_{ij},$$

we cannot add interaction effect δ_{ij}

$$y_{ij} = \underbrace{\mu + \alpha_i + \beta_j + \delta_{ij}}_{\mu_{ij}} + \epsilon_{ij},$$

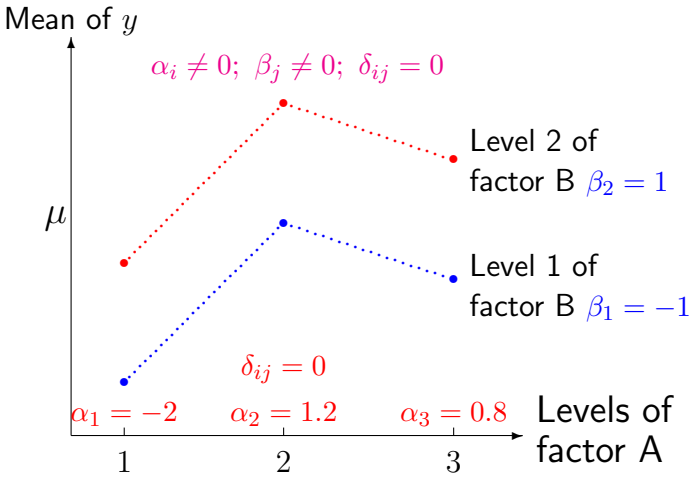
because it cannot be distinguished from the error ϵ_{ij}.

22.3 Interaction effect

Interaction effect between treatment j and block i is the special effects from some pairs of (i, j) which violate the trends of effects for treatment j alone and for block i alone. Examples of *interaction* plots:

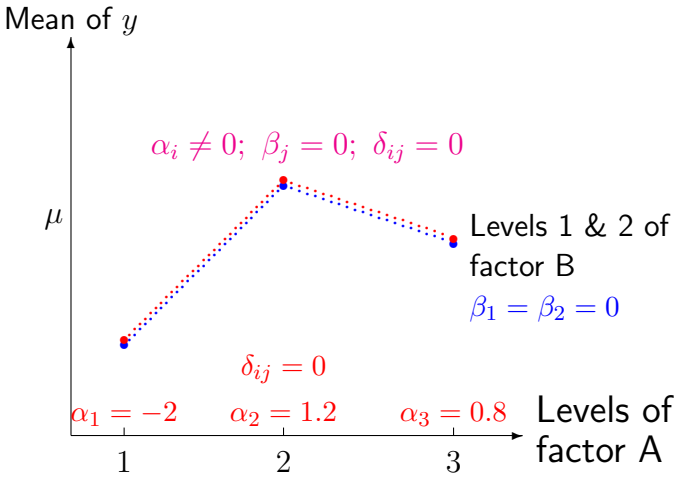
Example: $r = 3$ and $c = 2$. δ_{ij} allows for the inconsistency of the effect from one factor across levels of the other factor.

(a)



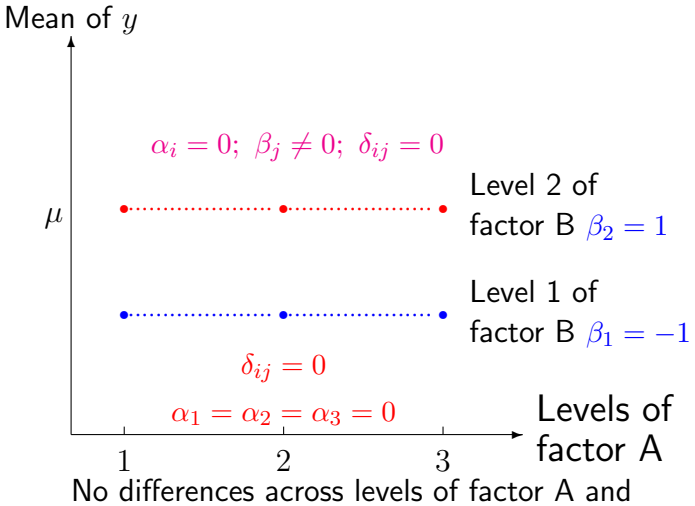
Differences across levels of factor A and differences across levels of factor B; no interaction

(b)



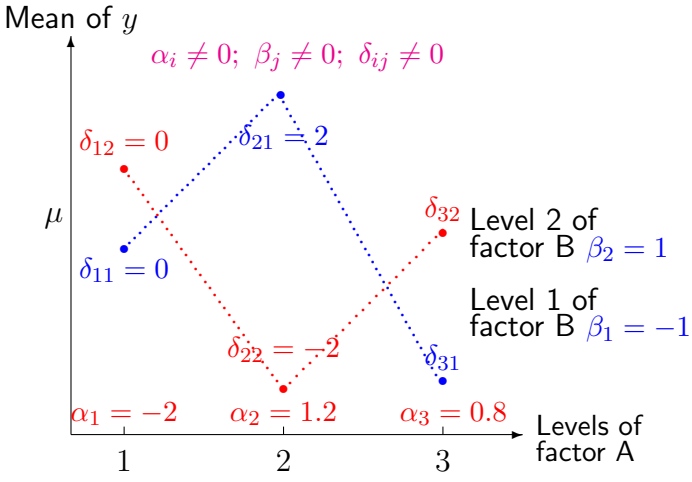
Differences across levels of factor A and no differences across levels of factor B; no interaction

(c)



No differences across levels of factor A and differences across levels of factor B; no interaction

(d)



Differences across levels of factor A and differences across levels of factor B; have interaction

$\mu_{11} = \mu + (-2) + (-1) + 0 = \mu - 3$

$\mu_{12} = \mu + (-2) + (1) + 0 = \mu - 1$ Larger than μ_{11}

$\mu_{21} = \mu + (1.2) + (-1) + (2) = \mu + 2.2$

$\mu_{22} = \mu + (1.2) + (1) + (-2) = \mu + 0.2$ Smaller than μ_{21}

22.4 ANOVA for two-way data with replicates

The analysis of variance for a two-way data with replicates proceeds much like that for a two-way data with single replicate.

The group means for $i = 1, 2, ..., r; j = 1, 2, ..., c$ and the overall mean are

$$\bar{y}_{ij.} = \frac{1}{m}\sum_{k=1}^{m} y_{ijk} \text{ and } \bar{y} = \frac{1}{rcm}\sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m} y_{ijk}.$$

As in ANOVA for one-way data, we can partition $y_{ijk} - \bar{y}$ as

$$\begin{aligned} y_{ijk} - \bar{y} &= (\bar{y}_{ij.} - \bar{y}) + (y_{ijk} - \bar{y}_{ij.}) \\ \text{i.e. } y_{ijk} - \mu &= \text{Group effect } \mu_{ij} + \text{Residual } \epsilon_{ijk} \end{aligned}$$

Hence, some algebra shows that

$$\underbrace{\sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m}(y_{ijk} - \bar{y})^2}_{SST_o} = \underbrace{m\sum_{i=1}^{r}\sum_{j=1}^{c}(\bar{y}_{ij.} - \bar{y})^2}_{SSG} + \underbrace{\sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m}(y_{ijk} - \bar{y}_{ij.})^2}_{SSR},$$

that is

$$\underbrace{\sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m} y_{ijk}^2 - N\bar{y}^2}_{SST_o} = \underbrace{m\sum_{i=1}^{r}\sum_{j=1}^{c}\bar{y}_{ij.}^2 - N\bar{y}^2}_{SSG} + \underbrace{(m-1)\sum_{i=1}^{r}\sum_{j=1}^{c} s_{ij.}^2}_{SSR},$$

with $s_{ij.}^2 = \frac{1}{m-1}\sum_{k=1}^{m}(y_{ijk} - \bar{y}_{ij.})^2$ being the sample variance in group i, j.

Furthermore we can partition $\bar{y}_{ij.} - \bar{y}$ as

$$\begin{aligned} \bar{y}_{ij.} - \bar{y} &= (\bar{y}_{i..} - \bar{y}) + (\bar{y}_{.j.} - \bar{y}) + (\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}) \\ \text{Group effect } \mu_{ij} &= \text{Block effect } \alpha_i + \text{Treatment effect } \beta_j + \text{Interaction effect } \delta_{ij}, \end{aligned}$$

where

$$\bar{y}_{i..} = \frac{1}{cm}\sum_{j=1}^{c}\sum_{k=1}^{m} y_{ijk} = \frac{1}{c}\sum_{j=1}^{c}\bar{y}_{ij.},$$

$$\bar{y}_{.j.} = \frac{1}{rm}\sum_{i=1}^{r}\sum_{k=1}^{m} y_{ijk} = \frac{1}{r}\sum_{i=1}^{r}\bar{y}_{ij.}.$$

Some algebra shows that

$$\underbrace{m\sum_{i=1}^{r}\sum_{j=1}^{c}(\bar{y}_{ij.}-\bar{y})^2}_{SSG} = \underbrace{mc\sum_{i=1}^{r}(\bar{y}_{i..}-\bar{y})^2}_{SSB} + \underbrace{mr\sum_{j=1}^{c}(\bar{y}_{.j.}-\bar{y})^2}_{SST} + \underbrace{m\sum_{i=1}^{r}\sum_{j=1}^{c}(\bar{y}_{ij.}-\bar{y}_{i..}-\bar{y}_{.j.}+\bar{y})^2}_{SSI}$$

The larger the SST, the stronger will be the evidence to indicate a difference between treatments;

the larger the SSB, the stronger will be the evidence to indicate a difference between blocks;

the larger the SSI, the stronger will be the evidence to indicate an interaction between treatments and blocks.

Note that in the randomized block design,

$$SSR = \sum_{i=1}^{r}\sum_{j=1}^{c}(y_{ij}-\hat{y}_{ij})^2 = \sum_{i=1}^{r}\sum_{j=1}^{c}(y_{ij}-\bar{y}_{i\cdot}-\bar{y}_{\cdot j}+\bar{y})^2$$

In the factorial design,

$$SSI = m\sum_{i=1}^{r}\sum_{j=1}^{c}(\bar{y}_{ij.}-\bar{y}_{i..}-\bar{y}_{.j.}+\bar{y})^2 \text{ and } SSR = \sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m}(y_{ijk}-\bar{y}_{ij.})^2$$

22.5 ANOVA test for two-way data with replicates

The two-way ANOVA tests for treatment and/or block and/or interaction effects in five-steps are:

1. **Hypothesis:** We test if all y_{ijk} are from the same population. Equivalently, we test three hypotheses:

   For treatment effects:

   $$\begin{aligned} H_0: &\quad \beta_1 = \beta_2 = ... = \beta_c = 0 \quad \text{vs} \\ H_1: &\quad \text{Not all } \beta_j \text{ equal;} \end{aligned}$$

   For block effects:

   $$\begin{aligned} H_0: &\quad \alpha_1 = \alpha_2 = ... = \alpha_r = 0 \quad \text{vs} \\ H_1: &\quad \text{Not all } \alpha_i \text{ equal.} \end{aligned}$$

   For interaction effects:

   $$\begin{aligned} H_0: &\quad \delta_{ij} = 0,\ i = 1, 2, ..., r;\ j = 1, 2, ..., c \quad \text{vs} \\ H_1: &\quad \text{Not all } \delta_{ij} \text{ equal.} \end{aligned}$$

2. **Test statistic:** For treatment, block and interaction effects respectively:

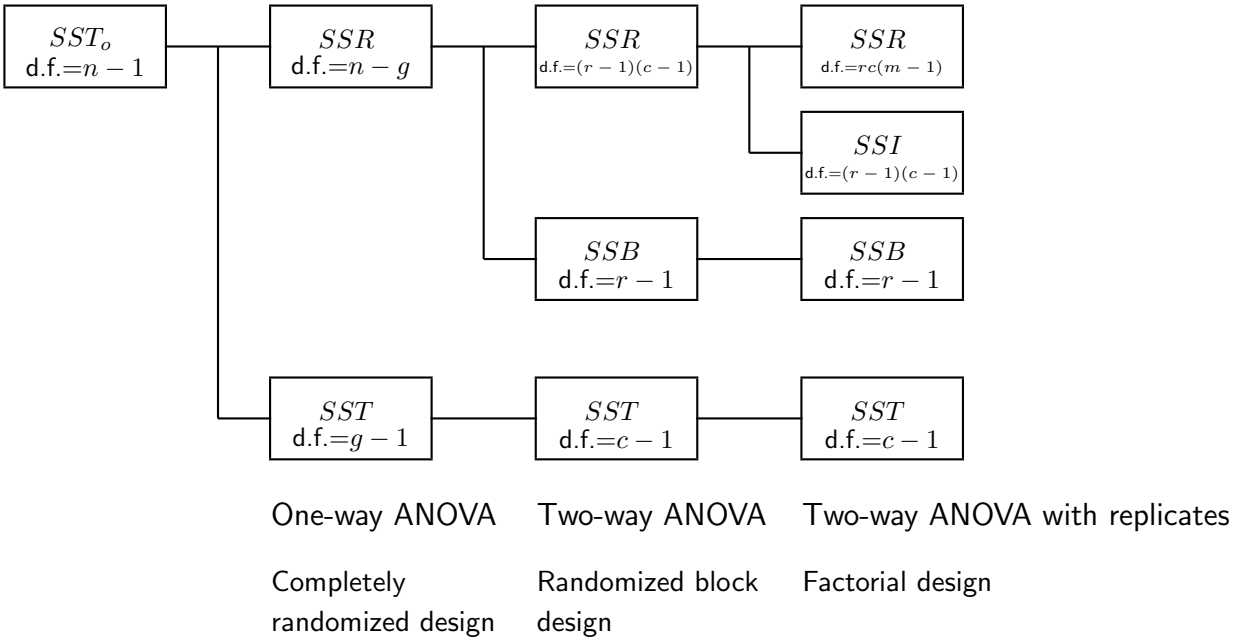
   $$\begin{aligned} f_{b0} &= \frac{SSB/(r-1)}{SSR/rc(m-1)} \sim F_{r-1,rc(m-1)}; \\ f_{t0} &= \frac{SST/(c-1)}{SSR/rc(m-1)} \sim F_{c-1,rc(m-1)}; \\ f_{i0} &= \frac{SSI/(r-1)(c-1)}{SSR/rc(m-1)} \sim F_{(r-1)(c-1),rc(m-1)}. \end{aligned}$$

3. **Assumption:** $Y_{ijk} \sim \mathcal{N}(\mu_{ij}, \sigma^2)$ and Y_{ijk} are independent.

4. ***P*-value:** For treatment, block and interaction effects respectively:

$$\begin{aligned} p\text{-value} &= \Pr(F_{c-1,rc(m-1)} \geq f_{t0}) \\ p\text{-value} &= \Pr(F_{r-1,rc(m-1)} \geq f_{b0}) \\ p\text{-value} &= \Pr(F_{(r-1)(s-1),rs(m-1)} \geq f_{i0}) \end{aligned}$$

5. **Decision:** reject H_0 if p-value $< \alpha$.



Decomposition of total variation in y for testing treatment effect

Note that there is *no nonparametric test* for this two-way ANOVA test with factorial design.

22.6 ANOVA table for two-way data with replicates

Two way ANOVA table for factorial design

Source	**df**	**SS**	**MS**	**F**
Treatments	$c-1$	$SST = rm\sum_{j=1}^{c}\overline{y}_{\cdot j\cdot}^2 - n\overline{y}^2$	$MST = \frac{SST}{c-1}$	$F_t = \frac{MST}{MSR}$
Blocks	$r-1$	$SSB = cm\sum_{i=1}^{r}\overline{y}_{i\cdot\cdot}^2 - n\overline{y}^2$	$MSB = \frac{SSB}{r-1}$	$F_b = \frac{MSB}{MSR}$
Interactions	$(r-1)(c-1)$	$SSI = SST_o - SST$ $-SSB - SSR$	$MSI = \frac{SSI}{(r-1)(c-1)}$	$F_i = \frac{MSI}{MSR}$
Residuals	$rc(m-1)$	$SSR = (m-1)\sum_{i=1}^{r}\sum_{j=1}^{c} s_{ij}^2$	$MSR = \frac{SSR}{rc(m-1)}$	
Total	$rcm-1$	$SST_o = \sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m} y_{ijk}^2 - n\overline{y}^2$		

$\overline{y}_{i\cdot\cdot} = \frac{1}{cm}\sum_{j=1}^{c}\sum_{k=1}^{m} y_{ijk}$, $\overline{y}_{\cdot j\cdot} = \frac{1}{rm}\sum_{j=1}^{r}\sum_{k=1}^{m} y_{ijk}$, $\overline{y} = \frac{1}{n}\sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m} y_{ijk}$ and
$s_{ij}^2 = \frac{1}{m-1}(\sum_{k=1}^{m} y_{ijk}^2 - m\overline{y}_{ij\cdot}^2)$.

Example: (Survival times) The data is summaried as below:

Poison	**Treatment** a	b	c	d	Bl. mean $\bar{y}_{i\cdot\cdot}$
I	3.23	1.22	2.33	2.22	
	2.22	0.91	2.22	1.41	
	2.17	1.14	1.59	1.52	
	2.33	1.39	1.32	1.61	
Gp. mean $\bar{y}_{ij\cdot}$	2.4875	1.165	1.8650	1.6900	1.8019
Gp. var. s^2_{ij}	0.2495	0.0398	0.2383	0.1315	
II	2.78	1.09	2.27	1.79	
	3.45	1.64	2.86	0.98	
	2.50	2.04	3.23	1.41	
	4.35	0.81	2.25	2.63	
Gp. mean $\bar{y}_{ij\cdot}$	3.2700	1.3950	2.6525	1.7025	2.2550
Gp. var. s^2_{ij}	0.6773	0.3038	0.2283	0.4918	
III	4.55	3.33	4.35	3.33	
	4.76	2.27	4.00	2.78	
	5.56	2.63	4.17	3.23	
	4.35	3.45	4.55	3.03	
Gp. mean $\bar{y}_{ij\cdot}$	4.8050	2.9200	4.2675	3.0925	3.7713
Gp. var. s^2_{ij}	0.2814	0.3185	0.0559	0.0590	
Tr. mean $\bar{y}_{\cdot j\cdot}$	3.5208	1.8267	2.9283	2.1617	2.6094

Furthermore, we have

$$\sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m} {y_{ijk}}^2 = 392.5927$$

The two-way ANOVA tests for treatment and/or block and/or interaction effects in five-steps are:

1. **Hypothesis:** for testing the treatment, block and interactin effects are respectively

$$H_0: \ \beta_1 = \beta_2 = ... = \beta_c = 0 \quad \text{vs} \quad H_1: \ \text{Not all } \beta_j \text{ equal;}$$
$$H_0: \ \alpha_1 = \alpha_2 = ... = \alpha_r = 0 \quad \text{vs} \quad H_1: \ \text{Not all } \alpha_i \text{ equal.}$$
$$H_0: \ \delta_{ij} = 0, \ i = 1, ..., r; \ j = 1, ..., c \quad \text{vs} \quad H_1: \ \text{Not all } \delta_{ij} \text{ are same.}$$

2. **Test statistic:** For treatment, block and interaction effects respectively:

$$f_{t0} = \frac{SST/(c-1)}{SSR/rc(m-1)} = \frac{20.9468/3}{9.225/(3(4)3)} = 27.2479$$
$$f_{b0} = \frac{SSB/(r-1)}{SSR/rc(m-1)} = \frac{34.0415/2}{9.225/(3(4)3)} = 66.4226$$
$$f_{i0} = \frac{SSI/(r-1)(c-1)}{SSR/rc(m-1)} = \frac{1.5553/6}{9.225/(3(4)3)} = 1.0116$$

where

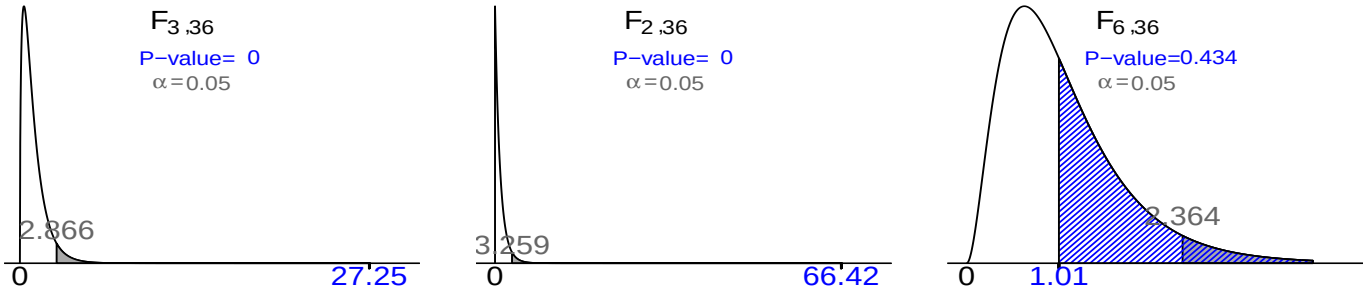
$$CM = rcm\,\bar{y}^2 = 3(4)4(2.6094^2) = 326.8242$$
$$SST_o = \sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{k=1}^{m} {y_{ijk}}^2 - rcm\,\bar{y}^2$$
$$= 392.5927 - 326.8242 = 65.7685$$
$$SST = rm\sum_{j=1}^{c}\bar{y}_{.j.}^2 - rcm\,\bar{y}^2$$
$$= 3(4)(3.5208^2 + \cdots + 2.1617^2) - 326.8242 = 20.9468$$
$$SSB = cm\sum_{i=1}^{r}\bar{y}_{i..}^2 - rcm\,\bar{y}^2$$
$$= 4(4)(1.8019^2 + \cdots + 3.7713^2) - 326.8242 = 34.0415$$

$$\begin{aligned} SSR &= (m-1)\sum_{i=1}^{r}\sum_{j=1}^{c} s_{ij.}^2 \\ &= 3(0.2495 + \cdots + 0.0590) = 9.225 \\ SSI &= SST_o - SSB - SST - SSR \\ &= 65.7685 - 20.9468 - 34.0415 - 9.225 = 1.5553 \end{aligned}$$

3. **Assumption:** $Y_{ijk} \sim \mathcal{N}(\mu_{ij}, \sigma^2)$ and Y_{ijk} are independent.
4. ***P*-value:** For treatment, block and interaction effects respectively:
   p-value $= \Pr(F_{3,36} \geq 27.2479) < 0.001$ ($F_{3,40,0.999} = 6.59$; 0.0000 from R)
   p-value $= \Pr(F_{2,36} \geq 66.4226) < 0.001$ ($F_{2,40,0.999} = 8.25$; 0.0000 from R)
   p-value $= \Pr(F_{6,36} \geq 1.0116) > 0.1$ ($F_{6,40,0.90} = 1.93$; 0.4332 from R)
5. **Decision:** we reject H_0 of no treatment and block effects. There are strong evidence in the data that means across treatment and means across poisson types differ. However there is no interaction effect between treatment and poison types in the data.

Two way ANOVA table for factorial design

Source	**df**	**SS**	**MS**	**F**
Treatments	3	20.9468	$\frac{20.9468}{3} = 6.9823$	$\frac{6.9823}{0.2562} = 27.25$
Blocks	2	34.0415	$\frac{34.0415}{2} = 17.0207$	$\frac{17.0207}{0.2562} = 66.42$
Interactions	6	1.5553	$\frac{1.5553}{6} = 0.2592$	$\frac{0.2592}{0.2562} = 1.01$
Residuals	36	9.225	$\frac{9.225}{36} = 0.2562$	
Total	47	65.7685		



Note that there are two formats of data file for ANOVA test:

1. **Matrix format:** outcomes are present in matrix where the column and/or row indicate levels of treatment (group) and/or block (discussed later) effects. You need to generate vectors of outcomes and `factor` labels for `aov`.

2. **Vector format:** the columns are already the vectors of outcomes and factor labels for treatment and/or block effects and hence you don't have to generate these vectors.

In R,

1. Conduct a 2-way ANOVA test.

A. Matrix format

```
> poison=read.csv("data/poison.csv")
> attach(poison)
> poison
   poison    a    b    c    d
1       I 3.23 1.22 2.33 2.22
2       I 2.22 0.91 2.22 1.41
3       I 2.17 1.14 1.59 1.52
4       I 2.33 1.39 1.32 1.61
5      II 2.78 1.09 2.27 1.79
6      II 3.45 1.64 2.86 0.98
```

```
7      II 2.50 2.04 3.23 1.41
8      II 4.35 0.81 2.25 2.63
9     III 4.55 3.33 4.35 3.33
10    III 4.76 2.27 4.00 2.78
11    III 5.56 2.63 4.17 3.23
12    III 4.35 3.45 4.55 3.03

> c=4
> r=3
> m=length(poison[,1])/r
> m
[1] 4

> poisonv=c(poison[,2],poison[,3],poison[,4],poison[,5]) #for matrix
> poisonv  #set a vector of obs excluding 1st col of labels
 [1] 3.23 2.22 2.17 2.33 2.78 3.45 2.50 4.35 4.55 4.76 5.56
     4.35 1.22 0.91 1.14
[16] 1.39 1.09 1.64 2.04 0.81 3.33 2.27 2.63 3.45 2.33 2.22
     1.59 1.32 2.27 2.86
[31] 3.23 2.25 4.35 4.00 4.17 4.55 2.22 1.41 1.52 1.61 1.79
     0.98 1.41 2.63 3.33
[46] 2.78 3.23 3.03

> factor.bl=factor(rep(rep(leters[1:3],c(4,4,4)),4)) #for matrix format
> factor.bl  #set a vector of block labels
 [1] a a a a b b b b c c c c a a a a b b b b c c c c a a a a
    b b b b c c c c a a
[39] a a b b b b c c c c
Levels: a b c

> factor.tr=factor(rep(letters[1:4],c(12,12,12,12))) #for matrix format
> factor.tr   #set a vector of treatment labels
 [1] a a a a a a a a a a a a b b b b b b b b b b b b c c c c
     c c c c c c c c d d
[39] d d d d d d d d d d
Levels: a b c d
```

```
> poison.aov=aov(poisonv~factor.tr*factor.bl)
> summary(poison.aov)
                    Df Sum Sq Mean Sq F value    Pr(>F)
factor.tr            3 20.947   6.982 27.2479 2.245e-09 ***
factor.bl            2 34.041  17.021 66.4225 8.292e-13 ***
factor.tr:factor.bl  6  1.555   0.259  1.0116    0.4332
Residuals           36  9.225   0.256
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

B. Vector format

```
> poisonv=read.csv("data/poisonv.csv")
> attach(poisonv)
> poisonv
> poisonv #data with 3 columns as vectors
      poisonv type treatment
 [1,]    3.23    1         1
 [2,]    2.22    1         1
...
[46,]    2.78    3         4
[47,]    3.23    3         4
[48,]    3.03    3         4

> poison1.aov=aov(poisonv~type*treatment) #wrong result
> summary(poison1.aov)
               Df Sum Sq Mean Sq F value   Pr(>F)
type            1 31.028  31.028  47.096 1.82e-08 ***
treatment       1  5.313   5.313   8.065  0.00681 **
type:treatment  1  0.440   0.440   0.668  0.41822
Residuals      44 28.988   0.659
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

The result of `poison1.aov` is incorrect as shown by the "1 df" for both factors because the labels of 1,2,3 are treated as numbers.

```
> treatment=as.factor(treatment)
> type=as.factor(type)
> poison2.aov=aov(poisonv~treatment*type)
> summary(poison2.aov)
              Df Sum Sq Mean Sq F value   Pr(>F)
treatment      3  20.95   6.982  27.248 2.25e-09 ***
type           2  34.04  17.021  66.423 8.29e-13 ***
treatment:type 6   1.56   0.259   1.012    0.433
Residuals     36   9.22   0.256
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

On dropping the interaction effect, the SSI is moved to SSR, i.e. $SSR' = SSI + SSR$.

```
> poison3.aov=aov(poisonv~treatment+type)
> summary(poison3.aov)
            Df Sum Sq Mean Sq F value   Pr(>F)
treatment    3  20.95   6.982   27.20 6.18e-10 ***
type         2  34.04  17.021   66.31 1.01e-13 ***
Residuals   42  10.78   0.257
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

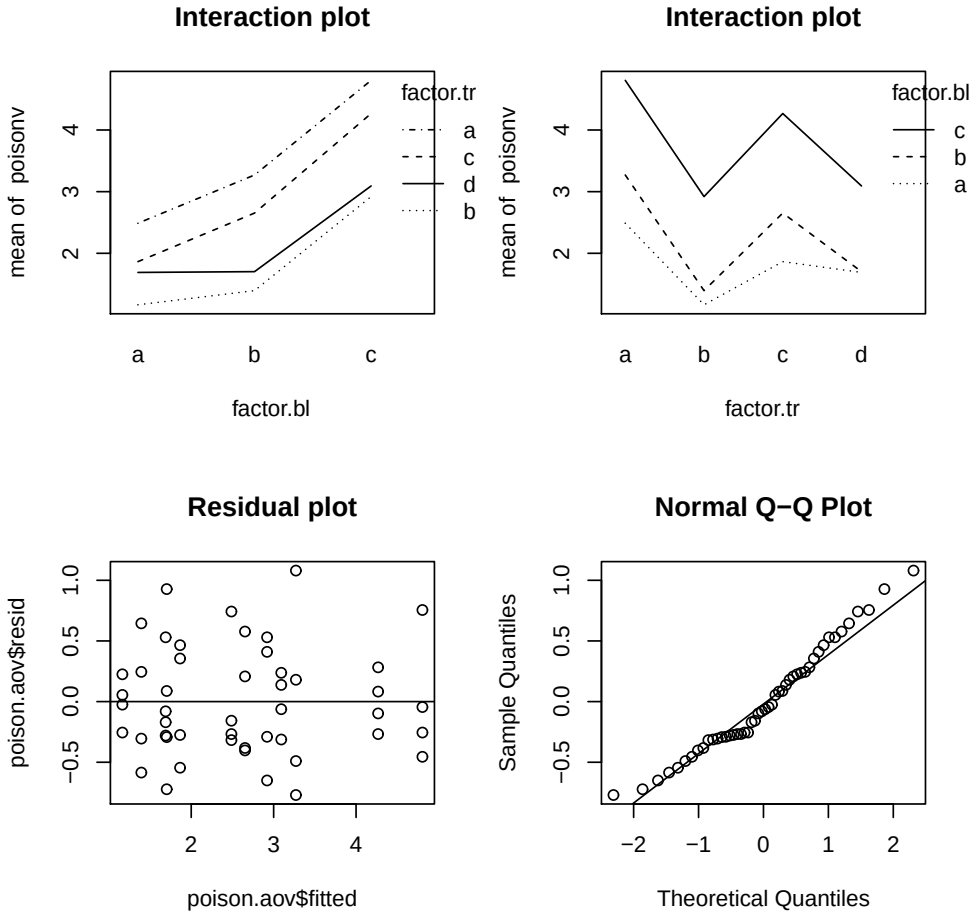
On further dropping the block effect, the SSB is moved to SSR', i.e. $SSR'' = SSB + SSR'$.

```
> poison4.aov=aov(poisonv~treatment)
> summary(poison4.aov)
            Df Sum Sq Mean Sq F value   Pr(>F)
treatment    3  20.95   6.982   6.854 0.000688 ***
Residuals   44  44.82   1.019
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

2. Check interaction effect and normality of residuals.

```
> par(mfrow=c(2,2))
> interaction.plot(factor.bl,factor.tr,poisonv)
> title("Interaction plot")
> interaction.plot(factor.tr,factor.bl,poisonv)
> title("Interaction plot")
> plot(poison.aov$fitted,poison.aov$resid)
> title("Residual plot")
> abline(h=0)
> qqnorm(poison.aov$resid)
> qqline(poison.aov$resid)
```

If there is no interaction effect, the lines on the interaction plots should be parallel. If residuals follow normal distribution, the normal qq-plot should be close to a straight line.



From the interaction plots, we conclude that

1. **Treatment effect:** treatment a has stronger effect than other treatments; Treatment effect drops from a to b, increase from b to c and drops again from c to d. Such trend is consistent for all levels of poison.

2. **Poison effect:** poison III has stronger effect than poisons I and II; Poison effect increases from type I to III. Such trend is consistent for all levels of treatment.

3. **Interaction effect:** Since the lines are parallel showing consistency of trends of one factor for all levels of the second factor, there is no interaction between the factors of treatment and poison.

To check for the *independence* and *equality of variance* for residuals assumptions, we obtain *residual plot* which should show a *random scatter* of points with no particular pattern around the horizontal axis and with similar spread across the fitted values. For the *boxplots of groups*, they should show similar *spreads*.

Since the residual plot shows a random scatter of points around the horizontal axis, we conclude that the equality of variance assumption is satisfied. We do not draw the 12 boxplots because each boxplot of size $m = 4$ does not have enough information to show the spread of each group clearly.

In the normal qq plot, the points lie close to the straight line which again confirms the normality of error assumption. To check p-values:

3. Calculation of group means and variances

```
> mean=mean(poisonv) #overall mean
> mean
[1] 2.609375

> mean.g=tapply(poisonv,list(factor.bl,factor.tr),mean)
> mean.g   #group means
         a     b      c      d
I   2.4875 1.165 1.8650 1.6900
II  3.2700 1.395 2.6525 1.7025
III 4.8050 2.920 4.2675 3.0925

> mean.bl=apply(mean.g,1,mean) #means for blocks
> mean.bl
       I       II      III
1.801875 2.255000 3.771250

> alpha=mean.bl-mean
> alpha  #block effect alpha sum to 0
        a         b         c
-0.807500 -0.354375  1.161875

> mean.tr=apply(mean.g,2,mean) #means for treatments
> mean.tr
       a        b        c        d
3.520833 1.826667 2.928333 2.161667

> beta=mean.tr-mean
> beta  #treatment effect beta sum to 0
         a          b          c          d
 0.9114583 -0.7827083  0.3189583 -0.4477083

> delta=mean.g-matrix(mean.tr,r,c,byrow=T)-
        matrix(mean.bl,r,c,byrow=F)+mean
> delta  #interaction effect delta sum to 0 by row & by col.
           a          b          c          d
```

```
a -0.2258333  0.14583333 -0.25583333  0.3358333
b  0.1035417 -0.07729167  0.07854167 -0.1047917
c  0.1222917 -0.06854167  0.17729167 -0.2310417
```

```
> var.g=tapply(poisonv,list(factor.bl,factor.tr),var)
> var.g   #group variances
            a          b          c          d
I   0.2494917 0.03976667 0.23830000 0.13153333
II  0.6772667 0.30376667 0.22829167 0.49182500
III 0.2813667 0.31853333 0.05589167 0.05895833
```

Note: Model: $y_{ijk} = \mu + \alpha_i + \beta_j + \delta_{ij} + \epsilon_{ijk}$,

$\mu = \bar{y}$,

$\alpha_i = \bar{y}_{i\cdot\cdot} - \bar{y}$,

$\beta_j = \bar{y}_{\cdot j\cdot} - \bar{y}$,

$\delta_{ij} = \bar{y}_{ij\cdot} - \bar{y}_{i\cdot\cdot} - \bar{y}_{\cdot j\cdot} + \bar{y}$

4. Calculation of SS and MS

```
> sumsq=sum(poisonv^2)   #sum of sq. of all obs.
> sumsq.bl=sum(mean.bl^2)  #sum of sq. of r block means
> sumsq.tr=sum(mean.tr^2)   #sum of sq. of c treatment means
> cm=m*c*r*mean^2   #correction for mean
> c(sumsq,sumsq.bl,sumsq.tr,cm)
[1] 392.5927 22.55411 28.98092 326.8242
```

```
> SSTo=sumsq-cm
> SST=m*r*sumsq.tr-cm
> SSB=m*c*sumsq.bl-cm
> SSR=(m-1)*sum(var.g)
> SSI=SSTo-SST-SSB-SSR
> c(SSTo,SST,SSB,SSR,SSI)
[1] 65.76848 20.94679 34.04146 9.224975 1.555254
```

```
> MST=SST/(c-1)
> MSB=SSB/(r-1)
```

```
> MSR=SSR/(r*c*(m-1))
> MSI=SSI/((r-1)*(c-1))
> c(MST,MSB,MSR,MSI)
[1] 6.982263 17.02073 0.2562493 0.2592090
```

5. Calculation of test statistics and p-values

```
> Ft=MST/MSR
> Fb=MSB/MSR
> Fi=MSI/MSR
> c(Ft,Fb,Fi)
[1] 27.24793 66.42255 1.011550

> pt=1-pf(Ft,c-1,r*c*(m-1))
> pb=1-pf(Fb,r-1,r*c*(m-1))
> pi=1-pf(Fi,(r-1)*(c-1),r*c*(m-1))
> c(pt,pb,pi)
[1] 6.22484e-08 9.547918e-15 0.4332494
```