STATISTICAL MODELLING

VII. Factorial experiments

So far in discussing experiments we have considered there to be a set of treatments to be applied and we have been concerned to group the units and apply these treatments so as to make the experiment as sensitive as possible.

Now I will turn to more sophisticated selection of treatments. The first point is that there will often be more than one factor of interest to the experimenter.

Definition VII.1: Experiments that involve more than one randomized or treatment factor are called **factorial experiments**. ■

VII.A Design of factorial experiments

In general, the number of treatments in a factorial experiments is the product of the numbers of levels of the treatment factors. Given the number of treatments, the experiment could be laid out as a Completely Randomized Design, a Randomized Complete Block Design or a Latin Square with that number of treatments. The incomplete block designs, such as BIBDs or Youden Squares are not suitable for factorial experiments.

a) Obtaining a layout for a factorial experiment in R

Layouts for factorial experiments can be obtained in R using the expressions for the chosen design when only a single-factor is involved. The difference with factorial experiments is that the several treatment factors need to be entered. Their values can be generated using the `fac.gen` function. It is likely to be necessary to use either the `each` or `times` arguments to generate the replicate combinations. The syntax of `fac.gen` and examples showing how to obtain layouts for a two-factor factorial laid out using a Completely Randomized Design, a Randomized Complete Block Design and a Latin Square are given in Appendix B, *Randomized layouts and sample size computations in R*.

Example VII.1 Fertilizing oranges

Suppose an experimenter is interested in investigating the effect of nitrogen and phosphorus fertilizer on yield of oranges. It was decided to investigate 3 levels of Nitrogen (viz 0,30,60 kg/ha) and 2 levels of Phosphorus (viz. 0,20 kg/ha). The yield after six months was measured.

For a factorial experiment, the treatments are all possible combinations of the 3 Nitrogen $\times$ 2 Phosphorus levels: $3 \times 2 = 6$ treatments. The treatment combinations, arranged in Yates order, are:

Treatment	N	P
1	0	0
2	30	0
3	60	0
4	0	20
5	30	20
6	60	20

A layout for this experiment in a CRD with three replicates of each treatment is generated in R as shown in the following output.

```
> #
> # CRD
> #
> n <- 18
> CRDFac2.unit <- list(Seedling = n)
> CRDFac2.ran <- fac.gen(list(N = c(0, 30, 60), P = c(0, 20)), times = 3)
> CRDFac2.lay <- fac.layout(unrandomized = CRDFac2.unit,
+                           randomized = CRDFac2.ran, seed = 105)
> remove("CRDFac2.unit", "CRDFac2.ran")
```

```
> CRDFac2.lay
   Units Permutation Seedling  N  P
1      1           2        1 30 20
2      2          18        2  0  0
3      3           4        3 30  0
4      4           5        4 30  0
5      5           7        5 30 20
6      6          12        6 30  0
7      7          15        7 60  0
8      8          13        8  0  0
9      9           6        9 60  0
10    10           1       10 60  0
11    11          10       11 30 20
12    12          16       12 60 20
13    13           8       13  0 20
14    14          14       14  0 20
15    15           3       15  0  0
16    16          11       16 60 20
17    17           9       17 60 20
18    18          17       18  0 20
```

Note the assignment of the generation of treatment values using `fac.gen` that creates 3 copies of the levels combinations of the two factors N and P, that have 3 and 2 levels respectively, and stores these in the `data.frame` `CRDFac2.ran`.

Suppose we had decided on a randomized complete block design with three blocks — how many units per block would be required?

In factorial experiments we are not limited to two factors — thus we may have looked at Potassium at 2 levels as well. How many treatments in this case? Answer $3\times2\times2 = 12$. ■

VII.B Advantages of factorial experiments

(Mead & Curnow sec. 6.2, 6.3 and 14.6)

a) Interaction in factorial experiments

The major advantage of factorial experiments is that they allow the detection of interaction.

Definition VII.2: Two factors are said to **interact** if the effect of one, on the response variable, depends upon the level of the other. If they do not interact, they are said to be **independent**. ■

Other terms that are synonymous with interact are dependent and nonadditive. To investigate whether two factors interact, the simple effects are computed.

Definition VII.3: A **simple effect** for the means computed for each combination of at least two factors is the difference between two of these means having different levels of one of the factors but the same levels for all other factors. ■

We talk of the simple effects of a factor for the levels of the other factors.

If there is an interaction, we can compute an interaction effect from the simple effects to measure the size of the interaction

Definition VII.4: An **interaction effect** is half the difference of two simple effects for two different levels of just one factor or is half the difference of two interaction effects.■

If there is not an interaction we can separately compute the main effects to see how each factor affects the response.

Definition VII.5: A **main effect** of a factor is the difference between two means with different levels of that factor, each mean having been formed from all observations having the same level of the factor. ■

Example VII.2 Chemical reactor experiment

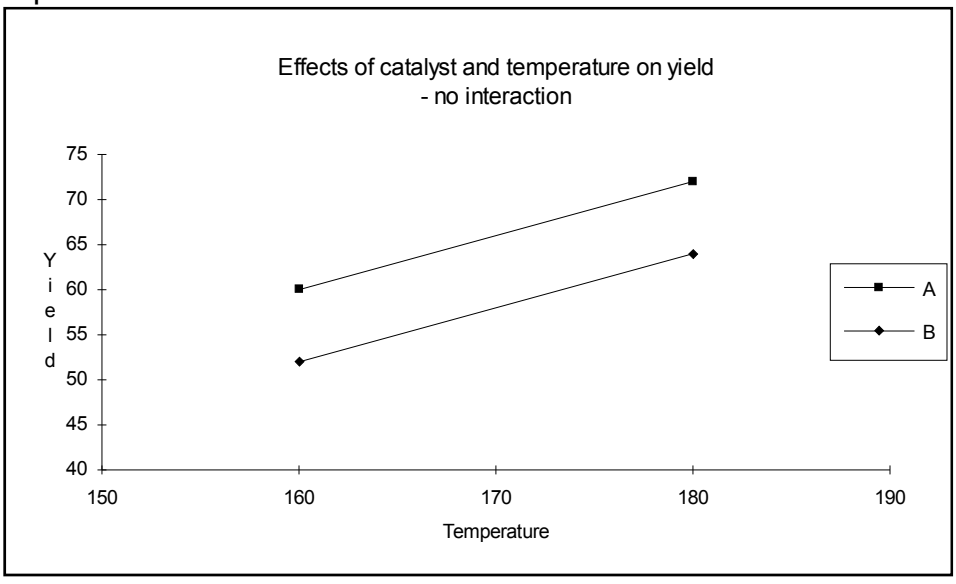
Consider a factorial experiment to investigate the effect of catalyst and temperature on the yield of chemical from a chemical reactor. Suppose there were two levels of each of the factors and that the table of means from the experiment was as follows:

		Temperature (°C)	
		160	180
Catalyst	A	60	72
	B	52	64

For A the temperature effect is $72-60 = 12$
For B the temperature effect is $64-52 = 12$

These are called the simple effects of temperature.

Clearly, the difference between (effect of) the temperatures is **independent** of which catalyst is used. The interaction effect is $[12 - 12]/2 = 0$. The situation can be illustrated using an **interaction plot**, in which the means for the combinations of the factors are plotted.



A set of parallel lines indicates that there is no interaction — the slope of these lines is proportional to the simple effects which are equal. If there was an interaction the simple effects would not be equal and so the lines would not be parallel.

Note that the statement about the independence of two factors is symmetrical in the two factors. Thus,

the simple catalyst effect at 160°C is $52-60 = -8$
the simple catalyst effect at 180°C is $64-72 = -8$

Thus the difference between (effect of) the catalysts is **independent** of which temperature is used. The interaction effect is still zero.

So we can say that temperature and catalyst are independent in their effects on yield. In reality, we need to qualify this to say they are *additively* independent (the ratios are not the same). We could also say that they are **additive** in their effects.

The practical import of this statement is that we can consider each factor separately. Indeed looking at the overall means for a factor will indicate what is happening in the experiment. For this experiment, the overall means are:

	Temperature (°C)	
	160	180
Mean	56	68

	Catalyst	
	A	B
Mean	66	58

So the differences between the means in these tables are the main effects of the factors. That is, the main effect of Temperature is 12 and that of Catalyst is -8. Note that in this case the main effects are the same as the individual difference calculated above and so they summarize the effect of the factors. Having used the two-way table of means to work out that there is no interaction, it can be abandoned for the purposes of summarizing the results of the analysis.

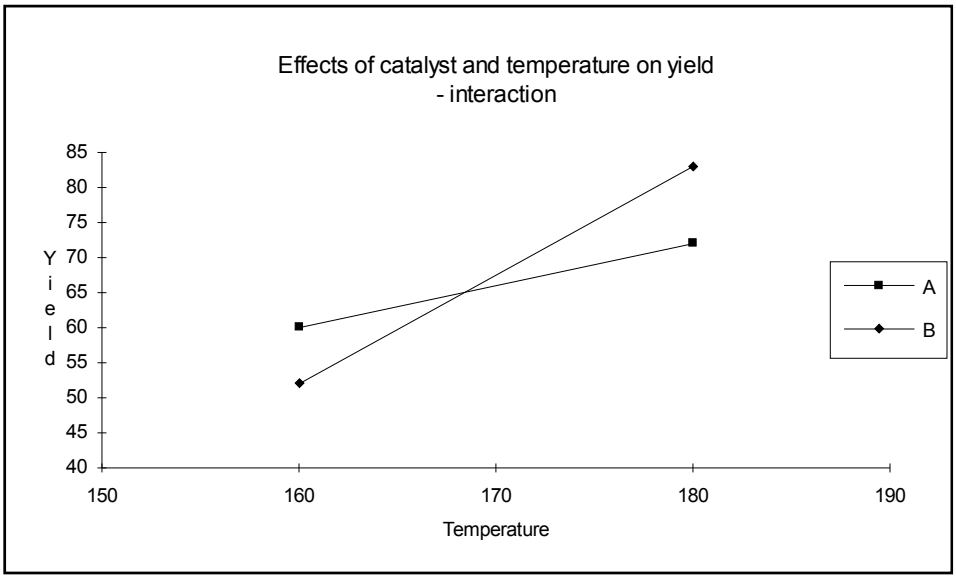
Example VII.3 Second chemical reactor experiment

Suppose the experiment was run with a second reactor and the results were as follows:

		Temperature (°C)	
		160	180
Catalyst	A	60	72
	B	52	83

The simple temperature effect for A is $72-60 = 12$
The simple temperature effect for B is $83-52 = 31$

Thus the difference between (effect of) the temperatures depends on which catalyst is used. Again, this statement is symmetrical in the factors and so we say that the two factors **interact**. The interaction plot for this example is shown in the following figure.



There is clearly an interaction as the lines have different slopes. In an experiment in which two factors interact, it is not appropriate to summarize the results using the overall means.

We first examine why using overall means is inappropriate. In the case of the example, the overall means are:

	Temperature (°C)	
	160	180
Mean	56	77.5

	Catalyst	
	A	B
Mean	66	67.5

The main effects cannot be equal to the simple effects in this case because the simple effects differ for the levels of the other factor. The main effects have no practical interpretation. It is the means for the combinations of the factors that must be examined to reveal the behaviour of the experimental material:

		Temperature (°C)	
		160	180
Catalyst	A	60	72
	B	52	83

Note that the interaction effect is computed as the half-difference between the catalyst effects at each temperature or vice-a-versa:

$$[(72–60) – (83–52)]/2 = [12 – 31]/2 = –9.5$$

or

$$[(52–60) – (83–72)]/2 = [–8 – 9]/2 = –9.5.$$ ■

The situation in which the two factors do not interact is the simpler of the two possibilities.

b) Advantages over one-factor-at-a-time experiments

It is sometimes suggested that rather than complicate things by putting several factors into a single experiment, it would be better to run several experiments each of which investigate one of the factors of interest. However, this is not the case as you will be unable to determine whether or not there is an interaction. Take our temperature-catalyst experiment again. One could run an experiment to examine just the temperature effect and would have to keep the catalyst used constant during the experiment. Suppose it is decided to use catalyst B. The implication of this is that the results of this experiment apply only to the conditions under which the experiment was run. That is, when catalyst B is used. To look at the other factor, a second experiment with 2 different catalysts would be run, but the same temperature used throughout say 160°C. WELL YOU HAVE ONLY APPLIED THREE OF THE FOUR POSSIBLE COMBINATIONS OF THE TWO FACTORS — catalyst A at 180°C has not been tested but catalyst B at 160°C has been tested twice as indicated in the following table:

			Experiment 1 Temperature (°C)	
			160	180
Experiment 2	Catalyst	A	60	?
		B	52	83

The results of the experiments would indicate that temperature increases yield by 31 gms and that the catalysts differ by 8 gms in yield. However, these conclusions are restricted — if we presume the factors act additively we would predict the yield for catalyst A at 160°C to be 60+31 = 83 + 8 = 91. This is quite clearly erroneous — we need the factorial experiment to determine if there is an interaction; exactly the same total amount of resources are involved in the two alternative strategies, assuming the number of replicates is the same in all the experiments.

In addition to allowing the detection of interaction, factorial experiment also have the advantage that, if the factors are additive then the main effects are estimated with greater precision. In the one-factor-at-a time experiments the effect of a particular factor is estimated as the difference between two means each based on *r* observations where *r* is the number of replicates of each treatments. In the factorial experiment the main effects of the factors are the difference between two means based on 2r observations which represents a $\sqrt{2}$ increase in precision. The improvement in precision will be greater for more factors and more levels; for a $3\times3\times3 = 3^3$ experiment the main effects are based on 9r observations leading to a 3 fold increase in precision over one-factor-at-a-time experiments.

To summarize, relative to one-factor-at-a-time experiments, factorial experiments have the advantages that:

1. if the factors interact, factorial experiments allow this to be detected and estimates of the interaction effect can be obtained, and
2. if the factors are independent, factorial experiments result in the estimation of the main effects with greater precision.

VII.C An example two-factor CRD experiment

The analysis of a factorial experiment is going to depend on the basic design that has been employed — that is, CRD, RCBD or LS. The design will determine the unrandomized factors and structure so that you basically perform the analysis appropriate to that design. The modification is that, instead of having just a single source in the analysis of variance corresponding to treatments, you will have a source for each factor and one for each possible combinations of factors.

a) Determining the ANOVA table for a two-Factor CRD

We will first use the procedure outlined in section VI.A for determining the analysis of variance table to establish the general form of the analysis for a two-factor CRD. Recall that, in general, such an experiment would have a total of *n* observations on two factors A and B with *a* and *b* levels, respectively.

a) Description of pertinent features of the study

1. Observational unit – a unit
2. Response variable – Y
3. Unrandomized factors – Units
4. Randomized factors – A, B
5. Type of study – Two-factor CRD

b) The experimental structure

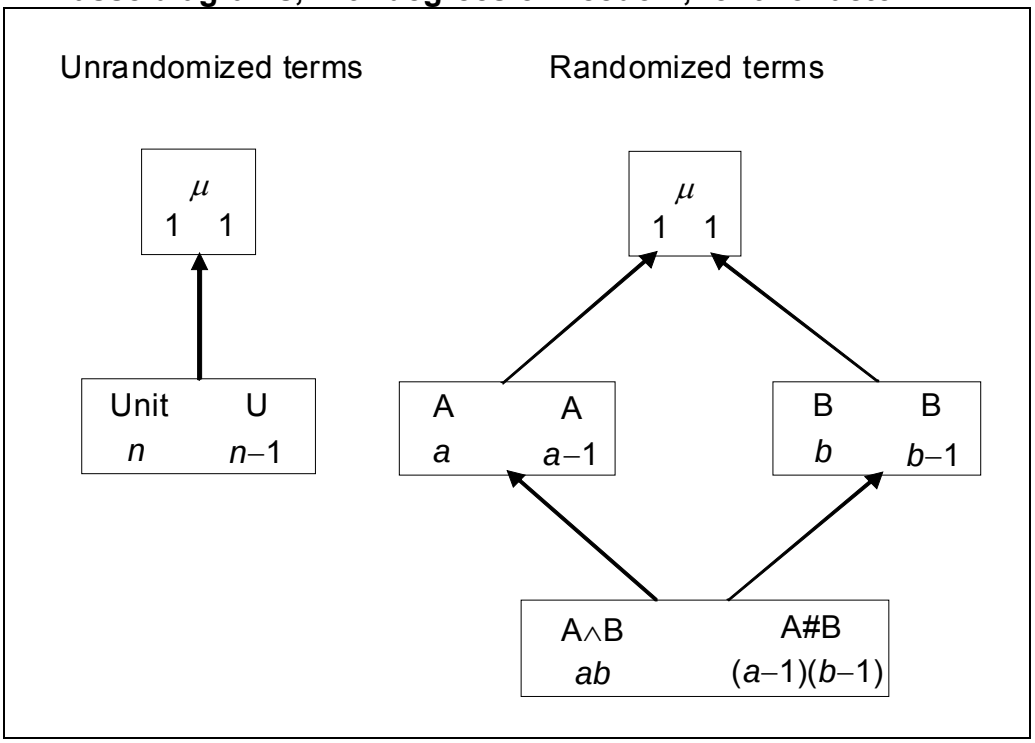
Structure	Formula
unrandomized	*n* Units
randomized	*a* A**b* B

c) Sources derived from the structure formulae

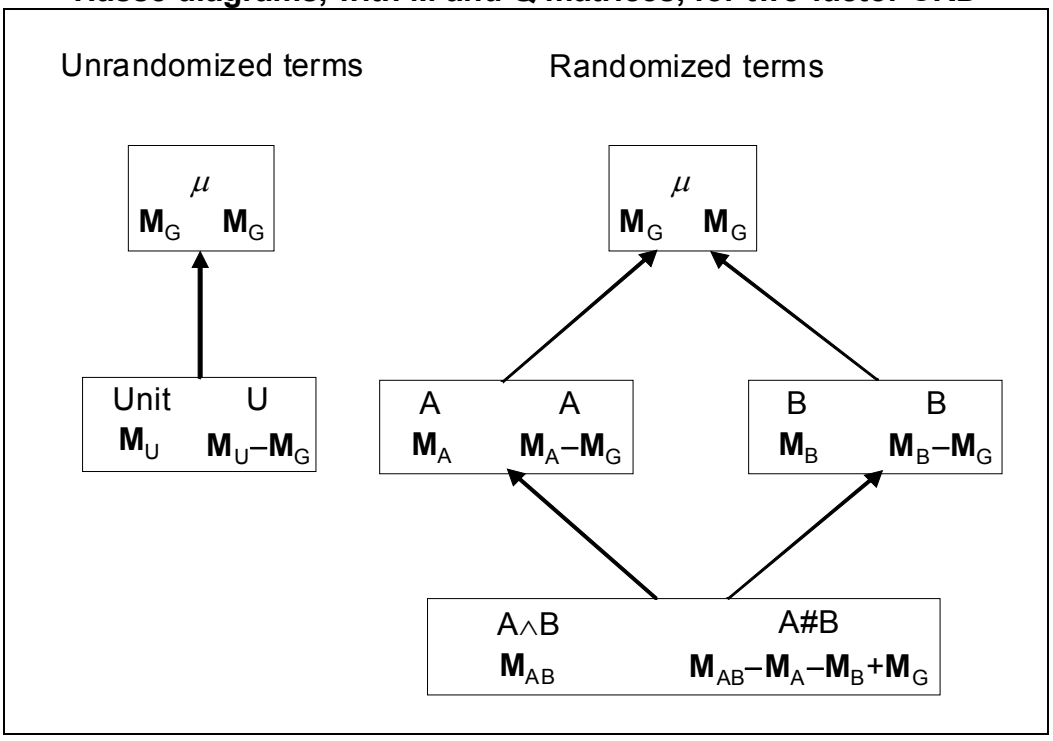
Units = Units
A*B = A + B + A#B.

d) Degrees of freedom and sums of squares

Hasse diagrams, with degrees of freedom, for two-factor CRD



Hasse diagrams, with M and Q matrices, for two-factor CRD



e) The analysis of variance table

Source	df	SSq
Units	$n-1$	$\mathbf{Y}'\mathbf{Q}_{U}\mathbf{Y}$
A	$a-1$	$\mathbf{Y}'\mathbf{Q}_{A}\mathbf{Y}$
B	$b-1$	$\mathbf{Y}'\mathbf{Q}_{B}\mathbf{Y}$
A#B	$(a-1)(b-1)$	$\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}$
Residual	$ab(r-1)$	$\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}$

f) Maximal expectation and variation models

Assume the randomized factors are fixed and that the unrandomized factor is a random factor. Then the potential expectation terms are A, B and A∧B. The variation term is: Units.

The maximal expectation model is

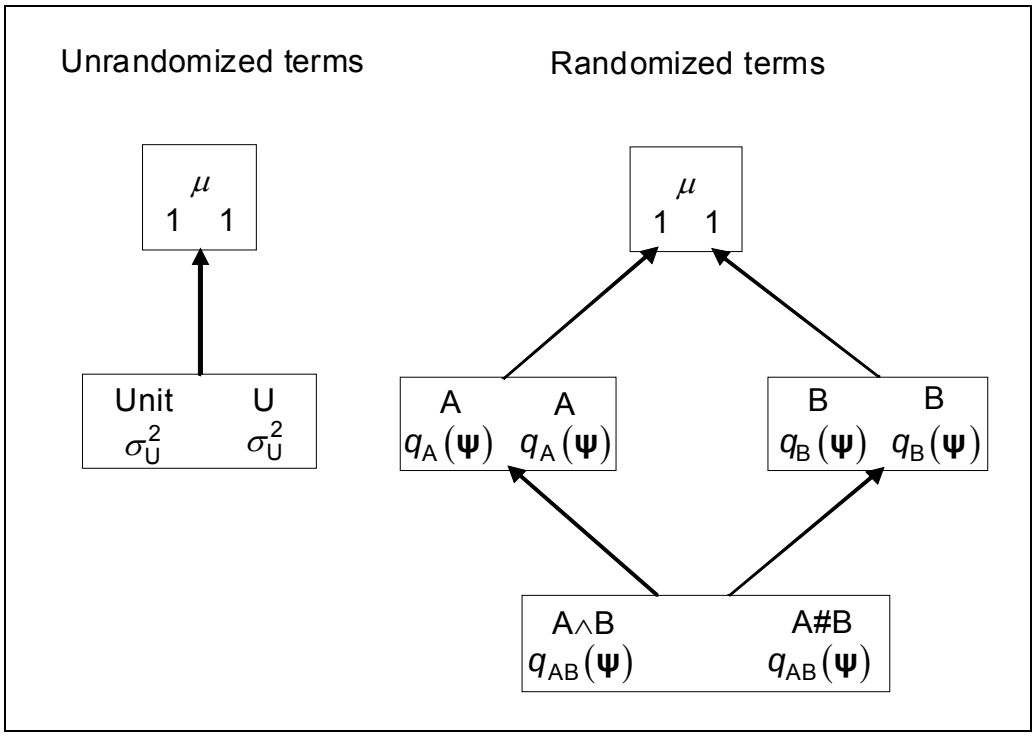
$$\psi = \mathrm{E}[\mathrm{Y}] = \mathrm{A}\wedge\mathrm{B}$$

and the variation model is

$$\mathrm{var}[\mathrm{Y}] = \mathrm{Units}$$

g) The expected mean squares.

Hasse diagrams, with expected mean squares, for two-factor CRD



Source	df	SSq	E[MSq]
Units	$n-1$	$\mathbf{Y}'\mathbf{Q}_U\mathbf{Y}$	
A	$a-1$	$\mathbf{Y}'\mathbf{Q}_A\mathbf{Y}$	$\sigma_U^2 + q_A(\psi)$
B	$b-1$	$\mathbf{Y}'\mathbf{Q}_B\mathbf{Y}$	$\sigma_U^2 + q_B(\psi)$
A#B	$(a-1)(b-1)$	$\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}$	$\sigma_U^2 + q_{AB}(\psi)$
Residual	$ab(r-1)$	$\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}$	σ_U^2

b) Analysis of an example

Example VII.4 Animal survival experiment

To demonstrate the analysis I will use the example from Box, Hunter and Hunter (sec. 7.7). In this experiment three poisons and four treatments (antidotes) were investigated. The 12 combinations of poisons and treatments were applied to animals using a CRD and the survival times of the animals measured (10 hours). The data are as follows:

		Treatment			
		1	2	3	4
Poison	I	0.31	0.82	0.43	0.45
		0.45	1.10	0.45	0.71
		0.46	0.88	0.63	0.66
		0.43	0.72	0.76	0.62
	II	0.36	0.92	0.44	0.56
		0.29	0.61	0.35	1.02
		0.40	0.49	0.31	0.71
		0.23	1.24	0.40	0.38
	III	0.22	0.30	0.23	0.30
		0.21	0.37	0.25	0.36
		0.18	0.38	0.24	0.31
		0.23	0.29	0.22	0.33

A. Description of pertinent features of the study

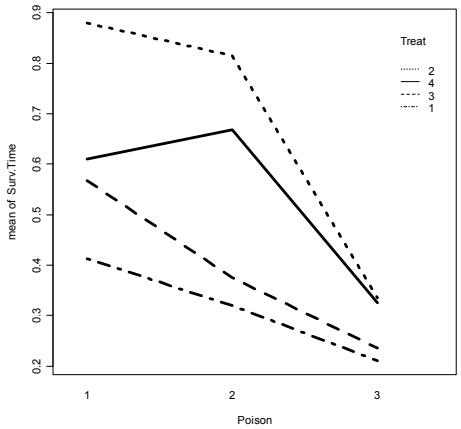
1. Observational unit – an animal
2. Response variable – Survival Time
3. Unrandomized factors – Animals
4. Randomized factors – Poisons, Treatments
5. Type of study – Two-factor CRD

B. The experimental structure

Structure	Formula
unrandomized	*48* Animals
randomized	*3* Poisons**4* Treatments

These are the steps that need to be performed before R is used to obtain the analysis. The remaining steps are left as an exercise for you.

The interaction plot for the initial graphical exploration is:



There is some evidence of an interaction in that the traces for each level of Treat look to be different.

The hypothesis test for the example is a follows:

Step 1: Set up hypotheses

a) H_0: there is no interaction between Poison and Treatment
H_1: there is an interaction between Poison and Treatment

b) H_0: $\rho_I = \rho_{II} = \rho_{III}$
H_1: not all population Poison means are equal

c) H_0: $\tau_A = \tau_B = \tau_C = \tau_D$
H_1: not all population Treatment means are equal

Set $\alpha = 0.05$.

Step 2: Calculate test statistics

The analysis of variance table for a two-factor CRD, with random factors being the unrandomized factors and fixed factors the randomized factors, is:

Source	df	SSq	MSq	E[MSq]	F	Prob
Animals	47	3.0051				
Poison	2	1.0330	0.5165	$\sigma^2_{\mathrm{A}} + q_{\mathrm{P}}(\psi)$	23.22	<.000
Treatment	3	0.9212	0.3071	$\sigma^2_{\mathrm{A}} + q_{\mathrm{T}}(\psi)$	13.81	<.001
Poison#Treat	6	0.2501	0.0417	$\sigma^2_{\mathrm{A}} + q_{\mathrm{PT}}(\psi)$	1.87	0.112
Residual	36	0.8007	0.0222	σ^2_{A}		

Step 3: Decide between hypotheses

The interaction of Poison and Treatment is not significant, so there is no interaction and the significance of the main effects is examined. Both main effects are highly significant. We will see that the model that best describes the data is the additive model $\boldsymbol{\psi}_{\mathrm{P+T}} = E[\mathbf{Y}] = \mathbf{X}_{\mathrm{P}}\boldsymbol{\rho} + \mathbf{X}_{\mathrm{T}}\boldsymbol{\tau}$.

Also, it remains to perform the usual diagnostic checking. ■

VII.D Indicator-variable models and estimation for factorial experiments

The models for the factorial experiments will depend on the design used in assigning the treatments — that is, CRD, RCBD or LS. The design will determine the unrandomized factors and the terms to be included involving those factors. They will also depend on the number of randomized factors.

a) Maximal model for two-factor CRD experiments

We will consider the models for the two-factor CRD. Let the total number of observations be *n* and the factors be A and B with *a* and *b* levels, respectively. Suppose that the combinations of A and B are each replicated *r* times — that is, $n = a \times b \times r$.

The maximal model for a two-factor CRD experiment, where the two randomized factors A and B are fixed, is:

$$\boldsymbol{\psi}_{\mathrm{AB}} = E[\mathbf{Y}] = \mathbf{X}_{\mathrm{AB}}(\alpha\beta) \text{ and } \mathbf{V} = \sigma^2_{\mathrm{U}}\mathbf{I}_n,$$

where $\mathbf{Y}$ is the *n*-random vector of random variables representing the response variable,

$(\alpha\beta)$ is the *ab*-vector of parameters for the A-B combinations,

$\mathbf{X}_{AB}$ is the $n \times ab$ matrix giving the combinations of A and B that occurred on each unit, i.e the **X** matrix for the generalized factor A∧B, and

σ_U^2 is the variability arising from different units.

Our model also involves assuming $\mathbf{Y} \sim N(\psi_{AB}, \mathbf{V})$.

We can give an expression for the **X** matrix in terms of direct products of **I**s and **1**s. To do this requires that the elements of the **Y** vector be ordered so that the values of the factors A and B are in standard order. We have previously used this term, but we here give a general definition.

Definition VII.6: Suppose we have k factors A_1, A_2, …, A_k with a_1, a_2, …, a_k levels, respectively, each of which has $n = r\prod_{i=1}^{k} a_i$ values where r is the number of times each levels combination of the k factors is repeated. The values of the factors are in **standard order** when

1. for any factor, the values of a factor consist of repetitions of the sequence of its levels that begins with the first level and goes to the last level; and
2. the number of consecutive values with the same level of a factor is a multiple of the product of the numbers of levels of all the factors to its right. ■

That is the values of the factors are systematically ordered in a hierarchical fashion — they are ordered according to A_1, then A_2, then A_3, … and then A_k. The repetitions of the levels combinations may be dispersed in any way that maintains the hierarchical pattern in the levels of the factors. For example, each of the levels combinations may be repeated consecutively or the complete set of levels combinations may be repeated or some combination of these two.

Suppose, the elements of the **Y** vector for our two-factor CRD are arranged so that the values of the factors A, B and the replicates are in standard order, as for a systematic layout. Then

$$\mathbf{X}_{AB} = \mathbf{I}_a \otimes \mathbf{I}_b \otimes \mathbf{1}_r$$

Example VII.5 2×2 Factorial experiment

Suppose A and B have two levels each and that each combination of A and B is replicated 3 times. Hence, $a = b = 2$, $r = 3$ and $n = 12$. Then

$$(\alpha\beta)' = (\alpha\beta_{11} \quad \alpha\beta_{12} \quad \alpha\beta_{21} \quad \alpha\beta_{22})$$

Now **Y** is arranged so that the values of A, B and the replicates are in standard order — that is

$$\mathbf{Y}' = (Y_{111} \quad Y_{112} \quad Y_{113} \quad Y_{121} \quad Y_{122} \quad Y_{123} \quad Y_{211} \quad Y_{212} \quad Y_{213} \quad Y_{221} \quad Y_{222} \quad Y_{223}).$$

Then,

$$\mathbf{X}_{AB} = \mathbf{I}_2 \otimes \mathbf{I}_2 \otimes \mathbf{1}_3$$

so that $\mathbf{X}_{AB}$ for the 4 level generalized factor A∧B is:

$$\mathbf{X}_{AB}$$

A	1	1	2	2
B	1	2	1	2

$$\begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

Notice that, as previously suggested, $\mathbf{X}_G$ can be written as a linear combination of the columns of each of the other three and that $\mathbf{X}_A$ and $\mathbf{X}_B$ can be written as linear combinations of the columns of $\mathbf{X}_{AB}$.

For the maximal model,

$$\psi_{AB} = E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} (\alpha\beta)_{11} \\ (\alpha\beta)_{12} \\ (\alpha\beta)_{21} \\ (\alpha\beta)_{22} \end{bmatrix} = \begin{bmatrix} (\alpha\beta)_{11} \\ (\alpha\beta)_{11} \\ (\alpha\beta)_{11} \\ (\alpha\beta)_{12} \\ (\alpha\beta)_{12} \\ (\alpha\beta)_{12} \\ (\alpha\beta)_{21} \\ (\alpha\beta)_{21} \\ (\alpha\beta)_{21} \\ (\alpha\beta)_{22} \\ (\alpha\beta)_{22} \\ (\alpha\beta)_{22} \end{bmatrix}$$

That is, the maximal model allows for a different response for each combination of A and B. ■

b) Alternative expectation models

The following rule is used in constructing this set of expectation models, which we term the **marginality-compliant models**.

Rule VII.1: The set of expectation models corresponds to the set of all possible combinations of potential expectation terms, subject to restriction that terms marginal to another expectation term are excluded from the model; it includes the minimal model that consists of a single term for the grand mean. ■

Remember that the marginality of terms is summarized in the Hasse diagrams of Generalized-factor Marginalities (see previous section) and can be deduced using definition VI.9. This definition states that one generalized factor is marginal to another if the factors in the marginal generalized factor are a subset of those in the other and this will occur irrespective of the replication of the levels of the generalized factors.

So for a two-factor CRD with all randomized factors fixed, then the potential expectation terms are A, B and A∧B. So the maximal model would presumably include all these terms: E[Y] = A + B + A∧B. However, marginal terms must be removed and so the maximal model reduces to E[Y] = A∧B. The next model leaves out A∧B and so we have the additive model E[Y] = A + B, and there are no marginal terms in this model. A simpler model than this leaves out one or other of A and B to produce the models E[Y] = A and E[Y] = B. The only other possible model is one that involves neither A nor B which is the model E[Y] = G.

Hence, in matrix terms, the alternative models for the expectation to be considered are:

$$\boldsymbol{\psi}_{AB} = \mathbf{X}_{AB}(\boldsymbol{\alpha\beta}) \qquad (\text{A and B interact in effect on response})$$
$$\boldsymbol{\psi}_{A+B} = \mathbf{X}_{A}\boldsymbol{\alpha} + \mathbf{X}_{B}\boldsymbol{\beta} \qquad (\text{A and B independently affect response})$$
$$\boldsymbol{\psi}_{A} = \mathbf{X}_{A}\boldsymbol{\alpha} \qquad (\text{A only affects response})$$
$$\boldsymbol{\psi}_{B} = \mathbf{X}_{B}\boldsymbol{\beta} \qquad (\text{B only affects response})$$
$$\boldsymbol{\psi}_{G} = \mathbf{X}_{G}\mu \qquad (\text{no factors affect response})$$

Again, suppose the elements of the **Y** vector for our two-factor CRD are arranged so that the values of the factors A, B and the replicates are in standard order, as for a systematic layout. Then the **X** matrices can be written as the following direct products:

$$\mathbf{X}_{G} = \mathbf{1}_{a} \otimes \mathbf{1}_{b} \otimes \mathbf{1}_{r} = \mathbf{1}_{abr},\ \mathbf{X}_{A} = \mathbf{I}_{a} \otimes \mathbf{1}_{b} \otimes \mathbf{1}_{r},\ \mathbf{X}_{B} = \mathbf{1}_{a} \otimes \mathbf{I}_{b} \otimes \mathbf{1}_{r} \text{ and } \mathbf{X}_{AB} = \mathbf{I}_{a} \otimes \mathbf{I}_{b} \otimes \mathbf{1}_{r}$$

Example VII.5 2×2 Factorial experiment (continued)

In this case,

$$\boldsymbol{\alpha}' = (\alpha_1 \quad \alpha_2),\ \boldsymbol{\beta}' = (\beta_1 \quad \beta_2) \text{ and } (\boldsymbol{\alpha\beta})' = (\alpha\beta_{11} \quad \alpha\beta_{12} \quad \alpha\beta_{21} \quad \alpha\beta_{22})$$

Now **Y** is arranged as follows:

$$\mathbf{Y}' = (Y_{111} \quad Y_{112} \quad Y_{113} \quad Y_{121} \quad Y_{122} \quad Y_{123} \quad Y_{211} \quad Y_{212} \quad Y_{213} \quad Y_{221} \quad Y_{222} \quad Y_{223}).$$

Then,

$$\mathbf{X}_{G} = \mathbf{1}_{2} \otimes \mathbf{1}_{2} \otimes \mathbf{1}_{3} = \mathbf{1}_{12},\ \mathbf{X}_{A} = \mathbf{I}_{2} \otimes \mathbf{1}_{2} \otimes \mathbf{1}_{3},\ \mathbf{X}_{B} = \mathbf{1}_{2} \otimes \mathbf{I}_{2} \otimes \mathbf{1}_{3} \text{ and } \mathbf{X}_{AB} = \mathbf{I}_{2} \otimes \mathbf{I}_{2} \otimes \mathbf{1}_{3}$$

so that the **X** matrices are as follows:

$$
\begin{array}{cccc}
\mathbf{X}_G & \mathbf{X}_A & \mathbf{X}_B & \mathbf{X}_{AB} \\
A & 1\ 2 & & 1\ 1\ 2\ 2 \\
B & & 1\ 2 & 1\ 2\ 1\ 2 \\
\begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} &
\begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \end{bmatrix} &
\begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \\ 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \end{bmatrix} &
\begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix}
\end{array}
$$

Notice that $\mathbf{X}_G$ can be written as a linear combination of the columns of each of the other three and that $\mathbf{X}_A$ and $\mathbf{X}_B$ can be written as linear combinations of the columns of $\mathbf{X}_{AB}$. ■

The relationships between the matrices noticed in the above example occur in general for two-factor factorial experiments arranged using a CRD, irrespective of the replication of the levels of A∧B.

Consequently, for indicator-variable terms (for generalized factors) as seen in the Hasse diagram,

- $\mathbf{X}_G\mu$ is marginal to $\mathbf{X}_A\alpha$, $\mathbf{X}_B\beta$ and $\mathbf{X}_{AB}(\alpha\beta)$; or $\mathbf{X}_G\mu \le \mathbf{X}_A\alpha$, $\mathbf{X}_B\beta$, $\mathbf{X}_{AB}(\alpha\beta)$;
- $\mathbf{X}_A\alpha$, $\mathbf{X}_B\beta$ are marginal to $\mathbf{X}_{AB}(\alpha\beta)$; or $\mathbf{X}_A\alpha$, $\mathbf{X}_B\beta \le \mathbf{X}_{AB}(\alpha\beta)$;

and, for models (made up of indicator-variable terms),

- $\psi_G = \mathbf{X}_G\mu$ is marginal to $\psi_A = \mathbf{X}_A\alpha$, $\psi_B = \mathbf{X}_B\beta$, $\psi_{A+B} = \mathbf{X}_A\alpha + \mathbf{X}_A\beta$ and $\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$; or $\psi_G \le \psi_A, \psi_B, \psi_{A+B}, \psi_{AB}$;
- $\psi_A = \mathbf{X}_A\alpha$ and $\psi_B = \mathbf{X}_B\beta$ are marginal to $\psi_{A+B} = \mathbf{X}_A\alpha + \mathbf{X}_A\beta$ and $\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$; or $\psi_A, \psi_B \le \psi_{A+B}, \psi_{AB}$;
- $\psi_{A+B} = \mathbf{X}_A\alpha + \mathbf{X}_A\beta$ is marginal to $\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$; or $\psi_{A+B} \le \psi_{AB}$.

More loosely, for terms, we say that G < A, B, A∧B and A, B < A∧B and, for models, we say that G < A, B, A+B, A∧B, A, B < A+B, A∧B, and A+B < A∧B.

The estimators of the expected values for the different expectation models considered for the two-factor CRD are all functions of means and so can be written in terms of mean operators, **M**s. Further, if **Y** is arranged so that the associated factors A, B and the replicates are in standard order, the **M** operators can be written as the direct product of **I** and **J** matrices. These expressions are summarized in the following table.

Model	Estimator
$\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$	$\hat{\psi}_{AB} = \left(\overline{\mathbf{A} \wedge \mathbf{B}}\right) = \mathbf{M}_{AB}\mathbf{Y} = r^{-1}\mathbf{I}_a \otimes \mathbf{I}_b \otimes \mathbf{J}_r\mathbf{Y}$
$\psi_{A+B} = \mathbf{X}_A\alpha + \mathbf{X}_B\beta$	$\hat{\psi}_{A+B} = \bar{\mathbf{A}} + \bar{\mathbf{B}} - \bar{\mathbf{G}}$
$\psi_A = \mathbf{X}_A\alpha$	$\hat{\psi}_A = \bar{\mathbf{A}} = \mathbf{M}_A\mathbf{Y} = (br)^{-1}\mathbf{I}_a \otimes \mathbf{J}_b \otimes \mathbf{J}_r\mathbf{Y}$
$\psi_B = \mathbf{X}_B\beta$	$\hat{\psi}_B = \bar{\mathbf{B}} = \mathbf{M}_B\mathbf{Y} = (ar)^{-1}\mathbf{J}_a \otimes \mathbf{I}_b \otimes \mathbf{J}_r\mathbf{Y}$
$\psi_G = \mathbf{X}_G\mu$	$\hat{\psi}_G = \bar{\mathbf{G}} = \mathbf{M}_G\mathbf{Y} = n^{-1}\mathbf{J}_a \otimes \mathbf{J}_b \otimes \mathbf{J}_r\mathbf{Y}$

where $\bar{\mathbf{G}}$ is the *n*-vector containing just the grand mean.
$\bar{\mathbf{A}}$ is the *n*-vector of A means.
$\bar{\mathbf{B}}$ is the *n*-vector of B means.
$\overline{\mathbf{A} \wedge \mathbf{B}}$ is the *n*-vector of means for the combinations of A and B, that is for the generalized factor A∧B.

Example VII.5 2×2 Factorial experiment (continued)

The mean vectors, produced by an **MY**, are as follows:

$$\bar{\mathbf{G}} \qquad \bar{\mathbf{A}} \qquad \bar{\mathbf{B}} \qquad \overline{\mathbf{A} \wedge \mathbf{B}}$$

$$\begin{bmatrix} \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \\ \bar{G} \end{bmatrix} \quad \begin{bmatrix} \bar{A}_1 \\ \bar{A}_1 \\ \bar{A}_1 \\ \bar{A}_1 \\ \bar{A}_1 \\ \bar{A}_1 \\ \bar{A}_2 \\ \bar{A}_2 \\ \bar{A}_2 \\ \bar{A}_2 \\ \bar{A}_2 \\ \bar{A}_2 \end{bmatrix} \quad \begin{bmatrix} \bar{B}_1 \\ \bar{B}_1 \\ \bar{B}_1 \\ \bar{B}_2 \\ \bar{B}_2 \\ \bar{B}_2 \\ \bar{B}_1 \\ \bar{B}_1 \\ \bar{B}_1 \\ \bar{B}_2 \\ \bar{B}_2 \\ \bar{B}_2 \end{bmatrix} \quad \begin{bmatrix} \overline{A_1 \wedge B_1} \\ \overline{A_1 \wedge B_1} \\ \overline{A_1 \wedge B_1} \\ \overline{A_1 \wedge B_2} \\ \overline{A_1 \wedge B_2} \\ \overline{A_1 \wedge B_2} \\ \overline{A_2 \wedge B_1} \\ \overline{A_2 \wedge B_1} \\ \overline{A_2 \wedge B_1} \\ \overline{A_2 \wedge B_2} \\ \overline{A_2 \wedge B_2} \\ \overline{A_2 \wedge B_2} \end{bmatrix}$$

■

VII.E Hypothesis testing using the ANOVA method for factorial experiments

An analysis of variance will be used to choose between the five alternative expectation models for a two-factor CRD, given in section VII.D, *Models and estimation for factorial experiments*. In this section we will use the generic names of A, B and Units for the factors in a two-factor CRD.

Recall the ANOVA table derived for the two factor experiment in section VII.C, *An example two-factor CRD experiment*.

Source	df	SSq	E[MSq]
Units	$n-1$	$\mathbf{Y}'\mathbf{Q}_{\mathrm{U}}\mathbf{Y}$	
A	$a-1$	$\mathbf{Y}'\mathbf{Q}_{\mathrm{A}}\mathbf{Y}$	$\sigma_{\mathrm{U}}^2 + q_{\mathrm{A}}(\psi)$
B	$b-1$	$\mathbf{Y}'\mathbf{Q}_{\mathrm{B}}\mathbf{Y}$	$\sigma_{\mathrm{U}}^2 + q_{\mathrm{B}}(\psi)$
A#B	$(a-1)(b-1)$	$\mathbf{Y}'\mathbf{Q}_{\mathrm{AB}}\mathbf{Y}$	$\sigma_{\mathrm{U}}^2 + q_{\mathrm{AB}}(\psi)$
Residual	$ab(r-1)$	$\mathbf{Y}'\mathbf{Q}_{\mathrm{U_{Res}}}\mathbf{Y}$	σ_{U}^2

In this section we look at the sums of squares and expected mean squares in more detail.

a) Sums of squares for the analysis of variance

Require the estimators of the following sum of squares for a two-factor CRD ANOVA: Total or Units, A, B, A#B and Residual. We will use the Hasse diagram giving expressions for the **Q** matrices in terms of **M** matrices.

Now a sum of squares $\mathbf{Y}'\mathbf{Q}\mathbf{Y}$ is the sum of squares of $\mathbf{Q}\mathbf{Y}$ from which we can derive an expression in terms of **M** and **Y**, and from these an expression in terms of mean vectors as follows:

Total or Units SSq: $\mathbf{Q}_{\mathrm{U}}\mathbf{Y} = (\mathbf{M}_{\mathrm{U}} - \mathbf{M}_{\mathrm{G}})\mathbf{Y} = \mathbf{Y} - \bar{\mathbf{G}} = \mathbf{D}_{\mathrm{G}}$

A SSq: $\mathbf{Q}_{\mathrm{A}}\mathbf{Y} = (\mathbf{M}_{\mathrm{A}} - \mathbf{M}_{\mathrm{G}})\mathbf{Y} = \bar{\mathbf{A}} - \bar{\mathbf{G}} = \mathbf{A}_e$

B SSq: $\mathbf{Q}_{\mathrm{B}}\mathbf{Y} = (\mathbf{M}_{\mathrm{B}} - \mathbf{M}_{\mathrm{G}})\mathbf{Y} = \bar{\mathbf{B}} - \bar{\mathbf{G}} = \mathbf{B}_e$

A#B SSq:
$$\mathbf{Q}_{\mathrm{AB}}\mathbf{Y} = (\mathbf{M}_{\mathrm{AB}} - \mathbf{M}_{\mathrm{A}} - \mathbf{M}_{\mathrm{B}} + \mathbf{M}_{\mathrm{G}})\mathbf{Y}$$
$$= \overline{\mathbf{A} \wedge \mathbf{B}} - \bar{\mathbf{A}} - \bar{\mathbf{B}} + \bar{\mathbf{G}} = (\mathbf{A} \wedge \mathbf{B})_e$$

Residual SSq:
$$\mathbf{Q}_{\mathrm{U_{Res}}}\mathbf{Y} = (\mathbf{M}_{\mathrm{U}} - \mathbf{M}_{\mathrm{AB}})\mathbf{Y} = \mathbf{Y} - \left(\overline{\mathbf{A} \wedge \mathbf{B}}\right) = \mathbf{D}_{\mathrm{AB}}$$
$$= \mathbf{Y} - (\mathbf{A} \wedge \mathbf{B})_e - \mathbf{A}_e - \mathbf{B}_e - \bar{\mathbf{G}}$$

Now all of the **Q**s and **M**s are symmetric and idempotent and FROM section VII.D, *Models and estimation for factorial experiments*, we have that

$$\bar{\mathbf{G}} = \mathbf{M}_{\mathrm{G}}\mathbf{Y} = n^{-1}\mathbf{J}_a \otimes \mathbf{J}_b \otimes \mathbf{J}_r\mathbf{Y}$$
$$\bar{\mathbf{A}} = \mathbf{M}_{\mathrm{A}}\mathbf{Y} = (br)^{-1}\mathbf{I}_a \otimes \mathbf{J}_b \otimes \mathbf{J}_r\mathbf{Y}$$
$$\bar{\mathbf{B}} = \mathbf{M}_{\mathrm{B}}\mathbf{Y} = (ar)^{-1}\mathbf{J}_a \otimes \mathbf{I}_b \otimes \mathbf{J}_r\mathbf{Y}$$
$$\left(\overline{\mathbf{A} \wedge \mathbf{B}}\right) = \mathbf{M}_{\mathrm{AB}}\mathbf{Y} = r^{-1}\mathbf{I}_a \otimes \mathbf{I}_b \otimes \mathbf{J}_r\mathbf{Y}$$

So, in order to compute the sums of squares, it is necessary to compute the vectors $\mathbf{D}_G$, $\mathbf{A}_e$, $\mathbf{B}_e$, $(\mathbf{A}\wedge\mathbf{B})_e$ and $\mathbf{D}_{AB}$. Then the sums of squares are the sums of squares of the elements of these vectors:

$$\mathbf{Y}'\mathbf{Q}_U\mathbf{Y} = \mathbf{D}_G'\mathbf{D}_G$$
$$\mathbf{Y}'\mathbf{Q}_A\mathbf{Y} = \mathbf{A}_e'\mathbf{A}_e$$
$$\mathbf{Y}'\mathbf{Q}_B\mathbf{Y} = \mathbf{B}_e'\mathbf{B}_e$$
$$\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y} = (\mathbf{A}\wedge\mathbf{B})_e'(\mathbf{A}\wedge\mathbf{B})_e$$
$$\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y} = \mathbf{D}_{AB}'\mathbf{D}_{AB}$$

So the analysis of variance table is constructed as follows:

Source	df	SSq	MSq	E[MSq]	F	p
Units	$n-1$	$\mathbf{Y}'\mathbf{Q}_U\mathbf{Y}$				
A	$a-1$	$\mathbf{Y}'\mathbf{Q}_A\mathbf{Y}$	$\frac{\mathbf{Y}'\mathbf{Q}_A\mathbf{Y}}{a-1} = s_A^2$	$\sigma_U^2 + q_A(\psi)$	$s_A^2/s_{U_{Res}}^2$	p_A
B	$b-1$	$\mathbf{Y}'\mathbf{Q}_B\mathbf{Y}$	$\frac{\mathbf{Y}'\mathbf{Q}_B\mathbf{Y}}{b-1} = s_B^2$	$\sigma_U^2 + q_B(\psi)$	$s_B^2/s_{U_{Res}}^2$	p_B
A#B	$(a-1)(b-1)$	$\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}$	$\frac{\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}}{(a-1)(b-1)} = s_{AB}^2$	$\sigma_U^2 + q_{AB}(\psi)$	$s_{AB}^2/s_{U_{Res}}^2$	p_{AB}
Residual	$ab(r-1)$	$\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}$	$\frac{\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}}{ab(r-1)} = s_{U_{Res}}^2$	σ_U^2		
Total	$abr-1$	$\mathbf{Y}'\mathbf{Q}_U\mathbf{Y}$				

Clearly, we can compute the sums of squares by decomposing **y** as follows:

$$\mathbf{y} = \bar{\mathbf{g}} + \mathbf{a}_e + \mathbf{b}_e + (\mathbf{a}\wedge\mathbf{b})_e + \mathbf{d}_{AB}$$

b) Expected mean squares

The expected mean squares involve three quadratic functions of the expectation vector: $q_A(\psi) = \psi'\mathbf{Q}_A\psi/(a-1)$, $q_B(\psi) = \psi'\mathbf{Q}_B\psi/(b-1)$ and $q_{AB}(\psi) = \psi'\mathbf{Q}_{AB}\psi/(a-1)(b-1)$. That is, their numerators are the sums of squares of

$$\mathbf{Q}_A\psi = (\mathbf{M}_A - \mathbf{M}_G)\psi,\ \mathbf{Q}_B\psi = (\mathbf{M}_B - \mathbf{M}_G)\psi \text{ and } \mathbf{Q}_{AB}\psi = (\mathbf{M}_{AB} - \mathbf{M}_A - \mathbf{M}_B + \mathbf{M}_G)\psi,$$

where ψ is the expectation vector for one of the five models $\psi_G = \mathbf{X}_G\mu$, $\psi_A = \mathbf{X}_A\alpha$, $\psi_B = \mathbf{X}_B\beta$, $\psi_{A+B} = \mathbf{X}_A\alpha + \mathbf{X}_B\beta$ and $\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$.

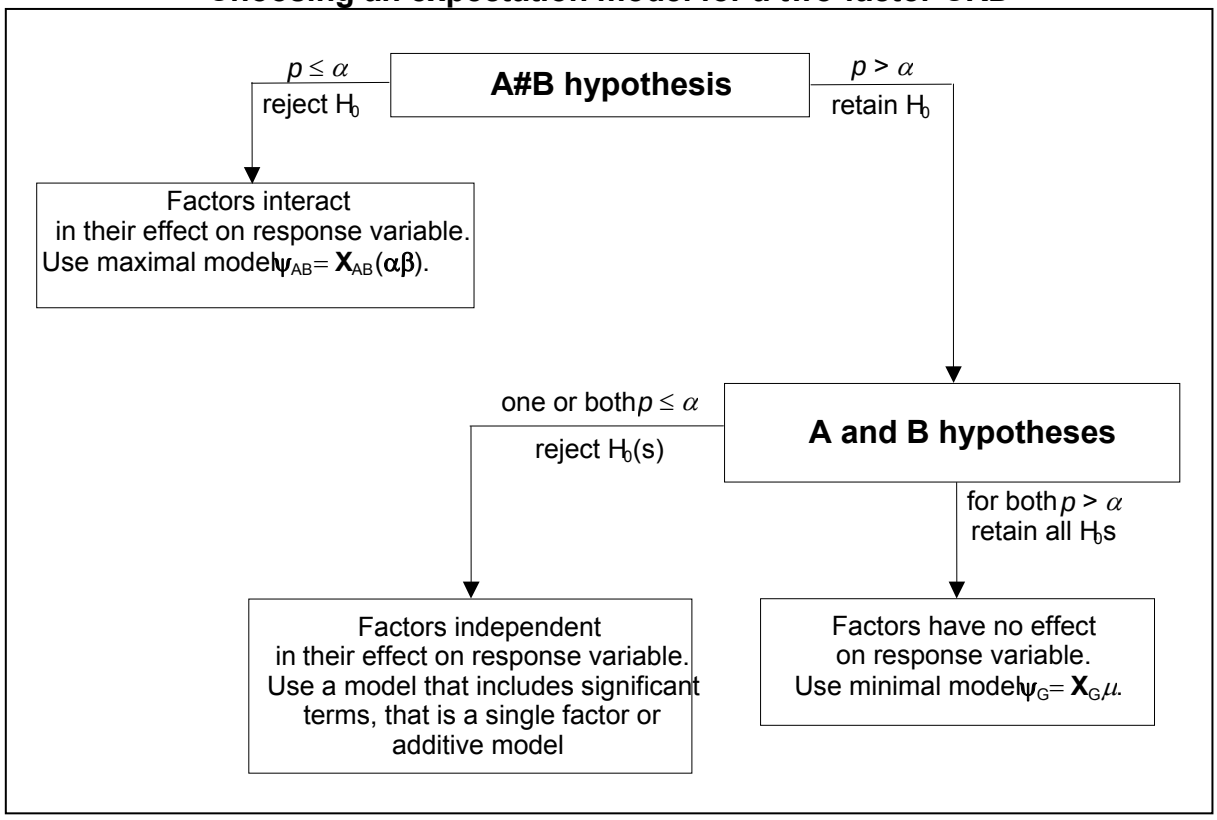
We require expressions for the quadratic functions under each of these models. The following table indicates when the quadratic functions are nonzero.

Quadratic functions in expected mean squares under alternative expectation models

	Source		
Expectation model	A	B	A#B
$\psi_G = \mathbf{X}_G\mu$	$q_A(\psi_G) = 0$	$q_B(\psi_G) = 0$	$q_{AB}(\psi_G) = 0$
$\psi_A = \mathbf{X}_A\alpha$	$q_A(\psi_A)$	$q_B(\psi_A) = 0$	$q_{AB}(\psi_A) = 0$
$\psi_B = \mathbf{X}_B\beta$	$q_A(\psi_B) = 0$	$q_B(\psi_B)$	$q_{AB}(\psi_B) = 0$
$\psi_{A+B} = \mathbf{X}_A\alpha + \mathbf{X}_B\beta$	$q_A(\psi_{A+B})$	$q_B(\psi_{A+B})$	$q_{AB}(\psi_{A+B}) = 0$
$\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$	$q_A(\psi_{AB})$	$q_B(\psi_{AB})$	$q_{AB}(\psi_{AB})$

Firstly, considering the column for source A#B, the only model for which $q_{AB}(\psi) \neq 0$ is $\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$. Consequently, A#B is significant indicates that $q_{AB}(\psi) > 0$ and that the maximal model is the appropriate model — no other model is consistent with a non-zero $q_{AB}(\psi)$. Secondly, considering the column for source A, $q_A(\psi) \neq 0$ occurs with either a model that includes $\mathbf{X}_A\alpha$ or the maximal model $\psi_{AB} = \mathbf{X}_{AB}(\alpha\beta)$. Now, if A#B is significant, we already know that the maximal model is appropriate and the test for A has no bearing on which model we should use. However, when A#B is not significant, we already know that the maximal model is not required and so a significant A indicates that the model should include $\mathbf{X}_A\alpha$. Thirdly for source B, provided A#B is not significant, a significant B indicates that the model should include $\mathbf{X}_B\beta$. This leads us to the following algorithm for selecting the appropriate model to describe the data.

Choosing an expectation model for a two-factor CRD



To determine the quadratic functions in the expected mean squares under the different models, as shown in the table above, note that

$$q_A(\psi) = \psi'\mathbf{Q}_A\psi/(a-1) = \psi'(\mathbf{M}_A - \mathbf{M}_G)\psi/(a-1) = \frac{rb\sum_{i=1}^{a}(\bar{\psi}_{i..} - \bar{\psi}_{...})^2}{(a-1)}$$

$$q_B(\psi) = \psi'\mathbf{Q}_B\psi/(b-1) = \psi'(\mathbf{M}_B - \mathbf{M}_G)\psi/(b-1) = \frac{ra\sum_{j=1}^{b}(\bar{\psi}_{.j.} - \bar{\psi}_{...})^2}{(b-1)}$$

where ψ_{ijk} is the element of the expectation vector for the *k*th unit and this unit received the *i*th level of A and the *j*th level of B,

$\bar{\psi}_{i..} = \sum_{j=1}^{b}\sum_{k=1}^{r}\psi_{ijk}/br$, $\bar{\psi}_{.j.} = \sum_{i=1}^{a}\sum_{k=1}^{r}\psi_{ijk}/ar$ and $\bar{\psi}_{...} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{r}\psi_{ijk}/abr$.

$$q_{AB}(\psi) = \psi'\mathbf{Q}_{AB}\psi/(a-1)(b-1) = \psi'(\mathbf{M}_{AB} - \mathbf{M}_A - \mathbf{M}_B + \mathbf{M}_G)\psi/(a-1)(b-1), = \frac{r\sum_{i=1}^{a}\sum_{j=1}^{b}(\bar{\psi}_{ij.} - \bar{\psi}_{i..} - \bar{\psi}_{.j.} + \bar{\psi}_{...})^2}{(a-1)(b-1)}$$

where $\bar{\psi}_{ij.} = \sum_{k=1}^{r}\psi_{ijk}/r$.

Example VII.5 2×2 Factorial experiment (continued)

The means $\bar{\psi}_{...}$, $\bar{\psi}_{i..}$, $\bar{\psi}_{.j.}$ and $\bar{\psi}_{ij.}$ are formed by applying the mean operators $\mathbf{M}_G$, $\mathbf{M}_A$, $\mathbf{M}_B$ and $\mathbf{M}_{AB}$ to the vector $\boldsymbol{\psi}$ as follows:

$$\mathbf{M}_G\boldsymbol{\psi} = \mathbf{M}_G \begin{bmatrix} \psi_{111} \\ \psi_{112} \\ \psi_{113} \\ \psi_{121} \\ \psi_{122} \\ \psi_{123} \\ \psi_{211} \\ \psi_{212} \\ \psi_{213} \\ \psi_{221} \\ \psi_{222} \\ \psi_{223} \end{bmatrix} = \begin{bmatrix} \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \\ \bar{\psi}_{...} \end{bmatrix}, \quad \mathbf{M}_A\boldsymbol{\psi} = \mathbf{M}_A \begin{bmatrix} \psi_{111} \\ \psi_{112} \\ \psi_{113} \\ \psi_{121} \\ \psi_{122} \\ \psi_{123} \\ \psi_{211} \\ \psi_{212} \\ \psi_{213} \\ \psi_{221} \\ \psi_{222} \\ \psi_{223} \end{bmatrix} = \begin{bmatrix} \bar{\psi}_{1..} \\ \bar{\psi}_{1..} \\ \bar{\psi}_{1..} \\ \bar{\psi}_{1..} \\ \bar{\psi}_{1..} \\ \bar{\psi}_{1..} \\ \bar{\psi}_{2..} \\ \bar{\psi}_{2..} \\ \bar{\psi}_{2..} \\ \bar{\psi}_{2..} \\ \bar{\psi}_{2..} \\ \bar{\psi}_{2..} \end{bmatrix}, \quad \mathbf{M}_B\boldsymbol{\psi}_{AB} = \mathbf{M}_B \begin{bmatrix} \psi_{111} \\ \psi_{112} \\ \psi_{113} \\ \psi_{121} \\ \psi_{122} \\ \psi_{123} \\ \psi_{211} \\ \psi_{212} \\ \psi_{213} \\ \psi_{221} \\ \psi_{222} \\ \psi_{223} \end{bmatrix} = \begin{bmatrix} \bar{\psi}_{.1.} \\ \bar{\psi}_{.1.} \\ \bar{\psi}_{.1.} \\ \bar{\psi}_{.2.} \\ \bar{\psi}_{.2.} \\ \bar{\psi}_{.2.} \\ \bar{\psi}_{.1.} \\ \bar{\psi}_{.1.} \\ \bar{\psi}_{.1.} \\ \bar{\psi}_{.2.} \\ \bar{\psi}_{\cdot 2.} \\ \bar{\psi}_{.2.} \end{bmatrix} \text{ and}$$

$$\mathbf{M}_{AB}\boldsymbol{\psi} = \mathbf{M}_{AB} \begin{bmatrix} \psi_{111} \\ \psi_{112} \\ \psi_{113} \\ \psi_{121} \\ \psi_{122} \\ \psi_{123} \\ \psi_{211} \\ \psi_{212} \\ \psi_{213} \\ \psi_{221} \\ \psi_{222} \\ \psi_{223} \end{bmatrix} = \begin{bmatrix} \bar{\psi}_{11.} \\ \bar{\psi}_{11.} \\ \bar{\psi}_{11.} \\ \bar{\psi}_{12.} \\ \bar{\psi}_{12.} \\ \bar{\psi}_{12.} \\ \bar{\psi}_{21.} \\ \bar{\psi}_{21.} \\ \bar{\psi}_{2.1} \\ \bar{\psi}_{22.} \\ \bar{\psi}_{22.} \\ \bar{\psi}_{22.} \end{bmatrix}.$$

where $\bar{\psi}_{i..} = \sum_{j=1}^{2} \sum_{k=1}^{3} \psi_{ijk} \big/ (2 \times 3)$. That is, $\bar{\psi}_{i..}$ is the mean of all parameters that have subscript *i* — it is said to be the mean over the subscripts that have been replaced by a dot. Similarly, $\bar{\psi}_{.j.} = \sum_{i=1}^{2} \sum_{k=1}^{3} \psi_{ijk} \big/ (2 \times 3)$ is the mean of all parameters that have subscript *j*, $\bar{\psi}_{...} = \sum_{i=1}^{2} \sum_{j=1}^{2} \sum_{k=1}^{3} \psi_{ijk} \big/ (2 \times 2 \times 3)$ is the mean over all subscripts, and $\bar{\psi}_{ij.} = \sum_{k=1}^{3} \psi_{ijk} \big/ 3$ is the mean of all parameters that have subscripts *i* and *j*. ■

Now we require $\bar{\psi}_{...}$, $\bar{\psi}_{i..}$, $\bar{\psi}_{.j.}$ and $\bar{\psi}_{ij.}$ under the alternative expectation models. To do this you have to realize that the elements of

- $\boldsymbol{\psi}_A$ are the α_i s, each α_i being repeated *rb* times in $\boldsymbol{\psi}_A$,
- $\boldsymbol{\psi}_B$ are the β_j s, each β_j being repeated *ra* times in $\boldsymbol{\psi}_B$ and
- $\boldsymbol{\psi}_{AB}$ are the $(\alpha\beta)_{ij}$ s, each $(\alpha\beta)_{ij}$ being repeated *r* times in $\boldsymbol{\psi}_{AB}$.

Also $\boldsymbol{\psi}_{A+B} = \boldsymbol{\psi}_A + \boldsymbol{\psi}_B$. Then the results of applying the mean operators $\mathbf{M}_G$, $\mathbf{M}_A$, $\mathbf{M}_B$ and $\mathbf{M}_{AB}$ to $\boldsymbol{\psi}_G$, $\boldsymbol{\psi}_A$, $\boldsymbol{\psi}_B$ and $\boldsymbol{\psi}_{AB}$ need to be obtained by substituting the parameters for a particular model into the elements ψ_{ijk} of $\boldsymbol{\psi}$.

Example VII.5 2×2 Factorial experiment (continued)

Here

$$\boldsymbol{\psi} = \begin{bmatrix} \psi_{111} \\ \psi_{112} \\ \psi_{113} \\ \psi_{121} \\ \psi_{122} \\ \psi_{123} \\ \psi_{211} \\ \psi_{212} \\ \psi_{213} \\ \psi_{221} \\ \psi_{222} \\ \psi_{223} \end{bmatrix} \text{ with } \boldsymbol{\psi}_G = \begin{bmatrix} \mu \\ \mu \\ \mu \\ \mu \\ \mu \\ \mu \\ \mu \\ \mu \\ \mu \\ \mu \\ \mu \\ \mu \end{bmatrix}, \boldsymbol{\psi}_A = \begin{bmatrix} \alpha_1 \\ \alpha_1 \\ \alpha_1 \\ \alpha_1 \\ \alpha_1 \\ \alpha_1 \\ \alpha_2 \\ \alpha_2 \\ \alpha_2 \\ \alpha_2 \\ \alpha_2 \\ \alpha_2 \end{bmatrix}, \boldsymbol{\psi}_B = \begin{bmatrix} \beta_1 \\ \beta_1 \\ \beta_1 \\ \beta_2 \\ \beta_2 \\ \beta_2 \\ \beta_1 \\ \beta_1 \\ \beta_1 \\ \beta_2 \\ \beta_2 \\ \beta_2 \end{bmatrix} \text{ and } \boldsymbol{\psi}_{AB} = \begin{bmatrix} (\alpha\beta)_{11} \\ (\alpha\beta)_{11} \\ (\alpha\beta)_{11} \\ (\alpha\beta)_{12} \\ (\alpha\beta)_{12} \\ (\alpha\beta)_{12} \\ (\alpha\beta)_{21} \\ (\alpha\beta)_{21} \\ (\alpha\beta)_{21} \\ (\alpha\beta)_{22} \\ (\alpha\beta)_{22} \\ (\alpha\beta)_{22} \end{bmatrix}.$$

That is, for $\boldsymbol{\psi}_G$, $\psi_{ijk} = \mu$, for $\boldsymbol{\psi}_A$, $\psi_{ijk} = \alpha_i$, for $\boldsymbol{\psi}_B$, $\psi_{ijk} = \beta_j$ and, for $\boldsymbol{\psi}_{AB}$, $\psi_{ijk} = (\alpha\beta)_{ij}$. Hence, for example for $\boldsymbol{\psi}_G$, $\bar{\psi}_{...} = \bar{\psi}_{i..} = \bar{\psi}_{.j.} = \bar{\psi}_{ij.} = \mu$. These can be obtained by substituting $\psi_{ijk} = \mu$ into the summation expressions for the different means or by applying the **M** operator matrices to $\boldsymbol{\psi}_G$.

You can derive expressions for the different expectation parameter means under the various models similarly. ■

The following table summarizes the general expressions for all the means under all the expectation models.

Expectation parameter means under alternative expectation models

Expectation model	Mean $\bar{\psi}_{...}$	$\bar{\psi}_{i..}$	$\bar{\psi}_{.j.}$	$\bar{\psi}_{ij.}$
$\boldsymbol{\psi}_G = \mathbf{X}_G\mu$	μ	μ	μ	μ
$\boldsymbol{\psi}_A = \mathbf{X}_A\boldsymbol{\alpha}$	$\bar{\alpha}_.$	α_i	$\bar{\alpha}_.$	α_i
$\boldsymbol{\psi}_B = \mathbf{X}_B\boldsymbol{\beta}$	$\bar{\beta}_.$	$\bar{\beta}_.$	β_j	β_j
$\boldsymbol{\psi}_{A+B} = \mathbf{X}_A\boldsymbol{\alpha} + \mathbf{X}_B\boldsymbol{\beta}$	$\bar{\alpha}_. + \bar{\beta}_.$	$\alpha_i + \bar{\beta}_.$	$\bar{\alpha}_. + \beta_j$	$\alpha_i + \beta_j$
$\boldsymbol{\psi}_{AB} = \mathbf{X}_{AB}(\boldsymbol{\alpha\beta})$	$\overline{(\alpha\beta)}_{..}$	$\overline{(\alpha\beta)}_{i.}$	$\overline{(\alpha\beta)}_{.j}$	$(\alpha\beta)_{ij}$

$\bar{\alpha}_. = \sum_{i=1}^{a}\alpha_i / a$, $\bar{\beta}_. = \sum_{j=1}^{b}\beta_j / b$, $\overline{(\alpha\beta)}_{i.} = \sum_{j=1}^{b}(\alpha\beta)_{ij} / b$, $\overline{(\alpha\beta)}_{.j} = \sum_{i=1}^{a}(\alpha\beta)_{ij} / a$ and $\overline{(\alpha\beta)}_{..} = \sum_{i=1}^{a}\ \sum_{j=1}^{b}(\alpha\beta)_{ij} / ab$

Now, $q_A(\psi) = \dfrac{rb\sum_{i=1}^{a}(\bar{\psi}_{i..} - \bar{\psi}_{...})^2}{(a-1)}$ so that $q_A(\psi_G) = q_A(\psi_B) = 0$,

$q_A(\psi_A) = q_A(\psi_{A+B}) = \dfrac{rb\sum_{i=1}^{a}(\alpha_i - \bar{\alpha}_.)^2}{(a-1)}$ and $q_A(\psi_{AB}) = \dfrac{rb\sum_{i=1}^{a}\left(\overline{(\alpha\beta)}_{i.} - \overline{(\alpha\beta)}_{..}\right)^2}{(a-1)}$.

Next, $q_B(\psi) = \dfrac{ra\sum_{j=1}^{b}(\bar{\psi}_{.j.} - \bar{\psi}_{...})^2}{(b-1)}$ so that $q_B(\psi_G) = q_B(\psi_A) = 0$,

$q_B(\psi_B) = q_B(\psi_{A+B}) = \dfrac{ra\sum_{j=1}^{b}(\beta_j - \bar{\beta}_.)^2}{(b-1)}$ and $q_B(\psi_{AB}) = \dfrac{ra\sum_{j=1}^{b}\left(\overline{(\alpha\beta)}_{.j} - \overline{(\alpha\beta)}_{..}\right)^2}{(b-1)}$.

Finally, $q_{AB}(\psi) = \dfrac{r\sum_{i=1}^{a}\sum_{j=1}^{b}(\bar{\psi}_{ij.} - \bar{\psi}_{i..} - \bar{\psi}_{.j.} + \bar{\psi}_{...})^2}{(a-1)(b-1)}$ so that

$q_{AB}(\psi_G) = q_{AB}(\psi_A) = q_{AB}(\psi_B) = 0$ and

$q_{AB}(\psi_{AB}) = \dfrac{r\sum_{i=1}^{a}\sum_{j=1}^{b}\left((\alpha\beta)_{ij} - \overline{(\alpha\beta)}_{i.} - \overline{(\alpha\beta)}_{.j} + \overline{(\alpha\beta)}_{..}\right)^2}{(a-1)(b-1)}$.

Now $q_A(\psi) = 0$ implies that $\bar{\psi}_{i..} - \bar{\psi}_{...} = 0$ or $\bar{\psi}_{i..} = \bar{\psi}_{...}$ for all *i*. That is, all $\bar{\psi}_{i..}$s are equal to the same value $\bar{\psi}_{...}$. Similarly, $q_B(\psi) = 0$ all $\bar{\psi}_{.j.}$s are equal to the same value $\bar{\psi}_{...}$. On the other hand, $q_{AB}(\psi) = 0$ implies that $\bar{\psi}_{ij.} - \bar{\psi}_{i..} - \bar{\psi}_{.j.} + \bar{\psi}_{...} = 0$ or $\bar{\psi}_{ij.} = \bar{\psi}_{i..} + \bar{\psi}_{.j.} - \bar{\psi}_{...}$. That is, that the $\bar{\psi}_{ij.}$s display an additive pattern. This will occur for all models except the maximal model where $\bar{\psi}_{ij.} - \bar{\psi}_{i..} - \bar{\psi}_{.j.} + \bar{\psi}_{...} = (\alpha\beta)_{ij} - \overline{(\alpha\beta)}_{i.} - \overline{(\alpha\beta)}_{.j} + \overline{(\alpha\beta)}_{..} \neq 0$.

c) Summary of the hypothesis test

Step 1: Set up hypotheses

a) H_0: there is no interaction between A and B

(or model simpler than $\mathbf{X}_{AB}(\alpha\beta)$ adequate)

$\left((\alpha\beta)_{ij} - \overline{(\alpha\beta)}_{i.} - \overline{(\alpha\beta)}_{.j} + \overline{(\alpha\beta)}_{..} = 0 \quad \text{for all } i, j\right)$

H_1: there is an interaction between A and B

$\left((\alpha\beta)_{ij} - \overline{(\alpha\beta)}_{i.} - \overline{(\alpha\beta)}_{.j} + \overline{(\alpha\beta)}_{..} \neq 0 \quad \text{for some } i, j\right)$

b) H_0: $\alpha_1 = \alpha_2 = ... = \alpha_a$ (or $\mathbf{X}_A\boldsymbol{\alpha}$ not required in model)
H_1: not all population A means are equal

c) H_0: $\beta_1 = \beta_2 = ... = \beta_b$ (or $\mathbf{X}_B\boldsymbol{\beta}$ not required in model)
H_1: not all population B means are equal

Set $\alpha = 0.05$.

Step 2: Calculate test statistics

The analysis of variance table is as follows:

Source	df	MSq	E[MSq]	F	p
Units	$n-1$				
A	$a-1$	$\frac{\mathbf{Y}'\mathbf{Q}_A\mathbf{Y}}{a-1} = s_A^2$	$\sigma_U^2 + q_A(\boldsymbol{\psi})$	$s_A^2 / s_{U_{Res}}^2$	p_A
B	$b-1$	$\frac{\mathbf{Y}'\mathbf{Q}_B\mathbf{Y}}{b-1} = s_B^2$	$\sigma_U^2 + q_B(\boldsymbol{\psi})$	$s_B^2 / s_{U_{Res}}^2$	p_B
A#B	$(a-1)(b-1)$	$\frac{\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}}{(a-1)(b-1)} = s_{AB}^2$	$\sigma_U^2 + q_{AB}(\boldsymbol{\psi})$	$s_{AB}^2 / s_{U_{Res}}^2$	p_{AB}
Residual	$ab(r-1)$	$\frac{\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}}{ab(r-1)} = s_{U_{Res}}^2$	σ_U^2		
Total	$abr-1$				

Step 3: Decide between hypotheses

The steps for choosing the model that best describes the expectation of the response is illustrated in the diagram given in the subsection d), *Expected mean squares*. The fundamental point of this diagram is that one first examines the A#B interaction that tests for whether $q_{AB}(\boldsymbol{\psi})$ is zero. If it is significant, the tests for A and B effects are not proceeded with as they are only relevant when A#B is not significant. For any hypothesis, if $\Pr\{F \geq F_O\} = p \leq \alpha$, then the evidence suggests that the null hypothesis be rejected.

If A#B is significant, we conclude that the maximal model $\boldsymbol{\psi}_{AB} = \mathbf{X}_{AB}(\boldsymbol{\alpha\beta})$ best describes the data. Having determined the model to be used for the data, there is no point to doing any further hypothesis tests; they will not provide any further information about the model.

However, if A#B is not significant, we conclude that the model $\psi = \mathbf{X}_{AB}(\alpha\beta)$ is not the best model for the data and that one of the models $\psi_G = \mathbf{X}_G\mu$, $\psi_A = \mathbf{X}_A\alpha$, $\psi_B = \mathbf{X}_B\beta$ or $\psi_{A+B} = \mathbf{X}_A\alpha + \mathbf{X}_B\beta$ will be better. The choice between these models depends on which of A and B are not significant. A term corresponding to the significant source must be included in the model. For example, if only B is significant, the model for the data would be $\psi = \mathbf{X}_B\beta$. If neither A nor B is significant, then the model for the data would be $\psi = \mathbf{X}_G\mu$.

d) Computation of ANOVA and diagnostic checking in R

The assumptions underlying a factorial experiment will be the same as for the basic design employed, except that residuals-versus-factor plots of residuals are also produced for all the factors in the experiment.

Example VII.4 Animal survival experiment (continued)

We previously determined the following experimental structure for this experiment.

Structure	Formula
unrandomized	*48* Animals
randomized	*3* Poisons**4* Treatments

From this we conclude that the model to be used for `aov` function is

```
Surv.Time ~ Poison * Treat + Error(Animals).
```

The following instructions will enter the data into the R `data.frame` `Fac2Pois.dat` and produce the analysis of variance for this example:

```
Fac2Pois.dat <- fac.gen(generate = list(Poison = 3, 4, Treat=4))
Fac2Pois.dat <- data.frame(Animals = factor(1:48), Fac2Pois.dat)
Fac2Pois.dat$Surv.Time <-
                  c(0.31,0.82,0.43,0.45,0.45,1.10,0.45,0.71,0.46,0.88,0.63,0.66,
                    0.43,0.72,0.76,0.62,0.36,0.92,0.44,0.56,0.29,0.61,0.35,1.02,
                    0.40,0.49,0.31,0.71,0.23,1.24,0.40,0.38,0.22,0.30,0.23,0.30,
                    0.21,0.37,0.25,0.36,0.18,0.38,0.24,0.31,0.23,0.29,0.22,0.33)
attach(Fac2Pois.dat)
Fac2Pois.dat
interaction.plot(Poison, Treat, Surv.Time, lwd=4)
Fac2Pois.aov <- aov(Surv.Time ~ Poison * Treat + Error(Animals), Fac2Pois.dat)
summary(Fac2Pois.aov)
```

Note the use of the function `interaction.plot` to produce this plot for the initial graphical exploration. We do not produce boxplots in this case, in part because they look at just the overall effects of one factor and are only relevant if the factors are independent.

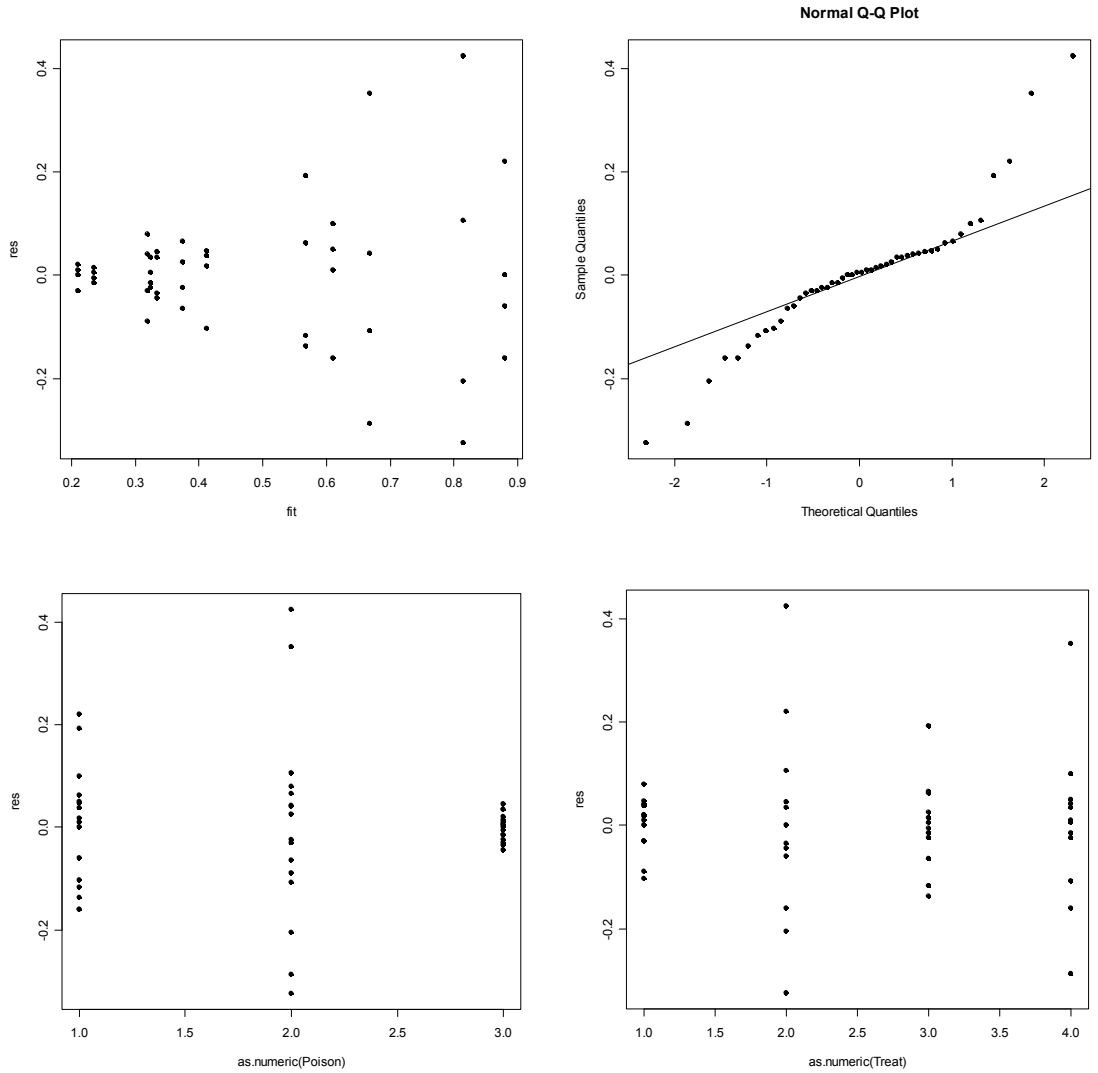
The R output produced by these instructions is:

```
> Fac2Pois.dat <- fac.gen(generate = list(Poison = 3, 4, Treat=4))
> Fac2Pois.dat <- data.frame(Animals = factor(1:48), Fac2Pois.dat)
> Fac2Pois.dat$Surv.Time <-
+                   c(0.31,0.82,0.43,0.45,0.45,1.10,0.45,0.71,0.46,0.88,0.63,0.66,
+                     0.43,0.72,0.76,0.62,0.36,0.92,0.44,0.56,0.29,0.61,0.35,1.02,
+                     0.40,0.49,0.31,0.71,0.23,1.24,0.40,0.38,0.22,0.30,0.23,0.30,
+                     0.21,0.37,0.25,0.36,0.18,0.38,0.24,0.31,0.23,0.29,0.22,0.33)
> attach(Fac2Pois.dat)
> Fac2Pois.dat
   Animals Poison Treat Surv.Time
1        1      1     1      0.31
2        2      1     2      0.82
3        3      1     3      0.43
4        4      1     4      0.45
5        5      1     1      0.45
6        6      1     2      1.10
7        7      1     3      0.45
8        8      1     4      0.71
9        9      1     1      0.46
10      10      1     2      0.88
11      11      1     3      0.63
12      12      1     4      0.66
13      13      1     1      0.43
14      14      1     2      0.72
15      15      1     3      0.76
16      16      1     4      0.62
17      17      2     1      0.36
18      18      2     2      0.92
19      19      2     3      0.44
20      20      2     4      0.56
21      21      2     1      0.29
22      22      2     2      0.61
23      23      2     3      0.35
24      24      2     4      1.02
25      25      2     1      0.40
26      26      2     2      0.49
27      27      2     3      0.31
28      28      2     4      0.71
29      29      2     1      0.23
30      30      2     2      1.24
31      31      2     3      0.40
32      32      2     4      0.38
33      33      3     1      0.22
34      34      3     2      0.30
35      35      3     3      0.23
36      36      3     4      0.30
37      37      3     1      0.21
38      38      3     2      0.37
39      39      3     3      0.25
40      40      3     4      0.36
41      41      3     1      0.18
42      42      3     2      0.38
43      43      3     3      0.24
44      44      3     4      0.31
45      45      3     1      0.23
46      46      3     2      0.29
47      47      3     3      0.22
48      48      3     4      0.33
> interaction.plot(Poison, Treat, Surv.Time, lwd=4)
> Fac2Pois.aov <- aov(Surv.Time ~ Poison * Treat + Error(Animals), Fac2Pois.dat)
> summary(Fac2Pois.aov)

Error: Animals
             Df  Sum Sq Mean Sq F value    Pr(>F)
Poison        2 1.03301 0.51651 23.2217 3.331e-07
Treat         3 0.92121 0.30707 13.8056 3.777e-06
Poison:Treat  6 0.25014 0.04169  1.8743    0.1123
Residuals    36 0.80073 0.02224
```

As the experiment was set up as a CRD, the assumptions underlying its analysis will be the same as for the CRD and its diagnostic checking the same. In particular, Tukey's one-degree-of-freedom-for-nonadditivity cannot be computed.

The R output produced by the expressions that deal with diagnostic checking is as follows:

```
> #
> # Diagnostic checking
> #
> res <- resid.errors(Fac2Pois.aov)
> fit <- fitted.errors(Fac2Pois.aov)
> plot(fit, res, pch=16)
> plot(as.numeric(Poison), res, pch=16)
> plot(as.numeric(Treat), res, pch=16)
> qqnorm(res, pch=16)
> qqline(res)
```



The residual-versus-fitted-values, residuals-versus-Poison, residuals-versus-Treat and normal probability plots both indicate a problem with the assumptions. The residual-versus-fitted-values plot is displaying strong funnel-shape so that variance is increasing with fitted values and this heterogeneity is reflected in the residuals-versus-factors plots. The normal probability plot is not displaying a straight-line trend

so that the data is displaying nonnormality. The question is would a transformation fix the problem and, if so, which one? ■

e) Box-Cox transformations for correcting transformable non-additivity

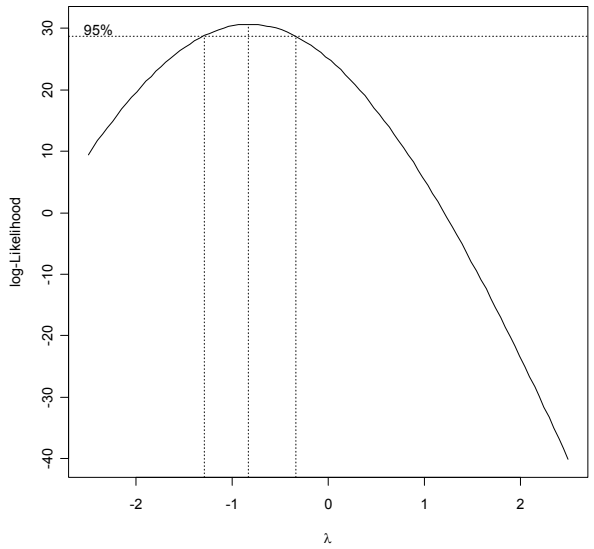
Box, Hunter and Hunter (sec. 7.9) describe the Box-Cox procedure for determining the appropriate power transformation for a set of data. It has been implemented in the R function `boxcox` supplied in the MASS library that comes with R. When you run this procedure you obtain a plot of the log-likelihood of λ, the power of the transformation to be used (for $\lambda = 0$ use the ln transformation). However, the function does not work with `aovlist` objects and so the `aov` function must be repeated without the `Error` function.

Example VII.4 Animal survival experiment (continued)

The following output has been obtained for the example and it indicates that, as the log likelihood is a maximum around $\lambda = -1$, the reciprocal transformation should be used. The reciprocal of the survival time will be the death rate — the number that die per unit time.

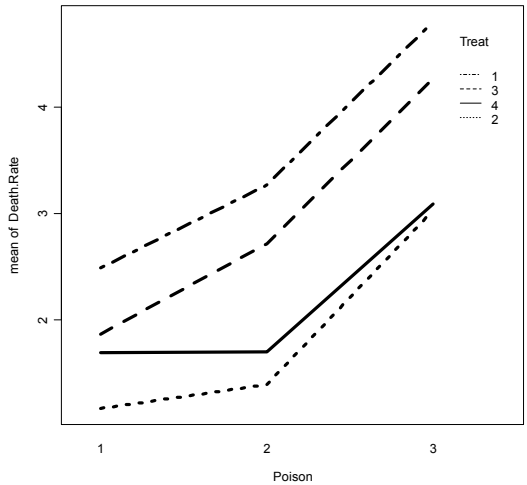
```
> Fac2Pois.NoError.aov <- aov(Surv.Time ~ Poison * Treat, Fac2Pois.dat)
> library(MASS)

        The following object(s) are masked from package:MASS :

         Animals

> boxcox(Fac2Pois.NoError.aov, lambda=seq(from = -2.5, to = 2.5, len=20),
+        plotit=T)
```

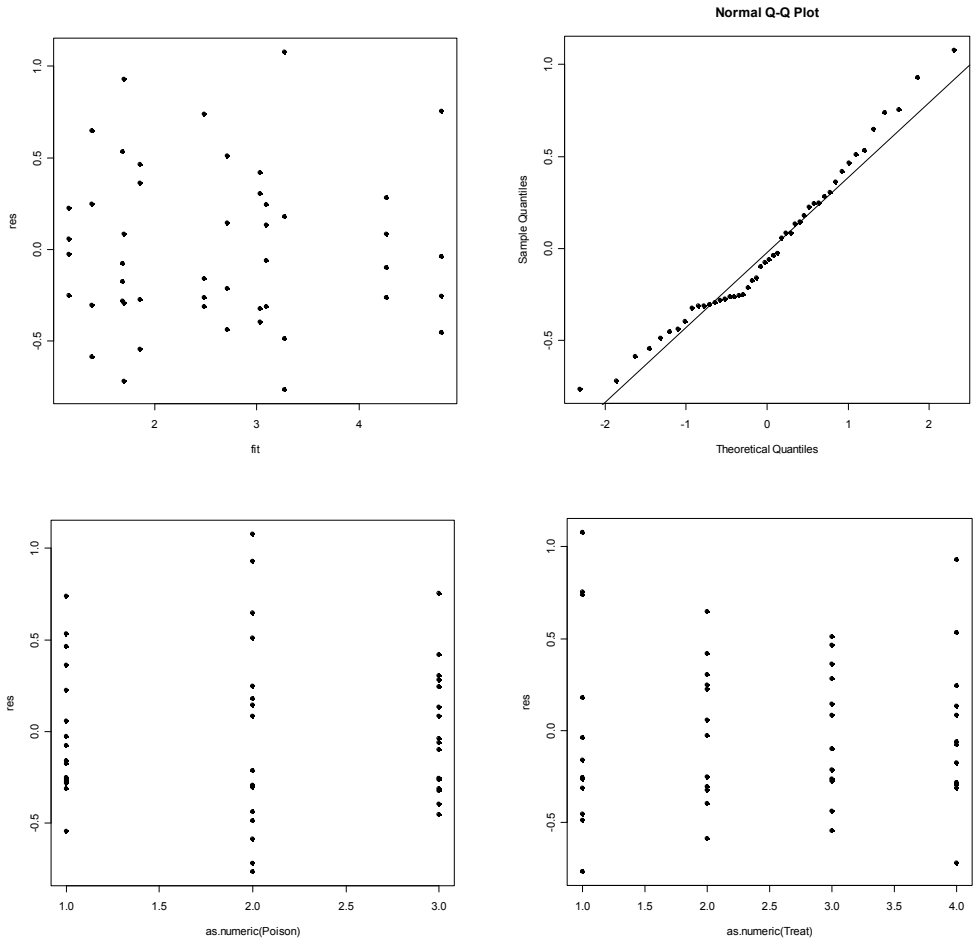
The message reporting the masking of Animals is saying that there is a vector Animals that is part of the MASS library that is being overshadowed by Animals in `Fac2Pois.dat`.



To repeat the analysis on the reciprocals I entered expressions that produced the following output. The first expression detachs the `Fac2Pois.dat` data.frame, the second adds `Death.Rate` to the data.frame and the last reattaches the data.frame to refresh the information available in R. The rest of the expressions repeat expressions from the original analysis with `Surv.time` replaced by `Death.Rate` appropriately.

```
> detach(Fac2Pois.dat)
> Fac2Pois.dat$Death.Rate <- 1/Fac2Pois.dat$Surv.Time
> attach(Fac2Pois.dat)

        The following object(s) are masked from package:MASS :

         Animals

> interaction.plot(Poison, Treat, Death.Rate, lwd=4)
> Fac2Pois.DR.aov <- aov(Death.Rate ~ Poison * Treat + Error(Animals),
Fac2Pois.dat)
> summary(Fac2Pois.DR.aov)

Error: Animals
            Df Sum Sq Mean Sq F value    Pr(>F)
Poison       2 34.877  17.439 72.6347 2.310e-13
Treat        3 20.414   6.805 28.3431 1.376e-09
Poison:Treat 6  1.571   0.262  1.0904    0.3867
Residuals   36  8.643   0.240
> res <- resid.errors(Fac2Pois.DR.aov)
> fit <- fitted.errors(Fac2Pois.DR.aov)
> plot(fit, res, pch=16)
> plot(as.numeric(Poison), res, pch=16)
> plot(as.numeric(Treat), res, pch=16)
> qqnorm(res, pch=16)
> qqline(res)
```





A comparison of the untransformed and transformed analyses follows:

		UNTRANSFORMED				TRANSFORMED		
Source	df	MSq	F	Prob	df	MSq	F	Prob
Animals	47				47			
Poison	2	0.5165	23.22	0.0000	2	17.4386	72.63	<0.001
Treatment	3	0.3071	13.81	0.0000	3	6.8048	28.34	<0.001
Poison#Treat	6	0.0417	1.87	0.1112	6	0.2618	1.09	0.387
Residual	36	0.0222			36	0.2401		

The analysis of the transformed data indicates that there is no interaction on the transformed scale with the interaction mean square being nearly equal to the Residual mean squares. This is confirmed by the interaction plot in which the traces are approximately parallel. The main effect mean squares are even larger than before indicating that we are able to separate the treatments even more on the transformed scale.

The diagnostic checking now indicates that all the assumptions are met. ■

VII.F Treatment differences

As usual the examination of treatment differences can be based on multiple comparisons or submodels. If all the factors are qualitative, multiple comparison procedures would be performed on the appropriate tables of means. If one or more of the factors are quantitative then submodels would be appropriate.

a) Multiple comparisons procedures

For two factor experiments, there will be altogether three tables of means, namely one for each of A, B and A∧B. Which table is of interest depends on the results of the hypothesis tests outlined above. However, in all cases Tukey's HSD procedure will be employed to determine which means are significantly different.

A#B Interaction significant

In this case you look at the table of means for the A∧B combinations.

		A						
		1	2	3	.	.	.	*a*
	1	x	x	x	.	.	.	x
	2	x	x	x	.	.	.	x
	.	.	.	.	.	.	.	.
B	.	.	.	.	.	.	.	.
	.	.	.	.	.	.	.	.
	b	x	x	x	.	.	.	x

$$w(5\%) = \frac{q_{ab,\upsilon,0.05}}{\sqrt{2}} s_{\bar{x}_d} = \frac{q_{ab,\upsilon,0.05}}{\sqrt{2}} s\sqrt{\frac{2}{r}}$$

There are at least two possibilities for which differences you investigate using this table. Which you do depends on which of the following is the researcher's objective(s):

1. finding the levels combination(s) of the factors that maximize (or minimize) the response variable or describing the response variable differences between all the levels combinations of the factors
2. for each level of one factor, finding the level of the other factor that maximizes (or minimizes) the response variable or describing the response variable differences between the levels of the other factor
3. finding a level of one factor for which there is no difference between the levels of the other factor

The first of these involves examining all possible pairs of differences between means for the levels combinations of the two factors. The other two involve examining the pairs of mean differences between the levels of one factor *for each level of the other factor*, i.e. in slices of the table for each level of the other factor; thus the simple effects are examined.

A#B interaction not significant

In this case examine the A and B tables of means for the significant lines.

	A						
	1	2	3	.	.	.	*a*
Means	x	x	x	.	.	.	x

$$w(5\%) = \frac{q_{a,\nu,0.05}}{\sqrt{2}} s_{\bar{x}_d} = \frac{q_{a,\nu,0.05}}{\sqrt{2}} s\sqrt{\frac{2}{rb}}$$

	B						
	1	2	3	.	.	.	*b*
Means	x	x	x	.	.	.	x

$$w(5\%) = \frac{q_{b,\nu,0.05}}{\sqrt{2}} s_{\bar{x}_d} = \frac{q_{b,\nu,0.05}}{\sqrt{2}} s\sqrt{\frac{2}{ra}}$$

That is, we examine each factor separately, using main effects. This is done in R using the function `model.tables`, to get the tables of means, and the function `qtukey`, to get the studentized range values.

Example VII.4 Animal survival experiment (continued)

For our example, the tables of means and studentized ranges are:

```
> #
> # multiple comparisons
> #
> model.tables(Fac2Pois.DR.aov, type="means")
Tables of means
Grand mean

2.622376

 Poison
Poison
    1     2     3
1.801 2.269 3.797

 Treat
Treat
    1     2     3     4
3.519 1.862 2.947 2.161

 Poison:Treat
      Treat
Poison 1     2     3     4
     1 2.487 1.163 1.863 1.690
     2 3.268 1.393 2.714 1.702
     3 4.803 3.029 4.265 3.092
> q.PT <- qtukey(0.95, 12, 36)
> q.PT
[1] 4.93606
```

```
> q.P <- qtukey(0.95, 3, 36)
> q.P
[1] 3.456758
> q.T <- qtukey(0.95, 4, 36)
> q.T
[1] 3.808798
```

For our example, as the interaction is not significant, the overall tables of means are examined.

For the Poison means,

$$w(5\%) = \frac{3.456758}{\sqrt{2}} \times \sqrt{\frac{0.240 \times 2}{16}} = 0.42$$

Clearly, all Poison means are significantly different.

For Treat means,

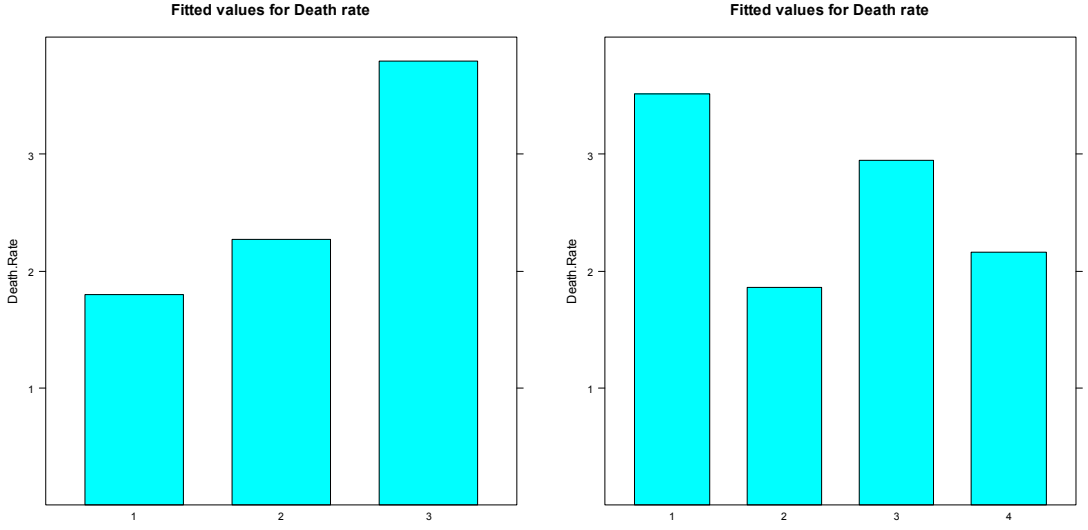
$$w(5\%) = \frac{3.808798}{\sqrt{2}} \times \sqrt{\frac{0.240 \times 2}{12}} = 0.54$$

Examination of the Treat means reveals that all but Treats 2 and 4 are different.

The expressions to produce the means for plotting in bar chart are as follows:

```
> #
> # Plotting means
> #
> Fac2Pois.DR.tab <- model.tables(Fac2Pois.DR.aov, type="means")
> Fac2Pois.DR.Poison.Means <-
+               data.frame(Poison = levels(Poison),
+                          Death.Rate = as.vector(Fac2Pois.DR.tab$tables$Poison))
> barchart(Death.Rate ~ Poison, main="Fitted values for Death rate", ylim=c(0,4),
+               data=Fac2Pois.DR.Poison.Means)
> Fac2Pois.DR.Treat.Means <-
+               data.frame(Treatment = levels(Treat),
+                          Death.Rate = as.vector(Fac2Pois.DR.tab$tables$Treat))
> barchart(Death.Rate ~ Treat, main="Fitted values for Death rate", ylim=c(0,4),
+               data=Fac2Pois.DR.Treat.Means)
```

The bar charts, produced using 2D-Graphs, are as follows:



Thus the maximum death rate would obtain with Poison 3 and Treat 1 and the minimum with Poison 1 and either Treat 2 or 4 (as these two Treats not significantly different.).

If the interaction had been significant, then we would have had to examine the 12 means in the Treat by Poison table, not the two overall tables examined above. Tukey's HSD would have been computed using the studentized range for 12 treatments. That is,

$$w(5\%) = \frac{4.93606}{\sqrt{2}} \times \sqrt{\frac{0.240 \times 2}{4}} = 1.21$$

Using this value, we might have looked to determine which combination of Treat and Poison resulted in the maximum death rate or, for each treatment, which poison gave the maximum death rate. ■

b) Polynomial submodels

As stated previously, the formal expression for maximal indicator-variable model for a two-factor CRD experiment, where the two randomized factors A and B are fixed, is:

$$\boldsymbol{\psi} = E[\mathbf{Y}] = \mathbf{X}_{\text{AB}}(\boldsymbol{\alpha\beta}) \text{ and } \mathbf{V} = \sigma_{\text{U}}^2 \mathbf{I}_n ,$$

where $\mathbf{Y}$ is the n-random vector of random variables representing the response variable,

$(\boldsymbol{\alpha\beta})$ is the ab-vector of parameters for the A-B combinations, and

σ_{U}^2 is the variability arising from different units.

In respect of fitting polynomial submodels, two situations are possible:

i) one factor only is quantitative, or
ii) both factors are quantitative.

One quantitative and one qualitative factor

In investigating submodels for a two-factor factorial with one factor, B say, quantitative, the following set of models, in terms of a single observation, for the expectation is considered:

$E\left[Y_{ijk}\right] = (\alpha\beta)_{ij}$	depends on combination of A and B
$E\left[Y_{ijk}\right] = \alpha_i + (\alpha\gamma)_{i1} x_{\beta_j} + (\alpha\gamma)_{i2} x_{\beta_j}^2$	quadratic response to B, differing for A
$E\left[Y_{ijk}\right] = \alpha_i + (\alpha\gamma)_{i1} x_{\beta_j}$	linear response to B, differing for A
$E\left[Y_{ijk}\right] = \alpha_i + \beta_j$	nonsmooth, independent response to A & B
$E\left[Y_{ijk}\right] = \alpha_i + \gamma_1 x_{\beta_j} + \gamma_2 x_{\beta_j}^2$	quadratic response to B, intercept differs for A
$E\left[Y_{ijk}\right] = \alpha_i + \gamma_1 x_{\beta_j}$	linear response to B, intercept differs for A
$E\left[Y_{ijk}\right] = \alpha_i$	nonsmooth response, depends on A only
$E\left[Y_{ijk}\right] = \beta_j$	nonsmooth response, depends on B only
$E\left[Y_{ijk}\right] = \mu + \gamma_1 x_{\beta_j} + \gamma_2 x_{\beta_j}^2$	quadratic response to B, A has no effect
$E\left[Y_{ijk}\right] = \mu + \gamma_1 x_{\beta_j}$	linear response to B, A has no effect
$E\left[Y_{ijk}\right] = \mu$	neither factor affects the response

where Y_{ijk} is the random variable representing the response variable for the *k*th unit that received the *i*th level of factor A and the *j*th level of factor B,

μ is the overall level of the response variable in the experiment,

α_i is the overall effect of the *i*th level of factor A on the response,

x_{β_j} is the value of the *j*th level of factor B,

γ_1 and γ_2 are the linear and quadratic coefficients of the equation describing the change in response as the level of B changes,

β_j is the overall effect of the *j*th level of factor B on the response,

$(\alpha\gamma)_{i1}$ and $(\alpha\gamma)_{i2}$ are the linear and quadratic coefficients of the equation describing, for the *i*th level of A, the change in response as the level of B changes,

$(\alpha\beta)_{ij}$ is the interaction between the *i*th level of A and the *j*th level of B.

The matrix expressions for these models are as follows:

$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta)$ depends on combination of A and B

$E[\mathbf{Y}] = \mathbf{X}_A\alpha + \mathbf{X}_{A1}(\alpha\gamma)_1 + \mathbf{X}_{A2}(\alpha\gamma)_2$ quadratic response to B, differing for A

$E[\mathbf{Y}] = \mathbf{X}_A\alpha + \mathbf{X}_{A1}(\alpha\gamma)_1$ linear response to B, differing for A

$E[\mathbf{Y}] = \mathbf{X}_A\alpha + \mathbf{X}_B\beta$ nonsmooth, independent response to A & B

$E[\mathbf{Y}] = \mathbf{X}_A\alpha + \mathbf{X}_1\gamma_1 + \mathbf{X}_2\gamma_2$ quadratic response to B, intercept differs for A

$E[\mathbf{Y}] = \mathbf{X}_A\alpha + \mathbf{X}_1\gamma_1$ linear response to B, intercept differs for A

$E[\mathbf{Y}] = \mathbf{X}_A\alpha$ nonsmooth response, depends on A only

$E[\mathbf{Y}] = \mathbf{X}_B\beta$ nonsmooth response, depends on B only

$E[\mathbf{Y}] = \mathbf{X}_G\mu + \mathbf{X}_1\gamma_1 + \mathbf{X}_2\gamma_2$ quadratic response to B, A has no effect

$E[\mathbf{Y}] = \mathbf{X}_G\mu + \mathbf{X}_1\gamma_1$ linear response to B, A has no effect

$E[\mathbf{Y}] = \mathbf{X}_G\mu$ neither factor affects the response

where $(\alpha\beta) = \{(\alpha\beta)_{ij}\}$ is an *ab*-vector of effects

$(\alpha\gamma)_1 = \{(\alpha\gamma)_{i1}\}$ is an *a*-vector of linear coefficients

$(\alpha\gamma)_2 = \{(\alpha\gamma)_{i2}\}$ is an *a*-vector of quadratic coeffients

$\alpha = \{\alpha_i\}$ is an *a*-vector of effects

$\beta = \{\beta_j\}$ is a *b*-vector of effects

$\gamma_2' = [\gamma_1 \quad \gamma_2]$

$\mathbf{X}_1$ is an *n*-vector containing the values of the levels of B

$\mathbf{X}_2$ is an *n*-vector containing the squared values of the levels of B

$\mathbf{X}_{A1}$ is an $n \times a$ matrix whose *i*th column contains the values of the levels of B for just those units that received the *i*th level of A

$\mathbf{X}_{A2}$ is an $n \times a$ matrix whose *i*th column contains the squared values of the levels of B for just those units that received the *i*th level of A

The models for non-smooth response are the indicator-variable models discussed previously. The first three models are interaction models, the next three are additive models involving both factors and the remainder, except the last, are single factor models.

Example VII.6 Effect of operating temperature on light output of an oscilloscope tube

Suppose an experiment was to be conducted to investigate the effect of the operating temperatures 75, 100, 125 and 150, for three glass types, on the light output of an oscilloscope tube. Further suppose that this was done using a completely randomized design with two replicates of each treatment combination. Then the following **X** matrices would be involved in the models for the analysis of the experiment:

$$\mathbf{X}_1\gamma_1 = \begin{bmatrix} 75 \\ 75 \\ 100 \\ 100 \\ 125 \\ 125 \\ 150 \\ 150 \\ 75 \\ 75 \\ 100 \\ 100 \\ 125 \\ 125 \\ 150 \\ 150 \\ 75 \\ 75 \\ 100 \\ 100 \\ 125 \\ 125 \\ 150 \\ 150 \end{bmatrix} \gamma_1$$

$$\mathbf{X}_{A1}(\alpha\gamma)_1 = \begin{bmatrix} 75 & 0 & 0 \\ 75 & 0 & 0 \\ 100 & 0 & 0 \\ 100 & 0 & 0 \\ 125 & 0 & 0 \\ 125 & 0 & 0 \\ 150 & 0 & 0 \\ 150 & 0 & 0 \\ 0 & 75 & 0 \\ 0 & 75 & 0 \\ 0 & 100 & 0 \\ 0 & 100 & 0 \\ 0 & 125 & 0 \\ 0 & 125 & 0 \\ 0 & 150 & 0 \\ 0 & 150 & 0 \\ 0 & 0 & 75 \\ 0 & 0 & 75 \\ 0 & 0 & 100 \\ 0 & 0 & 100 \\ 0 & 0 & 125 \\ 0 & 0 & 125 \\ 0 & 0 & 150 \\ 0 & 0 & 150 \end{bmatrix} \begin{bmatrix} (\alpha\gamma)_{11} \\ (\alpha\gamma)_{21} \\ (\alpha\gamma)_{31} \end{bmatrix}, \mathbf{X}_{A2}(\alpha\gamma)_2 = \begin{bmatrix} 5625 & 0 & 0 \\ 5265 & 0 & 0 \\ 10000 & 0 & 0 \\ 10000 & 0 & 0 \\ 15625 & 0 & 0 \\ 15625 & 0 & 0 \\ 22500 & 0 & 0 \\ 22500 & 0 & 0 \\ 0 & 5625 & 0 \\ 0 & 5625 & 0 \\ 0 & 10000 & 0 \\ 0 & 10000 & 0 \\ 0 & 15625 & 0 \\ 0 & 15625 & 0 \\ 0 & 22500 & 0 \\ 0 & 22500 & 0 \\ 0 & 0 & 5625 \\ 0 & 0 & 5625 \\ 0 & 0 & 10000 \\ 0 & 0 & 10000 \\ 0 & 0 & 15625 \\ 0 & 0 & 15625 \\ 0 & 0 & 22500 \\ 0 & 0 & 22500 \end{bmatrix} \begin{bmatrix} (\alpha\gamma)_{12} \\ (\alpha\gamma)_{22} \\ (\alpha\gamma)_{32} \end{bmatrix}$$

■

The above models are ordered from the most complex to the simplest. Why this set of expectation models? Along with rule VII.1, the following rule is used in formulating them.

Rule VII.2: An expectation model must include all polynomial terms of lower degree than a polynomial term that has been put in the model. ■

The following definitions allow you to determine if a polynomial term is of lower degree.

Definition VII.7: A **polynomial term** is one in which the **X** matrix involves the quantitative levels of a factor(s). ■

Definition VII.8: The **degree** for a polynomial term with respect to a quantitative factor is the power to which levels of that factor are to be raised in this term. ■

Definition VII.9: A polynomial term is said to be of **lower degree** than a second polynomial term if, for each quantitative factor in first term, its degree is less than or equal to its degree in the second term and the degree of at least one factor in the first term is less than that of the same factor in the second term. ■

As before, γs are used for the coefficients of polynomial terms and a numeric subscript for each quantitative fixed factor in the experiment is placed on the γs to indicate the degree(s) to which the factor(s) is(are) raised.

Note that the term $\mathbf{X}_1\gamma_1$ is not marginal to $\mathbf{X}_2\gamma_2$ — the column $\mathbf{X}_1$ is not a linear combination of the column $\mathbf{X}_2$. However, the degree of $\mathbf{X}_1\gamma_1$ is less than $\mathbf{X}_2\gamma_2$ and the degree rule above implies that if term $\mathbf{X}_2\gamma_2$ is included in the model, so must the term $\mathbf{X}_1\gamma_1$. As far as the marginality of *models* is concerned, the model involving just $\mathbf{X}_1\gamma_1$ is marginal to the model consisting of $\mathbf{X}_1\gamma_1$ and $\mathbf{X}_2\gamma_2$ — that is, the model $E[\mathbf{Y}] = \mathbf{X}_G\mu + \mathbf{X}_1\gamma_1$ is marginal to $E[\mathbf{Y}] = \mathbf{X}_G\mu + \mathbf{X}_1\gamma_1 + \mathbf{X}_2\gamma_2$. Also note that the term $\mathbf{X}_1\gamma_1$ is marginal to $\mathbf{X}_{A1}(\alpha\gamma)_1$ since $\mathbf{X}_1$ is the sum of the columns of $\mathbf{X}_{A1}$. Consequently, a model containing $\mathbf{X}_{A1}(\alpha\gamma)_1$ will not contain $\mathbf{X}_1\gamma_1$.

In general, the models to which a particular model is marginal will be found above it in the list; however, a model is marginal to only some, not all, of the models above it in this list. Note that the last four models differ from the four models immediately above them only in not including α.

The analysis of variance table for a two-factor CRD with one quantitative factor is:

Source	df	SSq
Units	$n-1$	$\mathbf{Y}'\mathbf{Q}_U\mathbf{Y}$
A	$a-1$	$\mathbf{Y}'\mathbf{Q}_A\mathbf{Y}$
B	$b-1$	$\mathbf{Y}'\mathbf{Q}_B\mathbf{Y}$
Linear	1	$\mathbf{Y}'\mathbf{Q}_{B_L}\mathbf{Y}$
Quadratic	1	$\mathbf{Y}'\mathbf{Q}_{B_Q}\mathbf{Y}$
Deviations	$b-3$	$\mathbf{Y}'\mathbf{Q}_{B_{Dev}}\mathbf{Y}$
A#B	$(a-1)(b-1)$	$\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}$
$A\#B_{Linear}$	$a-1$	$\mathbf{Y}'\mathbf{Q}_{AB_L}\mathbf{Y}$
$A\#B_{Quadratic}$	$a-1$	$\mathbf{Y}'\mathbf{Q}_{AB_Q}\mathbf{Y}$
Deviations	$(a-1)(b-3)$	$\mathbf{Y}'\mathbf{Q}_{AB_{Dev}}\mathbf{Y}$
Residual	$ab(r-1)$	$\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}$

In deciding between the various hypotheses one must take into account rules rules VII.1 and VII.2 about the marginality and degrees of terms in the models. The following strategy should be employed in determining which of the models is to be used to describe the data.

For Deviations

Only if the terms to which a term is marginal are not significant then, if $P(F \geq F_{calc}) \leq 0.05$, the evidence suggests that the null hypothesis be rejected and the term must be incorporated in the model. Deviations for B is marginal to Deviations for A#B so that if the latter is significant, the Deviations for B is not tested; indeed no further testing occurs as the maximal model has to be used to describe the data.

If deviations terms are significant, then one has to revert to using multiple comparisons.

For $A\#B_{Linear}$ and $A\#B_{Quadratic}$

Only if the polynomial terms are not of lower degree than a significant polynomial term then, if $P(F \geq F_{calc}) \leq 0.05$, the evidence suggests that the null hypothesis be rejected and the term be incorporated in the model. $A\#B_{Linear}$ is of lower degree than $A\#B_{Quadratic}$ so that if the latter is significant, $A\#B_{Linear}$ is not tested.

For A, Linear for B, Quadratic for B

Only if the terms to which a term is marginal and the polynomial terms are not of lower degree than a significant polynomial term then, if $P(F \geq F_{calc}) \leq 0.05$, the evidence suggests that the null hypothesis be rejected and the term be

incorporated in the model. For example, for the Linear term for B, it is of lower degree than the Quadratic term for B and it is marginal to $A\#B_{Linear}$ so that if either of these is significant, Linear for B is not tested.

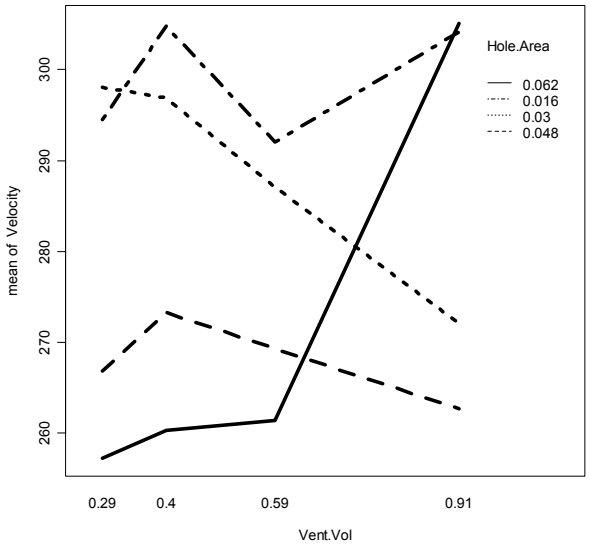
Both factors quantitative

Example VII.7 Muzzle velocity of an antipersonnel weapon

In a two-factor CRD experiment with two replicates the effect of Vent volume and Discharge hole area on the muzzle velocity of a mortar-like antipersonnel weapon was investigated. The muzzle velocity is given in the following table.

Vent	Discharge hole area			
volume	0.016	0.03	0.048	0.062
0.29	294.9	295.0	270.5	258.6
	294.1	301.1	263.2	255.9
0.40	301.7	293.1	278.6	257.1
	307.9	300.6	267.9	263.6
0.59	285.5	285.0	269.6	262.6
	298.6	289.1	269.1	260.3
0.91	303.1	277.8	262.2	305.3
	305.3	266.4	263.2	304.9

Notice that both factors are quantitative. Here is the `interaction.plot` produced using R.



Pretty clear that there is an interaction. ■

The maximal model for a two-factor factorial with both factors quantitative is the same as when there is only one qualitative factor.

The expression for the maximal polynomial submodel, in terms of a single observation, is:

$$E\left[Y_{ijk}\right] = \mu + \gamma_{10}x_{\alpha_i} + \gamma_{20}x_{\alpha_i}^2 + \gamma_{01}x_{\beta_j} + \gamma_{02}x_{\beta_j}^2 + \gamma_{11}x_{\alpha_i}x_{\beta_j} + \gamma_{12}x_{\alpha_i}x_{\beta_j}^2 + \gamma_{21}x_{\alpha_i}^2x_{\beta_j} + \gamma_{22}x_{\alpha_i}^2x_{\beta_j}^2$$

where Y_{ijk} is the random variable representing the response variable for the *k*th unit that received the *i*th level of factor A and the *j*th level of factor B,

μ is the overall level of the response variable in the experiment,

x_{α_i} is the value of the *i*th level of factor A,

x_{β_j} is the value of the *j*th level of factor B,

γs are the coefficients of the equation describing the change in response as the levels of A and/or B changes with the first subscript indicating the degree with respect to factor A and the second subscript indicating the degree with respect to factor B,

We could write this model as $E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{G}}\mu + \mathbf{X}\boldsymbol{\gamma}_{22}$ where $\boldsymbol{\gamma}'_{22} = \left[\gamma_{10} \quad \gamma_{20} \quad \gamma_{01} \quad \gamma_{02} \quad \gamma_{11} \quad \gamma_{12} \quad \gamma_{21} \quad \gamma_{22}\right]$ and $\mathbf{X} = \left[\mathbf{X}_{10} \quad \mathbf{X}_{20} \quad \mathbf{X}_{01} \quad \mathbf{X}_{02} \quad \mathbf{X}_{11} \quad \mathbf{X}_{12} \quad \mathbf{X}_{21} \quad \mathbf{X}_{22}\right]$ is an $n \times 8$ matrix whose columns are the products of the values of the levels of A and B as indicated by the subscripts in **X**. For example the third column consists of the values of the levels of B and the seventh column the product of the squared values of the levels of A with the values of the levels of B.

The following set of expectation models is considered when both factors are quantitative:

$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{AB}}\left(\boldsymbol{\alpha\beta}\right)$	depends on combination of A and B
$E\left[\mathbf{Y}\right] = \mathbf{X}_{G}\mu + \mathbf{X}\boldsymbol{\gamma}_{22}$	smooth response in A and B
$\left(\text{or some subset of } \mathbf{X}\boldsymbol{\gamma}_{22} \text{ that obeys the degrees rule}\right)$	
$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{A}}\boldsymbol{\alpha} + \mathbf{X}_{\mathrm{B}}\boldsymbol{\beta}$	nonsmooth, independent response to A & B
$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{A}}\boldsymbol{\alpha} + \mathbf{X}_{01}\gamma_{01} + \mathbf{X}_{02}\gamma_{02}$	quadratic response for B, intercept differs for A
$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{A}}\boldsymbol{\alpha} + \mathbf{X}_{01}\gamma_{01}$	linear response for B, intercept differs for A
$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{A}}\boldsymbol{\alpha}$	nonsmooth response, depends on A only
$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{B}}\boldsymbol{\beta} + \mathbf{X}_{10}\gamma_{10} + \mathbf{X}_{20}\gamma_{20}$	quadratic response for A, intercept differs for B
$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{B}}\boldsymbol{\beta} + \mathbf{X}_{10}\gamma_{10}$	linear response for A, intercept differs for B
$E\left[\mathbf{Y}\right] = \mathbf{X}_{\mathrm{B}}\boldsymbol{\beta}$	nonsmooth response, depends on B only

where $(\alpha\beta) = \{(\alpha\beta)_{ij}\}$

$\alpha = \{\alpha_i\}$

$\beta = \{\beta_j\}$

$\gamma'_{22} = [\gamma_{10} \quad \gamma_{20} \quad \gamma_{01} \quad \gamma_{02} \quad \gamma_{11} \quad \gamma_{12} \quad \gamma_{21} \quad \gamma_{22}]$

$\gamma'_{20} = [\gamma_{10} \quad \gamma_{20}]$

$\gamma'_{02} = [\gamma_{01} \quad \gamma_{02}]$

Again, rules rules VII.1 and VII.2 were used in deriving this set of models. Note that the subsets of terms from $\mathbf{X}\theta_{22}$ mentioned above include the null subset and must conform to rule VII.2 so that whenever a term from $\mathbf{X}\theta_{22}$ is added to the subset, all terms of lower degree must also be included in the subset. For example, $\mathbf{X}_{11}\gamma_{11} < \mathbf{X}_{12}\gamma_{12}$ so a model with $\mathbf{X}_{12}\gamma_{12}$ must include $\mathbf{X}_{11}\gamma_{11}$. However, $\mathbf{X}_{12}\gamma_{12} \not< \mathbf{X}_{21}\gamma_{21}$ so a model with $\mathbf{X}_{12}\gamma_{12}$does not need $\mathbf{X}_{21}\gamma_{21}$. Further, if for a term the Deviation for a marginal term is significant, polynomial terms are not considered for it.

In interpreting the fitted models, the following observations apply (for more see Box, Hunter and Hunter, section 15.4)

- models in which there are only single-factor polynomial terms define

  $\Rightarrow$ a plane if both terms linear
  $\Rightarrow$ a parabolic tunnel if one term is linear and the other quadratic
  $\Rightarrow$ a paraboloid if both involve quadratic terms

- models including interaction submodels define nonlinear surfaces

  $\Rightarrow$ they will be monotonic for factors involving only linear terms,

  $\Rightarrow$ for interactions involving quadratic terms, some candidate shapes are:

Alinear.Bquadratic Aquadratic.Bquadratic

- could also consider models in which one factor has a smooth response that differs for the levels of the other factor, but that would require a re-analysis where one factor is treated as it is qualitative.

The analysis of variance table for a two-factor CRD with both factors quantitative is:

Source	df	SSq
Units	$n-1$	$\mathbf{Y}'\mathbf{Q}_{U}\mathbf{Y}$
A	$a-1$	$\mathbf{Y}'\mathbf{Q}_{A}\mathbf{Y}$
Linear	1	$\mathbf{Y}'\mathbf{Q}_{A_L}\mathbf{Y}$
Quadratic	1	$\mathbf{Y}'\mathbf{Q}_{A_Q}\mathbf{Y}$
Deviations	$a-3$	$\mathbf{Y}'\mathbf{Q}_{B_{Dev}}\mathbf{Y}$
B	$b-1$	$\mathbf{Y}'\mathbf{Q}_{B}\mathbf{Y}$
Linear	1	$\mathbf{Y}'\mathbf{Q}_{B_L}\mathbf{Y}$
Quadratic	1	$\mathbf{Y}'\mathbf{Q}_{B_Q}\mathbf{Y}$
Deviations	$b-3$	$\mathbf{Y}'\mathbf{Q}_{B_{Dev}}\mathbf{Y}$
A#B	$(a-1)(b-1)$	$\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}$
$A_{Linear}\#B_{Linear}$	1	$\mathbf{Y}'\mathbf{Q}_{A_LB_L}\mathbf{Y}$
$A_{Linear}\#B_{Quadratic}$	1	$\mathbf{Y}'\mathbf{Q}_{A_LB_Q}\mathbf{Y}$
$A_{Quadratic}\#B_{Linear}$	1	$\mathbf{Y}'\mathbf{Q}_{A_QB_L}\mathbf{Y}$
$A_{Quadratic}\#B_{Quadratic}$	1	$\mathbf{Y}'\mathbf{Q}_{A_QB_Q}\mathbf{Y}$
Deviations	$(a-1)(b-1)-4$	$\mathbf{Y}'\mathbf{Q}_{AB_{Dev}}\mathbf{Y}$
Residual	$ab(r-1)$	$\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}$

Step 3: Decide between hypotheses

For Deviations

Only if the terms to which a term is marginal are not significant then, if $\Pr\{F \geq F_O\} = p \leq \alpha$, the evidence suggests that the null hypothesis be rejected and the term must be incorporated in the model. Deviations for A and B are marginal to Deviations for A#B so that if the latter is significant, neither the Deviations for A nor for B is tested; indeed no further testing occurs as the maximal model has to be used to describe the data and multiple comparisons used to investigate mean differences.

For all Linear and Quadratic terms

Only if the polynomial terms are not of lower degree than a significant polynomial term and the terms to which the term is marginal are not significant then, if $\Pr\{F \geq F_O\} = p \leq \alpha$, the evidence suggests that the null hypothesis be rejected; the term and all polynomial terms of lower degree must be incorporated in the model. For example, $A_{Linear}\#B_{Linear}$ is marginal to A#B and is of lower degree than all other polynomial interaction terms and so is not tested if any of them is significant.

Example VII.7 Muzzle velocity of an antipersonnel weapon (continued)

Here is the analysis produced using R, where both `factors` are converted to `ordered` and `split` used for all quantitative terms in the `summary` function.

```
> attach(Fac2Muzzle.dat)
> interaction.plot(Vent.Vol, Hole.Area, Velocity, lwd=4)
> Vent.Vol.lev <- c(0.29, 0.4, 0.59, 0.91)
> Fac2Muzzle.dat$Vent.Vol <- ordered(Fac2Muzzle.dat$Vent.Vol, levels=Vent.Vol.lev)
> contrasts(Fac2Muzzle.dat$Vent.Vol) <- contr.poly(4, scores=Vent.Vol.lev)
> contrasts(Fac2Muzzle.dat$Vent.Vol)
              .L         .Q          .C
0.29 -0.54740790  0.5321858 -0.40880670
0.4  -0.31356375 -0.1895091  0.78470636
0.59  0.09034888 -0.7290797 -0.45856278
0.91  0.77062277  0.3864031  0.08266312
> Hole.Area.lev <- c(0.016, 0.03, 0.048, 0.062)
> Fac2Muzzle.dat$Hole.Area <- ordered(Fac2Muzzle.dat$Hole.Area,
+                                                    levels=Hole.Area.lev)
> contrasts(Fac2Muzzle.dat$Hole.Area) <- contr.poly(4, scores=Hole.Area.lev)
> contrasts(Fac2Muzzle.dat$Hole.Area)
              .L   .Q         .C
0.016 -0.6584881  0.5 -0.2576693
0.03  -0.2576693 -0.5  0.6584881
0.048  0.2576693 -0.5 -0.6584881
0.062  0.6584881  0.5  0.2576693
> Fac2Muzzle.aov <- aov(Velocity ~ Vent.Vol * Hole.Area + Error(Test),
+                                                                Fac2Muzzle.dat)
> summary(Fac2Muzzle.aov, split = list(
+         Vent.Vol = list(L=1, Q=2, Dev=3),
+         Hole.Area = list(L=1, Q= 2, Dev=3),
+         "Vent.Vol:Hole.Area" = list(L.L=1, L.Q=2, Q.L=4, Q.Q=5, Dev=c(3,6:9))))
Error: Test
                          Df Sum Sq Mean Sq  F value    Pr(>F)
Vent.Vol                   3  379.5   126.5   5.9541 0.0063117
  Vent.Vol: L              1  108.2   108.2   5.0940 0.0383455
  Vent.Vol: Q              1   72.0    72.0   3.3911 0.0841639
  Vent.Vol: Dev            1  199.2   199.2   9.3771 0.0074462
Hole.Area                  3 5137.2  1712.4  80.6092 7.138e-10
  Hole.Area: L             1 4461.2  4461.2 210.0078 1.280e-10
  Hole.Area: Q             1  357.8   357.8  16.8422 0.0008297
  Hole.Area: Dev           1  318.2   318.2  14.9776 0.0013566
Vent.Vol:Hole.Area         9 3973.5   441.5  20.7830 3.365e-07
  Vent.Vol:Hole.Area: L.L  1 1277.2  1277.2  60.1219 8.298e-07
  Vent.Vol:Hole.Area: L.Q  1   89.1    89.1   4.1962 0.0572893
  Vent.Vol:Hole.Area: Q.L  1 2171.4  2171.4 102.2166 2.358e-08
  Vent.Vol:Hole.Area: Q.Q  1  308.5   308.5  14.5243 0.0015364
  Vent.Vol:Hole.Area: Dev  5  127.2    25.4   1.1975 0.3541807
Residuals                 16  339.9    21.2
```

The contrasts in the `summary` function are worked out using the following table:

Factor			B		
	Contrast	Contrast Label	1 L	2 Q	3 Dev
A	1	L	L.L (1)	L.Q (2)	Dev (3)
	2	Q	Q.L (4)	Q.Q (5)	Dev (6)
	3	Dev	Dev (7)	Dev (8)	Dev (9)

The analysis is summarized in the following table, in which the 5 interaction deviations lines have been pooled in that their df and SSq have been added together.

Source	df	SSq	MSq	F	p
Tests	31				
Vent.Vol	3	379.5	126.5	5.95	0.006
Linear	1	108.2	108.2	5.09	0.038
Quadratic	1	72.0	72.0	3.39	0.084
Deviations	1	199.2	199.2	9.38	0.007
Hole.Area	3	5137.2	1712.4	80.61	0.000
Linear	1	4461.2	4461.2	210.01	0.000
Quadratic	1	357.8	357.8	16.84	0.001
Deviations	1	318.2	318.2	14.98	0.001
Vent.Vol#Hole.Area	9	3973.5	441.5	20.78	0.000
V_{Linear}#H_{Linear}	1	1277.2	1277.2	60.12	0.000
V_{Linear}#$H_{Quadratic}$	1	89.1	89.1	4.20	0.057
$V_{Quadratic}$#H_{Linear}	1	2171.4	2171.4	102.22	0.000
$V_{Quadratic}$#$H_{Quadratic}$	1	308.5	308.5	14.52	0.002
Deviations	5	127.2	25.4	1.20	0.354
Residual	16	339.9	21.2		

While the Deviations for the interaction is not significant ($p = 0.354$), those for both the main effects are significant ($p = 0.007$ and $p = 0.001$). Hence a smooth response function cannot be fitted. Furthermore, the $V_{Quadratic}$#$H_{Quadratic}$ source is significant ($p = 0.002$) so that interaction terms are required. In this case, we must revert to the maximal model $E[\mathbf{Y}] = \mathbf{X}_{VH}(\alpha\beta)$ and use multiple comparisons. ■

Fitting these submodels in R is an extension of the procedure for a single factor. Having specified polynomial contrasts for each quantitative factor, the `list` argument of the `summary` function is used to obtain the sums of squares. The general form of the `summary` function for one factor, B say, quantitative is:

```
summary(Experiment.aov,
    split = list(B = list(L = 1, Q = 2, Dev = 3:(b-1)),
                 "A:B" = list(L = 1, Q = 2, Dev = 3:(b-1))))
```

and for two factors, A and B say, quantitative is

```
summary(Experiment.aov,
        split = list(A = list(L = 1, Q = 2, Dev = 3:(a-1)),
                     B = list(L = 1, Q = 2, Dev = 3:(b-1)),
                   "A:B" = list(L.L=1, L.Q=2, Q.L=b, Q.Q=(b+1),
                                Dev=c(3:(b-1),(b+2:(a-1)(b-1))))))
```

For more details see Appendix C.5, *Factorial experiments*.

VII.G Nested factorial structures

Nested factorial structures commonly arise when a control treatment is included or when an interaction can be described in terms of one cell being different to the others. In these situations one sets up a factor (One say) with two levels, one for the control treatment or the different cell and two for the other treatments or cells. A second factor (Treats say) is set up with the same number of levels as there are treatments or cells. Then the structure for these two factors is One/Treats so that the terms in the analysis are One + Treats[One]. One compares the control or single cell with the mean of the others. Treats[One] reflects the differences between the other treatments or cells. Note that this can also be achieved using an orthogonal contrast, but the output using the nested factors is more convenient.

More generally one set up a nested factorial structure so that in the analysis there is: a) a term that reflects the average differences between *g* groups; and b) a term that reflects the differences within groups or several terms each one of which reflects the differences within a group.

Example VII.8 Grafting experiment (Daniel, 1977, p.27)

For example, consider the following RCBD experiment involving two factors each at two levels. The response is the percent grafts that take.

	B	1		2	
	A	1	2	1	2
	I	64	23	30	15†
	II	75	14	50	33
Block	III	76	12	41	17
	IV	73	33	25	10

†observation missing; value inserted so that residual is zero.

a) Description of pertinent features of the study

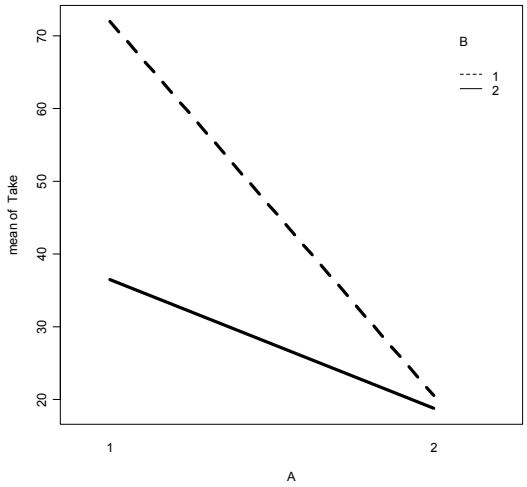
1. Observational unit – a plot
2. Response variable – % Take
3. Unrandomized factors – Blocks, Plots
4. Randomized factors – A, B
5. Type of study – Two-factor RCBD

b) The experimental structure

Structure	Formula
unrandomized	*4* Blocks/*4* Plots
randomized	*2* A**2* B

The following is the R output contains the analysis of the data:

```
> attach(Fac2Take.dat)
> Fac2Take.dat
   Blocks Plots A B Take
1       1     1 1 1   64
2       1     2 2 1   23
3       1     3 1 2   30
4       1     4 2 2   15
5       2     1 1 1   75
6       2     2 2 1   14
7       2     3 1 2   50
8       2     4 2 2   33
9       3     1 1 1   76
10      3     2 2 1   12
11      3     3 1 2   41
12      3     4 2 2   17
13      4     1 1 1   73
14      4     2 2 1   33
15      4     3 1 2   25
16      4     4 2 2   10
> interaction.plot(A, B, Take, lwd=4)
```



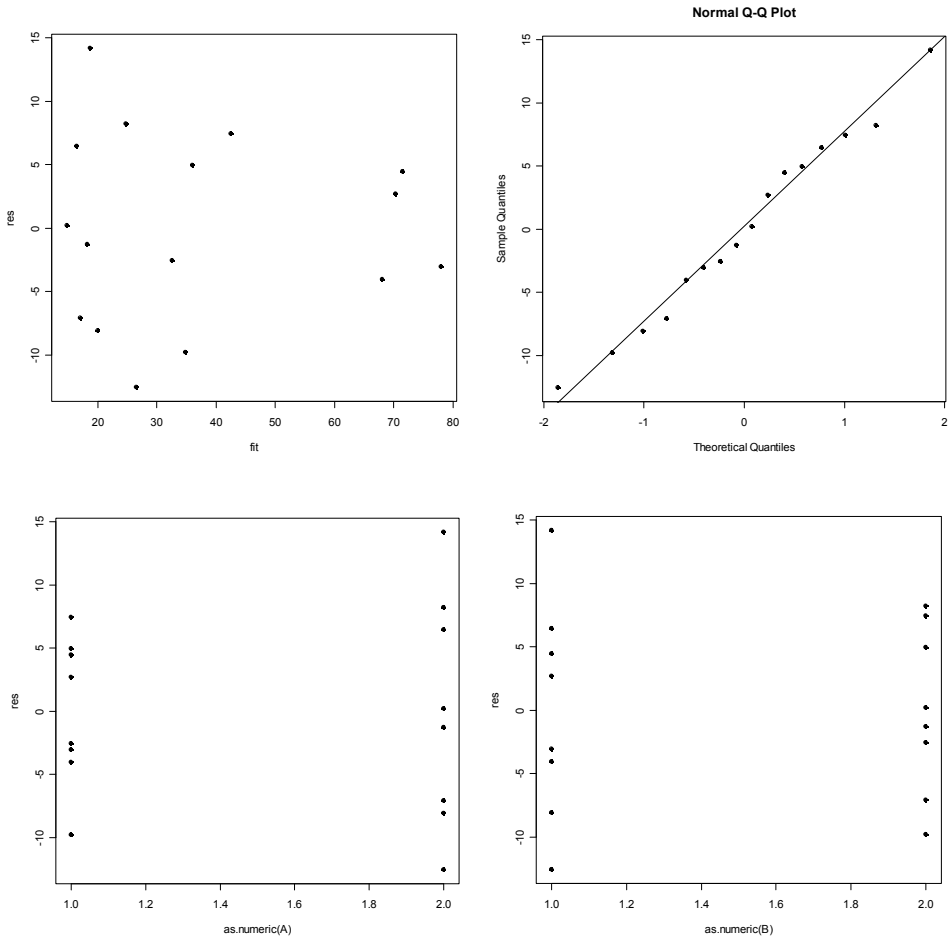
There appears to be an interaction.

```
> Fac2Take.aov <- aov(Take ~ Blocks + A * B + Error(Blocks/Plots), Fac2Take.dat)
> summary(Fac2Take.aov)

Error: Blocks
       Df  Sum Sq Mean Sq
Blocks  3 221.188  73.729

Error: Blocks:Plots
          Df Sum Sq Mean Sq F value    Pr(>F)
A          1 4795.6  4795.6  52.662 4.781e-05
B          1 1387.6  1387.6  15.238  0.003600
A:B        1 1139.1  1139.1  12.509  0.006346
Residuals  9  819.6    91.1
> res <- resid.errors(Fac2Take.aov)
> fit <- fitted.errors(Fac2Take.aov)
>
> plot(fit, res, pch=16)
> plot(as.numeric(A), res, pch=16)
> plot(as.numeric(B), res, pch=16)
> qqnorm(res, pch=16)
> qqline(res)
> tukey.1df(Fac2Take.aov, Fac2Take.dat, error.term = "Blocks:Plots")
$Tukey.SS
[1] 2.879712
```

```
$Tukey.F
[1] 0.02820886

$Tukey.p
[1] 0.870787

$Devn.SS
[1] 816.6828

> #
> # recompute for missing value
> #
> MSq <- c(73.729, 4795.6, 1387.6, 1139.1, 2.8797)
> Res <- c(rep(819.6/8, 4), 816.6828/7)
> df.num <- c(3,rep(1,4))
> df.den <- c(rep(8, 4),7)
> Fvalue <- MSq/Res
> pvalue <- 1-pf(Fvalue, df.num, df.den)
> data.frame(MSq,Res,df.num,df.den,Fvalue,pvalue)
        MSq      Res df.num df.den      Fvalue       pvalue
1   73.7290 102.4500      3      8  0.71965837 0.5677335580
2 4795.6000 102.4500      1      8 46.80917521 0.0001320942
3 1387.6000 102.4500      1      8 13.54416789 0.0062170009
4 1139.1000 102.4500      1      8 11.11859444 0.0103158259
5    2.8797 116.6690      1      7  0.02468266 0.8795959255
```

The recalculation of ANOVA quantities to take into account the missing value can be done either in R, as above, or in Excel. To use Excel you can cut the ANOVA quantities from R, paste them into Excel and then use *Data* > *Text to Columns* to separate the columns of the ANOVA table. You will need to use formulas to do the computation and, for the p-values, use =FDIST(F, ν_1, ν_2) where ν_1 is the numerator degrees of freedom and ν_2 is the denominator degrees of freedom. Note that you do not use 1 – FDIST(F, ν_1, ν_2) because of a bug in Excel. The following table illustrates this use of Excel — the new 8 degrees of freedom for the Residuals are manually entered, the unbolded items come from R output and the bolded items are recalculated using Excel formulae.

	Df	SSq	MSq	F	Pr(F)
Blocks	3	221.187	73.729	**0.719658**	**0.5677**
A	1	4795.563	4795.600	**46.809175**	**0.00013**
B	1	1387.563	1387.600	**13.544168**	**0.006217**
A#B	1	1139.062	1139.100	**11.118594**	**0.010316**
Residuals	*8*	819.563	**102.4500**		
Nonadditivity	1	2.880	**2.880**	**0.024683**	**0.879053**
Deviations	**7**	816.6833	**116.669**		



The hypothesis test for this example is a follows:

Step 1: Set up hypotheses

a) H_0: $(\alpha\beta)_{21} - (\alpha\beta)_{11} - (\alpha\beta)_{22} + (\alpha\beta)_{12} = 0$
H_1: $(\alpha\beta)_{21} - (\alpha\beta)_{11} - (\alpha\beta)_{22} + (\alpha\beta)_{12} \neq 0$

b) H_0: $\alpha_1 = \alpha_2$
H_1: $\alpha_1 = \alpha_2$

c) H_0: $\beta_1 = \beta_2$
H_1: $\beta_1 = \beta_2$

Set $\alpha = 0.05$.

Step 2: Calculate test statistics

The analysis of variance table for the two-factor RCBD is:

Source	df	SSq	MSq	E[MSq]	F	Prob
Blocks	3	221.9	73.7	$\sigma^2_{BP} + 4\sigma^2_B$	0.72	0.568
Plots[Blocks]	12	8141.8				
A	1	4795.5	4795.5	$\sigma^2_{BP} + q_A(\psi)$	46.81	<0.001
B	1	1387.6	1387.6	$\sigma^2_{BP} + q_B(\psi)$	13.54	0.006
A#B	1	1139.1	1139.1	$\sigma^2_{BP} + q_{AB}(\psi)$	11.12	0.010
Residual	8†	819.6	102.4	σ^2_S		
Nonadditivity	1	2.9	2.9		0.02	0.880
Deviations	7	816.7	116.7			

†Residual degrees of freedom have been reduced by one to allow for the missing observation and

Step 3: Decide between hypotheses

Note that the plot of residuals-versus-fitted-values reveals nothing untoward, the test for nonadditivity is not significant and the normal probability plot also appears to be satisfactory. There is a significant interaction between A and B so that the fitted model is $E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta)$.

The table of means for the combination of A and B needs to be examined. Suppose that the researcher wants to determine the level of A that has the greatest take for each level of B. The following output from R allows this.

```
> #
> # multiple comparisons
> #
> Fac2Take.tab <- model.tables(Fac2Take.aov, type="means")
> Fac2Take.tab$tables$"A:B"
   B
A    1     2
  1 72.00 36.50
  2 20.50 18.75
> q <- qtukey(0.95, 4, 8)
> q
[1] 4.52881
```

Tukey's HSD is given by

$$w(5\%) = \frac{4.52881}{\sqrt{2}} \times \sqrt{\frac{102.4 \times 2}{4}} = 22.91$$

Comparing differences between means in the above table with the Tukey's HSD it is concluded that there is no difference between A at level two of B but there is an A difference at level one of B. So at level one of B, level one of A gives the best take while at level two both levels of A give the same take. However, the results are only approximate because of the missing value.

It would appear that the results of this experiment are best described in terms of A and B both at level 1 is different from either A or B not at level 1. An analysis based on this can be achieved by setting up a factor for the 4 treatments and a two-level

factor that compares the cell with A and B both at level 1 with the remaining factors. The four-level factor for treatments is then specified as nested within the two-level factor.

The re-analysis for these new factors is achieved in R as follows:

```
> Fac2Take.dat$Cell.1.1 <- factor(1 + as.numeric(A != "1" | B != "1"))
> Fac2Take.dat$Treats <- fac.combine(list(A, B))
> detach(Fac2Take.dat)
> attach(Fac2Take.dat)
> Fac2Take.dat
   Blocks Plots A B Take Cell.1.1 Treats
1       1     1 1 1   64        1      1
2       1     2 2 1   23        2      3
3       1     3 1 2   30        2      2
4       1     4 2 2   15        2      4
5       2     1 1 1   75        1      1
6       2     2 2 1   14        2      3
7       2     3 1 2   50        2      2
8       2     4 2 2   33        2      4
9       3     1 1 1   76        1      1
10      3     2 2 1   12        2      3
11      3     3 1 2   41        2      2
12      3     4 2 2   17        2      4
13      4     1 1 1   73        1      1
14      4     2 2 1   33        2      3
15      4     3 1 2   25        2      2
16      4     4 2 2   10        2      4
> Fac2Take.aov <- aov(Take ~ Blocks + Cell.1.1/Treats + Error(Blocks/Plots),
+                                                                 Fac2Take.dat)
> summary(Fac2Take.aov)

Error: Blocks
       Df  Sum Sq Mean Sq
Blocks  3 221.188  73.729

Error: Blocks:Plots
               Df Sum Sq Mean Sq F value    Pr(>F)
Cell.1.1        1 6556.7  6556.7 72.0021 1.378e-05
Cell.1.1:Treats  2  765.5   382.8  4.2032   0.05139
Residuals        9  819.6    91.1
>
> #
> # recompute for missing value
> #
> MSq <- c(73.729,6556.7,382.8)
> Res <- rep(819.6/8, 3)
> df.num <- c(3, 1, 2)
> Fvalue <- MSq/Res
> pvalue <- 1-pf(Fvalue, df.num, 8)
> data.frame(MSq,Res,df.num,Fvalue,pvalue)
       MSq    Res df.num     Fvalue       pvalue
1   73.729 102.45      3  0.7196584 5.677336e-01
2 6556.700 102.45      1 63.9990239 4.367066e-05
3  382.800 102.45      2  3.7364568 7.146140e-02
```

The revised analysis of variance table is:

Source	df	SSq	MSq	F	Prob
Blocks	3	221.9	73.7	0.72	0.568
Plots[Blocks]	12	8141.8			
Cell 1,1 vs rest	1	6556.7	6556.7	64.00	<0.001
Among rest	2	765.5	382.8	3.74	0.071
Residual	8†	819.6	102.4		

† the Residual degrees of freedom have been reduced by one to allow for the missing observation

It would appear that the difference between the treatments is best summarized in terms of this single degree of freedom contrast between cell1,1 and the others. The mean for cell 1,1 is 72.0 and, for the other three treatments, the mean is 25.2, a difference of 46.8. ■

Such *one-cell interactions* are a very common form of interaction.

Example VII.9 Spraying sultanas

An experiment was conducted to investigate the effects of tractor speed and spray pressure on the quality of dried sultanas. The response was the lightness of the dried sultanas which is measured using a Hunterlab D25 L colour difference meter. Lighter sultanas are considered to be of better quality and these will have a higher lightness measurement (L). There were three tractor speeds and two spray pressures resulting in 6 treatment combinations which were applied to 6 plots, each consisting of 12 vines, using a randomized complete block design with three blocks. However, these 6 treatment combinations resulted in only 4 rates of spray application as indicated in the following table.

Table of application rates for the sprayer experiment

	Tractor Speed (km hour^{-1})		
Pressure (kPa)	3.6	2.6	1.8
140	**2090**	2930	**4120**
330	2930	**4120**	5770

To analyze this experiment we set up a factor, Rates, with four levels to compare the means of the four rates and two factors with three levels, Rate2 and Rate3, each of which compares the means of two treatment combinations with the same application rate. The levels of the factors Rate2 and Rate3 are shown in the following table.

Table of factor levels for Rate2 and Rate3 in the sprayer experiment

	Rate2			Rate3		
Tractor Speed (km hour^{-1})	3.6	2.6	1.8	3.6	2.6	1.8
Pressure (kPa)						
140	**1**	2	**1**	**1**	1	**2**
330	3	**1**	1	1	**3**	1

The experimental structure for this experiment is:

Structure	Formula
unrandomized	*3* Blocks/ *6* Plots
randomized	*4* Rates/(*3* Rate2+*3* Rate3)

The sources in the analysis of variance table are:

Source	df	E[MSq]
Blocks	2	$\sigma^2_{\mathrm{BP}} + \sigma^2_{\mathrm{B}}$
Plots[Blocks]	15	
Rates	3	$\sigma^2_{\mathrm{BP}} + q_{\mathrm{R}}(\psi)$
Rate2[Rates]	1	$\sigma^2_{\mathrm{BP}} + q_{\mathrm{R2}}(\psi)$
Rate3[Rates]	1	$\sigma^2_{\mathrm{BP}} + q_{\mathrm{R3}}(\psi)$
Residual	10	σ^2_{BP}
Total	17	

■

VII.H Models and hypothesis testing for three-factor experiments

In this section we sketch the analysis of the general three factor experiment. That is an experiment with factors A, B and C with *a*, *b* and *c* levels, respectively, and each of the *abc* combinations of A, B and C replicated *r* times. That is, there will be $n = abcr$ observations. We do this in preparation for discussing experiments with more than two factors in the next section. The analysis is an extension of that for a two-factor CRD.

The initial graphical exploration for these experiments involves examining the interaction between two factors for each level of the third. For example, look at the AB interaction for each of the *c* levels of C. This can be done using the nonstandard function `interaction.ABC.plot` from the *dae* library.

a) Using the rules to determine the ANOVA table for a 3-factor CRD experiment

a) Description of pertinent features of the study

1. Observational unit – a unit
2. Response variable – Response
3. Unrandomized factors – Units
4. Randomized factors – A, B, C
5. Type of study – Three-factor CRD

b) The experimental structure

Structure	Formula
unrandomized	*n* Units
randomized	*a* A**b* B**c* C

c) Sources derived from the structure formulae

The sources derived from the randomized structure formula are:

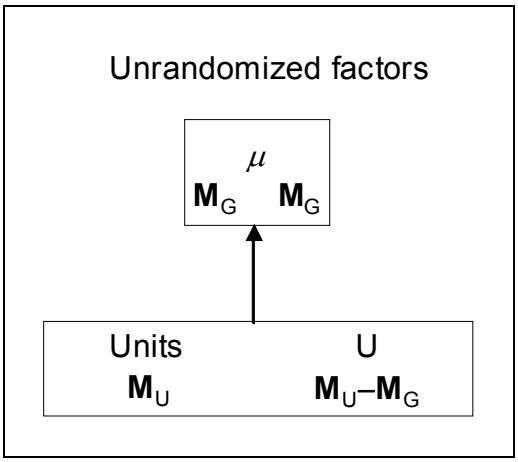
$$A*B*C = A + (B*C) + A\#(B*C)$$
$$= A + B + C + B\#C + A\#B + A\#C + A\#B\#C$$

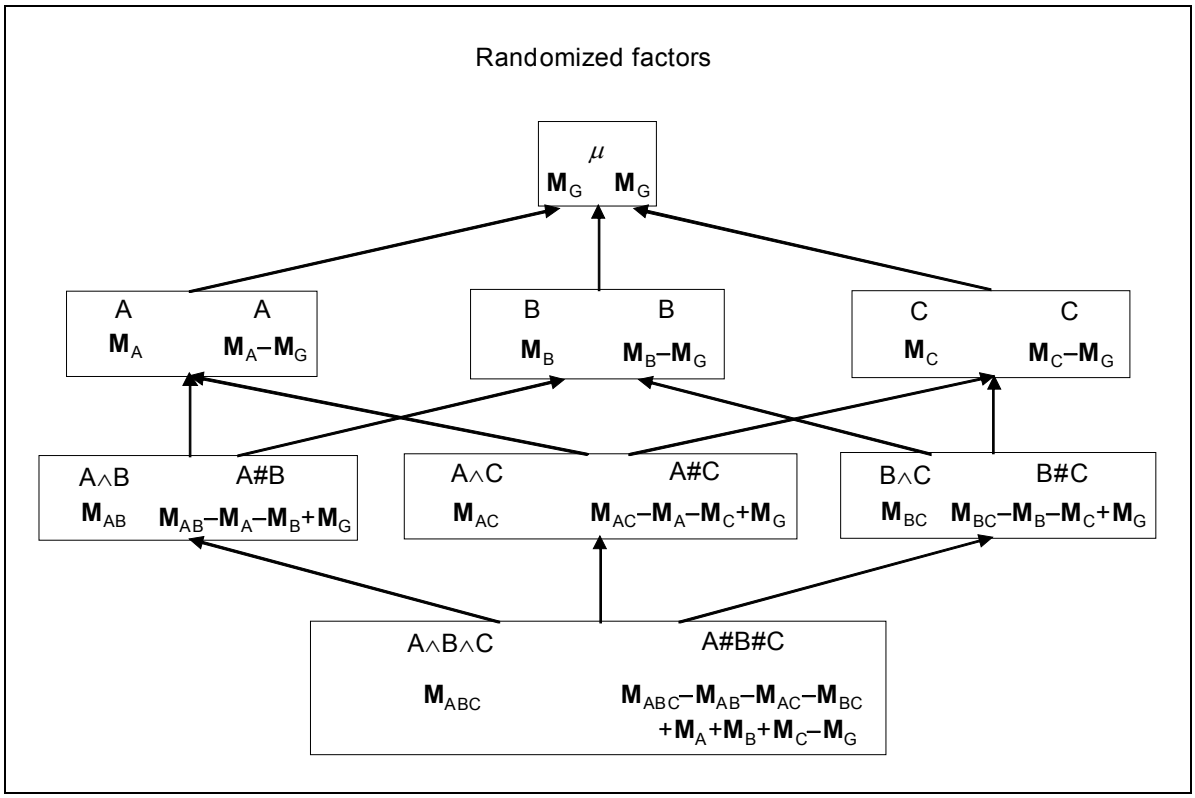
d) Degrees of freedom and sums of squares

The degrees of freedom of these terms can be derived by the cross product rule.

For each factor in the term, calculate the number of levels minus one and multiply these together.

The Hasse diagrams, with **M** and **Q** matrices, for this study are:





e) The analysis of variance table

Enter the sources for the study, their degrees of freedom and quadratic forms, into the analysis of variance table below.

f) Maximal expectation and variation models

Given that the only random factor is Units, the following are the symbolic expressions for the maximal expectation and variation models:

$$\psi = E[Y] = \mathrm{A} \wedge \mathrm{B} \wedge \mathrm{C}$$
$$\mathrm{var}[Y] = \mathrm{Units}$$

g) The expected mean squares.

Hence the analysis of variance table with sums of squares and expected mean squares is:

Source	df	SSq	E[MSq]
Units	$n-1$	$\mathbf{Y}'\mathbf{Q}_{U}\mathbf{Y}$	
A	$a-1$	$\mathbf{Y}'\mathbf{Q}_{A}\mathbf{Y}$	$\sigma_U^2 + q_A(\psi)$
B	$b-1$	$\mathbf{Y}'\mathbf{Q}_{B}\mathbf{Y}$	$\sigma_U^2 + q_B(\psi)$
A#B	$(a-1)(b-1)$	$\mathbf{Y}'\mathbf{Q}_{AB}\mathbf{Y}$	$\sigma_U^2 + q_{AB}(\psi)$
C	$c-1$	$\mathbf{Y}'\mathbf{Q}_{C}\mathbf{Y}$	$\sigma_U^2 + q_C(\psi)$
A#C	$(a-1)(c-1)$	$\mathbf{Y}'\mathbf{Q}_{AC}\mathbf{Y}$	$\sigma_U^2 + q_{AC}(\psi)$
B#C	$(b-1)(c-1)$	$\mathbf{Y}'\mathbf{Q}_{BC}\mathbf{Y}$	$\sigma_U^2 + q_{BC}(\psi)$
A#B#C	$(a-1)(b-1)(c-1)$	$\mathbf{Y}'\mathbf{Q}_{ABC}\mathbf{Y}$	$\sigma_U^2 + q_{ABC}(\psi)$
Residual	$abc(r-1)$	$\mathbf{Y}'\mathbf{Q}_{U_{Res}}\mathbf{Y}$	σ_U^2
Total	$abcr-1$	$\mathbf{Y}'\mathbf{Q}_{U}\mathbf{Y}$	

b) Indicator-variable models and estimation for the three-factor CRD

The models for the expectation that are considered for a three-factor factorial experiment are as follows:

$$E[\mathbf{Y}] = \mathbf{X}_{ABC}(\alpha\beta\delta)$$

$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) + \mathbf{X}_{AC}(\alpha\delta) + \mathbf{X}_{BC}(\beta\delta)$$

$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) + \mathbf{X}_{AC}(\alpha\delta) \quad \left(\begin{array}{l}\text{and equivalent models with a pair of}\\ \text{two-factors interactions}\end{array}\right)$$

$$E[\mathbf{Y}] = \mathbf{X}_{A}(\alpha) + \mathbf{X}_{BC}(\beta\delta) \quad \left(\begin{array}{l}\text{and equivalent models with two factors}\\ \text{interacting and one factor independent}\end{array}\right)$$

$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) \quad \left(\begin{array}{l}\text{and equivalent models with two factors}\\ \text{interacting}\end{array}\right)$$

$$E[\mathbf{y}] = \mathbf{X}_{A}(\alpha) + \mathbf{X}_{B}(\beta) + \mathbf{X}_{C}(\delta) \quad \left(\begin{array}{l}\text{and other models consisting of}\\ \text{only main effects}\end{array}\right)$$

$$E[\mathbf{Y}] = \mathbf{X}_{G}\mu$$

where

$$(\alpha\beta\delta) = \{(\alpha\beta\delta)_{ijk}\}$$
$$(\alpha\beta) = \{(\alpha\beta)_{ij}\}$$
$$(\beta\delta) = \{(\beta\delta)_{jk}\}$$
$$(\alpha\delta) = \{(\alpha\delta)_{ik}\}$$
$$\alpha = \{\alpha_i\}$$
$$\beta = \{\beta_j\}$$
$$\delta = \{\delta_k\}$$

Altogether there are 19 different models that are to be considered. Expressions for the estimators of the expected values for each of the models would be derived and these would be given in terms of the vectors of means $\bar{\mathbf{A}}$, $\bar{\mathbf{B}}$, $(\overline{\mathbf{A}\wedge\mathbf{B}})$, $\bar{\mathbf{C}}$, $(\overline{\mathbf{A}\wedge\mathbf{C}})$, $(\overline{\mathbf{B}\wedge\mathbf{C}})$ and $(\overline{\mathbf{A}\wedge\mathbf{B}\wedge\mathbf{C}})$ where the means in the vector are those for each combination of the factors in the vector's name. Being means vectors they can be written in terms of mean operators, **M**s. Further, if **Y** is arranged so that the associated factors A, B, C and the replicates are in standard order, the **M** operators can be written as the direct product of **I** and **J** matrices as follows:

$$\mathbf{M}_{\mathrm{G}} = \tfrac{1}{abcr}\,\mathbf{J}_a \otimes \mathbf{J}_b \otimes \mathbf{J}_c \otimes \mathbf{J}_r$$
$$\mathbf{M}_{\mathrm{A}} = \tfrac{1}{bcr}\,\mathbf{I}_a \otimes \mathbf{J}_b \otimes \mathbf{J}_c \otimes \mathbf{J}_r$$
$$\mathbf{M}_{\mathrm{B}} = \tfrac{1}{acr}\,\mathbf{J}_a \otimes \mathbf{I}_b \otimes \mathbf{J}_c \otimes \mathbf{J}_r$$
$$\mathbf{M}_{\mathrm{AB}} = \tfrac{1}{cr}\,\mathbf{I}_a \otimes \mathbf{I}_b \otimes \mathbf{J}_c \otimes \mathbf{J}_r$$
$$\mathbf{M}_{\mathrm{C}} = \tfrac{1}{abr}\,\mathbf{J}_a \otimes \mathbf{J}_b \otimes \mathbf{I}_c \otimes \mathbf{J}_r$$
$$\mathbf{M}_{\mathrm{AC}} = \tfrac{1}{br}\,\mathbf{I}_a \otimes \mathbf{J}_b \otimes \mathbf{I}_c \otimes \mathbf{J}_r$$
$$\mathbf{M}_{\mathrm{BC}} = \tfrac{1}{ar}\,\mathbf{J}_a \otimes \mathbf{I}_b \otimes \mathbf{I}_c \otimes \mathbf{J}_r$$
$$\mathbf{M}_{\mathrm{ABC}} = \tfrac{1}{r}\,\mathbf{I}_a \otimes \mathbf{I}_b \otimes \mathbf{I}_c \otimes \mathbf{J}_r$$

c) Expected mean squares under alternative models

We have previously given the expected mean squares under the maximal model. We also need to consider the expected mean squares under alternative models so that we know what models are indicated by the various hypothesis tests. Basically, we need to know under which models $q(\psi)$ is zero. From our discussion of the two-factor case, it is clear that $q(\psi)$ will be zero only when the model does not include a term to which the term for the source is marginal. So, provided terms to which it is marginal have been ruled out by prior tests, the hypothesis test for a mean square for a fixed term is a test for whether the expectation term corresponding to it is zero.

For example, consider the A#B mean square. Its expected value is

$$\sigma_U^2 + q_{AB}(\psi)$$

Now, $q_{AB}(\psi) \neq 0$ for models involving the A∧B term $\left[\mathbf{X}_{AB}(\alpha\beta)\right]$ or terms to which the AB term is marginal. That is, it is nonzero for the models

$$E[\mathbf{Y}] = \mathbf{X}_{ABC}(\alpha\beta\delta)$$
$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) + \mathbf{X}_{AC}(\alpha\delta) + \mathbf{X}_{BC}(\beta\delta)$$
$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) + \mathbf{X}_{BC}(\beta\delta)$$
$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) + \mathbf{X}_{AC}(\alpha\delta)$$
$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta) + \mathbf{X}_{C}\delta$$
$$E[\mathbf{Y}] = \mathbf{X}_{AB}(\alpha\beta)$$

It will only become zero when the A∧B∧C and A∧B terms are dropped from the model. Dropping the A∧B∧C term in the first model leads to a consideration of the next simplest model which is one involving the terms A∧B, A∧C, and B∧C. Dropping terms other than A∧B from the other models leaves A∧B in the model so that $q_{AB}(\psi)$ remains nonzero. It is only when the A∧B term is dropped that $q_{AB}(\psi)$ becomes zero. Hence the test for A#B, provides a test for whether the term A∧B should be included in the model, *provided that the test for A#B#C has already indicated that the term A∧B∧C can be omitted.*

d) The hypothesis test

The hypothesis test for choosing the model for a 3-factor experiment is as follows:

Step 1: Set up hypotheses

Term being tested

a) H_0: $\left(\begin{array}{l} (\alpha\beta\delta)_{ijk} - \overline{(\alpha\beta\delta)}_{ij.} - \overline{(\alpha\beta\delta)}_{i.k} - \overline{(\alpha\beta\delta)}_{.jk} \\ + \overline{(\alpha\beta\delta)}_{i..} + \overline{(\alpha\beta\delta)}_{.j.} + \overline{(\alpha\beta\delta)}_{..k} - \overline{(\alpha\beta\delta)}_{...} = 0 \quad \text{for all i,j,k} \end{array} \right)$ A∧B∧C

H_1: $\left(\begin{array}{l} (\alpha\beta\delta)_{ijk} - \overline{(\alpha\beta\delta)}_{ij.} - \overline{(\alpha\beta\delta)}_{i.k} - \overline{(\alpha\beta\delta)}_{.jk} \\ + \overline{(\alpha\beta\delta)}_{i..} + \overline{(\alpha\beta\delta)}_{.j.} + \overline{(\alpha\beta\delta)}_{..k} - \overline{(\alpha\beta\delta)}_{...} \neq 0 \quad \text{for some i,j,k} \end{array} \right)$

b) H_0: $\left((\alpha\beta)_{ij} - \overline{(\alpha\beta)}_{i.} - \overline{(\alpha\beta)}_{.j} + \overline{(\alpha\beta)}_{..} = 0 \quad \text{for all i,j}\right)$ A∧B

H_1: $\left((\alpha\beta)_{ij} - \overline{(\alpha\beta)}_{i.} - \overline{(\alpha\beta)}_{.j} + \overline{(\alpha\beta)}_{..} \neq 0 \quad \text{for some i,j}\right)$

c) H_0: $\left((\alpha\delta)_{ik} - \overline{(\alpha\delta)}_{i.} - \overline{(\alpha\delta)}_{.k} + \overline{(\alpha\delta)}_{..} = 0 \quad \text{for all i,k}\right)$ A∧C

H_1: $\left((\alpha\delta)_{ik} - \overline{(\alpha\delta)}_{i.} - \overline{(\alpha\delta)}_{.k} + \overline{(\alpha\delta)}_{..} \neq 0 \quad \text{for some i,k}\right)$

d) H_0: $\left((\beta\delta)_{jk} - \overline{(\beta\delta)}_{j.} - \overline{(\beta\delta)}_{.k} + \overline{(\beta\delta)}_{..} = 0 \quad \text{for all j,k}\right)$ B∧C

H_1: $\left((\beta\delta)_{jk} - \overline{(\beta\delta)}_{j.} - \overline{(\beta\delta)}_{.k} + \overline{(\beta\delta)}_{..} \neq 0 \quad \text{for some j,k}\right)$

e) H_0: $\alpha_1 = \alpha_2 = ... = \alpha_a$ A

H_1: not all population A means are equal

f) H_0: $\beta_1 = \beta_2 = ... = \beta_b$ B

H_1: not all population B means are equal

g) H_0: $\delta_1 = \delta_2 = ... = \delta_c$ C

H_1: not all population C means are equal

Set $\alpha = 0.05$.

Step 2: Calculate test statistics

The form of the analysis of variance table for a three-factor factorial CRD is:

Source	df	SSq	E[MSq]
Units	$n-1$	$\mathbf{Y'Q}_U\mathbf{Y}$	
A	$a-1$	$\mathbf{Y'Q}_A\mathbf{Y}$	$\sigma^2_U + q_A(\psi)$
B	$b-1$	$\mathbf{Y'Q}_B\mathbf{Y}$	$\sigma^2_U + q_B(\psi)$
A#B	$(a-1)(b-1)$	$\mathbf{Y'Q}_{AB}\mathbf{Y}$	$\sigma^2_U + q_{AB}(\psi)$
C	$c-1$	$\mathbf{Y'Q}_C\mathbf{Y}$	$\sigma^2_U + q_C(\psi)$
A#C	$(a-1)(c-1)$	$\mathbf{Y'Q}_{AC}\mathbf{Y}$	$\sigma^2_U + q_{AC}(\psi)$
B#C	$(b-1)(c-1)$	$\mathbf{Y'Q}_{BC}\mathbf{Y}$	$\sigma^2_U + q_{BC}(\psi)$
A#B#C	$(a-1)(b-1)(c-1)$	$\mathbf{Y'Q}_{ABC}\mathbf{Y}$	$\sigma^2_U + q_{ABC}(\psi)$
Residual	$abc(r-1)$	$\mathbf{Y'Q}_{U_{Res}}\mathbf{Y}$	σ^2_U
Total	$abcr-1$	$\mathbf{Y'Q}_U\mathbf{Y}$	

Of course, mean squares would be added to this table by taking each sum of squares and dividing by its degrees of freedom, F statistics computed by dividing all mean squares, except the Residual mean square, by the Residual mean square, and p values obtained for each F statistic.

Step 3: Decide between hypotheses

For A#B#C interaction source

If $\Pr\{F \geq F_O\} = p \leq \alpha$, the evidence suggests that the null hypothesis be rejected and the term should be incorporated in the model.

For A#B, A#C and B#C interaction sources

Only if A#B#C is not significant, then if $\Pr\{F \geq F_O\} = p \leq \alpha$, the evidence suggests that the null hypothesis be rejected and the term corresponding to the significant source should be incorporated in the model.

For A, B and C sources

For each term, only if the interactions involving the term are not significant, then if $\Pr\{F \geq F_O\} = p \leq \alpha$, the evidence suggests that the null hypothesis be rejected and the term corresponding to the significant source should be incorporated in the model.

VII.I Summary

In this chapter we have:

- described how to design factorial experiments using a completely randomized, a randomized complete block or a Latin square design;
- emphasized the advantage of factorial experiments over one-factor-at-a time experiments;
- formulated alternative linear expectation models using indicator variables to describe the results from a factorial experiment; given the estimators of the expected values as functions of **M** or mean operator matrices;
- used the rules from chapter VI, *Determining the analysis of variance table*, to formulate the ANOVA hypothesis test for choosing between expectation models in a two-factor factorial experiment and outlined the test;
  - the partition of the total sums of squares was given with the sums of squares expressed as the sums of squares of the elements of vectors and as quadratic forms where the matrices of the quadratic forms, **Q** matrices, are symmetric idempotents;
  - the expected mean squares under the alternative expectation models are used to justify the choice of F test statistic;
  - the order in which hypotheses should be tested was described and it was mentioned that in some cases not all hypotheses will be tested;
- shown how to obtain a layout and the analysis of variance in R;
- discussed procedures for checking the adequacy of the proposed models; demonstrated how to choose a Box-Cox transformation when the model is inadequate;
- subsequent to the hypothesis test, examined treatment differences in detail; in particular, outlined the fitting of submodels for the two cases of a) one factor quantitative and the other qualitative and b) both factors quantitative;
- used the rules from chapter VI, *Determining the analysis of variance table*, to formulate the analyses for nested and three-factor factorial experiments.

VII.J Exercises

VII.1 A completely randomized experiment was conducted to investigate the effect of vitamin B_{12} (0, 5 mg) and antibiotics (0, 40 mg) fed to swine. The response was the average daily gain in weight.

		Vitamin B_{12}	
		0	5
		1.30	1.26
	0	1.19	1.21
		1.08	1.19
Antibiotics			
		1.05	1.52
	40	1.00	1.56
		1.05	1.55

What are the components of this experiment?

1. Observational unit ______________________
2. Response variable ______________________
3. Unrandomized factors ______________________
4. Randomized factors ______________________
5. Type of study ______________________

What is the experimental structure for this experiment?

Structure	Formula
unrandomized	
randomized	

What are the degrees of freedom, sums of squares and expected mean squares for the lines in the analysis of variance table based on all unrandomized factors being random and all randomized factors being fixed?

Source	df	SSq	E[MSq]
Total			

Obtain the usual analysis for a two-factor factorial experiment using R, including diagnostic checking. Also, examine treatment differences using multiple comparison procedures on the appropriate table(s) of means with a view to identifying the levels combinations of the factors that produce the maximum weight gain.

VII.2 Examination of the interaction plot of swine weight gain in exercise VII.1 suggests that there might be a response when both Antibiotic is at 40 and Vitamin B_{12} is at 5 and not a significant difference between the other three combinations. To investigate this possibility set up an analysis with a nested factorial structure that examines the divergence between two groups of treatments thought to be different and differences within the groups where no divergence is expected.

VII.3 An experiment was conducted to investigate the effect of temperature and copper content on the warping of copper plates. Copper plates were produced using each of the combinations of temperature and copper content on one day and this was repeated on a second day; the order of the temperature-copper content combinations was randomized to the 16 production runs used each day in the experiment. The amount of warping of the copper plates produced was measured and the results are given in the following table.

	Temperature (°C)							
	50		75		100		125	
Day	1	2	1	2	1	2	1	2
Copper content (%)								
40	17	20	12	9	16	12	21	17
60	16	21	18	13	18	21	23	21
80	24	22	17	12	25	23	23	22
100	28	27	27	31	30	30	29	31

What are the components of this experiment?

1. Observational unit _____
2. Response variable _____
3. Unrandomized factors _____
4. Randomized factors _____
5. Type of study _____

What is the experimental structure for this experiment?

Structure	Formula
unrandomized	
randomized	

What are the degrees of freedom, sums of squares and expected mean squares for the lines in the analysis of variance table based on all unrandomized factors being random and all randomized factors being fixed?

Source	df	SSq	E[MSq]
Total			

Analyze the data using R, including diagnostic checking and obtaining a fitted equation and surface for an appropriate polynomial submodel.

VII.4 The following are data on the number of units produced per day by different operators in different machines. The order of the operator-machine combinations was randomized to the days in a particular period. The whole process was repeated in a second period with re-randomization of the operator-machine combinations. The first observation for each combination in the following table is for the first period and the second for the second period.

	Operator							
Machine	A		B		C		D	
1	18	17	16	18	17	20	27	27
2	17	13	18	18	20	16	28	23
3	16	17	17	19	20	16	31	30
4	15	17	21	22	16	16	31	24
5	17	18	16	18	14	13	28	22

What are the components of this experiment?

1. Observational unit ______________________________
2. Response variable ______________________________
3. Unrandomized factors ______________________________
4. Randomized factors ______________________________
5. Type of study ______________________________

What is the experimental structure for this experiment?

Structure	Formula
unrandomized	
randomized	

What are the Hasse diagrams of generalized-factor marginalities, with **M** and **Q** matrices, for this study?

What are the degrees of freedom, sums of squares and expected mean squares for the lines in the analysis of variance table based on all factors being random?

Source	df	SSq	E[MSq]
Total			

The data has been saved in *Fac2Prod.dat.rda* and is available from the web site. Analyze the data using R, including diagnostic checking.

VII.5 The yields of an undesirable by-product of a process were measured from 12 runs in which 2 different catalysts and 2 different pressures were used in a random order; that is each combination was replicated 3 times. This experiment was repeated at two different laboratories. The data, given below, are the percentage of by-product produced and it is available in the file *Fac2ByPr.dat.rda* from the web site.

	Catalyst	I		II	
	Laboratory	A	B	A	B
Pressure	High	53	27	40	45
		43	45	32	12
		45	57	29	69
	Low	42	32	61	54
		95	27	24	60
		60	98	11	26

The components of this experiment are:

1. Observational unit – a run
2. Response variable – % By-product
3. Unrandomized factors – Laboratories, Runs
4. Randomized factors – Catalyst, Pressure
5. Type of study – Two-factor RCBD

In this experiment interactions between laboratories and treatments are likely to be of interest so that the experimental structure for this experiment would be:

Structure	Formula
unrandomized	Labs/Runs
randomized	Catalyst*Pressure*Labs

What are the Hasse diagrams of generalized-factor marginalities, with **M** and **Q** matrices, for this study?

What are the degrees of freedom, sums of squares and expected mean squares for the lines in the analysis of variance table based on all unrandomized factors being random and all randomized factors being fixed?

Source	df	SSq	E[MSq]
Total			

Analyze the data using R, including diagnostic checking and the examination of treatment differences. Note that in producing the exploratory interaction plots, because there are 3 factors in the randomized structure, an interaction plot for two of the factors should be produced for each level of the third factor. In this case, an interaction plot of Catalyst by Pressure for each Lab seems the natural choice. Use the nonstandard function `interaction.ABC.plot` from the *dae* library.