



**The RCBD Model:**

$$Y_{hi} = \mu + \theta_h + \tau_i + \varepsilon_{hi}$$

$$\varepsilon_{hi} \sim N(0, \sigma^2)$$

$\varepsilon_{hi}$ 's independent

where

$Y_{hi}$  is the random variable representing the response for treatment  $i$  observed in block  $h$ ,

$\mu$  is a constant (which may be thought of as the overall mean – see below)

$\theta_h$  is the (additive) effect of the  $h^{\text{th}}$  block ( $h = 1, 2, \dots, b$ )

$\tau_i$  is the (additive) effect of the  $i^{\text{th}}$  treatment ( $i = 1, 2, \dots, v$ )

$\varepsilon_{hi}$  is the random error for the  $i^{\text{th}}$  treatment in the  $h^{\text{th}}$  block.

(Why is there no subscript  $t$  for observation number?)

*Note:*

- This model is also called the *block-treatment model*. Formally, it looks just like a two-way main effects model – *but* you need to remember that there is just one factor plus one block, and the randomization is just within each block. So we don't have the conditions for a two-way analysis of variance.
- Like the main-effects model, this is an additive model that does not provide for any interaction between block and treatment level – it assumes that treatments have the same effect in every block, and the only effect of the block is to shift the mean response up or down. If interaction between block and factor is suspected, then either a transformation is needed to remove interaction before using this model, or a design with more than one observation per block-treatment combination must be used. (Trying to add an interaction term in the RCBD would create the same problem as is encountered in two-way ANOVA with one observation per cell: the degrees of freedom for the error are zero, so the method of analysis breaks down. So if interaction is suspected, block size must be increased to allow an estimation of interaction.)
- This is an over-specified model; the additional constraints  $\sum_{h=1}^b \theta_h = 0$  and  $\sum_{i=1}^v \tau_i = 0$ , are typically added, so that the treatment and block effects are thought of as deviations from the overall mean.
- There is an alternate *means model*  $Y_{hi} = \mu_{ih} + \varepsilon_{hi}$ , where  $\mu_{ih} = \mu + \theta_h + \tau_i$ .
- Note that the  $i^{\text{th}}$  treatment mean is  $\mu_i = \frac{1}{b} \sum_{h=1}^b (\mu + \theta_h + \tau_i)$ . Assuming the constraint

$$\sum_{h=1}^b \theta_h = 0, \text{ this gives } \mu_i = \mu + \tau_i$$

**Estimating and Analysis:**

*Least squares fits:* Since the model is formally the same as the main-effects model, the process of finding least squares estimates is the same as for the latter model, yielding estimates (with notation appropriately changed)

$$\begin{aligned}
\mu^{\wedge} &= \bar{y}_{..} \\
\theta_h^{\wedge} &= \bar{y}_{h\cdot} - \bar{y}_{..} \\
\tau_i^{\wedge} &= \bar{y}_{\cdot i} - \bar{y}_{..} \\
y_{hi}^{\wedge} &= \mu^{\wedge} + \theta_h^{\wedge} + \tau_i^{\wedge} = \\
&= \bar{y}_{h\cdot} + \bar{y}_{\cdot i} - \bar{y}_{..}
\end{aligned}$$

Thus the error sum of squares for this model is

$$\text{ssE} =$$

As with the two-way main effects model,  $\text{MSE} = \text{SSE}/(b-1)(v-1)$  is an unbiased estimator of  $\sigma^2$ . (Note that  $(b-1)(v-1) = bv - b - v + 1 = n - b - v + 1$ , since  $n = bv$ .)

*Model checking:* As always, be sure to this before interpreting output! Look especially for potential problems with the normality assumption, unequal error variance by block or treatment, and treatment-block interaction. To check for possible block-treatment interaction, form an “interaction plot” by plotting each  $y_{hi}$  against each treatment level  $i$  and connecting points for each block  $h$ . If corresponding line segments are parallel, this suggests both no interaction and small error variability. (Note that since there is one observation per (block, treatment level) combination, there is no way to check the equal variance assumption at that fine a level.)

*Hypothesis test and Analysis of Variance Table:* We are interested in testing equality of treatment means. Thus we wish to test the null hypothesis

$$H_0: \mu_1 = \mu_2 = \dots = \mu_v$$

against the alternate

$$H_a: \mu_i \neq \mu_j \text{ for at least one pair } i, j.$$

*Note:* Since  $\mu_i = \mu + \tau_i$ , we can restate the hypotheses as

$$H_0: \tau_1 = \tau_2 = \dots = \tau_v = 0$$

and

$$H_a: \text{at least one } \tau_i \neq 0.$$

We can construct an F-test in the usual manner: We consider the submodel corresponding to the null hypothesis, namely

$$Y_{hi} = \mu + \theta_h + \varepsilon_{hi}$$

This has least squares fits

$$(y_{hi}^{\wedge})_0 = (\bar{y}_{..}) + (\bar{y}_{h\cdot} - \bar{y}_{..}) = \bar{y}_{h\cdot}$$

and hence error sum of squares

$$ssE_0 =$$

The difference  $ssT = ssE_0 - ssE$  is called the *sum of squares for treatment*. Our test statistic for  $H_0$  is

$$\frac{ssT/(v-1)}{ssE/(b-1)(v-1)}$$

As usual, the numerator is denoted  $msT$  (with  $v-1$  degrees of freedom) and the denominator  $msE$  (with  $(b-1)(v-1)$  degrees of freedom, as mentioned above). The test statistic has an F distribution with  $v-1$  degrees of freedom in the numerator,  $(b-1)(v-1)$  in the denominator.

*Note:*

- The above test is the same as the F-test for the treatment factor we would get by two-way ANOVA considering treatment and block as two factors in a main effects model. Thus we can test our hypothesis by using a two-way ANOVA main-effects software routine.
- We can define  $ssB$  and  $msB$  (using  $b-1$  degrees of freedom), but we *don't* get a legitimate F-test for the null hypothesis "No block effect," since the conditions for proving that the would-be test statistic has an F-distribution are not met, because the blocks are chosen, not randomly assigned.
- Nonetheless, the ratio  $msB/msE$  can be considered as an informal measure of the effect of the blocking factor – if the ratio is large, that suggests that the blocking "factor" has a large effect, and that the variance reduction obtained by blocking was probably helpful by improving the precision in the comparison of treatment means.
- The algebra works out to show that  $ssTot = ssB + ssT + ssE$ , and the degrees of freedom add accordingly.

*Contrasts:* In the RCBD, all contrasts (with coefficient sum zero) in the treatment effects  $\tau_i$  are estimable, and the techniques of Chapter 4 still apply, with the following observed:

- The estimate of  $\tau_i$  is  $\tau_i^{\wedge} = \bar{y}_{\cdot i} - \bar{y}_{\cdot\cdot}$ , but since in a contrast  $\sum c_i \tau_i$ , we have  $\sum c_i = 0$ , the estimate of the contrast is  $\sum c_i \bar{y}_{\cdot i}$
- The number of replicates is equal to the number  $b$  of blocks
- The error degrees of freedom are  $(b-1)(v-1)$ .
- The  $msE$  used is the one obtained by the block design analysis. (Thus the Minitab automatic procedures will not work for a block design.)