11.1 Introduction to Hierarchical Designs

In a hierarchical design, the levels of at least one treatment are nested in those of another treatment and the remaining treatments are completely crossed. If each level of treatment $B$ appears with only one level of treatment $A$, $B$ is said to be nested in $A$. This is denoted by $B(A)$ and read "$B$ within $A". The distinction between nested and crossed treatments is illustrated in Figure 11.1-1.

Experimental designs with one or more nested treatments are particularly well suited to research in the behavioral and medical sciences, education, and industry. Consider an example from education in which two types of programmed instruction materials (treatment levels $a_1$ and $a_2$) are to be evaluated using students in four sixth-grade classes (treatment levels $b_1$, $b_2$, $b_3$, and $b_4$). Two classrooms are randomly assigned to use each type of programmed material. For administrative reasons, all

![Diagram](image)

**Figure 11.1-1** Comparison of designs with nested and crossed treatments. In part (a), treatment $B(A)$ is nested in treatment $A$ because $b_1$ and $b_2$ appear only with $a_1$, whereas $b_3$ and $b_4$ appear only with $a_2$. In part (b), treatments $A$ and $B$ are crossed because each level of treatment $B$ appears once and only once with each level of treatment $A$, and vice versa.
children in a particular room must use the same type of programmed material. We assume that each classroom contains the same number of children. This hierarchical experiment corresponds to the design illustrated in Figure 11.1-1(a). Each classroom, \( b_k \), appears with only one level of programmed instruction. Thus, treatment \( B \) is nested in \( A \).

Nested treatments often occur in animal research where it is necessary to administer the same treatment level to all animals in the same cage or housing compound. Consider an experiment to investigate the effects of positive and negative ionization of air molecules (treatment levels \( a_1 \) and \( a_2 \), respectively) on the activity levels of rats. The animals are radiated continuously for a three-week period, after which their activity level is measured in an open field situation. Sixteen rats are housed in four cages (treatment levels \( b_1, b_2, b_3, \) and \( b_4 \)) with four rats per cage. Each cage is equipped with ionizing equipment for producing the required condition in a cage. The cages are randomly assigned to the ionization conditions, two to each condition, and the rats are randomly assigned to the cages. In this example, the cages are nested in the ionization conditions. This experiment also corresponds to the design shown in Figure 11.1-1(a). We assume that the activity level of a rat in the open field situation reflects the effects of (1) the ionization condition received, treatment \( A \); (2) the cage in which the rat is housed, treatment \( B(A) \); and (3) idiosyncratic characteristics of the rat and other uncontrolled variables, experimental error. These assumptions can be expressed more formally by means of the model equation

\[
Y_{ijk} = \mu + \alpha_i + \beta_{ij} + \epsilon_{ijk} \quad (i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q)
\]

where the symbol \( \beta_{ij} \) indicates that the \( j \)th level of treatment \( B(A) \) is nested in the \( i \)th level of \( A \). Note that an \( A \times B \) interaction term does not appear in the model.

In this and the programmed instruction experiment described earlier, treatment \( B(A) \) is really a nuisance variable. That is, the variable of classrooms or cages is included in the design and model equation because the researcher suspects that it might affect the dependent variable and not because of an interest in the variable per se. One could argue that if the cages in the ionization experiment are identical, this condition is constant for all subjects. This argument ignores such variables as differences in the location of the cages in a room and possible differences in the dispersion of air ions within the cages as well as differences in ambient lighting, temperature, and humidity. Also ignored are differences in the social environment in the cages due to the presence of dominant or neurotic rats in certain cages, undetected infectious diseases, and so on. The use of a hierarchical design enables a researcher to isolate the nuisance variables of cages, which might affect the rats' activity levels in the open field situation.

A common error in the analysis of hierarchical experiments is to ignore the nuisance variable and treat the design as if it were a CR-\( q \) design with \( nq_{ij} \) subjects in each level of treatment \( A \). Here, \( q_{ij} \) denotes the number of levels of treatment \( B(A) \) that are nested in the \( j \)th level of treatment \( A \). This incorrect analysis may result in a biased test of treatment \( A \). A correct analysis takes into account the effects of the nested treatment so that the analysis is congruent with the way the experiment was actually carried out. This point is discussed in Section 11.2.

Hierarchical designs that are constructed from completely randomized designs
are appropriate for experiments that meet, in addition to the assumptions of a CR-\(p\) design described in Chapter 5, the following conditions:

1. There are two or more treatments, with each treatment having two or more levels.
2. The levels of at least one treatment are nested in those of another treatment; nonnested treatments are completely crossed.
3. The levels (combinations) of the nested treatment(s) are randomly assigned to the nonnested treatment (treatment combinations), and the experimental units are randomly assigned to the treatment combinations.

Hierarchical designs are often used in research situations where the third requirement cannot be met. For example, the programmed instruction experiment might be performed in four schools using two sixth-grade classrooms in each school, a total of eight classrooms. In this design, the four schools can be randomly assigned to the two types of instruction materials but, obviously, classrooms in one school cannot be assigned to another school. Also, federal integration guidelines would probably preclude assigning students randomly to the treatment combinations. Many studies by their very nature preclude the kind of randomization described in the third requirement. Campbell and Stanley (1966, 34) refer to experiments in which the researcher has limited control over randomization as quasi-experiments. The interpretation of the results of such experiments presents a real challenge. It seems that the difficulty in interpreting the outcome of research varies inversely with the degree of control a researcher is able to exercise over randomization. Certainly, quasi-experiments and ex post facto studies are among the most difficult to interpret. Researchers will find Campbell and Stanley’s (1966) discussion and that in Cook and Campbell (1979) most helpful.

Types of Hierarchical Designs

In this chapter we describe hierarchical designs based on completely randomized and randomized block designs. Depending on the building block design that is used, a two-treatment hierarchical design is denoted by CRH-\(pq(A)\) or RBH-\(pq(A)\), where \(q(A)\) indicates that the \(q\) levels of treatment \(B(A)\) are nested in treatment \(A\). The design for the programmed instruction and ionization experiments described earlier is denoted by CRH-24(A). A completely randomized hierarchical design with three treatments can take any of the following forms: CRH-\(pq(A)r(AB)\), CRPH-\(pq(A)r\), CRPH-\(pqr(A)\), CRPH-\(pqr(B)\), CRPH-\(pq(A)r(A)\), and CRPH-\(pqr(AB)\). These designs are discussed in Section 11.6, so we limit our comments here to the treatment designation scheme. Treatments \(B(A)\) and \(C(AB)\) in a CRH-\(pq(A)r(AB)\) design are completely nested: \(B(A)\) is nested in \(A\), and \(C(AB)\) is nested in \(A\) and \(B(A)\). The other designs involve partial nesting, which is indicated by the use of \(P\) in their designation, and are referred to as completely randomized partial hierarchical designs. In the CRPH-

\(^1\)The merits of experiments, quasi-experiments, and other research strategies are discussed in Chapter 1.
11.2 Computational Example for CRH-pq(A) Design

pq(A)r design, for example, treatment B(A) is nested in A, but treatment C is crossed with A and B(A). In the CRPH-pqr(AB) design, treatment C(AB) is nested in A and B, but treatments A and B are crossed. These designs are described in Section 11.6.

Hierarchical designs are balanced if they have an equal number of experimental units in each treatment combination and an equal number of levels of the nested treatment in each level of the other treatment; otherwise, they are unbalanced. The analysis and interpretation of the results for unbalanced designs are more complex than the analysis and interpretation for balanced designs. We describe the analysis of balanced designs first using the classical sum-of-squares approach. The analysis of balanced and unbalanced designs using the cell means model is discussed in Section 11.8.

### 11.2 Computational Example for CRH-pq(A) Design

Assume that the ionization experiment described earlier has been performed. However, instead of four cages, eight were used. The cages, treatment B(A), were randomly assigned to the positive (a1) and negative (a2) ionization conditions, with the restriction that four cages were assigned to each condition. Thirty-two rats were randomly assigned to the p=q=2(4)=8 treatment combinations, with the restriction that four rats were assigned to each combination. For a balanced CRH-28(A) design, the number of levels of treatment B(A) that are nested in the jth level of treatment A, q(j) = 4, is constant for all j. The treatment effects for the ionization conditions are fixed; those for cages are assumed to be random. This is a common assumption for a nuisance variable. We are not interested in the eight cages used in the experiment, but rather in the population of cages from which the eight would have been a random sample if random sampling had been used.

The research hypotheses leading to the experiment can be evaluated by testing the following null hypotheses:

\[
H_0: \mu_1 = \mu_2 \quad H_0': \sigma^2 = 0 \\
H_1: \mu_1 \neq \mu_2 \quad H_1': \sigma^2 \neq 0
\]

If \( \sigma^2 = 0 \) is rejected, we conclude that \( \sigma^2 \neq 0 \) for \( a_1 \), or \( \sigma^2 \neq 0 \) for \( a_2 \), or both. The level of significance adopted is .05. The computational procedures are illustrated in Table 11.2-1. The results are summarized in Table 11.2-2. It is apparent that both null hypotheses can be rejected. From an examination of the data, we know that rats exposed to negative air ions are more active than those exposed to positive ions. The finding that there are differences in the activity levels among the various cages is of little substantive interest because the cages represent a nuisance variable. The significant \( F \) statistic for cages indicates that the decision to include this source of variation in the design was a good one.

Table 11.2-2 contains two error terms: one for testing MSA and another for testing

---

\(^2\text{For a discussion of the problems, see Gill (1978, 185-199), Gower (1962), and Snedecor (1956, 271).}\)
Table 11.2-1 Computational Procedures for CRH-28(A) Design

(i) Data and notation \( Y_{ijk} \) denotes a score for experimental unit \( i \) in treatment combination \( a_ib_k; \ i = 1, \ldots, n \) experimental units \( a_i; j = 1, \ldots, p \) levels of treatment \( A \) \( a_j; k = 1, \ldots, q \) levels of treatment \( B(A) (b_k) \).

**A B(A) S Summary Table**

<table>
<thead>
<tr>
<th>( a_1 )</th>
<th>( a_1 )</th>
<th>( a_1 )</th>
<th>( a_1 )</th>
<th>( a_2 )</th>
<th>( a_2 )</th>
<th>( a_2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( b_1 )</td>
<td>( b_2 )</td>
<td>( b_3 )</td>
<td>( b_4 )</td>
<td>( b_5 )</td>
<td>( b_6 )</td>
<td>( b_7 )</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>5</td>
<td>2</td>
<td>7</td>
<td>4</td>
<td>7</td>
</tr>
<tr>
<td>6</td>
<td>2</td>
<td>6</td>
<td>3</td>
<td>8</td>
<td>5</td>
<td>8</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>5</td>
<td>4</td>
<td>7</td>
<td>4</td>
<td>9</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>6</td>
<td>3</td>
<td>6</td>
<td>3</td>
<td>8</td>
</tr>
</tbody>
</table>

**A B(A) Summary Table**

Entry is \( \sum_{i=1}^{n} Y_{ijk} \)

<table>
<thead>
<tr>
<th>( b_1 )</th>
<th>( b_2 )</th>
<th>( b_1 )</th>
<th>( b_4 )</th>
<th>( b_5 )</th>
<th>( b_6 )</th>
<th>( b_7 )</th>
<th>( \sum_{i=1}^{n} \sum_{k=1}^{q} Y_{ijk} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( n = 4 )</td>
<td>15</td>
<td>7</td>
<td>22</td>
<td>12</td>
<td>28</td>
<td>16</td>
<td>32</td>
</tr>
<tr>
<td>( \sum_{i=1}^{n} )</td>
<td>28</td>
<td>16</td>
<td>32</td>
<td>40</td>
<td>116</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(ii) Computational symbols

\[
\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} Y_{ijk} = 3 + 1 + \cdots + 11 = 172.000
\]

\[
\frac{\left( \sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} Y_{ijk} \right)^2}{npq} = \frac{(172)^2}{4(2)(4)} = 924.500
\]

\[
\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} Y_{ijk}^2 = [AB5] = (3)^2 + (1)^2 + \cdots + (11)^2 = 1160.00
\]

\[
\frac{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} Y_{ijk}}{npq} = [A] = \frac{(56)^2}{4(4)} + \frac{(116)^2}{4(4)} = 1037.000
\]

\[
\frac{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} Y_{ijk}^2}{n} = [AB] = \frac{(15)^2}{4} + \frac{(7)^2}{4} + \cdots + \frac{(40)^2}{4} = 1141.500
\]
11.2 Computational Example for CRH-pq(A) Design

Table 11.2-1 Computational Procedures for CRF-28(A) Design (Continued)

(iii) Computational formulas

\[
\begin{align*}
SSTO &= \{ABS\} - \{Y\} = 235.500 \\
SSA &= \{A\} - \{Y\} = 112.500 \\
SSB(A) &= \{AB\} - \{A\} = 104.500 \\
SSWCELL &= \{ABS\} - \{AB\} = 18.500 \\
\end{align*}
\]

\[MSB(A)\]. The test of MSA for model III (see Table 11.2-2) uses MSB(A) in the denominator of the \( F \) statistic. For \( F \) to be distributed as central \( F \) when the null hypothesis is true, the population variance estimator \( MSB(A) \) should be composed of homogeneous sources of variation. It can be shown that \( SSB(A) \) represents a pooled sum of squares:

\[
SSB(A) = \sum_{j=1}^{q_0} SSB \text{ at } a_j 
\]

\[p(q_0 - 1) \]

Actually \( SSB(A) \) is the pooled simple main effects of treatment \( B \) at each level of treatment \( A \). The reader may recall from Section 9.6 that

\[
\sum_{j=1}^{p} SSB \text{ at } a_j = SSB + SSAB
\]

Table 11.2-2 ANOVA Table for CRH-28(A) Design

<table>
<thead>
<tr>
<th>Source</th>
<th>SS</th>
<th>df</th>
<th>MS</th>
<th>( F )</th>
<th>E(MS)</th>
<th>Model III (A fixed)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. A (ionization)</td>
<td>112.500</td>
<td>( p - 1 = 1 )</td>
<td>112.500</td>
<td>6.46*</td>
<td>( \sigma_i^2 + n_0 \sigma_p^2 + \sum_{j=1}^{q_0} a_j^2/(p-1) )</td>
<td></td>
</tr>
<tr>
<td>2. B(A) (cages)</td>
<td>104.500</td>
<td>( p(q_0 - 1) = 6 )</td>
<td>17.417</td>
<td>22.59**</td>
<td>( \sigma_i^2 + \sigma_p^2 )</td>
<td></td>
</tr>
<tr>
<td>3. WCELL</td>
<td>18.500</td>
<td>( q_0(q_0 - 1) = 24 )</td>
<td>0.771</td>
<td></td>
<td>( \sigma_i^2 )</td>
<td></td>
</tr>
<tr>
<td>4. Total</td>
<td>235.500</td>
<td>( n_p q_0 - 1 = 31 )</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*p < .05 \quad **p < .000001
## Table 11.2-3 Comparison of Correct and Incorrect Analyses for the Data in Table 11.2-1

<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>SS</th>
<th>df</th>
<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Incorrect analysis: CR-2 design</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2. Within groups</td>
<td>[AS] - [A]</td>
<td>123.000</td>
<td>p(n - 1) = 30</td>
<td>4.100</td>
<td></td>
</tr>
<tr>
<td><strong>Correct analysis: CRH-28(A) design</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3. WCELL</td>
<td>[ABS] - [AB]</td>
<td>18.500</td>
<td>pq_0(n - 1) = 24</td>
<td>0.771</td>
<td></td>
</tr>
</tbody>
</table>

*p < .05  **p < .000001

Thus, $SSB(A)$ in a hierarchical experiment is equivalent to $SSB + SSAB$ in the corresponding factorial experiment. Procedures for partitioning $SSB(A)$ into $p$ sources of variation for testing the assumption of homogeneity are described in Section 9.6. The other error-term estimator, $MSWCELL$, also should be composed of homogeneous sources of variation. Procedures for testing this assumption are described in Section 3.5.

Typically the number of degrees of freedom associated with $MSB(A)$, the error term for testing $MSA$, is quite small. If there is reason for believing that $\sigma^2 = 0$, then $MSB(A)$ and $MSWCELL$ are both estimators of the same population error variance and can be pooled. For a discussion of the issues involved in performing preliminary tests and pooling, see Section 9.11. Pooling is not appropriate for the ionization data in Table 11.2-1 because the hypothesis $\sigma^2 = 0$ was rejected.

### An Incorrect Analysis

A common error in analyzing experiments that involve a nested nuisance variable is to ignore the variable and use an analysis appropriate for a CR-$p$ design. Instead of including the variable of, say, cages or classrooms in the design, the researcher acts as if $nq_0$ experimental units were randomly assigned to each level of treatment $A$ and the $nq_0$ units were all treated alike. If $\sigma^2 \neq 0$, as is often the case, then the test of treatment $A$ using $MSWCELL$ as the error term is positively biased. An analysis of the data in Table 11.2-1 ignoring the variable of cages leads to the results shown in Table 11.2-3. The discrepancy between the incorrect analysis (CR-2) and the correct analysis (CRH-28(A)) is quite large. The two analyses lead to the same decision for treatment $A$ if $\sigma^2 = 0$ and the researcher uses a pooled error term based on $MSB(A)$ and $MSWCELL$. Then the test of $A$ is given by $F = MSA/MSRES = 112.500/4.100 = 27.44$, where
\[
MSRES = \frac{SSB(A) + SSWCELL}{pq(n-1) + pq(n-1)}
\]
\[
= \frac{104.500 + 18.500}{6 + 24}
\]
\[
= 4.100
\]

As noted earlier, the use of a pooled error term for these data is not appropriate.

### 11.3 Experimental Design Model for CRH-pq(A) Design

#### Assumptions for Mixed Model [A Fixed and B(A) Random]

A score \( Y_{ijk} \) in a completely randomized hierarchical design is a composite that reflects the effects of treatments \( A \) and \( B(A) \) plus all other sources of variation that affect \( Y_{ijk} \). The experimental design model for a CRH-pq(A) design is

\[(11.3-1)\]
\[
Y_{ijk} = \mu + \alpha_i + \beta_{kl} + \epsilon_{ijk} \quad (i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q)
\]

where

- \( Y_{ijk} \) is the observation for the \( i \)th experimental unit in the \( jk \)th treatment combination.
- \( \mu \) is the grand mean.
- \( \alpha_i \) is the treatment effect for population \( j \) and is equal to \( \mu_j - \mu \). The \( j \)th treatment effect is a constant for all scores in treatment level \( a_j \) and is subject to the restriction \( \sum_j a_j = 0 \).
- \( \beta_{kl} \) is the treatment effect for population \( k(j) \) and is equal to \( \mu_{jk} - \mu_j \cdot \beta_{k(j)} \) is \( NID(0, \sigma^2_{\beta}) \).
- \( \epsilon_{ijk} \) is \( NID(0, \sigma^2) \) and independent of \( \beta_{k(j)} \).

#### Partition of the Total Sum of Squares

The values of the parameters \( \mu, \alpha_i, \beta_{k(j)} \), and \( \epsilon_{ijk} \) in model (11.3-1) are unknown, but they can be estimated from sample data as follows:

Parameters of the model equation

\[
Y_{ijk} = \mu + \alpha_i + \beta_{kl} + \epsilon_{ijk}
\]

Sample estimators of the parameters

\[(11.3-2)\]
\[
Y_{ijk} = \overline{Y} + (\overline{Y}_j - \overline{Y}) + (\overline{Y}_k - \overline{Y}_j) + (Y_{ijk} - \overline{Y}_{ijk})
\]

<table>
<thead>
<tr>
<th>Score</th>
<th>Grand mean</th>
<th>Treatment effect</th>
<th>Treatment effect</th>
<th>Within-cell error effect</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>( \alpha_i )</td>
<td>( \beta_{k(j)} )</td>
<td>( \epsilon_{ijk} )</td>
</tr>
</tbody>
</table>
The partition of the total sum of squares, which is the basis for the analysis in Table 11.2-2, is obtained by rearranging the terms in equation (11.3-2) as follows:

\[
Y_{ijk} - \bar{Y}_{..} = (Y_{ij} - \bar{Y}_{..}) + (Y_{i} - \bar{Y}_{..}) + (Y_{ij} - \bar{Y}_{i})
\]

Squaring both sides of equation (11.3-3) and summing over all of the observations following the examples in Sections 3.2 and 7.1 lead to the following partition of the total sum of squares:

\[
\frac{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} (Y_{ijk} - \bar{Y}_{..})^2}{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} (Y_{ij} - \bar{Y}_{..})^2} + \frac{n \sum_{j=1}^{p} (Y_{ij} - \bar{Y}_{.})^2}{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} (Y_{ijk} - \bar{Y}_{..})^2} = \frac{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} (Y_{ijk} - \bar{Y}_{.})^2}{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} (Y_{ijk} - \bar{Y}_{..})^2} + \frac{n \sum_{i=1}^{n} (Y_{i} - \bar{Y}_{..})^2}{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} (Y_{ijk} - \bar{Y}_{..})^2} + \frac{\sum_{i=1}^{n} \sum_{j=1}^{p} (Y_{ij} - \bar{Y}_{.})^2}{\sum_{i=1}^{n} \sum_{j=1}^{p} \sum_{k=1}^{q} (Y_{ijk} - \bar{Y}_{..})^2}
\]

The sums-of-squares formulas in (11.3-4) are not the most convenient for computational purposes. More convenient formulas are given in Table 11.2-1. Mean squares are obtained by dividing the sums of squares by the degrees of freedom in Table 11.2-2.

**Assumptions for Other Models and Expectations of MS's**

The assumptions for a fixed-effects model are as follows:

\[
Y_{ijk} = \mu + \alpha_j + \beta_{i(j)} + \epsilon_{i(j)} \quad (i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q)
\]

where

- \(\alpha_j\) is a constant for all scores in treatment level \(a_j\) and is subject to the restriction \(\sum_{j=1}^{p} \alpha_j = 0\).
- \(\beta_{i(j)}\) is a constant for all scores in treatment level \(b_i\) and is subject to the restriction \(\sum_{i=1}^{n} \beta_{i(j)} = 0\) for all \(j\).
- \(\epsilon_{i(j)}\) is \(\text{NID}(0, \sigma^2_{\epsilon})\).

If treatments \(A\) and \(B(A)\) represent random effects, the assumptions are as follows:

- \(\alpha_j\) is \(\text{NID}(0, \sigma^2_{\alpha})\).
- \(\beta_{i(j)}\) is \(\text{NID}(0, \sigma^2_{\beta})\).
- \(\epsilon_{i(j)}\) is \(\text{NID}(0, \sigma^2_{\epsilon})\) and independent of \(\alpha_j\) and \(\beta_{i(j)}\).

Experiments in which treatment \(A\) is random but \(B(A)\) is fixed are rare. The assumptions for this mixed model are as follows:

- \(\alpha_j\) is \(\text{NID}(0, \sigma^2_{\alpha})\).
- \(\beta_{i(j)}\) is subject to the restriction \(\sum_{j=1}^{p} \beta_{i(j)} = 0\) for all \(j\).
- \(\epsilon_{i(j)}\) is \(\text{NID}(0, \sigma^2_{\epsilon})\), and independent of \(\alpha_j\).

See Review Exercise 6 for the derivation.
### Table 11.3.1 Expected Values of Mean Squares for CRH-\(pq(A)\) Design

<table>
<thead>
<tr>
<th>Mean Square</th>
<th>Model I A fixed</th>
<th>Model II A random</th>
<th>Model III* A random</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(B(A)) fixed</td>
<td>(B(A)) random</td>
<td>(B(A)) fixed</td>
</tr>
<tr>
<td>1. MSA</td>
<td>(\sigma^2 + nq_0 \sum \alpha_i^2 / (p-1))</td>
<td>(\sigma^2 + n\sigma^2_\alpha + nq_0\sigma^2_{\varepsilon})</td>
<td>(\sigma^2 + nq_0\sigma^2_{\varepsilon})</td>
</tr>
<tr>
<td>2. MSB(A)</td>
<td>(\sigma^2 + n \sum_{i=1}^{q_0} \sum_{t=1}^{p} \beta_{it\alpha} / (pq_0 - 1))</td>
<td>(\sigma^2 + n\sigma^2_{\varepsilon})</td>
<td>(\sigma^2 + n \sum_{i=1}^{q_0} \sum_{t=1}^{p} \beta_{it\alpha} / (pq_0 - 1))</td>
</tr>
<tr>
<td>3. MSWCELL</td>
<td>(\sigma^2_{\varepsilon})</td>
<td>(\sigma^2_{\varepsilon})</td>
<td>(\sigma^2_{\varepsilon})</td>
</tr>
</tbody>
</table>

*Expected values for model III (A fixed) are given in Table 11.2.-2.

The expected values for these models are given in Table 11.3.1. These expected values and those for other hierarchical designs are easily derived using the rules in Section 9.9.

#### 11.4 Procedures for Testing Differences Among Means

Tests of differences among means in a CRH-\(pq(A)\) design have the same general form as those given in Chapter 4. The test statistics for making comparisons among treatment \(A\) means for a mixed model (A fixed) have the form

\[
t = \frac{\hat{Y}_{(a)}}{\sigma_{(a)}} = \frac{c_1 \bar{Y}_{1\cdot} + c_2 \bar{Y}_{2\cdot} + \cdots + c_p \bar{Y}_{p\cdot}}{\sqrt{MSB(A)}}
\]

\[
q = \frac{\hat{Y}_{(a)}}{\sigma_{(a)}} = \frac{c_1 \bar{Y}_{1\cdot} + c_2 \bar{Y}_{2\cdot} + \cdots + c_p \bar{Y}_{p\cdot}}{\sqrt{MSWCELL/n}}
\]

For a fixed-effects model, the mean square in the denominator of the above statistics should be replaced by MSWCELL. The general rule is that the error term used in testing a treatment null hypothesis should be used in testing specific hypotheses concerning the population means. The number of degrees of freedom for these statistics is equal to the degrees of freedom associated with the mean square used in the denominator: \(pq_0 - 1\) or \(pq_0(n-1)\).

A researcher ordinarily is not interested in testing hypotheses concerning the nested treatment. However, if this test is desired, the statistics have the following form for both the fixed-effects model and the mixed model [\(B(A)\) fixed]:

\[
t = \frac{\hat{Y}_{(a)}}{\sigma_{(a)}} = \frac{c_1 \bar{Y}_{1\cdot} + c_2 \bar{Y}_{2\cdot} + \cdots + c_p \bar{Y}_{p\cdot}}{\sqrt{MSWCELL/n}}
\]

\[
q = \frac{\hat{Y}_{(a)}}{\sigma_{(a)}} = \frac{c_1 \bar{Y}_{1\cdot} + c_2 \bar{Y}_{2\cdot} + \cdots + c_p \bar{Y}_{p\cdot}}{\sqrt{MSWCELL/n}}
\]
### 11.5 Estimating Strength of Association, Effect Size, Power, and Sample Size

#### Strength of Association

Measures of strength of association for a fixed-effects model are given by

\[
\hat{\omega}_{H_0}^2 = \frac{\sum_{j=1}^{p} \hat{\alpha}_j^2 / p}{\hat{\sigma}_e^2 + \sum_{j=1}^{p} \hat{\alpha}_j^2 / p} \quad \hat{\omega}_{H_0,A}^2 = \frac{\sum_{j=1}^{p} \beta_{i,j}^2 / q}{\hat{\sigma}_e^2 + \sum_{j=1}^{p} \beta_{i,j}^2 / q}
\]

Comparable measures for a random-effects model are given by

\[
\hat{\eta}_{H_0}^2 = \frac{\sigma_a^2}{\hat{\sigma}_e^2 + \sigma_a^2} \quad \hat{\eta}_{H_0,A}^2 = \frac{\sigma_b^2}{\hat{\sigma}_e^2 + \sigma_b^2}
\]

The expectations of the mean squares in Table 11.2-2 and 11.3-1 are the basis for identifying the terms required to compute the measures of association. Procedures for using the E(MS)_i's to estimate \(\sum_{j=1}^{p} \hat{\alpha}_j^2 / p\) and so on were introduced in Section 5.5. If an estimated component is negative, that estimate is set equal to zero. A mixed model (A fixed) is appropriate for the ionization experiment described in Sections 11.1 and 11.2. Measures of partial omega squared and the partial intraclass correlation for the ionization data in Table 11.2-2 are as follows:

\[
\hat{\omega}_{H_0}^2 = \frac{\sum_{j=1}^{p} \hat{\alpha}_j^2 / p}{\hat{\sigma}_e^2 + \sum_{j=1}^{p} \hat{\alpha}_j^2 / p} = \frac{2.971}{0.771 + 2.971} = .79
\]

\[
\hat{\rho}_{H_0,A} = \frac{\sigma_b^2}{\hat{\sigma}_e^2 + \sigma_b^2} = \frac{4.162}{0.771 + 4.162} = .84
\]

where

\[
\sum_{j=1}^{p} \hat{\alpha}_j^2 = \frac{(p - 1)[MSA - MSB(A)]}{npq_{ij}} = \frac{(2 - 1)(112.500 - 17.417)}{(4)(2)(4)} = 2.971
\]

\[
\hat{\sigma}_b^2 = \frac{MSB(A) - MSWCELL}{n} = \frac{17.417 - 0.771}{4} = 4.162
\]

\[
\hat{\sigma}_e^2 = MSWCELL = 0.771
\]

Both the ionization treatment and the cages account for an appreciable portion of the variance in the dependent variable.
Effect Size

Cohen's measure of effect size can be computed from partial omega squared. For example, the formula for computing $\hat{f}_A$ for treatment A is

$$\hat{f}_A = \sqrt{\frac{\hat{\omega}^2_{\text{partial}}} {1 - \hat{\omega}^2_{\text{partial}}}}$$

Estimating Power and Sample Size

Procedures for estimating power and sample size were discussed in Section 5.6. Formulas for computing $\hat{\phi}$ are

$$\hat{\phi}_A = \sqrt{\frac{\hat{\lambda}_{A,0}}{p}} = \sqrt{\frac{\sum \hat{\lambda}_{1,p}}{\sum \hat{\lambda}_{1,n \sigma}}} \quad \nu_1 = p - 1$$

$$\hat{\phi}_{B(0)} = \sqrt{\frac{\hat{\lambda}_{B(0),0}}{q_{(0)}}} = \sqrt{\frac{\sum \hat{\beta}_{B(0),0}}{\sum \hat{\beta}_{B(0),n \sigma}}} \quad \nu_2 = pq(0)(n - 1)$$

11.6 Description of Other Completely Randomized Hierarchical Designs

This section gives a brief description of a variety of hierarchical designs that are constructed from completely randomized and randomized block designs. Suggestions for analyzing these designs using computer programs written for crossed treatments are given in the following section.

CRH-$pq(A)r(AB)$ Design

Consider an experiment to evaluate the efficacy of a new drug, denoted by $a_1$, and the current drug, denoted by $a_2$. Four hospitals, treatment $B(A)$, with two wards each, treatment $C(AB)$, are available to participate in the experiment. Because expensive equipment is needed to monitor the side effects of the new drug, it was decided to use the new drug in two of the four hospitals and the current drug in the other two hospitals. The hospitals were randomly assigned to the drug conditions, with the restriction that two hospitals were assigned to each condition. A total of $npq(0)r(0)$ patients were randomly assigned to the $pq(0)r(0) = (2)(2)(2) = 8$ treatment combinations, with the restriction that $n$ patients were assigned to each combination. The
Figure 11.6-1 Diagram of CRH-24(A)8(AB) design. The four hospitals, treatment B(A), are nested in the two drugs, treatment A; the eight wards, treatment C(AB), are nested in the hospitals and drugs. Patients are randomly assigned to the \( pqr_0r_{00} = (2)(2)(2) = 8 \) treatment combinations, with the restriction that \( n \) patients are assigned to each combination.

design is diagrammed in Figure 11.6-1. The experimental design model equation for this completely nested design in which hospitals are nested in the drugs, and wards are nested in hospitals and drugs is

\[
Y_{ij} = \mu + \alpha_i + \beta_{i0} + \gamma_{ij0} + \epsilon_{ijk0} \quad (i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q; l = 1, \ldots, r)
\]

The computational formulas and so on for this design are given in Table 11.6-1. The sums of squares \( SSB(A) \) and \( SSC(AB) \) represent pooled simple main effects and pooled simple simple main effects, respectively. It can be shown that these sums of squares correspond to

\[
SSB(A) = \sum_{j=1}^{q} SSB \text{ at } a_j = SSB + SSAB
\]

\[
SSC(AB) = \sum_{j=1}^{r_0} \sum_{l=1}^{q} SSC \text{ at } a_jb_l = SSC + SSAC + SSBC + SSABC
\]

<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>( df )</th>
<th>( E(MS) ) *</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. A</td>
<td>([A] - [Y])</td>
<td>( p - 1 )</td>
<td>( \sigma^2 + n(1 - \frac{r}{R})\sigma^2 + nq_0\gamma_0\sigma^2 + npq_0r_0\sigma^2 )</td>
</tr>
<tr>
<td>2. B(A)</td>
<td>([AB] - [A])</td>
<td>( p_0(q_0 - 1) )</td>
<td>( \sigma^2 + n(1 - \frac{r}{R})\sigma^2 + npq_0\sigma^2 )</td>
</tr>
<tr>
<td>3. C(AB)</td>
<td>([ABC] - [AB])</td>
<td>( pq_0r_0(n - 1) )</td>
<td>( \sigma^2 + n\sigma^2 )</td>
</tr>
<tr>
<td>4. WCELL</td>
<td>([ABCS] - [ABC])</td>
<td>( npr_0r_0(n - 1) )</td>
<td>( \sigma^2 )</td>
</tr>
<tr>
<td>5. Total</td>
<td>([ABCS] - [Y])</td>
<td>( npq_0r_0r_0(n - 1) )</td>
<td>( )</td>
</tr>
</tbody>
</table>

*The variances should be replaced by \( \Sigma \alpha_i^2/(p - 1) \), \( \Sigma \beta_{i0}^2/p(q_0 - 1) \), and \( \Sigma \gamma_{ij0}^2/pr_0r_0(n - 1) \) if the corresponding treatments are fixed.
11.6 Description of Other Completely Randomized Hierarchical Designs 489

\[ \begin{array}{c}
\text{Figure 11.6-2} \quad \text{Diagram of CRPH-24(A)2 design. The four levels of treatment B(A) are nested in the two levels of treatment A; treatment C is crossed with treatments A and B(A).}
\end{array} \]

in a factorial design. For \( MSB(A) \) and \( MSC(AB) \) to serve as denominators of \( F \) statistics, the mean squares should be composed of homogeneous sources of variation—for example,

\[
MSC \text{ at } a_i b_1 = MSC \text{ at } a_i b_2 = \cdots = MSC \text{ at } a_i b_g
\]

**CRPH-pq(A)r, CRPH-pqr(A), and CRPH-pqr(B) Designs**

The experimental design model equation for a CRPH-pq(A)r design in which treatment B(A) is nested in A, but treatment C is crossed with A and B(A) is

\[
Y_{ijl} = \mu + \alpha_i + \beta_k + \gamma_l + (\alpha\gamma)_{il} + (\beta\gamma)_{kl} + \varepsilon_{ikl} \quad (i = 1, \ldots, p; \quad j = 1, \ldots, r)
\]

The design is diagrammed in Figure 11.6-2; computational formulas are given in Table 11.6-2. It can be shown that \( SSB(A) \) and \( SSB(AB) \times C \) correspond to

\[
SSB(A) = \sum_{j=1}^{p} SSB \text{ at } a_j = SSB + SSAB
\]

\[
SSB(AB) \times C = \sum_{j=1}^{p} SSB \text{ at } a_j = SSBC + SSABC
\]

in a factorial design.

One variation on this design is to nest treatment C(A) in A and cross treatments A and B. The other variation is to nest treatment C(B) in B and cross treatments A and B. The experimental design model equations are, respectively,

\[
Y_{ijl} = \mu + \alpha_i + \beta_k + \gamma_l + (\alpha\beta)_{ik} + (\beta\gamma)_{kl} + \varepsilon_{ijkl} \\
Y_{ijl} = \mu + \alpha_i + \beta_k + \gamma_l + (\alpha\beta)_{ik} + (\alpha\gamma)_{il} + \varepsilon_{ijkl}
\]

These designs are diagrammed in Figures 11.6-3 and 11.6-4; the computational formulas are given in Tables 11.6-3 and 11.6-4.
Table 11.6-2  CRPH-pq(A)r Design

<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>df</th>
<th>E(MS)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. A</td>
<td>[A] - [Y]</td>
<td>p - 1</td>
<td>$\sigma^2_a + n\left(1 - \frac{q}{Q}\right)\left(1 - \frac{r}{R}\right)\sigma^2_{pr}$</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>$+ nq_0\left(1 - \frac{q}{Q}\right)\sigma^2_{ar} + nr\left(1 - \frac{q}{Q}\right)\sigma^2_{ar}$</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>$+ nq_0 r\sigma^2_a$</td>
</tr>
<tr>
<td>2. B(A)</td>
<td>[AB] - [A]</td>
<td>p(q_0 - 1)</td>
<td>$\sigma^2_a + n\left(1 - \frac{r}{R}\right)\sigma^2_{ar}$</td>
</tr>
<tr>
<td>3. C</td>
<td>[C] - [Y]</td>
<td>r - 1</td>
<td>$\sigma^2_a + n\left(1 - \frac{q}{Q}\right)\sigma^2_{ar} + nq_0\left(1 - \frac{p}{P}\right)\sigma^2_{ar}$</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>$+ nq_0 r\sigma^2_a$</td>
</tr>
<tr>
<td>4. AC</td>
<td>[AC] - [A] - [C] + [Y]</td>
<td>(p - 1)(r - 1)</td>
<td>$\sigma^2_a + n\left(1 - \frac{q}{Q}\right)\sigma^2_{ar} + nq_0\sigma^2_{ar}$</td>
</tr>
<tr>
<td>5. B(A) X C</td>
<td>[ABC] - [AB] - [AC] + [A]</td>
<td>p(q_0 - 1)(r - 1)</td>
<td>$\sigma^2_a + n\sigma^2_{ar}$</td>
</tr>
<tr>
<td>6. WCELL</td>
<td>[ABCS] - [ABC]</td>
<td>p(q_0)(n - 1)</td>
<td>$\sigma^2_a$</td>
</tr>
<tr>
<td>7. Total</td>
<td>[ABCS] - [Y]</td>
<td>npq_0r - 1</td>
<td></td>
</tr>
</tbody>
</table>

*The variances should be replaced by $\Sigma \sigma^2_i/(p - 1)$, $\Sigma \beta^2_{ij}/p(q_0 - 1)$, and $\Sigma \gamma^2_i/(r - 1)$ if the corresponding treatments are fixed.

Figure 11.6-3  Diagram of CRPH-224(A) design. Treatments A and B are crossed; the four levels of treatment C(A) are nested in A. Treatments B and C(A) are crossed.

Figure 11.6-4  Diagram of CRPH-224(B) design. Treatments A and B are crossed; the four levels of treatment C(B) are nested in B. Treatments A and C(B) are crossed.
### Table 11.6-3 CRPH-pqr(A) Design

<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>df</th>
<th>$E(\text{MS})^*$</th>
</tr>
</thead>
</table>
| 1. A   | $[A] - [Y]$ | $p - 1$ | $\sigma^2 + n(1 - \frac{q}{Q})(1 - \frac{r}{R})\sigma^2_{\beta r}$ 
+ $nq\sigma^2_{\alpha}$ |
| 2. B   | $[B] - [Y]$ | $q - 1$ | $\sigma^2 + n\left(1 - \frac{r}{R}\right)\sigma^2_{p r}$ 
+ $nq\sigma^2_{\beta r}$ |
| 3. C(A) | $[AC] - [A]$ | $p(r_{ii} - 1)$ | $\sigma^2 + n\left(1 - \frac{q}{Q}\right)\sigma^2_{\beta r}$ 
+ $nq\sigma^2_{\alpha}$ |
| 4. $AB$ | $[AB] - [A] - [B] + [Y]$ | $(p - 1)(q - 1)$ | $\sigma^2 + n\left(1 - \frac{r}{R}\right)\sigma^2_{p r}$ 
+ $nq\sigma^2_{\beta r}$ |
| 5. $B \times C(A)$ | $[ABC] - [AB] - [AC] + [A]$ | $p(q - 1)(r_{ii} - 1)$ | $\sigma^2 + n\sigma^2_{\beta r}$ |
| 6. WCELL | $[ABCS] - [ABC]$ | $pq(r_{iij}) - 1$ | $\sigma^2$ |
| 7. Total | $[ABCS] - [Y]$ | $npr_{iij} - 1$ | |

*The variances should be replaced by $\Sigma\sigma^2_{\beta}(p - 1)$, $\Sigma\beta^2_{\alpha}(q - 1)$, and $\Sigma\gamma^2_{\beta\alpha\gamma}(r_{iij} - 1)$ if the corresponding treatments are fixed.

### CRPH-pq(A)r(A) Design

The experimental design model equation for a CRPH-pq(A)r(A) design in which both treatments $B(A)$ and $C(A)$ are nested in treatment $A$ is

$$Y_{ijkl} = \mu + \alpha_j + \beta_{ik} + \gamma_{il} + (B\gamma)_{ijknl} + \epsilon_{ijkl} \quad (i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q; l = 1, \ldots, r)$$

This design is diagrammed in Figure 11.6-5; computational formulas are given in Table 11.6-5. It can be shown that $SSB(A)$, $SSC(A)$, and $SSB(A) \times C(A)$ correspond to

$$SSB(A) = \sum_{j=1}^{p} SSB \text{ at } a_j = SSB + SSAB$$

$$SSC(A) = \sum_{j=1}^{p} SSC \text{ at } a_j = SSC + SSAC$$

$$SSB(A) \times C(A) = \sum_{j=1}^{p} SSB \text{ at } a_j = SSBC + SSABC$$

in a factorial design.

### CRPH-pqr(AB) Design

A CRPH-pqr(AB) design is one in which treatment $C(AB)$ is nested in both $A$ and $B$, but treatments $A$ and $B$ are crossed. For example, suppose a new drug education
program for junior high students is to be evaluated. We denote the program by $a_i$ and the control condition by $a_0$. Two schools, treatment $B$, are available to the researcher. Eight social studies teachers, treatment $C(AB)$, are randomly assigned to the $pq$ treatment combinations, with the restriction that two teachers are assigned to each combination. The design is diagrammed in Figure 11.6-6.

The experimental design model equation is

$$Y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_{ij} + (\alpha\beta)_{ik} + \varepsilon_{ijkl} \quad (i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q; l = 1, \ldots, r)$$

![Diagram of CRPH-24(A)4(A) design](image.png)

Figure 11.6-5 - Diagram of CRPH-24(A)4(A) design. The four levels of treatment $B(A)$ are nested in treatment $A$; the four levels of treatment $C(A)$ are also nested in treatment $A$. The levels of treatments $B(A)$ and $C(A)$ are crossed.
### Table 11.6-5  CRPH-(pq)(A) Design

<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>df</th>
<th>( E(\text{MS}) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. A</td>
<td>([A] - [Y])</td>
<td>(p - 1)</td>
<td>(\sigma_r^2 + n\left(1 - \frac{q}{Q}\right)\left(1 - \frac{r}{R}\right)\sigma_y^2) + (nq_0\left(1 - \frac{r}{R}\right)\sigma_y^2 + nr_0\left(1 - \frac{q}{Q}\right)\sigma_y^2 + nq_0r_0\sigma_\theta^2)</td>
</tr>
<tr>
<td>2. B(A)</td>
<td>([AB] - [A])</td>
<td>(p(q_0 - 1))</td>
<td>(\sigma_r^2 + n\left(1 - \frac{r}{R}\right)\sigma_y^2 + nr_0\sigma_\theta^2)</td>
</tr>
<tr>
<td>3. C(A)</td>
<td>([AC] - [A])</td>
<td>(p(r_0 - 1))</td>
<td>(\sigma_r^2 + n\left(1 - \frac{q}{Q}\right)\sigma_y^2 + nr_0\sigma_\theta^2)</td>
</tr>
<tr>
<td>4. B(A) \times C(A)</td>
<td>([ABC] - [AB] - [AC] + [A])</td>
<td>(p(q_0 - 1)(r_0 - 1))</td>
<td>(\sigma_r^2 + nr_0\sigma_y^2)</td>
</tr>
<tr>
<td>5. WCELL</td>
<td>([ABCS] - [ABC])</td>
<td>(pq_0r_0(n - 1))</td>
<td>(\sigma_y^2)</td>
</tr>
<tr>
<td>6. Total</td>
<td>([ABCS] - [Y])</td>
<td>(npq_0r_0 - 1)</td>
<td>(\sigma_y^2)</td>
</tr>
</tbody>
</table>

*The variances should be replaced by \(\Sigma \sigma_j^2 (p - 1), \Sigma \sigma_{ij}^2 (q_0 - 1), \) and \(\Sigma \gamma_j^2 (n - 1)\) if the corresponding treatments are fixed.

The computational formulas are given in Table 11.6-6. The sum of squares \(SSC(AB)\) corresponds to

\[
SSC(AB) = \sum_{i=1}^{p} \sum_{j=1}^{q} \text{SSC at } a_i b_j = SSC + SSAC + SSBC + SSABC
\]

in a factorial design.

We have now described all of the three-treatment hierarchical designs that are based on a CR-\(p\) design. The patterns that underlie hierarchical designs with four or more treatments are straightforward extensions of those described. Accordingly, in the next section we describe only one of the four-treatment completely randomized partial hierarchical designs.

![Diagram of CRPH-228(AB) design. Treatments A and B are crossed; the eight levels of treatment C(AB) are nested in A and B.](image)
Table 11.6-6  CRPH-pqr(AB) Design

<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>df</th>
<th>( E(MS)* )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. A</td>
<td>([A] - [Y])</td>
<td>( p - 1 )</td>
<td>( \sigma^2_a + n\rho_{12}\left(1 - \frac{a}{Q}\right)\sigma^2_{ab} + n\left(1 - \frac{r}{R}\right)\sigma^2_\gamma )</td>
</tr>
<tr>
<td>2. B</td>
<td>([B] - [Y])</td>
<td>( q - 1 )</td>
<td>( \sigma^2_b + n\rho_{12}\left(1 - \frac{b}{p}\right)\sigma^2_{ab} + n\left(1 - \frac{r}{R}\right)\sigma^2_\gamma )</td>
</tr>
<tr>
<td>3. C(AB)</td>
<td>([ABC] - [AB])</td>
<td>( pq(n_i - 1) )</td>
<td>( \sigma^2 + \rho_{12}\sigma^2_\gamma )</td>
</tr>
<tr>
<td>4. AB</td>
<td>([AB] - [A] - [B] + [Y])</td>
<td>((p-1)(q-1) )</td>
<td>( \sigma^2_{ab} + n\rho_{12}\sigma^2_\gamma )</td>
</tr>
<tr>
<td>5. WCELL</td>
<td>([ABC] - [ABC])</td>
<td>( nqr(n_i - 1) )</td>
<td>( \sigma^2_\gamma )</td>
</tr>
<tr>
<td>6. Total</td>
<td>([ABC] - [Y])</td>
<td>( nqr(n_i) - 1 )</td>
<td>( )</td>
</tr>
</tbody>
</table>

*The variances should be replaced by \( \sum a^2_i/(p - 1), \sum b^2_i/(q - 1), \) and \( \sum \gamma^2_{i,j}/pq(n_i - 1) \) if the corresponding treatments are fixed.

CRPH-pqrt(C) Design

The experimental design model equation for a CRPH-pqrt(C) design in which treatments A, B, and C are crossed but D(C) is nested in C is

\[
Y_{ijkm} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_{i10} + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\alpha\delta)_{i10} + (\beta\gamma)_{jk} + (\beta\delta)_{j10} + (\alpha\beta\gamma)_{ijk} + (\alpha\beta\delta)_{ij1} + (\alpha\beta\gamma)_{ijk} + \epsilon_{ijk}\]

\[(i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q; l = 1, \ldots, r; m = 1, \ldots, l)\]

The design is diagrammed in Figure 11.6-7; computational formulas are given in Table 11.6-7. The sums of squares \( SSD(C), SSA \times D(C), SSB \times D(C), \) and \( SSA \times B \times D(C) \) correspond to

![Diagram of CRPH-2224(C) design](image)

Figure 11.6-7  Diagram of CRPH-2224(C) design. Treatments A, B, and C are crossed; the four levels of treatment D(C) are nested in treatment C.
11.6 Description of Other Completely Randomized Hierarchical Designs

\[ SSD(C) = \sum_{i=1}^{r} SSD \text{ at } c_i = SSD + SSCD \]
\[ SSA \times D(C) = \sum_{i=1}^{r} SSAD \text{ at } c_i = SSAD + SSACD \]
\[ SSB \times D(C) = \sum_{i=1}^{r} SSBD \text{ at } c_i = SSBD + SSBDC \]
\[ SSA \times B \times D(C) = \sum_{i=1}^{r} SSABD \text{ at } c_i = SSABD + SSABCD \]

in a factorial design.

**RBH-pq(A) Design**

Hierarchical designs can be constructed using an RB-p design as the building block design. In this section we describe an RBH-pq(A) design in which the q levels of treatment B(A) are nested in those of treatment A.

Suppose an educational researcher wants to compare the effectiveness of two ways of using reading pacers in increasing sixth-graders’ reading speed. In condition \( a_i \), the rate of presentation of reading material is increased by a small amount every 5 minutes. In condition \( a_j \), the child controls the speed and is encouraged to increase it as much as possible. Four reading pacers are modified to provide the constant and self-paced conditions, and the equipment is installed in four study rooms. The rooms are not identical, and there is no way to ensure that other extraneous conditions such as ambient noise, room illumination, and so on are the same from room to room. Accordingly, the rooms are designated as levels of treatment B(A). Twenty children are assigned to one of five blocks based on a pretest of their reading speed; subjects within a block have similar scores. The subjects in each block are randomly assigned to the four combinations of treatments A and B(A). A diagram of this design is shown in Figure 11.6-8; computational formulas are given in Table 11.6-8.

If blocks do not interact with treatments A and B(A), the experimental design model equation is

\[ Y_{ijk} = \mu + \alpha_i + \beta_{jk} + \pi_j + \epsilon_{ijk} \quad (i = 1, \ldots, n; j = 1, \ldots, p; k = 1, \ldots, q) \]

If the block-treatment interactions, \( \sigma^2_{\alpha\pi} \) and \( \sigma^2_{\beta\pi} \), are not equal to zero, the model equation must be amended as follows:

\[ Y_{ijk} = \mu + \alpha_i + \beta_{jk} + \pi_j + (\pi\alpha)_{ij} + (\pi\beta)_{jk} + \epsilon_{ijk} \]

Computational procedures for the additive and nonadditive models were discussed in Section 10.6.

The construction of randomized block hierarchical and partial hierarchical designs with three or more treatments follows the pattern illustrated earlier for the CR-p building block design. Additional information about hierarchical designs can be found
<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>( df )</th>
<th>( E(\text{MS})^a )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. ( A )</td>
<td>( [A] - [Y] )</td>
<td>( p - 1 )</td>
<td>( \sigma_i^2 + n\left(1 - \frac{p}{Q}\right)(1 - \frac{T}{r})\sigma_{aY}^2 + nt_0\left(1 - \frac{p}{Q}\right)(1 - \frac{T}{r})\sigma_{aY}^2 ) + ( nq\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 + nqf_p\left(1 - \frac{r}{Q}\right)\sigma_{aY}^2 + nqf_p\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 ) + ( nqf_p\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 )</td>
</tr>
<tr>
<td>2. ( B )</td>
<td>( [B] - [Y] )</td>
<td>( q - 1 )</td>
<td>( \sigma_i^2 + n\left(1 - \frac{p}{P}\right)(1 - \frac{T}{r})\sigma_{aY}^2 + nt_0\left(1 - \frac{r}{P}\right)(1 - \frac{T}{r})\sigma_{aY}^2 ) + ( np\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 + npf_p\left(1 - \frac{r}{P}\right)\sigma_{aY}^2 + npf_p\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 ) + ( npf_p\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 )</td>
</tr>
<tr>
<td>3. ( C )</td>
<td>( [C] - [Y] )</td>
<td>( r - 1 )</td>
<td>( \sigma_i^2 + n\left(1 - \frac{p}{P}\right)(1 - \frac{T}{r})\sigma_{aY}^2 ) + ( np\left(1 - \frac{r}{P}\right)(1 - \frac{T}{r})\sigma_{aY}^2 + npf_p\left(1 - \frac{r}{P}\right)(1 - \frac{T}{r})\sigma_{aY}^2 ) ( + npf_p\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 ) + ( npf_p\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 )</td>
</tr>
<tr>
<td>4. ( D(C) )</td>
<td>( [CD] - [C] )</td>
<td>( r(t_0 - 1) )</td>
<td>( \sigma_i^2 + n\left(1 - \frac{p}{P}\right)(1 - \frac{T}{r})\sigma_{aY}^2 + np\left(1 - \frac{r}{P}\right)\sigma_{aY}^2 ) + ( nq\left(1 - \frac{T}{r}\right)\sigma_{aY}^2 + npq\sigma_{aY}^2 )</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>---</td>
<td>---</td>
<td>---</td>
<td>---</td>
</tr>
<tr>
<td>5. $AB$</td>
<td>$[AB] - [A] - [B] + [Y]$</td>
<td>$(p - 1)(q - 1)$</td>
<td>$\sigma_1^2 + n(1 - \frac{r}{T})\sigma_{ab}^2 + n\tau_0(1 - \frac{r}{T})\sigma_{a}^2 + n\tau_0\sigma_{b}^2$</td>
</tr>
<tr>
<td>6. $AC$</td>
<td>$[AC] - [A] - [C] + [Y]$</td>
<td>$(p - 1)(r - 1)$</td>
<td>$\sigma_1^2 + n(1 - \frac{q}{Q})(1 - \frac{r}{T})\sigma_{ac}^2$</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7. $A \times D(C)$</td>
<td>$[ACD] - [AC] - [CD] + [C]$</td>
<td>$(p - 1)(t_0 - 1)$</td>
<td>$\sigma_1^2 + n(1 - \frac{q}{Q})\sigma_{ac}^2 + n\tau_0\sigma_{b}^2$</td>
</tr>
<tr>
<td>8. $BC$</td>
<td>$[BC] - [B] - [C] + [Y]$</td>
<td>$(q - 1)(r - 1)$</td>
<td>$\sigma_1^2 + n(1 - \frac{p}{P})(1 - \frac{r}{T})\sigma_{bc}^2 + n\tau_0(1 - \frac{p}{P})\sigma_{b}^2$</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9. $B \times D(C)$</td>
<td>$[BCD] - [BC] - [CD] + [C]$</td>
<td>$(q - 1)(t_0 - 1)$</td>
<td>$\sigma_1^2 + n(1 - \frac{p}{P})\sigma_{bc}^2 + n\tau_0\sigma_{b}^2$</td>
</tr>
<tr>
<td>10. $ABC$</td>
<td>$[ABC] - [AB] - [AC] - [BC]$</td>
<td>$(p - 1)(q - 1)(r - 1)$</td>
<td>$\sigma_1^2 + n(1 - \frac{r}{T})\sigma_{abc}^2 + n\tau_0\sigma_{b}^2$</td>
</tr>
<tr>
<td>11. $A \times B \times D(C)$</td>
<td>$[ABC] - [ACD] - [ABCD]$</td>
<td>$(p - 1)(q - 1)(t_0 - 1)$</td>
<td>$\sigma_1^2 + n\sigma_{abc}^2$</td>
</tr>
<tr>
<td>12. $WCELL$</td>
<td>$[ABCDS] - [ABCD]$</td>
<td>$pqrt_0(n - 1)$</td>
<td>$\sigma_1^2$</td>
</tr>
<tr>
<td>13. Total</td>
<td>$[ABCDS] - [Y]$</td>
<td>$nqrt_0 - 1$</td>
<td></td>
</tr>
</tbody>
</table>

*The variances should be replaced by $\Sigma\sigma_1^2/(p - 1), \Sigma\beta_1^2/(q - 1), \Sigma\gamma_1^2/(r - 1),$ and $\Sigma\delta_{ab}^2/(t_0 - 1)$ if the corresponding treatments are fixed.*
Figure 11.6-8 Block diagram of RBH-24(A) design. Treatment B(A) is nested in treatment A. Treatments A and B(A) are crossed with blocks. The blocks represent \( n \) sets of \( pq_{0} = (2)(2) = 4 \) matched subjects or \( n \) subjects who receive all four treatment combinations. In the former case, the subjects in a block are randomly assigned to the treatment combinations. In the latter case, the order in which the treatment combinations is presented is randomized independently for each block.

in Gill (1978, 185-210), Henderson (1953, 226-252), and Searle (1971a, chaps. 10 and 11).

11.7 Analyzing Hierarchical Designs Using Computer Programs for Crossed Treatments

Computer programs for analyzing experiments with crossed treatments are widely available. Such is not the case for experiments with nested treatments. Fortunately,

<table>
<thead>
<tr>
<th>Source</th>
<th>Formula</th>
<th>( df )</th>
<th>( E(MS)^{*} ) (additive model)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Blocks</td>
<td>([S] - [Y])</td>
<td>( n - 1 )</td>
<td>( \sigma_{a}^{2} + pq_{0}\sigma_{b}^{2} )</td>
</tr>
<tr>
<td>2. Treatments</td>
<td>([AB] - [Y])</td>
<td>( pq_{0} - 1 )</td>
<td>( \sigma_{a}^{2} + n(1 - \frac{q}{Q})\sigma_{b}^{2} + npq_{0}\sigma_{a}^{2} )</td>
</tr>
<tr>
<td>3. ( A )</td>
<td>([A] - [Y])</td>
<td>( p - 1 )</td>
<td>( \sigma_{a}^{2} + n\sigma_{b}^{2} )</td>
</tr>
<tr>
<td>4. ( B(A) )</td>
<td>([AB] - [A])</td>
<td>( p(q_{0} - 1) )</td>
<td>( \sigma_{a}^{2} + n\sigma_{b}^{2} )</td>
</tr>
<tr>
<td>5. Residual</td>
<td>([AB] - [A] - [S] + [Y])</td>
<td>( (n - 1)(pq_{0} - 1) )</td>
<td>( \sigma_{a}^{2} )</td>
</tr>
<tr>
<td>6. ( A \times BL )</td>
<td>([AS] - [A] - [S] + [Y])</td>
<td>( (n - 1)(p - 1) )</td>
<td>( \sigma_{a}^{2} )</td>
</tr>
<tr>
<td>7. ( B(A) \times BL )</td>
<td>([AB] - [A] - [AS] + [A])</td>
<td>( (n - 1)p(q_{0} - 1) )</td>
<td>( \sigma_{a}^{2} )</td>
</tr>
<tr>
<td>8. Total</td>
<td>([AB] - [Y])</td>
<td>( npq_{0} - 1 )</td>
<td>( \sigma_{a}^{2} )</td>
</tr>
</tbody>
</table>

*The variances should be replaced by \( \Sigma\tilde{\alpha}_{i}^{2}/p(p - 1) \) and \( \Sigma\tilde{\beta}_{ij}^{2}/p(q_{0} - 1) \) if the corresponding treatments are fixed.
11.8 Cell Means Model Approach to Hierarchical Designs

Table 11.7-1 Correspondence Between the Sums of Squares for CRPH-pq(A) and CRF-pq Designs

<table>
<thead>
<tr>
<th>Sum of Squares</th>
<th>CRPH-pq(A) Degrees of Freedom</th>
<th>CRF-pq Degrees of Freedom</th>
</tr>
</thead>
<tbody>
<tr>
<td>SSA = SSA</td>
<td>p - 1 = p - 1</td>
<td></td>
</tr>
<tr>
<td>SSB(A) = SSB + SSAB</td>
<td>p(q_0 - 1) = (q - 1) + (p - 1)(q - 1)</td>
<td>r - 1 = r - 1</td>
</tr>
<tr>
<td>SSC = SSC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SSAC = SSAC</td>
<td>(p - 1)(r - 1) = (p - 1)(r - 1)</td>
<td></td>
</tr>
<tr>
<td>SSB(A) x C = SSB + SSABC</td>
<td>p(q_0 - 1)(r - 1) = (q - 1)(r - 1) + (p - 1)(q - 1)(r - 1)</td>
<td>pqr(n - 1) = pqr(n - 1)</td>
</tr>
<tr>
<td>SSWCELL = SSWCELL</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

programs for crossed treatments can be used to analyze data for any balanced hierarchical design. We describe the procedure using the CRPH-24(A)2 design that was shown in Figure 11.6-2. The first step is to renumber the levels of the nested treatment, B(A), as if they were crossed with A: b_1 = b_0, b_2 = b_2, b_3 = b_3, b_4 = b_4. The data can be analyzed using a program appropriate for a three-treatment completely randomized factorial design. The computer printout will yield nine sums of squares as follows:

SSA  SSB  SSC
SSAB SSAC SSBC
SSABC SSWCELL SSTO

These sums of squares can be combined as shown in Table 11.7-1 to obtain the sums of squares for the CRPH-pq(A) design. Once these sums of squares have been computed, they are divided by the appropriate degrees of freedom to obtain mean squares. These steps and the subsequent tests of significance are performed by hand—a minor task compared to performing the entire analysis by hand or writing a computer program.

11.8 Cell Means Model Approach to Hierarchical Designs

A cell means model can be used to analyze data for a hierarchical design. The model for a CRH-pq(A) design is

\[ Y_{ij} = \mu + \alpha_i + \beta_j + \epsilon_{ijk} \]

where \( \epsilon_{ijk} \) is \( NID(0, \sigma^2) \). An important advantage of this model over the classical sum-of-squares model is that it can be used when there are missing observations and missing cells.

*The reader who is interested only in the classical sum-of-squares approach can, without loss of continuity, omit this section.
Cell Means Model with No Missing Observations

The ionization data in Table 11.2.1 are used to illustrate the computational procedures for the cell means model. For the purpose of forming coefficient matrices using Kronecker products, the null hypotheses for this CRH-28(A) design can be expressed in matrix notation as follows:

$$
\begin{bmatrix}
\mu_{11} \\
\mu_{12} \\
\mu_{13} \\
\mu_{14}
\end{bmatrix} = [0]
$$

The null hypothesis for treatment B(aj) requires a word of explanation. This null hypothesis is for those levels of treatment B that are nested in treatment level ai. The null hypothesis that we want to test for treatment B(A),

$$H_{(a)(b)} \mu_{(a)(b)} = 0_{(a)}$$

includes the levels of treatment B(aj) that are nested in both ai and aj. This is the hypothesis that is tested. However, when a Kronecker product is used to obtain the coefficient matrix, C', for a nested treatment, H_{(a)(b)} must be used instead of H_{(a)(b)}. In this example, the levels of treatment B(aj) that are nested in ai are used; identical results would be obtained if the levels in aj were used. The use of H_{(a)(b)} instead of H_{(a)} is the first of two modifications that are required for nested treatments. The coefficient matrices are obtained as follows:

$$
\begin{bmatrix}
1 & 1 & 1 & 1
\end{bmatrix}
\begin{bmatrix}
1 & 1 & 1 & 1
\end{bmatrix}
= [1 & 1 & 1 & 1 & -1 & -1 & -1 & -1]
$$

The other modification involves the use of \( I_p \) (p x p identity matrix) instead of \( I_p \) (1 x p sum vector) in obtaining \( C_{(a)(b)}' \). Because treatment B(aj) is nested in treatment A, \( C_{(a)(b)}' \) is obtained from the Kronecker product \( I_p \otimes H_{(a)(b)} \) instead of from \( I_p \otimes H_{(a)(b)} \). The computational procedures for the CRH-28(A) design are shown in Table 11.8.1. The sums of squares in Table 11.8.1 are identical to those in Table 11.2.1, where the classical sum-of-squares approach was used. In the next section, the cell means model is used to analyze data for an experiment that has a missing cell and two missing observations.
### Table 11.8-1 Computational Procedures for CRH-28(4) Design Using the Cell Means Model

Data and basic matrices \((N = 32, h = 8, u = 4, p = 2, q_0 = 4)\)

<table>
<thead>
<tr>
<th>(Y_{n\times1})</th>
<th>(X_{n\times8})</th>
</tr>
</thead>
<tbody>
<tr>
<td>(a_1, b_1)</td>
<td>1 0 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_1, b_2)</td>
<td>1 0 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_1, b_3)</td>
<td>1 0 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_1, b_4)</td>
<td>1 0 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_2, b_1)</td>
<td>0 1 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_2, b_2)</td>
<td>0 1 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_2, b_3)</td>
<td>0 1 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_2, b_4)</td>
<td>0 1 0 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_3, b_1)</td>
<td>0 0 1 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_3, b_2)</td>
<td>0 0 1 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_3, b_3)</td>
<td>0 0 1 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_3, b_4)</td>
<td>0 0 1 0 0 0 0 0</td>
</tr>
<tr>
<td>(a_4, b_1)</td>
<td>0 0 0 1 0 0 0 0</td>
</tr>
<tr>
<td>(a_4, b_2)</td>
<td>0 0 0 1 0 0 0 0</td>
</tr>
<tr>
<td>(a_4, b_3)</td>
<td>0 0 0 1 0 0 0 0</td>
</tr>
<tr>
<td>(a_4, b_4)</td>
<td>0 0 0 1 0 0 0 0</td>
</tr>
<tr>
<td>(a_5, b_1)</td>
<td>0 0 0 0 1 0 0 0</td>
</tr>
<tr>
<td>(a_5, b_2)</td>
<td>0 0 0 0 1 0 0 0</td>
</tr>
<tr>
<td>(a_5, b_3)</td>
<td>0 0 0 0 1 0 0 0</td>
</tr>
<tr>
<td>(a_5, b_4)</td>
<td>0 0 0 0 1 0 0 0</td>
</tr>
<tr>
<td>(a_6, b_1)</td>
<td>0 0 0 0 0 1 0 0</td>
</tr>
<tr>
<td>(a_6, b_2)</td>
<td>0 0 0 0 0 1 0 0</td>
</tr>
<tr>
<td>(a_6, b_3)</td>
<td>0 0 0 0 0 1 0 0</td>
</tr>
<tr>
<td>(a_6, b_4)</td>
<td>0 0 0 0 0 1 0 0</td>
</tr>
<tr>
<td>(a_7, b_1)</td>
<td>0 0 0 0 0 0 1 0</td>
</tr>
<tr>
<td>(a_7, b_2)</td>
<td>0 0 0 0 0 0 1 0</td>
</tr>
<tr>
<td>(a_7, b_3)</td>
<td>0 0 0 0 0 0 1 0</td>
</tr>
<tr>
<td>(a_7, b_4)</td>
<td>0 0 0 0 0 0 1 0</td>
</tr>
<tr>
<td>(a_8, b_1)</td>
<td>0 0 0 0 0 0 0 1</td>
</tr>
<tr>
<td>(a_8, b_2)</td>
<td>0 0 0 0 0 0 0 1</td>
</tr>
<tr>
<td>(a_8, b_3)</td>
<td>0 0 0 0 0 0 0 1</td>
</tr>
<tr>
<td>(a_8, b_4)</td>
<td>0 0 0 0 0 0 0 1</td>
</tr>
</tbody>
</table>

\[ \mathbf{y} = (X'X)^{-1}X'y = [3.75, 1.75, 5.50, 3.00, 7.00, 4.00, 8.00, 10.00] \]

\[ \text{SSY} = y'y - y'JyN^{-1} = 235.500 \]

\[ \text{SSA} = (C_{100})'(C_{100}(X'X)^{-1}C_{100})^{-1}(C_{100}) = 112.500 \]

\[ \text{SSB} = (C_{100})'(C_{100}(X'X)^{-1}C_{100})^{-1}(C_{100})F \]

\[ \text{df} = npq_0 - 1 = 31 \]

\[ \text{df} = p - 1 = 1 \]

\[ \text{df} = p(q_0 - 1) = 6 \]

\[ \text{SSWCELL} = y'y - \hat{\mu}'(X'y) = 18.500 \]

\[ \text{df} = pq_0(n - 1) = 24 \]
Table 11.8-2 Data for Ionization Experiment

<table>
<thead>
<tr>
<th>Entry is $Y_{ij}$</th>
<th>$A \ B(A)$ Summary Table</th>
<th>$A \ B(A)$ Summary Table</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$a_1$</td>
<td>$a_2$</td>
</tr>
<tr>
<td>$a_1$</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>$a_2$</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>$b_1$</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>$b_2$</td>
<td>3</td>
<td>3</td>
</tr>
</tbody>
</table>

$\sum_{j=1}^{a} \beta_j q_{ij} = \mu_1, \quad \mu_2, \quad 4.0278, \quad 7.2500$

Cell Means Model with a Missing Cell and Observations

Suppose that the ionization experiment described in Sections 11.1 and 11.2 is unbalanced because the equipment in the second cage malfunctioned and two of the animals in other cages died. We assume that the deaths were unrelated to the nature of the treatments. The data for this experiment are shown in Table 11.8-2. The four observations in cell $a_1b_1$ along with $Y_{113}$ and $Y_{127}$ are missing. To compute sums of squares for this design, coefficient matrices for the following hypotheses are formulated:

$H_0: \frac{\mu_{11} + \mu_{13} + \mu_{14}}{3} - \frac{\mu_{25} + \mu_{26} + \mu_{27} + \mu_{28}}{4} = 0 \quad \text{or} \quad \mu_{11} - \mu_{21} = 0$

$H_0: \quad \mu_{11} - \mu_{13} = \mu_{13} - \mu_{14} = 0$
\[ \mu_{25} - \mu_{26} = \mu_{26} - \mu_{27} = \mu_{27} - \mu_{28} = 0 \]

The null hypothesis for treatment $A$ involves a simple average of the means at each level of treatment $B(A)$. Alternatively, a hypothesis for treatment $A$ that involves weighted means could be tested (see Section 9.14). The coefficient matrices for testing treatments $A$ and $B(A)$ are

$C_{(A)}^{(i)} = \left[ \begin{array}{cccc} \frac{1}{3} & 1 & 1 & -1 \\ -\frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} \end{array} \right]$

$C_{(B(A))}^{(i)} = \left[ \begin{array}{cccc} 1 & -1 & 0 & 0 \\ 0 & 1 & -1 & 0 \\ 0 & 0 & 1 & -1 \\ 0 & 0 & 0 & 1 \end{array} \right]$

$\Sigma_{i=1}^{a} q_{ij} C_{(A)}^{(i)} = \left[ \begin{array}{cccc} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{array} \right]$
Table 11.8-3 ANOVA Table for CRH-27(A) Design with Missing Cell and Observations

<table>
<thead>
<tr>
<th>Source</th>
<th>SS</th>
<th>df</th>
<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. A (ionization)</td>
<td>64.7702</td>
<td>(p - 1 = 1)</td>
<td>64.7702</td>
<td></td>
</tr>
<tr>
<td>2. B(A) (cages)</td>
<td>83.8924</td>
<td>(\sum_{i} q_{i}(n_{i} - 1) = 5)</td>
<td>16.7785</td>
<td></td>
</tr>
<tr>
<td>3. WCELL</td>
<td>17.4167</td>
<td>(\sum_{i=1}^{4} (n_{i} - 1) = 19)</td>
<td>0.9167</td>
<td></td>
</tr>
<tr>
<td>4. Total</td>
<td>170.0385</td>
<td>(N - 1 = 25)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*\(p < .000002\)

where \(p = 2\), \(q_{10} = 3\), \(q_{10} = 4\), and \(h = 7\). The coefficients in \(C_{10A}\) are given by \(c_{i} = \pm 1/q_{10}\) or 0; the coefficients in \(C_{10A00}\) are given by \(c_{i} = \pm 1\) or 0. The sums of squares are

\[
SSA = (C_{10A0}^\prime \beta)(C_{10A}^\prime (X'X)^{-1} C_{10A} \beta) = 64.7702
\]

\[
SSB(A) = (C_{10A00}^\prime \beta)(C_{10A0}^\prime (X'X)^{-1} C_{10A00} \beta) = 83.8924
\]

\[
SSWCELL = y'y - \hat{\beta}^\prime (X'X) = 17.4167
\]

\[
SSTO = y'y - y'JyN^{-1} \hat{\beta} = 170.0385
\]

where

\[
\hat{\beta} = [(X'X)^{-1} (X'y)]^\prime = [3.75 \quad 5.33 \quad 3.00 \quad 7.00 \quad 4.00 \quad 8.00 \quad 10.00]
\]

\[
(X'X)^{-1} = \begin{bmatrix}
\frac{1}{4} & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \frac{1}{4} & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \frac{1}{4} & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \frac{1}{4} & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \frac{1}{4} & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \frac{1}{4} & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{4}
\end{bmatrix}
\]

\[
y' = [3 \quad 6 \quad 3 \quad 3 \quad 5 \quad 6 \quad 5 \quad 2 \quad 3 \quad 4 \quad 3 \quad 7 \ldots 11]
\]

The results of the analysis are summarized in Table 11.8-3.

**Formulating Coefficient Matrices for Hierarchical Designs**

The use of Kronecker products to formulate coefficient matrices for the cell means model is illustrated for a CRPH-236(B) design and a CRPH-2224(C) design. The pattern underlying the formulation of coefficient matrices for any hierarchical design should be apparent from these examples. The coefficient matrices for a CRPH-236(B) design are presented first.
CHAPTER 11  •  Hierarchical Designs

Treatment A
\[
\mathbf{H}_A^T \times \mathbf{1}_q^T \otimes \mathbf{1}_r^T \otimes \mathbf{1}_o^T = C_{(p-1) \times q}^{(p-1) \times r}^{(p-1) \times o}
\]

Treatment B
\[
\mathbf{1}_r^T \otimes \mathbf{H}_B^T \otimes \mathbf{1}_o^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]

Treatment C(B)
\[
\mathbf{1}_r^T \otimes \mathbf{1}_q^T \otimes \mathbf{H}_{C(B)}^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]

\(A \times B\)
\[
\mathbf{H}_A^T \otimes \mathbf{H}_B^T \otimes \mathbf{1}_o^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]

\(A \times C(B)\)
\[
\mathbf{H}_A^T \otimes \mathbf{I}_q^T \otimes \mathbf{H}_{C(B)}^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]

where
\[
\mathbf{H}_A = \begin{bmatrix} 1 & -1 \\ -1 & 1 \end{bmatrix}, \quad \mathbf{H}_B = \begin{bmatrix} 1 & -1 & 0 \\ 0 & 1 & -1 \end{bmatrix}, \quad \mathbf{H}_{C(B)} = \begin{bmatrix} 1 & -1 & 0 \\ 0 & 1 & -1 \end{bmatrix}
\]

\[
\mathbf{1}_r = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}, \quad \mathbf{1}_q = \begin{bmatrix} 1 \\ 1 \\ 1 \end{bmatrix}, \quad \mathbf{1}_o = \begin{bmatrix} 1 \\ 0 \\ 0 \\ 1 \end{bmatrix}
\]

For this example, in which treatment \(C(B)\) is nested in treatment \(B\), the formulation of coefficient matrices using Kronecker products requires two modifications. First, the \(H_{C(B)}\) and \(\mathbf{1}_{a}^{T}\) matrices involve only those levels of \(C(B)\) that are nested in the \(k\th\) level of \(B\). Second, when a coefficient matrix involves treatment \(C(B)\), the sum vector, \(\mathbf{1}_{e}\) for treatment \(B\) is replaced by an identity matrix, \(\mathbf{1}_{q}\). If treatment \(C\) had been nested in both \(A\) and \(B\), \(\mathbf{1}_{r}\) and \(\mathbf{1}_{o}\) would have been replaced by \(\mathbf{1}_{q}\) and \(\mathbf{1}_{r}\). The sum of squares for any treatment or interaction has the general form
\[
SS = (\mathbf{C}_a^T \cdot \mathbf{\beta}_a) (\mathbf{C}_a (\mathbf{X}_a)^{-1} \mathbf{C}_a^T)^{-1} (\mathbf{C}_a^T \cdot \mathbf{\beta}_a)
\]

The degrees of freedom for a treatment or interaction are equal to the number of rows in its coefficient matrix. The within-cell sum of squares and the total sum of squares are given by
\[
SSWCELL = \mathbf{y}^T \mathbf{y} - \mathbf{\hat{\mu}} \cdot (\mathbf{X} \cdot \mathbf{y}) \quad \text{and} \quad SSTO = \mathbf{y}^T \mathbf{y} - \mathbf{\hat{\mu}} \cdot (\mathbf{Y} \cdot \mathbf{N})^{-1}
\]

It is apparent that only three formulas are required to analyze any hierarchical design.

The coefficient matrices for a CRPH-2224(C) design in which the \(t = 4\) levels of treatment \(D(C)\) are nested in \(C\) are given by the following Kronecker products:

Treatment A
\[
\mathbf{H}_A^T \otimes \mathbf{1}_q^T \otimes \mathbf{1}_r^T \otimes \mathbf{1}_o^T = C_{(p-1) \times q}^{(p-1) \times r}^{(p-1) \times o}
\]

Treatment B
\[
\mathbf{1}_r^T \otimes \mathbf{H}_B^T \otimes \mathbf{1}_o^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]

Treatment C
\[
\mathbf{1}_r^T \otimes \mathbf{1}_q^T \otimes \mathbf{H}_{C(B)}^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]

Treatment D(C)
\[
\mathbf{1}_r^T \otimes \mathbf{1}_q^T \otimes \mathbf{1}_r^T \otimes \mathbf{H}_{D(C)}^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]

\(A \times B\)
\[
\mathbf{H}_A^T \otimes \mathbf{H}_B^T \otimes \mathbf{1}_o^T = C_{(p-1) \times q}^{(p-1) \times q}^{(p-1) \times q}
\]
11.9 Advantages and Disadvantages of Hierarchical Designs

The major advantages of hierarchical designs are as follows:

1. All subjects are used in simultaneously evaluating the effects of two or more treatments.
2. A researcher can isolate the effects of nuisance variables and evaluate treatments that cannot be crossed with other treatments.

The major disadvantages of hierarchical designs are as follows:

1. If numerous treatments are included in the experiment, the number of subjects required may be prohibitive.
2. The power of certain tests for mixed and random-effects models tends to be low because of the small number of degrees of freedom associated with the error term.
3. If, as is often the case, the nesting of treatment levels or the assignment of experimental units to treatment combinations is not random, the interpretation of the results may be ambiguous.

11.10 Review Exercises

1. Terms to remember
   a. hierarchical design
   b. partial hierarchical design
   c. balanced hierarchical design
   d. unbalanced hierarchical design

2. [11.1] Distinguish between the following.
   a. Hierarchical and partial hierarchical designs
   b. Balanced hierarchical and unbalanced hierarchical designs

3. An experiment was designed to evaluate the effectiveness of a pattern-practice approach in modifying the nonstandard dialect of the Chicano children living in San Antonio.
Texas. The essential elements of the approach, denoted by $a_1$, involved pattern drill in imitating audio recorded speech models and immediate feedback by a teacher. The control condition, $a_2$, involved reading stories aloud to the teacher. The children were praised for a good performance, but no corrections or guidance was given. Twenty-four 12-year-old Chicano children with similar scores on a standardized speech test were randomly assigned to six miniclases, with four children in each. The six miniclases, treatment $B(A)$, were randomly assigned to the levels of treatment $A$. The dependent variable was the difference between the children’s pre- and posttest scores on the test. The following data were obtained.

<table>
<thead>
<tr>
<th>$a_1$</th>
<th>$a_1$</th>
<th>$a_1$</th>
<th>$a_2$</th>
<th>$a_2$</th>
<th>$a_2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$b_1$</td>
<td>$b_2$</td>
<td>$b_3$</td>
<td>$b_4$</td>
<td>$b_5$</td>
<td>$b_6$</td>
</tr>
<tr>
<td>5</td>
<td>10</td>
<td>7</td>
<td>1</td>
<td>8</td>
<td>6</td>
</tr>
<tr>
<td>2</td>
<td>15</td>
<td>12</td>
<td>1</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td>10</td>
<td>11</td>
<td>14</td>
<td>0</td>
<td>1</td>
<td>6</td>
</tr>
<tr>
<td>11</td>
<td>8</td>
<td>15</td>
<td>6</td>
<td>3</td>
<td>10</td>
</tr>
</tbody>
</table>

*a. [11.2] Test the hypotheses $\mu_{a_1} = \mu_{a_2}$ and $\sigma^2_k = 0$; let $\alpha = .05$.

*b. [11.2] Is it reasonable to assume that the population variance estimated by $MSB(A)$ is composed of homogeneous sources of variation? Test the hypotheses $\sigma^2_k$ at $a_1 = \sigma^2_k$ at $a_2$; let $\alpha = .25$.

*c. [11.5] Calculate $\delta_{b_1B(A)}$ and $\beta_{b_1B(A)}$.

d. Prepare a "results and discussion section" for the *Journal of Educational Psychology.*

4 An industrial psychologist was interested in decreasing the time required to assemble an electronic component. Three assembly fixtures, treatment $A$, including the one currently in use, $a_1$, were evaluated. Five operators at each of six workplaces in the plant, treatment $B(A)$, were selected randomly to participate in the experiment. The six workplaces were randomly assigned to use the assembly fixtures, with the restriction that two workplaces were assigned to each fixture. The operators were randomly assigned to the treatment combinations. After a three-week familiarization period, the following data on the number of units assembled per hour were collected:

<table>
<thead>
<tr>
<th>$a_1$</th>
<th>$a_1$</th>
<th>$a_2$</th>
<th>$a_3$</th>
<th>$a_3$</th>
<th>$a_3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$b_1$</td>
<td>$b_2$</td>
<td>$b_3$</td>
<td>$b_4$</td>
<td>$b_5$</td>
<td>$b_6$</td>
</tr>
<tr>
<td>17</td>
<td>13</td>
<td>21</td>
<td>25</td>
<td>26</td>
<td>32</td>
</tr>
<tr>
<td>7</td>
<td>23</td>
<td>24</td>
<td>29</td>
<td>34</td>
<td>32</td>
</tr>
<tr>
<td>9</td>
<td>14</td>
<td>14</td>
<td>26</td>
<td>32</td>
<td>37</td>
</tr>
<tr>
<td>12</td>
<td>18</td>
<td>19</td>
<td>24</td>
<td>30</td>
<td>34</td>
</tr>
<tr>
<td>15</td>
<td>22</td>
<td>17</td>
<td>21</td>
<td>28</td>
<td>35</td>
</tr>
</tbody>
</table>
11.10  Review Exercises  507

*a. [11.2] Test the hypotheses $\mu_1 = \mu_2 = \mu_3$  and $\sigma_0^2 = 0$; let $\alpha = .05$.
*b. [11.2] Is it reasonable to assume that the population variance estimated by MSB(A) is composed of homogeneous sources of variation? Use Cochran's C statistic to test the hypothesis $\sigma_1^2 = \sigma_2^2 = \sigma_3^2$ at $a_1 = a_2 = a_3$; let $\alpha = .05$.
*d. [11.5] Calculate $\delta_{A|B=0}$ and $\lambda_{I|P_{0A}}$.
*e. Prepare a "results and discussion section" for the Journal of Applied Psychology.

5 The effects of early environment on the problem-solving ability of rats at maturity were investigated. Rats were raised in one of three environments: $a_1$ was a normal environment, $a_2$ was an enriched environment, and $a_3$ was a restricted environment. Nine cages were randomly assigned to the levels of treatment $A$, with the restriction that three cages were assigned to each level of $A$. Thirty-six rats were randomly assigned to the nine treatment combinations, with four rats to a cage. The dependent variable was the number of trials required to learn a visual discrimination task. The following data were obtained:

<table>
<thead>
<tr>
<th>$a_1$</th>
<th>$a_1$</th>
<th>$a_1$</th>
<th>$a_2$</th>
<th>$a_2$</th>
<th>$a_2$</th>
<th>$a_3$</th>
<th>$a_3$</th>
<th>$a_3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$b_1$</td>
<td>$b_2$</td>
<td>$b_3$</td>
<td>$b_4$</td>
<td>$b_5$</td>
<td>$b_6$</td>
<td>$b_7$</td>
<td>$b_8$</td>
<td>$b_9$</td>
</tr>
<tr>
<td>14</td>
<td>13</td>
<td>11</td>
<td>11</td>
<td>11</td>
<td>5</td>
<td>15</td>
<td>11</td>
<td>12</td>
</tr>
<tr>
<td>12</td>
<td>11</td>
<td>11</td>
<td>10</td>
<td>9</td>
<td>7</td>
<td>12</td>
<td>13</td>
<td>9</td>
</tr>
<tr>
<td>11</td>
<td>9</td>
<td>10</td>
<td>11</td>
<td>7</td>
<td>8</td>
<td>15</td>
<td>15</td>
<td>12</td>
</tr>
<tr>
<td>11</td>
<td>8</td>
<td>8</td>
<td>9</td>
<td>8</td>
<td>14</td>
<td>13</td>
<td>11</td>
<td></td>
</tr>
</tbody>
</table>

a. [11.2] Test the hypotheses $\mu_1 = \mu_2 = \mu_3$ and $\sigma_0^2 = 0$; let $\alpha = .05$.
b. [11.2] Is it reasonable to assume that the population variance estimated by MSB(A) is composed of homogeneous sources of variation? Use Cochran's C statistic to test the hypothesis $\sigma_1^2 = \sigma_2^2 = \sigma_3^2$ at $a_1 = a_2 = a_3$; let $\alpha = .05$.
d. [11.5] Calculate $\delta_{A|B=0}$ and $\lambda_{I|P_{0A}}$.
e. Prepare a "results and discussion section" for the Journal of Perceptual and Motor Skills.

*6 Show for a CRH-$pq(A)$ design that

$$
\sum_{i=1}^{n} \sum_{j=1}^{q_0} (Y_{ij} - \bar{Y}_j)^2 = nq_0 \sum_{j=1}^{q_0} (\bar{Y}_j - \bar{Y}_..)^2 + n \sum_{j=1}^{q_0} (\bar{Y}_j - \bar{Y}_..)^2 + n \sum_{i=1}^{p} \sum_{k=1}^{q_0} (Y_{ijk} - \bar{Y}_{ij})^2
$$

*7 [11.6] Identify the following designs; assume in each case that the building block design is a CR-$p$ design.
8 Explain why the following is not a hierarchical design.

*9 [11.6] For each of the following designs, (i) write the experimental design model equation and (ii) construct a diagram of the design. Use the minimum number of levels required for each treatment.

a. CRPH-pqrt(B) b. CRPH-pqrt(AB) c. CRPH-pq(A)-r(AB)\cdot r(ABC)
d. CRPH-pqrt(A) e. CRPH-pq(A)-r(A) f. CRPH-pq(A)-r(AB)

*10 [11.6] There is a correspondence between the sum of squares for a nested treatment and the sums of squares in a factorial design. For example, SSB(\text{A}) = SSB + SSAB and SSC(AB) = SSC + SSAC + SSBC + SSABC. (i) For each of the following, indicate the correspondence.

a. SSB(B) b. SSB \times D(C) c. SSA \times D(BC)
d. SSD(ABC) e. SSB(A) \times C(A) f. SSB(A) \times C(A) \times D(A)
g. SSD(BC) h. SSE(ABD) i. SSA \times C(B)
j. SSD \times E(ABC) k. SSC(AB) \times D l. SSC(A) \times E(D)

(ii) It is evident from part (i) that a simple rule governs the correspondence between a nested sum of squares and the sums of squares in the factorial design. State the rule.

*11 [11.7] Show by means of a table (see Table 11.7-1) how you would use a computer program for a CRPH-pqrt design to analyze data for the following designs.

a. CRPH-pqrt(AB) b. CRPH-pq(A)-r(A)

*12 [11.8] Exercise 3 describes an experiment that was concerned with modifying the dialect of Chicano children. Suppose that observation Y_{12} = 12 is missing.

a. Formulate the C' matrices for testing the null hypotheses for A and B(A).

b. Formulate (X'X)^{-1}

c. Analyze the data using the cell means model approach; test hypotheses concerning the simple averages of cell means. (This exercise requires the inversion of a 4 \times 4 matrix. It can be done without a computer or calculator that has a matrix inversion program, but the computations are tedious.)
*13 [11.8] Exercise 4 describes an experiment that was concerned with decreasing the time required to assemble an electronic component. Suppose that observation $Y_{111} = 9$ and cell $a_1b_2$ are missing.

*a. Formulate the $C'$ matrices for testing the null hypotheses for $A$ and $B(A)$.

*b. Formulate $(X'X)^{-1}$

*c. Analyze the data using the cell means model approach; test hypotheses concerning the simple averages of cell means. (This exercise requires the inversion of $2 \times 2$ matrices. It can be done without a computer or calculator that has a matrix inversion program.)

14 [11.8] Exercise 5 describes an experiment that investigated the effects of early environment on the problem-solving ability of rats.

a. Use Kronecker products to formulate the $C'$ matrices for testing the null hypotheses for $A$ and $B(A)$.

b. Formulate $(X'X)^{-1}$

c. Analyze the data using the cell means model approach. (This exercise requires the inversion of a $6 \times 6$ matrix. A computer with a matrix program should be used.)