MODELING THE EFFECTS OF RESTRICTED RANDOMIZATION

BY

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A Thesis
Submitted to the Faculty of Graduate Studies
in Partial Fulfilment of the Requirements
for the Degree of

DOCTOR OF PHILOSOPHY

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ABSTRACT

Because the usual linear model does not convey information pertinent to the randomization process, the linear model and associated expected mean squares are inadequate when randomization is restricted in some way. The linear model is extended to incorporate such information by viewing the realized observations as a fraction of the potential observations, and utilizing the idea of bias or aliasing in a manner similar to fractional designs. In particular, two areas of restricted randomization are examined 1) restricting the run-order of a sequential experiment and 2) restrictions resulting from inherent structure of the experimental material (blocking). In both cases treatment effects and effects associated with the randomization process may be non-additive, in contrast to some of the previous work that has assumed such effects are additive. In addition, the nature of the resulting bias is examined. Rules are specified that allow construction of pseudo expected mean squares that indicate the presence of bias that results from restricting the randomization process.

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CHAPTER 1

RANDOMIZATION AND THE LINEAR MODEL

1.1 INTRODUCTION

Randomization is a cornerstone of statistical experimental design and may be viewed as the foundation for inference (Kempthorne 1955). Randomizing the assignment of treatments to experimental units and randomizing the run-order of sequential trials averages out the influences of uncontrolled or unrecognized factors. Differences in the mean response among treatment levels can then be attributed to the treatments. However, in some settings complete randomization may be impossible, or at least impractical. Some designs are inherently or *intrinsically* restricted in the assignment of factor level combinations to experimental units as a natural consequence of the relationships among experimental units. For example, in animal experiments with litter as a blocking factor, litter, cannot be randomly assigned to the experimental units, rats. This inherent structure among experimental units will be called a *block structure*. Other designs are externally or *extrinsically* restricted at the discretion of the experimenter. For example, in an experiment with sequential trials, the randomization of run-order may be restricted due to cost or time constraints. This imposed structure will be called a *segment structure*. When randomization is restricted because of a block or a segment structure, it creates the potential for confounding.

An overview of the dual role of randomization in relation to block and segment structures is shown in **Figure 1**, a generalization of a paradigm originally presented by Milliken and Johnson (1984). The factor combinations to be studied for their effect on the

response make up the **treatment structure**, e.g., *Diet* and *Drug* studied for their effect on tumor growth in rats.

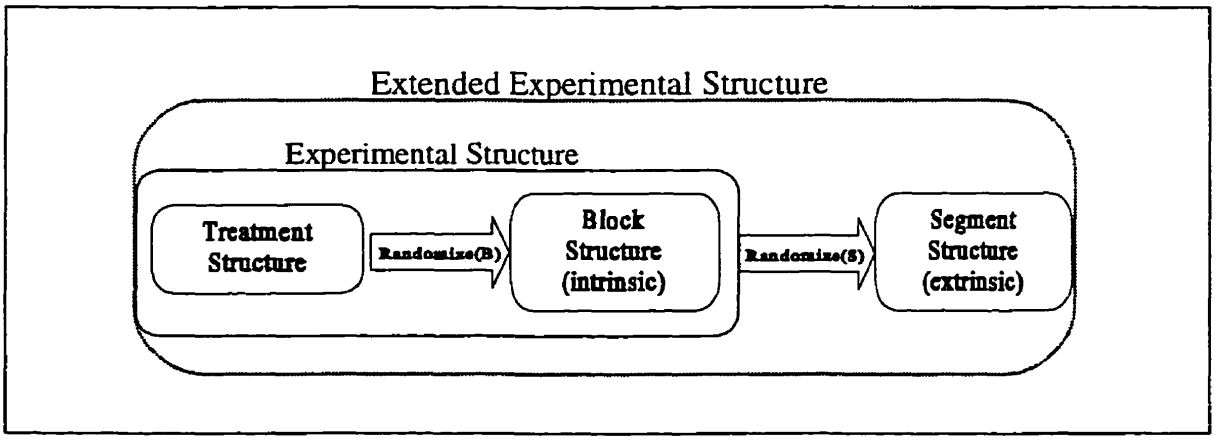


Figure 1 Paradigm relating treatment, block, and segment structure to randomization.

Factor combinations that naturally group homogeneous experimental units make up the **block structure**, e.g., several *Litters* of rats are available and rats within a *Litter* are considered more homogeneous. Ideally these two structures should be considered separately, i.e., the block structure should not dictate the treatment combinations considered and vice-versa. The randomization of treatments to experimental units is constrained by the block structure (**Randomization(B)**). Milliken defines the **experimental structure** as the union of treatment structure and block structure and the specification of the randomization process. For example, a Randomized Complete Block design (experimental structure) is defined by:

Table I Example of Experimental Structure

Treatment Structure	A factorial with Diet and Drug each at two levels
Block Structure	The natural grouping of Rats into Litters
Randomization(B) Process	The assignment of all treatment combinations to Rats is randomized independently within each Litter

Extending the paradigm, factor combinations that do not define natural grouping, but groupings of experimental runs imposed at the discretion of the experimenter, make up the **segment structure**. Consider an experiment in the automotive industry to investigate the effects of several factors on paint quality. The factors to be investigated involve two types of spray nozzle, and two oven temperatures for baking the painted panels. Because several hours are required to change the oven temperature, all runs at a given oven temperature will be completed before changing the oven temperature. The randomization of run-order is constrained by the segment structure defined by the experimenter (**Randomization(S)**).

Table II Example of Extension to Experimental Structure: Segment Structure

Treatment Structure	A factorial with Bake Temperature and Nozzle Type each at two levels
Randomization(S) Process	The level of Bake Temperature is randomly chosen, all runs at that Bake Temperature are run, in random order, before proceeding to the next Temperature

The **extended experimental structure** is the union of treatment structure, block structure, and segment structure, and the specification of both randomization processes. While both design and segment structures play an important role in experimental design, this information is not conveyed by the usual methods for modeling experiments.

In many experimental settings the data is analyzed by way of a linear model. Variation in the response variable is partitioned corresponding to terms in the model and summarized in an ANOVA table. To test whether terms in the model are useful in explaining the variability in the response variable, appropriate F statistics are formed by examination of the expected mean squares (EMS). To form appropriate F statistics the numerator EMS should equal the denominator EMS plus a component that is a function of the term involved in the hypothesis.

For example, suppose a researcher wants to test the following hypothesis based upon the accompanying ANOVA table.

$$\textit{Intended Hypothesis:}\quad H_o\colon \sigma_A^2 = 0 \qquad H_a\colon \sigma_A^2 > 0$$

Source	df	SS	MS	EMS	F
A	df_A	SS_A	MS_A	$\sigma_E^2 + \sigma_A^2$	MS_A/MS_E
E	df_E	SS_E	MS_E	σ_E^2	

(1)

The appropriate F statistic is MS_A/MS_E because the additional component in the EMS for term A, σ_A^2, is the object of the hypothesis. Under the null hypothesis the component σ_A^2 is zero and no variability in the response is attributable to the term A in the model. Under the alternative hypothesis the component σ_A^2 inflates the numerator mean square and leads to a larger F ratio. A sufficiently large F ratio is taken as evidence that the term is useful in explaining variation in the response variable. Under appropriate conditions this F ratio can be compared with an F-distribution with df_A and df_E degrees of freedom.

However, if the model is misspecified then additional bias components may appear in the numerator EMS and the hypothesis being tested is one of joint or combined effects as in (**2**). If the researcher forms the hypothesis test using the EMS of (**1**), when in reality the correct EMS are those of (**2**), then the hypothesis tested is not the one desired and such tests will be called biased (note: this is not the classical definition of biased, Mood 1974, p. 425).

$$\textit{Actual Hypothesis:}\quad H_o\colon \sigma_A^2 + \sigma_{Bias}^2 = 0 \qquad H_a\colon \sigma_A^2 + \sigma_{Bias}^2 > 0$$

Source	df	SS	MS	EMS	F
A	df_A	SS_A	MS_A	$\sigma_E^2 + \sigma_A^2 + \sigma_{Bias}^2$	MS_A/MS_E
E	df_E	SS_E	MS_E	σ_E^2	

(2)

So it is seen that the EMS, a function of the linear model, play a critical role in forming F-statistics and defining the hypotheses tested by those F statistics. Further, misspecification of the model can lead to biased tests.

While the use and the interpretation of the linear model are founded on the principle of randomization, the analysis is derived from normal theory and incorporates no information about the randomization process. If a linear model is used that assumes complete randomization, when in fact randomization is restricted in some way, then the model has been misspecified and there is potential for bias. This bias remains concealed because it is not represented in the misspecified model or corresponding EMS. Consider, for example, how the randomized complete block design (RCBD) with one factor is fundamentally different from a two-factor completely randomized design with no interaction (CRD). In the RCBD a block-treatment combination cannot be randomly assigned to an experimental unit, while in the CRD a treatment combination can be randomly assigned to an experimental unit. This fundamental difference in the randomization process is not represented by the linear model, and the resulting potential for bias is not expressed by the EMS. This fact, ignored in many design text books, is acknowledged by some who suggest that the test for treatment is valid, but the test for blocks is not, though both appear unbiased according to conventional EMS:

> Examination of (the EMS table for the RCBD) will show that the expected mean square for blocks is of the same form as the expected mean square for treatments, and this suggests that a logical procedure would be to test (for a block effect) by calculating F=B/E (where B=MSB, and E=MSE). Why is it then that the statistician says this should not be done? The answer may be found by noting the manner in which the randomization was performed. You will recall that the treatments were assigned at random to the experimental units within each block *but that the blocks were formed in a decidedly nonrandom fashion.* Because of this feature of the randomized complete block design, *a statistical test of the block effect should not be performed.* (Ostle and Mensing 1975, p. 380)

This paradox of "see one thing, say another" results from understanding the fundamental role of randomization in experimental design while employing a linear model that does not

represent it. This issue was addressed by Speed (1991) in his comments on Samuels, Casella, and McCabe (1991). Samuels et al. (1991) discuss the confusion arising from various parameterizations of the mixed model and the associated hypothesis tests. Speed indicates a weakness in the usual linear model approach, stating "this mixed model muddle is a self-inflicted wound that can only be healed by genuinely returning to those notions and principles . . . of units and sampling and randomization" (Speed 1991, p. 810).

Rather than ignore the potential for hidden bias, modeling the extended experimental structure is preferable (**Figure 1** on page 2), including the integral process of randomization. Explicit representation of the randomization process in the linear model makes its effects accessible for design, analysis, and interpretation. Potential bias is then evident, alerting the experimenter to limitations on the interpretation of results and desired inferences. With this understanding and armed with domain-specific knowledge the experimenter may choose to proceed or, perhaps at increased expense, to modify the design or randomization procedure.

Such a synthesis of vital randomization information into the linear model framework is presented by Kempthorne (1955), Wilk (1955), Scheffe (1959), Anderson and McLean (1974a, 1974b), White (1975), Lorenzen (1984), Lentner, Arnold, and Hinkelmann (1989), Lorenzen and Anderson (1993a), and Hinkelmann and Kempthorne (1994). This augmented linear model is used to compare the nature of hypothesis tests under complete randomization and under randomization with block restrictions. Similarly, for designs with segment restrictions, information pertinent to the randomization process is combined with the linear model (Anderson and McLean 1974a, 1974b; Lorenzen 1984; Lorenzen and Anderson 1993a). In both cases this synthesis allows the linear model to represent the effects of randomization explicitly. Much of the work on block restrictions examines the effects of nonadditivity or interaction of experimental unit and treatment effects. However, previous results from other authors dealing with segment restrictions are entirely dependent on the *implicit* assumption of additivity of segment effects and treatment effects (Anderson and McLean 1974a, 1974b; Lorenzen 1984; Lorenzen and Anderson 1993a). In summary, the

synthesis of randomization information into the linear model can be very instructive. Such a synthesis should address the potential for nonadditivity between treatment effects and the effects representing the randomization process. We can then examine the sensitivity of inferences under various restrictions on the randomization process.

We incorporate randomization information into the linear model in a novel fashion by casting the traditional experimental structure as a fractional factorial design. The full factorial describes, in some sense, the universe of potential observations. The randomization process determines which subsets, or fractions, of the potential observations can be realized. As in traditional fractional factorial designs, the effects of certain factors may be confounded with the effects of other factors. This confounding structure shows how the randomization process influences the EMS and corresponding test statistics. Finally, the traditional analysis of fractional factorial designs assumes that the effects of confounded factors cannot be disentangled unless the effects of one factor are assumed zero. We again generalize this to examine the extent of the entangling, or the sensitivity to departures from the underlying assumption of strictly null effects. This will allow us to examine the strength of any bias resulting from the specified randomization process.

1.2 RANDOMIZATION AS A FRACTIONAL DESIGN

A simple example will demonstrate the effects of restricted randomization, emphasizing concepts while leaving the details of derivation for Chapter 2. Both complete and restricted randomization are presented in the framework of fractional designs. The experiment is first presented assuming complete randomization and then modified, due to some real world constraint, to incorporate a segment, or run-order, restriction.

Suppose that the true average response in an experiment is an additive function of two factors, Temperature (T) and Humidity (H) (i.e., there is no interaction). The researcher, who is not omniscient, is unaware of the effects of Humidity and designs a single factor

experiment involving Temperature at two levels with two replications. Humidity changes over time and is at lower levels for the first two runs and at higher levels for the last two runs. The omission of Humidity from design considerations may not pose a problem (which bodes well for all those researchers who are not omniscient). With the experiment completely randomized there are six potential experimental sequences as shown in **Table III**.

Table III Six Potential Experimental Sequences Under Complete Randomization. Dotted line delineates the low vs. high levels of Humidity.

Run Order	Humidity Levels	Temperature Levels for the 6 Sequences					
		1	2	3	4	5	6
1	1	1	1	1	2	2	2
2	2	1	2	2	1	1	2
3	3	2	1	2	1	2	1
4	4	2	2	1	2	1	1

As far as the experimenter is concerned, no matter which one of the six potential experiments is realized, the two observed responses at each temperature are considered as replicates from a one-factor design and the analysis proceeds as such. In this experimental design the effects of the lurking variable (Humidity) are removed, on average, by selecting one of these six potential experimental sequences at random (i.e., complete randomization) coupled with the additive relationship between T and H. This "averaging out" takes place because any humidity effects (above dotted line vs. below dotted line) are just as likely to show up in the "within" treatment variability as the "between" treatment variability. For example, the average of the runs with low humidity (above the dotted line) is taken across the same temperature in some sequences and across different temperatures in other sequences, and likewise for runs with high humidity (below the dotted line) (**Table III**).

However, because changes in Temperature settings are difficult and costly the researcher decides not to completely randomize run-order. Once a level of Temperature is randomly selected, all runs at that Temperature setting are completed, in random order, before proceeding with the second Temperature setting. In this restricted randomization only two of the original six sequences are possible, as shown in **Table IV**.

Table IV Two Potential Experimental Sequences Under Restricted Randomization. Dotted line delineates low vs. high levels of Humidity.

Run Order	Humidity Levels	Temperature Levels for the two sequences	
1	1	1	2
2	2	1	2
3	3	2	1
4	4	2	1

The potential for confounding between the effects of Temperature and Humidity is clear. Any difference between Temperature 1 and 2 is *always* observed with the difference between low Humidity (above the dotted line) and high Humidity (below the dotted line) (**Table IV**). The effect of low humidity vs. high humidity shows up only in the "between" temperature variation and not the "within" temperature variation, resulting in confounding of the temperature and humidity effects.

How can this intuitive argument be formalized? If we take a "hyper" view of the experiment (**Table V**), the six potential sequences under complete randomization in **Table III**, can be viewed as a half fraction of a more general factorial experiment involving both temperature and humidity. The shaded portions of **Table V** correspond to the six potential sequences in **Table III**. The levels of Humidity have a one-to-one association with run-order so only shaded combinations are possible.

Table V Hyper-view of experiment. Shaded sections are a ½ fraction, and are the potential sequences from **Table III**.

	FACTORS											
	T	H	T	H	T	H	T	H	T	H	T	H
LEVELS							1	1	1	1	1	1
			1	2	1	2					1	2
	1	3			1	3			1	3		
	1	4	1	4			1	4				
	2	1	2	1	2	1						
	2	2					2	2	2	2		
			2	3			2	3			2	3
					2	4			2	4	2	4

Now let

z_{ijk}= response of the k^{th} replicate receiving the ij^{th} treatment combination (i^{th} level of T and the j^{th} level of H, i=1,...,2, j=1,...,4, k =1)

μ = overall mean,

t_i = effect of the i^{th} level of temperature, T,

h_j = effect of the j^{th} level of humidity, H,

th_{ij} = additional effect of the i^{th} level of temperature in conjunction with the j^{th} level of humidity,

ϵ_{ijk} = effect of the k^{th} level of error, E, additional effect when the ij^{th} treatment is applied to the k^{th} replicate,

$Q_p(\bullet)$ = quadratic function of effects associated with the p^{th} term in the model.

If the assumption of additivity between Temperature and Humidity effects is relaxed then the true response follows the model:

$$z_{ijk} = \mu + t_i + h_j + th_{ij} + \epsilon_{ijk} \qquad (3)$$

However, because the experimenter is unaware of the lurking variable humidity, a model for a one-factor completely randomized design is proposed. The treatment combinations for this design are the shaded portions of the complete design, or a half fraction of the complete design (**Table V**). The variability in the response variable can be partitioned according to the proposed effects model:

$$y_{ij} = \mu + t_i + \epsilon_{ij} \qquad (4)$$

where

y_{ij} = response of the j^{th} replicate receiving the i^{th} level of treatment (i=1,...,2, j=1,...,2)

μ = overall mean,

t_i = effect of the i^{th} level of temperature, T,

ϵ_{ij} = effect of the j^{th} level of error, E, additional effect when the i^{th} treatment is applied to the j^{th} replicate,

Partitioning the variability according to the proposed model (**4**), and taking the expectation of the mean squares according to the true model (**3**) yields the following EMS table:

SOURCE	*EMS*	
T	$Q_E(\epsilon_{ijk}, h_j, th_{ij}) + Q_T(t_i, th_{ij})$	**(5)**
E	$Q_E(\epsilon_{ijk}, h_j, th_{ij})$	

This shows the reason for the additivity assumption that underlies the usual analysis of variance, i.e. additivity of treatment effects and effects associated with run-order. If the effects of Temperature and Humidity are additive then all th_{ij} terms are zero and the EMS table reduces to:

SOURCE	*EMS*	
T	$Q_E(\epsilon_{ijk}, h_j) + Q_T(t_i)$	**(6)**
E	$Q_E(\epsilon_{ijk}, h_j)$	

The extra component in the numerator EMS of the usual F-statistic is a function of Temperature effects only, and one would expect a large F-statistic to indicate that Temperature is associated with a significant amount of variability in the response. The lack of bias is the result of the realized fraction being randomly selected from *all possible fractions*, i.e., *complete randomization*, coupled with the assumption of *additivity* between Temperature and Humidity.

Under restricted randomization, the realized experiment is still a ½ fraction of the complete two factor design, but only two of the six potential sequences are candidates as shown in **Table VI**.

Table VI Hyper-view of experiment. Shaded sections are a ½ fraction, and are the potential sequences from **Table IV**.

	FACTORS			
	T	H	T	H
LEVELS			1	1
			1	2
	1	3		
	1	4		
	2	1		
	2	2		
			2	3
			2	4

This restricted randomization leads to the following EMS table where the expectation is taken over the true model **(3)**:

SOURCE	*EMS*	
T	$Q_E(\epsilon_{ijk}, h_j, th_{ij}) + Q_T(t_i, h_j, th_{ij})$	**(7)**
E	$Q_E(\epsilon_{ijk}, h_j, th_{ij})$	

As before, we assume that the effects of Temperature and Humidity are additive and the EMS table reduces to:

SOURCE	*EMS*	
T	$Q_E(\epsilon_{ijk}, h_j) + Q_T(t_i, h_j)$	**(8)**
E	$Q_E(\epsilon_{ijk}, h_j)$	

In contrast to complete randomization, even under the assumption of additivity the extra component in the numerator EMS contains a Humidity bias component. Unless all humidity effects are zero, attributing a large F-ratio to the effects of temperature alone is impossible. This bias occurs because the realized experiment, while still randomly chosen, is selected from a specific, nonrandom, subset of the six potential fractional designs (compare **Table III** and **Table IV**). The act of **restricting randomization has disturbed the randomization-additivity combination that usually ensures unbiased tests**. To achieve an unbiased test requires further assumptions about Humidity effects. An important aspect of restricted randomization comes to light by considering the strength of the bias component. For example, if Temperature and Humidity are nonadditive, the bias component will generally be much stronger (larger) for restricted randomization **(7)** than for complete randomization **(5)**. The nature of the bias component is discussed more fully in Chapter 2.

Understanding that the effects of non-additivity depend on the randomization process

is important. Some vague notion of this relationship is not sufficient, the functions defining the bias components should be explicitly defined and carefully examined to understand the cost of restricting randomization. Assessing the cost of randomizing without recognizing the cost of **not** randomizing can lead to poor design decisions.

1.3 LITERATURE REVIEW

Kempthorne (1955) discusses the importance of randomization tests, introduced by Fisher, in validating tests based on normal theory. Normal theory results, relying on distributional assumptions and often too little data to validate those assumptions, is presented as a reasonable approximation to results of more robust randomization tests. The essence of randomization tests is to calculate the same test statistic used for the observed data for all possible combinations of the observed responses and treatment combinations. According to H_o, the treatment has no effect, and the observed test statistic comes from the same distribution as those calculated from the permuted data and is simply an observation from that distribution. If the observed test statistic is extreme, relative to the distribution of permuted test statistics (e.g., larger than 95% of them), then it may be taken as evidence that the observed test statistic is not from the same distribution as the permuted test statistics and that the treatment affects the response. This is done without appeal to the usual assumptions of normality and homogeneity.

Kempthorne (1955) showed for a one-factor design that if randomization is complete and if treatment effects and experimental unit effects are additive then randomization tests lead to the same ANOVA table as that derived from normal theory. He also showed that the distribution of test statistics based on randomization theory and normal theory are asymptotically equivalent. First he defined

$$G = \frac{SS(Treatment)}{SS(Total_{Corrected})}$$

a 1-to-1 transformation of the usual F statistic

$$F = \frac{MS(Treatment)}{MS(Error)}$$

Tests based on these two statistics are equivalent and under normal theory G has a Beta distribution and F has an F distribution. It was then shown that the first two moments of the randomization distribution asymptotically approach the first two moments of this Beta distribution as the number of replications increases. So, given sufficient sample size, the usual F-statistic yield's reasonable results even when the normal theory assumptions are violated because it closely approximates the more robust randomization test.

The key to developing the nonparametric randomization tests involves modeling the act of randomization (assignment of treatments to experimental units). This is done by defining a delta-dirac function (an indicator function) representing whether a particular experimental unit receives a particular treatment combination. The joint probability distribution of the delta-dirac function is used to derive the expected mean squares and allows for the effects of the randomization to be modeled and appear in the EMS. Examples are presented for the randomized complete block design, Latin square design, and designs involving subsampling (Wilk 1955; Wilk and Kempthorne 1957; Hinkelmann and Kempthorne 1994).

Anderson and McLean (1974a, 1974b) presented a method that uses an explicit term in the linear model to represent the randomization process. An example was given contrasting the completely randomized two-factor design (CRD) with a single replication and the randomized complete block design (RCBD) pointing out fundamental differences and indicating areas of confusing similarity. As pointed out earlier, the fundamental difference in the manner that treatments are assigned to experimental units is obscured by the fact that the linear model and ANOVA calculations are similar for both designs. Anderson and McLean (1974a, 1974b) incorporated a term in the linear model, which they called a

restriction error, to represent the effects of the restricted randomization. This demonstrates the difference between the two designs. The restriction error provides a high level or abstract method of representing the complex effects of restricted randomization as derived by Kempthorne (1955), Wilk (1955), and Scheffe (1959). It is easily integrated with EMS algorithms (Lorenzen and Anderson 1993b), making the results of more complex theory available to a broad range of practicing experimenters.

Anderson and McLean (1974a, 1974b), Lorenzen (1984), and Lorenzen and Anderson (1993a) discussed randomization of run-order and the effects of restricting it in certain ways. Lorenzen (1984) provided a theoretical foundation for the results presented by Anderson and McLean (1974a, 1974b) with slight modification. The effects of the restriction error are still represented in the EMS but the row in the ANOVA table corresponding to the restriction error term (δ) is removed because it has zero degrees of freedom. However, the model implicitly assumed strict additivity between treatment and run-order (an experimental time unit). This is like assuming that temperature and humidity in Example 1.1 do not interact, or more generally, that there are no unknown or lurking variables associated with time that interact with the variables under study. Rather than assume that all nonadditive effects are zero, their effects on bias should be examined, especially because this bias depends on the randomization process.

White (1975) focuses on the weakness of the linear model as a description of the experiment similarly to Anderson and McLean (1974a, 1974b), but goes further in characterizing the natural structure of the experimental material. This inherent structure is considered separately from any imposed by the particular design. For example, an experiment may be conducted so that only one level of a factor is applied to a particular subset of the experimental material (i.e., by definition, the subset of the experimental material is the experimental unit, and is nested in the factor levels) or so that all levels of a factor are applied to each subset of experimental material (i.e., the subset of experimental material is not the experimental unit, and is crossed with the factor levels). This structure

is imposed as a result of the design, or treatment, and the combinations of factor levels can be randomly assigned to experimental units. On the other hand, nesting may be the result of inherent structure between experimental units and this structure is not subject to randomization. For example, a design may be chosen such that a rat is either crossed or nested with a factor such as drug type, but the rat is inherently nested in factors Litter and Gender. While the drug treatment is subject to random assignment to the rats, the Litter or Gender treatment cannot be applied by the experimenter and so cannot be randomly assigned to a rat. While the label "treatment" may be a misnomer when applied to Litter and Gender, the usual linear models approach makes no differentiation between such imposed vs. inherent labeling.

1.4 SUMMARY

Randomization is an integral part of, and fundamental to, experimental design. Restrictions on the randomization process may be the natural result of structure among experimental units (design structure), or imposed in response to realistic constraints (segment structure). The usual linear model does not convey information about the randomization process, and extensions to the linear model have been presented in the literature to model the randomization process for design and segment structures.

The weaknesses of previous work on modeling restricted randomization are:

(1) Segment restriction involved implicit assumptions of additivity so the strength of nonadditive bias components was never examined.

(2) Block restrictions have been presented in design specific format, i.e., not generalized.

(3) Derivation of the effects of segment and block restrictions used extensive summation notation that obscures the underlying structure and is cumbersome.

(4) Results of segment and block restrictions were not unified.

The remaining chapters of this thesis correct these previous weaknesses. In particular:

(1) A general model formulation in the language of linear models, matrix algebra, will be developed (Chapter 2). Extensive and tedious summation notation used in previous formulations is replaced by a compact and efficient representation which abstracts the algebraic detail and reveals the inherent structure. The randomization process is viewed as acting upon potential responses to produce sets of realizable responses. This relationship is mapped into the familiar setting of complete and fractional designs where, as described in Example 1.1, aliasing or biasing would be expected.

(2) The two important elements:

(i) description of the randomization process and

(ii) definition of the model parameters

are separated in the development in (1). The two elements are in effect independent and modification in one does not require adjustment to the other. Model parameters can be redefined or removed without affecting the mathematical description of the randomization process.

(3) Additivity between treatment and experimental unit is *not* implicitly assumed. The strength of the bias is examined for both complete and restricted randomization. Examples are presented to show the effects of lurking variables under complete and restricted randomization when additivity is not assumed.

(4) Simple rules are presented for generating expected mean squares (indicating presence or absence of bias components) under restricted randomization and allowing for nonadditivity. They can be used to identify the general conditions required for unbiased tests.

(5) The results for block restrictions will be derived using the same general framework as segment restrictions. Results will be general enough to cover cases involving

split-plot structures and subsampling.

(6) The results for Segment and Block restrictions are unified.

(7) Results for segment restrictions are extended to allow fractional designs, e.g., Taguchi designs (Chapter 4).

(8) A computer program has been developed that produces the quadratic form and/or function of covariances involved in the EMS under complete and restricted randomization. It can handle arbitrary number of factors each at an arbitrary number of levels with multiple restrictions on factor levels or treatment combinations involving several factors.

CHAPTER 2

MODELING SEGMENT RESTRICTIONS

This chapter deals with segment restrictions, i.e., those applied at the discretion of the experimenter regarding the run-order of a sequential experiment. The derivation (section 2.1) focuses on the *structure* of the problem and the *function* of randomization at the expense of extensive calculations. Section 2.2 parallels the derivation with a detailed example of a one factor design under complete and restricted randomization. Subsequently, a general method is proposed in section 2.3 that greatly reduces the burden of calculation by directly modeling the probability structure of the randomization process. This is done for a useful, but specific, subset of segment restrictions. An example of a two-factor design is presented (Section 2.4) for complete randomization and randomization that involves single and multiple restrictions on factor levels and a restriction on combined factor levels. The detail presented in the one-factor example is not attempted and the focus is on results and interpretation. The existence and strength of bias components are discussed for various restrictions on randomization. Finally, general rules are presented for generating EMS that show the presence and relative strength of bias components.

2.1 DERIVATION

The derivation of the general result is first presented in terms of a two-factor design (A and B) but is easily generalized to any number of factors. The two factor design is sufficient to demonstrate many aspects of more complex designs including restricted factors,

nonrestricted factors, interactions between restricted and nonrestricted factors, and replication.

Consider an experiment with two factors (A and B) at I and J levels respectively. A total of K replicates of each treatment combination will be run. The IJ treatment combinations are applied to the IJK experimental units and the experiment is run in a particular order indexed by l=1,...,L, where L=IJK. The experimental units are labeled l=1,...,IJK. To improve readability the symbol @ (read "at" or "applied to") will be placed between subscripts representing treatment combinations and those representing run-order.

Note: In the following notation the vectors $\boldsymbol{\mu}$ and matrices $\boldsymbol{\Sigma}$ are not uniquely identified by subscripts. For example, $\boldsymbol{\mu}$ used in reference to the mean of the $\alpha U_{i@l}$ is different from $\boldsymbol{\mu}$ used in reference to the mean of the $\beta U_{j@l}$. Such terms will always be used in an identifiable context, alleviating the need for extra subscripts.

The notation used in the initial derivation is as follows:

$z_{ij@l}$ = potential response when the ij^{th} treatment is applied to the l^{th} run-order,

α_i = effect of the i^{th} level of factor A (i=1,...,I),

β_j = effect of the j^{th} level of factor B (j=1,...,J),

$\alpha\beta_{ij}$ = effect of the interaction between the i^{th} level of A and j^{th} level of B,

U_l = effect of the l^{th} level of run-order (l=1,...,IJK), $\boldsymbol{U}$ ~MVN($\boldsymbol{\mu}$, $\boldsymbol{\Sigma}$) (can be viewed as representing the main effects of any lurking variables with a 1-to-1 correspondence to run-order),

$\alpha U_{i@l}$ = effect of the interaction between the i^{th} level of A and l^{th} run-order, $\boldsymbol{\alpha U}$ ~MVN($\boldsymbol{\mu}$, $\boldsymbol{\Sigma}$),

$\beta U_{j@l}$ = effect of the interaction between the j^{th} level of B and l^{th} run-order, $\boldsymbol{\beta U}$ ~MVN($\boldsymbol{\mu}$, $\boldsymbol{\Sigma}$),

$\alpha\beta U_{ij@l}$ = effect of the interaction between the i^{th} level of A, the j^{th} level of B, and the l^{th} run-order, $\boldsymbol{\alpha\beta U}$ ~MVN($\boldsymbol{\mu}$, $\boldsymbol{\Sigma}$),

$\epsilon_{ij@l}$ = error term for the l^{th} run-order receiving the ij^{th} treatment, $\epsilon_{ijl} \sim N(0, \sigma^2_\epsilon)$,

Q_p = matrix of a quadratic form for p^{th} term.

y_{ijk} = observed response for the k^{th} replicate of the ij^{th} treatment.

α_i, β_j, and $\alpha\beta_{ij}$ may be defined as fixed or random effects.

For segmented designs the run-order of the IJK units can be indexed by multiple subscripts. For example, $l=mn$, where m represents ordered segments and n represents run-order within segment m. If a two-factor design is restricted on A then m=1,...,I and n=1,...,JK, or if restricted on AB then m=1,...,IJ and n=1,...,K. Distinctions can be drawn between run-orders in the same segment or different segments without performing mental gymnastics with the subscript l.

The variable $z_{ij@l}$ is the potential response when the ij^{th} treatment is applied to the l^{th} run-order, and is a function of both the observable and unobservable factors.

$$z_{ij@l}=\mu+\alpha_i+\beta_j+\alpha\beta_{ij}+U_l+\alpha U_{i@l}+\beta U_{j@l}+\alpha\beta U_{ij@l}+\epsilon_{ij@l} \quad . \qquad \textbf{(11)}$$

The potential observations in **(11)** can be written in matrix notation where left and right subscripts indicate the row and column size respectively.

$$_{IJL}z_l = {}_{IJL}X_P \; {}_P\theta_l + {}_{IJL}\epsilon_l$$

where $\theta' = [\mu, \alpha_1, \alpha_2, \ldots, \alpha\beta U_{IJ@L}]$ (with P effects)

X = design matrix relating z and θ

$\epsilon' = [\epsilon_{111}, \epsilon_{112}, \ldots, \epsilon_{IJ@L}]$

Of course not all $z_{ij@l}$ are, or can be observed, only a subset or fraction of the potential responses appears in each possible realization of the experiment. For example, the first unit run (l=1) can only receive one of the IJ treatment combinations. For any realizable experiment a selection matrix, T, can be defined that links the observed responses (similar

to Kempthorne 1955), $\boldsymbol{y}$ (in standard lexicographic order), to the potential responses, z.

$$_{IJK}\boldsymbol{y}_1 = {}_{IJK}\boldsymbol{T}_{IJL}\ {}_{IJL}z_1$$

where $\boldsymbol{T} = [t_{11@1}, t_{11@2}, \cdots, t_{IJ@L}]$ and
$t_{ij@l}$ is a column vector

Each of the IJK rows of $\boldsymbol{T}$ corresponds to a realized response and each of the IJL columns of $\boldsymbol{T}$ corresponds to a potential response. If a potential response is realized then the corresponding row and column of $\boldsymbol{T}$ contains a one, otherwise it contains a zero. Note that $\boldsymbol{T}$ is a random variable because it represents the realization of a random event, the realized run-order. $\boldsymbol{Z}$ is also a random variable because it depends on the random variable ϵ and any random effects defined in θ. The $\boldsymbol{T}$ matrix (and its theoretical moments) carries information about the randomization process while z (and its theoretical moments) carries information about the effects specified in the linear model.

In an ANOVA table the sum of squares for the p^{th} row in the ANOVA table can be expressed as

$$SS_p = y' Q_p y$$

$$= z' T' Q_p T z$$

for some quadratic form Q_p.

Since $\boldsymbol{y}$ is in standard lexicographic order and the formation of sums of squares is not dependent on the realized run order, Q_p is constant over all possible realizations of the experiment. SS_p is a function of two random variables, z and $\boldsymbol{T}$, and its expectation can be taken conditionally.

$$E(SS_p) = E(z' T' Q_p T z) = E_z(z' [\, E_{T/z}(T' Q_p T) \,]\ z)$$

The inner brackets contain the expectation of a multivariate quadratic form. This

multivariate quadratic form can be expressed as a matrix of univariate quadratic forms by appropriate partitioning. The expectation can then be expressed as the univariate elements:

$$R_p = E_{T\cdot z}(T' Q_p T) = \begin{bmatrix} E(t'_{11@1} Q_p t_{11@1}) & E(t'_{11@1} Q_p t_{11@2}) & \cdots & E(t'_{11@1} Q_p t_{IJ@L}) \\ E(t'_{11@2} Q_p t_{11@1}) & E(t'_{11@2} Q_p t_{11@2}) & \cdots & E(t'_{11@2} Q_p t_{IJ@L}) \\ \vdots & \vdots & \ddots & \vdots \\ E(t'_{IJ@L} Q_p t_{11@1}) & E(t'_{IJ@L} Q_p t_{11@2}) & \cdots & E(t'_{IJ@L} Q_p t_{IJ@L}) \end{bmatrix}$$

Each element of R_p can be reexpressed as the expectation of a bilinear form (Searle 1971):

$$E(t'_{ij@l} Q_p t_{i'j'@l'}) = tr\,(Q_p\, COV(t_{ij@l}, t_{i'j'@l'})) + E(t_{ij@l})' Q_p\, E(t_{i'j'@l'}) \qquad (17)$$

The randomization process determines the first two moments of T, required to solve for the elements of R_p. As one might expect, determining the moments of T can be calculation intensive. A "brute force" approach is used in Section 2.2, i.e., produce all possible T matrices and average the appropriate columns or cross products of columns. (The general method developed in section 2.3 does not require the generation of the T matrices.)

Having determined R_p, the expectation of SS_p is now a quadratic form in z and is handled conventionally.

$$E(SS_p) = E_z(z' R_p\, z)$$

$$= tr(R_p\, COV(z)) + E(z)' R_p\, E(z)$$

By substituting $z = X\theta + \epsilon$, and using standard results for manipulating covariances and traces, $E(SS_p)$ can be expressed as a function of the effects of interest as follows:

$$E(SS_p) = tr(X' R_p X\, COV(\theta)) + tr(R_p)\,\sigma^2_\epsilon + E(\theta')\, X' R_p X\, E(\theta) \qquad (19)$$

The EMS_p are found by dividing the $E(SS_p)$ by the degrees of freedom associated with the p^{th} term in the ANOVA. The EMS_p, a function of θ, contain all the usual components (observable effects) one would see in an ANOVA table, but may also include components

representing lurking variables associated with run-order (unobservable effects). For a specified F-test the bias component can be isolated by expressing:

$$EMS_{num} = EMS_{den} + [EMS_{num} - EMS_{den}]$$

Under H_o $[EMS_{num} - EMS_{den}]$ represents the bias component. Under H_A $[EMS_{num} - EMS_{den}]$ represents the bias plus treatment components. This bias component can be found by defining:

$$R_{bias} = \left(\frac{R_{num}}{df_{num}} - \frac{R_{den}}{df_{den}} \right)$$

and substituting back into **(19)** in place of R_p. In this way an EMS table can be presented which clearly demonstrates the existence and form of any bias components corresponding to the specified F-tests.

Taking the conditional expectation, as described, functionally separates T, which represents the randomization process, and z, which represents the observable and unobservable linear model effects. These effects subsequently appear in the expected means squares, which are used in deriving appropriate F tests. Elements of z can be defined independently of T, allowing various model definitions to be examined without recalculating of the moments of T.

2.2 ONE-FACTOR EXAMPLE

A detailed example will now be presented to illustrate the ideas of the previous section. Suppose an experiment is designed to study the effects of a factor, A (with two levels), on a response of interest, y. The experiment is to be replicated twice for a total of four experimental units. The experiment is sequential in that only one treatment can be applied to one experimental unit at a given time or run-order. Six cases will be examined, outlined as follows:

Complete randomization of treatments over run-order:

Case 1.1: No Run-order effects (usual ANOVA),

Case 1.2: Run-order effects are additive,

Case 1.3: Run-order effects are nonadditive.

Restricted randomization of treatments over run-order:

Case 2.1: No Run-order effects

Case 2.2: Run-order effects are additive,

Case 2.3: Run-order effects are nonadditive.

2.2.1 Complete Randomization of Run-Order

Define:

$z_{i@l}$ = response when the i^{th} treatment is applied to the l^{th} run-order,

α_i = effect of the i^{th} level of factor A, considered fixed or random (i=1,...,I, I=2),

U_l = effect of the l^{th} run-unit (l=1,...,IJ, J=2 replicates), $\boldsymbol{U} \sim$ MVN($\boldsymbol{\mu}$, $\boldsymbol{\Sigma}$), (can be viewed as representing the main effects of any lurking variables),

$\alpha U_{i@l}$ = effect of the interaction between the i^{th} level of A and the l^{th} run-unit where $\alpha\boldsymbol{U} \sim$ MVN($\boldsymbol{\mu}$, $\boldsymbol{\Sigma}$),

$\epsilon_{i@l}$ = error term for the l^{th} run-order receiving the i^{th} treatment, $\epsilon_{i@l} \sim N(0, \sigma^2_{\epsilon})$,

Q_P = matrix of a quadratic form for p^{th} term.

$\boldsymbol{T}$ = selection matrix linking y_{ij} and $z_{i@l}$.

y_{ij} = observed response for the j^{th} replicate of the i^{th} treatment.

The ANOVA tables are presented in general form, but to examine the structure of the bias components it is assumed that the run-order effects, U_l and $\alpha U_{i@l}$, are random effects with

constant variances (diagonal of corresponding Σ is constant). The bias components are written as a function of σ, where σ is an element of Σ. The assumption of constant variances allows us to examine bias components as a function of the correlation matrix.

Now z defines the potential observations.

$$z = \begin{bmatrix} z_{1@1} \\ z_{1@2} \\ z_{1@3} \\ z_{1@4} \\ z_{2@1} \\ z_{2@2} \\ z_{2@3} \\ z_{2@4} \end{bmatrix} = X\theta = \begin{bmatrix} 1 & 1 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mu \\ \alpha_1 \\ \alpha_2 \\ U_1 \\ U_2 \\ U_3 \\ U_4 \\ \alpha U_{1@1} \\ \alpha U_{1@2} \\ \alpha U_{1@3} \\ \alpha U_{1@4} \\ \alpha U_{2@1} \\ \alpha U_{2@2} \\ \alpha U_{2@3} \\ \alpha U_{2@4} \end{bmatrix} + \begin{bmatrix} \epsilon_{1@1} \\ \epsilon_{1@2} \\ \epsilon_{1@3} \\ \epsilon_{1@4} \\ \epsilon_{2@1} \\ \epsilon_{2@2} \\ \epsilon_{2@3} \\ \epsilon_{2@4} \end{bmatrix} \qquad (22)$$

For any realized experiment, y is linked to z by a selection matrix T.

$$\begin{bmatrix} y_{11} \\ y_{12} \\ y_{21} \\ y_{22} \end{bmatrix} = \boldsymbol{T} \begin{bmatrix} z_{1@1} \\ z_{1@2} \\ z_{1@3} \\ z_{1@4} \\ z_{2@1} \\ z_{2@2} \\ z_{2@3} \\ z_{2@4} \end{bmatrix}$$

The matrix $\boldsymbol{T}$ is dependent on the randomization scheme employed (complete or restricted) while z is dependent on the linear model definition, run-order effect either nonexistent, additive, or nonadditive.

$\boldsymbol{Q}_A$ and $\boldsymbol{Q}_E$, the matrices of the quadratic forms for "A" and "Error" in the ANOVA table are:

$$\boldsymbol{Q}_A = \begin{bmatrix} .25 & .25 & -.25 & -.25 \\ .25 & .25 & -.25 & -.25 \\ -.25 & -.25 & .25 & .25 \\ -.25 & -.25 & .25 & .25 \end{bmatrix} \qquad \boldsymbol{Q}_E = \begin{bmatrix} .5 & -.5 & 0 & 0 \\ -.5 & .5 & 0 & 0 \\ 0 & 0 & .5 & -.5 \\ 0 & 0 & -.5 & .5 \end{bmatrix} \tag{24}$$

The sums of squares of the usual ANOVA are:

$$\begin{aligned} SS(A) &= y'\boldsymbol{Q}_A y = \sum_{i=1}^{2}\sum_{j=1}^{2}(\bar{y}_{i.}-\bar{y}_{..})^2 \\ SS(E) &= y'\boldsymbol{Q}_E y = \sum_{i=1}^{2}\sum_{j=1}^{2}(y_{ij}-\bar{y}_{i.})^2 \end{aligned} \tag{25}$$

Under complete randomization 24 potential experimental sequences can be realized

with equal probability:

Table VII Twenty-four potential experimental sequences under complete randomization.

y_{ij}	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
y_{11}	1	1	1	1	1	1	2	2	2	2	2	2	3	3	3	3	3	3	4	4	4	4	4	4
y_{12}	2	2	3	3	4	4	1	1	3	3	4	4	1	1	2	2	4	4	1	1	2	2	3	3
y_{21}	3	4	2	4	2	3	3	4	1	4	1	3	2	4	1	4	1	2	2	3	1	3	1	2
y_{22}	4	3	4	2	3	2	4	3	4	1	3	1	4	2	4	1	2	1	3	2	3	1	2	1

The realizable observations (y's for each sequence) can be obtained from z using a 4x8 T matrix (the subscript on T is an index to the sequence in **Table VII**):

$$T_1=\begin{bmatrix}1&0&0&0&0&0&0&0\\0&1&0&0&0&0&0&0\\0&0&0&0&0&0&1&0\\0&0&0&0&0&0&0&1\end{bmatrix}$$

$$T_2=\begin{bmatrix}1&0&0&0&0&0&0&0\\0&1&0&0&0&0&0&0\\0&0&0&0&0&0&0&1\\0&0&0&0&0&0&1&0\end{bmatrix}$$

$$\vdots$$

$$T_{24}=\begin{bmatrix}0&0&0&1&0&0&0&0\\0&0&1&0&0&0&0&0\\0&0&0&0&0&1&0&0\\0&0&0&0&1&0&0&0\end{bmatrix}$$

For example, if the realized experiment consists of randomly selecting run-order 1 then

$y = T_1 z$, where z is defined as in **(22)**.

To evaluate the EMS_A requires, according to **(17)**,

$$E(t_{i@l}),\ \text{a column of}\ E(T) \tag{27}$$

and

$$COV(t_{i@l}, t_{i'@l'}) = E(t_{i@l} t'_{i'@l'}) - E(t_{i@l}) E(t'_{i'@l'}) \tag{28}$$

E(T) in **(27)** is the average of the 24 T matrices each selected with probability 1/24, and

$$E(T) = \begin{bmatrix} .25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\ .25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & .25 & .25 & .25 & .25 \\ 0 & 0 & 0 & 0 & .25 & .25 & .25 & .25 \end{bmatrix} \tag{29}$$

Equation **(28)** on the other hand requires that the appropriate outer product $(t_{i@l} t_{i'@l'})$ be taken for each of the 24 T matrices and then averaged. For example using the first two columns of T_1 the outer product is:

$$t_{1@1} t'_{1@2} = \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \begin{bmatrix} 0 & 1 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

This outer product is computed for each of the remaining 23 T matrices and the results averaged.

$$E(t_{1@1}t'_{1@2}) = \begin{bmatrix} 0 & .083 & 0 & 0 \\ .083 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{31}$$

From these moments the $\mathbf{COV}(t_{1@1}, t_{1@2})$ is derived.

$$COV(t_{1@1}, t_{1@2}) = E(t_{1@1}t'_{1@2}) - E(t_{1@1})E(t'_{1@2})$$

$$= \begin{bmatrix} -.0625 & .02083 & 0 & 0 \\ .02083 & -.0625 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

These moments are used with Q_A in **(17)** to solve for $\mathbf{R}_{p:1@1,1@2}$ (the element of R_p in row one, column 2). For example,

$$R_{A:[1@1,1@2]} = E(t'_{1@1}Q_A t_{1@2})$$

$$= tr(Q_A\, COV(t_{1@1}, t_{1@2})) + E(t'_{1@1})\, Q_A\, E(t_{1@2})$$

$$= tr\left(\begin{bmatrix} .25 & .25 & -.25 & -.25 \\ .25 & .25 & -.25 & -.25 \\ -.25 & -.25 & .25 & .25 \\ -.25 & -.25 & .25 & .25 \end{bmatrix} \begin{bmatrix} -.0625 & .0208 & 0 & 0 \\ .0208 & -.0625 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \right)$$

$$+ \begin{bmatrix} .25 & .25 & 0 & 0 \end{bmatrix} \begin{bmatrix} .25 & .25 & -.25 & -.25 \\ .25 & .25 & -.25 & -.25 \\ -.25 & -.25 & .25 & .25 \\ -.25 & -.25 & .25 & .25 \end{bmatrix} \begin{bmatrix} .25 \\ .25 \\ 0 \\ 0 \end{bmatrix}$$

$$= .04165 \approx .0417$$

The remaining elements of R_p are solved similarly (at least the upper or lower triangular

submatrix, due to symmetry). For example, having gone through the necessary calculations as described, $\boldsymbol{R}_A$ is :

$$\boldsymbol{R}_A = \begin{bmatrix} 0.1250 & 0.0417 & 0.0417 & 0.0417 & 0 & -0.0833 & -0.0833 & -0.0833 \\ 0.0417 & 0.1250 & 0.0417 & 0.0417 & -0.0833 & 0 & -0.0833 & -0.0833 \\ 0.0417 & 0.0417 & 0.1250 & 0.0417 & -0.0833 & -0.0833 & 0 & -0.0833 \\ 0.0417 & 0.0417 & 0.0417 & 0.1250 & -0.0833 & -0.0833 & -0.0833 & 0 \\ 0 & -0.0833 & -0.0833 & -0.0833 & 0.1250 & 0.0417 & 0.0417 & 0.0417 \\ -0.0833 & 0 & -0.0833 & -0.0833 & 0.0417 & 0.1250 & 0.0417 & 0.0417 \\ -0.0833 & -0.0833 & 0 & -0.0833 & 0.0417 & 0.0417 & 0.1250 & 0.0417 \\ -0.0833 & -0.0833 & -0.0833 & 0 & 0.0417 & 0.0417 & 0.0417 & 0.1250 \end{bmatrix}$$

The zero elements represent a unit run at a particular time receiving both treatments, clearly an impossible event. Having determined $\boldsymbol{R}_A$, the $E(SS_A)$ is the expectation of a univariate quadratic form and is found in the usual manner, incorporating an appropriate definition of z.

Before interpreting results a brief explanation of subsequent EMS tables is in order. Common definitions, such as $\Phi(A)$, found in many textbooks that deal with analysis of variance are not given. The bias components for the p^{th} term are functions of $[MS_p - MS_E]$, which can be expressed as cross-products of observations *within* the levels of the p^{th} term minus cross-products of observations *between* levels of the p^{th} term. Such bias components will be labeled as (W-B) for (*Within-Between*). This is simply a re expression of the usual formulas for sums of squares that parallels the form of the quadratic matrices, $_{QP}$ and $\boldsymbol{Q}_E$. For example:

$$MS_A - MS_E$$

$$= \frac{\left[\sum_i \sum_j (\bar{y}_{i.} - \bar{y}_{..})^2\right]}{[I-1]} - \frac{\left[\sum_i \sum_j (y_{ij} - \bar{y}_{i.})^2\right]}{[I(J-1)]}$$

$$= \frac{\left[(I-1)J\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ^2} - \frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{I(I-1)J^2K^2}\right]\right]}{[I-1]} - \frac{\left[I(J-1)\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ} - \frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ(J-1)}\right]\right]}{[I(J-1)]} \quad \textbf{(35)}$$

$$= \left[J\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{[IJ(J-1)]}\right]\right] - \left[J\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{[I(I-1)J^2]}\right]\right]$$

The extra components in the EMS_E are a function of MS_E and can be expressed as cross-products of observations on a *diagonal* (squared observations) minus cross-products of observations *within* levels of factor E. Such bias components will be labeled as (D-W) for (*Diagonal-Within*). For example:

$$MS_E = \frac{\left[\sum_i \sum_j (y_{ij} - \bar{y}_{i.})^2\right]}{[I(J-1)]}$$

$$= \frac{\left[I(J-1)\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ} - \frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ(J-1)}\right]\right]}{[I(J-1)]} \quad \textbf{(36)}$$

Case 1.1: No Run-order effects (usual ANOVA)

The usual linear model and ANOVA provide no means for representing randomization information and are equivalent to assuming no run-order effects. This is accomplished by setting all effects involving U_l to zero and $z_{i@l} = \mu + \alpha_i + \epsilon_{i@l}$. The general results are presented in **Table VIII**, Case 1.1. The test for main effect A is unbiased using MSE as the denominator of the F-test.

Case 1.2: Run-order effects are additive (reduces to the usual ANOVA)

When the run-order effects are additive, all $\alpha U_{i@l}$ effects are zero and $z_{i@l} = \mu + \alpha_i + U_l + \epsilon_{i@l}$. Results in **Table VIII**, Case 1.2 show that an unbiased test for A exists using MSE as the denominator. The combination of complete randomization and additivity of treatment and run-order effects leads to an unbiased test for A. The effects of U are confounded with, or inflate the error term, ϵ, but do not bias the test for A. Effects of unrecognized or uncontrolled factors do not bias tests if their effects are additive with the effects of factors controlled by the experimenter.

Lorenzen (1984) noted that the distributional assumptions of the F-test only hold if the effects of U are not fixed. If there are fixed U effects then the denominator of the F statistic involves a noncentral χ^2, and does not follow an F-distribution. The test can be modified to adjust for the noncentrality of the denominator χ^2, but throughout this thesis it is assumed that such effects are only random or serially correlated. Under these conditions the EMS(E) components can be combined, or pooled, resulting in EMS similar to Case 1.1.

Table VIII EMS for One-factor design- complete randomization

Case 1.1: No Run-order effects (usual ANOVA)
A: $\sigma_\epsilon^2 + J\Phi(A)$
E: σ_ϵ^2
Case 1.2: Run-order effects are additive
A: $\sigma_\epsilon^2 + \sigma_U^2(D-W) + J\Phi(A)$
E: $\sigma_\epsilon^2 + \sigma_U^2(D-W)$
Case 1.3: Run-order effects are nonadditive
A: $\sigma_\epsilon^2 + \sigma_U^2(D-W) + \sigma_{AU}^2(D-W) + J\sigma_{AU}^2(W-B) + J\Phi(A)$
E: $\sigma_\epsilon^2 + \sigma_U^2(D-W) + \sigma_{AU}^2(D-W)$

COMPONENT DEFINITION

$$\sigma^2_U(D-W)=(IJ)^{-1}\sum_{l}\sum_{l'}\sigma_{l,l'} - (IJ(IJ-1))^{-1}\sum_{l}\sum_{l'\neq l}\sigma_{l,l'}$$

$$\sigma^2_{AU}(D-W)=(I^2J)^{-1}\sum_{i}\sum_{i'}\sum_{l}\sum_{l'}\sigma_{i@l,i'@l'} - (I^2J(IJ-1))^{-1}\sum_{i}\sum_{i'\neq i}\sum_{l}\sum_{l'\neq l}\sigma_{i@l,i'@l'}$$

$$\sigma^2_{AU}(W-B)=(I^2J(IJ-1))^{-1}\sum_{i}\sum_{i'\neq i}\sum_{l}\sum_{l'\neq l}\sigma_{i@l,i'@l'} - (I(I-1)IJ(IJ-1))^{-1}\sum_{i}\sum_{i'\neq i}\sum_{l}\sum_{l'\neq l}\sigma_{i@l,i'@l'}$$

Case 1.3: Run-order effects are nonadditive

With nonadditive run-order effects $z_{i@l} = \mu + \alpha_i + U_l + \alpha U_{i@l} + \epsilon_{i@l}$. General results are presented in **Table VIII**, Case 1.3. Even with complete randomization the test for A is biased because components involving the $\alpha U_{i@l}$ effects appear in the numerator EMS. The bias component is a function of the average correlation between units receiving the same treatment minus the average correlation between units receiving different treatments:

$$\frac{\sigma^2_{AU}(W-B)}{\sigma^2_{AU}} = (I^2J(IJ-1))^{-1}\sum\sum\sum\sum_{i=i'\,l\neq l'}\rho_{i@l,i'@l'} - (I(I-1)IJ(IJ-1))^{-1}\sum\sum\sum\sum_{i\neq i'\,l\neq l'}\rho_{i@l,i'@l'}$$

where σ^2_{AU} is the diagonal of Σ_{AU}

This constraint can be viewed directly from the correlation matrix (elements that are not part of the constraint equation are denoted by a •):

$$\rho_{AU} = \begin{bmatrix} \blacksquare & \begin{matrix} \cdot & \rho_{1@1,2@2} & \rho_{1@1,2@3} & \rho_{1@1,2@4} \\ \rho_{1@2,2@1} & \cdot & \rho_{1@2,2@3} & \rho_{1@2,2@4} \\ \rho_{1@3,2@1} & \rho_{1@3,2@2} & \cdot & \rho_{1@3,2@4} \\ \rho_{1@4,2@1} & \rho_{1@4,2@2} & \rho_{1@4,2@3} & \cdot \end{matrix} \\ \begin{matrix} \cdot & \rho_{2@1,1@2} & \rho_{2@1,1@3} & \rho_{2@1,1@4} \\ \rho_{2@2,1@1} & \cdot & \rho_{2@2,1@3} & \rho_{2@2,1@4} \\ \rho_{2@3,1@1} & \rho_{2@3,1@2} & \cdot & \rho_{2@3,1@4} \\ \rho_{2@4,1@1} & \rho_{2@4,1@2} & \rho_{2@4,1@3} & \cdot \end{matrix} & \blacksquare \end{bmatrix} \quad (42)$$

The bias component is the average of the shaded submatrices minus the average of the nonshaded submatrices. It should be noted that the number of lags of a given order is the same in the shaded and nonshaded submatrices. Thus, if correlations are of the same order of magnitude, they tend to cancel. This bias component is a measure of "interaction", in other words, it measures the strength of the dependency of the covariance structure on the treatment levels. Unless lurking variables exhibit extemely unusual covariance structures as a function of treatment effects, randomization protects the experimenter from the effects

of unrecognized or uncontrolled factors, to some degree. Bias that is a measure of interaction will be *weak* bias.

2.2.2 Restricted Randomization of Run-Order

Consider now the case where due to the nature of the treatment or cost constraints run-order is restricted on A. The restriction implies that once a level of A is randomly selected, all runs at that level are completed (in random order) before proceeding with the other level of A. This implies there are two segments in this experiment, so run-order will be indexed by two subscripts, m for ordered segments, and n for run-order within the m^{th} segment.

Define:

$z_{i@mn}$ = response when the i^{th} treatment is applied to the n^{th} run-order within the m^{th} segment,

α_i = effect of the i^{th} level of factor A, considered fixed or random (i=1,...,I, I=2),

U_{mn} = effect of the n^{th} run-order within the m^{th} segment (m=1,...,I, n=1,...,J, J=2 replicates), $U \sim \text{MVN}(\mu, \Sigma)$, (can be viewed as representing the main effects of any lurking variables),

$\alpha U_{i@mn}$ = effect of the interaction between the i^{th} level of A and the mn^{th} run-order, where $\alpha U \sim \text{MVN}(\mu, \Sigma)$,

$\epsilon_{i@mn}$ = error term for the mn^{th} run-order receiving the i^{th} treatment, $\epsilon_{i@mn} \sim N(0, \sigma^2_{\epsilon})$,

Q_P = matrix of a quadratic form for p^{th} term.

T = selection matrix linking y_{ij} and $z_{i@mn}$.

y_{ij} = observed response for the j^{th} replicate of the i^{th} treatment.

It is assumed that the run-order effects, U_{mn} and $\alpha U_{i@mn}$, are random effects with constant variance (diagonal of corresponding Σ is constant).

Now z defines the potential observations.

$$z = \begin{bmatrix} z_{1@11} \\ z_{1@12} \\ z_{1@21} \\ z_{1@22} \\ z_{2@11} \\ z_{2@12} \\ z_{2@21} \\ z_{2@22} \end{bmatrix} = X\theta = \begin{bmatrix} 1 & 1 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mu \\ \alpha_1 \\ \alpha_2 \\ U_{11} \\ U_{12} \\ U_{21} \\ U_{22} \\ \alpha U_{1@11} \\ \alpha U_{1@12} \\ \alpha U_{1@21} \\ \alpha U_{1@22} \\ \alpha U_{2@11} \\ \alpha U_{2@12} \\ \alpha U_{2@21} \\ \alpha U_{2@22} \end{bmatrix} + \begin{bmatrix} \epsilon_{1@11} \\ \epsilon_{1@12} \\ \epsilon_{1@21} \\ \epsilon_{1@22} \\ \epsilon_{2@11} \\ \epsilon_{2@12} \\ \epsilon_{2@21} \\ \epsilon_{2@22} \end{bmatrix} \quad (43)$$

For any realized experiment, y is linked to z by a selection matrix $\boldsymbol{T}$.

$$\begin{bmatrix} y_{11} \\ y_{12} \\ y_{21} \\ y_{22} \end{bmatrix} = \boldsymbol{T} \begin{bmatrix} z_{1@11} \\ z_{1@12} \\ z_{1@21} \\ z_{1@22} \\ z_{2@11} \\ z_{2@12} \\ z_{2@21} \\ z_{2@22} \end{bmatrix}$$

With the restricted run-order of the experiment only eight sequences are possible, as shown in **Table IX** (there were 24 under complete randomization, compare **Table VII** on page 29).

Table IX Eight potential experimental sequences under restricted randomization. The dotted line delineates the segments.

y_{ij}	1	2	3	4	5	6	7	8
y_{11}	1	1	2	2	3	3	4	4
y_{12}	2	2	1	1	4	4	3	3
y_{21}	3	4	3	4	1	2	1	2
y_{22}	4	3	4	3	2	1	2	1

Each potential realization of a run-order can be obtained from z using a 4x8 T matrix:

$$T_1 = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

$$T_2 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{bmatrix}$$

$$\vdots$$

$$T_8 = \begin{bmatrix} 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \end{bmatrix}$$

For example, if an experiment is realized by randomly assigning run-order 1 to the

experimental units then $y=T_1 z$, where z is defined in **(43)**.

To evaluate the EMS_A requires

$$E(t_{i@mn}), \text{ a column of } E(T) \tag{46}$$

and

$$COV(t_{i@mn}, t_{i'@m'n'}) = E(t_{i@mn} t'_{i'@m'n'}) - E(t_{i@mn}) E(t'_{i'@m'n'}) \tag{47}$$

$E(T)$ in **(46)** is the average of the eight T matrices and is:

$$E(T) = \begin{bmatrix} .25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\ .25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & .25 & .25 & .25 & .25 \\ 0 & 0 & 0 & 0 & .25 & .25 & .25 & .25 \end{bmatrix} \tag{48}$$

$E(T)$ under restricted randomization is the same as under complete randomization **(19)** because $E(T)$ is a function only of the marginal probabilities, e.g., P(run-order n within segment m gets treatment i). The restricted randomization only affects the joint probabilities, e.g., P(mn^{th} run-order gets treatment i and m' n'^{th} run-order gets treatment i'). According to **(47)** the appropriate outer product $(t_{i@mn} t'_{i'@m'n'})$ is averaged over the eight T matrices. For example using the first two columns of T_1 the outer product is:

$$t_{1@11} t'_{1@12} = \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \begin{bmatrix} 0 & 1 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

This outer product is computed for each of the remaining seven T matrices and the results averaged, giving:

$$E(t_{1@11}t'_{1@12}) = \begin{bmatrix} 0 & .25 & 0 & 0 \\ .25 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad \textbf{(50)}$$

Because the joint probabilities are affected by the restricted randomization **(40)** differs from its counterpart under complete randomization **(31)**. The $\mathbf{COV}(t_{1@11},t_{1@12})$ under restricted randomization is:

$$COV(t_{1@11}, t_{1@12}) = E(t_{1@11}t'_{1@12}) - E(t_{1@11})\,E(t'_{1@12})$$

$$= \begin{bmatrix} -.0625 & .1875 & 0 & 0 \\ .1875 & -.0625 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

These moments are used with $\boldsymbol{Q}_A$ in **(17)** to solve for $\boldsymbol{R}_{A:1@11,1@12}$, the element from row 1, column 2 of $\boldsymbol{R}_A$. For example,

$$\begin{aligned} \boldsymbol{R}_{A:1@11,1@12} &= E(t'_{1@11}\boldsymbol{Q}_A t_{1@12}) \\ &= tr(\boldsymbol{Q}_A\,COV(t_{1@11},t_{1@12})) + E(t'_{1@11})\,\boldsymbol{Q}_A\,E(t_{1@12}) \\ &= tr\left(\begin{bmatrix} .25 & .25 & -.25 & -.25 \\ .25 & .25 & -.25 & -.25 \\ -.25 & -.25 & .25 & .25 \\ -.25 & -.25 & .25 & .25 \end{bmatrix}\begin{bmatrix} -.0625 & .1875 & 0 & 0 \\ .1875 & -.0625 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}\right) \\ &\quad + \begin{bmatrix} .25 & .25 & 0 & 0 \end{bmatrix}\begin{bmatrix} .25 & .25 & -.25 & -.25 \\ .25 & .25 & -.25 & -.25 \\ -.25 & -.25 & .25 & .25 \\ -.25 & -.25 & .25 & .25 \end{bmatrix}\begin{bmatrix} .25 \\ .25 \\ 0 \\ 0 \end{bmatrix} \\ &= .1250 \end{aligned}$$

The remaining elements of $\boldsymbol{R}_A$ are solved similarly and yield:

$$\boldsymbol{R}_A = \begin{bmatrix} .125 & .125 & 0 & 0 & 0 & 0 & -.125 & -.125 \\ .125 & .125 & 0 & 0 & 0 & 0 & -.125 & -.125 \\ 0 & 0 & .125 & .125 & -.125 & -.125 & 0 & 0 \\ 0 & 0 & .125 & .125 & -.125 & -.125 & 0 & 0 \\ 0 & 0 & -.125 & -.125 & .125 & .125 & 0 & 0 \\ 0 & 0 & -.125 & -.125 & .125 & .125 & 0 & 0 \\ -.125 & -.125 & 0 & 0 & 0 & 0 & .125 & .125 \\ -.125 & -.125 & 0 & 0 & 0 & 0 & .125 & .125 \end{bmatrix}$$

$\boldsymbol{R}_A$ now contains more zero elements than it did with complete randomization (**34**). These extra zero elements represent a run segment containing two different treatment levels or the same treatment level present in different run segments. For example, the zero in the first row and sixth column of $\boldsymbol{R}_A$ represents the first run-order receiving treatment 1 and the second run-order receiving treatment 2, while the zero in the first row and third column of $\boldsymbol{R}_A$ represents treatment 1 applied to the first and third run-units. Under the restricted randomization scheme, as defined, such events are not possible. Since $\boldsymbol{R}_A$, the matrix of the quadratic form in z, is different under complete and restricted randomization the resulting EMS will reflect this difference. Once $\boldsymbol{R}_A$ is calculated, the $E(SS_A)$ is the expectation of a univariate quadratic form and is found using standard methods, incorporating an appropriate definition of z. Again consider three cases:

Case 2.1: No Run-order effects (Usual ANOVA)

With no run-order effects Case 2.1 of **Table X** is the same as if randomization where complete (Case 1.1 of **Table VIII**). If an experimenter is absolutely certain that no uncontrolled variables change over time that might affect the response, and if the experimenter can convince his colleagues of this fact, then randomization is not required.

Case 2.2: Run-order effects are additive

It was previously shown that complete randomization in combination with additivity

of treatment and run-order effects leads to unbiased tests (**Table VIII**, Case 1.2). Now, with restricted randomization, the test for A is biased by U components (**Table X**, Case 2.2). Even for the additive case, further assumptions are required about the effects of U to obtain an unbiased test for A. This is the price that must be paid for disturbing the randomization-additivity combination that usually assures unbiased tests.

The bias component is a function of the correlation matrix associated with U:

$$\frac{\sigma_U^2(W-B)}{\sigma_U^2} = (IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\rho_{mn,m'n'} - (I(I-1)J^2)^{-1}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\rho_{mn,m'n'}$$

where σ_U^2 is the diagonal of $\boldsymbol{\Sigma}_U$ and
m indexes the segment and n indexes run-order within segment m

This is the average correlation of units in the same segment minus the average correlation of units in different segments. This constraint can be viewed directly as a function of the correlation matrix of U:

$$\boldsymbol{\rho}_U = \begin{bmatrix} \blacksquare & \rho_{11,21} & \rho_{11,22} \\ & \rho_{12,21} & \rho_{12,22} \\ \rho_{21,11} & \rho_{21,12} & \blacksquare \\ \rho_{22,11} & \rho_{22,12} & \end{bmatrix}$$

The bias component is the average of the shaded submatrices minus the average of the nonshaded submatrices. It should be noted that the number of lags of a given order in the shaded submatrices is different from in the nonshaded submatrices. If observations close in time are more highly correlated than observations farther apart in time then the shaded and nonshaded submatrices will not cancel and the bias component may be appreciable. This is additional bias, above and beyond the bias that is a function of the interaction between the correlation structure and treatment level and will be called *strong* bias.

Table X: EMS for the One-factor design- restricted on A

Case 2.1: No Run-order effects (usual ANOVA)
A: $\sigma_\epsilon^2 + J\Phi(A)$
E: σ_ϵ^2
Case 2.2: Run-order effects are additive
A: $\sigma_\epsilon^2 + \sigma_U^2(D-W) + J\sigma_U^2(W-B) + J\Phi(A)$
E: $\sigma_\epsilon^2 + \sigma_U^2(D-W)$
Case 2.3: Run-order effects are nonadditive
A: $\sigma_\epsilon^2 + \sigma_U^2(D-W) + \sigma_{AU}^2(D-W) + J\sigma_U^2(W-B) + J\sigma_{AU}^2(W-B) + J\Phi(A)$
E: $\sigma_\epsilon^2 + \sigma_U^2(D-W) + \sigma_{AU}^2(D-W)$

COMPONENT DEFINITION

$$\sigma_U^2(D-W)=(IJ)^{-1}\sum_{m=m'}\sum_{n=n'}\sum\sum\sigma_{mn,m'n'}-(IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{mn,m'n'}$$

$$\sigma_U(W-B)=(IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{mn,m'n'}-(I(I-1)J^2)^{-1}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sigma_{mn,m'n'}$$

$$\sigma_{AU}^2(D-W)=(I^2J)^{-1}\sum_{i=i'm=m'n=n'}\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'}-(I^2J(J-1))^{-1}\sum_{i=i'm=m'n\neq n'}\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'}$$

$$\sigma_{AU}^2(W-B)=(I^2J(J-1))^{-1}\sum_{i=i'm=m'n\neq n'}\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'}-(I^2(I-1)^2J^2)^{-1}\sum_{i\neq i'm\neq m'n\ n'}\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'}$$

Case 2.3: Run-order effects are nonadditive

With nonadditive run-order effects $z_{i@mn} = \mu + \alpha_i + U_{mn} + \alpha U_{i@mn} + \epsilon_{i@mn}$. General results are presented in **Table X**, Case 2.3. There is additional bias in the test for A due to the nonadditive effects $\alpha U_{i@mn}$. This bias component is a function of the correlations of:

$$\frac{\sigma^2_{AU}(W-B)}{\sigma^2_{AU}} = (I^2J(J-1))^{-1}[\sum_{i\neq i'}\sum_{m\neq m'}\sum_{n\neq n'}\rho_{i@mn,i'@m'n'}] - (I^2(I-1)^2J^2)^{-1}[\sum_{i\neq i'}\sum_{m\neq m'}\sum_{n\neq n'}\rho_{i@mn,i'@m'n'}]$$

It can be viewed as the correlation matrix (as before, components that are not involved in the constraint are denoted by a ·):

$$\rho_{AU} = \begin{bmatrix} \blacksquare & \cdot & \cdot & \cdot & \cdot & \rho_{1@11,2@21} & \rho_{1@11,2@22} \\ & \cdot & \cdot & \cdot & \cdot & \rho_{1@12,2@21} & \rho_{1@12,2@22} \\ \cdot & \cdot & \blacksquare & & \rho_{1@21,2@11} & \rho_{1@21,2@12} & \cdot & \cdot \\ \cdot & \cdot & & & \rho_{1@22,2@11} & \rho_{1@22,2@12} & \cdot & \cdot \\ \cdot & \cdot & \rho_{2@11,1@21} & \rho_{2@11,1@22} & \blacksquare & & \cdot & \cdot \\ \cdot & \cdot & \rho_{2@12,1@21} & \rho_{2@12,1@22} & & & \cdot & \cdot \\ \rho_{2@21,1@11} & \rho_{2@21,1@12} & \cdot & \cdot & \cdot & \cdot & \blacksquare & \\ \rho_{2@22,1@11} & \rho_{2@22,1@12} & \cdot & \cdot & \cdot & \cdot & & \end{bmatrix}$$

The bias component is the average of the shaded submatrices minus the average of the nonshaded submatrices. It should be noted that the number of lags of a given order in the shaded submatrices is different from in the nonshaded submatrices. If observations close in time are more highly correlated than observations farther apart in time then the shaded and nonshaded submatrices will not cancel and the bias component may be appreciable. This is additional bias, above and beyond the bias that is a function of the interaction between the correlation structure and treatment level and will be called *strong* bias.

2.2.3 Simulation of Size of Total Restriction Error

The conditions for unbiased tests and a description of any bias components were presented for complete and restricted randomization. It was shown that under complete randomization there are weak bias components due to nonadditive effects of run-order and treatment. It was also shown that under restricted randomization there are strong bias components due to main effects associated with run-order and nonadditive effects between run-order and treatment. If the structure of Σ_U and Σ_{AU} is completely general the total bias is a function of so many parameters it would be difficult to gain insight into the nature of the bias. For this reason we narrowly define the structures for Σ_U and Σ_{AU} and examine the bias under four scenarios by plotting total bias as a function of ρ. For completeness, ρ is varied from -1 to 1, however, a more realistic range might be $-0.3 < \rho < 0.3$ or perhaps even $0 < \rho < 0.3$. In general the correlation matrices for U and AU have an AR(1) structure:

$$\rho_U = \begin{bmatrix} 1 & \rho & \rho^2 & \rho^3 \\ \rho & 1 & \rho & \rho^2 \\ \rho^2 & \rho & 1 & \rho \\ \rho^3 & \rho^2 & \rho & 1 \end{bmatrix}$$

$$\rho_{AU} = \begin{bmatrix} 1 & \rho_{11} & \rho_{11}^2 & \rho_{11}^3 & 1 & \rho_{12} & \rho_{12}^2 & \rho_{12}^3 \\ \rho_{11} & 1 & \rho_{11} & \rho_{11}^2 & \rho_{21} & 1 & \rho_{12} & \rho_{12}^2 \\ \rho_{11}^2 & \rho_{11} & 1 & \rho_{11} & \rho_{21}^2 & \rho_{21} & 1 & \rho_{12} \\ \rho_{11}^3 & \rho_{11}^2 & \rho_{11} & 1 & \rho_{21}^3 & \rho_{21}^2 & \rho_{21} & 1 \\ 1 & \rho_{21} & \rho_{21}^2 & \rho_{21}^3 & 1 & \rho_{22} & \rho_{22}^2 & \rho_{22}^3 \\ \rho_{12} & 1 & \rho_{21} & \rho_{21}^2 & \rho_{22} & 1 & \rho_{22} & \rho_{22}^2 \\ \rho_{12}^2 & \rho_{12} & 1 & \rho_{21} & \rho_{22}^2 & \rho_{22} & 1 & \rho_{22} \\ \rho_{12}^3 & \rho_{12}^2 & \rho_{12} & 1 & \rho_{22}^3 & \rho_{22}^2 & \rho_{22} & 1 \end{bmatrix}$$

Each of the four quadrants of ρ_{AU} are AR(1) where the correlation depends on the sequence of treatments, hence each quadrant is not necessarily symmetric. We will assume constant variance and further, let $\rho_{11}=a\rho$, $\rho_{12}=b\rho$, $\rho_{21}=c\rho$, $\rho_{22}=d\rho$ and $\sigma^2_{AU}=e\sigma^2_U$. As a result, the covariance matrices can be defined as:

$$\Sigma_U = \begin{bmatrix} \sigma_U^2 & \rho\sigma_U^2 & \rho^2\sigma_U^2 & \rho^3\sigma_U^2 \\ \rho\sigma_U^2 & \sigma_U^2 & \rho\sigma_U^2 & \rho^2\sigma_U^2 \\ \rho^2\sigma_U^2 & \rho\sigma_U^2 & \sigma_U^2 & \rho\sigma_U^2 \\ \rho^3\sigma_U^2 & \rho^2\sigma_U^2 & \rho\sigma_U^2 & \sigma_U^2 \end{bmatrix}$$

$$\Sigma_{AU} = \begin{bmatrix} e\sigma_U^2 & e\sigma_U^2(a\rho) & e\sigma_U^2(a\rho)^2 & e\sigma_U^2(a\rho)^3 & e\sigma_U^2 & e\sigma_U^2(b\rho) & e\sigma_U^2(b\rho)^2 & e\sigma_U^2(b\rho)^3 \\ e\sigma_U^2(a\rho) & e\sigma_U^2 & e\sigma_U^2(a\rho) & e\sigma_U^2(a\rho)^2 & e\sigma_U^2(c\rho) & e\sigma_U^2 & e\sigma_U^2(b\rho) & e\sigma_U^2(b\rho)^2 \\ e\sigma_U^2(a\rho)^2 & e\sigma_U^2(a\rho) & e\sigma_U^2 & e\sigma_U^2(a\rho) & e\sigma_U^2(c\rho)^2 & e\sigma_U^2(c\rho) & e\sigma_U^2 & e\sigma_U^2(b\rho) \\ e\sigma_U^2(a\rho)^3 & e\sigma_U^2(a\rho)^2 & e\sigma_U^2(a\rho) & e\sigma_U^2 & e\sigma_U^2(c\rho)^3 & e\sigma_U^2(c\rho)^2 & e\sigma_U^2(c\rho) & e\sigma_U^2 \\ e\sigma_U^2 & e\sigma_U^2(c\rho) & e\sigma_U^2(c\rho)^2 & e\sigma_U^2(c\rho)^3 & e\sigma_U^2 & e\sigma_U^2(d\rho) & e\sigma_U^2(d\rho)^2 & e\sigma_U^2(d\rho)^3 \\ e\sigma_U^2(b\rho) & e\sigma_U^2 & e\sigma_U^2(c\rho) & e\sigma_U^2(c\rho)^2 & e\sigma_U^2(d\rho) & e\sigma_U^2 & e\sigma_U^2(d\rho) & e\sigma_U^2(d\rho)^2 \\ e\sigma_U^2(b\rho)^2 & e\sigma_U^2(b\rho) & e\sigma_U^2 & e\sigma_U^2(c\rho) & e\sigma_U^2(d\rho)^2 & e\sigma_U^2(d\rho) & e\sigma_U^2 & e\sigma_U^2(d\rho) \\ e\sigma_U^2(b\rho)^3 & e\sigma_U^2(b\rho)^2 & e\sigma_U^2(b\rho) & e\sigma_U^2 & e\sigma_U^2(d\rho)^3 & e\sigma_U^2(d\rho)^2 & e\sigma_U^2(d\rho) & e\sigma_U^2 \end{bmatrix}$$

In the following simulation we set e=0.6 (variance for interaction effects is smaller than variance for main effect). ρ_{11}, ρ_{12}, ρ_{21}, ρ_{22} are defined by the four scenarios described below and are appropriately labeled in **Figure 2.**

Results are graphed for four experimental scenarios:

(1) Run-order effects are additive (the serial correlation of run-order effects is independent of the treatments involved). This is the usual assumption that leads to unbiased tests when coupled with complete randomization (a=0, b=0, c=0, d=0).

This could occur if run-order effects were due to some lurking variable that is unaffected by treatment level, for example, ambient humidity changes over time and has the same effect on the response regardless of the treatment being applied. No bias exists under complete randomization, but when randomization is restricted a bias component exists for all $\rho \neq 0$ and increases in absolute value as $|\rho|$ increases. The absolute value of the bias component is larger for negative values of ρ than for corresponding positive values of ρ.

(2) Run-order effects are nonadditive. Within one of the treatments, run-order effects have higher serial correlation (a=1, b=0, c=0, d=0).

This could occur if the run-order effects were due to some lurking variable associated with one of the treatments, for example, treatment 1 involves water and treatment 2 involves oil and the lurking variable is humidity. We might expect the correlation of run-order effects among treatment 1 responses to be higher than among treatment 2 responses. Under complete randomization the bias component is smaller than under restricted randomization, for all $\rho \neq 0$ (in the range of interest) and increases in absolute value as $|\rho|$ increases. The absolute value of the bias component is larger for negative values of ρ than for corresponding positive values of ρ.

(3) Run-order effects are nonadditive. When treatment 2 is followed by treatment 1, run-order effects have higher serial correlation. This is different from case (2) because one treatment is followed by a different treatment, which crosses a segment boundary in the case of restricted randomization (a=0, b=0, c=1, d=0).

This could occur if the treatments involved the same equipment, e.g., treatments are two synthetic compounds being produced by the same equipment. Residual material from the first compound acts as a catalyst for the second compound but reverse is not true. Under complete randomization the bias component is smaller than under

restricted randomization, for all $\rho \neq 0$ (in the range of interest).

(4) Run-order effects are nonadditive. When treatment 1 is followed by treatment 1 or treatment 2 run-order effects have higher negative serial correlation, and when treatment 2 is followed by treatment 1 run-order effects have higher correlation, (a=-1, b=-1, c=1, d=0).

This is an unusual case where no simple example is apparent. Under complete randomization the bias component may be **larger** than under restricted randomization for $\rho \neq 0$ (in the range of interest). The absolute value of the bias component is larger for negative values of ρ than for corresponding positive values of ρ. If one had enough domain knowledge to recognize a situation such as this, where restricting randomization would reduce bias, an experiment would be superfluous.

From the graph of the total bias component based on scenarios (1), (2), and (3) in **Figure 2**, the power of randomization is apparent. In the additive case (scenario (1)), complete randomization leads to unbiased tests whereas restricted randomization leads to a sizable bias component. Even when the effects of treatment and run-order are nonadditive, i.e., the assumptions of ANOVA are violated, complete randomization exhibits less bias than restricted randomization (scenarios (2) & (3)).

Under complete randomization there is usually complete or substantial canceling out of effects compared with restricted randomization (e.g., the shaded and nonshaded submatrices of the correlation matrices of the previous examples tend to be more equal under complete randomization). Under complete randomization the proportion of correlations of specific lags is the same for elements with positive and negative coefficients. Bias components of this type are called *weak* bias components. Under restricted randomization the proportion of correlations of specific lags is **not** the same for elements with positive and

negative coefficients. Bias components of this type are called *strong* bias components. While a weak bias component can be larger than a strong bias component, this occurs for unusual correlation structures, as in scenario (4).

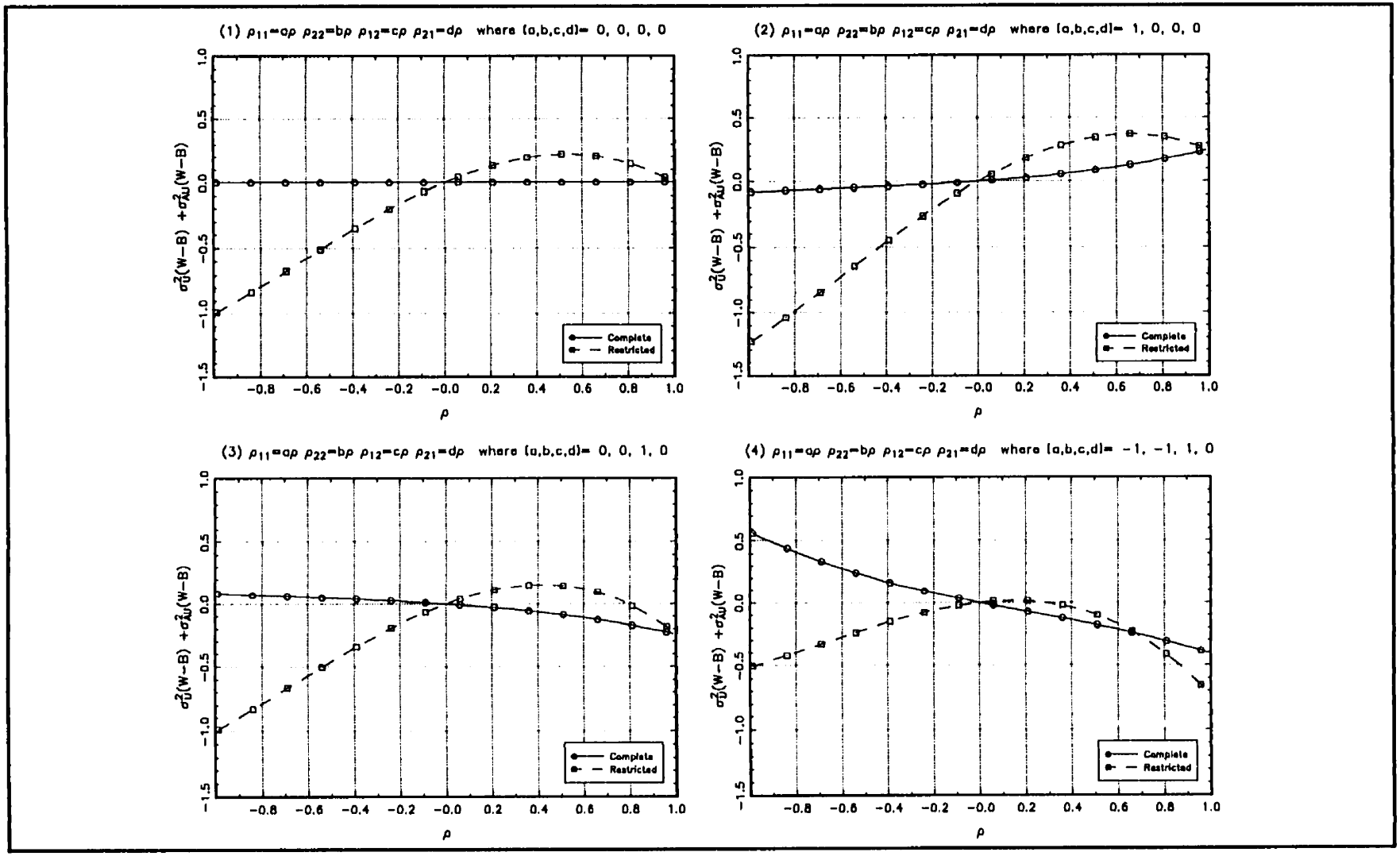


Figure 2 Total bias simulated for a One-factor Design with 2 levels and 2 replications assuming an AR(1) structure for run-order effects.

2.2.4 Summary of the One Factor Example

The one factor example, because of its simplicity, demonstrates details of the derivation and yields some interesting results. Under complete randomization, additive run-order effects lead to unbiased tests. Nonadditive run-order effects lead to a weak bias for tests. When randomization is restricted the test for the treatment effect, A, is biased even assuming additivity of treatment and run-order effects. The test for A has a strong bias component that is a function of the main effects of run-order, U. Nonadditivity between treatment and run-order effects introduces additional strong bias components ignored in previous work (Anderson and McLean 1974a, 1974b; Lorenzen 1984; Lorenzen and Anderson 1993a). These results are summarized below, where the benefit of randomization is apparent.

Table XI Bias summary for One-factor design. W: Weak, S: Strong

	Bias Components	
Restriction on:	**U**	**AU**
None	-	W
A	S	S

2.3 EXTENDED NOTATION FOR MULTIPLE RESTRICTIONS

The notation for representing the effects of restricted randomization is extended by directly modeling the segment and within-segment structure. The previous examples for the one-factor design modeled run-order effects as a function of U (U_{mn} and $\alpha U_{i@mn}$). This was a clear way to introduce the methodology, however, representing multiple restrictions on randomization by multiple restriction terms will be convenient, i.e., a term for each subscript that indexes run-order. With each restriction represented by a term in the model, rather than an additional subscript on an existing term, effects of specific restrictions are more clearly delineated. After defining the new notation, we revisit the one-factor design with restricted randomization to show the equivalency of the two representations.

For our purposes, multiple restrictions must be hierarchical in nature, that is, have a nesting relationship. Once a factor defines a restriction, subsequent restrictions are applied within the previously defined segments. For example, consider a factorial design with three factors, A, B, and C. Suppose a run order restriction is defined by factor A, resulting in I segments with JK run-orders within each segment. A second restriction could be defined on combinations of B and C **within** each level of A.

For each factor that defines a hierarchical restriction, define a segment factor, nested in any previously defined segment factors. The segment factor will have the same number of levels as the factor that defined the restriction. After all such segment factors have been defined, define a final segment factor, nested in all previous segment factors, with the same number of levels as there are runs. Construct the "true" effects model representing all the usual design factors and segment factors, and appropriate interactions between. Note that there will be no interactions among segment factors because they are fully nested.

Multiple restriction terms can be viewed as a redefinition of the run-order effect, U, in terms of hierarchically nested effects that correspond to segments. For example, with two restrictions U can be modeled as:

$$U_{mno} = \eta_m + \kappa_{mn} + \lambda_{mno}$$

$$\text{where } \eta_m = U_{m\cdot\cdot}\,,\ \kappa_{mn} = U_{mn\cdot}\,,\ \lambda_{mno} = U_{mno} - \eta_m - \kappa_{mn}$$

Equivalently, U can be expressed in matrix form as:

$$U = P_\eta \eta + P_\kappa \kappa + \lambda$$

where P_η and P_κ are design matrices relating U to η and κ, and
$\eta = c_\eta U$, $\kappa = c_\kappa U$, $\lambda = U - P_\eta \eta - P_\kappa \kappa$
with c_i defined to average within appropriate segments defined by U

Consider, for example, a two-factor design with fixed factors A and B, with two and three levels respectively and two replications. Suppose that the following run-order, or segment, restrictions are defined: Restrict on factor A, and restrict on factor B within A. Accordingly we define two segment factors, say H and K, with two and three levels respectively. A final segment factor is defined, Λ, with 12 levels. The "true" model over which the expectation is to be taken is:

$$\begin{aligned} z = X_U U + \epsilon &= X_U[P_\eta \eta + P_\kappa \kappa + \lambda] + \epsilon \\ &= X_U P_\eta \eta + X_U P_\kappa \kappa + X_U \lambda + \epsilon \\ &= X_\eta \eta + X_\kappa \kappa + X_\lambda \lambda + \epsilon \end{aligned}$$

The covariance of **U** can be expressed as:

$$\Sigma_U = P_\eta \Sigma_\eta P_\eta' + P_\kappa \Sigma_\kappa P_\kappa' + \Sigma_\cdot$$

$$\text{where } \Sigma_\cdot = \Sigma_\lambda + \left[P_\eta \Sigma_{\eta\kappa} P_\kappa + P_\eta \Sigma_{\eta\lambda} + P_\kappa \Sigma_{\kappa\lambda}\right] + \left[P_\eta \Sigma_{\eta\kappa} P_\kappa + P_\eta \Sigma_{\eta\lambda} + P_\kappa \Sigma_{\kappa\lambda}\right]'$$

$$\text{with } \Sigma_\eta = c_\eta \Sigma_U c_\eta'\,,\ \Sigma_\kappa = c_\kappa \Sigma_U c_\kappa'\,,\ \Sigma_\lambda = \Sigma_U - P_\eta \Sigma_\eta P_\eta' - P_\kappa \Sigma_\kappa P_\kappa'$$

The covariance of any terms involving U, such as AU, can be similarly expressed as a function of η, κ, and λ. The covariance of z is then expressed as:

$$\Sigma_z = X_U \Sigma_U X_U'$$

The EMS for the terms in the assumed model (the one to be analyzed once data is gathered) is taken over the true model utilizing z and Σ_z as defined above.

An Example of the One-factor ANOVA using notation for multiple restrictions

The results for restricted randomization were given in **Table X** on page 45, where run-order was modeled with a single term with multiple subscripts. Results using multiple terms, one for each subscript, are given in **Table XII**. Assuming additivity, the test for A is biased by the segment main effect. Under nonadditivity additional bias exists as a result of treatment-segment nonadditivity.

Table XII EMS for the One-factor design- restriction on A, using new notation for multiple restrictions

Case 3.1: No Run-order effects (Usual ANOVA)
A: $\sigma^2_\epsilon + J\Phi(A)$
E: σ^2_ϵ
Case 3.2: Run-order effects are additive
A: $\sigma^2_\epsilon + \sigma^2_\kappa(D-W) + J\sigma^2_\eta(W-B) + J\Phi(A)$
E: $\sigma^2_\epsilon + \sigma^2_\kappa(D-W)$
Case 3.3: Run-order effects are nonadditive
A: $\sigma^2_\epsilon + \sigma^2_\kappa(D-W) + \sigma^2_{A\kappa}(D-W) + J\sigma^2_\eta(W-B) + J\sigma^2_\kappa(W-B) + J\sigma^2_{A\eta}(W-B) + J\sigma^2_{A\kappa}(W-B) + J\Phi(A)$
E: $\sigma^2_\epsilon + \sigma^2_\kappa(D-W) + \sigma^2_{A\kappa}(D-W)$

COMPONENT DEFINITION

$$\sigma^2_{\eta}(W-B) = I^{-1} \sum_{m=m'} \sigma_{m,m'} - (I(I-1))^{-1} \sum_{m \neq m'} \sigma_{m,m'}$$

$$\sigma^2_{\kappa}(W-B) = (IJ(J-1))^{-1} \sum_{m=m'} \sum_{n \neq n'} \sum \sum \sigma_{mn,m'n'} - (I(I-1)J^2)^{-1} \sum_{m \neq m'} \sum_{n \; n'} \sum \sum \sigma_{mn,m'n'}$$

$$\sigma^2_{A\eta}(W-B) = (I^2)^{-1} \sum_{i=i'} \sum_{m=m'} \sum \sum \sigma_{i@m,i'@m'} - (I(I-1)I(I-1))^{-1} \sum_{i \neq i'} \sum_{m \neq m'} \sum \sum \sigma_{i@m,i'@m'}$$

$$\sigma^2_{A\kappa}(W-B) = (I^2J(J-1))^{-1} \sum_{i=i'} \sum_{m=m'} \sum_{n \neq n'} \sum \sum \sum \sigma_{i@mn,i'@m'n'} - (I^2(I-1)J^2)^{-1} \sum_{i=i'} \sum_{m \neq m'} \sum_{n \; n'} \sum \sum \sum \sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{\kappa}(D-W) = (IJ)^{-1} \sum_{m=m'} \sum_{n=n'} \sum \sum \sigma_{mn,m'n'} - (IJ(J-1))^{-1} \sum_{m=m'} \sum_{n \neq n'} \sum \sum \sigma_{mn,m'n'}$$

$$\sigma^2_{A\kappa}(D-W) = (IJK)^{-1} \sum_{i=i'} \sum_{m=m'} \sum_{n=n'} \sum \sum \sum \sigma_{i@mn,i'@m'n'} - (IJK(K-1))^{-1} \sum_{i=i'} \sum_{m=m'} \sum_{n \neq n'} \sum \sum \sum \sigma_{i@mn,i'@m'n'}$$

Table XII (run-order modeled by multiple terms) was derived as an equivalent expression of **Table X** (run-order modeled by a single term with multiple subscripts). This equivalence can be shown, for example, between

$\sigma^2_U(W\text{-}B)$ and $[\sigma^2_\eta(W\text{-}B) + \sigma^2_\kappa(W\text{-}B)]$.

The elements of Σ_η and Σ_κ are defined respectively as:

$$\sigma_{\eta:m,m'} = J^{-2}\sum_{n}\sum_{n'}\sigma_{U:mn,m'n'}$$

$$\sigma_{\kappa:mn,m'n'} = \sigma_{U:mn,m'n'} - \sigma_{\eta:m,m'}$$

The bias components defined in terms of segment and within-segment effects are:

$$\sigma^2_\eta(W\text{-}B) = I^{-1}\sum_{m=m'}\sum\sigma_{\eta:m,m'} - (I(I-1))^{-1}\sum_{m\neq m'}\sum\sigma_{\eta:m,m'}$$
$$= (IJ^2)^{-1}\sum_{m=m'}\sum_{n}\sum_{n'}\sum\sigma_{U:mn,m'n'} - (I(I-1)J^2)^{-1}\sum_{m\neq m'}\sum_{n}\sum_{n'}\sum\sigma_{U:mn,m'n'}$$

$$\sigma^2_\kappa(W\text{-}B) = \left[(IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sigma_{\kappa:mn,m'n'}\right] - \left[(I(I-1)J^2)^{-1}\sum_{m\neq m'}\sum_{n}\sum_{n'}\sum\sigma_{\kappa:mn,m'n'}\right]$$
$$= \left[(IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sigma_{U:mn,m'n'} - (IJ^2)^{-1}\sum_{m=m'}\sum_{n}\sum_{n'}\sum\sigma_{U:mn,m'n'}\right]$$
$$- \left[(I(I-1)J^2))^{-1}\sum_{m\neq m'}\sum_{n}\sum_{n'}\sum\sigma_{U:mn,m'n'} - (I(I-1)J^2)^{-1}\sum_{m\neq m'}\sum_{n}\sum_{n'}\sum\sigma_{U:mn,m'n'}\right]$$
$$= \left[(IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sigma_{U:mn,m'n'} - (IJ^2)^{-1}\sum_{m=m'}\sum_{n}\sum_{n'}\sum\sigma_{U:mn,m'n'}\right] - [\,0\,]$$

The sum of the above bias components is equivalent to $\sigma^2_U(W\text{-}B)$:

$$\sigma^2_\kappa(W\text{-}B) + \sigma^2_\eta(W\text{-}B) =$$
$$= (IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sigma_{U:mn,m'n'} - (I(I-1)J^2)^{-1}\sum_{m\neq m'}\sum_{n}\sum_{n'}\sum\sigma_{U:mn,m'n'}$$
$$= \sigma^2_U(W\text{-}B)$$

2.4 A GENERAL METHOD

The "brute force" approach used to find the moments of $\boldsymbol{T}$ in the preceding one-factor example can be generalized and used for many different restriction methods, and even for unbalanced data. It does not appear too difficult in the example because there are so few possible $\boldsymbol{T}$ matrices (24 under complete randomization) and they are of reasonable size (4x8). However, as more complex designs are considered, a more sophisticated approach is apparently needed. For instance, in the more complex case of two factors each at two levels with two replications there are 40,320 $\boldsymbol{T}$ matrices with size 8x32 (under complete randomization), which is clearly not amenable to the "brute force" approach.

The general method presented for solving for the moments of $\boldsymbol{T}$ allows for any number of factors and restrictions on their randomization assuming the restrictions are applied hierarchically. The necessary design structure is set up and the marginal and joint probabilities of realizing potential observations are solved for complete and restricted randomization.

2.4.1 Notation

We will now generalize the notation used earlier. In particular we allow for K factors, the first K_1 of which are restricted in their randomization.

Let:

K_1 = # of restricted factors
K_2 = # of non-restricted factors
$K = K_1+K_2$ = # of factors in the experiment

$F_1,\ldots,F_{K_1},F_{K_1+1},\ldots,F_K$ = factors $1, \ldots, K$. The first K_1 are hierarchically restricted. The last K_2 are not restricted
F_{K+1} = Replicate or Error Factor
$L_1,\ldots,L_{K+1}$ = # of levels of factor $F_1,\ldots,F_{K+1}$
$f_1,\ldots f_{K+1}$ = index of factor $F_1,\ldots,F_{K+1}$, $1 \le f_i \le L_i$

The notation for indexing run-order uses segments (sets of run-orders within the same level of a restricted factor) and run-order within segments.

$S_1,\ldots,S_{K_1},S_{K_1+1},\ldots,S_{K+1}$ = run-order factors. The first K_1 correspond to segments. The last K_2+1 are dummy factors that index run-order within segments.
$L_1,\ldots,L_{K+1}$ = # of levels of segment factor $S_1,\ldots,S_{K+1}$
$s_1,\ldots,s_{K+1}$ = index of segment factor $S_1,\ldots,S_{K+1}$, $1 \le s_i \le L_i$

Then

$\prod_{i=1}^{K} L_i$ = # of treatment combinations (factor level combinations)
$\prod_{i=1}^{K+1} L_i$ = # of run-orders

We can now write the linear model:

$$y = T z$$

where

$$\mathbf{y} = \begin{bmatrix} y_{1,1,\ldots,1} \\ y_{1,1,\ldots,2} \\ \vdots \\ y_{L_1,L_2,\ldots,L_{K-1}} \end{bmatrix}$$

A vector of realizable observations with factors and replicates in lexicographic order. **y** is size $\left(\prod_{i=1}^{K-1} L_i\right)$ x 1.

$$\mathbf{z} = \begin{bmatrix} z_{1,1,\ldots,1 \,@\, 1,1,\ldots,1} \\ z_{1,1,\ldots,1 \,@\, 1,1,\ldots,2} \\ \vdots \\ z_{L_1,L_2,\ldots,L_K \,@\, L_1,L_2,\ldots,L_{K-1}} \end{bmatrix}$$

A vector of potential observations when treatment combination $f_1, f_2, \ldots, f_K$ is applied to run-order $s_1, s_2, \ldots, s_K$. **y** is size $\left(\left(\prod_{i=1}^{K-1} L_i\right)\left(\prod_{i=1}^{K} L_i\right)\right)$ x 1

$\boldsymbol{T}$

A selection matrix indicating which potential observations are realized. $\boldsymbol{T}$ is size $\left(\prod_{i=1}^{K-1} L_i\right)$ x $\left(\left(\prod_{i=1}^{K-1} L_i\right)\left(\prod_{i=1}^{K} L_i\right)\right)$

2.4.2 Obtaining moments of T

We saw earlier (17) that to find the expected value of a quadratic form we need to evaluate $E(t_{f_1 f_2 \cdots f_K @ s_1, s_2 \cdots s_{K-1}})$, a column of E($T$), and

$E(t_{f_1 f_2 \cdots f_K @ s_1, s_2 \cdots s_{K-1}} t'_{f'_1 f'_2 \cdots f'_K @ s'_1, s'_2 \cdots s'_{K-1}})$, an outer product of the columns of T.

Theorem 1.1

$$E(T) = \frac{I_{\left(\prod_{i=1}^{K} L_i\right)} \otimes (L_{K-1}) J_{\left(\prod_{i=1}^{K+1} L_i\right)}}{\left(\prod_{i=1}^{K-1} L_i\right)}$$

where I_a is an identity matrix of size a. (Any matrix with only one subscript is assumed square).
$_aJ_b$ is a matrix of ones of size $a \times b$
$\otimes$ is the Kronecker product. (Each element of the first operand is replaced by its product with the second operand).

Proof:

For a given treatment combination there are L_{K-1} realizable observations (eg. **Figure 3** boxed submatrix of **y**) and $\prod_{i=1}^{K-1} L_i$ potential observations (eg. **Figure 3** boxed submatrix of **z**). The potential observations are mapped to the realizable observations by T^*, an L_{K-1} by $\prod_{i=1}^{K-1} L_i$ indicator matrix (eg. **Figure 3** boxed submatrix of T). Each of the $\prod_{i=1}^{K-1} L_i$ potential

observations is mapped to a realizable observation with equal probability $\frac{1}{\prod_{i=1}^{K-1} L_i}$, yielding

$E(T') = \left({}^{(L_{K-1})}J_{\left(\prod_{i=1}^{K-1}\right)} \right) \left(\frac{1}{\prod_{i=1}^{K-1} L_i} \right)$. This mapping is identical for each of the $\prod_{i=1}^{K} L_i$ treatment

combinations, thus, $E(T) = \left(I_{\prod_{i=1}^{K} L_i} \right) \otimes (E(T')) = \left(I_{\prod_{i=1}^{K} L_i} \right) \otimes \left(\frac{{}^{(L_{K-1})}J_{\left(\prod_{i=1}^{K-1} L_i\right)}}{\prod_{i=1}^{K-1} L_i} \right)$.

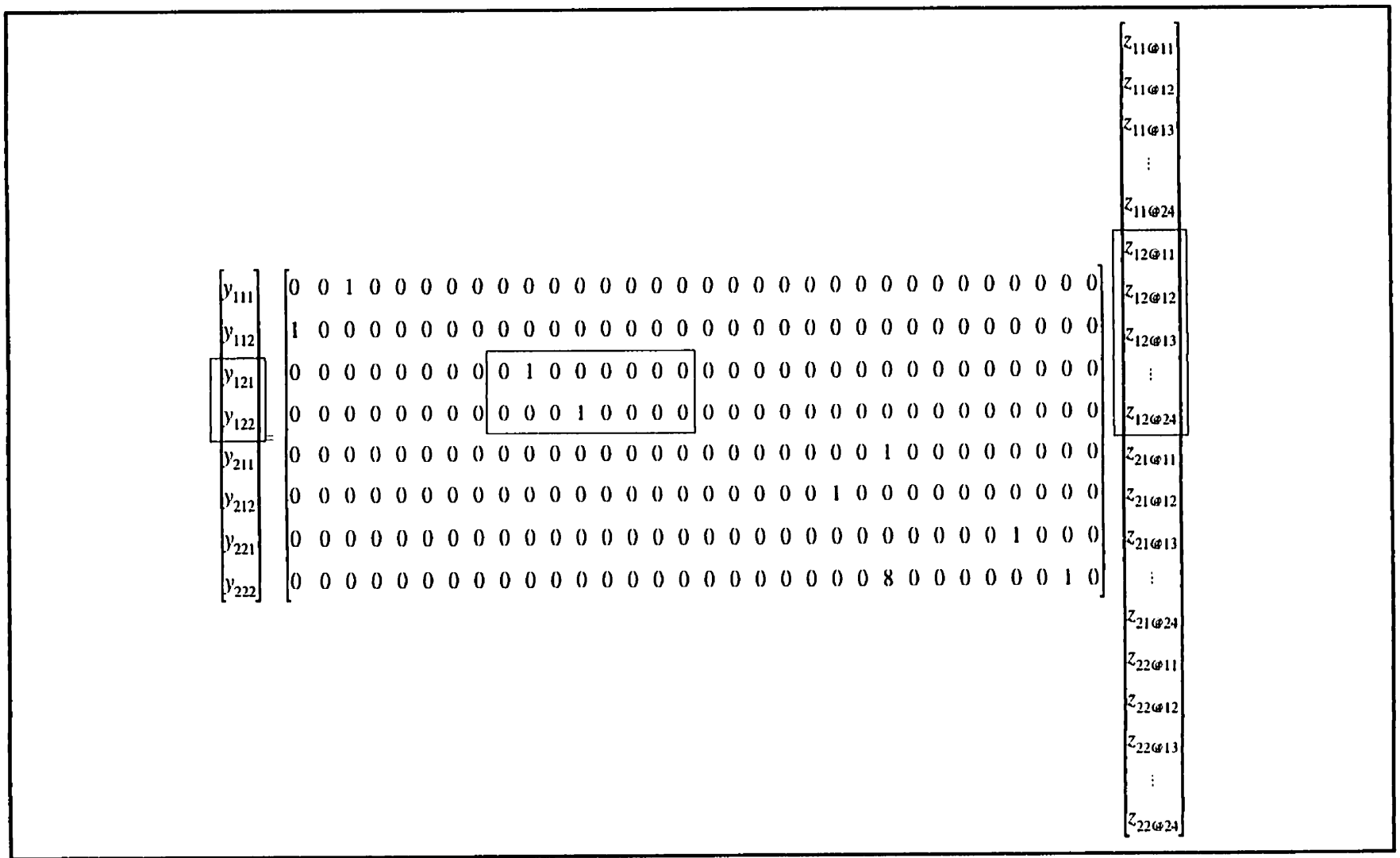


Figure 3 Example of a realized experiment for a Two-factor design restricted on A. Boxed submatrices represent mapping from z to y

Theorem 1.2:

$$E(t_{f_1 f_2 \cdots f_K @ s_1 s_2 \cdots s_{K-1}} \; t'_{f'_1 f'_2 \cdots f'_K @ s'_1 s'_2 \cdots s'_{K-1}}) = \boldsymbol{E}_{rc} \otimes \boldsymbol{P}$$

where E_{rc} is a $\left(\prod_{i=1}^{K} L_i\right) \times \left(\prod_{i=1}^{K} L_i\right)$ elementary matrix with a 1 in row r column c with r and c given by

$$r = f_K + \sum_{i=1}^{K-1} (f_i - 1) \prod_{j=i+1}^{K} L_j$$

$$c = f'_K + \sum_{i=1}^{K-1} (f'_i - 1) \prod_{j=i+1}^{K} L_j$$

(Continued on the next page)

and P is determined according to the 4 possible cases as follows:

(1) *if* $(f_i=f_i' \ \forall\ i,\ 1\le i\le K)$ *and* $(s_i=s_i' \ \forall\ i,\ 1\le i\le K+1)$
(i.e.) same treatment is applied to same run-order

$$\textit{then}\quad P = \left(\frac{I_{L_{K+1}}}{\prod_{i=1}^{K+1} L_i}\right)$$

(2) *if* $(f_i=f_i' \ \forall\ i,\ 1\le i\le K)$ *and* $(s_i=s_i' \ \forall\ i,\ 1\le i\le K_1)$ *and*
$(s_i\neq s_i'$ *for at least one* $i,\ K_1+1\le i\le K+1)$
(i.e.) same treatment combination is applied to a different run-order within the same lowest level segment

$$\textit{then}\quad P = \frac{\left(I_{L_{K+1}} - I_{L_{K+1}}\right)}{\left(\left(\prod_{i=K_1+1}^{K+1} L_i\right)-1\right)\left(\prod_{i=1}^{K+1} L_i\right)}$$

(3) *if* $(f_i=f_i' \ \forall\ i,\ 1\le i\le K_1)$ *and* $(f_i\neq f_i'$ *for at least one* $i,\ K_1+1\le i\le K)$ *and*
$(s_i=s_i' \ \forall\ i,\ 1\le i\le K_1)$ *and* $(s_i\neq s_i'$ *for at least one* $i,\ K_1+1\le i\le K+1)$
(i.e.) different treatment combination is applied to a different run-order within the same lowest level segment

$$\textit{then}\quad P = \frac{\left(I_{L_{K+1}}\right)}{\left(\left(\prod_{i=K_1+1}^{K+1} L_i\right)-1\right)\left(\prod_{i=1}^{K+1} L_i\right)}$$

(4) *if* $(f_i\neq f_i'$ *for at least one* $i,\ 1\le i\le K_1)$ *and* $(s_i\neq s_i'$ *for at least one* $i,\ 1\le i\le K_1)$
and $(r=r')$ where

r equals the subscript of the first inequality in $(f_i=f_i')$, $(1\le r\le K_1)$
r'equals the subscript of the first inequality in $(s_i=s_i')$, $(1\le r\le K_1)$

(i.e) different treatment combination applied to a different run-order in a different segment

$$\textit{then}\quad P = \frac{\left(I_{L_{K+1}}\right)}{\left(L_r-1\right)\left(\prod_{i=r+1}^{K+1} L_i\right)\left(\prod_{i=1}^{K+1} L_i\right)}$$

Proof:

The column vector t_i, a column of T, has a single element equal to 1- the rest being zero. This nonzero component can only occur in one of the L_{K-1} rows that correspond to the treatment combination being mapped from **z** to **y**. Call this potentially nonzero subvector t_i^*. The outer product of $t_i^* t_{i'}^{*\prime}$ is size L_{K-1} x L_{K-1} with $E(t_i^* t_{i'}^{*\prime}) = P$. The rows and columns of P are indexed by the replication factor L_{K+1}.

E_{rc} is a square elementary matrix with the number of rows and number of columns equal to the number of treatment combinations ($\prod_{i=1}^{K} L_i$ x $\prod_{i=1}^{K} L_i$). A 1 indicates the joint treatment combination associated with t_i^* and $t_{i'}^*$. It follows that

$E(t_i t_{i'}^{\prime}) = E_{rc} \otimes E(t_i^* t_{i'}^{*\prime}) = E_{rc} \otimes P$.

To find **P**, first define the events:

A = {treatment combination $f_1 f_2 \ldots f_K$ assigned to run-order $s_1 s_2 \ldots s_{K-1}$}

B = {treatment combination $f_1' f_2' \ldots f_K'$ assigned to run-order $s_1' s_2' \ldots s_{K-1}'$}

Let p be defined as the probability of joint realization, i.e.:

$p = P(A \text{ and } B) = P(B|A)\, P(A)$

S is an L_{K-1} x L_{K-1} matrix with nonzero elements defined by possible nonzero values of t_i^* and $t_{i'}^*$. Let the nonzero values of S equal the reciprocal of the number of nonzero elements (all possibilities are equally likely). Then $P = S\, p$

Four general cases give rise to $\boldsymbol{P}$:

(1) Same treatment combination, same run-order.

There are $\prod_{i=1}^{K} L_i$ treatment combinations so $P(A) = \frac{1}{\prod_{i}^{K} L_i}$. (This is constant for cases (1) through (4)). Since A=B in this case P(B|A)=1, therefore $p = \frac{1}{\prod_{i}^{K} L_i}$.

Only diagonal elements of $\boldsymbol{P}$ are nonzero because in we are dealing with the same run-order, and hence the same replication, so $S = \frac{I_{L_{K-1}}}{L_{K-1}}$ and

$$P = S\,p = \left(\frac{I_{L_{K-1}}}{L_{K-1}}\right)\left(\frac{1}{\prod_{1}^{K} L_i}\right) = \frac{I_{L_{K-1}}}{\prod_{1}^{K-1} L_i}.$$

(2) Same treatment combination, different run-order in the same segment.

Given A, there are $(L_{K-1}-1)$ ways to realize B out of $\left(\left(\prod_{i=K_1-1}^{K} L_i\ L_{K-1}\right)-1\right)$ total possibilities. Therefore, $p = P(B|A)\,P(A) = \frac{(L_{K-1}-1)}{\left(\left(\prod_{i=K_1-1}^{K} L_i\ L_{K-1}\right)-1\right)}\left(\frac{1}{\prod_{i=1}^{K} L_i}\right)$.

Only off-diagonal elements of $\boldsymbol{P}$ are nonzero because we are dealing with a

different run-order, and hence a different replication, so

$$S = \frac{J_{L_{K-1}} - I_{L_{K-1}}}{L_{K-1}\left(L_{K-1}-1\right)} \text{ and } P = Sp = \frac{\left(J_{L_{K-1}} - I_{L_{K-1}}\right)}{\left(\left(\prod_{i=K_1-1}^{K-1} L_i\right)-1\right)\left(\prod_{i=1}^{K-1} L_i\right)}.$$

(3) **Different treatment combination, different run-order in the same segment.**

Given A, there are L_{K-1} ways to realize B out of $\left(\left(\prod_{i=K_1-1}^{K} L_i\ L_{K-1}\right)-1\right)$ total possibilities. $p = P(B|A)\,P(A) = \frac{L_{K-1}}{\left(\prod_{i=K_1-1}^{K-1} L_i\right)-1}\left(\frac{1}{\prod_{i=1}^{K} L_i}\right)$. Since the run-orders are

under different treatment combinations all elements of P are nonzero because any replicate in the first treatment combination may be realized with any replicate in the second treatment combination, hence $S = \frac{J_{L_{K-1}}}{\left(L_{K-1}\right)^2}$ and

$$P = Sp = \frac{\left(J_{L_{K-1}}\right)}{\left(\left(\prod_{i=K_1-1}^{K-1} L_i\right)-1\right)\left(\prod_{i=1}^{K-1} L_i\right)}.$$

(4) **Different segment, any treatment combination, where r is the subscript of the first segment to be different.**

Given A, there are L_{K-1} way to realize B out of $(L_r-1)\prod_{i=r-1}^{K-1} L_i$ total possibilities.

$p = P(B|A)\,P(A) = \dfrac{L_{K-1}}{\left((L_r-1)\prod_{i=r-1}^{K-1} L_i\right)}\left(\dfrac{1}{\prod_{i=1}^{K} L_i}\right)$. Since the run-orders are in

different treatment combinations, all elements of P are nonzero because any replicate in the first treatment combination may be realized with any replicate in the second treatment combination , so $S = \dfrac{J_{L_{K-1}}}{(L_{K-1})^2}$ and

$$P = Sp = \frac{\left(J_{L_{K-1}}\right)}{(L_r-1)\left(\prod_{i=r-1}^{K-1} L_i\right)\left(\prod_{i=1}^{K-1} L_i\right)}.$$

2.4.3 One-factor Example Revisited

We illustrate the application of the previous results by first considering a one-factor example under complete and restricted randomization

2.4.3.1 Complete Randomization

Consider a one-factor design with a single factor with two levels and two replications under complete randomization. Then:

$$
\begin{aligned}
K_1 &= 0 \\
K_2 &= 1 \\
K &= 1
\end{aligned}
$$

$$
\begin{aligned}
F_1 &= \text{factor A} \\
F_2 &= \text{replicates} \\
L_1 &= 2 \quad (\#\text{ of levels of factor A}) \\
L_2 &= 2 \quad (\#\text{ of replicates}) \\
f_1 &= \text{index for level of A} \\
f_2 &= \text{index for level of replicate}
\end{aligned}
$$

$$
\begin{aligned}
S_1,\ldots,S_2 &= \text{segment factors} \\
L_1,\ldots,L_2 &= \#\text{ of levels of } S_1,\ldots,S_2
\end{aligned}
$$

Consequently, the treatments are indexed by f_1 where f_1 takes on the values 1 and 2. These treatments are applied to run-units labeled $s_1 s_2$ which take on the values 11, 12, 21, 22. Because randomization is not restricted, there is only one segment consisting of four run-orders.

The E(T) is:

$$
E(T) = \frac{I_{\left(\prod_{i=1}^{K} L_i\right)} \otimes (L_{K-1}) J_{\left(\prod_{i=1}^{K-1} L_i\right)}}{\left(\prod_{i=1}^{K-1} L_i\right)} = \frac{I_2 \otimes {}_2J_4}{4}
$$

$$
= \begin{bmatrix}
.25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\
.25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & .25 & .25 & .25 & .25 \\
0 & 0 & 0 & 0 & .25 & .25 & .25 & .25
\end{bmatrix}
$$

which matches **(29)** on page 30.

The value of $E(t_{f_1@s_1s_2} t'_{f_1'@s_1's_2'})$ is dependent on which of the four scenarios it corresponds to:

1. **Same** run-order gets the **same** treatment. For example, the first unit run gets treatment one:

$$E(t_{f_1@s_1s_2} t'_{f_1'@s_1's_2'}) = E(t_{1@11} t'_{1@11})$$

$\mathbf{E}_{rc}$ is given by:

$$\boldsymbol{E}_{rc} = \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix}$$

where r=1 and c=1

and $\boldsymbol{P}$ is defined as:

$$\boldsymbol{P} = \left(\frac{\boldsymbol{I}_{L_{K-1}}}{\prod_{i=1}^{K-1} L_i} \right) = \frac{\boldsymbol{I}_2}{4} = \begin{bmatrix} .25 & 0 \\ 0 & .25 \end{bmatrix}$$

So,

$$\begin{aligned} E(t_{1@11} t'_{1@11}) &= \boldsymbol{E}_{rc} \otimes \boldsymbol{P} \\ &= \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix} \otimes \begin{bmatrix} .25 & 0 \\ 0 & .25 \end{bmatrix} \\ &= \begin{bmatrix} .25 & 0 & 0 & 0 \\ 0 & .25 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \end{aligned}$$

2. **Different** run-order within the same segment gets the **same** treatment. For example, the

first unit run gets treatment one and the second unit run gets treatment one.

$$E(t_{f_1@s_1s_2}\, t'_{f_1'@s_1's_2'}) = E(t_{1@11}\, t'_{1@12})$$

$\mathbf{E}_{rc}$ is given by:

$$\boldsymbol{E}_{rc} = \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix}$$

where r=1 and c=1

and $\boldsymbol{P}$ is defined as:

$$\boldsymbol{P} = \frac{\left(\boldsymbol{J}_{L_{K-1}} - \boldsymbol{I}_{L_{K-1}}\right)}{\left(\left(\prod_{i=K_1-1}^{K-1} L_i\right) - 1\right)\left(\prod_{i=1}^{K-1} L_i\right)} = \frac{(\boldsymbol{J}_2 - \boldsymbol{I}_2)}{((4)-1)(4)} = \begin{bmatrix} 0 & .083 \\ .083 & 0 \end{bmatrix}$$

So,

$$\begin{aligned} E(t_{1@11}\, t'_{1@12}) &= \boldsymbol{E}_{rc} \otimes \boldsymbol{P} \\ &= \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix} \otimes \begin{bmatrix} 0 & .083 \\ .083 & 0 \end{bmatrix} \\ &= \begin{bmatrix} 0 & .083 & 0 & 0 \\ .083 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \end{aligned}$$

which matches (**31**) on page 31.

3. **Different** run-unit gets a **different** treatment in the **same** segment. For example, the first unit run gets treatment one and the second unit run gets treatment two.

$$E(t_{f_1@s_1s_2}\, t'_{f_1'@s_1's_2'}) = E(t_{1@11}\, t'_{2@12})$$

$\mathbf{E}_{rc}$ is given by:

$$E_{rc} = \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix}$$

where r=1 and c=2

and P is defined as:

$$P = \frac{\left(J_{L_{K-1}}\right)}{\left(\left(\prod_{i=K_1-1}^{K-1} L_i\right)-1\right)\left(\prod_{i=1}^{K-1} L_i\right)} = \frac{J_2}{12} = \begin{bmatrix} .083 & .083 \\ .083 & .083 \end{bmatrix}$$

So,

$$E(t_{1@11}\, t'_{2@12}) = E_{rc} \otimes P$$

$$= \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix} \otimes \begin{bmatrix} .083 & .083 \\ .083 & .083 \end{bmatrix}$$

$$= \begin{bmatrix} .083 & .083 & 0 & 0 \\ .083 & .083 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

4. **Different** unit run gets a **different** treatment in a **different** segment. Since randomization is not restricted there is only one segment, so this case does not exist.

2.4.3.2 Restricted Randomization

Now suppose that the experiment has a run-order restriction on the factor, i.e., levels

of A are randomized, but all reps at a given level of A must be run consecutively. Then:

$$
\begin{aligned}
K_1 &= 1 \\
K_2 &= 0 \\
K &= 1
\end{aligned}
$$

$$
\begin{aligned}
F_1 &= \text{factor A} \\
F_2 &= \text{replicates} \\
L_1 &= 2 \quad (\#\text{ of levels of factor A}) \\
L_2 &= 2 \quad (\#\text{ of replicates}) \\
f_1 &= \text{index for factor A} \\
f_2 &= \text{index for replicates}
\end{aligned}
$$

$$
\begin{aligned}
S_1,\ldots,S_2 &= \text{segment factors} \\
L_1,\ldots,L_2 &= \#\text{ of levels of } S_1,\ldots,S_2
\end{aligned}
$$

Consequently, the treatments are indexed by f_1 where f_1 takes on the values 1 and 2. These treatments are applied to run-orders labeled s_1s_2 which take on the values 11, 12, 21, 22, where s_1 indexes segments and s_2 indexes run-order within segment.

The E(T) is identical to the completely randomized example:

$$
E(T) = \frac{I_{\left(\prod_{i=1}^{K} L_i\right)} \otimes (L_{K-1})J_{\left(\prod_{i=1}^{K-1} L_i\right)}}{\left(\prod_{i=1}^{K-1} L_i\right)} = \frac{I_2 \otimes {}_2J_4}{4}
$$

$$
= \begin{bmatrix}
.25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\
.25 & .25 & .25 & .25 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & .25 & .25 & .25 & .25 \\
0 & 0 & 0 & 0 & .25 & .25 & .25 & .25
\end{bmatrix}
$$

which matches **(48)** on page 41.

The value of $E(t_{f_1@s_1s_2}\, t'_{f_1'@s_1's_2'})$ is dependent on which of the four scenarios it corresponds to:

1. **Same** run-order gets the **same** treatment. For example, the first unit run gets treatment one.

$$E(t_{f_1@s_1s_2}\, t'_{f_1'@s_1's_2'}) = E(t_{1@11}\, t'_{1@11})$$

$\mathbf{E}_{rc}$ is given by:

$$\boldsymbol{E}_{rc} = \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix}$$

where r=1 and c=1

and $\boldsymbol{P}$ is defined as:

$$\boldsymbol{P} = \left(\frac{\boldsymbol{I}_{L_{K-1}}}{\prod_{i=1}^{K-1} L_i} \right) = \frac{\boldsymbol{I}_2}{4} = \begin{bmatrix} .25 & 0 \\ 0 & .25 \end{bmatrix} .$$

Hence,

$$\begin{aligned} E(t_{1@11}\, t'_{1@11}) &= \boldsymbol{E}_{rc} \otimes \boldsymbol{P} \\ &= \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix} \otimes \begin{bmatrix} .25 & 0 \\ 0 & .25 \end{bmatrix} \\ &= \begin{bmatrix} .25 & 0 & 0 & 0 \\ 0 & .25 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \end{aligned}$$

2. **Different** run-order gets the **same** treatment within the same segment. For example, the first unit run gets treatment one and the second unit run gets treatment one.

$$E(t_{f_1@s_1s_2}\, t'_{f_1'@s_1's_2'}) = E(t_{1@11}\, t'_{1@12})$$

$\mathbf{E}_{rc}$ is given by:

$$E_{rc} = \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix}$$

where r=1 and c=1

and $\boldsymbol{P}$ is defined as:

$$P = \frac{\left(J_{L_{K-1}} - I_{L_{K-1}}\right)}{\left(\left(\prod_{i=K_1-1}^{K-1} L_i\right) - 1\right)\left(\prod_{i=1}^{K-1} L_i\right)} = \frac{(J_2 - I_2)}{((2)-1)(4)} = \begin{bmatrix} 0 & .25 \\ .25 & 0 \end{bmatrix}$$

Hence,

$$E(t_{1@11}\, t'_{1@12}) = E_{rc} \otimes P$$

$$= \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix} \otimes \begin{bmatrix} 0 & .25 \\ .25 & 0 \end{bmatrix}$$

$$= \begin{bmatrix} 0 & .25 & 0 & 0 \\ .25 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

which matches **(50)** on page 42.

3. **Different** run-order gets a **different** treatment in the **same** segment. For a single factor design with restricted randomization this scenario does not exist.

4. **Different** run-order gets a **different** treatment involving a **different** segment. For example, the first unit run gets treatment one and the third unit run gets treatment two.

$$E(t_{f_1@s_1s_2}\, t'_{f'_1@s'_1s'_2}) = E(t_{1@11}\, t'_{2@21})$$

$\mathbf{E}_{rc}$ is given by:

$$E_{rc} = \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix}$$

where r=1 and c=2

and $\boldsymbol{P}$ is defined as:

$$P = \left(\frac{I_{L_{K-1}}}{\prod_{i=1}^{K-1} L_i} \right) = \frac{I_2}{4} = \begin{bmatrix} .25 & 0 \\ 0 & .25 \end{bmatrix}$$

Hence,

$$E(t_{1@11}\, t'_{2@21}) = E_{rc} \otimes P$$

$$= \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix} \otimes \begin{bmatrix} .25 & 0 \\ 0 & .25 \end{bmatrix}$$

$$= \begin{bmatrix} 0 & 0 & .25 & 0 \\ 0 & 0 & 0 & .25 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

2.5 TWO-FACTOR EXAMPLE

Using the general method it is now feasible to investigate larger and more complex designs. Results, including a brief description, an ANOVA table, and summary, are presented for a two factor design, with fixed factors A and B, according to the following restriction scenarios:

1. complete randomization,

2. restrict on a single factor (e.g. A: levels of A are randomized and then all replications at a given level of A are run consecutively in random order),
3. restrict on a factor combination (e.g. AB: AB combinations are randomized and then all replications of a given AB combination are run consecutively in random order),
4. restrict on a factor then restrict on another factor within the given levels of the first (e.g. A, B(A): levels of A are randomized and then, within each level of A, the levels of B are randomized and then all runs for the specified levels of A and B are run consecutively in random order).

Similar to the one-factor examples, three cases are considered for each of the design scenarios:

Case 1: No Run-order effects (usual ANOVA),

Case 2: Run-order effects are additive,

Case 3: Run-order effects are nonadditive.

The complexity of the underlying model and ANOVA is increased due to the number of terms involved, so the detail present in the one-factor example is not attempted. Components that shed light on the nature of tests and the conditions leading to unbiased tests are discussed in greater detail. Again we shall assume that effects that involve run-order can be modeled as random effects with some general covariance structure Σ. It is further assumed that any three factor interaction components between A, B, and U are negligible, and while shown in the EMS table for completeness, they are not discussed in detail.

The design under consideration is a complete factorial with two factors A and B with I and J levels respectively, and K replications. The ANOVA tables are specified in these general terms while, for purposes of demonstrating the basic structure of the EMS components, I, J, and K are set equal to two.

2.5.1 Complete Randomization

Consider a two-factor design with factors A and B where run-order is completely randomized. Since there is no restriction or segmentation, run-order is indexed by a single subscript:

$$z_{ij@l} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + U_l + \alpha U_{i@l} + \beta U_{i@l} + \epsilon_{ij@l}$$

where $l = 1 \ldots IJK$

Results are summarized in **Table XIX**.

Case 1: No Run-order effects (usual ANOVA)

As expected all tests for main effects and interaction are unbiased, but there must be **no** uncontrolled variables associated with time that affect the response.

Case 2: Run-order effects are additive (reduces to the usual ANOVA)

When run-order effects are additive, tests for main effects and interactions remain unbiased although MSE is inflated to due to the presence of U components. The combination of randomization and additivity result in unbiased tests for all effects. This assumption of additivity is implicit in Lorenzen (1984) and Anderson and McLean (1974a, 1974b), and serves as the underlying foundation for standard ANOVA. Lorenzen and Anderson (1993a) did comment that nonadditivity could exist but did not pursue the issue.

Case 3: Run-order effects are nonadditive

When run-order effects are nonadditive, the main effect tests for A and B are biased by AU and BU components respectively (third order interactions are assumed negligible). The form of the AU and BU bias components is the same, so only the AU component is examined in any detail. The AU bias component is a function of correlations among the $\alpha U_{i@l}$ effects:

$$\frac{\sigma^2_{AU}(W-B)}{\sigma^2_{AU}} = (I^2JK(IJK-1))^{-1}[\sum_{i\neq i'}\sum_{l\neq l'}\sum\rho_{i@l,i'@l'}] - (I(I-1)IJK(IJK-1))^{-1}[\sum_{i\neq i'}\sum_{l\neq l'}\sum\rho_{i@l,i'@l'}]$$

where σ^2_{AU} is from the diagonal of $\mathbf{\Sigma_{AU}}$

The average correlation within the same treatment must equal the average correlation in different treatments. This is a *weak* bias component, due only to the interaction between treatment and run-order, i.e., the run-order correlation is dependent on the level of treatment.

Table XIII EMS for the Two-factor design- complete randomization

Case 1: No Run-order effects (Usual ANOVA)
A: $\sigma_\epsilon^2 + JK\Phi(A)$
B: $\sigma_\epsilon^2 + IK\Phi(B)$
AB: $\sigma_\epsilon^2 + K\Phi(AB)$
E: σ_ϵ^2
Case 2: Run-order effects are additive (Usual ANOVA)
A: $\sigma_\epsilon^2 + JK\Phi(A)$
B: $\sigma_\epsilon^2 + IK\Phi(B)$
AB: $\sigma_\epsilon^2 + K\Phi(AB)$
E: σ_ϵ^2

Case 3: Run-order effects are nonadditive

A: $\sigma^2_{\epsilon*} + JK\sigma^2_{A(}(W-B) + JK\sigma^2_{AB(}(A:W-B) + JK\,\Phi(A)$

B: $\sigma^2_{\epsilon*} + IK\sigma^2_{B(}(W-B) + IK\sigma^2_{AB(}(B:W-B) + IK\,\Phi(B)$

AB: $\sigma^2_{\epsilon*} + K\sigma^2_{AB(}(AB:W-B)$

E: $\sigma^2_{\epsilon*}$ where $\sigma^2_{\epsilon*} = \sigma^2_{\epsilon} + \sigma^2_{A(}(D-W) + \sigma^2_{B(}(D-W) + \sigma^2_{AB(}(D-W)$

COMPONENT DEFINITION

$$\sigma^2_{U}(D-W) = (IJK)^{-1}\sum\sum\sigma_{l,l'} - (IJK(IJK-1))^{-1}\sum\sum\sigma_{l,l'}$$
$$l=l' \qquad\qquad l\neq l'$$

$$\sigma^2_{AU}(D-W) = (I^2JK)^{-1}\sum\sum\sum\sum\sigma_{i@l,i'@l'} - (I^2JK(IJK-1))^{-1}\sum\sum\sum\sum\sigma_{i@l,i'@l'}$$
$$i=i' \; l=l' \qquad\qquad i\neq i' \; l=l'$$

$$\sigma^2_{BU}(D-W) = (IJ^2K)^{-1}\sum\sum\sum\sum\sigma_{j@l,j'@l'} - (IJ^2K(IJK-1))^{-1}\sum\sum\sum\sum\sigma_{j@l,j'@l'}$$
$$j=j' \; l=l' \qquad\qquad j\neq j' \; l=l'$$

$$\sigma^2_{ABU}(D-W) = (IJ(IJK))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'} - (I^2J^2K(IJK-1))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'}$$
$$i=i' \; j=j' \; l=l' \qquad\qquad i\neq i' \; j\neq j' \; l=l'$$

$$\sigma^2_{AU}(W-B) = (I^2JK(IJK-1))^{-1}\sum\sum\sum\sum\sigma_{i@l,i'@l'} - (I(I-1)IJK(IJK-1))^{-1}\sum\sum\sum\sum\sigma_{i@l,i'@l'}$$
$$i=i' \; l\neq l' \qquad\qquad i\neq i' \; l\neq l'$$

$$\sigma^2_{BU}(W-B) = (IJ^2K(IJK-1))^{-1}\sum\sum\sum\sum\sigma_{j@l,j'@l'} - (J(J-1)IJK(IJK-1))^{-1}\sum\sum\sum\sum\sigma_{j@l,j'@l'}$$
$$j=j' \; l\neq l' \qquad\qquad j\neq j' \; l\neq l'$$

$$\sigma^2_{ABU}(A:W-B) = (IJ^2IJK(IJK-1))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'} - (I(I-1)J^2IJK(IJK-1))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'}$$
$$i=i' \; j\neq j' \; l\neq l' \qquad\qquad i\neq i' \; j\neq j' \; l\neq l'$$

$$\sigma^2_{ABU}(B:W-B) = (I^2JIJK(IJK-1))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'} - (I^2J(J-1)IJK(IJK-1))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'}$$
$$i\neq i' \; j=j' \; l\neq l' \qquad\qquad i\neq i' \; j\neq j' \; l\neq l'$$

$$\sigma^2_{ABU}(AB:W-B) = \left[(IJIJK(IJK-1))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'} + (I(I-1)J(J-1)IJK(IJK-1))\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'}\right] -$$
$$i=i' \; j=j' \; l\neq l' \qquad\qquad i\neq i' \; j\neq j' \; l\neq l'$$

$$\left[(IJ(J-1)IJK(IJK-1))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'} + (I(I-1)JIJK(IJK-1))\sum\sum\sum\sum\sum\sum\sigma_{ij@l,ij'@l'}\right]$$
$$i=i' \; j\neq j' \; l\neq l' \qquad\qquad i\neq i' \; j=j' \; l\neq l'$$

2.5.2 Randomization restricted on a main effect: A

Consider a factorial design involving factors A and B with a run-order restriction on A. Once a level of factor A is randomly chosen, all levels of B and all replications are run in random order before proceeding to another level of A. If the restriction were instead on the second factor B, the results would hold by simply re labeling the two factors. There are now two segments corresponding to the two levels of A. The vector of potential responses can be re written as:

$$z_{ij@mn} = \mu+\alpha_i+\beta_j+\alpha\beta_{ij}+\eta_m+\kappa_{mn}+\alpha\eta_{i@m}+\alpha\kappa_{i@mn}+\beta\eta_{j@n}+\beta\kappa_{j@mn}+\alpha\beta\eta_{ij@m}+\alpha\beta\kappa_{ij@mn}+\epsilon_{ij@mn}$$

where $m=1...I$, $n=1...JK$

Case 1: No Run-order effects (usual ANOVA)

Results are identical to Case 1.1 because there are no run-order effects. Tests for main effects and interaction are unbiased.

Case 2: Run-order effects are additive (reduces to the usual ANOVA)

When run-order effects are additive, the test for the effect of factor A is biased, while the tests for the effects of B and AB are not biased. This is the same result arrived at in Lorenzen (1984). The bias component on the test for A is a function of the correlation of the η_m and the κ_{mn} which can be rewritten as a function of U_l as shown on page 60. The bias component is the average correlation of effects within the same segment minus the average correlation of effects in different segments. If observations close in time are more highly correlated than observations farther apart in time then this is a *strong* bias component. In practice, it would usually be necessary to assume that there are no uncontrolled effects that change over time and affect the response. This is the price that must be paid for restricting randomization. Under complete randomization no such bias existed (see **Table XXI**).

If one were willing to live with a potential bias on the restricted term then it would appear that tests involving other terms are unaffected. One might conclude that restricting

factors of secondary importance leaves tests for factors of primary importance unbiased and yields potential benefits in time and cost. For example, if the main effects of B or interaction effects of AB are of primary interest, then this restricted randomization appears to be a good design candidate. Such a conclusion is premature until the nature of potential bias due to nonadditivity is examined.

Case 3: Run-order effects are non additive

When run-order effects are non additive, tests for A, B, and AB are all biased and the nature of these bias components is summarized in **Table XXII**. The additional bias components, for testing B and AB, are all weak bias components. In other words, unless the correlation is strongly dependent on the level of treatment, test for the effects of B and the interaction effects of AB are relatively unbiased. Restricting on factors of less importance creates a strong bias in tests for those factors, but creates only weak bias in tests for the effects of other factors deemed more important.

Table XIV EMS for the Two-factor design- restricted on A

Case 1: No Run-order effects (usual ANOVA)

A: $\sigma_\epsilon^2 + JK\Phi(A)$

B: $\sigma_\epsilon^2 + IK\Phi(B)$

AB: $\sigma_\epsilon^2 + K\Phi(AB)$

E: σ_ϵ^2

Case 2: Run-order effects are additive

A: $\sigma_\epsilon^2 + \sigma_\kappa^2(D-W) + JK\sigma_\eta^2(W-B) + JK\sigma_\kappa^2(W-B) + JK\Phi(A)$

B: $\sigma_\epsilon^2 + \sigma_\kappa^2(D-W) + IK\Phi(B)$

AB: $\sigma_\epsilon^2 + \sigma_\kappa^2(D-W) + K\Phi(AB)$

E: $\sigma_\epsilon^2 + \sigma_\kappa^2(D-W)$

Case 3: Run-order effects are nonadditive

$$A:\ \sigma^2_{\epsilon\bullet} + JK\sigma^2_{AB\kappa}(A:W-B) + JK\sigma^2_{AB\eta}(A:W-B) + JK\sigma^2_{B\kappa}(A:W-B) + JK\sigma^2_{B\eta}(A:W-B) + JK\sigma^2_{A\kappa}(W-B) + JK\sigma^2_{A\eta}(W-B) + JK\sigma^2_{\kappa}(W-B) + JK\sigma^2_{\eta}(W-B) + JK\Phi(A)$$

$$B:\ \sigma^2_{\epsilon\bullet} + IK\sigma^2_{AB\kappa}(B:W-B) + IK\sigma^2_{AB\eta}(B:W-B) + IK\sigma^2_{B\kappa}(B:W-B) + IK\sigma^2_{B\eta}(B:W-B) + IK\Phi(B)$$

$$AB:\ \sigma^2_{\epsilon\bullet} + K\sigma^2_{AB\kappa}(AB:W-B) + K\sigma^2_{AB\eta}(AB:W-B) + K\sigma^2_{B\kappa}(AB:W-B) + K\sigma^2_{B\eta}(AB:W-B) + K\Phi(AB)$$

$$E:\ \sigma_{\epsilon\bullet}$$

where $\sigma^2_{\epsilon\bullet} = \sigma^2_{\epsilon} + \sigma^2_{AB\kappa}(D-W) + \sigma^2_{B\kappa}(D-W) + \sigma^2_{A\kappa}(D-W) + \sigma^2_{\kappa}(D-W)$

COMPONENT DEFINITION

$$\sigma^2_{\eta}(W-B) = (I)^{-1}\sum\sum_{m=m'}\sigma_{m,m'} - (I(I-1))^{-1}\sum\sum_{m\neq m'}\sigma_{m,m'}$$

$$\sigma^2_{\kappa}(W-B) = (IJK(JK-1))^{-1}\sum\sum\sum\sum\sum_{m=m'\,n\neq n'}\sigma_{mn,m'n'} - (I(I-1)J^2K^2)^{-1}\sum\sum\sum\sum\sum_{m\neq m'\,n\,n'}\sigma_{mn,m'n'}$$

$$\sigma^2_{A\eta}(W-B) = (I^2)^{-1}\sum\sum\sum\sum\sum_{i=i'\,m=m'}\sigma_{i@m,i'@m'} - (I^2(I-1)^2)^{-1}\sum\sum\sum\sum\sum_{i\neq i'\,m\neq m'}\sigma_{i@m,i'@m'}$$

$$\sigma^2_{A\kappa}(W-B) = (I^2JK(JK-1))^{-1}\sum\sum\sum\sum\sum\sum\sum_{i=i'\,m=m'\,n\neq n'}\sigma_{i@mn,i'@m'n'} - (I^2(I-1)^2J^2K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum_{i\neq i'\,m\neq m'\,n\,n'}\sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{B\eta}(A:W-B) = (J^2I)^{-1}\sum\sum\sum\sum\sum_{j\,j'\,m=m'}\sigma_{j@m,j'@m'} - (J^2I(I-1))^{-1}\sum\sum\sum\sum\sum_{j\,j'\,m\neq m'}\sigma_{j@m,j'@m'}$$

$$\sigma^2_{B\kappa}(A:W-B) = (J^2I^2JK(JK-1))^{-1}\sum\sum\sum\sum\sum\sum\sum_{j\,j'\,m=m'\,n\neq n'}\sigma_{j@mn,j'@m'n'} - (J^2I(I-1)J^2K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum_{j\,j'\,m\neq m'\,n\,n'}\sigma_{j@mn,j'@m'n'}$$

$$\sigma^2_{AB\eta}(A:W-B) = (IJ^2I)^{-1}\sum\sum\sum\sum\sum\sum\sum_{i=i'\,j\,j'\,m=m'}\sigma_{ij@m,ij'@m'} - (I(I-1)J^2I(I-1))^{-1}\sum\sum\sum\sum\sum\sum\sum_{i\neq i'\,j\,j'\,m\neq m'}\sigma_{ij@m,ij'@m'}$$

$$\sigma^2_{AB\kappa}(A:W-B) = (IJ^2IJK(JK-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum_{i=i'\,j\,j'\,m=m'\,n\neq n'}\sigma_{ij@mn,ij'@m'n'} - (I(I-1)J^2I(I-1)J^2K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum_{i\neq i'\,j\,j'\,m\neq m'\,n\,n'}\sigma_{ij@mn,ij'@m'n'}$$

COMPONENT DEFINITION

$$\sigma^2_{B\eta}(B:W-B) = (JI^2)^{-1}\sum\sum\sum\sum\sigma_{j@m,j'@m'} - (J(J-1)I^2)^{-1}\sum\sum\sum\sum\sigma_{j@m,j'@m'}$$
$$j=j' \; m \; m' \qquad\qquad j\neq j' \; m \; m'$$

$$\sigma^2_{B\kappa}(B:W-B) = [(JIJK(JK-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (JI(I-1)J^2K^2))^{-1}\sum\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'}] -$$
$$j=j' \; m=m' \; n\neq n' \qquad\qquad j=j' \; m\neq m' \; n \; n'$$
$$[(J(J-1)IJK(JK-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (J(J-1)I(I-1)J^2K^2)^{-1}\sum\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'}]$$
$$j\neq j' \; m=m' \; n\neq n' \qquad\qquad j\neq j' \; m\neq m' \; n \; n'$$

$$\sigma^2_{AB\eta}(B:W-B) = [(IJI)^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)JI(I-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m}] -$$
$$i=i' \; j=j' \; m=m' \qquad\qquad i\neq i' \; j=j' \; m\neq m'$$
$$[(IJ(J-1)I(I-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)J(J-1)I(I-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m}]$$
$$i=i' \; j\neq j' \; m=m' \qquad\qquad i\neq i' \; j\neq j' \; m\neq m'$$

$$\sigma^2_{AB\kappa}(B:W-B) = [(IJIJK(JK-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)JI(I-1)J^2K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}] -$$
$$i=i' \; j=j' \; m=m' \; n\neq n' \qquad\qquad i\neq i' \; j=j' \; m\neq m' \; n \; n'$$
$$[(IJ(J-1)IJ^2K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)J(J-1)I(I-1)J^2K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}]$$
$$i=i' \; j\neq j' \; m=m' \; n\neq n' \qquad\qquad i\neq i' \; j\neq j' \; m\neq m' \; n \; n'$$

COMPONENT DEFINITION

$$\sigma^2_{B\eta}(AB{:}W{-}B) = [(JI)^{-1}\sum_{j=j'}\sum_{m=m'}\sum\sum\sigma_{j@m,j'@m'} + (J(J-1)I(I-1))^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sum\sigma_{j@m,j'@m'}] -$$
$$[(JI(I-1))^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum\sum\sigma_{j@m,j'@m'} + (J(J-1)I)^{-1}\sum_{j\neq j'}\sum_{m=m'}\sum\sum\sigma_{j@m,j'@m'}]$$

$$\sigma^2_{B\kappa}(AB{:}W{-}B) = [(JIJK(JK-1))^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (J(J-1)I(I-1)J^2K^2)^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'}] -$$
$$[(J(J-1)IJK(JK-1))^{-1}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (JI)I-1)J^2K^2)^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'}]$$

$$\sigma^2_{AB\eta}(AB{:}W{-}B) = [(IJI)^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)J(J-1)JK(JK-1))^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m'}] -$$
$$[(IJ(J-1)I)^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m=m'}\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)JI(I-1))^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m'}]$$

$$\sigma^2_{AB\kappa}(AB{:}W{-}B) = [(IJIJK(JK-1))^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)J(J-1)I(I-1)J^2K^2)^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}] -$$
$$[(IJ(J-1)IJK(JK-1))^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)JI(I-1)J^2K^2)^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}]$$

COMPONENT DEFINITION

$$\sigma^2_{\kappa}(D-W) = (IJK)^{-1}\sum_{m=m'}\sum_{n=n'}\sum\sum\sigma_{mn,m'n'} - (IJK(JK-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{mn,m'n'}$$

$$\sigma^2_{A\kappa}(D-W) = (I^2JK)^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n=n'}\sum\sum\sigma_{i@mn,i'@m'n'} - (I^2JK(JK-1))^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{B\kappa}(D-W) = (JIJK)^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum\sum\sigma_{j@mn,j'@m'n'} - (JIJK(JK-1))^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{j@mn,j'@m'n'}$$

$$\sigma^2_{AB\kappa}(D-W) = (IJIJK)^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} - (IJIJK(JK-1))^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}$$

2.5.3 Randomization restricted on a treatment combination: AB

Consider now a factorial design involving factors A and B with a run-order restriction placed on AB, i.e., an AB combination is randomly chosen and all replications are run in random order before proceeding to another AB combination. Segments, then, are defined by unique combinations of the levels of A and B.

Case 1: No Run-order effects (usual ANOVA)

Results are the usual unbiased tests.

Case 2: Run-order effects are additive

All terms now have a strong U bias component.

Case 3: Run-order effects are non additive

Additional AU and BU bias components appear for terms A, B, and AB. These are all strong bias components. In practice, one must assume **no** lurking variables affect the response of interest.

Table XV EMS for the Two-factor design- restricted on AB

Case 1: No Run-order effects (usual ANOVA)

A: $\sigma_\epsilon^2 + JK\Phi(A)$

B: $\sigma_\epsilon^2 + IK\Phi(B)$

AB: $\sigma_\epsilon^2 + K\Phi(AB)$

E: σ_ϵ^2

Case 2: Run-order effects are additive

A: $\sigma_{\epsilon+}^2 + K\sigma_\kappa^2(A:W-B) + K\sigma_\eta^2(A:W-B) + JK\Phi(A)$

B: $\sigma_{\epsilon+}^2 + K\sigma_\kappa^2(B:W-B) + K\sigma_\eta^2(B:W-B) + IK\Phi(B)$

AB: $\sigma_{\epsilon+}^2 + K\sigma_\kappa^2(AB:W-B) + K\sigma_\eta^2(AB:W-B) + K\Phi(AB)$

E: $\sigma_{\epsilon+}$

where $\sigma_{\epsilon+}^2 = \sigma_\epsilon^2 + \sigma_{AB\kappa}^2(D-W) + \sigma_{B\kappa}^2(D-W) + \sigma_{A\kappa}^2(D-W) + \sigma_\kappa^2(D-W)$

Case 3: Run-order effects are nonadditive

$$A\text{: } \sigma^2_{\epsilon\cdot} + K\sigma^2_{AB\kappa}(A{:}W\text{-}B) + K\sigma^2_{AB\eta}(A{:}W\text{-}B) + K\sigma^2_{B\kappa}(A{:}W\text{-}B) + K\sigma^2_{B\eta}(A{:}W\text{-}B) + K\sigma^2_{A\kappa}(A{:}W\text{-}B) + K\sigma^2_{A\eta}(A{:}W\text{-}B) + K\sigma^2_{\kappa}(A{:}W\text{-}B) + K\sigma^2_{\eta}(A{:}W\text{-}B) + JK\Phi(A)$$

$$B\text{: } \sigma^2_{\epsilon\cdot} + K\sigma^2_{AB\kappa}(B{:}W\text{-}B) + K\sigma^2_{AB\eta}(B{:}W\text{-}B) + K\sigma^2_{B\kappa}(B{:}W\text{-}B) + K\sigma^2_{B\eta}(B{:}W\text{-}B) + K\sigma^2_{A\kappa}(B{:}W\text{-}B) + K\sigma^2_{A\eta}(B{:}W\text{-}B) + K\sigma^2_{\kappa}(B{:}W\text{-}B) + K\sigma^2_{\eta}(B{:}W\text{-}B) + IK\Phi(B)$$

$$AB\text{: } \sigma^2_{\epsilon\cdot} + K\sigma^2_{AB\kappa}(AB{:}W\text{-}B) + K\sigma^2_{AB\eta}(AB{:}W\text{-}B) + K\sigma^2_{B\kappa}(AB{:}W\text{-}B) + K\sigma^2_{B\eta}(AB{:}W\text{-}B) + K\sigma^2_{A\kappa}(AB{:}W\text{-}B) + K\sigma^2_{A\eta}(AB{:}W\text{-}B) + K\sigma^2_{\kappa}(AB{:}W\text{-}B) + K\sigma^2_{\eta}(AB{:}W\text{-}B) + K\Phi(AB)$$

$$E\text{: } \sigma_{\epsilon\cdot}$$

where $\sigma^2_{\epsilon\cdot} = \sigma^2_{\epsilon} + \sigma^2_{AB\kappa}(D\text{-}W) + \sigma^2_{B\kappa}(D\text{-}W) + \sigma^2_{A\kappa}(D\text{-}W) + \sigma^2_{\kappa}(D\text{-}W)$

COMPONENT DEFINITION

$$\sigma^2_{\eta}(A:W-B) = (IJ)^{-1}\sum\sum\sigma_{m,m'} - (IJ(JI-1))^{-1}\sum\sum\sigma_{m,m'}$$
$$m=m' \qquad m\neq m'$$

$$\sigma^2_{\kappa}(A:W-B) = (IJK(K-1))^{-1}\sum\sum\sum\sum\sigma_{mn,m'n'} - (IJ(IJ-1)K^2)^{-1}\sum\sum\sum\sum\sigma_{mn,m'n'}$$
$$m=m' \; n\neq n' \qquad m\neq m' \; n \; n'$$

$$\sigma^2_{A\eta}(A:W-B) = [(I^2J)^{-1}(\sum\sum\sum\sum\sigma_{i@m,i'@m'} + (I^2J(IJ-1))^{-1}\sum\sum\sum\sum\sigma_{i@m,i'@m'}] - [(I(I-1)IJ(IJ-1))^{-1}\sum\sum\sum\sum\sigma_{i@m,i'@m'}]$$
$$i=i' \; m=m' \qquad i\neq i' \; m\neq m'$$

$$\sigma^2_{A\kappa}(A:W-B) = [(I^2JK(K-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'} + (I^2J(J-1)K^2)^{-1}\sum\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'}] -$$
$$i=i' \; m=m' \; n\neq n' \qquad i=i' \; m\neq m' \; n \; n'$$

$$[(I(I-1)IJ(IJ-1)K)^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'} + (I(I-1)IJ(IJ-1)K(K-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'}]$$
$$i\neq i' \; m\neq m' \; n=n' \qquad i\neq i' \; m\neq m' \; n\neq n'$$

$$\sigma^2_{B\eta}(A:W-B) = (JIJ)^{-1}\sum\sum\sum\sum\sigma_{j@m,j'@m'} - (JIJ(IJ-1))^{-1}\sum\sum\sum\sum\sigma_{j@m,j'@m'}$$
$$j=j' \; m=m' \qquad j=j' \; m\neq m'$$

$$\sigma^2_{B\kappa}(A:W-B) = (JIJK(K-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'} - (JIJ(IJ-1)K^2)^{-1}\sum\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'}$$
$$j=j' \; m=m' \; n\neq n' \qquad j=j' \; m\neq m' \; n \; n'$$

$$\sigma^2_{AB\eta}(A:W-B) = [(IJIJ)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m'} + (IJ(J-1)IJ(IJ-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m}] -$$
$$i=i' \; j\neq j' \; m=m' \qquad i=i' \; j\neq j' \; m\neq m'$$

$$[(I(I-1)JIJ(IJ-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)J(J-1)IJ(IJ-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m'}]$$
$$i\neq i' \; j\neq j' \; m=m' \qquad i\neq i' \; j\neq j' \; m\neq m'$$

$$\sigma^2_{AB\kappa}(A:W-B) = [(IJIJK(K-1))^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (IJ(J-1)IJ(IJ-1)K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}] -$$
$$i=i' \; j\neq j' \; m=m' \; n \; n' \qquad i=i' \; j\neq j' \; m\neq m' \; n \; n'$$

$$[(I(I-1)JIJ(IJ-1)K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)J(J-1)IJ(IJ-1)K^2)^{-1}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}]$$
$$i\neq i' \; j\neq j' \; m=m' \; n \; n' \qquad i\neq i' \; j\neq j' \; m\neq m' \; n \; n'$$

COMPONENT DEFINITION

$$\sigma^2_{\eta}(B{:}W{-}B) = (IJ)^{-1}\sum_{m=m'}\sum\sigma_{m,m'} - (IJ(JI-1))^{-1}\sum_{m\neq m'}\sum\sigma_{m,m'}$$

$$\sigma^2_{\kappa}(B{:}W{-}B) = (IJK(K-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{mn,m'n'} - (IJ(IJ-1)K^2)^{-1}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sigma_{mn,m'n'}$$

$$\sigma^2_{A\eta}(B{:}W{-}B) = (IIJ)^{-1}\sum_{i=i'}\sum_{m=m'}\sum\sum\sigma_{i@m,i'@m'} - (IIJ(IJ-1))^{-1}\sum_{i=i'}\sum_{m\neq m'}\sum\sum\sigma_{i@m,i'@m'}$$

$$\sigma^2_{A\kappa}(B{:}W{-}B) = (IIJK(K-1))^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'} - (IIJ(IJ-1)K^2)^{-1}\sum_{i=i'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{B\eta}(B{:}W{-}B) = [(JIJ)^{-1}(\sum_{j=j'}\sum_{m=m'}\sum\sum\sigma_{j@m,j'@m'} + (JIJJ(IJ-1))^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum\sum\sigma_{j@m,j'@m}] - [(J(J-1)IJ(IJ-1))^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sum\sigma_{j@m,j'@m'}]$$

$$\sigma^2_{B\kappa}(B{:}W{-}B) = [(JIJK(K-1))^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (JIJ(J-1)K^2)^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'}] -$$
$$[(J(J-1)IJ(IJ-1)K)^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n=n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (J(J-1)IJ(IJ-1)K(K-1))^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'}]$$

$$\sigma^2_{AB\eta}(B{:}W{-}B) = [(IJIJ)^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)JIJ(IJ-1))^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m}] -$$
$$[(IJ(J-1)IJ(IJ-1))^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)J(J-1)IJ(IJ-1))^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m'}]$$

$$\sigma^2_{AB\kappa}(B{:}W{-}B) = [(IJIJK(K-1))^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)JIJ(IJ-1)K^2)^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}] -$$
$$[(IJ(J-1)IJ(IJ-1)K^2)^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n=n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)J(J-1)IJ(IJ-1)K^2)^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}]$$

COMPONENT DEFINITION

$$\sigma^2_{\eta}(AB{:}W{-}B) = (IJ)^{-1}\sum_{m=m'}\sum\sigma_{m,m'} - (IJ(JI-1))^{-1}\sum_{m\neq m'}\sum\sigma_{m,m'}$$

$$\sigma^2_{\kappa}(AB{:}W{-}B) = (IJK(K-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{mn,m'n'} - (IJ(IJ-1)K^2)^{-1}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sigma_{mn,m'n'}$$

$$\sigma^2_{A\eta}(AB{:}W{-}B) = (IIJ)^{-1}\sum_{i=i'}\sum_{m=m'}\sum\sum\sigma_{i@m,i'@m'} - (IIJ(IJ-1))^{-1}\sum_{i=i'}\sum_{m\neq m'}\sum\sum\sigma_{i@m,i'@m'}$$

$$\sigma^2_{A\kappa}(AB{:}W{-}B) = (IIJK(K-1))^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'} - (IIJ(IJ-1)K^2)^{-1}\sum_{i=i'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{B\eta}(AB{:}W{-}B) = (JIJ)^{-1}\sum_{j=j'}\sum_{m=m'}\sum\sum\sigma_{j@m,j'@m'} - (JIJ(IJ-1))^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum\sum\sigma_{j@m,j'@m'}$$

$$\sigma^2_{B\kappa}(AB{:}W{-}B) = (JIJK(K-1))^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'} - (JIJ(IJ-1)K^2)^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'}$$

$$\sigma^2_{AB\eta}(AB{:}W{-}B) = [(IJIJ)^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)J(J-1)IJ(IJ-1))^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m'}] -$$
$$[(IJ(J-1)IJ(IJ-1))^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m'} + (I(I-1)JIJ(IJ-1))^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum\sum\sum\sigma_{ij@m,ij'@m'}]$$

$$\sigma^2_{AB\kappa}(AB{:}W{-}B) = [(IJIJK(K-1))^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)J(J-1)IJ(IJ-1)K^2)^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}] -$$
$$[(IJ(J-1)IJ(IJ-1)K^2)^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'} + (I(I-1)JIJ(IJ-1)K^2)^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sum\sigma_{ij@mn,ij'@m'n'}]$$

2.5.4 Randomization restricted hierarchically: A, then B within A

Consider a factorial design involving factors A and B with a run-order restriction placed on A and then B within A. A level of A is randomly chosen, then within that level of A, a level of B is randomly chosen and all replications are run in random order before proceeding to another level of B. When all levels of B have been completed, another level of A is selected at random and the process repeats itself. This is considered a hierarchical restriction, a restriction within a restriction.

Case 1: No Run-order effects (usual ANOVA)

All tests are unbiased.

Case 2: Run-order effects are additive

All terms now exhibit a strong bias component that is a function of κ, but the test on factor A is further biased by a component involving η. This makes intuitive sense because the levels of B are randomized to a greater degree than the levels of A (hierarchical nature of the restriction).

Case 3: Run-order effects are non additive

All terms now exhibit strong interaction bias components that involve κ, but the test on factor A is further biased by interaction components that involve η. This makes intuitive sense because there is more randomization among the levels of B than among the levels of A (hierarchical nature of the restriction)

Table XVI EMS for the Two-factor design- restricted on A, and B within A

Case 1: No Run-order effects (usual ANOVA)

A: $\sigma_\epsilon^2 + JK\Phi(A)$

B: $\sigma_\epsilon^2 + IK\Phi(B)$

AB: $\sigma_\epsilon^2 + K\Phi(AB)$

E: σ_ϵ^2

Case 2: Run-order effects are additive

A: $\sigma_{\epsilon*}^2 + K\sigma_\lambda^2(A:W-B) + JK\sigma_\kappa^2(A:W-B) + JK\sigma_\eta^2(A:W-B) + JK\Phi(A)$

B: $\sigma_{\epsilon*}^2 + K\sigma_\lambda^2(B:W-B) + K\sigma_\kappa^2(B:W-B) + IK\Phi(B)$

AB: $\sigma_{\epsilon*}^2 + K\sigma_\lambda^2(AB:W-B) + K\sigma_\kappa^2(AB:W-B) + K\Phi(AB)$

E: $\sigma_{\epsilon*}$

where $\sigma_{\epsilon*}^2 = \sigma_\epsilon^2 + \sigma_{AB\kappa}^2(D-W) + \sigma_{B\kappa}^2(D-W) + \sigma_{A\kappa}^2(D-W) + \sigma_\kappa^2(D-W)$

Case 3: Run-order effects are nonadditive

$$A:\ \sigma^2_{\epsilon+} + K\sigma^2_{AB\lambda}(A{:}W\text{-}B) + JK\sigma^2_{AB\kappa}(A{:}W\text{-}B) + JK\sigma^2_{AB\eta}(A{:}W\text{-}B) + K\sigma^2_{B\lambda}(A{:}W\text{-}B) + JK\sigma^2_{B\kappa}(A{:}W\text{-}B) + JK\sigma^2_{B\eta}(A{:}W\text{-}B)$$
$$+ K\sigma^2_{A\lambda}(A{:}W\text{-}B) + JK\sigma^2_{A\kappa}(A{:}W\text{-}B) + JK\sigma^2_{A\eta}(A{:}W\text{-}B) + K\sigma^2_{\lambda}(A{:}W\text{-}B) + JK\sigma^2_{\kappa}(A{:}W\text{-}B) + JK\sigma^2_{\eta}(A{:}W\text{-}B) + JK\Phi(A)$$

$$B:\ \sigma^2_{\epsilon+} + K\sigma^2_{AB\lambda}(B{:}W\text{-}B) + K\sigma^2_{AB\kappa}(B{:}W\text{-}B) + K\sigma^2_{AB\eta}(B{:}W\text{-}B) + K\sigma^2_{B\lambda}(B{:}W\text{-}B) + K\sigma^2_{B\kappa}(B{:}W\text{-}B) + IK\sigma^2_{B\eta}(B{:}W\text{-}B)$$
$$+ K\sigma^2_{A\lambda}(B{:}W\text{-}B) + K\sigma^2_{A\kappa}(B{:}W\text{-}B) + K\sigma^2_{\lambda}(B{:}W\text{-}B) + K\sigma^2_{\kappa}(B{:}W\text{-}B) + IK\Phi(B)$$

$$AB:\ \sigma^2_{\epsilon+} + K\sigma^2_{AB\lambda}(AB{:}W\text{-}B) + K\sigma^2_{AB\kappa}(AB{:}W\text{-}B) + K\sigma^2_{AB\eta}(AB{:}W\text{-}B) + K\sigma^2_{B\lambda}(AB{:}W\text{-}B) + K\sigma^2_{B\kappa}(AB{:}W\text{-}B) + K\sigma^2_{B\eta}(AB{:}W\text{-}B)$$
$$+ K\sigma^2_{A\lambda}(AB{:}W\text{-}B) + K\sigma^2_{A\kappa}(AB{:}W\text{-}B) + K\sigma^2_{\lambda}(AB{:}W\text{-}B) + K\sigma^2_{\kappa}(AB{:}W\text{-}B) + K\Phi(AB)$$

$$E:\ \sigma_{\epsilon+}$$

where $\sigma^2_{\epsilon+} = \sigma^2_{\epsilon} + \sigma^2_{AB\lambda}(D\text{-}W) + \sigma^2_{B\lambda}(D\text{-}W) + \sigma^2_{A\lambda}(D\text{-}W) + \sigma^2_{\lambda}(D\text{-}W)$

COMPONENT DEFINITION

$$\sigma^2_{\eta}(A:W-B) = (I)^{-1}\sum_{m=m'}\sum\sigma_{m,m'} - (I(I-1))^{-1}\sum_{m\neq m'}\sum\sigma_{m,m'}$$

$$\sigma^2_{\kappa}(A:W-B) = (IJ^2)^{-1}\sum_{m=m'\ n\ n'}\sum\sum\sum\sigma_{mn,m'n'} - (I(I-1)J^2)^{-1}\sum_{m\neq m'\ n\ n'}\sum\sum\sum\sigma_{mn,m'n'}$$

$$\sigma^2_{\lambda}(A:W-B) = [(IJK(K-1))^{-1}(\sum_{m=m'\ n=n'\ o\neq o'}\sum\sum\sum\sum\sum\sigma_{mno,m'n'o'} + (IJ(J-1)K^2)^{-1}\sum_{m=m'\ n\neq n'\ o\ o'}\sum\sum\sum\sum\sum\sigma_{mno,m'n'o'}] -$$
$$[(I(I-1)JK^2)^{-1}\sum_{m\neq m'\ n=n'\ o\ o'}\sum\sum\sum\sum\sum\sigma_{mno,m'n'o'} + (I(I-1)J(J-1)K^2)^{-1}\sum_{m\neq m'\ n\neq n'\ o\ o'}\sum\sum\sum\sum\sum\sigma_{mno,m'n'o'}$$

$$\sigma^2_{A\eta}(A:W-B) = (I^2)^{-1}\sum_{i=i'\ m=m'}\sum\sum\sum\sigma_{i@m,i'@m'} - (I(I-1)I(I-1))^{-1}\sum_{i\neq i'\ m\neq m'}\sum\sum\sum\sigma_{i@m,i'@m'}$$

$$\sigma^2_{A\kappa}(A:W-B) = (I^2J^2)^{-1}\sum_{i=i'\ m=m'\ n\ n'}\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'} - (I(I-1)I(I-1)J^2)^{-1}\sum_{i\neq i'\ m\neq m'\ n\ n'}\sum\sum\sum\sum\sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{A\lambda}(A:W-B) = [(I^2JK(K-1))^{-1}\sum_{i=i'\ m=m'\ n=n'\ o\neq o'}\sum\sum\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'} + (I^2J(J-1)K^2)^{-1}\sum_{i=i'\ m=m'\ n\neq n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'}] -$$
$$[(I(I-1)I(I-1)JK^2)^{-1}\sum_{i\neq i'\ m\neq m'\ n=n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'} + (I(I-1)I(I-1)J(J-1)K^2)^{-1}\sum_{i\neq i'\ m\neq m'\ n\neq n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'}]$$

COMPONENT DEFINITION

$$\sigma^2_{B\eta}(A;W-B) = (J^2I)^{-1}\sum_{j\ j'\ m=m'}\sum\sum\sum\sigma_{j@m,j'@m'} - (J^2I(I-1))^{-1}\sum_{j\ j'\ m\neq m'}\sum\sum\sum\sigma_{j@m,j'@m'}$$

$$\sigma^2_{B\kappa}(A;W-B) = [(JIJ)^{-1}\sum_{j=j'\ m=m'\ n=n'}\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (J(J-1)IJ(J-1))^{-1}\sum_{j\neq j'\ m=m'\ n\neq n'}\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'}] -$$
$$[(JI(I-1)K^2)^{-1}\sum_{j=j'\ m\neq m'\ n\ n'}\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (J(J-1)I(I-1)K^2)^{-1}\sum_{j\neq j'\ m\neq m'\ n\ n'}\sum\sum\sum\sum\sum\sigma_{j@mn,j'@m'n'}]$$

$$\sigma^2_{B\lambda}(A;W-B) = [(JIJK(K-1))^{-1}\sum_{j=j'\ m=m'\ n=n'\ o\neq o'}\sum\sum\sum\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'} + (J(J-1)IJ(J-1)K^2)^{-1}\sum_{j\neq j'\ m=m'\ n\neq n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'}] -$$
$$[(JI(I-1)J^2K^2)^{-1}\sum_{j=j'\ m\neq m'\ n\ n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'} + (J(J-1)I(I-1)J^2K^2)^{-1}\sum_{j\neq j'\ m\neq m'\ n\ n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'}]$$

$$\sigma^2_{AB\eta}(A;W-B) = (IJ^2I)^{-1}\sum_{i=i'\ j\ j'\ m=m'}\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m'} - (I(I-1)J^2I(I-1))^{-1}\sum_{i\neq i'\ j\ j'\ m\neq m'}\sum\sum\sum\sum\sum\sigma_{ij@m,ij'@m'}$$

$$\sigma^2_{AB\kappa}(A;W-B) = [(IJIJ)^{-1}\sum_{i=i'\ j=j'\ m=m'\ n=n'}\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'} + (IJ(J-1)IJ(J-1))^{-1}\sum_{i=i'\ j\neq j'\ m=m'\ n\neq n'}\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'}] -$$
$$[(I(I-1)JI(I-1)K^2)^{-1}\sum_{i\neq i\ j=j'\ m\neq m'\ n\ n'}\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'} + (I(I-1)J(J-1)I(I-1)K^2)^{-1}\sum_{i\neq i'\ j\neq j'\ m\neq m'\ n\ n'}\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'}]$$

$$\sigma^2_{AB\lambda}(A;W-B) = [(IJIJK(K-1))^{-1}\sum_{i=i'\ j=j'\ m=m'\ n=n'\ o\neq o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'} + (IJ(J-1)IJ(J-1)K^2)^{-1}\sum_{i=i'\ j\neq j'\ m=m'\ n\neq n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'}] -$$
$$[(I(I-1)JI(I-1)J^2K^2)^{-1}\sum_{i\neq i'\ j=j'\ m\neq m'\ n\ n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'} + (I(I-1)J(J-1)I(I-1)J^2K^2)^{-1}\sum_{i\neq i'\ j\neq j'\ m\neq m'\ n\ n'\ o\ o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'}]$$

COMPONENT DEFINITION

$$\sigma^2_{\kappa}(B;W-B) = (IJ)^{-1}\sum_{m=m'}\sum_{n=n'}\sum\sum\sigma_{mn,m'n'} - (IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{mn,m'n'}$$

$$\sigma^2_{\lambda}(B;W-B) = (IJK(K-1))^{-1}\sum_{m=m'}\sum_{n=n'}\sum_{o\neq o'}\sum\sum\sum\sigma_{mno,m'n'o'} - (IJ(J-1)K^2)^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum_{o\ o'}\sum\sum\sum\sigma_{mno,m'n'o'}$$

$$\sigma^2_{A\kappa}(B;W-B) = (I^2J)^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n=n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'} - (I^2J(J-1))^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{A\lambda}(B;W-B) = (I^2JK(K-1))^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n=n'}\sum_{o\neq o'}\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'} - (I^2J(J-1)K^2)^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n\neq n'}\sum_{o\ o'}\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'}$$

$$\sigma^2_{B\eta}(B;W-B) = (JI)^{-1}(\sum_{j=j'}\sum_{m\ m'}\sum\sum\sigma_{j@m,j'@m'} - (J(J-1)I)^{-1}\sum_{j\neq j'}\sum_{m\ m'}\sum\sum\sigma_{j@m,j'@m'}$$

$$\sigma^2_{B\kappa}(B;W-B) = [(JIJ)^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (JIJ^2)^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'}] -$$
$$[(J(J-1)IJ^2)^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'} + (J(J-1)IJ(J-1))^{-1}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{j@mn,j'@m'n'}]$$

$$\sigma^2_{B\lambda}(B;W-B) = [(JIJK(K-1))^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum_{o\neq o'}\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'} + (JIJ^2K^2)^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum_{o\ o'}\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'}] -$$
$$[(J(J-1)IJ^2K^2)^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\ n'}\sum_{o\ o'}\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'} + (J(J-1)IJ(J-1)K^2)^{-1}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\neq n'}\sum_{o\ o'}\sum\sum\sum\sum\sigma_{j@mno,j'@m'n'o'}]$$

COMPONENT DEFINITION

$$\sigma^2_{AB\eta}(B:W-B) = [(IJI)^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum\sigma_{ij@m,i'j'@m'} + (I(I-1)JI)^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum\sigma_{ij@m,i'j'@m'}] -$$
$$[(IJ(J-1)I)^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m=m'}\sum\sigma_{ij@m,i'j'@m'} + (I(I-1)J(J-1)I)^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sigma_{ij@m,i'j'@m'}]$$

$$\sigma^2_{AB\kappa}(B:W-B) = [(IJIJ)^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum\sigma_{ij@mn,i'j'@m'n'} + (I(I-1)JIJ^2)^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sigma_{ij@mn,i'j'@m'n'}] -$$
$$[(IJ(J-1)IJ(J-1))^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\ n'}\sum\sigma_{ij@mn,i'j'@m'n'} + (I(I-1)J(J-1)IJ^2)^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\ n'}\sum\sigma_{ij@mn,i'j'@m'n'}]$$

$$\sigma^2_{AB\lambda}(B:W-B) = [(IJIJK(K-1))^{-1}\sum_{i=i'}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum_{o\neq o'}\sum\sigma_{ij@mno,i'j'@m'n'o'} + (I(I-1)JIJ^2K^2)^{-1}\sum_{i\neq i'}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum_{o\ o'}\sum\sigma_{ij@mno,i'j'@m'n'o'}] -$$
$$[(I(I-1)J(J-1)IJ^2K^2)^{-1}\sum_{i\neq i'}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\ n'}\sum_{o\ o'}\sum\sigma_{ij@mno,i'j'@m'n'o'} + (IJ(J-1)IJ(J-1)K^2)^{-1}\sum_{i=i'}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\neq n'}\sum_{o\ o'}\sum\sigma_{ij@mno,i'j'@m'n'o'}]$$

COMPONENT DEFINITION

$$\sigma^2_{\kappa}(AB{:}W{-}B) = (IJ)^{-1}\sum_{m=m'}\sum_{n=n'}\sum\sum\sigma_{mn,m'n'} - (IJ(J-1))^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{mn,m'n'}$$

$$\sigma^2_{\lambda}(AB{:}W{-}B) = (IJK(K-1))^{-1}\sum_{m=m'}\sum_{n=n'}\sum_{o\neq o'}\sum\sum\sum\sigma_{mno,m'n'o'} - (IJ(J-1)K^2)^{-1}\sum_{m=m'}\sum_{n\neq n'}\sum_{o\ o'}\sum\sum\sum\sigma_{mno,m'n'o'}$$

$$\sigma^2_{A\kappa}(AB{:}W{-}B) = (I^2J)^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n=n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'} - (I^2J(J-1))^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sum\sigma_{i@mn,i'@m'n'}$$

$$\sigma^2_{A\lambda}(AB{:}W{-}B) = (I^2JK(K-1))^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n=n'}\sum_{o\neq o'}\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'} - (I^2J(J-1)K^2)^{-1}\sum_{i=i'}\sum_{m=m'}\sum_{n\neq n'}\sum_{o\ o'}\sum\sum\sum\sum\sigma_{i@mno,i'@m'n'o'}$$

$$\sigma^2_{B\eta}(AB{:}W{-}B) = [(JI)^{-1}\sum_{j=j'}\sum_{m=m'}\sum\sigma_{j@mj'@m'} + (J(J-1)I(I-1))^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum\sigma_{j@mj'@m'}] -$$
$$[(JI(I-1))^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum\sigma_{j@mj'@m'} + (J(J-1)I)^{-1}\sum_{j\neq j'}\sum_{m=m'}\sum\sigma_{j@mj'@m'}]$$

$$\sigma^2_{B\kappa}(AB{:}W{-}B) = [(JIJ)^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum\sum\sigma_{j@mnj'@m'n'} + (J(J-1)I(I-1)K^2)^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sigma_{j@mnj'@m'n'}] -$$
$$[(JI(I-1)K^2)^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum\sum\sigma_{j@mnj'@m'n'} + (J(J-1)IK(K-1))^{-1}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\neq n'}\sum\sum\sigma_{j@mnj'@m'n'}]$$

$$\sigma^2_{B\lambda}(AB{:}W{-}B) = [(JIJK(K-1))^{-1}\sum_{j=j'}\sum_{m=m'}\sum_{n=n'}\sum_{o\neq o'}\sum\sum\sum\sigma_{j@mnoj'@m'n'o'} + (J(J-1)I(I-1)J^2K^2)^{-1}\sum_{j\neq j'}\sum_{m\neq m'}\sum_{n\ n'}\sum_{o\ o'}\sum\sum\sum\sigma_{j@mnoj'@m'n'o'}]$$
$$[(J(J-1)IJ(J-1)K^2)^{-1}\sum_{j\neq j'}\sum_{m=m'}\sum_{n\neq n'}\sum_{o\ o'}\sum\sum\sum\sigma_{j@mnoj'@m'n'o'} + (JI(I-1)J^2K^2)^{-1}\sum_{j=j'}\sum_{m\neq m'}\sum_{n\ n'}\sum_{o\ o'}\sum\sum\sum\sigma_{j@mnoj'@m'n'o'}]$$

COMPONENT DEFINITION

$$\sigma^2_{AB\eta}(AB:W-B) = [(IJI)^{-1}\sum_{i=i'\ j=j'\ m=m'}\sum\sum\sum\sum\sum\sigma_{ij@m,i'j'@m'} + (I(I-1)J(J-1)I(I-1))^{-1}\sum_{i\neq i'\ j\neq j'\ m\neq m'}\sum\sum\sum\sum\sum\sigma_{ij@m,i'j'@m}] -$$
$$[(IJ(J-1)I)^{-1}\sum_{i=i'\ j\neq j'\ m=m'}\sum\sum\sum\sum\sum\sigma_{ij@m,i'j'@m'} + (I(I-1)JI(I-1))^{-1}\sum_{i\neq i'\ j=j'\ m\neq m'}\sum\sum\sum\sum\sum\sigma_{ij@m,i'j'@m}]$$

$$\sigma^2_{AB\kappa}(AB:W-B) = [(IJIJ)^{-1}\sum_{i=i'\ j=j'\ m=m'\ n=n'}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'} + (I(I-1)J(J-1)I(J-1)J^2)^{-1}\sum_{i\neq i'\ j\neq j'\ m\neq m'\ n\ \ n'}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'}] -$$
$$[(IJ(J-1)IJ(J-1))^{-1}\sum_{i=i'\ j\neq j'\ m=m'\ n\neq n'}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'} + (I(I-1)JI(I-1)J^2)^{-1}\sum_{i\neq i'\ j=j'\ m\neq m'\ n\ \ n'}\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mn,i'j'@m'n'}]$$

$$\sigma^2_{AB\lambda}(AB:W-B) = [(IJIJK(K-1))^{-1}\sum_{i=i'\ j=j'\ m=m'\ n=n'\ o\neq o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'} + (I(I-1)J(J-1)I(J-1)J^2K^2)^{-1}\sum_{i\neq i'\ j\neq j'\ m\neq m'\ n\ \ n'\ o\ \ o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'}] -$$
$$[(IJ(J-1)IJ(J-1)K^2)^{-1}\sum_{i=i'\ j\neq j'\ m=m'\ n\neq n'\ o\ \ o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'} + (I(I-1)JI(I-1)J^2K^2)^{-1}\sum_{i\neq i'\ j=j'\ m\neq m'\ n\ \ n'\ o\ \ o'}\sum\sum\sum\sum\sum\sum\sum\sum\sum\sigma_{ij@mno,i'j'@m'n'o'}]$$

2.5.5 Summary of the Two Factor Example

In each of the preceding four sections specific restrictions on the randomization process have been addressed. All those results are now summarized in **Table XVII** where the presence of bias components is shown and each bias component is labeled as strong or weak. Under complete randomization the subscript that defines *between* and *within*, does not change in conjunction with the subscript that defines run-order. The result is a weak bias component that is a measure of interaction only. For example, run-order is defined by l and for the bias component that involves $\alpha U_{i@l}$ the same levels of the subscript l appear in the *between* and the *within* sections:

$$\frac{\sigma^2_{AU}(W-B)}{\sigma^2_{AU}} = \frac{\sum\sum\sum\sum_{i\neq i'\ l\neq l'}\rho_{il,i'l'}}{IIJ(IJ-1)} - \frac{\sum\sum\sum\sum_{i\neq i'\ l\neq l'}\rho_{il,i'l'}}{I(I-1)IJ(IJ-1)}$$

When randomization is restricted, then the subscript that defines *between* and *within* changes in conjunction with a subscript that defines segments. Contrasts among the levels of subscript that define *between* and *within* are also contrasts among segments, i.e., they are confounded. The result is a strong bias component, one that contrasts observations closer in time with those further apart in time. For example, the subscript i changes in conjunction with the segment subscript m, resulting in a strong bias component.

$$\frac{\sigma^2_{AU}(W-B)}{\sigma^2_{AU}} = \frac{\sum\sum\sum\sum\sum\sum\sum\rho_{imn,i'm'n'}}{IIJ(IJ-1)} - \frac{\sum\sum\sum\sum\sum\sum\rho_{imn,i'm'n'}}{I(I-1)IJ(IJ-1)}$$

This also explains why strong main effect bias components and strong non additive bias components that involve the main effect always appear in conjunction.

In particular, the following points are summarized in **Table XVII**:

- With complete randomization **no** strong bias components exist.

- With a restriction on A, there are strong bias components in the test for the effect of A, but only weak bias components in tests for the effects of B and AB. If weak bias components are negligible then one can restrict on factors of lesser importance and maintain reasonably unbiased tests on factors of greater importance. In some practical settings this may reduce cost or increase efficiency.
- With the restriction on AB, tests for all effects exhibit strong bias components. The effect of segmenting has been spread among the tests for the effects of A, B, and AB. The magnitude of each component is less than the strong bias component when the restriction is on A only. This is because there is increased randomization, i.e., more segments of smaller size are being randomized.
- With the restriction on A and then B within A, there are two levels of bias components: those that are a function of the restriction on A and those that are a function of the restriction on B within A. Strong bias components exist for all tests, but for the tests of B effects and AB effects there are no strong bias components involving η. This is expected because components involving η contrast the levels of A and these contrasts are averaged out when looking at the sums of squares for B or AB. Thus the bias associated with A effects is generally larger than the bias associated with B and AB effects.

Table XVII Summary of bias for the Two-factor design under various randomization scenarios

Restriction	Effect	Bias Components (S: Strong, W: Weak, Shaded: undefined)											
		η	κ	λ	Aη	Aκ	Aλ	Bη	Bκ	Bλ	ABη	ABκ	ABλ
None (η represents U)	A				W						W		
	B							W			W		
	AB										W		
On A	A	S	S		S	S		S	S		S	S	
	B							W	W		W	W	
	AB							W	W		W	W	
On AB	A	S	S		S	S		S	S		S	S	
	B	S	S		S	S		S	S		S	S	
	AB	S	S		S	S		S	S		S	S	
On A, then B within A	A	S	S	S	S	S	S	S	S	S	S	S	S
	B		S	S		S	S	W	S	S	W	S	S
	AB		S	S		S	S	W	S	S	W	S	S

2.6 EMS RULES THAT MODEL THE RANDOMIZATION PROCESS

General rules are now developed, assuming nonadditivity of treatment and run-order effects. These rules are amendments to Bennett-Franklin type rules and only indicate the presence and strength of any bias components, not the exact form. EMS are generated for any hierarchically restricted, balanced, complete factorial design. Anderson and McLean (1974a, 1974b) modified the usual linear model to represent restrictions on randomization and then applied the usual algorithms to generate EMS (Lorenzen and Anderson 1993b). The linear model is further modified to allow for nonadditivity of treatment and run-order effects. There has been much discussion in the literature about expected mean squares in the mixed model (Scheffe 1959; Searle 1971; Hocking 1973; Samuels et al. 1991). In brief, two methods for calculating EMS compete, whose primary differences lie in the parameter definitions for interactions between fixed and random factors, and the associated covariance structure. Regardless of which of the competing mixed model definitions is used, the following adaptations generate EMS components that represent restrictions on the randomization process.

The rules work on the following basis: For any term in the proposed model, say A, the bias components are a function of $[MS_{num} - MS_{den}]$ which can be written as a function of cross-products *within* the same level minus cross-products *between* levels. For example, the bias components for A, from a one-factor design, can be expressed as:

$$MS_A - MS_E$$

$$= \frac{\left[\sum_i \sum_j (\bar{y}_{i.} - \bar{y}_{..})^2\right]}{[I-1]} - \frac{\left[\sum_i \sum_j (y_{ij} - \bar{y}_{i.})^2\right]}{[I(J-1)]}$$

$$= \frac{\left[(I-1)J\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ^2} - \frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{I(I-1)J^2K^2}\right]\right]}{[I-1]} - \frac{\left[I(J-1)\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ} - \frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{IJ(J-1)}\right]\right]}{[I(J-1)]}$$

$$= \left[J\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{[IJ(J-1)]}\right]\right] - \left[J\left[\frac{\sum\sum\sum\sum y_{ij}y_{i'j'}}{[I(I-1)J^2]}\right]\right]$$

2.6.1 General Ems Rules

The following rules will reproduce the bias components found in **Table XVII** and indicate the strong/weak nature of the bias:

1. Define factors and relationships.
   - Define the usual design factors and their relationships.
   - Starting at the top of the hierarchy, for each factor, or factor combination, that defines a hierarchical restriction, define a segment factor nested in the defining factors and any previously defined segment factors.
   - After all segment factors are defined, define a final segment factor, nested in all previous segment factors.
2. Create the full effects model using all defined factors and append an error term that includes all previous subscripts. Label terms in the model as fixed, random, or mixed (random with the restriction that the sum over subscripts associated with fixed factors is 0), in the usual manner (according to either of the two competing methods for mixed models). However, any term that contains a segment effect should be considered random. To avoid introducing an excess of symbols (e.g., H for the factor and η for the effect), segment factors and effects will be labeled with the same symbol.
3. Calculate the EMS for terms that are not associated with segment effects and the error term, using standard algorithms for generating EMS (Lorenzen and Anderson 1993b). The expectation is taken over all terms created in step 2.
4. Expand any component that includes both design and segment factors into multiple component, representing the segment factor main effect the interactions between the segment factor and design factor. For example, just as we can expand B(A) as [B + AB] we can also expand η(A)B as [η + Aη]B and write it as [Bη + ABη]. The EMS terms from Step 3 are expanded in sequential order and shown in [ ].
5. Components associated with segment main effects are strong bias components. For example, σ^2_η is a strong bias component. Components associated with interactions that involve segment effects are strong bias components if they appear in conjunction with

the segment main effect component, otherwise it is a weak bias. For example, the component $\sigma^2_{A\eta}$ is a strong bias component if it appears in conjunction with σ^2_{η}, otherwise it is a weak bias component. Indicate weak bias components in some manner, for example weak bias components are underlined.

The Pseudo EMS constructed according to these rules now contains all components shown in shown in **Table XVII** and their strong and weak nature is indicated. They are referred to as Pseudo EMS because only the presence of run-order bias components is indicated, not the form of the component. The rules will now be applied to all the previous examples in this chapter:

Table XVIII Index to examples of Pseudo EMS generation

DESIGN	RESTRICTION ON:	TABLE
One-factor	None	**Table XIX**
	A	**Table XX**
Two-factor	None	**Table XXI**
	A	**Table XXII**
	AB	**Table XXIII**
	A, then B within A	**Table XXIV**

Table XIX Pseudo EMS for the One-factor design: no restriction

Step 1	**Step 2**	**Step 3**
A η	$z_{il} = \mu + \alpha_i + \eta_l + \alpha\eta_{il} + \epsilon_{il}$	*SOURCE* *EMS* A $\sigma^2_\epsilon + \sigma^2_{A\eta} + J\Phi(A)$ E σ^2_ϵ

(No Step 4) Step 5

SOURCE *EMS*

A $\sigma^2_\epsilon + \sigma^2_{A\eta} + J\Phi(A)$

E σ^2_ϵ

Table XX Pseudo EMS for the One-factor design: restriction on A

Step 1	**Step 2**	**Step 3**
A $\eta(A)$ $\kappa(A\eta)$	$z_{imn} = \mu + \alpha_i + \eta_{im} + \kappa_{imn} + \epsilon_{imn}$	*SOURCE* *EMS* A $\sigma^2_\epsilon + \sigma^2_{\kappa(A\eta)} + \sigma^2_{\eta(A)} + J\Phi(A)$ E σ^2_ϵ

Step 4 (No Step 5)

SOURCE *EMS*

A $\sigma^2_\epsilon + [\sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\sigma^2_{A\eta} + \sigma^2_{\eta}] + J\Phi(A)$

E σ^2_ϵ

Table XXI Pseudo EMS for the Two-factor design: no restriction

Step 1	Step 2	Step 3
A B η	$z_{ijl}=\mu+\alpha_i+\beta_j+\alpha\beta_{ij}+\eta_l+\alpha\eta_{il}+\beta\eta_{jl}+\alpha\beta\eta_{ijl}+\epsilon_{ijl}$	*SOURCE* *EMS* A $\sigma^2_\epsilon + \sigma^2_{AB\eta} + \sigma^2_{A\eta} + JK\Phi(A)$ B $\sigma^2_\epsilon + \sigma^2_{AB\eta} + \sigma^2_{B\eta} + IK\Phi(B)$ AB $\sigma^2_\epsilon + \sigma^2_{AB\eta} + K\Phi(AB)$ E σ^2_ϵ

(No Step 4) Step 5

SOURCE *EMS*

A $\sigma^2_\epsilon + \underline{\sigma^2_{AB\eta}} + \underline{\sigma^2_{A\eta}} + JK\Phi(A)$

B $\sigma^2_\epsilon + \underline{\sigma^2_{AB\eta}} + \underline{\sigma^2_{B\eta}} + IK\Phi(B)$

AB $\sigma^2_\epsilon + \underline{\sigma^2_{AB\eta}} + K\Phi(AB)$

E σ^2_ϵ

Table XXII Pseudo EMS for the Two-factor design: restriction on A

Step 1

A
B
$\eta(A)$
$\kappa(A\eta)$

Step 2

$$z_{ijmn} = \mu + \alpha_i + \eta_{im} + \kappa_{imn} + \beta_j + \alpha\beta_{ij} + \eta\beta_{ijm} + \kappa\beta_{ijmn} + \epsilon_{ijmn}$$

Step 3

SOURCE	*EMS*
A	$\sigma^2_\epsilon + \sigma^2_{\kappa(A\eta)\beta} + \sigma^2_{\eta(A)\beta} + \sigma^2_{\kappa(A\eta)} + \sigma^2_{\eta(A)} + JK\,\Phi(A)$
B	$\sigma^2_\epsilon + \sigma^2_{\kappa(A\eta)\beta} + \sigma^2_{\eta(A)\beta} + JK\,\Phi(B)$
AB	$\sigma^2_\epsilon + \sigma^2_{\kappa(A\eta)\beta} + \sigma^2_{\eta(A)\beta} + K\,\Phi(AB)$
E	σ^2_ϵ

Step 4 & 5

SOURCE	*EMS*
A	$\sigma^2_\epsilon + [\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)}] + [\sigma^2_{AB\eta} + \sigma^2_{B\eta}] + [\sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\sigma^2_{A\eta} + \sigma^2_{\eta}] + JK\Phi(A)$
B	$\sigma^2_\epsilon + [\underline{\sigma^2_{AB\kappa(\eta)}} + \underline{\sigma^2_{B\kappa(\eta)}}] + [\underline{\sigma^2_{AB\eta}} + \underline{\sigma^2_{B\eta}}] + IK\Phi(B)$
AB	$\sigma^2_\epsilon + [\underline{\sigma^2_{AB\kappa(\eta)}} + \underline{\sigma^2_{B\kappa(\eta)}}] + [\underline{\sigma^2_{AB\eta}} + \underline{\sigma^2_{B\eta}}] + K\Phi(AB)$
E	σ^2_ϵ

Table XXIII Pseudo EMS for the Two-factor design: restriction on AB

Step 1

A
B
$\eta(AB)$
$\kappa(AB\eta)$

Step 2

$$z_{ijmn} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \eta_{ijm} + \kappa_{ijmn} + \epsilon_{ijmn}$$

Step 3

SOURCE	*EMS*
A	$\sigma^2_\epsilon + \sigma^2_{\kappa(AB\eta)} + \sigma^2_{\eta(AB)} + JK\Phi(A)$
B	$\sigma^2_\epsilon + \sigma^2_{\kappa(AB\eta)} + \sigma^2_{\eta(AB)} + IK\Phi(B)$
AB	$\sigma^2_\epsilon + \sigma^2_{\kappa(AB\eta)} + \sigma^2_{\eta(AB)} + K\Phi(AB)$
E	σ^2_ϵ

Step 4 (No Step 5)

SOURCE	*EMS*
A	$\sigma^2_\epsilon + [\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)} + \sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\sigma^2_{AB\eta} + \sigma^2_{B\eta} + \sigma^2_{A\eta} + \sigma^2_{\eta}] + JK\Phi(A)$
B	$\sigma^2_\epsilon + [\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)} + \sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\sigma^2_{AB\eta} + \sigma^2_{B\eta} + \sigma^2_{A\eta} + \sigma^2_{\eta}] + IK\Phi(B)$
AB	$\sigma^2_\epsilon + [\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)} + \sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\sigma^2_{AB\eta} + \sigma^2_{B\eta} + \sigma^2_{A\eta} + \sigma^2_{\eta}] + K\Phi(AB)$
E	σ^2_ϵ

Table XXIV Pseudo EMS for the Two-factor design: restriction on A, then B within A

Step 1

A
B
$\eta(A)$
$\kappa(AB\eta)$
$\lambda(AB\eta\kappa)$

Step 2

$$y_{ijk} = \mu + \alpha_i + \eta_{im} + \beta_j + \alpha\beta_{ij} + \eta\beta_{ijm} + \kappa_{ijmn} + \lambda_{ijmno} + \epsilon_{ijmno}$$

Step 3

SOURCE	*EMS*
A	$\sigma^2_\epsilon + \sigma^2_{\lambda(AB\eta\kappa)} + \sigma^2_{\kappa(AB\eta)} + \sigma^2_{\eta(A)B} + \sigma^2_{\eta(A)} + JK\Phi(A)$
B	$\sigma^2_\epsilon + \sigma^2_{\lambda(AB\eta\kappa)} + \sigma^2_{\kappa(AB\eta)} + IK\Phi(B)$
AB	$\sigma^2_\epsilon + \sigma^2_{\lambda(AB\eta\kappa)} + \sigma^2_{\kappa(AB\eta)} + K\Phi(AB)$
E	σ^2_ϵ

Step 4 & 5

SOURCE	*EMS*
A	$\sigma^2_\epsilon + [\sigma^2_{AB\lambda(\eta\kappa)} + \sigma^2_{B\lambda(\eta\kappa)} + \sigma^2_{A\lambda(\eta\kappa)} + \sigma^2_{\lambda(\eta\kappa)}] + [\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)} + \sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\sigma^2_{AB\eta} + \sigma^2_{B\eta}] + [\sigma^2_{A\eta} + \sigma^2_{\eta}] + JK\Phi(A)$
B	$\sigma^2_\epsilon + [\sigma^2_{AB\lambda(\eta\kappa)} + \sigma^2_{B\lambda(\eta\kappa)} + \sigma^2_{A\lambda(\eta\kappa)} + \sigma^2_{\lambda(\eta\kappa)}] + [\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)} + \sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\underline{\sigma^2_{AB\eta}} + \underline{\sigma^2_{B\eta}}] + IK\Phi(B)$
AB	$\sigma^2_\epsilon + [\sigma^2_{AB\lambda(\eta\kappa)} + \sigma^2_{B\lambda(\eta\kappa)} + \sigma^2_{A\lambda(\eta\kappa)} + \sigma^2_{\lambda(\eta\kappa)}] + [\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)} + \sigma^2_{A\kappa(\eta)} + \sigma^2_{\kappa(\eta)}] + [\underline{\sigma^2_{AB\eta}} + \underline{\sigma^2_{B\eta}}] + K\Phi(AB)$
E	σ^2_ϵ

2.6.2 Rule Subset for Strong Bias Indication

Under certain conditions the general rules can be simplified. This may be helpful for consulting work when a model and associated EMS need to be constructed "on the fly," or for instructional purposes in experimental design courses. This subset of the general rules is equivalent to those produced by Anderson and McLean (1974a, 1974b), Lorenzen (1984), and Lorenzen and Anderson (1993a). There are two conditions under which the following subset of rules can be applied:

1. Run-order effects are additive (the assumption made in previous work by Anderson (1974a, 1974b), Lorenzen (1984), and Lorenzen and Anderson (1993a)), or

2. Only strong bias components are of interest. Because strongly biased non additive components are present when the main effect bias component is present we can interpret the main effect bias component as representing strong bias including any non additive effects that involve the main effect.

The subset rules are as follows:

1. Define factors and relationships.
   - Define the usual design factors and their relationships.
   - Starting at the top of the hierarchy, for each factor, or factor combination, that defines a hierarchical restriction, define a segment factor nested in the defining factors and any previously defined segment factor.

2. Create the full effects model using all defined factors but do not create interactions that involve segment factors, append an error term that includes previous subscripts. Label terms in the model as fixed, random, or mixed, in the usual manner (according to either of the two competing methods for mixed

models). Segment effect are considered random.

3. Calculate the EMS for terms that are not associated with segment effects and the error term, using standard EMS algorithms (Lorenzen and Anderson 1993b). The expectation is taken over all terms created in step 2.

The subset rules are now applied to the Two-factor design, restricted on A, then B within A (see **Table XXV**). The time-consuming steps, 4 and 5, are no longer required. The tests for all effects, A, B, and AB, exhibit strong bias due to the restriction on B within A. The test for the effects of A exhibits additional strong bias due to the restriction on A. Under nonadditivity these strong bias components include non additive components that involve the respective main effect.

Table XXV Subset of Pseudo EMS for the Two-factor design: restriction on A, then B within A

Step 1	Step 2	Step 3
A B $\eta(A)$ $\kappa(AB\eta)$ $\lambda(AB\eta\kappa)$ $E(AB\eta\kappa\lambda)$	$z_{ijmno}=\mu+\alpha_i+\eta_{im}+\beta_j+\alpha\beta_{ij}+\eta\beta_{ijm}+\kappa_{ijmn}+\lambda_{ijmno}+\epsilon_{ijmno}$	$\underline{SOURCE}$ $\underline{EMS}$ A $\sigma^2_\epsilon + \sigma^2_{\kappa(AB\eta)} + \sigma^2_{\eta(A)} + JK\Phi(A)$ B $\sigma^2_\epsilon + \sigma^2_{\kappa(AB\eta)} + IK\Phi(B)$ AB $\sigma^2_\epsilon + \sigma^2_{\kappa(AB\eta)} + K\Phi(AB)$ E σ^2_ϵ

2.7 SUMMARY OF SEGMENT RESTRICTIONS

Randomization, assignment of treatments to experimental units or run-order of experimental trials, is a cornerstone of statistical design of experiments. However, because of real world constraints it may be impractical to completely randomize. This introduces potential bias in tests concerning model parameters. This bias usually remains hidden when analyzing data using textbook linear model methods because the model provides no means for representing the underlying randomization process. Previous authors have suggested modifications to the linear model to allow for the representation of pertinent randomization information. Such modifications produced useful results but involved implicit strict additivity assumptions.

This chapter generalized previous results to allow for nonadditivity of run-order effects and treatment effects. This generalization also allows for the separation of information pertinent to treatment structure and information pertinent to randomization. Bias components, including those due to non additive effects are explicit in the expected mean squares. The existence and nature of both strong and weak bias components were discussed. It was shown that, while non additive bias components may be weak or strong, the presence of strong non additive bias components is indicated by main effect bias components. If restrictions are placed on factors of lesser importance then factors of greater importance will be weakly biased.

Rules were developed for construction of EMS that show the potential bias present when restricting randomization of run-order. These rules are adaptations of Bennet/Franklin type rules and are applicable to the class of hierarchically restricted balanced complete factorial designs. The rules indicate both the presence of bias due to restricted randomization and the strong or weak nature of the bias. A subset of these rules, effectively those used by Anderson and McLean (1974a, 1974b), Lorenzen (1984), and Lorenzen and Anderson (1993a), were also demonstrated and interpreted according to two alterative conditions.

CHAPTER 3

MODELING BLOCK RESTRICTIONS

3.1 INTRODUCTION

Chapter Two dealt with restrictions in time at the discretion of the experimenter. This chapter deals with designs that involve inherent relationships among the experimental material that result in restrictions on the randomization process. These designs involve blocking- the non random grouping of similar experimental material. The effects of such restriction on randomization are not completely represented by the classical linear model, as pointed out previously by authors such as Wilk (1955), Kempthorne (1955), Scheffe (1959), Anderson and McLean (1974a), and Hinkelmann and Kempthorne (1994). In particular, there has been discussion and disagreement on the whether and how to test for block effects (Hocking 1973; Samuels et al. 1991). In his review of Samuels et al. (1991), Speed summarized eloquently:

> ... this mixed-model muddle is a self-inflicted wound that can only be healed by genuinely returning to those notions and principles that authors claimed guided their thinking: populations of units and sampling and randomization procedures (Speed 1991, p. 810).

Example 3.1 The CRD and RCBD: Confusing Similarities

Two experiments are described in parallel to illustrate the apparent similarities and the differences between the CRD and RCBD. The CRD has two factors and is replicated once. The RCBD has one blocking factor and one treatment factor and is replicated once. The effects of the two treatment factors in the CRD are assumed additive, as are the block and treatment effects in the RCBD.

Table XXVI The CRD and RCBD: Confusing similarities

CRD: An experiment is conducted to assess the effects of drug type and dietary salt on a response of interest. Four rats serve as the experimental subjects (all from the same litter).	**RCBD**: An experiment is conducted to assess the effect of drug type on a response of interest. Rats from two litters serve as the experimental subjects with both drugs randomly assigned to the rats from each litter.
DRUG A B SALT Low O O High O O	DRUG A B Litter 1 O O 2 O O
The linear model is $y_{ijk}=\mu+s_i+d_j+\epsilon_{ijk}$ where y_{ijk} = response of the kth rat receiving the ijth treatment (i=1,...,I, j=1,...,J, k=1,...,K, where I=2, J=2, and K=1) μ = overall mean, s_i = effect of the ith level of salt, d_j = effect of the jth level of drug, ϵ_{ijk} = additional error effect when the ijth treatment is applied to the kth rat to receive that treatment. $\epsilon_{ijk} \sim N(0, \sigma_\epsilon^2)$ and independent, all other effects are considered fixed.	The linear model is $y_{ijk}=\mu+l_i+d_j+\epsilon_{ijk}$ where y_{ijk} = response of the kth rat of the ith lab receiving the ijth treatment (i=1,...,I, j=1,...,J, k=1,...,K, where I=2, J=2, and K=1) μ = overall mean, l_i = effect of the ith level of litter, d_j = effect of the jth level of drug, ϵ_{ijk} = additional error effect when the jth treatment is applied to the kth rat to receive that treatment from the ith litter. $l_i \sim N(0, \sigma_l^2)$ and independent, $\epsilon_{ijk} \sim N(0, \sigma_\epsilon^2)$ and independent, all other effects are considered fixed.
Partitioning the sums of squares and calculating the EMS according to the defined model yields the standard EMS table for the CRD:	Partitioning the sums of squares and calculating the EMS according to the defined model yields the standard EMS table for the RCBD:

SOURCE	*df*	*EMS*
Salt	$I-1$	$\sigma_\epsilon^2 + J\Phi(S)$
Drug	$J-1$	$\sigma_\epsilon^2 + I\Phi(D)$
Error	$(I-1)(J-1)$	σ_ϵ^2

From inspection of the EMS it appears that there are unbiased tests for both the Salt and Drug effect using MSE as the denominator of the F-test.

Design Information Absent from the Linear Model: Randomization Process

Salt-Drug combinations are randomly assigned to rats.

SOURCE	*df*	*EMS*
Litter	$I-1$	$\sigma_\epsilon^2 + J\sigma_l^2$
Drug	$J-1$	$\sigma_\epsilon^2 + I\Phi(D)$
Error	$(I-1)(J-1)$	σ_ϵ^2

From inspection of the EMS it appears that there are unbiased tests for both the Litter and Drug effect using MSE as the denominator of the F-test.

Design Information Absent from the Linear Model: Randomization Process

Drug levels are randomly assigned to rats. Litter of origin is not subject to experimental control.

Comparing the models and EMS tables for the two designs it is not clear that a fundamental difference exists, in fact they appear virtually identical. The difference lies in the process of assigning treatments to experimental units. In the CRD any Salt-Drug combination can be assigned to a rat whereas in the RCBD only a level of Drug can be assigned to a rat because its Litter of origin is not subject to experimental control. The similarity of designs in **Table XXVI** is due to the absence of this information in the description of the linear model and associated EMS. The "apparent" unbiased test for Litter is, in fact, biased, but the process of randomization must be explicitly modeled in order to demonstrate this.

This chapter examines "Blocking" (which, for now, we generalize as the non random grouping of experimental material) as a restriction on randomization. The approach used is similar to that used for restrictions in time, or "Segmentation", discussed in Chapter Two. Analogous methods can be used to model the effects of blocking i.e., treating the realized

observations as a randomly selected fraction of the potential observations. The difference lies in the population of potential observations and the manner in which randomization is restricted. The methodology developed is general to the class of hierarchically blocked complete factorial designs. Hierarchical blocking infers a hierarchy of experimental material, such as School, Class within School, and Student within Class. The levels of each of these factors can serve as experimental units to which a factorial treatment structure can be randomly assigned. Designs in this class include CRD, RCBD, Split-Plot, Split-Split-Plot, etc., and can involve subsampling at any level of experimental material. Once the methodology is developed, alternative models are presented based on varying assumptions (e.g., the usual assumption of no block-treatment interaction is relaxed). In particular, the conditions leading to tests of Block and Treatment effects are examined.

3.2 DERIVATION

While the methodology is similar, the parameter definitions for blocking differ from those of segmenting as given in Chapter Two. Here, we focus on the intrinsic structure of the experimental material. Consider a Generalized RCBD (GRCBD: an RCBD where treatment is replicated within each block, see Gates 1995) with a single treatment factor and subsampling. First define the conceptual mean, Δ_{ijmn}, according to Wilk (1955). Δ_{ijmn} is the conceptual deterministic component of the response if treatment j is applied to unit m (implies all subunits of unit m as well) of block i. For segmentation (Chapter Two) a notational convenience, @, was introduced to separate subscripts associated with the usual effects from subscripts associated with the effects describing the randomization process. For blocking the distinction is not as clear because the subscripts associated with the usual effects are also associated with the randomization process. The use of such a separator contorts the order, familiar to most users, that portrays the hierarchy of experimental material and its relationship to other factors. For this reason the notational convenience of Chapter Two is not adopted for use here. An equivalent algebraic expression for Δ_{ijmn} in terms of means and deviations from means is given by

$$\Delta_{ijmn} = \left[\bar{\Delta}_{....}\right] + \left[(\bar{\Delta}_{i...} - \bar{\Delta}_{....})\right] + \left[(\bar{\Delta}_{.j..} - \bar{\Delta}_{....})\right] + \left[(\bar{\Delta}_{ij..} - \bar{\Delta}_{i...}) - (\bar{\Delta}_{.j..} - \bar{\Delta}_{....})\right] + \left[(\bar{\Delta}_{i.m.} - \bar{\Delta}_{i...})\right] +$$
$$\left[(\bar{\Delta}_{ijm.} - \bar{\Delta}_{i.m.}) - (\bar{\Delta}_{ij..} - \bar{\Delta}_{i...})\right] + \left[(\bar{\Delta}_{i.mn} - \bar{\Delta}_{i.m.})\right] + \left[(\bar{\Delta}_{ijmn} - \bar{\Delta}_{i.mn}) - (\bar{\Delta}_{ijm.} - \bar{\Delta}_{i.m.})\right]$$

If "effects" are defined according to **Table XXVII** then Δ_{ijmn} may be reparameterized as

$$\Delta_{ijmn} = \mu + \beta_i + \tau_j + \beta\tau_{ij} + u_{im} + \tau u_{ijm} + v_{imn} + \tau v_{ijmn}$$

These parameters are conceptual because all treatments cannot be applied to a given experimental unit in a realized experiment. The following conditions are implicit in the parameter definitions:

$$\sum_i \beta_i = \sum_j \tau_j = \sum_i \beta\tau_{ij} = \sum_j \beta\tau_{ij} = \sum_m u_{im} = \sum_j \tau u_{ijm} = \sum_m \tau u_{ijm} = \sum_n v_{imn} = \sum_j \tau v_{ijmn} = \sum_n \tau v_{ijmn} = 0$$

Table XXVII Parameter definition for the GRCBD with subsampling

$\mu = [\bar{\Delta}_{....}]$	Grand mean: overall mean response of all treatments applied to all units in all blocks.
$\beta_i = [(\bar{\Delta}_{i...} - \bar{\Delta}_{....})]$	Block effect: difference between the mean response of all treatments applied to all units of block i and the overall mean response.
$\tau_j = [(\bar{\Delta}_{j..} - \bar{\Delta}_{....})]$	Treatment effect: difference between the mean response of treatment j applied to all units of all blocks and the overall mean response.
$\beta\tau_{ij} = [(\bar{\Delta}_{ij..} - \bar{\Delta}_{i...}) - (\bar{\Delta}_{j..} - \bar{\Delta}_{....})]$	Block-Treatment interaction: difference between the treatment effect within block i and the overall treatment effect.
$u_{im} = [(\bar{\Delta}_{i.m.} - \bar{\Delta}_{i...})]$	Unit-error effect: difference between the mean response of all treatments applied to unit m of block i and the mean response of all treatments applied to all units of block i.
$\tau u_{ijm} = [(\bar{\Delta}_{ijm.} - \bar{\Delta}_{i.m.}) - (\bar{\Delta}_{ij..} - \bar{\Delta}_{i...})]$	Treatment-Unit-error interaction: difference between the treatment effect within unit m of block i and the treatment effect within block i.
$v_{imn} = [(\bar{\Delta}_{i.mn} - \bar{\Delta}_{i.m.})]$	Subsampling-error effect: difference between the response of all treatments applied to sub unit n of unit m of block i and the mean response of all treatments applied to all sub units of unit m of block i.
$\tau v_{ijmn} = [(\bar{\Delta}_{ijmn} - \bar{\Delta}_{i.mn}) - (\bar{\Delta}_{ijm.} - \bar{\Delta}_{i.m.})]$	Treatment-Subsampling-error interaction: difference between the treatment effect within subunit n of unit m of block i and treatment effect within unit m of block i.

Let z_{ijmn} be the potential response if treatment j is applied to unit m, and hence subunit n of unit m of block i:

$$z_{ijmn} = \Delta_{ijmn} + \epsilon_{ijm} + \delta_{ijmn}$$

The stochastic component, ϵ_{ijm}, is part of experimental error and assumed to be distributed iid $N(0,\sigma_\epsilon^2)$ (Unit-error effect and Treatment-Unit-error interaction from **Table XXVII** are deterministic components of experimental error). ϵ_{ijm} may be an expression of treatment

error (the inability to reproduce treatment conditions exactly) or random fluctuations in the state of the experimental unit (Hinkelmann and Kempthorne 1994). δ_{ijmn} is part of subsampling error or may be an expression of random fluctuations in the subunits, and is assumed to be distributed iid $N(0,\sigma^2_\delta)$.

The model for the potential responses can be written in matrix notation.

$$_{IJMN}z_1 = {}_{IJMN}X_{P\ P}\theta_1$$

where $\theta' = [\mu, \beta_1, \beta_2, ..., \tau\nu_{IJMN}, \epsilon_{111}, \epsilon_{112}, ..., \epsilon_{IJM}\delta_{1111}, \delta_{1112}, ..., \delta_{IJMN}]$
X = design matrix relating z and θ
P = # of parameters in the model

(To avoid the use of multiple design matrices (X matrices) all effects are included in the vector θ). Not all potential responses can be realized for a given experiment. For example, in a standard RCBD (a single replication within each block), if unit 1 from block 1 is assigned treatment 1, then no other unit from block 1 can be assigned treatment 1. For any realizable experiment a selection matrix, T, is constructed that links the realizable observations, y (in standard lexicographic order), to the potential responses, z.

$$_{IJK}y_1 = {}_{IJK}T_{IJMN}\ {}_{IJMN}z_1 + {}_{IJK}\eta_1$$

where $T = [t_{1111}, t_{1112}, ..., t_{IJMN}]$ and t_{ijmn} is column vector, and
$\eta \sim MV(0, I\sigma^2_\eta)$ and represents observational error

T is a random matrix that represents the randomization used in the experiment. Each of the IJK rows of T corresponds to a realizable response and each of the IJMN columns of T corresponds to a potential response. If a potential response is realized for a particular experiment then the corresponding row and column of T contains a one, otherwise it contains a zero.

We have added an extra component, η, or observational error. While not necessarily a function of the experimental material, observational error is, in practice, often "lumped" with experimental error or subsampling error. Because the nature of the experimental material is central to the results of this chapter, we briefly consider observational error in order to clearly distinguish from experimental error or subsampling error. Conceptually, η is realized when the *observation* is made, not necessarily when the treatment is applied to the experimental unit. In fact, it may be possible to modify observational error after the experiment has been performed. For example, consider an experiment performed to study the degradation of vitamins under various freeze-dried storage conditions. The lab technician who made the original observations used a flawed measurement technique. A second set of observations is made by another technician using a correct measurement technique and observational error is greatly reduced (a basic assumption is that the experimental material remains in a stable state once the treatment is applied). One final point should be made regarding observational error. If observations are made sequentially in time and are subject to outside influences (fatigue of the observer, equipment warm-up, etc.) then observation-order ought to be randomized just as run-order is randomized. Consequently all the results of Chapter Two could be applied to observation order as well as run-order of the experiment. With an understanding of when observational error is produced, η will be ignored resulting in the model:

$$z = X\theta$$

and

$$y = Tz$$

In an ANOVA table the sum of squares for the p^{th} term in the model can be expressed as

$$SS_p = y'Q_p y = z'T'Q_p Tz$$

$E(SS_p)$ is found in a similar fashion as in Chapter 2:

$$E(SS_p) = tr(X'R_pX\ COV(\theta)) + E(\theta')X'R_pX\,E(\theta) \qquad (163)$$

where $R_p = E(T'Q_pT)$. The EMS_p are found by dividing the $E(SS_p)$ by the appropriate degrees of freedom. The evaluation of the EMS_p requires R_p which, in turn, requires:

$$E(t_{ijmn}),\ \text{a column of}\ E(T)$$

and

$$COV(t_{ijmn}t_{i'j'm'n'}) = E(t_{ijmn}t'_{i'j'm'n'}) - E(t_{ijmn})E(t'_{i'j'm'n'})$$

These moments contain information pertinent to the randomization process. Up to this point, the development of the results has closely paralleled those for segmentation, presented in Chapter Two. However, in blocked designs the population of potential observations and randomization process differ from those of segmentation, so the general methodology for finding the moments of T is a point of departure. Before deriving the general methodology for finding these moments, an example is presented to demonstrate the results thus far.

Example 3.2a Modeling the Potential Observations for an RCBD

An experiment is conducted to test the effects of two levels of a Drug. Tests will be performed using two rats from each of two Litters. A single observation will be made on each rat. Within each Litter the two Drugs are randomly assigned to the rats. Three subscripts, *ijm*, index the levels of Litter, Drug, and Rat, respectively. Given the experiment as described, the vector of potential responses, z is modeled as follows:

$$z = \begin{bmatrix} z_{111} \\ z_{112} \\ z_{121} \\ z_{122} \\ z_{211} \\ z_{212} \\ z_{221} \\ z_{222} \end{bmatrix} = X\theta = \begin{bmatrix} 1 & 1 & 0 & 1 & 0 & 1 & & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 & & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 & \cdots & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 & & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & & 0 & 1 \end{bmatrix} \begin{bmatrix} \mu \\ \beta_1 \\ \beta_2 \\ \tau_1 \\ \tau_2 \\ \beta\tau_{11} \\ \vdots \\ \epsilon_{221} \\ \epsilon_{222} \end{bmatrix} \quad \textbf{(166)}$$

For any realizable experiment y is linked to z by a selection matrix T, where the subscripts of y, ijk, index the levels of Lab, Drug, and replication within a Lab-Drug combination, respectively.

$$\begin{bmatrix} y_{111} \\ y_{121} \\ y_{211} \\ y_{221} \end{bmatrix} = T \begin{bmatrix} z_{111} \\ z_{112} \\ z_{121} \\ \vdots \\ z_{222} \end{bmatrix} \quad \textbf{(167)}$$

There is not a 1-to-1 correspondence between y and z based on similar subscripts, i.e., y_{111} may be realized as either z_{111} or z_{112}. Specifically, a subscript of z that indexes unique experimental units within a block is mapped to a subscript of y that indexes the number of experimental units within a block *for a given treatment* level. For example, m indexes the m^{th} Rat from Lab i regardless of the level of Drug, while k indexes the k^{th} Rat from Lab i to receive the j^{th} level of Drug. It is important to clearly define the subscripts because they are involved in defining the probabilities associated with the randomization process.

For this experiment there are only four (equally probable) potential assignments of Drug

to Rats and they can be represented by four **T** matrices:

$$T_1=\begin{bmatrix}1&0&0&0&0&0&0&0\\0&0&0&1&0&0&0&0\\0&0&0&0&1&0&0&0\\0&0&0&0&0&0&0&1\end{bmatrix}$$

$$T_2=\begin{bmatrix}1&0&0&0&0&0&0&0\\0&0&0&1&0&0&0&0\\0&0&0&0&0&1&0&0\\0&0&0&0&0&0&1&0\end{bmatrix}$$

$$T_3=\begin{bmatrix}0&1&0&0&0&0&0&0\\0&0&1&0&0&0&0&0\\0&0&0&0&1&0&0&0\\0&0&0&0&0&0&0&1\end{bmatrix}$$

$$T_4=\begin{bmatrix}0&1&0&0&0&0&0&0\\0&0&1&0&0&0&0&0\\0&0&0&0&0&1&0&0\\0&0&0&0&0&0&1&0\end{bmatrix}$$

To evaluate the EMS requires both

$$E(t_{ijm}),\ \text{a column of } E(T)$$

and

$$COV(t_{ijm},t_{i'j'm'})=E(t_{ijm}t'_{i'j'm'})-E(t_{ijm})E(t'_{i'j'm'})$$

Because there are only a few possible T matrices it is easy to show, for example, that

$$E(\boldsymbol{T}) = \begin{bmatrix} .5 & .5 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & .5 & .5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & .5 & .5 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & .5 & .5 \end{bmatrix}$$

and

$$COV(t_{111}, t_{211}) = E(t_{111} t'_{211}) - E(t_{111}) E(t'_{211})$$

$$\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 0 & .25 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} - \begin{bmatrix} 0 & 0 & .25 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

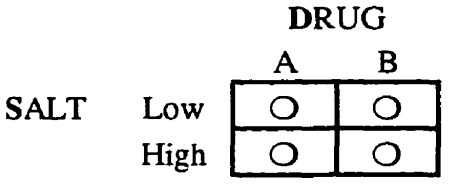
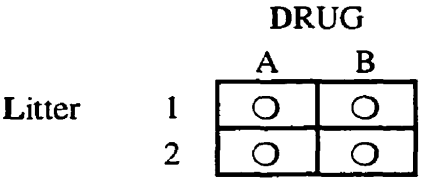
where t_{111} and t_{211} are the 1^{st} and 5^{th} column of $\boldsymbol{T}$ respectively

All remaining pair-wise moments are found in a similar manner. With these moments computed, the EMS_p can be found according to (**163**). The computation of these moments can be accomplished by brute force, however, this is tedious for the simple case and infeasible for designs of increased complexity. As was done for segment restrictions, a general solution is developed to calculate moments of $\boldsymbol{T}$ for designs that involve blocking.

Example 3.2b Contrasting the Potential Observations for the CRD and RCBD

To further clarify the difference between segmentation and blocking, we continue with the previous example and show the vector of potential observations, z, for the CRD and RCBD. The populations of potential observations differ because in the CRD randomization is restricted at the discretion of the experimenter (i.e., there may be none), whereas in the RCBD randomization is restricted due to the inherent structure of the experimental material. The $\boldsymbol{T}$ selection matrices associated with each z are not even the same dimension.

Table XXVIII Potential Observations for the CRD and RCBD

CRD: An experiment is conducted to assess the effects of drug type and dietary salt on a response of interest. Four rats serve as the experimental subjects (all from the same litter).	**RCBD**: An experiment is conducted to assess the effect of drug type on a response of interest. Rats from two litters serve as the experimental subjects with both drugs randomly assigned to the rats from each litter.
	

Elements of z are z_{ijm} where i=1,...,2, j=1,...,2, and m=1,...,4 index the level of SALT, DRUG, and RAT respectively for a total of 16 potential observations:

$$z = \begin{bmatrix} z_{111} \\ z_{112} \\ z_{113} \\ z_{114} \\ z_{121} \\ z_{122} \\ z_{123} \\ z_{124} \\ z_{211} \\ z_{212} \\ z_{213} \\ z_{214} \\ z_{221} \\ z_{222} \\ z_{223} \\ z_{224} \end{bmatrix}$$

Elements of z are z_{ijm} where i=1..2, j=1..2, and m=1..2 index the level of LITTER, DRUG, and RAT within LITTER respectively for a total of eight potential observations:

$$z = \begin{bmatrix} z_{111} \\ z_{112} \\ z_{121} \\ z_{122} \\ z_{211} \\ z_{212} \\ z_{221} \\ z_{222} \end{bmatrix}$$

3.3 A GENERAL METHOD

A general method will now be developed for calculating moments of $\boldsymbol{T}$ for the class of complete factorial designs with hierarchical structure on the experimental material. This hierarchical structure implies a hierarchical grouping of the experimental material. The factors that define these groupings will be called *cluster factors* (Milliken and Johnson 1984), calls them design factors). For example, the cluster factor *School* groups *Classes*, and the cluster factor *Classes* groups *Students*. Factors that define the treatments or treatment combinations that are to be applied to the experimental material will be called *treatment factors*. For example, the treatment factors Temperature and Humidity, with two and three levels respectively, define six treatment combinations. *Experimental units* (EU's) are the smallest units of experimental material to which treatments are independently applied. Different sets of treatments may be applied to experimental material from different levels in the hierarchy, resulting in a hierarchy of experimental units (i.e., split-plot type experimental structures). A *Block* is a cluster of experimental units, where all appropriate treatments are randomly assigned to the experimental units within the cluster. Here, appropriate treatments are those belonging to the set of treatments that define the experimental units. *Observational units* (OU's) are the units of experimental material on which observations are made, and may or may not be the same as experimental units.

The class of experimental structures defined above is quite broad as demonstrated in **Figure 4** (a modified structure diagram, Taylor and Hilton 1981) where the hierarchical relationships among cluster factors and treatment factors are shown.. If a cluster factor is connected to any other factors by a strictly upward path (the path may include other factors) then it is considered nested in those factors. If there is no nesting relationship between two factors then they are considered crossed. The structure diagram is modified by imposing a *design level* super structure on it, represented by *design levels* 0, 1, and 2 in **Figure 4**. A design level k (k=1,...,K) includes experimental unit EU_k, the treatment factors that define EU_k, and any cluster factors nested in EU_k that are not EU factors themselves or nested in other EU factors. Design level 0 includes any blocking factor for EU_1 and any cluster factors

above the blocking factor. Cluster factors are indexed from the top of the hierarchy using two subscripts: the first ($i=1,...,I_k$) indexes cluster factor within design level, the second ($k=1,...,K$) indexes design level. Treatment factors with a common design level are indexed arbitrarily (from $j=1,...,J$). The smallest cluster units for a given level k will be called *subsampling units* (SSU's), where SSU's for design level k are the blocks for design level (k+1), and SSU's for level K are also the OU's. The structure diagram demonstrates the repetitive and hierarchical framework used in development of the general methodology. For example, SSU's from one level of the hierarchy can serve as blocking units for the next level (e.g., Cluster Factor 3,1).

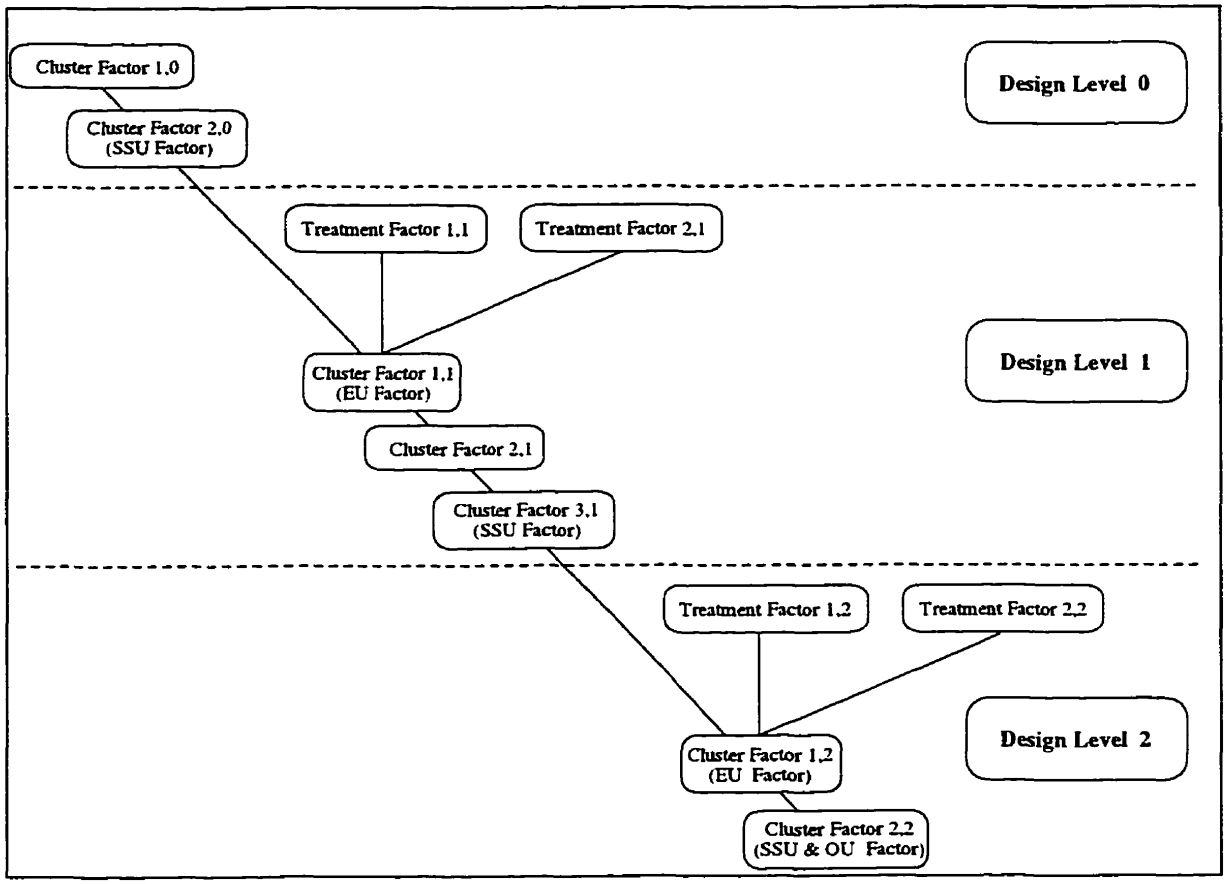


Figure 4 Modified Structure Diagram for designs with blocking, replication, multiple levels of E.U.'s, and subsampling.

In summary, the SSU's of design level 0 are the blocks for design level 1. Each design

level k (k=1,...,K) is defined by the independent application of treatment combinations to experimental units (EU's) which may be further subdivided into hierarchical subsets of experimental material (the smallest of which is the SSU). The SSU's for level k are the blocks for the next design level, k+1. The structure of design level k+1 is repeated for each SSU at design level k. The SSU's of design level 0 are the blocks for design level 1. This basic pattern of hierarchical design levels with independent randomizations at each level is exploited in the development of the general methodology.

The following example is for a split-plot design and demonstrates the modified structure diagram for a specific design (**Figure 5**):

> A school district wants to evaluate two methods of teaching science (based on right/left brain learning styles). They are also interested in comparing three individual review methods: computer assisted review, standard homework assignments, and a combination of the two. Two *schools* will be randomly selected to be involved in the evaluation, with two grade seven *classes* from each *school*. Each of the *teaching methods* will be randomly assigned to a *class* from each *school*. The *students* in each *class* will be randomly assigned to the three *review methods*. The final exam scores will be used to assess the effects of the *teaching methods* and *review methods*.

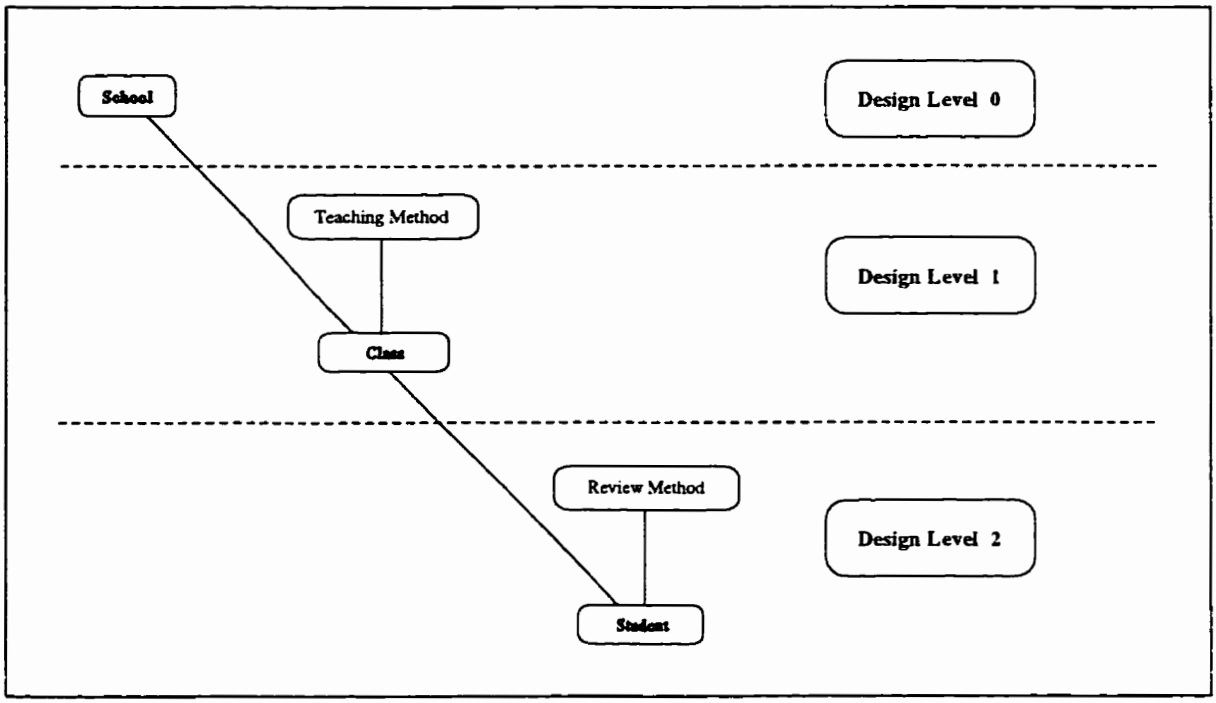


Figure 5 Modified Structure Diagram for Split-Plot Experimental Design

Class is the experimental unit to which the treatment *Teaching Method* is applied and these two factors constitute *design level 1*. *School* serves as a blocking factor for *Classes* and constitutes *design level 0*. *Student* is the experimental unit to which the treatment *Review Method* is applied and these two factors constitute *design level 2*. *Class* also serves as a blocking factor for *Students*.

The randomization of treatment combinations to EU's is performed independently for each of the K hierarchical design levels. This means that the probability structure associated with the entire design can be built up from K independent and hierarchical substructures, where $P(event_k \text{ and } event_{k'}) = P(event_k)P(event_{k'})$ for $k \neq k'$. Given the hierarchical nature of the probability structure and the independence between the design levels, the Kronecker product is a natural operator to use because it multiplies each element of the first matrix by the every element of the second matrix. The theorems that define a general solution for the moments of $\boldsymbol{T}$ make effective use of this property.

3.3.1 Notation

We now define a general notation similar to segmentation but with an added layer of complexity to distinguish between treatment factors and cluster factors that model the inherent structure of the experimental material.

Let:

U_{ik} = i th cluster factor in the k th design level
(i=1,...,I_k, k=[0,]1,...,K where k=0 is optional)

F_{jk} = j th treatment factor in the k th design level
(j=1,...,J_k, k=1,...,K)

$L_{U_{ik}}$ = # of levels of U_{ik} nested within each level of the previous cluster factor
($U_{(i-1)k}$ for i>1, $U_{I_{(k-1)}(k-1)}$ for i=1)

$L_{F_{jk}}$ = # of levels of F_{jk}

u_{ik} = 1,...,$L_{U_{ik}}$, index for factor U_{ik}

f_{jk} = 1,...,$L_{F_{jk}}$, index for factor F_{jk}

The hierarchy of factors in a structure diagram (**Figure 4**) can be equivalently represented as an ordered list, where factors within a common design level are bracketed:

$$[U_{10}, U_{20},..., U_{I_0 0}]\,[F_{11}, F_{21},..., F_{J_1 1}, U_{11}, U_{21},..., U_{I_1 1}]... \\ [F_{1K}, F_{2K},..., F_{J_K K}, U_{1K}, U_{2K},..., U_{I_K K}] \qquad \textbf{(176)}$$

The structure diagram gives a visual, or more heuristic, description while the ordered list is amenable to algorithmic development and can be thought of as the basis for the theorems to be presented. This is the order of hierarchical models familiar to most users and will often be referenced in shorthand (e.g., $U_{10},U_{20},...,U_{I_K K}$).

The U_{ik} factors and corresponding indices uniquely identify the experimental material prior to treatment assignment (e.g., a specific rat from a specific litter). Factors and corresponding indices associated with realizable observations do not uniquely identify the

experimental material, instead they identify replications within a treatment. Such replication factors can be defined prior to the actual treatment assignment and are defined as follows: for each cluster factor U_{ik} define a replicate factor R_{ik} (R for replicate instead of U for Unit) and index R_{ik} in terms of replication (e.g., the r[th] rat from a specific litter to receive a specific treatment):

R_{ik} = i^{th} replicate factor in the k^{th} design level
(i=1,...,I_k, k=[0,]1,...,K where k=0 is optional)

$$L_{R_{1k}} = \left(\frac{L_{U_{1k}}}{\prod_{j=1}^{J_k} F_{jk}} \right) \quad \text{for } i=1 \text{ and } k=1,...,K$$

= # of *replicates* of R_{1k} nested within the previous cluster factor ($R_{I_{k-1}(k-1)}$) and all treatment factors of the same design level (F_{jk} for j=1...J_k)

$L_{R_{ik}} = L_{U_{ik}}$ for i=2,...,I_k and k=1,...,K
= # of *replicates* of R_{ik} nested within the previous cluster factor ($R_{(i-1)k}$)

We can now write the linear model:

$$y = Tz \tag{178}$$

where

$$y = \begin{bmatrix} y_{1,1,...,1} \\ y_{1,1,...,2} \\ \vdots \\ y_{L_{R_{10}}, L_{R_{20}}, ..., L_{R_{I_K K}}} \end{bmatrix}$$

A vector of realized observations with factors and replicates in lexicographic order. y is size $\left(\left(\prod_{i=1}^{I_k} \prod_{k=0}^{K} L_{R_{ik}} \right) \left(\prod_{j=1}^{J_k} \prod_{k=1}^{K} L_{F_{jk}} \right) \right)$ x 1.

$$z = \begin{bmatrix} z_{1,1,\ldots,1} \\ z_{1,1,\ldots,2} \\ \vdots \\ z_{L_{U_{10}},L_{U_{20}},\ldots,L_{U_{I_K K}}} \end{bmatrix}$$

A vector of potential observations with factors and units in lexicographic order. z is size $\left(\left(\prod_{i=1}^{I_k}\prod_{k=0}^{K} L_{U_{ik}}\right)\left(\prod_{j=1}^{J_k}\prod_{k=1}^{K} L_{F_{jk}}\right)\right)$ x 1.

T

A selection matrix indicating which potential observations are realized and is size

$$\left(\left(\prod_{i=1}^{I_k}\prod_{k=0}^{K} L_{R_{ik}}\right)\left(\prod_{j=1}^{J_k}\prod_{k=1}^{K} L_{F_{jk}}\right)\right) \text{ x } \left(\left(\prod_{i=1}^{I_k}\prod_{k=0}^{K} L_{U_{ik}}\right)\left(\prod_{j=1}^{J_k}\prod_{k=1}^{K} L_{F_{jk}}\right)\right)$$

For T, as defined in **(178)**, the columns indicate potential observations and the rows indicate realizable observations. For a given experiment, if a potential observation is realized then the appropriate row-column of T is one, otherwise it is zero. The $E(T)$ and $E(t_{u_{10},u_{20},\ldots,u_{I_K K}} t'_{u'_{10},u'_{20},\ldots,u'_{I_K K}})$ (the columns of T) can be computed using the Kronecker operator,

with potential observations associated with columns of the Kronecker operands and realizable observations associated with rows of the Kronecker operands. Working with an ordered list of factors, such as that found in **(176)**, the first two moments of T are given in Theorems 3 and 4 respectively. We will state and prove the general results, then show a specific example. It should be noted that the elements of T are equal to one if an event occurs, and are equal to zero otherwise, so the expected value of an element of T is equivalent to the probability that the event occurs. In such circumstances the expression "expected value" may be replaced by "probability".

Theorem 3

$$E(T) = \left[I\left(\prod_{i=1}^{I_0} L_{U_{i0}}\right)\right] \otimes \left[\bigotimes_{k=1}^{K} \left[\left[I\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)\right] \otimes \left[\frac{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)^{J\left(\prod_{i=1}^{I_k} L_{U_{ik}}\right)}}{\left(\prod_{i=1}^{I_k} L_{U_{ik}}\right)}\right]\right]\right] \quad \textbf{(182)}$$

where the Kronecker multiplier operator, $\bigotimes_{k=1}^{K}$, is defined such that

$\bigotimes_{k=1}^{K} \mathrm{M}_k = \mathrm{M}_1 \otimes \mathrm{M}_2 \otimes \ldots \otimes \mathrm{M}_K$, given M_k is a matrix

This can be rewritten in terms of three components, **B**, **C**, and **D** as:

$$E(T) = \mathbf{B}_0 \otimes \left[\bigotimes_{k=1}^{K} \mathbf{B}_k\right]$$

where

$$\mathbf{B}_0 = \left[I\left(\prod_{i=1}^{I_0} L_{U_{i0}}\right)\right]$$

$$\mathbf{B}_k = [\mathbf{C} \otimes \mathbf{D}]$$

$$\mathbf{C} = \left[I\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)\right]$$

$$\mathbf{D} = \left[\frac{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)^{J\left(\prod_{i=1}^{I_k} L_{U_{ik}}\right)}}{\left(\prod_{i=1}^{I_k} L_{U_{ik}}\right)}\right]$$

Proof:

Substructure **D** (defines the conditional probability that a potential observation is realized for a given treatment and for a given design level k):

For each of the $\prod_{j=1}^{J_k} L_{F_{jk}}$ treatment combinations for a given design level k, there are $L_{R_{1k}}$ replications and $\prod_{i=2}^{I_k} L_{R_{ik}}$ subsamples per replicate, for a total of $\prod_{i=1}^{I_k} L_{R_{ik}}$ realizable observations. There are $L_{U_{1k}}$ potential EU's and $\prod_{i=2}^{I_k} L_{U_{ik}}$ potential SSU's per EU for a total of $\prod_{i=1}^{I_k} L_{U_{ik}}$ potential observations. The probability that a potential observation becomes one specific realized observation is $\left(\frac{1}{\prod_{i=1}^{I_k} L_{U_{ik}}} \right)$.

The probability that the potential observations (represented by the columns of $\boldsymbol{T}$) become specific realized observations (represented by the rows of $\boldsymbol{T}$) can be represented by the matrix $\mathbf{D} = \left(\frac{\prod_{i=1}^{I_k} L_{R_{ik}} \prod_{i=1}^{J_k} L_{U_{ik}}}{\prod_{i=1}^{I_k} L_{U_{ik}}} \right)$.

Substructure **C** (defines the marginal probability that a potential treatment is realized for a given design level k, because all treatments are realized the probability is 1):

Each of the $\prod_{j=1}^{J_k} L_{F_{jk}}$ potential treatment combinations for a given k is realized with

probability=1, represented by the matrix $\mathbf{C} = \left(\begin{matrix} I_{J_k} \\ \prod_{j=1} L_{F_{jk}} \end{matrix} \right)$.

Substructure $\mathbf{B}_k$ (for a given design level k, defines the probability that a potential observation for a specified treatment is realized by combining the conditional probabilities of substructure **D** and the marginal probabilities of substructure C):

Multiplying each element of the treatment probability structure, **C**, by the within treatment probability structure, **D**, results in $\mathbf{B}_k = \left(\begin{matrix} I_{J_k} \\ \prod_{j=1} L_{F_{jk}} \end{matrix} \right) \otimes \left(\frac{\prod_{i=1}^{I_k} L_{R_{ik}} \quad \prod_{i=1}^{J_{I_k}} L_{U_{ik}}}{\prod_{i=1}^{I_k} L_{U_{ik}}} \right)$.

Complete Structure E(*T*) (independent randomizations are performed at each of the k hierarchical design levels, the probabilities associated with design level K are multiplied by the probabilities associated with design level (K-1), and this is done for all k until k=0):

$\mathbf{B}_{k-1}$ represents the probability that the potential blocks for level k are realized. Blocks (for k>1) are not realized with probability 1 because the realized blocks are a function of the randomization performed at level (k-1). Multiplying each probability in $\mathbf{B}_{k-1}$ by the within block probability structure, $\mathbf{B}_k$, can be performed by $\left(\mathbf{B}_{k-1} \otimes \mathbf{B}_k\right)$, which is the within block structure for level (k-1). $\mathbf{B}_{k-2}$ represents the probability that the potential blocks for level (k-1) are realized. Multiplying each probability in $\mathbf{B}_{k-2}$ by the within block probability structure, $\mathbf{B}_{k-1}$, can be performed by $\left(\mathbf{B}_{k-2} \otimes \mathbf{B}_{k-1}\right)$, which is the within block structure for level (k-2).

This continues until the within block probability structure, $\mathbf{B}_1$, is multiplied by each probability in its block structure, $\mathbf{B}_0$, where

$$\mathbf{B}_0 = \begin{cases} \begin{pmatrix} \boldsymbol{I}_{I_0} \\ \prod_{i=1}^{I_0} L_{R_{i0}} \end{pmatrix}, & \text{if } \prod_{i=1}^{I_0} L_{R_{i0}} \text{ exists} \\ 1, & \text{otherwise} \end{cases}.$$

Setting k=K results in $E(\boldsymbol{T}) = \mathbf{B}_0 \otimes \left[\bigotimes_{k=1}^{K} \mathbf{B}_k \right]$.

□

Application of Theorem 3 is demonstrated for Example 3.2a (page 133) where the moments of $\boldsymbol{T}$ were found by brute force. First, define the following:

$$\begin{aligned} L_{U_{10}} &= 2 \\ L_{U_{11}} &= 2 \\ L_{F_{11}} &= 2 \\ L_{R_{11}} &= 1 \end{aligned}$$

Then

$$E(\boldsymbol{T}) = \boldsymbol{I}_2 \otimes \left[\boldsymbol{I}_2 \otimes \left[\frac{\boldsymbol{J}_2}{2} \right] \right]$$

$$= \begin{bmatrix} .5 & .5 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & .5 & .5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & .5 & .5 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & .5 & .5 \end{bmatrix}$$

These results agree with those of Example 3.2a.

Theorem 4

$$E(t_{u_{10},u_{20},\ldots,u_{I_K K}} t'_{u'_{10},u'_{20},\ldots,u'_{I_K K}}) = \left[E_0^{rc}\otimes\right] \bigotimes_{k=1}^{K} \left[E_k^{rc}\otimes P_k\right]$$

where E_0^{rc} is a $\left(\prod_{i=1}^{I_0} L_{U_{i0}}\right)\times\left(\prod_{i=1}^{I_0} L_{U_{i0}}\right)$ zero matrix with a 1 in row r and column c

$$r = \sum_{i=1}^{I_0-1}\left((u_{i0}-1)\prod_{i'=i+1}^{I_0} L_{U_{i'0}}\right) + u_{I0}\,, \qquad c \equiv \sum_{i=1}^{I_0-1}\left((u'_{i0}-1)\prod_{i'=i+1}^{I_0} L_{U_{i'0}}\right) + u'_{I0}$$

and where E_k^{rc} is a $\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)\times\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)$ zero matrix with a 1 in row r and column c

$$r = \sum_{j=1}^{J_k-1}\left((f_{jk}-1)\prod_{j'=j+1}^{J_k} L_{F_{j'k}}\right) + f_{Jk}\,, \qquad c \equiv \sum_{j=1}^{J_k-1}\left((f'_{jk}-1)\prod_{j'=j+1}^{J_k} L_{F_{j'k}}\right) + f'_{Jk}$$

and P_k (written as the product of S_k and p_k to facilitate the proof) is defined in one of six possible ways:

(1) same Block: $(u_{im}= u'_{im}$ *and* $f_{im}=f'_{im}) \;\forall\; (m=0,\ldots,(k-1)$ *and* $i=1,\ldots,I_m)$
same Treatment: $f_{jk}=f'_{jk} \;\forall\; j=1,\ldots,J_k$
same EU: $u_{Ik}=u'_{Ik}$
same SSU: $u_{mk}=u'_{mk} \;\forall\; m=2,\ldots,I_k$

$$P_k = S_k p_k = \left[\frac{I_{I_k}}{\prod_{i=1}^{I_k} L_{R_{ik}}}\right]\left[\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right]$$

(2) same Block: ($u_{im} = u'_{im}$ *and* $f_{im} = f'_{im}$) $\forall$ ($m=0,\ldots,(k-1)$ *and* $i=1,\ldots,I_m$)
same Treatment: $f_{jk} = f'_{jk}$ $\forall$ $j=1,\ldots,J_k$
same EU: $u_{1k} = u'_{1k}$
different SSU: $u_{mk} \neq u'_{mk}$ *for at least some* $m=2,\ldots,I_k$

$$P_k = S_k p_k = \left[\frac{\left[I_{L_{R_{1k}}}\right] \otimes \left[J_{\prod_{i=2}^{I_k} L_{R_{ik}}} - I_{\prod_{i=2}^{I_k} L_{R_{ik}}}\right]}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)\left(\prod_{i=2}^{I_k} L_{R_{ik}} - 1\right)}\right]\left[\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right]$$

(3) same Block: ($u_{im} = u'_{im}$ *and* $f_{im} = f'_{im}$) $\forall$ ($m=0,\ldots,(k-1)$ *and* $i=1,\ldots,I_m$)
same Treatment: $f_{jk} = f'_{jk}$ $\forall$ $j=1,\ldots,J_k$
different EU: $u_{1k} \neq u'_{1k}$

$$P_k = S_k p_k = \left[\frac{\left[J_{L_{R_{1k}}} - I_{L_{R_{1k}}}\right] \otimes \left[J_{\prod_{i=2}^{I_k} L_{R_{ik}}}\right]}{L_{R_{1k}}\left(L_{R_{1k}} - 1\right)\left(\prod_{i=2}^{I_k} L_{R_{ik}}\right)^2}\right]\left[\left(\frac{L_{R_{1k}} - 1}{L_{U_{1k}} - 1}\right)\left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right)\right]$$

(4) same Block: ($u_{im} = u'_{im}$ *and* $f_{im} = f'_{im}$) $\forall$ ($m=0,\ldots,(k-1)$ *and* $i=1,\ldots,I_m$)
different Treatment: $f_{jk} \neq f'_{jk}$ *for at least some* $j=1,\ldots,J_k$

$$P_k = S_k p_k = \left[\frac{J_{\prod_{i=1}^{I_k} L_{R_{ik}}}}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)^2}\right]\left[\left(\frac{L_{R_{1k}}}{L_{U_{1k}} - 1}\right)\left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right)\right]$$

(5) different Block: ($u_{im} \neq u'_{im}$ *or* $f_{im} \neq f'_{im}$) *for at least some* $m=0,\ldots,(k-1)$ *and* $i=1,\ldots,I_m$

$$P_k = S_k p_k = \left[\frac{J_{I_k}}{\prod_{i=1} L_{R_{ik}}}\right]\left[\frac{1}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)^2}\right]\left[\frac{1}{\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)^2}\right]$$

(6) anything not defined by cases (1) through (5)

$$P_k = S_k p_k = \left[J_{I_k} \prod_{i=1} L_{R_{ik}}\right] 0$$

The proof parallels substructures **B**, **C**, and **D** from which the $E(t_{u_{10},u_{20},\ldots,u_{I_K K}} t'_{u'_{10},u'_{20},\ldots,u'_{I_K K}})$ is built up using the Kronecker operator.

Proof:

Substructure **D** (defines the probability that potential observations are jointly realized for a given design level k):

Given that the randomization of treatments to EU's is independent for the K hierarchical levels, for some level k there are $\prod_{i=1}^{I_k} L_{U_{ik}}$ realizable observations (potentially nonzero rows) for each $t_{u_{10},u_{20},\ldots,u_{I_K K}}$, denoted by the subvector

$t^{*}_{u_{10},u_{20},\ldots,u_{I_K K}}$. Let $P_k = E(t^{*}_{u_{10},u_{20},\ldots,u_{I_K K}} t^{*'}_{u'_{10},u'_{20},\ldots,u'_{I_K K}})$ be the matrix of probabilities that potential observations are jointly realized for a given k (P_k is determined later).

Substructure **C** (defines the probability that potential treatments are jointly realized given design level k, because all treatments are jointly realized the probability is 1):

Because we are dealing with complete factorial designs where the joint probability of realizing any two treatments is 1, E_k^{rc} is a $\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)$ elementary matrix with a 1 indicating the joint treatments associated with t_i^{*} and $t_{i'}^{*}$.

Substructure B_k (for a given design level k, defines the probability that potential observations and treatments are jointly realized by combining the conditional probabilities associated with substructure **D** and the marginal probabilities associated with substructure **C**):

Multiplying each element of the joint treatment structure, **C**, by the within treatment probability structure, P_k, results in $B_k = (E_k^{rc} \otimes P_k)$.

Complete Structure $E(t_{u_{10},u_{20},\ldots,u_{I_K K}} t'_{u'_{10},u'_{20},\ldots,u'_{I_K K}})$ (independent randomizations are performed at each of the k hierarchical design levels, the probabilities associated with design level K are multiplied by the probabilities associated with design level (K-1), and this is done for all k until k=0):

$\mathbf{B}_{k-1}$ represents the probability that two potential blocks for level k are jointly realized. Blocks (for k>1) are not realized with probability 1 because the realized blocks are a function of the randomization performed at level (k-1). Multiplying

each probability in $\mathbf{B}_{k-1}$ by the within block probability structure, $\mathbf{B}_k$, is accomplished by $(\mathbf{B}_{k-1} \otimes \mathbf{B}_k)$, which yields the within block probability structure for level (k-1). $\mathbf{B}_{k-2}$ represents the probability that two potential blocks for level (k-1) are jointly realized. Multiplying each probability in $\mathbf{B}_{k-2}$ by the within block probability structure, $\mathbf{B}_{k-1}$, is accomplished by $(\mathbf{B}_{k-2} \otimes \mathbf{B}_{k-1})$, which yields the within block probability structure for level (k-2). This continues up to and including (k=1) where $\mathbf{B}_0$ is the probability that two potential blocks for level 1 are jointly realized, and where $\mathbf{B}_0 = \begin{cases} E_0^{rc}, & \text{if } \prod_{i=1}^{I_0} L_{U_{i0}} \text{ exists} \\ 1, & \text{otherwise} \end{cases}$.

Setting k=K results in $E(t_{u_{10}u_{20}\cdots u_{I_K K}} t'_{u'_{10}u'_{20}\cdots u'_{I'_K K}}) = \mathbf{B}_0 \otimes \left[\bigotimes_{k=1}^{K} \mathbf{B}_k\right]$.

Specification of $\boldsymbol{P}_k = S_k p_k$:

(**Table XXIX** can be used as a visual aid to indicate nonzero elements for cases (1) through (6). For cases (1), (2), and (3) the nonzero elements are indicated with the respective case number. For case (4) and (5) all elements are nonzero, and for case (6) all elements are zero.)

Given events A and B defined as:

$$A = \{\text{treatment } f_{1k}f_{2k}\cdots f_{J_k k} \text{ assigned to EU } u_{1k}\}$$
$$B = \{\text{treatment } f'_{1k}f'_{2k}\cdots f'_{J'_k k} \text{ assigned to EU } u'_{1k}\}$$

then $p_k = P(A \text{ and } B) = P(B|A)P(A)$ and S_k is a $\left(\prod_{i=1}^{K} L_{R_{ik}}\right)\left(\prod_{i=1}^{K} L_{R_{ik}}\right)$ matrix of r

nonzero weights equal to $\frac{1}{r}$. Hence, $\boldsymbol{P}_k$ is a matrix whose r elements, equal to $\frac{p}{r}$, spread the probability of an event over the possible ways of realizing the event.

(1) same Block: $(u_{im} = u'_{im}$ *and* $f_{im} = f'_{im}) \ \forall \ (m=0,...,(k-1)$ *and* $i=1,...,I_m)$
same Treatment: $f_{jk} = f'_{jk} \ \forall \ j=1,...,J_k$
same EU: $u_{1k} = u'_{1k}$
same SSU: $u_{mk} = u'_{mk} \ \forall \ m=2,...,I_k$

There are $\prod_{j=1}^{J_k} L_{F_{jk}}$ treatments so $P(A) = \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right)$. Since event A equals event B the

P(B|A)=1 $\therefore \ p_k = P(A) = \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right)$.

Events A (or B) is realized for all $\prod_{i=1}^{I_k} L_{R_{ik}}$ SSU's (diagonal elements of

Table XXIX) so $\boldsymbol{S}_k = \left(\frac{I_{\left(\prod_{i=1}^{I_k} L_{R_{ik}} \right)}}{\prod_{i=1}^{I_k} L_{R_{ik}}} \right)$ and $\boldsymbol{P}_k = \boldsymbol{S}_k p_k = \left[\frac{I_{\prod_{i=1}^{I_k} L_{R_{ik}}}}{\prod_{i=1}^{I_k} L_{R_{ik}}} \right] \left[\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right]$.

(2) same Block: ($u_{im} = u'_{im}$ *and* $f_{im} = f'_{im}$) $\forall$ (m=0,...,(k−1) *and* i=1,...,I_m)
same Treatment: $f_{jk} = f'_{jk}$ $\forall$ j=1,...,J_k
same EU: $u_{1k} = u'_{1k}$
different SSU: $u_{mk} \neq u'_{mk}$ *for at least some* m=2,...,I_k

p_k is defined as in (1) because it is only a function of treatment and EU.

Two SSU's from a given EU can be realized in $\left(\prod_{i=2}^{I_k} L_{R_{ik}}\right)\left(\prod_{i=2}^{I_k} L_{R_{ik}} - 1\right)$ ways,

represented by the off diagonal submatrix $\left[\boldsymbol{J}_{\prod_{i=2} L_{U_{ik}}} - \boldsymbol{I}_{\prod_{i=2} L_{U_{ik}}}\right]$ (see **Table XXIX**).

Applying this within EU structure to all $L_{R_{1k}}$ EU's and dividing by the number of nonzero elements yields

$$\boldsymbol{S}_k = \left[\frac{\left[\boldsymbol{I}_{L_{R_{1k}}}\right] \otimes \left[\boldsymbol{J}_{\prod_{i=2} L_{R_{ik}}} - \boldsymbol{I}_{\prod_{i=2} L_{R_{ik}}}\right]}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)\left(\prod_{i=2}^{I_k} L_{R_{ik}} - 1\right)}\right] \text{ and } \boldsymbol{P}_k = \boldsymbol{S}_k p_k = \left[\frac{\left[\boldsymbol{I}_{L_{R_{1k}}}\right] \otimes \left[\boldsymbol{J}_{\prod_{i=2} L_{R_{ik}}} - \boldsymbol{I}_{\prod_{i=2} L_{R_{ik}}}\right]}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)\left(\prod_{i=2}^{I_k} L_{R_{ik}} - 1\right)}\right]\left[\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right].$$

(3) same Block: ($u_{im} = u'_{im}$ *and* $f_{im} = f'_{im}$) $\forall$ (m=0,...,(k−1) *and* i=1,...,I_m)
same Treatment: $f_{jk} = f'_{jk}$ $\forall$ j=1,...,J_k
different EU: $u_{1k} \neq u'_{1k}$

$P(A) = \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right)$. Conditional on event A, only $\left(L_{R_{1k}} - 1\right)$ of the remaining

$\left(L_{U_{1k}} - 1\right)$ EU's can be assigned the treatment defined by event A, so

$P(B|A) = \left(\frac{L_{R_{1k}} - 1}{L_{U_{1k}} - 1} \right)$ and $p_k = \left[\left(\frac{L_{R_{1k}} - 1}{L_{R_{1k}} - 1} \right) \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right) \right]$. For a given treatment, any of

the $\prod_{i=2}^{I_k} L_{R_{ik}}$ SSU's from one EU can be jointly realized with any of the $\prod_{i=2}^{I_k} L_{R_{ik}}$ SSU's

from another EU, represented by the submatrix of jointly realized SSU's $\left(J_{\prod_{i=2}^{I_k} L_{R_{ik}}} \right)$

(see **Table XXIX**). There are $\left(L_{R_{1k}}\right)\left(L_{R_{1k}} - 1\right)$ pairs of EU's for which this can occur

represented by the matrix of jointly realized EU's $\left[J_{L_{R_{1k}}} - I_{L_{R_{1k}}}\right]$. Applying the

within EU structure to the EU structure and weighting by the inverse of the

number on nonzero elements yields $S_k = \left[\frac{\left[J_{L_{R_{1k}}} - I_{L_{R_{1k}}}\right] \otimes \left[J_{\prod_{i=2}^{I_k} L_{R_{ik}}}\right]}{L_{R_{1k}}\left(L_{R_{1k}} - 1\right)\left(\prod_{i=2}^{I_k} L_{R_{ik}}\right)^2} \right]$. So

$$P_k = S_k p_k = \left[\frac{\left[J_{L_{R_{1k}}} - I_{L_{R_{1k}}}\right] \otimes \left[J_{\prod_{i=2}^{I_k} L_{R_{ik}}}\right]}{L_{R_{1k}}\left(L_{R_{1k}} - 1\right)\left(\prod_{i=2}^{I_k} L_{R_{ik}}\right)^2} \right] \left[\left(\frac{L_{R_{1k}} - 1}{L_{U_{1k}} - 1} \right) \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right) \right].$$

(4) same Block: $(u_{im} = u'_{im}$ *and* $f_{im} = f'_{im}) \ \forall \ (m=0,\ldots,(k-1)$ *and* $i=1,\ldots,J_m)$
different Treatment: $f_{jk} \neq f'_{jk}$ *for at least some* $j=1,\ldots,J_k$

$P(A) = \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right)$. Conditional on event A, $L_{R_{1k}}$ of the remaining $\left(L_{U_{1k}} - 1\right)$ EU's can be assigned the treatment defined by event B, so $P(B|A) = \left(\frac{L_{R_{1k}}}{L_{U_{1k}} - 1} \right)$ and

$p_k = \left[\left(\frac{L_{R_{1k}}}{L_{R_{1k}} - 1} \right) \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}} \right) \right]$. Any of the $\prod_{i=2}^{I_k} L_{R_{ik}}$ SSU's from any of the $L_{R_{1k}}$ EU's assigned one treatment can be jointly realized with any of the $\prod_{i=2}^{I_k} L_{R_{ik}}$ SSU's from any of the $L_{R_{1k}}$ EU's assigned another treatment. This is represented by the weight matrix $S_k = \left[\frac{J^{\prod_{i=1}^{I_k} L_{R_{ik}}}}{\left(\prod_{i=1}^{I_k} L_{R_{ik}} \right)^2} \right]$ (all elements of **Table XXIX**). So

$$P_k = S_k p_k = \left[\frac{J_{I_k} \prod_{i=1} L_{R_{ik}}}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)^2}\right]\left[\left(\frac{L_{R_{1k}}}{L_{U_{1k}} - 1}\right)\left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right)\right]$$

(5) different Block: $(u_{im} \neq u'_{im}$ *or* $f_{im} \neq f'_{im})$ *for at least some* $m=0,\ldots,(k-1)$ *and* $i=1,\ldots,I_m$

$P(A) = \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right)$. Because randomization of treatments to EU's is independent among blocks $P(B|A) = P(B) = P(A) = \left(\frac{1}{\prod_{j=1}^{J_k} L_{F_{jk}}}\right)$ and $p_k = \left[\frac{1}{\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)^2}\right]$. Any of the $\prod_{i=2}^{I_k} L_{R_{ik}}$ SSU's from any of the $L_{R_{1k}}$ EU's from one block can be jointly realized with any of the $\prod_{i=2}^{I_k} L_{R_{ik}}$ SSU's from any of the $L_{R_{1k}}$ EU's from another block. This is represented by the weight matrix $S_k = \left[\frac{J_{I_k} \prod_{i=1} L_{R_{ik}}}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)^2}\right]$ (all elements of **Table XXIX**). So

$$P_k = S_k p_k = \left[\frac{\prod_{i=1}^{I_k} L_{R_{ik}}}{\left(\prod_{i=1}^{I_k} L_{R_{ik}}\right)^2}\right]\left[\frac{1}{\left(\prod_{j=1}^{J_k} L_{F_{jk}}\right)^2}\right]$$

(6) joint realizations of SSU's that are not possible (anything not defined by cases (1) through (5))

$$P_k = \left[\prod_{i=1}^{I_k} L_{R_{ik}}\right] 0$$

□

Table XXIX Location of nonzero elements of P_k for cases (1) through (3). For cases (4) and (5) all elements are nonzero, and for case (6) all elements are zero.
(1) = same SSU
(2) = same EU but different SSU
(3) = different EU

	EU	1			...			$L_{R_{1k}}$		
EU	SSU	1	...	$\prod_{i=2}^{l_k} L_{R_{ik}}$	1	...	$\prod_{i=2}^{l_k} L_{R_{ik}}$	1	...	$\prod_{i=2}^{l_k} L_{R_{ik}}$
1	1	(1)	-2	-2	-3	-3	-3	-3	-3	-3
	⋮	-2	-1	-2	-3	-3	-3	-3	-3	-3
	$\prod_{i=2}^{l_k} L_{R_{ik}}$	-2	-2	-1	-3	-3	-3	-3	-3	-3
⋮	1	-3	-3	-3	(1)	-2	-2	-3	-3	-3
	⋮	-3	-3	-3	-2	-1	-2	-3	-3	-3
	$\prod_{i=2}^{l_k} L_{R_{ik}}$	-3	-3	-3	-2	-2	-1	-3	-3	-3
$L_{R_{1k}}$	1	-3	-3	-3	-3	-3	-3	(1)	-2	-2
	⋮	-3	-3	-3	-3	-3	-3	-2	-1	-2
	$\prod_{i=2}^{l_k} L_{R_{ik}}$	-3	-3	-3	-3	-3	-3	-2	-2	-1

Application of Theorem 4 is demonstrated for Example 3.2a (page 133) where the moments of T were found by brute force. First, define the following:

$$L_{U_{10}} = 2$$
$$L_{U_{11}} = 2$$
$$L_{F_{11}} = 2$$
$$L_{R_{11}} = 1$$

Then

$$E(t_{u_{10}f_{11}u_{11}}\, t'_{u'_{10}f'_{11}u'_{11}}) = E(t_{111}t'_{211}) = E_0^{rc} \otimes E_1^{rc} \otimes P_1$$

$$= \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix} \otimes \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix} \otimes [.25]$$

$$= \begin{bmatrix} 0 & 0 & .25 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

These results agree with those of Example 3.2a.

3.4 EXAMPLE APPLIED TO A GRCBD WITH SUBSAMPLING

The results of this section, specifically the EMS given in **Table XXXI**, are based on Theorems 3 and 4 developed in the last section. We will consider the effect of various models on the EMS and hypothesis tests based on those EMS. We begin with a fixed effects model with additional random components that represent experimental error and sampling error (the model defined in Section 3.2) and through a series of assumptions evolve to a completely random model. In all, four models are considered and for each we discuss the nature of tests for Block effects, Treatment effects, Block-Treatment interaction effects, and the effects of experimental error. A high level map of the effects provides an overview of the evolution from model 1 to model 4 (**Table XXX**). The corresponding EMS are found in **Table XXXI**. The effects are defined as fixed, random, or both, and we also consider a mixed Block-Treatment interaction effect (i.e., a random effect with a sum-to-zero restriction over the subscript associated with the fixed factor). Two alternative definitions for the Block-Treatment interaction effects are of greater interest to us, specifically random and mixed, because they are at the root of the "whether/how to test block effects" controversy arising from normal theory (Hocking 1973; Samuels et al. 1991). For a more detailed discussion of random and mixed Block-Treatment interaction effects the reader is referred

to Searle (1971) and Scheffe (1959).

Table XXX Summary of effects associated with the four models. F:fixed, R:random, M:mixed (random with sum-to-zero constraints over subscript associated with the fixed factor).

		Effects						
		β_i	τ_j	$\beta\tau_{ij}$	u_{ik}	τu_{ijk}	δ_{ikl}	$\tau\delta_{ijkl}$
Models	1	F	F	F	F, R	F	F, R	F
	2	F	F	F	F, R		R	
	3	R	F	R or M	F, R		R	
	4	R	F	R or M	R		R	

Model 1: Fixed Effects Model

From a practitioners point of view this model is of limited use because the assumption of fixed blocks effects restricts inferences to those blocks actually run in the study. However, it serves as a starting point from which to explore more useful models.

Block: The test for Block effects is biased whether MS(Block-Treatment interaction) or MS(Error) is used as the denominator because their EMS contain a Unit component that is not present in the EMS for Block.

Treatment: The usual test for Treatment effects using MS(Block-Treatment interaction) in the denominator is biased because there is an additional $\beta\tau$ component in the EMS(Block-Treatment interaction). One would expect this in a two-factor fixed effects model, which is what we have by assuming Block effects, as well as treatment effects, are fixed. The test using MS(Error) in the denominator is also biased because, while τu components are present in both

EMS(Treatment) and EMS(Error), the coefficients differ.

Block-Treatment interaction: The test for Block-Treatment interaction effects using MS(Error) in the denominator is biased because, while τu components are present in both EMS(Block-Treatment interaction) and EMS(Error), the coefficients differ.

Model 2: Unit and subunit effects are additive, subunit effects are random

The results based on model 2 are similar to those of Wilk (1955) with the addition of random components due to experimental and observational error. As in Model 1, we are limited by the assumption of fixed Block effects, however, because there is a test for Treatment effects, it serves as a stepping stone to Model 3. Wilk (1955) argued in favor of assuming Treatment-Unit additivity because blocks are formed, or chosen, in order to minimize the heterogeneity of the experimental material within a block. While there may be large differences in experimental material from block to block, there should be relatively small differences between the units within a block. So, while Treatment may exhibit nonadditive behavior across blocks, it may be reasonable to assume additive behavior across units within a block. We are also assuming that the effects of subsampling or taking repeated measures within a unit are modeled as random effects.

Block: Tests for Block effects are biased for reasons stated for Model 1.

Treatment: There is an unbiased test using MS(Error) as the denominator. This requires replication of treatments within blocks.

Block-Treatment interaction: The test for Block-Treatment interaction effect using MS(Error) in the denominator is unbiased. This requires replication of treatments within blocks. If this test is nonsignificant, the SS and df associated with the Block-Treatment interaction effects can be pooled with those for Error,

resulting in a more powerful test for Treatment effects.

One could test for the joint effects of experimental error and unit effects by forming the ratio MS(Error)/MS(Subsample). If nonsignificant then further pooling could be done to increase the power of the test on treatments.

(Comments on pooling are not meant to address the issue of whether and when to pool, but only to point out the existence of unbiased tests and the potential for pooling.)

Model 3: Block effects are random

With random Block effects inferences can be made to the population of blocks represented by those actually run in the experiment. This assumption is common in the development of the normal theory RCBD as well, and allows us to address the "whether/how to test block effects" controversy. The controversy has two levels:

i) Normal theory: Should Block-Treatment interaction effects be modeled as random or mixed, resulting in an unbiased or biased test of Block effects respectively (Searle 1971; Hocking 1973)?

ii) Recognition of the randomization process: Regardless of which definition is used for Block-Treatment interaction effects, the test for Block effects is not performed because the peculiar nature of the randomization process is recognized (Ostle and Mensing 1975, p. 380).

We do not attempt to resolve the controversy in the normal theory arena because it deals with secondary issues as far as blocking is concerned, i.e., How to define the parameters and covariance structures. The essence of blocking is a modification of the randomization process and by directly modeling this process, randomization theory provides an alternative and more complete resolution.

Block: The test for Block effects is biased for the reasons stated for Model 1. It does not matter whether the Block-Treatment interaction effects are defined as random or mixed, the Unit effects introduce bias.

Treatment: The test for Treatment effects using MS(Block-Treatment interaction) in the denominator is unbiased regardless of whether the Block-Treatment interaction effects are defined as random or mixed (this is true under normal theory as well). It is not necessary to replicate treatment within blocks, which can greatly reduce the required size of the experiment.

Block-Treatment interaction: The test for Block-Treatment interaction effects using MS(Error) in the denominator is unbiased. This requires replication of treatments within blocks. If this test is nonsignificant, the SS and df associated with the Block-Treatment interaction effects can be pooled with those for Error, resulting in a more powerful test for Treatment effects.

One could test for the joint effects of experimental error and unit effect by forming the ratio MS(Error)/MS(Subsample). If this test is not significant then further pooling could be done.

Model 4: Unit effects are random

If blocks are made up of a large number of units, from which a random sample of units is drawn for the purposes of the experiment then the resultant tests are equivalent to those of normal theory:

Block: If Block-Treatment interaction effects are modeled as random effects then there is an unbiased test for Block effects using MS(Block-Treatment) in the denominator. If Block-Treatment interaction effects are modeled as mixed effects then there is not an unbiased test for Block effects. In this case the model should be appropriately defined by considering the parameters and their

associated covariance structure (Hocking 1973).

Treatment: The test for Treatment effects using MS(Block-Treatment interaction) as the denominator is unbiased.

Block-Treatment interaction: The test for Block-Treatment interaction effects using MS(Error) in the denominator is unbiased. This requires replication of treatments within a block.

Error: The test for experimental error effects using MS(Subsample) in the denominator is unbiased. This requires subsampling or repeated measures on a unit.

Table XXXI GRCBD with Subsampling: Four Models

Model 1: Full Model, Mostly Fixed Effects

Block:	$\sigma_\delta^2 + \sigma_\epsilon^2 +$		$\frac{L}{IJ(JK-1)}\sum_i\sum_j\sum_k \tau u_{ijk}^2$	$+ \frac{JKL}{(I-1)}\sum_i \beta_i^2$
Treatment:	$\sigma_\delta^2 + \sigma_\epsilon^2 +$		$\frac{L \quad (J-2)}{IJ(K-1)(J-1)\ (J-1)}\sum_i\sum_j\sum_k \tau u_{ijk}^2 + \frac{L}{I(JK-1)}\sum_i\sum_k u_{ik}^2 +$	$\frac{IKL}{(J-1)}\sum_j \tau_j^2$
Block-Treatment interaction:	$\sigma_\delta^2 + \sigma_\epsilon^2 +$		$\frac{L \quad (J-2)}{IJ(K-1)(J-1)\ (J-1)}\sum_i\sum_j\sum_k \tau u_{ijk}^2 + \frac{L}{I(JK-1)}\sum_i\sum_k u_{ik}^2 +$	$\frac{KL}{(I-1)(J-1)}\sum_i\sum_j \beta\tau_{ij}^2$
Error:	$\sigma_\delta^2 + \sigma_\epsilon^2 +$		$\frac{L}{IJ(JK-1)}\sum_j\sum_k \tau u_{jik}^2 + \frac{L}{I(JK-1)}\sum_i\sum_k u_{ik}^2$	
Subsample:	$\sigma_\delta^2 +$	$\frac{1}{(L-1)IJ^2K}\sum_i\sum_j\sum_k\sum_l \delta_{ijkl}^2 +$	$\frac{1}{(L-1)IJK}\sum_i\sum_j\sum_k\sum_l \tau\delta_{ijkl}^2$	

Model 2: All $\tau u_{ijk} = 0$, all $\tau\delta_{ijkl} = 0$, $\delta_{ikl} \sim (0, \sigma^2_\delta)$

Block:	$\sigma^2_\delta + \sigma^2_\epsilon +$			$\frac{JKL}{(I-1)_i}\Sigma\beta_i^2$
Treatment:	$\sigma^2_\delta + \sigma^2_\epsilon +$	$\frac{L}{I(JK-1)_{i,k}}\Sigma\Sigma u_{ik}^2 +$		$\frac{IKL}{(J-1)_j}\Sigma\tau_j^2$
Block-Treatment interaction:	$\sigma^2_\delta + \sigma^2_\epsilon +$	$\frac{L}{I(JK-1)_{i,k}}\Sigma\Sigma u_{ik}^2 +$	$\frac{KL}{(I-1)(J-1)_{i,j}}\Sigma\Sigma\beta\tau_{ij}^2$	
Error:	$\sigma^2_\delta + \sigma^2_\epsilon +$	$\frac{L}{I(JK-1)_{i,k}}\Sigma\Sigma u_{ik}^2$		
Subsample:	σ^2_δ			

Model 3: $\beta_i \sim (0, \sigma^2_\beta)$ ($\left[KL\,\sigma^2_{\beta\tau}\right]$ exists for random definition of Block-Treatment interaction effects but not for the mixed definition)

Block:	$\sigma^2_\delta + \sigma^2_\epsilon +$		$\left[KL\,\sigma^2_{\beta\tau}\right] +$	$JKL\,\sigma^2_\beta$
Treatment:	$\sigma^2_\delta + \sigma^2_\epsilon +$	$\frac{L}{I(JK-1)_{i,k}}\Sigma\Sigma u_{ik}^2 +$	$KL\,\sigma^2_{\beta\tau} +$	$\frac{IKL}{(J-1)_j}\Sigma\tau_j^2$
Block-Treatment interaction:	$\sigma^2_\delta + \sigma^2_\epsilon +$	$\frac{L}{I(JK-1)_{i,k}}\Sigma\Sigma u_{ik}^2 +$	$KL\,\sigma^2_{\beta\tau}$	
Error:	$\sigma^2_\delta + \sigma^2_\epsilon +$	$\frac{L}{I(JK-1)_{i,k}}\Sigma\Sigma u_{ik}^2$		
Subsample:	σ^2_δ			

Model 4: u_{il}~$(0,\sigma_u^2)$ ($\left[KL\,\sigma^2_{\beta\tau}\right]$ exists for random definition of Block-Treatment interaction effects but not for the mixed definition)

Block:	$\sigma^2_\delta + \sigma^2_{\epsilon'} + \left[KL\,\sigma^2_{\beta\tau}\right] + JKL\,\sigma^2_\beta$
Treatment:	$\sigma^2_\delta + \sigma^2_{\epsilon'} + KL\,\sigma^2_{\beta\tau} + \frac{IKL}{(J-1)}\sum_j \tau_j^2$
Block-Treatment interaction:	$\sigma^2_\delta + \sigma^2_{\epsilon'} + KL\,\sigma^2_{\beta\tau}$
Error:	$\sigma^2_\delta + \sigma^2_{\epsilon'}$
Subsample:	σ^2_δ

where $\sigma^2_{\epsilon'} = \sigma^2_\epsilon + \sigma^2_u$

In summary, the test of primary importance is that of treatment effects and there are two conditions under which an unbiased test exists, both requiring Treatment-Unit additivity:

1. If Block effects are fixed and treatments are replicated within blocks then MS(Error) serves as the denominator, but inferences are restricted to those blocks actually run in the experiment (see Model 2).
2. If Block effects are random then MS(Block-Treatment interaction) serves as the denominator (see Model 3). It is not necessary to replicate treatments within blocks. Inferences apply to the population of blocks represented by those actually run in the experiment.

The test for blocks is usually of secondary importance, because blocking is used as a variance reduction technique. In order to test for Block effects the Units within blocks that are run in the experiment must represent a random sample from a large population of units within those blocks (see Model 4). If this is true then the resulting tests are equivalent to those derived according to normal theory and one must still decide whether to define the Block-Treatment interaction effects as random or mixed in order to determine if there is an unbiased test for Block effects. However, it is common to encounter the situation where Block effects are considered random while Units are not considered a random sample from a large population of units within a Block (Model 3) resulting in a biased test for Block effects.

3.5 GENERAL RULES FOR PSEUDO EMS

We will show how to augment the usual linear model to incorporate information about the randomization process. We will also show how to construct pseudo EMS (indicate the existence, but not form, of components associated with the randomization process). Treatment-Unit additivity is assumed but the experimenter is free to define Blocks effects, Treatment effects, and Block-Treatment interaction effects as desired.

The following definitions are used in generating the EMS:

If the levels of a first factor change for each level combination of a second set of factors, the index for the levels of the first factor are *nested* in the indices for level combinations of the second set of factors, or alternatively the indices for level combinations of the second set of factors *contain* the index for levels of the first factor. For example, if the levels of factor B (indexed by j) are different for each level of factor A (indexed by i) then j is *nested* in i, or alternatively i *contains* j. We shall refer to indices (or subscripts) that contain other indices as *container* indexes (or subscripts). Any subscript that is not a container subscript is called a noncontainer subscript. For example, the effects for A and B respectively are:

$$\alpha_i, \text{ and } \beta_{ij}$$

where i is a non-container subscript with respect to α and
i is a container subscript with respect to β because it nests or contains j

The concept of container subscripts is expressed by some authors (e.g., Lorenzen and Anderson 1993b) with notation that places container subscripts in parentheses, for example:

$$\alpha_i, \text{ and } \beta_{(i)j}$$

Given that the order of terms in a model corresponds to the natural hierarchy of factors (see **Figure 4** on page 140), the effects of blocking can be described as follows:

> If the Units within a block (or more generally a cluster factor) are associated with fixed effects then a corresponding fixed component appears in the EMS associated with all terms from the Unit term up to, but not including the term associated with the block (or cluster) factor.

This is demonstrated in Model 3 of **Table XXXI**, where a fixed component associated with the Unit effects (u_{ik}) appears in the EMS(Error) which is associated with Units, the EMS(Block-Treatment interaction), and the EMS(Treatment), but not the EMS(Block). Previous work by Anderson (1974a, 1974b), Lorenzen (1984), and Lorenzen and Anderson (1993a) incompletely modeled the complement or lack of this bias component. Here its

existence (but not form) is directly modeled using the following process:

1. Define the usual effects model.
2. For each term in the model associated with clustered units that are not a random sample from a much larger population of units within the cluster:
    a. immediately follow it with a duplicate term marked with an asterisk,
    b. delete any container subscripts from the asterisked term that are not in common with the term associated with the cluster factor.
3. For each nonasterisked term in the model (term of interest) the EMS are generated by taking the expectation over all subsequent terms in the augmented model (candidate terms). For nonasterisked candidate terms the EMS are calculated in the usual manner (Lorenzen and Anderson 1993b). For asterisked candidate terms the following rule is applied:

    If any noncontainer subscript of the term of interest is not a container subscript of the (subsequent) candidate term then a fixed effects candidate component (Φ) is included in the EMS.

This rule is the result of modeling units within blocks or clusters as fixed effects and the restriction that units are not randomly assigned to blocks or clusters.

This process is demonstrated in the following example.

Example 3.5a General Rules Applied to a GRCBD with subsampling

Two coating processes are to be tested for their ability to decrease brittleness of extruded plastic parts subjected to sunlight. Six Parts are extruded from a mold at a time, separated, and then coated. The position of the mold in the extruder cannot be precisely controlled.

The experiment will consist of five extrusion runs (Blocks). The two coatings (Treatments) are randomly assigned to the six parts (Experimental Units) in each run. After a specified amount of time in an artificial sunlight chamber the parts are

tested for brittleness. Two areas (Subsamples) of the part are tested due to variability in the testing procedure.

Step 1: The usual effects model for this experiment can be written as:

$$y_{ijkl} = \mu + \beta_i + \tau_j + \beta\tau_{ij} + \epsilon_{ijk} + \delta_{ijkl}$$

$$\text{where } \beta_i \sim N(0, \sigma^2_\beta),\ \sum_{j=1}^{2} \tau_j = 0,\ \beta\tau_{ij} \sim N(0, \sigma^2_{\beta\tau}),\ \epsilon_{ijk} \sim N(0, \sigma^2_\epsilon),\ \delta_{ijkl} \sim N(0, \sigma^2_\delta) \quad \textbf{(209)}$$

Step 2: While it might be argued that Parts within the mold for each run are representative of a large population of potential Parts that could have been created, because of the positional effects within the mold we will assume that Parts from a mold run do not represent a random sample from a large number of such parts.

a: The term representing part effects is duplicated with an asterisk.

$$\epsilon^{*}_{ijk}$$

b: The container subscript j of the asterisked term is not in common with the subscripts of the term associated with the clustering factor, β_i, and is deleted.

$$\epsilon^{*}_{ik}$$

The augmented model is:

$$y_{ijkl} = \mu + \beta_i + \tau_j + \beta\tau_{ij} + \epsilon_{ijk} + \epsilon^{*}_{ik} + \delta_{ijkl}$$

$$\text{where the additional term is defined such that } \sum_{k=1}^{K} \epsilon^{*}_{ik} = 0 \quad \textbf{(212)}$$

Step 3: For each term in **(209)** the expectation is taken over the terms in **(212)**. **Table XXXII** summarizes the application of the new rule for each term of interest. The resulting EMS are shown in **Table XXXIII**.

Table XXXII Application of new rule to the candidate term $\epsilon^{\cdot}_{ik}$

Term of Interest	Subscript		Candidate term $\epsilon^{\cdot}_{ik}$ where i is a container subscript and k is a noncontainer subscript
	Noncontainer	Container	
β_i	i		The noncontainer subscript i associated with Block is a container subscript of the candidate term therefore no component is added to the EMS(Block).
τ_j	j		The noncontainer subscript j associated with Treatment is not a container subscript of the candidate term therefore a component Φ_{ϵ}. is added to the EMS(Treatment).
$\beta\tau_{ij}$	ij		The noncontainer subscript j associated with Block-Treatment interaction is not a container subscript of the candidate term therefore a component Φ_{ϵ}. is added to the EMS(Block-Treatment interaction).
ϵ_{ijk}	k	ij	The noncontainer subscript k associated with replication is not a container subscript of the candidate term therefore a component Φ_{ϵ}. is added to the EMS(Error).
δ_{ijkl}	l	ijk	The candidate term is not subsequent to δ_{ijkl} in the model. No component is added to the EMS(Subsample)

Table XXXIII Example of General Rules for EMS for Blocking: a GRCBD with Subsampling

Block (Run):	σ^2_δ	+		σ^2_ϵ	+	$JKL\,\sigma^2_\beta$		
Treatment:	σ^2_δ	+	Φ_ϵ.	+ σ^2_ϵ	+	$KL\,\sigma^2_{\beta\tau}$	+	$\frac{IKL}{(J-1)_j}\sum\tau^2_j$
Block-Treatment interaction:	σ^2_δ	+	Φ_ϵ.	+ σ^2_ϵ	+	$KL\,\sigma^2_{\beta\tau}$		
Error (Parts):	σ^2_δ	+	Φ_ϵ.	+ σ^2_ϵ				
Subsample (Area of Part):	σ^2_δ							

The test for Treatment effects is unbiased using MS(Block-Treatment interaction) in the denominator. However, there is no unbiased test for Block effects because no term for the denominator can be found that includes an asterisked component. The test for Block-Treatment interaction effects using MS(Error) in the denominator is unbiased. The test for Error effects (Parts) using MS(Subsample) in the denominator is biased. These results are comparable with those in **Table XXXI** where form, as well as presence, of components is shown.

Example 3.5b General Rules Applied to a Split-Plot structure

A school district wants to evaluate two methods of teaching science (based on right/left brain learning styles). They are also interested in comparing three individual review methods: computer assisted review, standard homework assignments, and a combination of the two. Two *schools (S)* will be randomly selected to be involved in the evaluation, with two grade seven *classes (C)* from each *school.* Each of the *teaching methods (T)* will be randomly assigned to a *class* from each *school.* The three *review methods (R)* will be randomly assigned to the *pupils (P)* in each *class.* The final exam scores will be used to assess the effects of the *teaching methods* and *review methods.*

The linear model associated with this design is:

$$y_{ijklm}=\mu+S_i+T_j+ST_{ij}+C_{ijk}+R_l+SR_{il}+TR_{jl}+STR_{ijl}+CR_{ijkl}+P_{ijklm}$$

where $S_i \sim N(0,\sigma_S^2)$, $ST_{ij} \sim N(0,\sigma_{ST}^2)$, $C_{ijk} \sim N(0,\sigma_C^2)$, $SR_{il} \sim N(0,\sigma_{SR}^2)$,
$STR_{ijl} \sim N(0,\sigma_{STR}^2)$, $CR_{ijkl} \sim N(0,\sigma_{CR}^2)$, $P_{ijklm} \sim N(0,\sigma_P^2)$,
and $\sum_{j=1}^{J} T_j = \sum_{l=1}^{L} R_l = \sum_{j=1}^{J} TR_{jl} = \sum_{l=1}^{L} TR_{jl} = 0$

Neither classes within a school nor students within a class are a random sample from a large population so application of Step 2 yields the augmented model:

$$y_{ijklm}=\mu+S_i+T_j+ST_{ij}+C_{ijk}+C'_{ik}+R_l+SR_{il}+TR_{jl}+STR_{ijl}+CR_{ijkl}+P_{ijklm}+P'_{ijkm}$$

where the additional terms are defined such that $\sum_{k=1}^{K} C'_{ik} = \sum_{m=1}^{M} P'_{ijkm} = 0$

Application of Step 3 to the augmented model yields the EMS found in **Table XXXIV**.

Table XXXIV EMS table for Split-Plot Example

School		σ_P^2	+	$IJM\ \sigma_{CR}^2$	+	$KM\ \sigma_{STR}^2$	+	$JKM\ \sigma_{SR}^2$	+		$IJLM\ \sigma_C^2$	+	$KLM\ \sigma_{ST}^2$	+ $JKLM\ \sigma_S^2$
Teaching		σ_P^2	+	$IJM\ \sigma_{CR}^2$	+	$KM\ \sigma_{STR}^2$	+		$\Phi(C^*)$	+	$IJLM\ \sigma_C^2$	+	$KLM\ \sigma_{ST}^2$	+ $IKLM\Phi(T)$
School-Teaching interaction		σ_P^2	+	$IJM\ \sigma_{CR}^2$	+	$KM\ \sigma_{STR}^2$	+		$\Phi(C^*)$	+	$IJLM\ \sigma_C^2$	+	$KLM\ \sigma_{ST}^2$	
Class		σ_P^2	+	$IJM\ \sigma_{CR}^2$	+				$\Phi(C^*)$	+	$IJLM\ \sigma_C^2$			
Review	$\Phi(P^*)$	+ σ_P^2	+	$IJM\ \sigma_{CR}^2$	+	$KM\ \sigma_{STR}^2$	+	$JKM\ \sigma_{SR}^2$	+	$IJKM\ \Phi(R)$				
School-Review interaction	$\Phi(P^*)$	+ σ_P^2	+	$IJM\ \sigma_{CR}^2$	+	$KM\ \sigma_{STR}^2$	+	$JKM\ \sigma_{SR}^2$						
Teach-Review interaction	$\Phi(P^*)$	+ σ_P^2	+	$IJM\ \sigma_{CR}^2$	+	$KM\ \sigma_{STR}^2$	+	$IKM\ \Phi(TR)$						
School-Teach-Review interaction	$\Phi(P^*)$	+ σ_P^2	+	$IJM\ \sigma_{CR}^2$	+	$KM\ \sigma_{STR}^2$								
Class-Review interaction	$\Phi(P^*)$	+ σ_P^2	+	$IJM\ \sigma_{CR}^2$										
Pupil	$\Phi(P^*)$	+ σ_P^2												

The test for Teaching method is unbiased using MS(School-Teaching interaction) in the denominator. The test for Review method is unbiased using MS(School-Review interaction) in the denominator. The test for the Teaching method by Review method interaction is unbiased using MS(School-Teach-Review interaction) in the denominator. These tests of treatment effects are usually of primary interest. Additionally, the test for the School by Teaching method by Review method interaction is unbiased using MS(Class-Review interaction) in the denominator. The test for the Class by Review method interaction is unbiased using MS(Pupil) in the denominator. The test for Class, which under normal theory would be unbiased using MS(Class-Review interaction) in the denominator, is biased due to additional Φ components.

3.6 SUMMARY OF MODELING BLOCK RESTRICTIONS

The usual linear model and associated EMS do not incorporate information pertinent to the randomization process. This means there is relatively little difference in the models and EMS of designs that involve blocking (a restriction on the randomization process) and those that do not. This has resulted in some confusion over testing for block effects (Searle 1971; Ostle and Mensing 1975, p. 380; Samuels et al. 1991). The methods presented in this chapter extend the linear model and associated EMS to incorporate information pertinent to the randomization process and make the effects of blocking explicit.

The methods are general to a rich class of hierarchical designs which includes the CRD, RCBD, and Split-plot, and may involve subsampling. Additionally, simple rules for generating EMS (Lorenzen and Anderson 1993b) were extended to model the effects the restricted randomization process. Several examples were given, and it was shown that in general the tests for fixed effects are similar to normal theory, but the same is not true for tests of effects associated with factors that block or cluster units. Only if units used in the experiment are considered a random sample from a large population of units within each block or cluster, are the tests for block or cluster effects unbiased. The controversy over

testing for block effects is resolved by modeling the randomization process.

CHAPTER 4

PUTTING IT ALL TOGETHER

4.1 INTRODUCTION

In this chapter two extensions to modeling restricted randomization are considered. First, the segmentation of fractional designs, and second, the combination of the results for segmentation and blocking. Rather than derive results from first principles, this chapter will focus on ways to directly apply the results of previous chapters. In conclusion, we will review the work presented in this, and previous chapters, and indicate how the computer code used to find EMS for segmenting and blocking can be accessed via the Internet.

4.2 SEGMENTATION OF FRACTIONAL DESIGNS

The purpose of a fractional design is to reduce the required size of an experiment by sacrificing information relative to effects of secondary importance while maximizing information relative to effects of primary importance. This is accomplished by selecting a subset of the treatment combinations to be run in the experiment according to well defined criteria (Box, Hunter, and Hunter 1978; Peterson 1985; Das and Giri 1986). The general approach to model the effects of segmenting and blocking also views the realizable observations as a fraction, or subset, of the potential observations. However, this fraction is selected according to a random process, unlike fractional designs where no random process comes into play in the selection of the treatment combinations. Segmentation of a fractional design can then be modeled as a two stage fractional design- the first stage is the nonrandom selection of a subset of treatment combinations, and the second stage is the random selection

of the treatment-run-order combinations to be realized. Our intent is not to present methods for creating fractional designs but to model the effects of segmenting a specified fractional design. For a review of fractional design the reader is referred to other sources (Box et al. 1978; Peterson 1985; Das and Giri 1986).

Consider the following example:

Initially an experiment is planned that involves three factors, A, B, and C, each at two levels and a single replication. There are eight treatment combinations indexed by the levels of A, B, and C:

111 112 121 122 211 212 221 222

There are 64 potential observations, the union of the eight treatment combinations and the eight possible run-orders, indexed by the levels of A, B, C, and run-order.

$$z = \begin{bmatrix} z_{111@1} \\ z_{111@2} \\ z_{111@3} \\ z_{111@4} \\ z_{111@5} \\ z_{111@6} \\ z_{111@7} \\ z_{111@8} \\ z_{112@1} \\ \vdots \\ z_{222@8} \end{bmatrix}$$

Because of cost constraints a decision is made to run a fraction of the original eight treatment combinations. The fraction is chosen in such a way that the effects of factor C are completely confounded with the interaction effects associated with factors A and B, or we

may simply state that C is confounded with AB (implies that A is confounded with BC, and B is confounded with AC). Often effects of higher order are assumed negligible (e.g. interaction effect associated with factors A and B) and information obtained on the confounded effects is attributed entirely to effects of lower order (e.g. main effects associated with factor C). Applying the methods described in Box et. al. (1978) the selected treatment combinations for the fractional design are indexed by the levels of A, B, and C respectively:

112 121 211 222

These four treatment combinations define a half fraction of the original eight treatment combinations.

There are now only 16 potential observations z^*, the union of the four treatment combinations and the four possible run-orders, and they are indexed by the levels of factors A, B, C, and run-order. It should be noted that the indices associated with A, B, and C only run over the levels defined by the half fraction, not all possible levels of A, B, and C. The potential observations associated with the fraction z^* can be selected from the original potential observations z with a nonrandom selection matrix T^* where T^* is defined according to the criteria for fractional designs (Box et.al. 1978):

$$z^{*} = \begin{bmatrix} z_{112@1} \\ z_{112@2} \\ z_{112@3} \\ z_{112@4} \\ z_{121@1} \\ \vdots \\ z_{222@4} \end{bmatrix} = T^{*}z = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & & 0 \\ & & & & & \vdots & & & & & \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & & 0 \end{bmatrix} \begin{bmatrix} z_{111@1} \\ z_{111@2} \\ z_{111@3} \\ z_{111@4} \\ z_{111@5} \\ z_{111@6} \\ z_{111@7} \\ z_{111@8} \\ z_{112@1} \\ \vdots \\ z_{222@8} \end{bmatrix}$$

In a manner similar to Chapter Two, the four realizable observations y can be written as a randomly selected subset of the potential observations associated with the fractional design, z^{*}, and a two stage selection process unfolds:

$$y = \begin{bmatrix} y_{111} \\ y_{121} \\ y_{211} \\ y_{221} \end{bmatrix} = Tz^{*} = TT^{*}z$$

Using the same approach as in Chapter Two it can be shown that

$$\begin{aligned} E(y'Q_p y) &= E_z(z'T^{*'}E_{Tz}(T'Q_p T)T^{*}z) \\ &= E_z(z'T^{*'}R_p T^{*}z) \\ &= E_z(z'R_p^{*}z) \end{aligned}$$

This solution involves $R_p = E_{Tz}(T'Q_p T)$, similar to the expectation seen in Chapter Two, pre

and post multiplied by the nonrandom matrices $T^{*'}$ and T^{*} respectively. While such a general approach could be used to derive the EMS components resulting from fractionation and segmentation, the general class of fractional designs, such as those described by Das and Giri (1986), does not lead to an easily defined expression for R_p such as that in Chapter Two. The difficulty is not a function of modeling the randomization process, because even if the randomization process is ignored there are no simple rules for generating the EMS for these designs. However, there is a small yet important subclass of fractional designs for which the results of Chapter Two can be directly applied i.e. the matrix R_p can be expressed as described in Chapter Two. This subclass is defined by those designs where each factor has 2^s levels, where s is a positive integer and can be unique for each factor (Das and Giri 1986). For designs of this subclass a fractional design can be expressed as a complete design in a subset of the original factors with an appropriate relabeling of confounded effects. Because of this the pseudo EMS rules of Chapter Two can be directly applied by viewing the fractional design as a complete design in a subset of the original factors. We will demonstrate the application of these rules in the following example.

Example 4.1 Segmentation of a Fractional Design

Consider a half fraction of a design with three factors, A, B, and C, each at two levels and two replications. The effects of factor C are completely confounded with the interaction effects associated with factors A and B, and we will assume all such interaction effects are negligible, thus allowing us to focus strictly on the effects of segmentation. Because of the high cost associated with changing the levels of A the randomization of run-order will be restricted. A level of factor A is randomly selected and all combinations of factors B and C associated with that level of A and all replications are run in random order before proceeding with the next level of factor A. For example, a potential realization of the experiment is:

Order	A	B	C
1	2	1	1
2	2	2	2
3	2	2	2
4	2	1	1
5	1	2	1
6	1	1	2
7	1	1	2
8	1	2	1

The results of applying the segmentation rules from Section 2.6.1 are shown in **Table XXXV** where the test for the effects of factor A exhibits strong bias, while tests for the effects of factors B and C exhibit weak bias. The presence of strong bias is also indicated by application of the simplified rules of Section 2.6.2 and the resulting pseudo EMS are shown in **Table XXXVI**.

Table XXXV Pseudo EMS for a Segmented Fractional Design: restriction on A

Step 1

A
B
C
$\eta(A)$
$\kappa(A\eta)$

Step 2

$$z_{ijk@mn} = \mu + \alpha_i + \eta_{i@m} + \kappa_{i@mn} + \beta_j + \eta\beta_{ij@m} + \kappa\beta_{ij@mn} + \gamma_k + \eta\gamma_{ik@m} + \kappa\gamma_{ik@mn} + \epsilon_{ijk@mn}$$

Step 3

SOURCE	*EMS*
A	$\sigma_e^2 + \sigma^2_{C\kappa(A\eta)} + \sigma^2_{C\eta(A)} + \sigma^2_{B\kappa(A\eta)} + \sigma^2_{B\eta(A)} + \sigma^2_{\kappa(A\eta)} + \sigma^2_{\eta(A)} + JKL\,\Phi(A)$
B	$\sigma_e^2 + \sigma^2_{B\kappa(A\eta)} + \sigma^2_{B\eta(A)} + IKL\,\Phi(B)$
C	$\sigma_e^2 + \sigma^2_{C\kappa(A\eta)} + \sigma^2_{C\eta(A)} + IJL\,\Phi(C)$
E	σ_e^2

Steps 4 & 5

SOURCE	*EMS*
A	$\sigma_e^2 + \left[\sigma^2_{AC\kappa(\eta)} + \sigma^2_{C\kappa(\eta)}\right] + \left[\sigma^2_{AC\eta} + \sigma^2_{C\eta}\right] + \left[\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)}\right] + \left[\sigma^2_{AB\eta} + \sigma^2_{B\eta}\right] + \sigma^2_{\kappa(A\eta)} + \sigma^2_{\eta(A)} + JKL\,\Phi(A)$
B	$\sigma_e^2 + \left[\sigma^2_{AB\kappa(\eta)} + \sigma^2_{B\kappa(\eta)}\right] + \left[\sigma^2_{AB\eta} + \sigma^2_{B\eta}\right] + IKL\,\Phi(B)$
C	$\sigma_e^2 + \left[\sigma^2_{AC\kappa(\eta)} + \sigma^2_{C\kappa(\eta)}\right] + \left[\sigma^2_{AC\eta} + \sigma^2_{C\eta}\right] + IJL\,\Phi(C)$
E	σ_e^2

Table XXXVI Simplified Pseudo EMS for a Segmented Fractional Design: restriction on A

Step 1	Step 2	Step 3
A *B* *C* $\eta(A)$	$z_{ijk@l} = \mu + \alpha_i + \eta_{i@l} + \beta_j + \gamma_k + \epsilon_{ijk@l}$	*SOURCE* *EMS* *A* $\sigma_\epsilon^2 + \sigma_{\eta(A)}^2 + JKL\,\Phi(A)$ *B* $\sigma_\epsilon^2 + IKL\,\Phi(B)$ *C* $\sigma_\epsilon^2 + IJL\,\Phi(C)$ *E* σ_ϵ^2

4.3 COMBINING RESULTS FOR SEGMENTING AND BLOCKING

We will now define conditions under which the pseudo EMS rules for segmenting and blocking developed previously can both be applied to a design. Such a design would involve inherent restrictions due to the structure among the experimental material and restrictions on run-order applied at the discretion of the experimenter. For example, a sequential RCBD where all runs within a block will be run in random order before proceeding with another block. We will approach the problem using a simple example which is easily generalized: an RCBD with two blocks, two treatments, and a single replication.

Define z as the potential observations where $z_{ijk@l}$ represents treatment j applied to unit k in block i in run-order l:

$$ {}_{32}z_1 = \begin{bmatrix} z_{111@1} \\ z_{111@2} \\ z_{111@3} \\ z_{111@4} \\ z_{112@1} \\ \vdots \\ z_{222@4} \end{bmatrix} $$

It is helpful to think of the first three subscripts of z as being "stretched", or repeated, to accommodate the possible run-orders indexed by the fourth subscript. Combining segmenting and blocking involves a two stage randomization process. First treatment combinations are assigned to experimental units, which involves the first three subscripts in the selection process (the fourth is carried along for the second stage). Second the run-order is determined according to the fourth subscript. Using such a two stage randomization process the realizable observations y can be linked to the potential observations z as follows:

$$ {}_4y_1 = {}_4T_{16}^{S}\left[{}_4T_8^{B} \otimes {}_4I_4 \right] {}_{32}z_1 $$

T^S and T^B are the selection matrices for segmenting and blocking respectively, and are the same matrices obtained when segmenting and blocking are modeled separately. T^B selects the treatment combinations that are applied to the experimental units and is "stretched" to accommodate all the possible run-orders by use of the Kronecker product $\left[{}_4T_8^B \otimes {}_4I_4 \right]$. Having selected the appropriate assignment of treatment combinations to experimental units, T^S then selects the assignment of run-order.

With the problem formulated in this way, the effects model can incorporate interaction effects involving unit and run-order. However, such generality comes at a price- requiring the joint moments of T^S and T^B. If we are willing to assume independence of effects that involve unit and run-order then the problem can be reformulated to show that the previously developed rules for segmenting and blocking can be directly applied. The reformulation expresses the multiplicative model involving T^S and T^B as a simpler additive model. Under the assumption of independence the effects can be divided into two subsets which are the objects of the two selection matrices T^S and T^B respectively. Wilk (1955) put forth an argument concerning assumptions in the RCBD that can serve as a rationale for the assumption of independence of effects that involve unit and run-order. Wilk argued that if blocking is effective then units within a block are homogeneous, and while it may be unrealistic to assume that block-by-treatment interactions are negligible, it may not be unrealistic to assume that the unit-by-treatment interactions are negligible. Since run-order effects can be viewed as an aggregate of treatment effects associated with lurking variables, unit-by-run-order interactions can be viewed as unit-by-treatment interactions, and Wilk's argument applies.

The vector of effects can written as two subvectors: one that involves unit effects (u) and another that involves run-order effects (o). The block and treatment effects are arbitrarily put into the subvector that contains the unit effects.

$$\beta' = \beta^{B'} | \beta^{S'} = \left[\beta_1, \beta_2, ..., \beta\tau_{22}, u_1, u_2, ..., \tau u_{22}\right] | \left[o_1, o_2, ..., \beta\tau o_{22@4}\right]$$

Because the potential observations can be modeled as $z = X\beta$, indices associated with specific elements of z are also associated with specific effects or elements of β. First z^* is formed as elements of z are selected by $\left[{}_4T_8^B \otimes {}_4I_4\right]$, where T^B selects or chooses which treatments are assigned to which units and carries along all the effects associated with block and treatment. The Kronecker product with I effectively "stretches" T^B so that all effects associated with run-order are carried along. The selection matrix T^B is effectively only making choices among effects contained in the subvector β^B. T^S then selects elements of z^* associated with run-order effects, those contained in subvector β^S. Because of the assumption of independence of effects involving unit and run-order T^S and T^B do not have any effects in common from which choices are made i.e. T^B selects from β^B and T^S selects from β^S. The same result can be achieved by use of an additive model rather than a multiplicative model, where the additive model is a function of the potential observations for segmenting and blocking considered independently.

For segmenting the potential observations are indexed by block, treatment, and run-order:

$$z^S = \begin{bmatrix} z^S_{11@1} \\ z^S_{11@2} \\ z^S_{11@3} \\ z^S_{11@4} \\ z^S_{12@1} \\ \vdots \\ z^S_{22@4} \end{bmatrix}$$

The model for segmentation can be written as (see Chapter Two for details):

$$y = T^S z^S \text{ where } z^S = X^S \beta^S$$

For blocking the potential observations are indexed by block, treatment, and unit within block:

$$z^B = \begin{bmatrix} z^B_{111} \\ z^B_{112} \\ z^B_{121} \\ z^B_{122} \\ z^B_{211} \\ z^B_{212} \\ z^B_{221} \\ z^B_{222} \end{bmatrix}$$

The model for blocking can be written as (see Chapter Three for details):

$$y = T^B z^B \text{ where } z^B = X^B \mathrm{B}^B$$

If both segmentation and blocking are involved the realizable observations can be modeled as:

$$y = T^S z^S + T^B z^B$$

The sum of squares for the p^{th} term in the model can be expressed as:

$$\begin{aligned} y'Q_p y &= \left[T^S z^S + T^B z^B\right]' Q_p \left[T^S z^S + T^B z^B\right] \\ &= \left[z^{S'} T^{S'} Q_p T^S z^S\right] + \left[z^{S'} T^{S'} Q_p T^B z^B\right] + \\ &\quad \left[z^{B'} T^{B'} Q_p T^S z^S\right] + \left[z^{B'} T^{B'} Q_p T^B z^B\right] \end{aligned}$$

The expectation of the sum of squares is:

$$\begin{aligned} E(y'Q_p y) &= E_{z^S}\left[z^{S'} E_{T^S|z^S}\left[T^{S'} Q_p T^S\right] z^S\right] + E_{z^S z^B}\left[z^{S'} E_{T^S T^B|z^S z^B}\left[T^{S'} Q_p T^B\right] z^B\right] + \\ &\quad E_{z^B z^S}\left[z^{B'} E_{T^B T^S|z^B z^S}\left[T^{B'} Q_p T^S\right] z^S\right] + E_{z^B}\left[z^{B'} E_{T^B|z^B}\left[T^{B'} Q_p T^B\right] z^B\right] \\ &= E_{z^S}\left[z^{S'} R_p^S z^S\right] + E_{z^S z^B}\left[z^{S'} R_p^{SB} z^B\right] + \\ &\quad E_{z^B z^B}\left[z^{B'} R_p^{BS} z^S\right] + E_{z^S}\left[z^{B'} R_p^B z^B\right] \\ &= \left[tr(R_p^S \Sigma_{z^S}) + \mu_{z^S}' R_p^S \mu_{z^S}\right] + \left[tr(R_p^{SB} \Sigma_{z^S z^B}) + \mu_{z^S}' R_p^{SB} \mu_{z^B}\right] + \\ &\quad \left[tr(R_p^{BS} \Sigma_{z^B z^S}) + \mu_{z^B}' R_p^{BS} \mu_{z^S}\right] + \left[tr(R_p^B \Sigma_{z^B}) + \mu_{z^B}' R_p^B \mu_{z^B}\right] \end{aligned}$$

Similar to Chapter Two, it is assumed that effects involving run-order are random, hence $\mu_z^S = 0$ and terms multiplied by μ_z^S vanish. It is also assumed that the covariance between effects associated with run-order and other effects is zero, i.e. $\Sigma_{z^S z^B} = \Sigma_{z^B z^S} = 0$, hence terms multiplied by $\Sigma_{z^S z^B}$ or $\Sigma_{z^B z^S}$ also vanish. Such an assumption should not prove overly restrictive, for example $\sigma_{\tau\mu_{jk}, \tau o_{j(l)}} = 0$. The expected sum of squares reduces to:

$$E(y'Q_p y) = \left[tr(R_p^S \Sigma_{z^S}) + \mu_{z^S}' R_p^S \mu_{z^S}\right] + \left[tr(R_p^B \Sigma_{z^B}) + \mu_{z^B}' R_p^B \mu_{z^B}\right]$$

The expression in the first set of brackets is the expected sum of squares associated with segmentation as derived in Chapter Two. The expression in the second set of brackets is the expected sum of squares associated with blocking as defined in Chapter Three. Under the specified conditions the pseudo EMS rules for segmenting and blocking can be jointly applied to a design.

For the following example the simplified rules for segmenting (Section 2.6.2) will be combined with the rules for blocking (Section 3.5).

Example 4.2 Combining the Results of Segmenting and Blocking

An RCBD with two blocks and two treatments is replicated twice (i.e. treatments are replicated within blocks). The units involved in the experiment do not represent a random sample of units from within each block. The experiment is run sequentially and a segment restriction is imposed on blocks (a block is randomly selected and all runs within that block are run in random order before proceeding with the next block).

2. Define factors and relationships.
   - Define the usual design factors and their relationships.

     B (block)
     T (treatment)
     E(BT) (Error)
   - Starting at the top of the hierarchy, for each factor, or factor combination, that defines a hierarchical restriction, define a segment factor nested in the defining factors and any previously defined segment factor.

     B (block)
     η(B)

T (treatment)
E(BT) (Error)

2. Build the effects model.
   - Create the full effects model using all defined factors but do not create interactions that involve segment factors. Label terms in the model as fixed, random, or mixed, in the usual manner (according to either of the two competing methods for mixed models), segment effect are considered random.

$$z_{ijkm}=\mu+\beta_i+\eta_{im}+\tau_j+\beta\tau_{ij}+\epsilon_{ijk}$$

   - For each term in the model associated with clustered units that are not a random sample from a much larger population of units within the cluster:
     a. immediately follow it with a duplicate term marked with an asterisk,
     b. delete any container subscripts from the asterisked term that are not in common with the term associated with the cluster factor.

$$z_{ijkm}=\mu+\beta_i+\eta_{im}+\tau_j+\beta\tau_{ij}+\epsilon_{ijk}+\epsilon^{*}_{ik}$$

3. Calculate Pseudo EMS.

   Calculate the EMS for each term not associated with segment effects or asterisked effects (the term of interest). The EMS are generated by taking the expectation over all subsequent terms in the augmented model (candidate terms). For nonasterisked candidate terms the EMS are calculated in the usual manner (Lorenzen and Anderson 1993b). For asterisked candidate terms the following rule is applied:
   - If any noncontainer subscript of the term of interest is not a container subscript of the (subsequent) candidate term then a fixed effects candidate component (Φ) is included in the EMS.

For example, consider the EMS for block and treatment. β_i has a noncontainer subscript i which is a container subscript of the candidate term ϵ'_{ik} hence there is no $\Phi(\epsilon')$ component. τ_j has a noncontainer subscript j which is not a container subscript of the candidate term ϵ'_{ik} hence there is a $\Phi(\epsilon')$ component.

The factors, model, and pseudo EMS are summarized in **Table XXXVII.** The test for Block effects using the MS(Block-Treatment interaction) in the denominator is biased due to blocking (lacks a $\Phi(\epsilon')$ component) and due to segmenting (additional $\sigma^2_{\gamma(B)}$ component). The test for Treatment effects using MS(Block-Treatment interaction) in the denominator is unbiased. The test for Block-Treatment interaction effect using MS(Error) in the denominator is also unbiased.

Table XXXVII Combined Application of Segmenting and Blocking

Step 1	Step 2	Step 3
B T $\eta(B)$ $E(BT)$	$z_{ijkm}=\mu+\beta_i+\eta_{im}+\tau_j+\beta\tau_{ij}+\epsilon_{ijk}+\epsilon^{\bullet}_{ik}$	*SOURCE* *EMS* B $\sigma^2_\epsilon + K\sigma^2_{BT} + \sigma^2_{\eta(B)} + JK\sigma^2_B$ T $\Phi(\epsilon^{\bullet}) + \sigma^2_\epsilon + K\sigma^2_{BT} + IK\Phi(T)$ BT $\Phi(\epsilon^{\bullet}) + \sigma^2_\epsilon + K\sigma^2_{BT}$ E $\Phi(\epsilon^{\bullet}) + \sigma^2_\epsilon$

4.4 SUMMARY AND SUGGESTIONS FOR FURTHER WORK

Randomization is the cornerstone of experimental design and has been viewed as the foundation for inference (Kempthorne 1955). While the usual methods for linear models ignore fundamental information relative to the randomization process, several authors have adapted the linear model to incorporate such information to varying degrees (Kempthorne 1955; Wilk 1955; Scheffe 1959; Anderson and McLean 1974a, 1974b; White 1975; Lorenzen 1984; Lorenzen and Anderson 1993a; Hinkelmann and Kempthorne 1994). In this body of literature two fundamental roles of randomization are identified: the assignment of treatments to experimental units where those units are grouped into blocks, and the assignment of run-order in sequential trials where run-order may be restricted in some way. The dual role of randomization has been dealt with by implicitly modeling block restrictions (the inherent grouping of similar experimental material) and segment restrictions (the discretionary restriction of run-order). However, some weaknesses of the previous work include:

- Derivation of the effects of segment and block restriction used extensive summation notation which can obscure the inherent and simple structure of the problem.
- Segment restrictions involved implicit assumptions of additivity.
- Block restrictions were presented in design specific format i.e. not generalized.
- Results for Segment and Block restrictions were not unified.

In this and previous chapters we have attempted to address these weaknesses using a general matrix based framework for modeling the effects of restricted randomization.

This general method is based on selecting the realizable observations y from a vector of potential observations z using a selection matrix T, where $y = Tz$. The realizable observations are a subset, or fraction, of the potential observations and the concept of alias, or confounding, carries over and can be represented in the EMS. The simplicity and compactness of the matrix model notation extends to the expression of quadratic forms and their expectations. This tends to focus attention on the fundamental problem structure rather than the machinery required to solve it. In some of the previous work this structure is

obscured by excessive summation notation. A matrix based approach lends itself to implementation using commercially available matrix based computer languages (all code was written using GAUSS 1992, and can be downloaded from http://www.math.sfu.ca/~cschwarz/Restrict). While the problem was formulated using matrix notation and the resulting EMS bias components can be viewed as "within" and "between" submatrices, it was useful to reexpress these components using summation notation to express the functional form. The use of a symbolic programming language to automate this reexpression was explored (MAPLE V 1993) but it was deemed too complex to implement. Specifically, no simple way was found to implement the constraints on summations, for example $\sum_{i=1}^{I}\sum_{i'=1}^{I}\sigma_{i,i'}$ where $i \neq i'$ (written in shorthand as $\sum\sum_{i \neq i'}\sigma_{i,i'}$) and to track the number of elements in the summation ($I(I-1)$ in this example).

Segment restrictions- restrictions on the run-order of a sequential experiment- were the topic of Chapter Two. Previous results made the implicit assumption of additivity of treatment effects and run-order effects (Anderson and McLean 1974a, 1974b; Lorenzen 1984; Lorenzen and Anderson 1993a), in fact, it was this implicit assumption that first drew my attention to the area of modeling restricted randomization. The general solution allows unlimited hierarchical restrictions on the randomization of run-order and allows nonadditivity of treatment and run-order effects. The issue of additivity is important because it is also underlies the usual linear model. When randomization is complete (the usual case) departure from additivity generally results in small or weak bias, but when randomization is restricted departure from additivity can result in substantial or strong bias. However, it was also shown that strong nonadditive bias components always occur in conjunction with run-order main effect components (which are always strong). This means that the simpler additive model is sufficient to indicate the presence of strong bias when randomization is restricted. This substantiates previous results which relied on the implicit assumption of additivity. Simple rules were developed for generation of pseudo EMS (which indicate the existence but not the form of bias components) for both the additive and nonadditive models.

In Section 4.2 it was shown that these same rules can be applied to the small but important subclass of fractional designs where each factor has 2^s levels (where s can be unique for each factor).

Designs that include sequential structures in parallel were not discussed in detail, however it should be possible to extend current results to cover such designs. An example of such a design might be an experiment carried out in several labs or using several machines in parallel. For each lab or machine the observations are sequential and subject to unique restrictions on randomization. The methods presented in previous chapters could be adapted by constraining time effects to be identical within blocks, however, this would assume that the runs within all blocks started and progressed at the same rate. It would also assume that the effects of run-order are global, for example, the effects of some lurking variable such as humidity are the same in different geographic locations. This is probably an unrealistic assumption in many experiments. A more general solution would allow run-order to be restricted within blocks while allowing unique run-order effects within each block. In general, it is unclear whether the run-order effects would be independent between blocks, as this would depend on the specific problem at hand. However, the methods for segmentation presented in Chapter 2 are probably sufficient to indicate potential bias due to restrictions even in such parallel sequential experiments. Consider a sequential experiment carried out simultaneously in several blocks, with a restriction on a factor, say factor A, within each block. Represent this design as though it is segmented on blocks and then segmented on factor A within blocks (hierarchical restriction). Because blocks are not actually run sequentially, the bias component associated with a test of blocks would not the correct structure. However, primary interest is in the bias associated with the test for factor A, in fact, typically one would not be interested in testing for the block effect. The bias component associated with the restriction on factor A within each block exhibits the correct structure because it is a function of correlations within a block.

The general approach used in segmenting should be applicable to blocking as well, and

this was the topic of Chapter Three. The resulting pseudo EMS rules are sufficient to model unlimited hierarchical restrictions and unlimited levels of subsampling in a broad class of designs. However, application of such rules is not as simple as it is with segmentation, and in general, it is may be simpler just to adopt a "don't test blocks" viewpoint. Designs with nonhierarchical blocking, such as Latin squares, are excluded. For the simple case of an RCBD it was confirmed (see Wilk 1955) that according to randomization theory there is no unbiased test for blocks. Whether and how to test blocks has long been a source of confusion and controversy in the field of linear models. The bias in the test for blocks exists because the units used in the experiment do not represent a random sample from a large population of units within a block. This type of bias can occur whenever homogenous experimental material is grouped and thus can occur as a result of subsampling as well as traditional blocking. If the units do represent a random sample of a large population of units within a block then the bias vanishes (though this is rarely the case in practice).

Finally the results for segmenting and blocking were combined. A general two stage randomization model was first proposed: first randomize the assignment of treatment to experimental units then randomize the run-order. Use of this two stage model requires the joint moments of the selection matrices $\boldsymbol{T}^s$ and $\boldsymbol{T}^b$. If it is assumed that the effects of unit and run-order are independent then it is possible to model the various effects using an additive rather than a multiplicative model and circumvent the need for the joint moments of the selection matrices $\boldsymbol{T}^s$ and $\boldsymbol{T}^b$. Such an assumption is not unreasonable, and under other mild conditions the additive model simplifies to two pieces which are the EMS associated with blocking and the EMS associated with segmenting.

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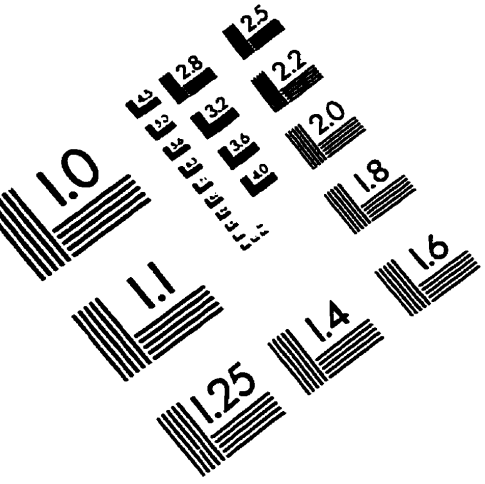
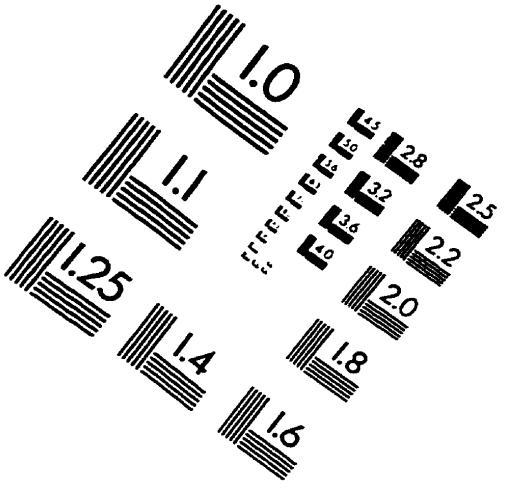
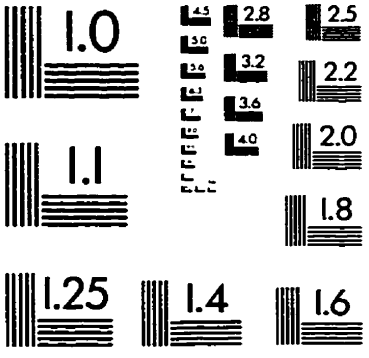
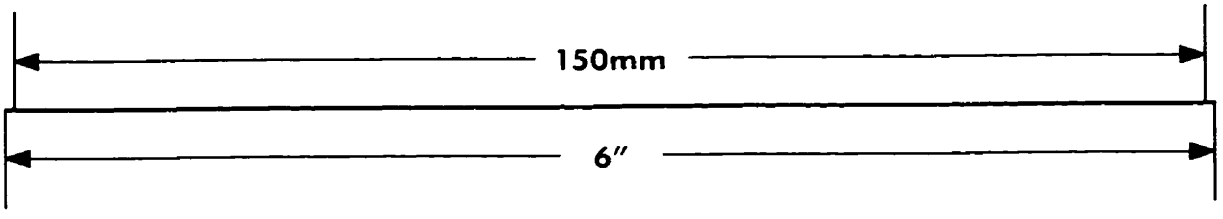
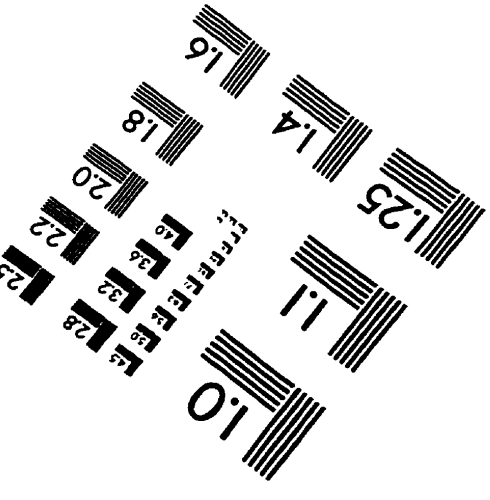
IMAGE EVALUATION
TEST TARGET (QA-3)

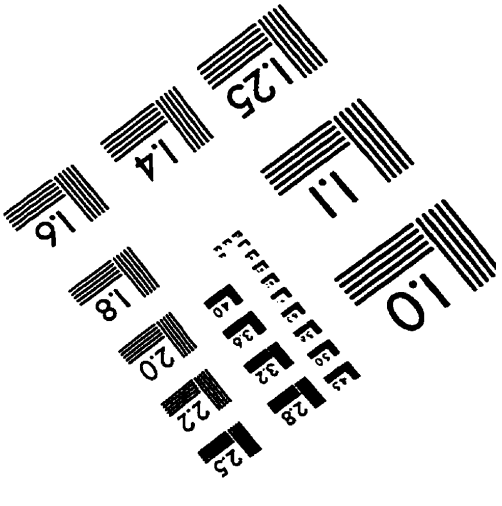












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