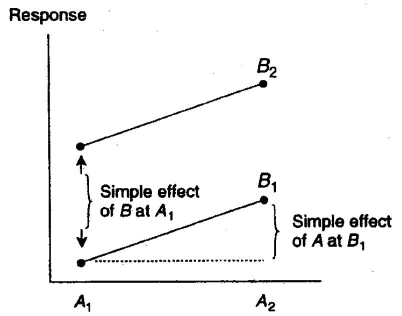
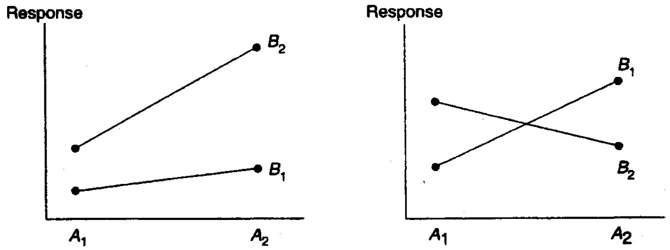


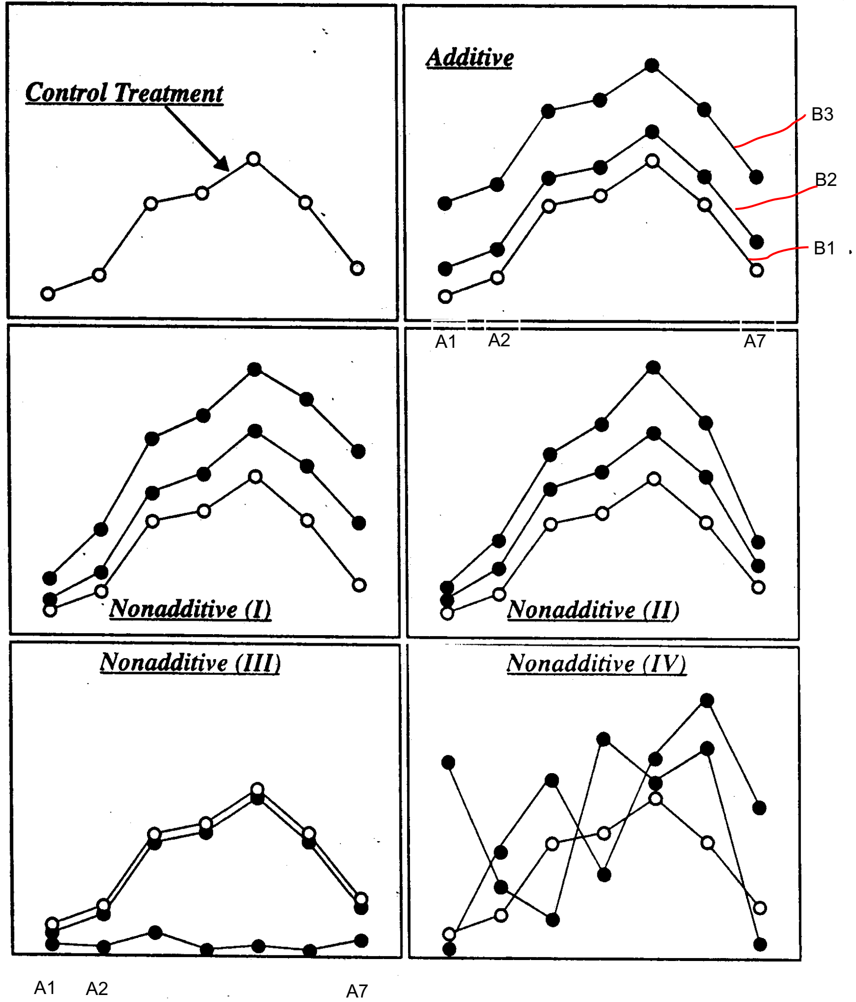
Figure 6.1 Illustration of no interaction in a factorial arrangement



(a) Interaction as a difference in *magnitude* of response

(b) Interaction as a difference in *direction* of response

Figure 6.2 Illustration of interaction in a factorial arrangement



Completely Randomized Factorial (CRF) Designs

$$\begin{array}{c|c|c|c} & B_1 & B_2 & \\ \hline A_1 & \mu_{11} & \mu_{12} & \bar{\mu}_{1\bullet} \\ \hline A_2 & \mu_{21} & \mu_{22} & \bar{\mu}_{2\bullet} \\ \hline & \bar{\mu}_{\bullet 1} & \bar{\mu}_{\bullet 2} & \end{array} \qquad \begin{array}{c|c|c|c} & B_1 & B_2 & \\ \hline A_1 & \bar{Y}_{11\bullet} & \bar{Y}_{12\bullet} & \bar{Y}_{1\bullet\bullet} \\ \hline A_2 & \bar{Y}_{21\bullet} & \bar{Y}_{22\bullet} & \bar{Y}_{2\bullet\bullet} \\ \hline & \bar{Y}_{\bullet 1\bullet} & \bar{Y}_{\bullet 2\bullet} & \end{array}$$

$$Y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijk} \qquad \varepsilon_{ijk} \overset{iid}{\sim} N(0, \sigma_e^2) \qquad \begin{array}{l} i = 1, \ldots, a \\ j = 1, \ldots, b \\ k = 1, \ldots, r \end{array}$$

Simple Effect Contrast

$S_{A,B_1} = \mu_{21} - \mu_{11}$ simple effect of factor A, at level 1 of factor B

$S_{A,B_2} = \mu_{22} - \mu_{12}$ simple effect of factor A, at level 2 of factor B

Main Effect Contrast

$M_A = \mu_{2\bullet} - \mu_{1\bullet}$ main effect of factor A [averaged over levels of the other factor(s)]

Interaction Effect Contrast

$$\begin{aligned} I_{AB} = S_{A,B_1} - S_{A,B_2} &= (\mu_{22} - \mu_{12}) - (\mu_{21} - \mu_{11}) \\ &= \mu_{22} - \mu_{12} - \mu_{21} + \mu_{11} \end{aligned}$$

Main Effect *Contrasts* vs. Main Effects

- M_A and I_{AB} above are *contrasts* and thus not defined in the same way as in the ANOVA where $\bar{\mu}_{\bullet\bullet}$ or $\bar{Y}_{\bullet\bullet\bullet}$ are taken as the reference (baseline).
- $M_{A1} = \bar{\mu}_{1\bullet} - \bar{\mu}_{\bullet\bullet}$ and $M_{A2} = \bar{\mu}_{2\bullet} - \bar{\mu}_{\bullet\bullet}$ are Main Effects (not contrasts)

"*Simple Main Effects*"

$\mu_{21} - \bar{\mu}_{\bullet 1}$ "*Simple Main Effect*" of treatment A_2 at level B_1

$\mu_{22} - \bar{\mu}_{\bullet 2}$ "*Simple Main Effect*" of treatment A_2 at level B_2

Decomposition of the *SS(Total)*

$$\left(Y_{ijk} - \bar{Y}_{\bullet\bullet\bullet}\right) = \left(Y_{ijk} - \bar{Y}_{ij\bullet}\right) + \left(\bar{Y}_{i\bullet\bullet} - \bar{Y}_{\bullet\bullet\bullet}\right) + \left(\bar{Y}_{\bullet j\bullet} - \bar{Y}_{\bullet\bullet\bullet}\right) + \left(\bar{Y}_{ij\bullet} - \bar{Y}_{i\bullet\bullet} - \bar{Y}_{\bullet j\bullet} + \bar{Y}_{\bullet\bullet\bullet}\right)$$

$$total \qquad Error \qquad FactorA_i \qquad FactorB_j \qquad Interaction$$

CRF - ab (Fixed Effects Model)

$$Y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijk} \qquad \varepsilon_{ijk} \overset{iid}{\sim} N(0, \sigma_e^2) \qquad \begin{array}{l} i = 1, \ldots, a \\ j = 1, \ldots, b \\ k = 1, \ldots, r \end{array}$$

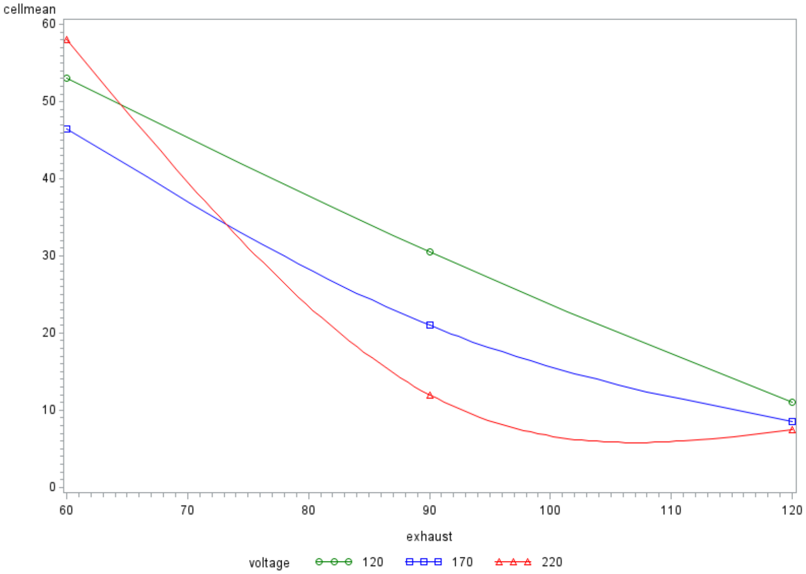
Source	**d.f.**	**SS**	**MS**	**E(MS)**
Factor A		$\sum_i \sum_j \sum_k \left(\bar{Y}_{i\bullet\bullet} - \bar{Y}_{\bullet\bullet\bullet}\right)^2$	MSA	$\sigma_e^2 + \frac{\sum\sum\sum \alpha_i^2}{a-1}$
Factor B		$\sum_i \sum_j \sum_k \left(\bar{Y}_{\bullet j\bullet} - \bar{Y}_{\bullet\bullet\bullet}\right)^2$	MSB	$\sigma_e^2 + \frac{\sum\sum\sum \beta_i^2}{b-1}$
Interaction (A*B)		$\sum_i \sum_j \sum_k \left(\bar{Y}_{ij\bullet} - \bar{Y}_{i\bullet\bullet} - \bar{Y}_{\bullet j\bullet} + \bar{Y}_{\bullet\bullet\bullet}\right)^2$	$MS(AB)$	$\sigma_e^2 + \frac{\sum\sum\sum (\alpha\beta)_{ij}^2}{(a-1)(b-1)}$
Error		$\sum_i \sum_j \sum_k \left(Y_{ijk} - \bar{Y}_{ij\bullet}\right)^2$	MSE	σ_e^2
Total	$rab-1$	$\sum_i \sum_j \sum_k \left(Y_{ijk} - \bar{Y}_{\bullet\bullet\bullet}\right)^2$		

Example: Vacuum Tubes in specialized audio equipment

DV: pressure inside vacuum tube (micrometers of Hg)
IV1: Exhaust index (60, 90, 120 seconds)
IV2: Voltage (120, 170, 220 volts)

Design: Completely Randomized Factorial (CRF-33)

	E1	E2	E3
V1			
V2			
V3			



CRF Designs

Simple Effect Contrast comparing V_{220} & V_{170} at E=60 *seconds*

$$C = \bar{\mu}_{220,60} - \bar{\mu}_{170,90}$$

Consider the following Main Effect contrast comparing the 60 & 90 sec Exhaust indices:

$$C = \bar{\mu}_{\bullet 60 \bullet} - \bar{\mu}_{\bullet 90 \bullet} \rightarrow \hat{C} = \bar{Y}_{\bullet 60 \bullet} - \bar{Y}_{\bullet 90 \bullet}$$

1) Estimate the contrast and its standard error.
2) Compute the test statistic for testing $H_0 : C = 0$ and test the hypothesis at $\alpha=0.05$.
3) Compute a 95% CI for the contrast

The null hypothesis of no nonadditivity is tested with the statistic $F_0 = MS(\text{Nonadditivity})/MS(\text{Residual}) = 269.6/33.6 = 8.02$. The null hypothesis is rejected with a critical region $F_0 > F_{.05,1,35} = 4.12$.

Several methods have been developed to ascertain the source of nonadditivity in a two-way table. Daniel (1978) used a method based on the residuals in each of the cells, $y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..}$. Technical discussions and examples of several other methods and models for nonadditivity can be found in Johnson and Graybill (1972), Bradu and Gabriel (1978), and Mandel (1971).

6.8 How Many Replications to Test Factor Effects?

Procedures were given in Section 2.14 to estimate replication numbers based on the test for differences among treatment means with the F_0 statistic. The values of Φ (Equation (2.25)) can be applied directly to a test for differences among cell means in the factorial arrangement with the null hypothesis H_0: $\mu_{11} = \mu_{12} = \cdots = \mu_{ab}$. In this case, the factorial structure is ignored and the cell means model $y_{ijk} = \mu_{ij} + e_{ijk}$ expressed in the effects model form is $y_{ijk} = \mu + \tau_{ij} + e_{ijk}$, where τ_{ij} is the effect of the ijth treatment combination in the factorial arrangement. Then

$$\Phi^2 = \frac{r\sum_{i=1}^{a}\sum_{j=1}^{b}\tau_{ij}^2}{ab\sigma^2} \tag{6.34}$$

is used to estimate replication numbers from the charts based on the values of τ_{ij} required to be significant.

If replication numbers based on the factorial effects are required, the noncentrality parameters are

$$\lambda_a = br\sum_{i=1}^{a}\frac{\alpha_i^2}{\sigma^2},\quad \lambda_b = ar\sum_{j=1}^{b}\frac{\beta_j^2}{\sigma^2},\quad \text{and}\quad \lambda_{ab} = r\sum_{i=1}^{a}\sum_{j=1}^{b}\frac{(\alpha\beta)_{ij}^2}{\sigma^2} \tag{6.35}$$

respectively, for A and B main effects and AB interaction. Then Φ is determined as $\Phi = \sqrt{\lambda/(\nu_1 + 1)}$, where ν_1 are the numerator degrees of freedom for the F_0 statistic.

6.9 Unequal Replication of Treatments

Missing data in research studies is inevitable. The design is no longer balanced with a complete data set, and standard computing formulae no longer apply. Before the advent of modern computing, a complete data set was most advantageous because relatively simple formulae could be used for manual computations. Much effort was put into developing methods for the analysis of variance sum of squares partitions when there were unequal numbers of observations among the cells of the

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ONE DEGREE OF FREEDOM FOR NON-ADDITIVITY*†

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INTRODUCTION

IN DISCUSSING the possible shortcomings of the analysis of variance, much attention has been paid to non-constancy and non-normality of the "error" contribution. (The recent papers in *Biometrics* by Eisenhart [4], Cochran [3] and Bartlett [1] discuss these matters and give references.) The present writer is usually much more concerned with and worried about non-additivity, and until recently has suffered from the lack of a systematic way to seek it out, and then to measure it. (Conversations with Frederick F. Stephan have contributed greatly to this development and presentation.)

The purpose of the present paper is to indicate such a way, when the data is in the form of a row-by-column table. (The professional practitioner of the analysis of variance will have no difficulty in extending the process to more complex designs.) We shall show how to isolate one degree of freedom from the "residue", "error", "interaction" or "discrepance", call it what you will. There are two known situations to which this single degree of freedom is expected to react by swelling:

(1) when one or more observations are unusually discrepant;
(2) when the analysis has been conducted in terms where the effects of rows and columns are not additive.

The first situation is quite familiar and requires little explanation. The second occurs often enough, but may not be noticed. An example may help to fix the ideas.

Let us construct an artificial example with 3 rows and 4 columns, with each entry contributed to overall, by rows, by columns, and by cells. Suppose that these contributions are as follows:

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*Prepared in connection with research sponsored by the Office of Naval Research.
†Presented to the Biometrics Section and the Biometric Society at Cleveland, December 29, 1948.

Tukey’s 1 d.f. Test for Transformable/Multiplicative Non-additivity (*r = 1 observation/cell*)

Source	d.f.	SS
A	*a-1*	*SS(A)*
B	*b-1*	*SS(B)*
A*B	*(a-1)(b-1)*	*SS(AB)*
Error	*ab(r-1)*	*SS(Error)*

1) $Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}$

2) $Y_{ij} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ij}$

3) $Y_{ij} = \mu + \alpha_i + \beta_j + m(\alpha_i)(\beta_j) + \varepsilon_{ij}$

- Residuals from (1) represent deviations from an additive model
- If (3) is the correct model, then residuals from (1) should be linearly related to $(\alpha_i)(\beta_j)$

H_0: There is <u>no</u> Transformable Non-additivity

$$SS(NonAdd) = \frac{\left[\sum_{i=1}^{a}\sum_{j=1}^{b}\left(\hat{\alpha}_i\right)\left(\hat{\beta}_j\right)Y_{ij}\right]^2}{\sum_{i=1}^{a}\left(\hat{\alpha}_i\right)^2\sum_{j=1}^{b}\left(\hat{\beta}_j\right)^2}$$

$$SS(REM) = SS(A*B) - SS(NonAdd)$$

$$df(REM) = df(A*B) - 1$$

$$F_{NonAdd} == \frac{SS(NonAdd)/1}{SS(REM)/df(REM)}$$

```
Class         Levels    Values
salinity           3    0 6 12
days               3    14 21 28

Number of Observations Used          9

Dependent Variable: water
                            Sum of
Source           DF       Squares    Mean Square   F Value   Pr > F
Model             8   116.3800000     14.5475000       .      .
Error             0     0.0000000      .
Corrected Total   8   116.3800000

R-Square     Coeff Var      Root MSE    water Mean
1.000000           .               .      6.700000

Source           DF     Type I SS    Mean Square   F Value   Pr > F
salinity          2   22.64666667    11.32333333       .      .
days              2   80.68666667    40.34333333       .      .
salinity*days     4   13.04666667     3.26166667       .      .

Source           DF   Type III SS    Mean Square   F Value   Pr > F
salinity          2   22.64666667    11.32333333       .      .
days              2   80.68666667    40.34333333       .      .
salinity*days     4   13.04666667     3.26166667       .      .


SS(Non-Additivity) for Tukey 1 d.f. test for Transformable Non-Additivity

dfnonadd    ssnonadd
    1        11.9559


If a transformation is needed (W=Y^p)
Tukey's suggested power is p = (1 - slope * ¯Y_..)
   y_gm  = ¯Y_.. = Grand Mean of all Observations
   slope = Estimate of the slope relating e_ij and (¯Y_i.-¯Y..)*(¯Y_.j-¯Y..)

y_gm     slope         p
 6.7    0.24267    -0.62587
```

```
*--------------------------------------;
*Read in SAS macros;
 FILENAME macro231 URL "http://www.uvm.edu/~rsingle/stat231/macros-stat231.sas";
 %INCLUDE macro231;

* Compute SS(NonAdd)
 %tukey1df(DATA=b1,DEP=water,INDEP1=salinity,INDEP2=days);

* Look for a transformation to remove any multiplicative non-addititvity;
 %tukey1df_transf(DATA=b1,DEP=water,INDEP1=salinity,INDEP2=days);
```