

Topic 6. Two-way designs: Randomized Complete Block Design

[ST&D Chapter 9 sections 9.1 to 9.7 (except 9.6) and section 15.8]

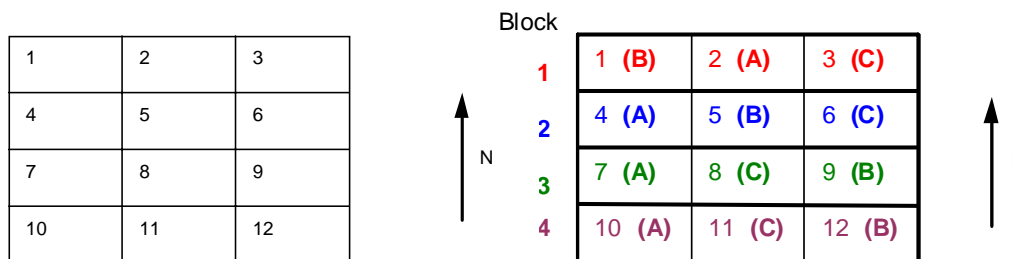
The completely randomized design

- It is assumed that the experimental units are uniform.
- It is always advocated to include as much of the native variability of the experiment as possible *within* each experimental unit
- Since experimental units are more variable, experimental error (MSE) is large, F (MST/MSE) is small, and the experiment is not very sensitive.
- The experiment can not be replicated in a variety of situations to increase the scope of the experiment.

6. 2. Randomized complete block design (RCBD)

- The population of experimental units is divided into a number of relatively homogeneous subpopulations or *blocks*.
- The treatments are randomly assigned to experimental units such that each treatment occurs equally often in each block.
- Blocks usually represent naturally occurring differences not related to the treatments.
- The variation among blocks can be partitioned out, usually reducing the experimental error (MSE).

6. 2. 2. Example: Three cultivars with 4 replications. N level varies from north to south. In a CRD error terms will tend to be negative at one end of the field and positive at the other.



The field can be divided into four blocks of three plots each, and the soil in each of these blocks will be uniform.

RCBD: INDEPENDENT RANDOMIZATIONS IN EACH BLOCK!

6. 2. 3. Statistical model

The new model is

$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}.$$

The sum of squares equation becomes:

$$\sum_{i=1}^t \sum_{j=1}^r (Y_{ij} - \bar{Y}_{..})^2 = r \sum_{i=1}^t (\bar{Y}_{i.} - \bar{Y}_{..})^2 + t \sum_{j=1}^r (\bar{Y}_{.j} - \bar{Y}_{..})^2 + \sum_{i=1}^t \sum_{j=1}^r (Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2$$

or, SS = SST + **SSB** + SSE.

Variance of means of n observations is $\sigma^2/n \Rightarrow$ multiplication by **r** and **t** in the SSB and SST result in all MS being **estimates of the same σ^2** when there are no block or treatment effects.

Partitioning of variance: is possible because the sums of squares of blocks and treatments are *orthogonal* (each block has all treatments).

6. 2. 4. ANOVA

ANOVA table for the **RCBD**

Source	Df	SS	MS	F
Blocks	r - 1	SSB	SSB/(r-1)	
Treatments	t - 1	SST	SST/(t-1)	MST/MSE
Error	(t-1)(r-1)	SS-SST-SSB	SSE/(r-1)(t-1)	
Total	rt - 1	SS		

If >1 rep. \Rightarrow add **BLOCK*TRT** In the model

ANOVA table for the **CRD**

Source	Df	SS	MS	F
Treatments	t - 1	SST	SST/(t-1)	MST/MSE
Error	t(r - 1)	SS - SST	SSE/r(t-1)	
Total	rt - 1	SS		

- The **RCBD** design has r - 1 fewer degrees of freedom than the **CRD**.
- If blocks were no different, the MSE for the CRD would be smaller than the MSE for the RCBD and the **CRD would be more powerful**.
- If there was a **substantial difference between blocks**, the MSE for the RCBD would be smaller than the MSE for the CRD and **the RCBD would be more powerful**.
- Obviously one should only use the RCBD when it is appropriate, but how can this be determined? The concept of **efficiency**, discussed in section 6. 3., answers this.

6. 2. 5. *Example* response of sheep to estrogen

The sheep are blocked by ranch, with four treatments per block. The treatments are combinations of sex of the sheep (M or F) and level of estrogen treatment (S0 or S3).

RCBD. Effect of estrogen on weight gains. Blocks are 4 different ranches.

Treatment	Block				Treatment	
	I	II	III	IV	Total	Mean
F-S0	47	52	62	51	212	53
M-S0	50	54	67	57	228	57
F-S3	57	53	69	57	236	59
M-S3	54	65	74	59	252	63
Block Total	208	224	272	224	928	
Block Mean	52	56	68	56		58

Table 6.2 **RCBD** ANOVA

Source of Variation	df	SS	MS	F
Totals	15	854		
Blocks	3	576	192.00	24.69**
Treatments	3	208	69.33	8.91**
Error	9	70	7.78	

Table 6.3 **CRD** ANOVA

Source of Variation	df	SS	MS	F
Totals	15	854		
Treatments	3	208	69.33	1.29 NS
Error	12	646	53.83	

- Each treatment occurs the same number of times in each block.
- Differences among blocks do not result from treatments but from other differences associated with the blocks.
- This component of the total sum of squares can be removed and the experimental error reduced accordingly.
- Compare the SS_{error} in Tables 6.2 and 6.3

6. 3. Relative efficiency [ST&D p. 221, and Topic 1 section 1.4.4.6]

Relative efficiency (RE) formalizes the comparison between 2 exp. designs.

Experimental design affects primarily the MSE since the degrees of freedom for treatments is always $t - 1$.

The information in the design is 1/MSE

$$\text{RE of design 1 to design 2} = (1/\text{MSE}_1) / (1/\text{MSE}_2) = \text{MSE}_2 / \text{MSE}_1$$

When the $df \text{ MSE} < 20 \Rightarrow$ a correction factor is used.

$$\text{RE}_{1 \text{ to } 2} = \frac{(n_1+1)/[(n_1+3)\text{MSE}_1]}{(n_2+1)/[(n_2+3)\text{MSE}_2]} = \frac{(n_1+1)(n_2+3)\text{MSE}_2}{(n_2+1)(n_1+3)\text{MSE}_1}$$

If RE is >1 , **design 1 provides more information** and is more efficient.

If $\text{RE}_{1 \text{ to } 2} = 2.0 \Rightarrow$ each rep of design 1 gives as much information as two reps of design 2.

To estimate MSE for other design: weighted average MSB and MSE

$$\text{MSE}_{\text{CR}} \cong \frac{f_b \text{MSB}_{\text{RCB}} + (f_t + f_e) \text{MSE}_{\text{RCB}}}{f_b + f_t + f_e}$$

To obtain this formula the total SS of the two designs are assumed equal, and then the MS are replaced by the variance components of the expected MS (Biometry p.838-839)

Example: Sheep experiment: $\text{MSE}_{\text{RCBD}} = 7.78$, and $\text{MSB}_{\text{RCBD}} = 192.0$, so

$$\text{MSE}_{\text{CRD}} \cong \frac{3 * 192.0 + (3 + 9) 7.78}{3 + 3 + 9} = 44.62$$

$$\text{RE}_{\text{RCBD to CRD}} = \frac{(f_{\text{rcbd}} + 1)(f_{\text{crd}} + 3)\text{MSE}_{\text{crd}}}{(f_{\text{crd}} + 1)(f_{\text{RCBD}} + 3)\text{MSE}_{\text{RCBD}}} = \frac{(9 + 1)(12 + 3)44.62}{(12 + 1)(9 + 3)7.78} = 5.51$$

which says that it takes 5.51 replications of the CRD to produce the same amount of information as one replication of the RCBD.

Derivation of the expected MSE_{CRD}

Randomized-complete-blocks design			
Source of variation	df	MS	Expected MS
Blocks	$b - 1$	MS_B	$\sigma_{(RB)}^2 + a\sigma_B^2$
Treatments	$a - 1$	$MS_{A(RB)}$	$\sigma_{(RB)}^2 + \frac{b}{a-1} \sum \alpha^2$
Error	$(a-1)(b-1)$	$MS_{E(RB)}$	$\sigma_{(RB)}^2$
Total	$ab - 1$		

Completely randomized design			
Source of variation	df	MS	Expected MS
Treatments	$a - 1$	$MS_{A(CR)}$	$\sigma_{(CR)}^2 + \frac{b}{a-1} \sum \alpha^2$
Error	$a(b-1)$	$MS_{E(CR)}$	$\sigma_{(CR)}^2$
Total	$ab - 1$		

To estimate MSE_{CRD} from the MS of an RCBD:

- Assume that the total SS of the two designs is the same.
- Rewrite the total SS as the addition of its different components

- Rewrite each total SS as the product between df*MS

$$(b-1)MS_B + (a-1)MS_{A(RB)} + (a-1)(b-1)MS_{E(RB)} = (a-1)MS_{A(CR)} + a(b-1)MS_{E(CR)}$$

- Replace each MS by the variance components of the EXPECTED MS

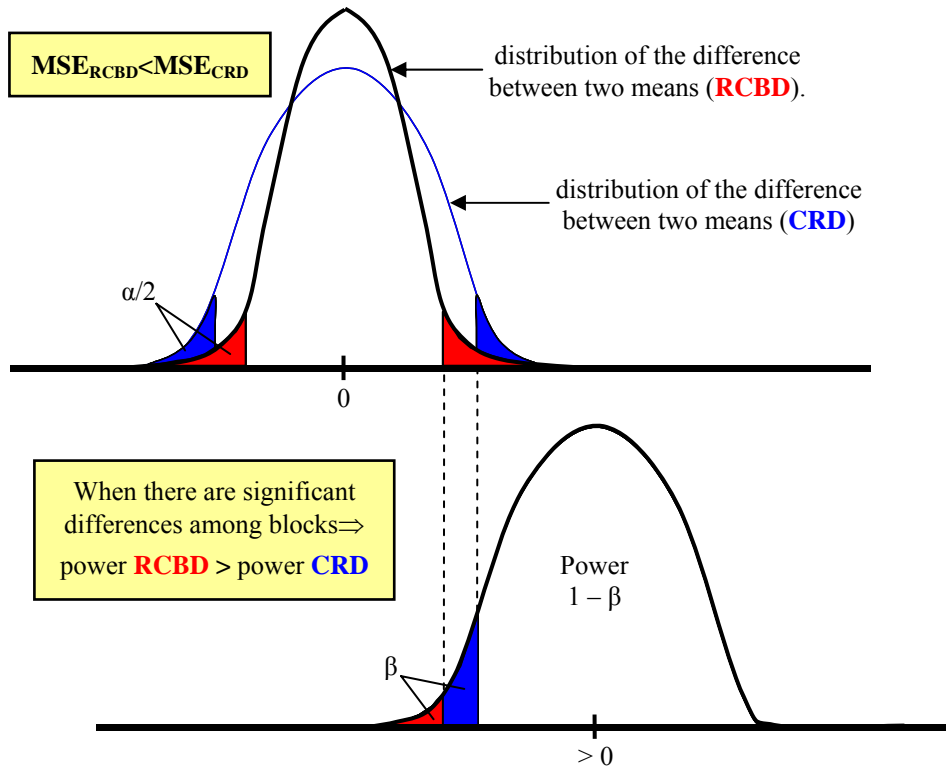
$$\begin{aligned} (b-1)(\sigma_{(RB)}^2 + a\sigma_B^2) + (a-1)\left(\sigma_{(RB)}^2 + \frac{b}{a-1} \sum \alpha^2\right) + (a-1)(b-1)\sigma_{(RB)}^2 \\ = (a-1)\left(\sigma_{(CR)}^2 + \frac{b}{a-1} \sum \alpha^2\right) + a(b-1)\sigma_{(CR)}^2 \\ [(b-1) + (a-1) + (a-1)(b-1)]\sigma_{(RB)}^2 + a(b-1)\sigma_B^2 + b \sum \alpha^2 \\ = [(a-1) + a(b-1)]\sigma_{(CR)}^2 + b \sum \alpha^2 \\ (ab-1)\sigma_{(RB)}^2 + a(b-1)\sigma_B^2 = (ab-1)\sigma_{(CR)}^2 \\ \sigma_{(CR)}^2 = \sigma_{(RB)}^2 + \frac{a(b-1)}{ab-1} \sigma_B^2 \end{aligned}$$

- Rewrite this formula in terms of the MS. Since
 - $\sigma_{(RB)}^2 = MS_{E(RB)}$ and $\sigma_B^2 = (MS_B - MS_{E(RB)})/a$ we obtain

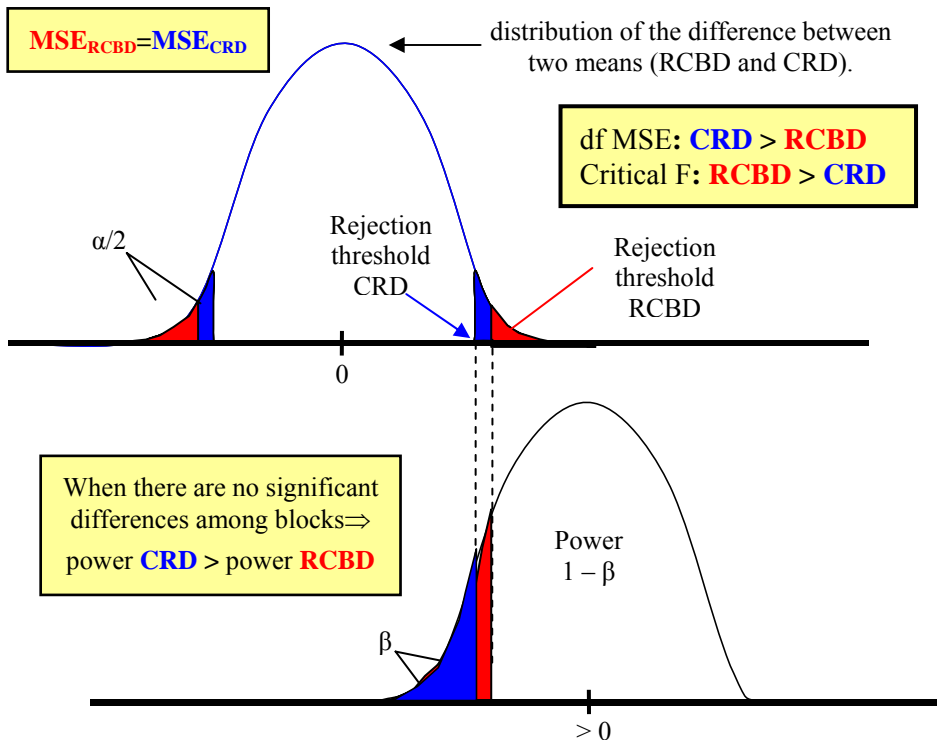
$$\begin{aligned} MS_{E(CR)} &= MS_{E(RB)} + a(b-1) \frac{MS_B - MS_{E(RB)}}{a(ab-1)} \\ &= MS_{E(RB)} + (b-1) \frac{MS_B}{ab-1} - (b-1) \frac{MS_{E(RB)}}{ab-1} \\ &= [(ab-1) - (b-1)] \frac{MS_{E(RB)}}{ab-1} + (b-1) \frac{MS_B}{ab-1} \\ &= \frac{\text{ft+fe} \cdot MS_{E(RB)} + \text{fb} \cdot MS_B}{\text{fb+ft+fe}} \end{aligned}$$

Power comparison between CRD and RCBD designs

1. Significant differences among blocks.



2. Not significant differences among blocks.



6. 4. Assumptions of the model

The model for the RCBD is $Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$. It is assumed that the ε_{ij} are independent, homogeneous and normally distributed (same as CRD).

In two-way or higher-order ANOVA **without replication** it is necessary to assume that interaction is not present if one is to make tests of the main effect using the MSE. Assumption of **additivity** of the main effects.

If **interaction is present** \Rightarrow **F-test is inefficient** and possibly misleading.

$F = \text{MST}/\text{MSE}$ but if no replication the expected **MSE** = $\sigma^2_{\varepsilon} + r\sigma^2_{\alpha\beta}$

The interaction term **$r\sigma^2_{\alpha\beta} \neq 0$** if treatment and block effects are not additive.

Table 6.4. Additive and multiplicative effects. Assume that $\mu=0$.

	Factor A			
Factor B	$\tau_1 = +1$	$\tau_2 = +2$	$\tau_3 = +3$	
$\beta_1 = +1$	2	3	4	Additive effects
	1	2	3	Multiplicative effects
	0	0.30	0.48	Log of multiplicative effects
$\beta_2 = +5$	6	7	8	Additive effects
	5	10	15	Multiplicative effects
	0.70	1.00	1.18	Log of multiplicative effects

- If multiplicative data of this sort is analyzed by a conventional ANOVA, the interaction SS is large.
- By transforming the variable into logs the additivity of the data is restored.
- This is a good illustration of how transformations of scale can be used to meet the assumptions of analysis of variance.

6. 4. 1. Tukey's test for non-additivity

A test devised by Tukey (ST&D p395) to test if there are multiplicative main effects (significant interactions).

Tukey's test partitions the interaction sum of squares into one degree of freedom due to multiplicative effects of the main effects and a residual SS.

If the single-degree-of-freedom SS for **non-additivity** is not significant, the assumptions for the ANOVA model are satisfied.

If the test is significant, then an analysis of the log of the variable may be more appropriate.

SS (non-additivity) = $Q^2 / \text{Cross Product}$, $df = 1$, where

$$Q^2 = \left\{ \sum_i \sum_j (\bar{y}_{i\cdot} - \bar{y}_{\cdot\cdot})(\bar{y}_{\cdot j} - \bar{y}_{\cdot\cdot}) y_{ij} \right\}^2$$

$$\text{and Cross Product} = \sum_i (\bar{y}_{i\cdot} - \bar{y}_{\cdot\cdot})^2 \sum_j (\bar{y}_{\cdot j} - \bar{y}_{\cdot\cdot})^2$$

6. 2. 5. 2. SAS Program

```
Data lambs;  
    Input sex_est $ block gain @@;  
Cards;  
xx  xx  xx  
;  
Proc GLM Data =lambs;  
    Class block sex_est;  
    Model gain= block sex_est;  
    Output out= lambs1 p= pgain r= resigain;  
  
Proc GLM Data = lambs1;  
    Class block sex_est;  
    Model gain= block sex_est pgain*pgain;  
run; quit;
```

pgain*pgain: Not in Class, last in Model

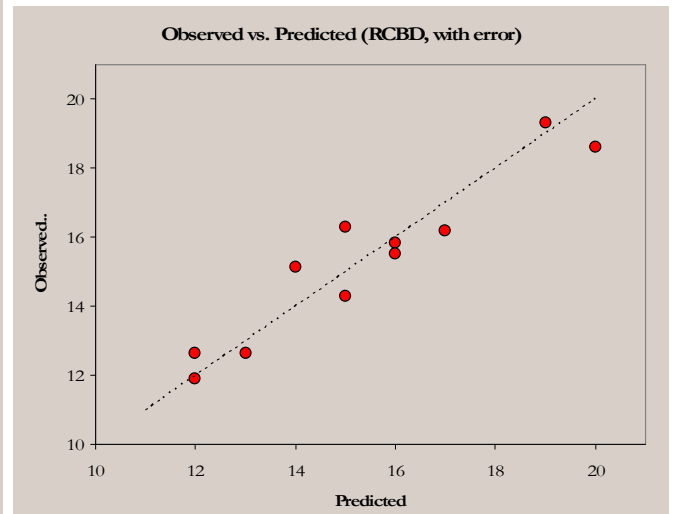
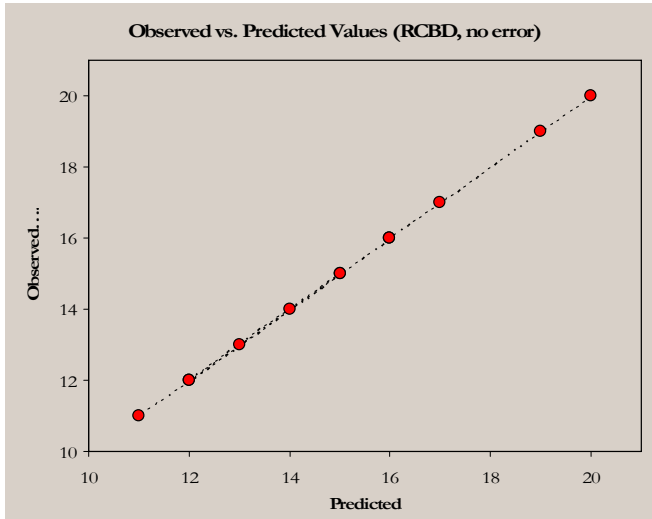
The Tukey 1-df Test for Nonadditivity

How does a regression of the observed data against the squares of its predicted values tell you anything about the existence of nonadditive (i.e. multiplicative) effects?

Under the linear model, each observation is characterized as:

$$y_{ij} = \mu + \beta_i + \tau_j + \varepsilon_{ij}$$

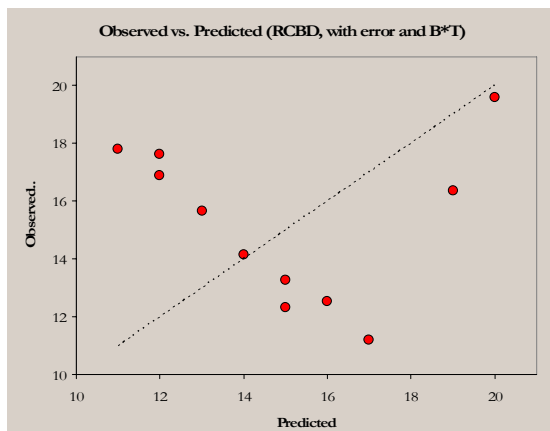
Therefore:



If the errors are in fact random and independent then ε_{ij} will be a *random variable* that causes *no systematic deviation* from this linear relationship.

If there is an interaction $\varepsilon_{ij} = \varepsilon_{RANDOMij} + \mathbf{B*T Interaction Effects}$

The following plot illustrates the deviation from linearity that results from significant multiplicative effects.



If the quadratic effect $\text{pred}*\text{pred}$ is significant, it indicates a **significant departure from the linearity** expected from the additive effects.

Edited SAS Output

First Proc GLM

Dependent Variable: GAIN

Source	DF	Type I SS	MS	F Value	Pr > F
BLOCK	3	576.00	192.00	24.69	0.0001
SEX_EST	3	208.00	69.33	8.91	0.0046
Error	9	70.00	7.78		
Total	15	854.00			

Second Proc GLM

Source	DF	Type I SS	MS	F Value	Pr > F
Model	7	787.4	112.5	13.5	0.0007
Error	8	66.6	8.3		
BLOCK	3	576.0	192.0	23.1	0.0003
SEX_EST	3	208.0	69.3	8.3	0.0076
pgain*pgain	1	3.4	3.4	0.4	0.5395

$70.0 - 3.4 = 66.6$ and $66.6/8 = 8.3$ Then $3.4/8.3 = 0.4$

Since $P = 0.5395$, NS, we do not reject the null hypothesis of additive effects

The first **PROC GLM** is a standard RCBD analysis. The **OUTPUT** statement is not essential but is very useful in any **PROC GLM** procedures to check the assumptions of the model.

The **OUTPUT** statement produces a new output data set: **lambs1**

It contains the old variables plus

“**p**=” includes the PREDICTED and

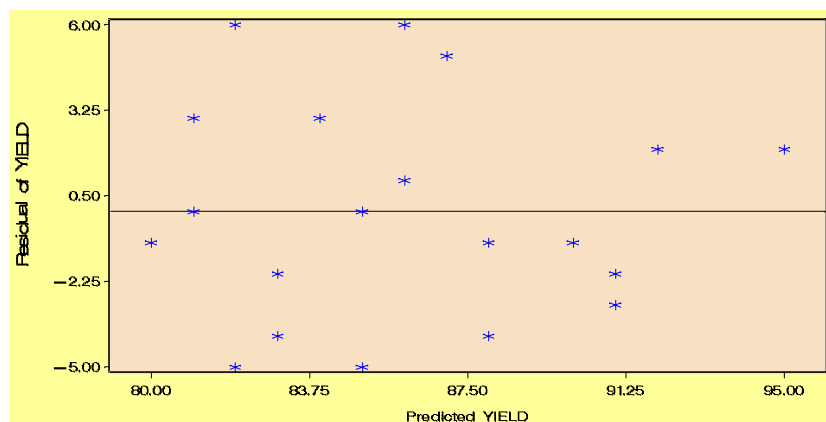
“**r**=” includes the RESIDUALS.

The second data step adds an additional variable that is the square of the predicted values: **pgain*pgain**, which is used in the **non-additivity test**.

Non-additivity test: Tukey 1-degree-of-freedom test with block, treatment, and squared predictions as sources (the latter appearing last in the model).

Table 6.5. Yield of penicillin in four treatments A, B, C, D. Blocks are different stocks of a raw material. The numbers below each observation are the predicted (P: Grand Mean + Treatment effect + Block effect) and residual (R) values.

Block	Treatment				Block Mean	Block Effect
	A	B	C	D		
Stock 1	O: 89 P: 90 R: -1	O: 88 P: 91 R: -3	O: 97 P: 95 R: 2	O: 94 P: 92 R: 2	92	+6
Stock 2	O: 84 P: 81 R: 3	O: 77 P: 82 R: -5	O: 92 P: 86 R: 6	O: 79 P: 83 R: -4		
Stock 3	O: 81 P: 83 R: -2	O: 87 P: 84 R: 3	O: 87 P: 88 R: -1	O: 85 P: 85 R: 0		
Stock 4	O: 87 P: 86 R: 1	O: 92 P: 87 R: 5	O: 89 P: 91 R: -2	O: 84 P: 88 R: -4		
Stock 5	O: 79 P: 80 R: -1	O: 81 P: 81 R: 0	O: 80 P: 85 R: -5	O: 88 P: 82 R: 6		
Treat.	84	85	89	86	Mean=86	
Treat.	-2	-1	3	0		



In this example no particular pattern is observed in the residuals. This observation parallels the **normal distribution of the residuals**, the **homogeneous variances** of the residuals among treatments and a non-significant **Tukey's test for nonadditivity**.

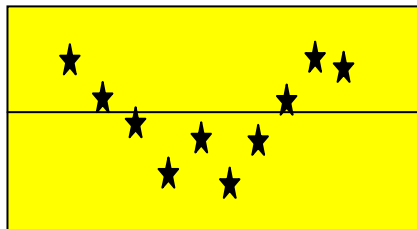
```

data penicil;
  input block trtmnt yield;
cards;
1 1 89
. . .
5 4 88
;
proc GLM;
  class block trtmnt;
  model yield=block trtmnt;
  output out=resplot p=predyiel r=resiyiel;
proc plot data=resplot;
  plot resiyiel*predyiel=trtmnt;
proc univariate data=resplot normal;
  var resiyiel;
run; quit;

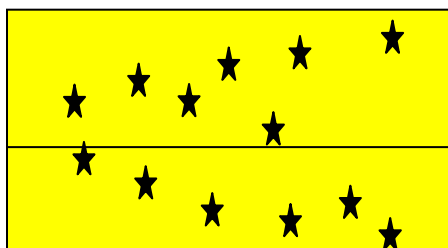
```

Discrepancies between the tentative model and the data can be detected by studying residuals. These residuals are the quantities remaining after the systematic contributions associated with the assumed model are removed.

Sometimes the plot of the residuals versus the predicted values shows a curvilinear relationship. This appearance suggests nonadditivity between the block and the treatment effects



Other times the plot of the residuals versus the predicted shows a funnel-like appearance. This indicates that the variance increases as the value of the response increases (a situation that is common when the variance is a constant percentage of the mean).

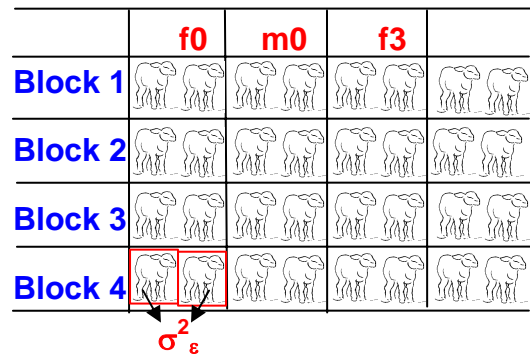


EXAMPLE LAMBS RCBD with 2 reps per cell

32 animals distributed in 4 blocks. We randomly assign 8 animals to the four treatments in each block. When we have more than one rep per block/treatment combination we include the interaction **Block*Treatment** in the model and **do not perform a Tukey's test for non-additivity**.

```
data lambs;
input sex_est $ block gain @@;
cards;
f0 1 46    f0 2 51    f0 3 61    f0 4 50
m0 1 49    m0 2 53    m0 3 66    m0 4 56
f3 1 56    f3 2 52    f3 3 68    f3 4 56
m3 1 53    m3 2 64    m3 3 73    m3 4 58

f0 1 48    f0 2 53    f0 3 62    f0 4 52
m0 1 51    m0 2 55    m0 3 68    m0 4 58
f3 1 58    f3 2 54    f3 3 70    f3 4 58
m3 1 55    m3 2 66    m3 3 75    m3 4 60
```



```
proc glm data=lambs order=data;
*Without order=data, SAS reads alphabetically f0 f3 m0 m3;
class block sex_est;
model gain= block sex_est block*sex_est;
output out=check p= pred r= resi;

contrast 'sex'          sex_est 1 -1 1 -1;
contrast 'estrogen'     sex_est 1 1 -1 -1;
contrast 'interaction'  sex_est 1 -1 -1 1;
*The Contrasts in this proc glm will use the error term of the complete model;

means sex_est/tukey;
*Example of mean comparisons in an RCBD;

proc univariate data=check normal;
var resi;
*In this artificial data the residuals are not Normal, is just presented as an example of the programming;

proc glm data=lambs;
*Homogeneity of  $\sigma^2$  with LEVENE should be tested in one-way ANOVA;
class sex_est;
model gain= sex_est;
means sex_est/ HOVTEST = LEVENE;
run; quit;
```

Output LAMB Reps

ANOVA Dependent Variable: gain

Source	DF	SS	MS	F Value	Pr > F
Model	15	1700.5	113.4	59.47	<.0001
Error	16	30.5	1.9		
Corrected Total	31	1731.0			

Source	DF	SS	MS	F Value	Pr > F
block	3	1132.1	377.4	198.0	<.0001
sex_est	3	426.1	142.0	74.5	<.0001
block*sex_est	9	142.3	15.8	8.3	0.0002

Contrast	DF	SS	MS	F Value	Pr > F
sex	1	132.0	132.0	69.26	<.0001
estrogen	1	294.0	294.0	154.25	<.0001
interaction	1	0.0	0.0	0.02	0.8997

Tukey's Studentized Range (HSD) Test for gain

Minimum Significant Diff. 1.97

Grouping	Mean	N	sex_est
A	63.000	8	m3
B	59.000	8	f3
C	57.000	8	m0
D	52.875	8	f0

Tests for Normality

Test --Statistic-- p Value-----
Shapiro-Wilk W 0.667284 Pr < W <0.0001

Not Normal residues. A transformation is required.

Levene's Test for Homogeneity of Variance

ANOVA of Squared Deviations from Group Means

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
sex_est	3	3181.5	1060.5	0.54	0.6567
Error	28	54660.5	1952.2		

Homogeneity of variance not rejected

EXAMPLE LAMBS NESTED

















16 animals, 4 ranches. Randomly assign animals to the four treatments in each ranch and make 2 measurements per animal

Animal = pot in our CRD nested example and the two measurements are like the two plants measured in each pot.

The Animal is **nested within the block*TRT combination**

```
data lambs;
input sex_est $ block animal gain @@;
cards;
f0 1 1 46  f0 2 1 51  f0 3 1 61  f0 4 1 50
m0 1 2 49  m0 2 2 53  m0 3 2 66  m0 4 2 56
f3 1 3 56  f3 2 3 52  f3 3 3 68  f3 4 3 56
m3 1 4 53  m3 2 4 64  m3 3 4 73  m3 4 4 58

f0 1 1 48  f0 2 1 53  f0 3 1 62  f0 4 1 52
m0 1 2 51  m0 2 2 55  m0 3 2 68  m0 4 2 58
f3 1 3 58  f3 2 3 54  f3 3 3 70  f3 4 3 58
m3 1 4 55  m3 2 4 66  m3 3 4 75  m3 4 4 60
```

	f0	m0	f3	m3
Block 1				
Block 2				
Block 3				
Block 4				

2 measurements

```
proc glm data=lambs order=data;
*Without order=data, SAS reads alphabetically f0 f3 m0 m3;
*With order=data, SAS reads f0 m0 f3 m3: Contrast are different!;
class block sex_est animal;
model gain= block sex_est animal(block*sex_est);
random animal(block*sex_est);
test h=sex_est e=animal(block*sex_est);

contrast 'sex' sex_est 1 -1 1 -1 / e=animal(block*sex_est);
contrast 'estrogen' sex_est 1 1 -1 -1 / e=animal(block*sex_est);
contrast 'interaction' sex_est 1 -1 -1 1 / e=animal(block*sex_est);
means sex_est/tukey e=animal(block*sex_est);
*Above is Tukey test wih correct error for comparison;
*Below is Tukey test wih incorrect error for comparison;
means sex_est/tukey;

proc varcomp Method= Typel;
class block sex_est animal;
model gain= block sex_est animal(block*sex_est);

run;
quit;
```

Output LAMB NESTED

ANOVA Dependent Variable: gain

Source	DF	SS	MS	F Value	Pr > F
Model	15	1700.5	113.4	59.47	<.0001
Error	16	30.5	1.9		
Corrected Total	31	1731.0			

Source	DF	SS	MS	F Value	Pr > F
block	3	1132.1	377.4	198.0	<.0001
sex_est	3	426.1	142.0	74.5	<.0001
animal(block*sex_est)	9	142.3	14.8	8.3	0.0002

Tests of Hypotheses Using MS for animal(block*sex_est) as Error Term

Source	DF	SS	MS	F Value	Pr > F
sex_est	3	426.1	142.0	8.98	0.0045

Contrast	DF	SS	MS	F Value	Pr > F
sex	1	132.0	132.0	8.35	0.0179
estrogen	1	294.0	294.0	18.60	0.0020
interaction	1	0.03	0.03	0.00	0.9655

Tukey's Studentized Range (HSD) Test for gain

	Correct	Incorrect
Critical Value	4.4	4.0
Minimum Significant Diff.	6.2	2.0

Correct Grouping	Incorrect Grouping	Mean	N	sex_est
A	A	63.000	8	m3
B	B	59.000	8	f3
B	C	57.000	8	m0
B	D	52.875	8	f0

Variance Components

Source	Expected Mean Square
block	Var(Error) + 2 Var(animal(block*sex_est)) + 8 var (block)
sex_est	Var(Error) + 2 Var(animal(block*sex_est)) + 8 var (sex_est)
animal(block*sex_est)	Var(Error) + 2 Var(animal(block*sex_est))
Error	Var(Error)

Variance Component	Estimate	%
Var(block)	45.3	64.7
Var(sex_est)	15.8	22.6
Var animal(block*sex_est)	7.0	10.0
Var(Error)	1.9	2.7

- The calculation of the variance comp. is the objective of the nested design
- This % contribution can be used to optimize the allocation of resources.