Lecture 9

Topic 6: Randomized Complete Block Designs (RCBD's)

The Completely Randomized Design (CRD)

1. It is assumed that all experimental units (EU's) are uniform.

2. Treatments are randomly assigned to EUs such that each treatment occurs equally often in the experiment. (1 randomization per experiment)

3. It is advocated to include as much of the native variability of the experiment as possible *within* each EU.

4. When EU's are not uniform, experimental error (MSE) increases, F (MST/MSE) decreases, and the experiment loses sensitivity. If the experiment is replicated in a variety of situations to increase its scope, the variability increases even further.

The Randomized Complete Block Design (RCBD)

1. The population of EU's is divided into a number of relatively homogeneous subpopulations or ***blocks***, and it is assumed that all EU's *within a given block* are uniform.

2. Within each block, treatments are randomly assigned to EU's such that each treatment occurs equally often (usually once) in each block. (1 randomization per block)

3. It is advocated to minimize the native variability as much as possible within blocks and to maximize the native variability as much as possible among blocks.

4. Variation among blocks can be partitioned out of the experimental error (MSE), thereby reducing this quantity and increasing the power of the test. Additional variability introduced when increasing the scope of the experiment can also be partitioned out of the MSE.

Blocks usually represent levels of naturally-occurring differences or sources of variation that are unrelated to the treatments, and *the characterization of these differences is not of interest to the researcher*.

Example: A field trial comparing three cultivars (A, B, and C) of mustard with four replications.

North end of field

1	2	3
4	5	6
7	8	9
10	11	12

South end of field

Hi N

Low N

CRD: One randomization per experiment

North end of field

B	C	B
C	A	C
A	B	A
C	B	A

South end of field

Hi N

Low N

RCBD: One randomization per block

Block	North end of field		
1	1	2	3
2	1	2	3
3	1	2	3
4	1	2	3

South end of field

Hi N

Low N

Block	North end of field		
1	B	A	C
2	A	B	C
3	A	C	B
4	A	C	B

South end of field

Hi N

Low N

The linear model

The model underlying each observation in the experiment:

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

$$Y_{ij} = \overline{Y}_{..} + (\overline{Y}_{i.} - \overline{Y}_{..}) + (\overline{Y}_{.j} - \overline{Y}_{..}) + (Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})$$

And the sum of squares:

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

TSS = SST + SSB + SSE

This *partitioning* of variance is possible because the sums of squares of treatments, blocks, and error are *orthogonal* to one another.

This orthogonality is a direct result of the *completeness* of the block design.

CRD

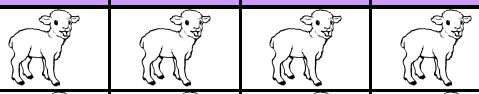
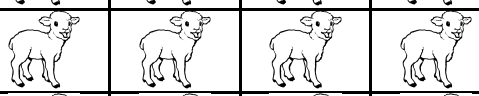
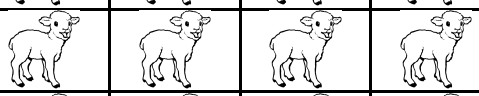
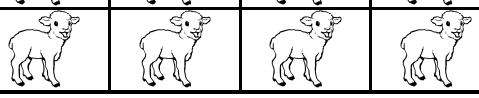
Source	df	SS	MS	F
Total	rt - 1	TSS		
Treatments	t - 1	SST	SST/(t-1)	MST/MSE
Error	t(r - 1)	TSS-SST	SSE/r(t-1)	

RCBD (one replication per block-treatment combination)

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

1. RCBD has (r - 1) fewer df_e than the CRD.
2. If there are no differences among blocks (SSB = 0), $MSE_{CRD} < MSE_{RCBD}$.
3. If there are large enough differences among blocks (SSB >> 0), $MSE_{CRD} > MSE_{RCBD}$.

Example: An experiment was conducted to investigate the effect of estrogen on weight gain in sheep. The treatments are combinations of sex of sheep (M, F) and level of estrogen (Est_0, Est_3). The sheep are blocked by ranch, with one replication of each treatment level at each ranch.

	Ranch			
Trtmt	**1**	**2**	**3**	**4**
M Est_0				
M Est_3				
F Est_0				
F Est_3				

Effect of estrogen on weight gain in sheep (lbs).

	Ranch (i.e. block)				Treatment	
Treatment	**I**	**II**	**III**	**IV**	**Total**	**Mean**
M Est_0	47	52	62	51	212	53
M Est_3	50	54	67	57	228	57
F Est_0	57	53	69	57	236	59
F Est_3	54	65	74	59	252	63
Block Total	208	224	272	224	928	
Block Mean	52	56	68	56		58

CRD ANOVA (treating blocks as reps)

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

RCBD ANOVA

Source	df	SS	MS	F
Total	15	854		
Treatment	3	208	69.33	8.91**
Blocks	3	576	192.00	24.69**
Error	9	70	7.78	

Expected mean squares and F tests

EMS table for this two-way (RCBD) classification experiment, featuring **t** treatments, **b** blocks, and **1** replication per Block*Trtmt combination:

Source	df	MS	EMS
Trtmt	t-1	MST	$\sigma_\varepsilon^2 + b\sum \frac{\tau^2}{t-1}$
Block	b-1	MSB	$\sigma_\varepsilon^2 + t\sigma_\beta^2$
Error	(t-1)(b-1)	MSE	σ_ε^2

The appropriate test statistic (F) is a ratio of mean squares that is chosen such that the expected value of the *numerator* differs from the expected value of the *denominator* only by the specific factor being tested.

Relative efficiency: When to block?

$$F = \frac{MST}{MSE} \qquad MSE = \frac{SSE}{df_e} \qquad F_{crit} = F_{\alpha, df_{trt}, df_e}$$

Blocking reduces SSE, which reduces MSE.

Blocking reduces df_e, which increases MSE and increases F_{crit}.

The concept of *relative efficiency* formalizes the comparison between two experimental methods by quantifying this balance between loss of degrees of freedom and reduction in experimental error.

The information per replication in a given design is:

$$I = \frac{1}{\sigma_\varepsilon^2} \approx \left(\frac{df_{MSE} + 1}{df_{MSE} + 3} \right) \frac{1}{MSE}$$

$$RE_{1:2} = \frac{I_1}{I_2} \approx \frac{\left(\frac{df_{MSE1} + 1}{df_{MSE1} + 3} \right) \frac{1}{MSE_1}}{\left(\frac{df_{MSE2} + 1}{df_{MSE2} + 3} \right) \frac{1}{MSE_2}} = \frac{(df_{MSE1} + 1)(df_{MSE2} + 3)MSE_2}{(df_{MSE2} + 1)(df_{MSE1} + 3)MSE_1}$$

The main complication is how to estimate MSE for the alternative design.

If an experiment was conducted as an RCBD, MSE_{CRD} can be *estimated* by the following formula (ST&D 222):

$$\hat{MSE}_{CRD} \cong \frac{df_B MSB_{RCBD} + (df_T + df_e) MSE_{RCBD}}{df_B + df_T + df_e}$$

Assume TSS of the two designs is the same.
Rewrite TSS in terms of its components and simplify the expression.

For the interested: Derivation of the expected MSE_{CRD}

1. Set the total sums of squares of each design equal to each other and rewrite in terms of mean squares and degrees of freedom:

$$TSS_{RCBD} = TSS_{CRD}$$
$$SST_{RCBD} + SSB_{RCBD} + SSE_{RCBD} = SST_{CRD} + SSE_{CRD}$$
$$df_{T(R)}MST_R + df_{B(R)}MSB_R + df_{e(R)}MSE_R = df_{T(C)}MST_C + df_{e(C)}MSE_C$$
$$(t-1)MST_R + (r-1)MSB_R + (t-1)(r-1)MSE_R = (t-1)MST_C + t(r-1)MSE_C$$

2. Replace each mean square with the variance components of its expected mean square:

$$(t-1)(\sigma^2_{e(R)} + r\sigma^2_{T(R)}) + (r-1)(\sigma^2_{e(R)} + t\sigma^2_{B(R)}) + (t-1)(r-1)\sigma^2_{e(R)} = (t-1)(\sigma^2_{e(C)} + r\sigma^2_{T(C)}) + t(r-1)\sigma^2_{e(C)}$$
$$[(t-1) + (r-1) + (t-1)(r-1)]\sigma^2_{e(R)} + (t-1)(r-1)\sigma^2_{B(R)} + r(t-1)\sigma^2_{T(R)} = [(t-1) + t(r-1)]\sigma^2_{e(C)} + r(t-1)\sigma^2_{T(C)}$$
$$\sigma^2_{e(C)} = \sigma^2_{e(R)} + \frac{t(r-1)\sigma^2_{B(R)}}{(tr-1)}$$

3. Finally, rewrite this expression in terms of mean squares and degrees of freedom:

$$MSE_{CRD} = MSE_{RCBD} + t(r-1)\frac{MSB - MSE_{RCBD}}{t(tr-1)}$$
$$MSE_{CRD} = MSE_{RCBD} + (r-1)\frac{MSB}{tr-1} - (r-1)\frac{MSE_{RCBD}}{tr-1}$$
$$MSE_{CRD} = [(tr-1) - (r-1)]\frac{MSE_{RCBD}}{tr-1} + (r-1)\frac{MSB}{tr-1}$$
$$MSE_{CRD} = \frac{r(t-1)MSE_{RCBD} + (r-1)MSB}{tr-1}$$
$$MSE_{CRD} = \frac{(df_{T(R)} + df_{e(R)})MSE_{RCBD} + df_B MSB}{df_{T(R)} + df_{B(R)} + df_{e(R)}}$$

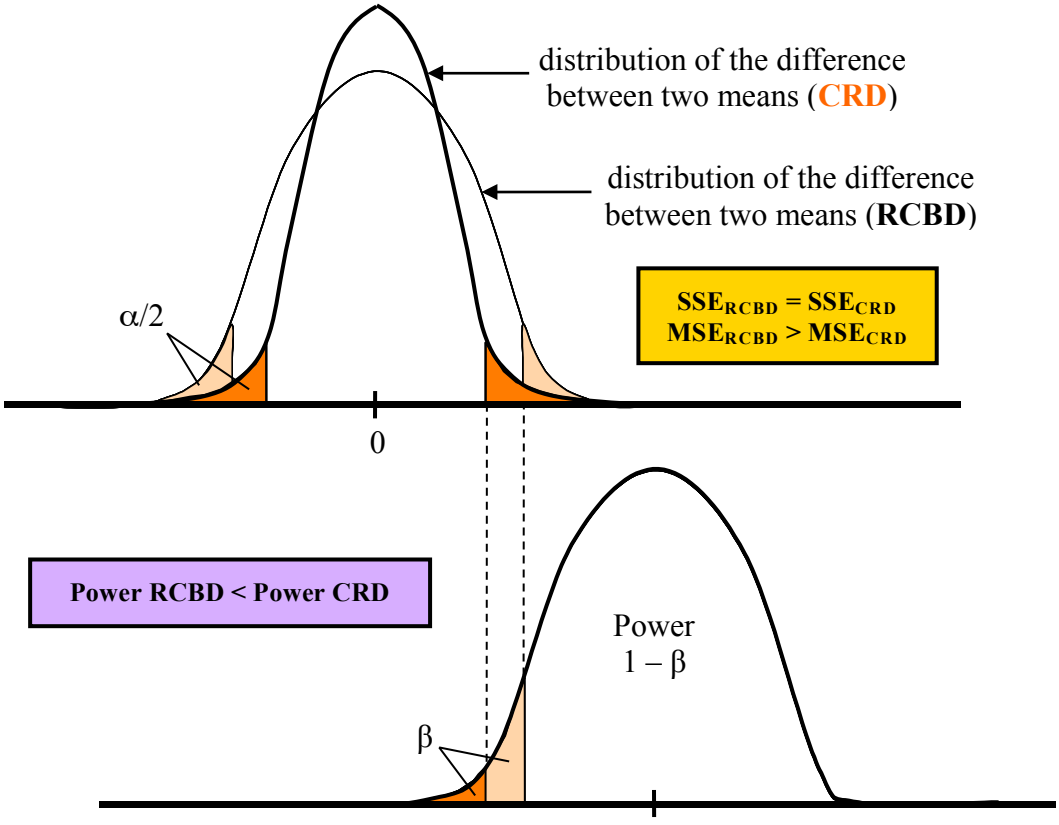
Example: From the sheep experiment, $MSE_{RCBD} = 7.78$ and $MSB_{RCBD} = 192.0$. Therefore:

$$\hat{MSE}_{CRD} \cong \frac{df_B MSB_{RCBD} + (df_T + df_e)MSE_{RCBD}}{df_B + df_T + df_e} = \frac{3(192) + (3+9)7.78}{3+3+9} = 44.62$$

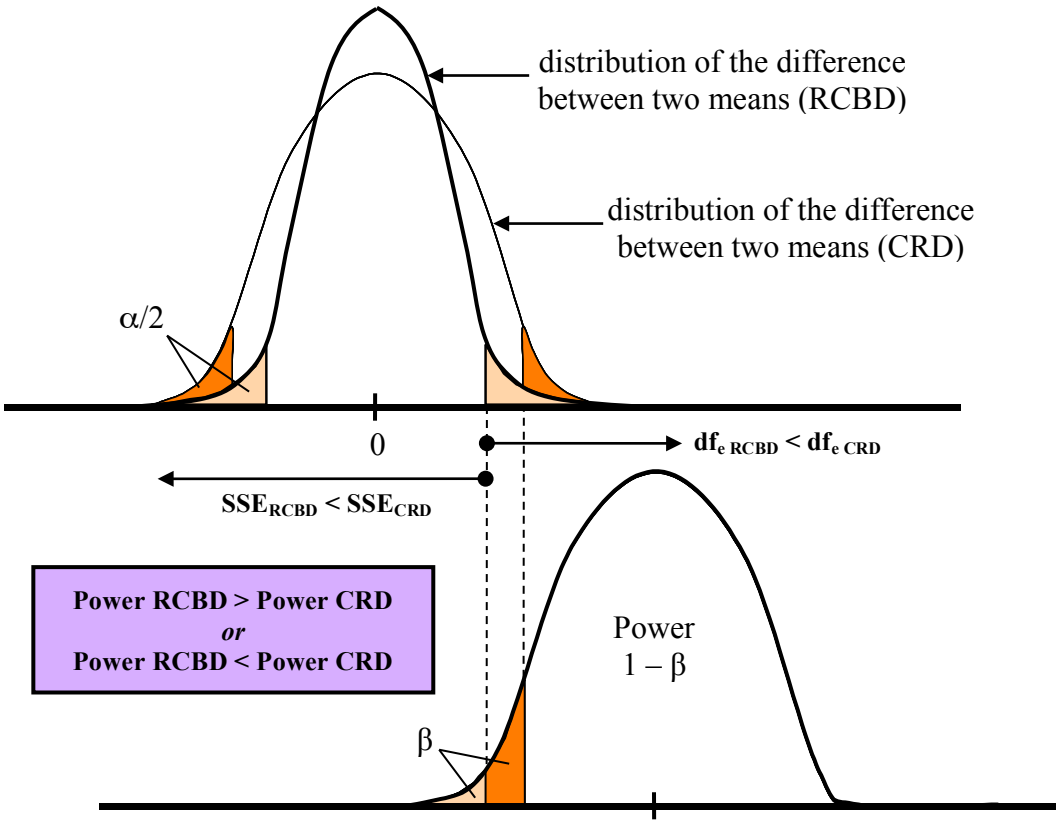
$$RE_{RCBD:CRD} \cong \frac{(df_{MSE1}+1)(df_{MSE2}+3)\hat{MSE}_{CRD}}{(df_{MSE2}+1)(df_{MSE1}+3)MSE_{RCBD}} = \frac{(9+1)(12+3)44.62}{(12+1)(9+3)7.78} = 5.51$$

Interpretation: It takes 5.51 replications in the CRD to produce the same amount of information as one replication in the RCBD. Or, the RCBD is 5.51 times more efficient than the CRD in this case.

1. When there are no significant differences among blocks



2. When there *are* significant differences among blocks



Assumptions of the model

The model for the RCBD with a single replication per block-treatment combination:

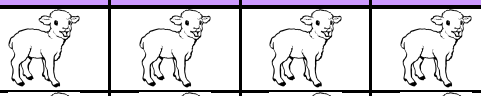
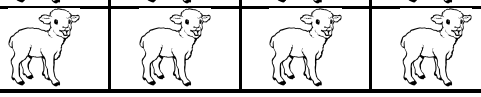
$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

1. The residuals (ε_{ij}) are independent, homogeneous, and normally distributed.

2. The variance within each treatment levels is homogeneous across all treatment levels.

3. The main effects are additive.

Recall that experimental error is defined as the variation among experimental units *that are treated alike*.

	Ranch			
Trtmt	**1**	**2**	**3**	**4**
M Est$_0$				
M Est$_3$				
F Est$_0$				
F Est$_3$				

There is an *expected* value for each sheep, given by:

$$\text{Expected } Y_{ij} = \mu + \tau_i + \beta_j$$

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

With only one replication per cell (i.e. treatment-block combination), the residuals are the combined effects of experimental error **and** any non-additive treatment*block interactions:

$$\varepsilon_{ij} = \tau_i * \beta_j + \text{error}_{ij}$$

So when we use ε_{ij} as estimates of the true experimental error, we are assuming that $\tau_i * \beta_j \simeq 0$.

This assumption of no interaction is referred to as the assumption of **additivity** of the main effects. If this assumption is violated, it's an indication that your blocks are not behaving as you expect (i.e. additively). In other words, something of great interested is lurking with your blocking variable that you need to better understand.

Tukey's 1-df test for nonadditivity

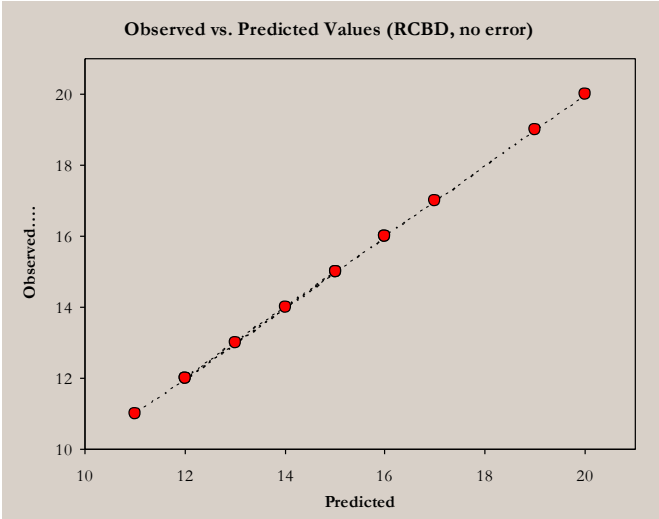
Under our linear model, each observation is characterized as:

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

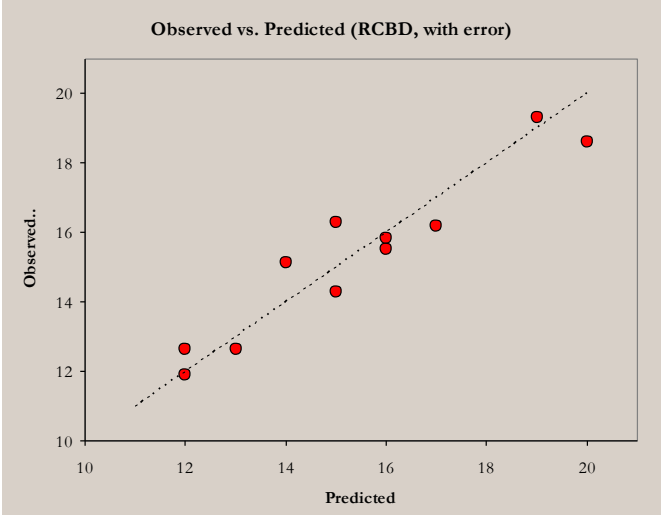
The predicted value of each individual is given by:

$$pred_{ij} = \mu + \beta_i + \tau_j$$

So, if we had no error in our experiment (i.e. if $\varepsilon_{ij} = 0$), the observed data would exactly match its predicted values and a correlation plot of the two would yield a perfect line with slope = 1:

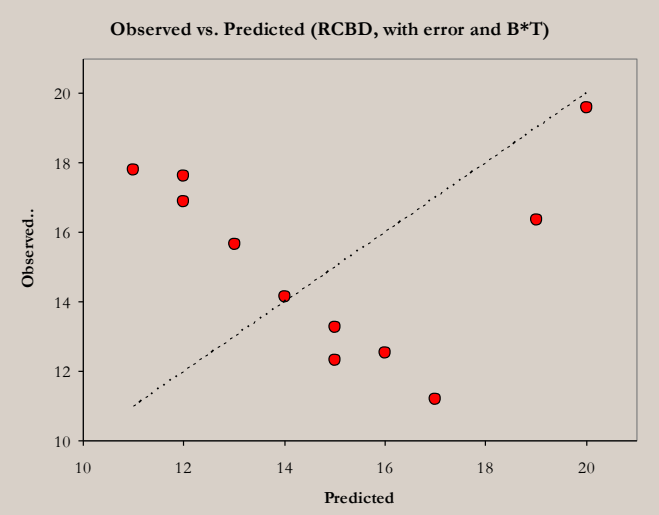


Now let's introduce some error:



But what happens when you have an interaction (e.g. Block * Treatment) but lack the degrees of freedom necessary to include it in the linear model?

$$\varepsilon_{ij} = \varepsilon_{RANDOMij} + \text{B*T Interaction Effects}$$



SO, if the observed and predicted values obey a linear relationship, then the non-random Interaction Effects buried in the error term are sufficiently small to uphold our assumption of additivity of main effects.

This test is easily implemented using R:

```
#The ANOVA [RCBD]
sheep_mod<-lm(Gain ~ Sex_Est + Ranch, sheep_dat)

sheep_dat$sq_preds <- predict(sheep_mod)^2

#The Tukey 1-df Test for Non-additivity
sheep_1df_mod<-lm(Gain ~ Sex_Est + Ranch + sq_preds, sheep_dat)
anova(sheep_1df_mod)
```

Output:

```
           Df Sum Sq Mean Sq F value     Pr(>F)
Sex_Est     3 208.00  69.333  8.3307 0.0076360 **
Ranch       3 576.00 192.000 23.0696 0.0002716 ***
preds2      1   3.42   3.419  0.4108 0.5394942
Residuals   8  66.58   8.323
```

This test is necessary **ONLY** when
there is **one observation** per block-treatment combination.
If there are two or more replications per block-treatment combination,
the block*treatment interaction can be tested directly in an exploratory model.

Example: Yield of penicillin from four different protocols (A – D). Blocks are different stocks of an important reagent. The numbers below each observation (**O**) are the predicted values (**P** = Grand Mean + Treatment effect + Block effect) and the residuals (**R**).

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	83	-3
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	85	-1
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	88	2
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	82	-4
Treatment mean	84	85	89	86	**Mean = 86**	
Treatment effect	-2	-1	3	0		

The R script for a full analysis of this dataset:

```
#The ANOVA
Penicillin_mod<-lm(Penicillin ~ Protocol + Stocks, Penicillin_dat)
anova(Penicillin_mod)

#TESTING ASSUMPTIONS
#Generate residual and predicted values
Penicillin_dat$resids <- residuals(Penicillin_mod)
Penicillin_dat$preds <- predict(Penicillin_mod)
Penicillin_dat$sq_preds <- Penicillin_dat$preds^2

#Look at a plot of residual vs. predicted values
plot(resids ~ preds, data = Penicillin_dat,
 xlab = "Predicted Values",
 ylab = "Residuals")

#Perform a Shapiro-Wilk test for normality of residuals
shapiro.test(Penicillin_dat$resids)

#Perform a Levene's Test for homogenity of variances
#install.packages("car")
library(car)
leveneTest(Penicillin ~ Variety, data = Penicillin_dat)
```

```
#Perform a Tukey 1-df Test for Non-additivity
Penicillin _1df_mod<-lm(Penicillin ~ Protocol + Stocks + sq_preds,
 Penicillin_dat)
anova(Penicillin _1df_mod)
```

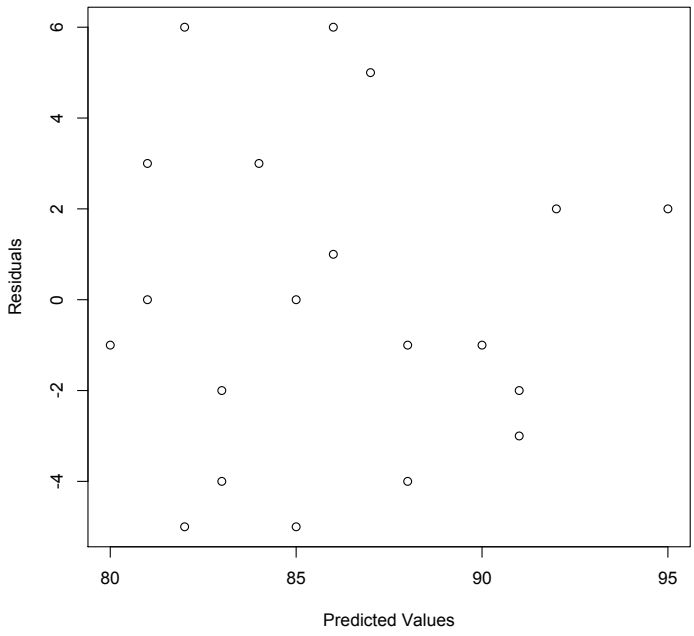
This dataset meets all assumptions: normality, variance homogeneity, and additivity:

```
      Shapiro-Wilk normality test
data:  Penicillin_dat$resids
W = 0.9505, p-value = 0.3743  <- NS
```

```
Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  3  0.1333 0.9388  <- NS
```

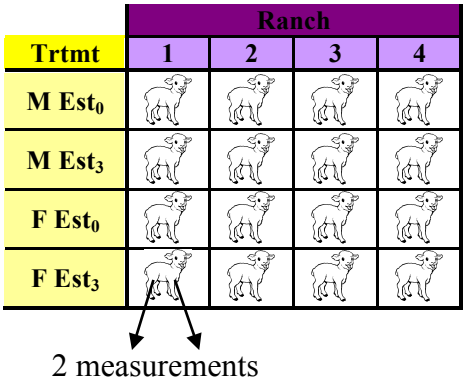
Tukey 1-df Test for Non-Additivity

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
~~Protocol~~	~~3~~	~~70.000~~	~~23.333~~	~~1.1458~~	~~0.37360~~
~~Stocks~~	~~4~~	~~264.000~~	~~66.000~~	~~3.2411~~	~~0.05488~~
sq_preds	1	2.001	2.001	0.0983	0.75978 <- NS
Residuals	11	223.999	20.364		



No particular pattern presents itself in the plot of residuals.

Nesting within an RCBD



Nested RCBD, table of Expected Mean Squares (EMS)

Source of variation	Expected MS	F
Blocks (β_i)	$\sigma_\delta^2+2\sigma_\varepsilon^2+8\sigma_\beta^2$	**MSB / MSEE**
Treatments (τ_j)	$\sigma_\delta^2+2\sigma_\varepsilon^2+8\Sigma\tau^2/3$	**MST / MSEE**
Exp. Error ($\varepsilon_{k(ij)}$)	$\sigma_\delta^2+2\sigma_\varepsilon^2$	MSEE / MSSE
Samp. Error ($\delta_{l(ijk)}$)	σ_δ^2	

R script for calculating components of variance

```
#Calculating components of variance
#install.packages("lme4")
library(lme4)
sheep1_mod<-lmer(gain ~ sex_est + (1|ranch) +
                   (1|animal:ranch:sex_est), data = sheep_dat)
summary(sheep1_mod)
```

```
Random effects:
 Groups                 Name        Variance Std.Dev.
 animal:ranch:sex_est (Intercept)   6.778    2.603
 ranch                (Intercept) 46.056    6.786
 Residual                          2.000    1.414
Number of obs: 32, groups:  animal:ranch:sex_est, 16; ranch, 4
```

Another way, using the within() function:

```
sheep_dat<-within(sheep_dat, animal<-(ranch:sex_est)[drop=TRUE])

sheep2_mod<-lmer(gain ~ sex_est + (1|ranch) +
                      (1|animal), data = sheep_dat)
summary(sheep2_mod)
```

```
Random effects:
 Groups   Name        Variance Std.Dev.
 animal   (Intercept)  6.778    2.603
 ranch    (Intercept) 46.056    6.786
 Residual              2.000    1.414
Number of obs: 32, groups:  animal, 16; ranch, 4
```

Again, the only reason to analyze this dataset as a nested RCBD is to calculate the variance components. If you do not need the variance components, simply average the subsamples for each experimental unit and analyze it as a simple RCBD.

As stated before, the objective of analyzing the experiment with the individual subsample values is to better understand the sources of variation in the experiment, not to test their significances (hypothesis testing is much simpler if you first average all the subsamples within each experimental unit).

The optimal allocation of resources

If one animal (EU) costs $150 US to establish and maintain, and one subsample (weighing) costs $5 to do…

$$n_{sub} = \sqrt{\frac{C_{e.u.} * s^2_{sub}}{C_{sub} * s^2_{e.u.}}} = \sqrt{\frac{150 * 2.00}{5 * 6.778}} = 2.97$$

…the optimum allocation of resources would be to weigh each sheep three times.

```
#The ANOVA
#Note: ALL Trtmt F-tests must be done BY HAND, using the correct
 error term (this includes contrasts)
sheep_mod<-lm(gain ~ sex_est + ranch + animal, sheep_dat)
anova(sheep_mod)

contrastmatrix<-cbind(c(1,1,-1,-1),c(1,-1,1,-1),c(1,-1,-1,1))
contrasts(sheep_dat$sex_est)<-contrastmatrix

sheep_contrast_mod<-aov(gain ~ sex_est + ranch + animal, sheep_dat)
summary(sheep_contrast_mod, split = list(sex_est = list("Sex" = 1,
"Estrogen" = 2, "Sex*Estrogen" = 3)))
```

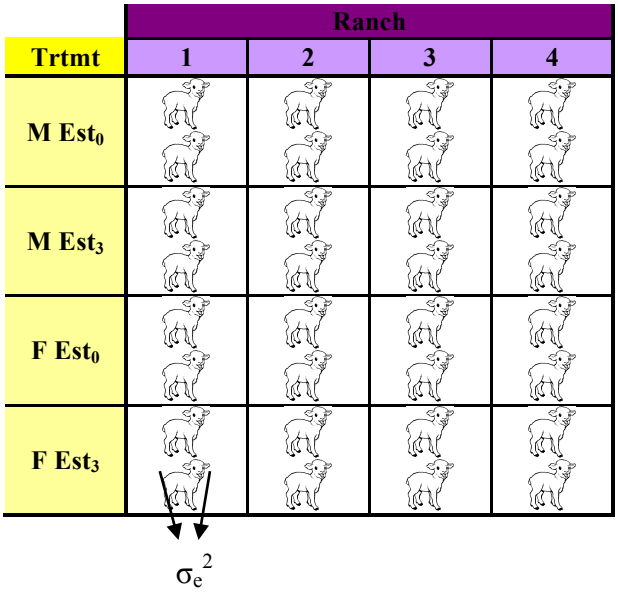
Output

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
sex_est	3	416	138.7	~~69.333~~	~~2.19e-09~~	~~***~~
sex_est: Sex	1	128	128.0	~~64.000~~	~~5.55e-07~~	~~***~~
sex_est: Estrogen	1	288	288.0	~~144.000~~	~~2.06e-09~~	~~***~~
sex_est: Sex*Estrogen	1	0	0.0	~~0.000~~	~~1.000000~~	
ranch	3	1152	384.0	~~192.000~~	~~9.39e-13~~	~~***~~
animal	9	140	**15.6**	7.778	0.000223	***
Residuals	16	32	2.0			

The correct error term for all Trtmt and Block F-tests is the MSEE (15.6). These F- and p-values need to be calculated manually (e.g. using the **pf()** function). The corrected table:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
sex_est	3	416	138.7	8.89	0.00469	**
sex_est: Sex	1	128	128.0	8.21	0.0186	*
sex_est: Estrogen	1	288	288.0	18.46	0.002	**
sex_est: Sex*Estrogen	1	0	0.0	0.000	1.000000	
ranch	3	1152	384.0	24.62	0.000113	***
animal	9	140	15.6	7.778	0.000223	***
Residuals	16	32	2.0			

RCBD with multiple replications per block-treatment combination




```
#The Exploratory ANOVA
sheep_mod<-lm(gain ~ sex_est*ranch, sheep_dat)
anova(sheep_mod)
```

```
Response: gain
              Df  Sum Sq Mean Sq F value    Pr(>F)
sex_est        3 951.63  317.21  20.716 9.323e-06 ***
ranch          3 176.12   58.71   3.834   0.03039 *
sex_est:ranch  9 137.12   15.24   0.995   0.48114
Residuals     16 245.00   15.31
```

```
pTrtmt<-pf(317.21/15.24,3,9,lower.tail=FALSE)
pBlock<-pf(58.71/15.24,3,9,lower.tail=FALSE)
```

```
#The final ANOVA
```

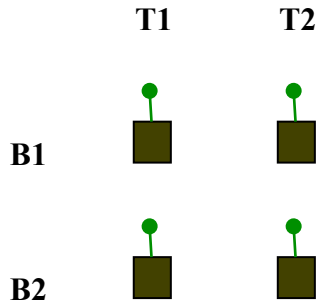
```
Response: gain
              Df  Sum Sq Mean Sq F value    Pr(>F)
sex_est        3 951.63  317.21  20.814   0.00022 ***
ranch          3 176.12   58.71   3.852   0.05031
sex_est:ranch  9 137.12   15.24   0.995   0.48114
Residuals     16 245.00   15.31
```

```r
#TESTING ASSUMPTIONS

#Generate residual values
sheep_dat$resids <- residuals(sheep_final_mod)
sheep_dat

#Perform a Shapiro-Wilk test for normality of residuals
shapiro.test(sheep_dat$resids)

#Perform Levene's Test for homogenity of variances
library(car)
#Testing HOV among treatments
leveneTest(gain ~ sex_est, data = sheep_dat)
```

```
     Shapiro-Wilk normality test

data:  sheep_dat$resids
W = 0.9662, p-value = 0.4022
```

```
Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  3   1.601 0.2114
```

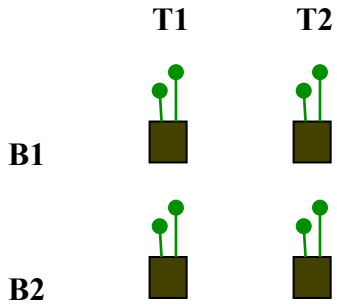
RCBD 1 rep/cell



lm(Y ~ Block + Trtmt, X_dat)

Tukey Test Required

RCBD 1 rep/cell with subsamples

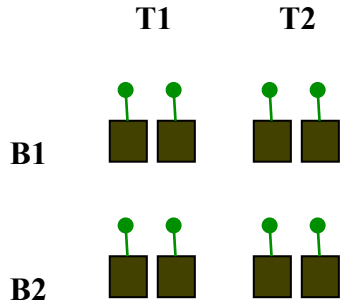


within(X_dat, Pot <- (Block:Trtmt))
lm(Y ~ Block + Trtmt + Pot, X_dat)

Custom F tests for Block and Trtmt
MSEE = MS_{Pot}

Tukey Test Required

RCBD >1 rep/cell



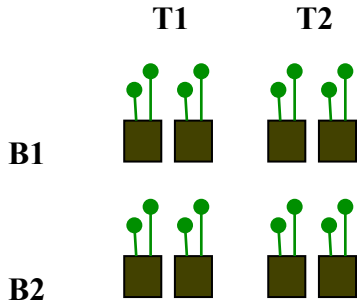
Exploratory model:

lm(Y ~ Block*Trtmt, X_dat)

Tukey Test not Required

Custom F tests for Block and Trtmt
error = $MS_{Block:Trtmt}$

RCBD >1 rep/cell with subsamples



Exploratory model:

within(X_dat, Pot <- (Block:Trtmt))
lm(Y ~ Block*Trtmt + Pot, X_dat)

Tukey Test not Required

Custom F test for Block:Trtmt
MSEE = MS_{Pot}

Custom F tests for Block and Trtmt
error = $MS_{Block:Trtmt}$