

RANDOMIZED COMPLETE BLOCK DESIGN (RCBD)

Description of the Design

- Probably the most used and useful of the experimental designs.
- Takes advantage of grouping similar experimental units into blocks or replicates.
- The blocks of experimental units should be as uniform as possible.
- The purpose of grouping experimental units is to have the units in a block as uniform as possible so that the observed differences between treatments will be largely due to “true” differences between treatments.

Randomization Procedure

- Each replicate is randomized separately.
- Each treatment has the same probability of being assigned to a given experimental unit within a replicate.
- Each treatment must appear at least once per replicate.

Example

Given four fertilizer rates applied to ‘Amidon’ wheat and three replicates of each treatment.

Rep 1	Rep 2	Rep 3	
A	B	A	A=0 kg N/ha
D	A	B	B=50 kg N/ha
C	D	C	C=100 kg N/ha
B	C	D	D=150 kg N/ha

Advantages of the RCBD

1. Generally more precise than the CRD.
2. No restriction on the number of treatments or replicates.
3. Some treatments may be replicated more times than others.
4. Missing plots are easily estimated.
5. Whole treatments or entire replicates may be deleted from the analysis.

6. If experimental error is heterogeneous, valid comparisons can still be made.

Disadvantages of the RCBD

1. Error df is smaller than that for the CRD (problem with a small number of treatments).
2. If there is a large variation between experimental units within a block, a large error term may result (this may be due to too many treatments).
3. If there are missing data, a RCBD experiment may be less efficient than a CRD

NOTE: The most important item to consider when choosing a design is the uniformity of the experimental units.

RCBD – No Sampling

Example

Grain yield of rice at six seeding rates (Mg/ha):

Rep	Seeding rate (kg/ha)						Y _j
	25	50	75	100	125	150	
1	5.1	5.3	5.3	5.2	4.8	5.3	31.0
2	5.4	6.0	5.7	4.8	4.8	4.5	31.2
3	5.3	4.7	5.5	5.0	4.4	4.9	29.8
4	4.7	4.3	4.7	4.4	4.7	4.1	26.9
Y _i	20.5	20.3	21.2	19.4	18.7	18.8	118.9
$\sum Y_{ij}^2$	105.35	104.67	112.92	94.44	87.53	89.16	594.07

Step 1. Calculate the correction factor (CF).

$$CF = \frac{Y^2_{..}}{tr} = \frac{118.9^2}{6*4} = 589.050$$

Step 2. Calculate the Total SS.

$$\begin{aligned} \text{Total SS} &= \sum Y_{ij}^2 - CF \\ &= (5.1^2 + 5.4^2 + 5.3^2 + \dots + 4.1^2) - CF \\ &= 5.02 \end{aligned}$$

Step 3. Calculate the Replicate SS (Rep SS)

$$\begin{aligned} \text{Rep SS} &= \sum \frac{Y_{.j}^2}{t} - CF \\ &= \frac{(31.0^2 + 31.2^2 + 29.8^2 + 26.9^2)}{6} - CF \\ &= 1.965 \end{aligned}$$

Step 4. Calculate the Treatment SS (Trt SS)

$$\begin{aligned} \text{Trt SS} &= \sum \frac{Y_{.i}^2}{r} - CF \\ &= \frac{(20.5^2 + 20.3^2 + 21.2^2 + 19.4^2 + 18.7^2 + 18.8^2)}{4} - CF \\ &= 1.2675 \end{aligned}$$

Step 5. Calculate the Error SS

$$\begin{aligned} \text{Error SS} &= \text{Total SS} - \text{Rep SS} - \text{Trt SS} \\ &= 1.7875 \end{aligned}$$

Step 6. Complete the ANOVA Table

SOV	Df	SS	MS	F
Rep	r-1 = 3	1.9650	0.6550	Rep MS/Error MS = 5.495**
Trt	t-1 = 5	1.2675	0.2535	Trt MS/Error MS = 2.127 ^{ns}
Error	(r-1)(t-1) = 15	1.7875	0.1192	
Total	tr-1 = 23	5.0200		

Step 7. Look up Table F -values for Rep and Trt:

Rep

$$F_{.05;3,15} = 3.29$$

$$F_{.01;3,15} = 5.42$$

Trt

$$F_{.05;5,15} = 2.90$$

$$F_{.01;5,15} = 4.56$$

Step 8. Make conclusions.

Rep: Since $F_{calc.}(5.495) > F_{Tab.}$ at the 95 and 99% levels of confidence, we reject H_0 : All replicate means are equal.

TRT: Since $F_{calc.}(2.127) < F_{Tab.}$ at the 95 and 99% levels of confidence, we fail to reject H_0 : All treatment means are equal.

Step 9. Calculate Coefficient of Variation (CV).

$$CV = \frac{s}{\bar{Y}} * 100$$

$$= \frac{\sqrt{.1192}}{4.95} * 100$$

$$= 6.97\%$$

Step 10. Calculate LSD's if necessary

- There is no need to calculate a LSD for replicate since you generally are not interested in comparing differences between replicate means.
- Since the F -test for treatment was non-significant, one would not calculate the F -protected LSD. However, if the F -test for treatment was significant, the LSD would be:

$$LSD_{TRT} = t_{.05/2} \sqrt{\frac{2ErrorMS}{r}}$$

$$= 2.131 \sqrt{\frac{2(0.1192)}{4}}$$

$$= 0.76$$

Significance of F -tests on Replicate

- This is a valid F -test but requires careful interpretation.
- If the F -test for replicate is significant, this indicates that the precision of the experiment has been increased by using this design instead of a CRD.
- This suggests that the scope of the experiment may have been increased since the experiment was conducted over a wider range of conditions.
- One needs to be careful when replicate effects are large because this suggests heterogeneity of error may exist.
- If replicate effects are small, this suggests that either the experimenter was not successful in reducing error variance of the individual experimental units or that the experimental units were homogenous to start.
- To know which situation is true in your case, you need to have the experience of knowing the “typical” size of the Rep MS.

Missing Data

- For each missing value in the experiment, you lose one degree of freedom from error and total.
- Reasons for missing data include:
 1. Animal dies
 2. Break a test tube.
 3. Animals eat grain in the plot.
 4. Spill grain sample.

- The value for a missing plot can be estimated by using the formula:

$$Y_{ij} = \frac{(rB + tT - G)}{(r-1)(t-1)}$$

where: r = number of replicates

t = number of treatments

B = replicate total of replicate with missing value

T = treatment total of treatment with missing value

G = Experiment total (Y_{..})

Example

Suppose you have the following data and analysis with no missing data:

Rep	Treatment				Y _j
	A	B	C	D	
1	9	11	3	7	30
2	8	13	5	10	36
3	7	12	8	4	31
Y _i	24	36	16	21	97

SOV	Df	SS	MS	F
Rep	2	5.167	2.584	0.526 ^{ns}
Trt	3	72.250	24.083	4.898*
Error	6	29.500	4.917	
Total	11	106.917		

Now assume the value for Y₃₂ is missing.

Rep	Treatment				Y _j
	A	B	C	D	
1	9	11	3	7	30
2	8	13		10	31
3	7	12	8	4	31
Y _i	24	36	11	21	92

Step 1. Estimate the missing value for Y_{32} using the formula:

$$Y_{ij} = \frac{(rB + tT - G)}{(r-1)(t-1)}$$

$$= \frac{[(3*31) + (4*11) - 92]}{(3-1)(4-1)}$$

$$= 7.5$$

Step 2. Substitute the calculate value into the missing spot in the data.

Rep	Treatment				$Y_{.j}$
	A	B	C	D	
1	9	11	3	7	30
2	8	13	7.5	10	38.5
3	7	12	8	4	31
$Y_{.i}$	24	36	18.5	21	99.5

Step 3. Complete the analysis.

- Remember that you will loose one degree of freedom in error and total for each missing value.

SOV	Df	SS	MS	F
Rep	2	10.792	5.396	1.023 ^{ns}
Trt	3	60.063	20.021	3.795 ^{ns}
Error	5	26.375	5.275	
Total	10	97.229		

Facts About the Missing Value Analysis

- Use of the estimated value does not improve the analysis or supply additional information. It only facilitates the analysis of the remaining data.
- The Error MS calculated using the estimate of the missing value is a minimum. Use of any other value but the one calculated would result in a larger value.
- The TRT SS and Rep SS are biased values. Unbiased values can be calculated using Analysis of Covariance.
- The mean calculated using the estimate of the missing value is called a **Least Square Mean**.

Calculating the LSD When You Have One Missing Value

- You will need to calculate two LSD's.
 1. LSD to compare treatments with no missing values.

$$\begin{aligned}LSD_{TRT} &= t_{.05/2} \sqrt{\frac{2ErrorMS}{r}} \\ &= 2.571 \sqrt{\frac{2(5.275)}{3}} \\ &= 4.821\end{aligned}$$

2. Compare the treatment with the missing value with the treatments with no missing values (note the calculation of $s_{\bar{Y}_1 - \bar{Y}_2}$).

$$\begin{aligned}LSD_{TRT} &= t_{.05/2} \sqrt{s^2 \left[\frac{2}{r} + \frac{t}{r(r-1)(t-1)} \right]} \\ &= 2.571 \sqrt{5.275 \left[\frac{2}{3} + \frac{4}{3(3-1)(4-1)} \right]} \\ &= 5.567\end{aligned}$$

Missing Data – More than One Missing Value

Given the following data and analysis with no missing data:

Rep	Treatment				Y _j
	A	B	C	D	
1	3.1	3.3	3.6	3.9	13.9
2	3.1	3.4	3.4	4.0	13.9
3	3.0	3.2	3.6	4.2	14.0
Y _i	9.2	9.9	10.6	12.1	41.8

SOV	Df	SS	MS	F
Rep	2	0.002	0.001	0.063 ^{ns}
Trt	3	1.537	0.512	32.000 ^{**}
Error	6	0.098	0.016	
Total	11	1.637		

Now assume Y_{22} and Y_{41} are missing.

Rep	Treatment				Y_j
	A	B	C	D	
1	3.1	3.3	3.6		10.0
2	3.1		3.4	4.0	10.5
3	3.0	3.2	3.6	4.2	14.0
Y_i	9.2	6.5	10.6	8.2	34.5

Step 1. Estimate all but one of the missing values by using means.

$$Y_{22} = \left(\frac{3.3 + 3.2}{2} + \frac{3.1 + 3.4 + 4.0}{3} \right) / 2$$

$$= 3.375$$

Step 2. Substitute this value into the table for Y_{22} .

Rep	Treatment				Y_j
	A	B	C	D	
1	3.1	3.3	3.6		10.0
2	3.1	3.375	3.4	4.0	13.875
3	3.0	3.2	3.6	4.2	14.0
Y_i	9.2	9.875	10.6	8.2	37.875

Step 3. Estimate Y_{41} .

$$Y_{41} = \frac{(rB + tT - G)}{(r-1)(t-1)}$$

$$= \frac{[(3 * 10) + (4 * 8.2) - 37.875]}{(3-1)(4-1)}$$

$$= 4.15$$

Step 4. Substitute this value into the table for Y_{41} and estimate Y_{22} again.

Rep	Treatment				Y_j
	A	B	C	D	
1	3.1	3.3	3.6	4.15	14.15
2	3.1		3.4	4.0	10.5
3	3.0	3.2	3.6	4.2	14.0
Y_i	9.2	6.5	10.6	12.35	38.65

.

$$\begin{aligned}
 Y_{22} &= \frac{(rB + tT - G)}{(r-1)(t-1)} \\
 &= \frac{[(3 * 10.5) + (4 * 6.5) - 38.65]}{(3-1)(4-1)} \\
 &= 3.14
 \end{aligned}$$

Step 5. Redo the estimate of Y_{41} using the new estimate of Y_{22} .

$$\begin{aligned}
 Y_{41} &= \frac{(rB + tT - G)}{(r-1)(t-1)} \\
 &= \frac{[(3 * 10) + (4 * 8.2) - 37.64]}{(3-1)(4-1)} \\
 &= 4.19
 \end{aligned}$$

Step 6. Redo the estimate of Y_{22} using the new estimate of Y_{41} .

$$\begin{aligned}
 Y_{22} &= \frac{(rB + tT - G)}{(r-1)(t-1)} \\
 &= \frac{[(3 * 10.5) + (4 * 6.5) - 38.69]}{(3-1)(4-1)} \\
 &= 3.14
 \end{aligned}$$

- You keep going through these steps until the estimated values don't change.
- For this problem I would probably estimate Y_{41} one more time.
- Calculation of the LSD's when there is more than one missing value is not similar to that used when there is one missing value.

RCBD with Sampling

- As we had with the CRD with sampling, we will have a source of variation for sampling error.
- Calculation of the Experimental Error df is done the same way as if there was no sampling.
- Calculation of the Sampling Error df is done the same way as was done for the CRD with sampling.

ANOVA Table

SOV	Df	F
Rep	$r-1$	Rep MS/Expt. Error MS
Trt	$t-1$	Trt MS/Expt. Error MS
Experimental Error	$(r-1)(t-1)$	
Sampling Error	$(rts-1)-(tr-1)$	
Total	$trs-1$	

Example

Rep	Sample	Treatment			
		A	B	C	
1	1	78	68	89	
1	2	82	64	87	
		$Y_{11.}=160$	$Y_{21.}=132$	$Y_{31.}=176$	$Y_{.1.}=468$
2	1	74	62	88	
2	2	78	66	92	
		$Y_{12.}=152$	$Y_{22.}=128$	$Y_{32.}=180$	$Y_{.2.}=460$
3	1	80	70	90	
3	2	84	60	96	
		$Y_{13.}=164$	$Y_{23.}=130$	$Y_{33.}=186$	$Y_{.3.}=480$
$Y_{i..}$		476	390	542	$Y_{...}=1408$

Step 1. Calculate the Correction Factor (CF).

$$\frac{Y_{...}^2}{rts} = \frac{1408^2}{3(3)(2)} = 110,136.889$$

Step 2. Calculate the Total SS:

$$\begin{aligned} Total\ SS &= \sum Y_{ijk}^2 - CF \\ &= (78^2 + 82^2 + 74^2 + \dots + 96^2) - CF \\ &= 2121.111 \end{aligned}$$

Step 3. Calculate the Replicate SS.

$$\begin{aligned} Rep\ SS &= \sum \frac{Y_{.j.}^2}{ts} - CF \\ &= \left(\frac{468^2}{3(2)} + \frac{460^2}{3(2)} + \frac{480^2}{3(2)} \right) - CF \\ &= 33.778 \end{aligned}$$

Step 4. Calculate the Treatment SS:

$$\begin{aligned} Treatment\ SS &= \sum \frac{Y_{i..}^2}{rs} - CF \\ &= \left(\frac{476^2}{3(2)} + \frac{390^2}{3(2)} + \frac{542^2}{3(2)} \right) - CF \\ &= 1936.444 \end{aligned}$$

Step 5. Calculate the SS Among Experimental Units Total (SSAEUT)

$$SS\ AEUT = \sum \frac{Y_{ij.}^2}{s} - CF$$

$$= \left(\frac{160^2}{2} + \frac{152^2}{2} + \frac{164^2}{2} + \dots + \frac{186^2}{2} \right) - CF$$

$$= 2003.111$$

Step 6. Calculate the Experimental Error SS:

$$\text{Experimental Error SS} = \text{SAEUT} - \text{SS TRT} - \text{SS REP}$$

$$= 2003.111 - 1936.444 - 33.778$$

$$= 32.889$$

Step 7. Calculate the Sampling Error SS:

$$\text{Sampling Error SS} = \text{Total SS} - \text{SSAEUT}$$

$$= 2121.111 - 2003.111$$

$$= 118.0$$

Step 8. Complete the ANOVA Table:

SOV	Df	SS	MS	F
Rep	r-1=2	33.778	16.889	2.054 ^{ns}
Trt	t-1 = 2	1936.444	968.222	117.76 ^{**}
Experimental Error	(r-1)(t-1) = 4	32.889	8.222	
Sampling Error	(trs-1) - (tr-1) = 9	118.0		
Total	trs-1 = 17	2121.111		

Step 9. Calculate LSD.

$$LSD_{TRT} = t_{.05/\frac{1}{2}} \sqrt{\frac{2Expt.ErrorMS}{rs}}$$

$$= 2.78 \sqrt{\frac{2(8.222)}{3 * 2}}$$

$$= 4.602$$

Step 10. Compare treatment means

Treatment	Mean
B	65.0 a
A	79.3 b
C	90.3 c

RCBD – When a Treatment Appears More Than Once in a Replicate

-As mentioned earlier, one advantage of the RCBD is that some treatments can appear more than once per replicate.

-Often, some researchers like to have checks appear more than once per replicate, while the other treatments appear only once per replicate.

Example

100-kernel weight of barley (g)

Rep	Drummond (check)	Stander	Robust	Morex	Y _j
1	3.5, 3.3, 3.5	3.7	4.0	3.1	21.1
2	3.6, 3.7, 3.5	3.7	3.8	3.3	21.6
3	3.4, 3.4, 3.5	3.5	3.7	3.1	20.6
Y _i	31.4	10.9	11.5	9.5	63.3

Step 1. Calculate the correction factor (CF).

$$CF = \frac{Y^2_{..}}{\text{Total \# of obs.}} = \frac{63.3^2}{18} = 222.605$$

Step 2. Calculate the Total SS.

$$\begin{aligned} \text{Total SS} &= \sum Y_{ij}^2 - CF \\ &= (3.5^2 + 3.3^2 + 3.5^2 + \dots + 3.1^2) - CF \\ &= 0.925 \end{aligned}$$

Step 3. Calculate the Replicate SS (Rep SS)

$$\begin{aligned} \text{Rep SS} &= \sum \frac{Y_{.j}^2}{t'} - CF \\ &= \frac{(21.1^2 + 21.6^2 + 20.6^2)}{6} - CF \\ &= 0.083 \end{aligned}$$

Step 4. Calculate the Treatment SS (Trt SS)

$$\begin{aligned} \text{Trt SS} &= \sum \frac{Y_{.i}^2}{r'} - CF \\ &= \left(\frac{31.4^2}{9} \right) + \frac{(10.9^2 + 11.5^2 + 9.5^2)}{3} - CF \\ &= 0.716 \end{aligned}$$

Step 5. Calculate the Checks within Reps SS = Checks(Rep) SS

$$\begin{aligned} \text{Checks(Rep)SS} &= (3.5^2 + 3.3^2 + \dots + 3.5^2) - \left[\frac{(3.5 + 3.3 + 3.5)^2}{3} + \dots + \frac{(3.4 + 3.4 + 3.5)^2}{3} \right] \\ &= 0.053 \end{aligned}$$

Step 6. Calculate the Error SS

$$\begin{aligned}\text{Error SS} &= \text{Total SS} - \text{Rep SS} - \text{Trt SS} - \text{Check(Reps) SS} \\ &= 0.073\end{aligned}$$

Step 7. Complete the ANOVA Table

SOV	Df	SS	MS	F
Rep	$r-1 = 2$	0.083	0.042	Rep MS/Error MS = 3.5
Trt	$t-1 = 3$	0.716	0.239	Trt MS/Error MS = 19.92**
Check(Reps)	$r(\#\text{cks per rep} - 1) = 6$	0.053		
Error	$(r-1)(t-1) = 6$	0.073	0.012	
Total	$\#\text{ of obs.} - 1 = 17$	0.925		

Step 8. Calculate LSD's if necessary

This problem will require two LSD's in order to make all comparisons:

1. Comparison of non-check treatments.

$$\begin{aligned}LSD_{TRT} &= t_{.05/2} \sqrt{\frac{2\text{ErrorMS}}{r}} \\ &= 2.447 \sqrt{\frac{2(0.012)}{3}} \\ &= 0.18\end{aligned}$$

2. Comparison of a non-check treatment to the check.

$$\begin{aligned}LSD_{TRT} &= t_{.05/2} \sqrt{s^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)} \\ &= 2.447 \sqrt{0.012 \left(\frac{1}{9} + \frac{1}{3} \right)} \\ &= 0.22\end{aligned}$$

Step 9. Show differences between treatment means.

Treatment	N	Mean
Drummond	9	3.49
Robust	3	3.17
Stander	3	3.63
Morex	3	3.83
¹ LSD(0.05)		0.18
² LSD(0.05)		0.22

¹LSD for comparing treatments not including Drummond.

²LSD for comparing Drummond vs. any other treatment.

Linear Models for the RCBD

No Sampling

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

where: Y_{ij} is the j^{th} observation of the i^{th} treatment,
 μ is the population mean,
 τ_i is the treatment effect of the i^{th} treatment,
 β_j is the rep effect of the j^{th} , replicate, and
 ε_{ij} is the random error.

With Sampling

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

where: Y_{ijk} is the j^{th} observation of the i^{th} treatment,
 μ is the population mean,
 τ_i is the treatment effect of the i^{th} treatment,
 β_j is the rep effect of the j^{th} , replicate,
 δ_{ij} is the sampling error, and
 ε_{ijk} is the random error.

Experimental Error in the RCBD

-The failure of treatments observations to have the same relative rank in all replicates.

Example 1

Rep	Treatments				
	A	B	C	D	E
1	2	3	4	5	6
2	3	4	5	6	7
3	4	5	6	7	8

*Note that each treatment increases by one from replicate to replicate.

Example 2

Fill in the given table so the Experimental Error SS = 0.

Rep	Treatments				
	A	B	C	D	E
1	2	6	1	8	4
2	4				
3	1				
4	5				

Answer

Rep	Treatments				
	A	B	C	D	E
1	2	6	1	8	4
2	4	8	3	10	6
3	1	5	0	7	3
4	5	9	4	11	7

SAS Commands

RCBD with no missing values.

```
options pageno=1;
data rcbdmiss
input trt $    rep    yield;
datalines;
a    1    3.1
a    2    3.1
a    3    3.0
b    1    3.3
b    2    3.4
b    3    3.2
c    1    3.6
c    2    3.4
c    3    3.6
d    1    3.9
d    2    4.0
d    3    4.2
;;
ods rtf file='rcbd nomiss.rtf';
proc anova;
class rep trt;
model yield=rep trt;
means trt/lsd;
title 'ANOVA for RCBD with no Missing Data';
run;
ods rtf close;
```

SAS commands for one missing data point

```
options pageno=1;
data rcbdmiss;
input trt $    rep    yield;
datalines;
a    1    3.1
a    2    3.1
a    3    3.0
b    1    3.3
b    2    .
b    3    3.2
c    1    3.6
c    2    3.4
c    3    3.6
d    1    3.9
d    2    4.0
d    3    4.2
;;
ods graphics off;
ods rtf file='rcbd nomiss.rtf';
```

SAS uses a period for missing data.
Other programs may use different
values, such as a dash (-) or -999.

```
proc glm;  
class rep trt;  
model yield=rep trt;  
lsmeans trt/pdiff;  
title 'ANOVA for RCBD with Missing Data';  
run;  
ods rtf close;
```

ANOVA for RCBD with no Missing Data

The ANOVA Procedure

Class Level Information		
Class	Levels	Values
rep	3	1 2 3
trt	4	a b c d

Number of Observations Read	12
Number of Observations Used	12

ANOVA for RCBD with no Missing Data

The ANOVA Procedure

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	1.53833333	0.30766667	18.77	0.0013
Error	6	0.09833333	0.01638889		
Corrected Total	11	1.63666667			

R-Square	Coeff Var	Root MSE	yield Mean
0.939919	3.675189	0.128019	3.483333

Source	DF	Anova SS	Mean Square	F Value	Pr > F
rep	2	0.00166667	0.00083333	0.05	0.9508
trt	3	1.53666667	0.51222222	31.25	0.0005

ANOVA for RCBD with no Missing Data

The ANOVA Procedure

Note This test controls the Type I comparisonwise error rate, not the : experimentwise error rate.

Alpha	0.05
Error Degrees of Freedom	6
Error Mean Square	0.016389
Critical Value of t	2.44691
Least Significant Difference	0.2558

Means with the same letter are not significantly different.			
t	Grouping	Mean	N trt
	A	4.0333	3 d
	B	3.5333	3 c
	B		
C	B	3.3000	3 b
C			
C		3.0667	3 a

ANOVA for RCBD with Missing Data

The GLM Procedure

Class Level Information		
Class	Levels	Values
rep	3	1 2 3
trt	4	a b c d

Number of Observations Read	12
Number of Observations Used	11

ANOVA for RCBD with Missing Data

The GLM Procedure

Dependent Variable: yield

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	1.55422980	0.31084596	20.76	0.0023
Error	5	0.07486111	0.01497222		
Corrected Total	10	1.62909091			

R-Square	Coeff Var	Root MSE	yield Mean
0.954047	3.505134	0.122361	3.490909

Source	DF	Type I SS	Mean Square	F Value	Pr > F
rep	2	0.00159091	0.00079545	0.05	0.9488
trt	3	1.55263889	0.51754630	34.57	0.0009

Source	DF	Type III SS	Mean Square	F Value	Pr > F
rep	2	0.01013889	0.00506944	0.34	0.7279
trt	3	1.55263889	0.51754630	34.57	0.0009

Ignore the table that has results for the Type I SS.

We use the Type III SS for ANOVA of data with missing values.

ANOVA for RCBD with Missing Data

The GLM Procedure

Dependent Variable: yield

trt	yield LSMEAN	LSMEAN Number
a	3.0666667	1
b	3.2277778	2
c	3.5333333	3
d	4.0333333	4

Least Squares Means for effect trt				
Pr > t for H0: LSMean(i)=LSMean(j)				
Dependent Variable: yield				
i/j	1	2	3	4
1		0.2214	0.0055	0.0002
2	0.2214		0.0455	0.0009
3	0.0055	0.0455		0.0041
4	0.0002	0.0009	0.0041	

Note: To ensure overall protection level, only probabilities associated with pre-planned comparisons should be used.

SAS Commands for the RCBD With Sampling

```
options pageno=1;
data rcbdsamp;
input Rep    Sample    Trt $ yield;
datalines;
1      1      a      78
1      2      a      82
2      1      a      74
2      2      a      78
3      1      a      80
3      2      a      84
1      1      b      68
1      2      b      64
2      1      b      62
2      2      b      66
3      1      b      70
3      2      b      60
1      1      c      89
1      2      c      87
2      1      c      88
2      2      c      92
3      1      c      90
3      2      c      96
;;
ods rtf file='rcbdsamp.rtf';
proc anova;
class rep trt;
model yield=rep trt rep*trt;
*test h=rep trt e=rep*trt;
*means trt/lsd e=rep*trt;
Means trt/lsd;
title 'RCBD With Sampling Using the Experimental Error as the Error
Term';
run;
ods rtf close;
```

RCBD With Sampling Using the Experimental Error as the Error Term

The ANOVA Procedure

Class Level Information		
Class	Levels	Values
Rep	3	1 2 3
Trt	3	a b c

Number of Observations Read	18
Number of Observations Used	18

RCBD With Sampling Using the Experimental Error as the Error Term

The ANOVA Procedure

Dependent Variable: yield

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	2003.111111	250.388889	19.10	<.0001
Error	9	118.000000	13.111111		
Corrected Total	17	2121.111111			

Sampling Error source of variation

R-Square	Coeff Var	Root MSE	yield Mean
0.944369	4.629026	3.620927	78.22222

Source	DF	Anova SS	Mean Square	F Value	Pr > F
Rep	2	33.777778	16.888889	1.29	0.3221
Trt	2	1936.444444	968.222222	73.85	<.0001
Rep*Trt	4	32.888889	8.222222	0.63	0.6552

Experimental Error source of variation

RCBD With Sampling Using the Experimental Error as the Error Term

The ANOVA Procedure

t Tests (LSD) for yield

Note: This test controls the Type I comparisonwise error rate, not the experimentwise error rate.

Alpha	0.05
Error Degrees of Freedom	9
Error Mean Square	13.11111
Critical Value of t	2.26216
Least Significant Difference	4.7291

Means with the same letter are not significantly different.			
t Grouping	Mean	N	Trt
A	90.333	6	c
B	79.333	6	a
C	65.000	6	b

The calculation SAS did for the LSD and mean separation above is incorrect because it used the Model mean square, which is the Sampling Error SOV, for determining the df and calculating the LSD.

You need to calculate the LSD using the Rep * TRT mean square, which is the Experimental Error mean square.