RANDOMIZED COMPLETE BLOCK DESIGN RCBD

1 DESCRIPTION

The simple RCBD is probably the most frequently used design. The experimental units are divided into homogeneous groups of material (called BLOCKs) each of which constitutes a single replication of the experiment.

At all stages during the experiment, the techniques applied within a block should be as uniform as possible, thus keeping experimental error within blocks as small as possible. Differences between blocks are permitted to be large, but are not of major concern in the analysis, since the comparisons of treatments and the computation of experimental error is done within blocks. Blocking will be effective only if the error variance among units within blocks is smaller than the error variance over all units.

The division into blocks needs to be made only at those stages during the study where failure to do so would increase experimental error. For example, blocking may not be required until data are being collected or laboratory analyses are being conducted.

The key to successful blocking is to minimize the variance among units within blocks while maximizing the variance among blocks. Precision usually decreases as the number of experiment units (or size of units) per block increases. Therefore block size should be kept as small as possible.

2 ADVANTAGES OF BLOCKING

2.1 Improves precision (relative to CRD)

2.1.1 effective blocking reduces S^2_e, thus resulting in greater precision or reduces the number of replications needed to achieve equal precision.

2.1.2 creates better treatment balance

2.2 Flexible

2.2.1 any number of treatments

2.2.2 any number of block replicates

2.2.3 extra replications for certain treatments may be included (2x, 3x, . . .)

2.2.4 not all blocks need to contain the same number of units

2.3 Scope of inference is increased and block means provide a comparison of the differences among blocks

3 DISADVANTAGES OF BLOCKING

3.1 Certain assumptions may be required for some tests of hypotheses.

3.2 Block*treatment interactions may make interpretation of treatment effects more difficult.

3.3 Blocking for a single factor may not provide sufficient error control (precision).

3.4 The gain in precision due to blocking generally decreases as the number of experimental units in a block increases.

3.5 Block degrees of freedom result in a reduction in error degrees of freedom, thus reducing sensitivity in small experiments or when EU heterogeneity is small.

3.6 Requires some prior knowledge about variability of experimental units for successful blocking.

4 RANDOMIZATION OF BLOCK DESIGNS

After the experimental units have been blocked, treatments are assigned at random within each block such that each treatment occurs once in every block for the simple RCBD or as planned if more or less than once per block. During the conduct of the experiment where the order of processing the material may make a difference, units are processed by block and in a completely random order within each block.

5 WHERE SHOULD THE RCB DESIGN BE USED?

5.1 Where sufficient knowledge exists about the heterogeneity of the experimental units to provide for effective blocking.

5.1.1 field experiments

5.1.2 experiments where lack of uniformity information is available

5.1.3 experiments with potential position and location effects

5.2 If more than one source of heterogeneity exists in the experimental material, sources may be confounded or multi-factor blocking may be required.

5.2.1 animal studies - weight, age, housing location, repetitions in time of year?

5.2.2 field studies - adjacent plots, location, previous land use?

5.2.3 laboratory studies - lab tech, time, batch of reagents?

5.3 When it is desirable to compare the treatments over a wide range of experimental material (e.g., as in variety trials) to increase generalizability.

6 MODEL FOR SIMPLE RCB DESIGN

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

where: Y_{ij} is the observed value for the j^{th} replicate of the i^{th} treatment (where i=1 to t and j=1 to b).

μ is the grand mean.

τ_i is the treatment effect for the i^{th} treatment; the treatment effects may be either fixed or random.

β_j is the block effect for the j^{th} block; the block effect may be either fixed or random, however if treatments are fixed then random blocks are required for exact tests of treatment hypotheses.

ϵ_{ij} is the random error associated with the Y_{ij} experimental unit.

7 EXAMINATION OF MODEL EFFECTS

7.1 Equations for sample estimates

Parameter	*Population value*	*Sample estimate*
μ	$\mu_{..}$	$\bar{Y}_{..}$
β_j	$\mu_{.j} - \mu_{..}$	$\bar{Y}_{.j} - \bar{Y}_{..}$
τ_i	$\mu_{i.} - \mu_{..}$	$\bar{Y}_{i.} - \bar{Y}_{..}$
ϵ_{ij}	$Y_{ij} - \mu_{i.} - \mu_{.j} + \mu_{..}$	$Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..}$

8 EXPECTED MEAN SQUARES (components in [ ] are confounded if both exist, θ^2 is the sums of squares of the fixed effects divided by degrees of freedom or the variance of a fixed effect)

8.1 Expected MS Random Model

Sources of variation	df	MS	Components of variance	VC estimate	Assumps.
Block	b-1	MSb	$[\sigma^2_e + \sigma^2_{bt}] + t\sigma^2_b$	S^2_b=(MSb-MSe)/t	none
Treatment	t-1	MSt	$[\sigma^2_e + \sigma^2_{bt}] + b\sigma^2_t$	S^2_t=(MSt-MSe)/b	none
Error	(b-1)(t-1)	MSe	$[\sigma^2_e + \sigma^2_{bt}]$	S^2_e=MSe	$\sigma^2_{bt} = 0$

8.2 Expected MS Fixed Model

Sources of variation	df	MS	Components of variance	VC estimate or F ratio	Assumptions
Block	b-1	MSb	$\sigma^2_e + t\theta^2_b$	Msb/MSe	$\theta^2_{bt} = 0$
Treatment	t-1	MSt	$\sigma^2_e + b\theta^2_t$	MSt/MSe	$\theta^2_{bt} = 0$
Error	(b-1)(t-1)	MSe	$[\sigma^2_e + \theta^2_{bt}]$	S^2_e=MSe	$\theta^2_{bt} = 0$

8.3 Expected MS Mixed Model (block random)

Sources of variance	df	MS	Components of variance	VC estimate or F ratio	Assumps.
Block	b-1	MSb	$\sigma^2_e + t\sigma^2_b$	S^2_b=(MSb-MSe)/t	$\sigma^2_{bt} = 0$
Treatment	t-1	MSt	$[\sigma^2_e + \sigma^2_{bt}] + b\theta^2_t$	MSt/MSe	none
Error	(b-1)(t-1)	MSe	$[\sigma^2_e + \sigma^2_{bt}]$	S^2_e=MSe	$\sigma^2_{bt} = 0$

9 STANDARD ERRORS

9.1 Standard error of treatment means

9.1.1 Fixed blocks

$$\sqrt{\frac{S_e^2}{b}}$$

9.1.2 Random blocks

$$\sqrt{\frac{S_e^2 + S_b^2}{b}}$$

9.2 Standard error of the difference between treatment means

$$\sqrt{\frac{2S_e^2}{b}}$$

10 PAIRED T TEST AS A RCBD

10.1 The data

BLOCK	YA	YB	DIFF
1	24	20	4
2	22	21	1
3	25	23	2
4	23	25	-2
5	28	28	0
6	30	27	3
7	29	24	5
8	31	30	1
9	33	26	7
$\bar{Y}$	27.22	24.89	2.33
S^2	14.94	10.61	7.50
COV_{XY}		9.03	

10.2 The Paired t test

$$SED = \sqrt{S_D^2 / r} = .913$$

$$t = \frac{\bar{Y}_A - \bar{Y}_B}{SED} = 2.556, \quad P<.0339$$

11.3 The Randomized Complete Block Anova

Source	DF	Sum of Squares	Mean Square	F Value	Prob<
Block	8	174.44	21.81		
Treatment	1	24.50	24.50	6.53	0.0339
Error	8	30.00	3.75		
Total	17	228.94			

$$SED = \sqrt{2MSE / r} = .913$$

11.4 Another approach - Correlated observations

$$V(X-Y) = V_X + V_Y - 2COV_{XY}$$

$$V(X-Y) = 14.94 + 10.61 - 2(9.03) = 7.50$$

$$S^2_{pooled} = MSE = \frac{8(14.94) + 8(10.61)}{8 + 8} = 12.78$$

$$SED = \sqrt{2(MSE - COV) / r} = .913$$

$t = 2.556$, $P<.0339$