Frequently asked questions

1. Define RBD

RBD: A two way layout is called RBD if there are N = pxk experimental units. Group these N experimental units in to k blocks of p units each such that with in the blocks the experiment units are relatively homogeneous in nature. With in each block the p treatments are randomly assigned to the p experimental units such that assigning the treatments to these experimental units has the same probability to appear and the assignment in different blocks are statistically independent.

2. Explain how RBD utilises the principles of randomisations, replication and local control

Randomisation: The p treatments to the p experimental units in each block are randomly applied

Replication: Since each treatment appears once and only once in each block, every treatment will appear in all the blocks. Hence each treatment replicated the number of times as the number of blocks.

Local Control:

Local control is adopted in the following way: First from the homogeneous blocks of the experimental units, then allocate each treatment randomly in each block. The error variance now will be smaller because of homogeneous blocks and some variance will be parted away from the error variance due to the difference among the blocks.

	Blocks			Block	Block	
				Totals	Averages	
Treatments	1	2		k		
1	y ₁₁	Y ₁₂		Y _{1n}	y _{1.}	$\overline{y_{1.}}$
2	y ₂₁	Y ₂₂ .		Y _{2n}	У2.	$\overline{\mathcal{Y}_{2.}}$

3. Give the Layout of RBD

•		•				
		•		•	•	•
		•		•	•	•
р	У _{р1}	y _{p2}		Урп	У р.	$\overline{\mathcal{Y}_{p.}}$
Treatment Total	y.1	y.2		y.n	у	
Treatment Averages	y ₁	<u><i>Y</i>.2</u>	<u>y.</u> 3	<u>y_{.n}</u>		

4. Explain the statistical Model used in RBD

 Y_{ij} represent the jth observation taken from treatment i.

We define the model

 $Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}, i = 1,2...p, j = 1,2\ldots k$

(4)

Where μ general effect

 $\alpha_i - i^{th}$ treatment effect;

 $\beta j - j^{th} blockeffect;$

 εij - error term, independent and identically distributed random variables with mean 0 and variance $\sigma 2$

5. Write the statistical hypothesis tested in RBD

1. Related to the treatment effects

 $H_A: \alpha_1 = \alpha_2 = \dots \alpha_p = 0$

And the alternative hypothesis is

- H_{A1} : at least one $\alpha_i = \alpha_j$ for all I, j
- 2. Related to the block effects

 $H_{B}: \beta_{1} = \beta_{2} = \dots \beta_{p} = 0$

And the alternative hypothesis is

 H_{B1} : at least one $\beta_i = \beta_j$ for all I, j

6. Derive the Least square estimates of the model parameters in RBD:

The parameters μ , α_i and β_j are estimated by the method of least squares. i.e. by

minimising error sum of squares. L = $\sum_{i=1}^{p} \sum_{j=1}^{k} \varepsilon_{ij} \sum_{j=1}^{p} \sum_{i=1}^{k} (y_{ij} - \mu - \alpha_i - \beta_j)^2$

And solving the normal equations $\frac{\partial L}{\partial \mu} = 0$, $\frac{\partial L}{\partial \alpha_i} = 0$ i= 1,2...p and $\frac{\partial L}{\partial \alpha_i}$

we obtain p+k+1 normal equations as ,

$$N\mu + \sum_{i=1}^{p} k\alpha_{i} + \sum_{j=1}^{k} p\beta_{j} = \sum_{i=1}^{p} \sum_{j=1}^{k} y_{ij}$$

1**PJ — <u>L</u> ^yij**, i= 1,2 …p

And

$$p\mu + \sum_{i=1}^{p} \alpha_i + p\beta_j = \sum_{i=1}^{p} y_{ij}$$
, j=1.2,...k

These normal equations are not linearly independent, as first equation is equal to the sum of p equations corresponding to α and equal to the sum of k equations corresponding to β . Hence no unique solution exists for μ and $\alpha_{i, i=}$ 1,2..p. and β_j j=1,2...k. Since we have defined the treatment effects as deviations from overall

mean, hence we add independent constraint, $\sum_{i=1}^{p} \alpha i = 0$, $\sum_{j=1}^{k} \beta_j = 0$ and solve

the simultaneous normal equations. Solving we get the solutions as

$$\hat{\mu} = \overline{y}_{..}_{and} \quad \hat{\alpha}_i = \overline{y}_{i.} - \overline{y}_{..}_{i=1,2..p} _{\beta j} = \hat{\beta}_i = \overline{y}_{.j} - \overline{y}_{..}$$

7. Show that with usual notations SST = SSTR+SSB+SSE

The fitted model after substituting the estimates
$$\hat{\mu}$$
 and $\hat{\alpha}_{i}_{j}$ and $\hat{\beta}_{j}$
in the linear model we get
Yij= $\hat{\mu}_{i} + \hat{\alpha}_{i} + \hat{\beta}_{j} + \epsilon_{ij}$
Or
Y_{ij}= $\overline{\hat{y}}_{...+} + (\overline{\hat{y}}_{i.} - \overline{\hat{y}}_{...+}) + (\overline{\hat{y}}_{...+} - \overline{\hat{y}}_{...+})_{+} (\overline{\hat{y}}_{...+} - \overline{\hat{y}}_{...+})_{+} (\overline{\hat{y}}_{...+} - \overline{\hat{y}}_{...+})_{+} + \overline{\hat{y}}_{...+})$
Or
(Yij- $\overline{y}_{...}) = (\overline{y}_{...+} - \overline{y}_{...+}) + (\overline{\hat{y}}_{...+} - \overline{\hat{y}}_{...+} - \overline{\hat{y}}_{...+} + \overline{\hat{y}}_{...+})$, the error term is chosen that
both sides of the equation are equal
Squaring both sides and summing over all the observations we get

$$\sum_{i=1}^{p} \sum_{j=1}^{k} (y_{ij} - \overline{y}_{..})^{2} = \sum_{i=1}^{p} k(\overline{y}_{...+} - \overline{y}_{...+})^{2} + \sum_{j=1}^{k} p(\overline{y}_{...+} - \overline{y}_{...+})^{2} + \sum_{i=1}^{k} (y_{ij} - \overline{y}_{...+} + \overline{y}_{...+})^{2}_{...+} all the
cross product vanishes.
Or
SST = SSTR + + SSB+ SSE
Where
SST = $\sum_{i=1}^{p} \sum_{j=1}^{k} (y_{ij} - \overline{y}_{...})^{2} = \sum_{i=1}^{p} \sum_{j=1}^{k} \frac{x_{ij}^{2}}{y_{ij}^{2}} - \frac{y_{ij}^{2}}{N}$$$

SST = $\sum_{i=1}^{p} \sum_{j=1}^{k} (y_{ij} - \overline{y_{..}})^{2} = \sum_{i=1}^{p} \sum_{j=1}^{k} y_{ij}^{2} - \frac{y_{..}^{2}}{N}$ SSTR = $\sum_{i=1}^{p} k (\overline{yi.} - \overline{y_{..}})^{2} = \sum_{i=1}^{p} \frac{y_{i.}^{2}}{k} - \frac{y_{..}^{2}}{N}$ SSB= $\sum_{j=1}^{k} p(\overline{y.}j - \overline{y_{..}})^{2} = \sum_{i=1}^{k} \frac{y_{.j}^{2}}{p} - \frac{y_{..}^{2}}{N}$ And SSE = $\sum_{i=1}^{p} \sum_{j=1}^{k} (y_{ij.} - \overline{y_{i.}} + \overline{y_{.j}} + \overline{y_{..}})^{2}$

8. Write the test Statistic used to test different hypothesis in RBD

. a. To test the null hypothesis H_A: α_1 = α_2 = $\ldots \alpha_p$ = 0

The test Statistics is

$$F_A = \frac{SSTR/(p-1)}{SSE/(p-1)(k-1)} = \frac{MSSTR}{MSSE}$$
(1)

Which is distributed as F with p-1 and (p-1)(k-1) degrees of freedom.

- . b. Similarly to test the null hypothesis $H_B\!\!:\beta_1$ = β_2 = $\ldots\beta_p$ = 0
- , the test Statistics is

$$F_B = \frac{SSB/(K-1)}{SSE/(p-1)(k-1)} = \frac{MSSB}{MSSE}$$
(2)

Which is distributed as F with k-1 and (p-1)(k-1) degrees of freedom.

4. Write the Analysis of variance Table(ANOVA Table) RBD

Sources of	Degree of	Sum of	Mean sum of	F-Value
variation	freedom	squares	squares	
Treatments	p-1	SSTR	MSSTR =	MSSTR/
			SSTR/(p-1)	MSSE
replicates	k-1	SSB	MSSB =	MSS B / MSSE
			SSB/(k-1)	
Error	(p-1) (k-1)	SSE	MSSE =	
			SSE/(p-1) (k-1)	
total	N-1	TSS		

5. Write the Advantages of RBD ::

- a) Blocking increases precision
- b) Any number of blocks and any no. of treatments with in blocks can be used
- c) Statistical analysis relatively simple
- d) Easy to construct the design
- e) When significant blocking can be achieved, differences due to error variance are eliminated from treatment contrasts.
- f) RBD has greater precision than CRD

6. Write the Disadvantages of the RBD:

- a) Missing observations within blocks complicates analysis
- b) Degree of freedom for RBD smaller than for a comparable CRD

- c) The design is not suitable for testing a large number of treatments, as with increase in block size, the blocks are not likely to consists of homogeneous plots and hence error sum will increase.
- d) If block and treatment effects interact (that is, they are not additive). The RBD analysisis not appropriate.

Sources of	Degree of	Sum of	Mean sum of	F-Value
variation	freedom	squares	squares	
Treatments	5		0.2535	
replicates	3	1.965		
Error			0.1192	
total	23	5.02		

7. Complete the following Anova Table:

Ans:	

Sources of	Degree of	Sum of	Mean sum of	F-Value
variation	freedom	squares	squares	
Treatments	5	1.2675	0.2535	2.1267
replicates	3	1.965	0.655	5.5788
Error	15	1.7875	0.1192	
total	23	5.02		