Chapter 28

Balanced Incomplete Block Design

BIBD
product formulation

Block	1	2	3	4	5
1	X	X	X		
2	X	X		X	
3	X	X			X
4	X		X	X	
5	X		X		X
6	X			X	X
7		X	X	X	
8		X	X		X
9		X		X	X
10			X	X	X

- When the number of experimental units in each block is less than the number of treatment combinations
- Balanced when every treatment appears w/ every other treatment in the same block the same number of times
  - 1 & 2 appear together in 3 blocks
  - 1 & 3 — 3
  - 1 & 4 — 3
  - 1 & 5 — 3
  - ⋮ — ⋮
  - 4 & 5 — 3

  } Thus balanced

With r = # of treatments, r_b = block size, n_b = # of blocks and no restriction on n_b we can construct a BIBD by listing $\binom{r}{r_b}$ subsets of size r_b from all treatments

Advantages and Disadvantages

1) Helpful with studies that have a lot of treatments
2) Simplifies analysis
3) equal precision across groups
4) May waste collected data
5) Restrictive assumptions
6) More complex than RCBD

Model $Y_{ij} = \mu_{..} + \rho_i + \tau_j + \epsilon_{ij}$

- $\mu_{..}$ is a constant
- ρ_i are constants for the block row effects $\ni \Sigma \rho_i = 0$
- τ_j are constants for the treatment effects $\ni \Sigma \tau_j = 0$
- ϵ_{ij} are ind $N(0, \sigma^2)$
- no block-treatment interactions are present
- Sum of squares & tests are the same as the fixed effects model (Chapter 21)

Regression Approach $Y_{ij} = \mu_{..} + \rho_1 Z_{ij1} + \cdots + \rho_9 Z_{ij9} + \tau_1 X_{ij1} + \cdots + \tau_4 X_{ij4} + \epsilon_{ij}$

$\ni X_{ijk} = \begin{cases} 1 & \text{if from treatment } k \\ -1 & \text{if from treatment 5} \\ 0 & \text{o.w.} \end{cases}$

$Z_{ijk} = \begin{cases} 1 & \text{if from block } k \\ -1 & \text{if from block 10} \\ 0 & \text{o.w.} \end{cases}$

Tests $R_1 \rightarrow Y_{ij} = \mu_{..} + \rho_1 Z_{ij1} + \cdots + \rho_9 Z_{ij9} + \epsilon_{ij}$

$R_2 \rightarrow Y_{ij} = \mu_{..} + \tau_1 X_{ij1} + \cdots + \tau_4 X_{ij4} + \epsilon_{ij}$

① $H_0: \tau_1 = \tau_2 = \tau_3 = \tau_4 = 0$

H_a: not H_0

$$F^* = \frac{SSE(R) - SSE(F)}{df_R - df_F} \div MSE(F)$$

Reject if $F^* > F(1-\alpha, df_R, df_F)$

② $H_0: \rho_1 = \rho_2 = \cdots \rho_{10} = 0$

H_a: not H_0

$$F^* = \frac{SSE(R) - SSE(F)}{df_R - df_F} \div MSE(F)$$

Reject if $F^* > F(1-\alpha, df_R, df_F)$

- $\hat{\mu}_{\cdot j} = \hat{\mu}_{\cdot\cdot} + \hat{\tau}_j$
- $\sigma^2(\hat{L}) = \sigma^2\left(\sum_{j=1}^{t} c_j \hat{\mu}_{\cdot j}\right) = \sigma \frac{n_b}{mp} \sum_{j=1}^{t} c_j^2$
- Confidence Intervals: $\hat{L} \pm \frac{1}{\sqrt{2}} q_{\nu}[1-\alpha, r, n_b r_b - n_b - r + 1] s(\hat{L})$ pairwise-tukey
  $\hat{L} \pm (r-1) F[1-\alpha, r-1, n_b r_b - n_b - r + 1] s(\hat{L})$ scheffe
  $\hat{L} \pm t[1-\alpha/2g, n_b r_b - n_b - r + 1]$ Bonferroni

SAS Look at chapter 21

Latin Square Designs · When it isn't feasible to use two blocking variables simultaneously in RCBD

Factor B	FACTOR A 1	2	3
1	T2	T1	T3
2	T1	T3	T2
3	T3	T2	T1

- There are r treatments and r levels in each block
- Each Row and each column has all treatments
- No interactions
- Can have random blocks

Advantages
1.) Greater reduction in variability
2.) Good for pilot studies
3.) Keeps track of order

Disadvantages
1.) # of levels must = number of treatments
2.) Restrictive assumptions
3.) Very small degrees of freedom w/ few treatments
4.) large degrees of freedom w/ a lot of treatments

Model $y_{ijk} = \mu_{\cdots} + \rho_i + \kappa_j + \tau_k + \epsilon_{ijk}$
- $\mu_{\cdots}$ is a constant
- ρ_i, κ_j, τ_k are constants $\ni \sum \rho_i = \sum \kappa_j = \sum \tau_k = 0$
- $\epsilon_{ijk} \sim N(0, \sigma^2)$

$Y_{i\cdot\cdot} = \sum_j Y_{ijk}$ $\quad \bar{Y}_{i\cdot\cdot} = \frac{Y_{i\cdot\cdot}}{r}$

$Y_{\cdot j\cdot} = \sum_i Y_{ijk}$ $\quad \bar{Y}_{\cdot j\cdot} = \frac{Y_{\cdot j\cdot}}{r}$

$Y_{\cdot\cdot k} = \sum_{ij} Y_{ijk}$ $\quad \bar{Y}_{\cdot\cdot k} = \frac{Y_{\cdot\cdot k}}{r}$

$Y_{\cdots} = \sum_i \sum_j Y_{ijk}$ $\quad \bar{Y}_{\cdots} = \frac{Y_{\cdots}}{r^2}$

$\hat{\mu}_{\cdots} = \bar{Y}_{\cdots}$

$\hat{\rho}_i = \bar{Y}_{i\cdot\cdot} - \bar{Y}_{\cdots}$

$\hat{\kappa}_j = \bar{Y}_{\cdot j\cdot} - \bar{Y}_{\cdots}$

$\hat{\tau}_k = \bar{Y}_{\cdot\cdot k} - \bar{Y}_{\cdots}$

$\therefore \hat{Y}_{ijk} = \bar{Y}_{i\cdot\cdot} + \bar{Y}_{\cdot j\cdot} + \bar{Y}_{\cdot\cdot k} - 2\bar{Y}_{\cdots}$

$e_{ijk} = Y_{ijk} - \hat{Y}_{ijk} = Y_{ijk} - \bar{Y}_{i\cdot\cdot} - \bar{Y}_{\cdot j\cdot} - \bar{Y}_{\cdot\cdot k} + 2\bar{Y}_{\cdots}$

Sum of squares & Mean Squares Table 28.5 p 1189

Test ① H_0: all $\tau_k = 0$

H_a: not H_0

$F^* = \frac{MSTR}{MSRem}$

Reject if $F^* > F[1-\alpha, r-1, (r-1)(r-2)]$

② H_0: all row blocking variables $= 0$

H_a: not H_0

$F^* = \frac{MSRow}{MSRem}$

③ H_0: all column blocking variables $= 0$

H_a: not H_0

$F^* = \frac{MSCol}{MSRem}$

- $s^2(\hat{L}) = \frac{2MSRem}{r}$
- Confidence Intervals: $\hat{L} \pm t[1-\alpha/2, (r-1)(r-2)]$
  $\hat{L} \pm \frac{1}{\sqrt{2}} q[1-\alpha, r, (r-1)(r-2)]$
  $\hat{L} \pm (r-1) F[1-\alpha, r-1, (r-1)(r-2)]$
  $\hat{L} \pm t[1-\alpha/2g, (r-1)(r-2)]$
- Diagnostics
  - Look at Y_{ij} vs pred
  - Look at Y_{ij} vs blocks
  - Look at normal probability plot

Power of ~~F test~~ $\phi = \frac{1}{\sigma}\sqrt{\Sigma \tau_k^2}$

- Efficiency of Blocking

$E_1 = \sigma_r^2/\sigma_L^2$ $\quad \hat{E}_1 = \frac{MSRow + MSCol + (r-1)MSRem}{(r+1)MSRem}$

$E_2 = \sigma_{br}^2/\sigma_L^2$ $\quad \hat{E}_2 = \frac{MSCol + (r-1)MSRem}{rMSRem}$

$E_3 = \sigma_{bc}^2/\sigma_L^2$ $\quad \hat{E}_3 = \frac{MSRow + (r-1)MSRem}{rMSRem}$

Model w/ Replications within Cells $Y_{ijkm} + \mu_{...} + \rho_i + \kappa_j + \tau_k + \epsilon_{ijkm}$

- $\mu_{...}$ is a constant
- ρ_i, κ_j, τ_k are constants ∋ $\Sigma\rho_i = \Sigma\kappa_j = \Sigma\tau_k = 0$
- $\epsilon_{ijkm} \sim N(0, \sigma^2)$

Sum of Squares & Mean Squares table 28.7 p 1196

Skipped 28.8

SAS

```
/* To find the sample size necessary to get 80% Power */
proc power;
  onewayanova;
  group means μ1 | μ2 | μ3 | μ4;
  stddev = σ;
  alpha = α;
  npergroup = .
  power = .8;
 run;
/* Latin Squares */
proc glm plots=all;
  class A B Treatments;
  model Y = A B Treatments;
  ls means treatment / pdiff adjust=Tukey alpha=.05 cl;
run;
```