6. Two-way Layout

Treatments and blocks

- In a two-way layout, the main focus remains on the treatment effects, but the data in each treatment are no longer considered as identically distributed.
- Let $X_{1j},\ldots,X_{nj}$ denote the random variables for treatment j, $j=1,\ldots,k$.
- The cdf F_{ij} of X_{ij} is not common for $i=1,\ldots,n$ (as in one-way layout). This allows to account for differences *within* the same treatment.
- When F_{ij} within each treatment j are allowed to vary with i, the variables $X_{i1},\ldots,X_{ik}$ are said to be in *block* i, $i=1,\ldots,n$.
- Thus the data are divided into k treatments and n blocks. Each combination of treatment-block has one observation. The total sample size is $N=nk$.
- Variations in the data may be influenced by both treatment effects and block effects (differences between blocks). Hence it is desirable to separate these two types of effects. This is the key idea of the two-way layout problem.

Assumption 6.1

(i) The N random variables X_{ij}, $i = 1, \ldots, n$, $j = 1, \ldots, k$, are independent.

(ii) The cdf F_{ij} of X_{ij} satisfy the following relations:

$$F_{ij}(t) = F(t - \beta_i - \tau_j),\ t \in \mathbb{R},\ \text{for } i \in \{1, \ldots, n\} \text{ and } j \in \{1, \ldots, k\}, \qquad (6.1)$$

where F is a continuous cdf with unknown median θ, β_i is the unknown effect of block i, and τ_j is the unknown effect of treatment j.

If F is normal, Assumption 6.1 is equivalent to the two-way ANOVA model:

$$X_{ij} = \theta + \beta_i + \tau_j + e_{ij} \text{ with i.i.d. } e_{ij} \sim N(0, \sigma^2),\ i = 1, \ldots, n,\ j = 1, \ldots, k.$$

The two-way layout model under Assumption 6.1 is known as the *randomized complete block design* (RCBD) in the contexts of *experimental design*.

We first focus on the problems with one observation in each (treatment-block) combination. The cases with no observation in some combinations and multiple observations in each combination will be discussed later.

6.1 Tests in a randomized complete block design

A nonparametric test for general alternatives

Hypotheses: $H_0 : \tau_1 = \cdots = \tau_k$ against $H_1 : \tau_1, \ldots, \tau_k$ are not all equal.

Test statistic: Let r_{ij} denote the rank of X_{ij} among $X_{i1}, \ldots, X_{ik}$ (in block i),

$$R_j = \sum_{i=1}^{n} r_{ij}, \quad j = 1, \ldots, k. \tag{6.2}$$

The test statistic S of the *Friedman, Kendall-Babington Smith test* is defined by

$$S = \frac{12}{nk(k+1)} \sum_{j=1}^{k} \left[R_j - \frac{n(k+1)}{2} \right]^2 = \frac{12}{nk(k+1)} \sum_{i=1}^{k} R_j^2 - 3n(k+1), \tag{6.3}$$

where

$$\frac{n(k+1)}{2} = \frac{n}{k} \sum_{j=1}^{k} j = \frac{n}{k} \sum_{j=1}^{k} r_{ij} = \frac{1}{k} \sum_{i=1}^{n} \sum_{j=1}^{k} r_{ij} = \frac{1}{k} \sum_{j=1}^{k} R_j$$

Note that $(r_{i1}, \ldots, r_{ik})$ are the ranks within block i (a permutation of $(1, \ldots, k)$ if no ties), not over all X_{ij}'s with $r_{ij} \in \{1, 2, \ldots, N\}$ as in one-way layout.

Example 6.1 The following tables show the differences in ranks $\{r_{ij}\}$ between the one-way layout and the randomized complete block design (RCBD):

One-way layout	Treatments				Row sum of ranks
	1	2	3	4	
X_{ij} (r_{ij})	3.2 (3)	2.5 (1)	3.5 (4)	3.8 (5)	13
	4.6 (7)	5.8 (9)	6.6 (11)	7.5 (12)	39
	2.9 (2)	4.2 (6)	6.1 (10)	5.4 (8)	26
R_j	$R_1 = 12$	$R_2 = 16$	$R_3 = 25$	$R_4 = 25$	78

RCBD	Treatments				Row sum of ranks
Blocks	1	2	3	4	
1	3.2 (2)	2.5 (1)	3.5 (3)	3.8 (4)	10
2	4.6 (1)	5.8 (2)	6.6 (3)	7.5 (4)	10
3	2.9 (1)	4.2 (2)	6.1 (4)	5.4 (3)	10
R_j	$R_1 = 4$	$R_2 = 5$	$R_3 = 10$	$R_4 = 11$	30

Removal of block effects

By taking the ranks $\{r_{ij}\}$ within each block, the ranks in each block take the same range $\{1,2,\ldots,k\}$. This removes the differences between the blocks (block effects).

Consider the data in Example 6.1. Then the test for one-way layout in (5.2) is

$$H = \frac{12}{12(13)} \cdot \frac{12^2 + 16^2 + 25^2 + 25^2}{3} - 3(13) = \frac{1650}{39} - 39 = 3.3077$$

with p-value $\approx \Pr\left(\chi_3^2 \geq 3.3077\right) = 0.3466$. The test for RCBD in (6.3) is

$$S = \frac{12}{3(4)(5)}\left(4^2 + 5^2 + 10^2 + 11^2\right) - 3(3)(5) = \frac{262}{5} - 45 = 7.4$$

with p-value $\approx \Pr\left(\chi_3^2 \geq 7.4\right) = 0.0602$, which is much smaller than the p-value 0.3466 produced by the one-way layout test.

This shows that if block effects exist, the test ignoring such effects may be unable to detect the treatment effects even if they are significant.

Distribution of S: Assume no ties. Then there are $k!$ ways to arrange $r_{i1},\ldots,r_{ik}$ in block i. Totally, there are $(k!)^n$ ways to arrange the ranks $\{r_{ij}\}$ for all data. By (6.3), the order of $R_1,\ldots,R_k$ does not affect the value of S, hence there are $k!$ ways to produce an equal value of S. For example, if $k=3$ and $n=2$, then the following $3!=6$ rank assignments produce the same value of $S=1$:

Block 1: (r_{11},r_{12},r_{13})	(1,2,3)	(1,3,2)	(2,1,3)	(2,3,1)	(3,1,2)	(3,2,1)
Block 2: (r_{21},r_{22},r_{23})	(3,1,2)	(3,2,1)	(1,3,2)	(1,2,3)	(2,3,1)	(2,1,3)
(R_1,R_2,R_3)	(4,3,5)	(4,5,3)	(3,4,5)	(3,5,4)	(5,4,3)	(5,3,4)

$$\Rightarrow\ S=\frac{12}{2(3)(4)}(3^2+4^2+5^2)-3(2)(4)=\frac{50}{2}-24=1$$

Hence we can fix the ranks in one block, such as $(r_{11},r_{12},\ldots,r_{1k})=(1,2,\ldots,k)$, to obtain the distribution of S under H_0 by

$$\Pr(S=s)=\frac{\text{No. of }(R_1,\ldots,R_k)\text{ with }r_{ij}\text{ fixed in one block}: S=s}{(k!)^{n-1}} \tag{6.4}$$

Example 6.2 For $k=4$, $n=2$ and $(k!)^{n-1}=4!=24$, fix the ranks in Block 1 at $(r_{11},r_{12},r_{13},r_{14})=(1,2,3,4)$ and calculate $S=0.3\left(R_1^2+\cdots+R_4^2\right)-30$ by (6.3) for each case $(r_{21},r_{22},r_{23},r_{24})$ of Block 2 ranks.

Let 1234 represent $(r_{21},r_{22},r_{23},r_{24})=(1,2,3,4)$, and so on. Then

$1234 \Rightarrow (R_1,R_2,R_3,R_4)=(2,4,6,8) \Rightarrow S=0.3\left(2^2+4^2+6^2+8^2\right)-30=6$,

$1324 \Rightarrow S=0.3\left(2^2+5^2+5^2+8^2\right)-30=5.4$, and similarly for all other Block 2 ranks. The distribution of S is obtained as follows:

Block 2 ranks	4321	3421 4231 4312	3412	2431 3241 4132 4213	2341 4123	2413 3142	1432 3214	1342 1423 2314 3124	2143	1243 1324 2134	1234
s	0	0.6	1.2	1.8	2.4	3	3.6	4.2	4.8	5.4	6
$\Pr(S=s)$	1/24	3/24	1/24	4/24	2/24	2/24	2/24	4/24	1/24	3/24	1/24

See Comment 8 on page 297 of the textbook for more details.

Asymptotic distribution of S: Under H_0, $S \sim \chi^2_{k-1}$ approximately for large n.

Rejection rule: Reject H_0 at level α if $S \geq s_\alpha$, where s_α is a value of S such that $\Pr(S \geq s_\alpha) = \alpha$, which can be found from the exact distribution of S.

Approximate rejection rule: Reject H_0 at level α if $S \geq \chi^2_{k-1,\alpha}$.

Ties: If there are ties within a block, assign the average block ranks to tied values. To retain χ^2_{k-1} approximately under H_0, the test statistic S in (6.3) is adjusted to

$$S' = \frac{S}{1-B} \quad \text{with} \quad B = \frac{1}{nk(k+1)(k-1)} \sum_{\text{tied } i} \left(\sum_{j=1}^{g_i} t_{i,j}^3 - k \right), \tag{6.5}$$

where g_i is the number of tied groups in block i, $t_{i,j}$ is the size of the j-th tied group in block i, $j = 1, \ldots, g_i$, $i = 1, \ldots, n$, and the summation index "tied i" is over the blocks with at least two tied ranks within the block. For example, if the ranks in block i are (1.5, 1.5, 3), then $g_i = 2$, $t_{i,1} = 2$ and $t_{i,2} = 1$.

This adjustment is not needed for exact distribution of S conditional on ties.

Example 6.3 In Example 7.1 of the textbook (page 293), Table 7.1 (page 294) presents a set of data with 3 treatments and 22 blocks. Tied ranks $\{2.5, 2.5\}$ exist in 4 blocks of $i = 7, 15, 17, 22$ with $g_i = 2$, $t_{i,1} = 2$ and $t_{i,2} = 1$. The sums of block ranks for the 3 treatments are $R_1 = 53$, $R_2 = 47$ and $R_3 = 32$. Hence

$$B = \frac{1}{nk(k+1)(k-1)} \sum_{i=7,15,17,22} \left(\sum_{j=1}^{g_i} t_{i,j}^3 - k \right) = \frac{4(2^3 + 1^3 - 3)}{22(3)(4)(2)} = \frac{8+1-3}{22(6)} = \frac{1}{22}$$

and by (6.3) and (6.5),

$$S' = \frac{S}{1 - 1/22} = \frac{22}{21}\left[\frac{12(53^2 + 47^2 + 32^2)}{22(3)(4)} - 3(22)(4) \right] = 11.1$$

The approximate p-value is $\Pr(S' \ge 11.1) \approx \Pr(\chi_{3-1}^2 \ge 11.1) = 0.0039$.

This shows very strong evidence to reject H_0 and conclude that τ_1, τ_2, τ_3 are not equal. Therefore, the three methods of rounding first base, namely "round out", "narrow angle" and "wide angle", produce significantly different results.

A nonparametric test for ordered alternatives

Hypotheses: $H_0 : \tau_1 = \cdots = \tau_k$ against $H_1 : \tau_1 \le \cdots \le \tau_k$ are not all equal.

Test statistic: Let $R_1, \ldots, R_k$ be defined in (6.2). The *Page test* statistic for ordered alternatives H_1 is given by

$$L = \sum_{j=1}^{k} jR_j = R_1 + 2R_2 + \cdots + kR_k \tag{6.6}$$

The distribution of L: Unlike the test statistics S in (6.3), the value of L in (6.6) varies with the order of $R_1, \ldots, R_k$. Hence a total of $(k!)^n$ equally likely outcomes for within-block $\{r_{ij}\}$ need to be counted. As a result, the distribution of L under H_0 is given by

$$\Pr(L = l) = \frac{\text{No. of } \{(r_{i1}, \ldots, r_{ik}), i = 1, \ldots, n\} : L = l}{(k!)^n} \tag{6.7}$$

Rejection rule: Reject H_0 at level α and conclude $\tau_1 \le \cdots \le \tau_k$ if $L \ge l_\alpha$, where l_α is a value of L such that $\Pr(L \ge l_\alpha) = \alpha$.

Example 6.4 Consider $k=3$ and $n=2$. There are $(3!)^2=36$ outcomes of $\{r_{ij}\}$.

$$\left.\begin{array}{l}(r_{11},r_{12},r_{13})=(1,2,3)\\(r_{21},r_{22},r_{23})=(3,1,2)\end{array}\right\} \quad \begin{array}{l}\Rightarrow\ (R_1,R_2,R_3)=(4,3,5)\ \Rightarrow\\ L=R_1+2R_2+3R_3=4+2(3)+3(5)=25\end{array}$$

$$\left.\begin{array}{l}(r_{11},r_{12},r_{13})=(1,3,2)\\(r_{21},r_{22},r_{23})=(3,2,1)\end{array}\right\} \quad \begin{array}{l}\Rightarrow\ (R_1,R_2,R_3)=(4,5,3)\ \Rightarrow\\ L=R_1+2R_2+3R_3=4+2(5)+3(3)=23\end{array}$$

Similarly calculate L for all outcomes of $\{r_{ij}\}$ (cf. Comment 17 from page 307 of the textbook). Then use (6.7) to obtain the distribution of L as follows:

l	20	21	22	23	24	25	26	27	28
$\Pr(L=l)$	$\frac{1}{36}$	$\frac{4}{36}$	$\frac{4}{36}$	$\frac{4}{36}$	$\frac{10}{36}$	$\frac{4}{36}$	$\frac{4}{36}$	$\frac{4}{36}$	$\frac{1}{36}$

Achievable level α and corresponding l_α include

$\Pr(L\ge 28)=1/36 \ \Rightarrow\ \alpha=1/36$ with $l_\alpha=l_{1/36}=28$

$\Pr(L\ge 27)=5/36 \ \Rightarrow\ \alpha=5/36$ with $l_\alpha=l_{5/36}=27$, and so on.

Mean and variance of L: Under H_0, we have

$$(r_{1j},\ldots,r_{nj}) \sim (r_{11},\ldots,r_{n1}), \quad r_{ij} \sim r_{11} \quad \text{and} \quad (r_{iu},r_{iv}) \sim (r_{11},r_{12})$$

for $i=1,\ldots,n$, $j=1,\ldots,k$ and $u \neq v \in \{1,\ldots,k\}$. Let

$$Q_i = r_{i1} + 2r_{i2} + \cdots + kr_{ik}, \quad i=1,\ldots,n.$$

Then $Q_1,\ldots,Q_n$ are i.i.d. and

$$L = \sum_{j=1}^{k} jR_j = \sum_{j=1}^{k}\sum_{i=1}^{n} jr_{ij} = \sum_{i=1}^{n}\sum_{j=1}^{k} jr_{ij} = \sum_{i=1}^{n} Q_i$$

Since r_{11} is equally likely to take one of $1,\ldots,k$, $\mathrm{E}[r_{11}] = (k+1)/2 \;\Rightarrow$

$$\mathrm{E}[Q_1] = \sum_{j=1}^{k} j\mathrm{E}[r_{1j}] = \mathrm{E}[r_{11}]\sum_{j=1}^{k} j = \frac{k+1}{2}\cdot\frac{k(k+1)}{2} = \frac{k(k+1)^2}{4} \quad \Rightarrow$$

$$\mathrm{E}_0[L] = \sum_{i=1}^{n}\mathrm{E}[Q_i] = n\mathrm{E}[Q_1] = \frac{nk(k+1)^2}{4} \tag{6.8}$$

Next,

$$\mathrm{Var}(r_{11}) = \frac{1}{k}\sum_{j=1}^{k} j^2 - (\mathrm{E}[r_{11}])^2 = \frac{(k+1)(2k+1)}{6} - \frac{(k+1)^2}{4} = \frac{(k+1)(k-1)}{12} \qquad (6.9)$$

Since (r_{11}, r_{12}) is equally likely to take any of the $k(k-1)$ pairs $u \neq v \in \{1,\ldots,k\}$,

$$\sum_{u\neq v}^{k} uv = \sum_{u=1}^{k}\sum_{v=1}^{k} uv - \sum_{u=1}^{k} u^2 = \left[\frac{k(k+1)}{2}\right]^2 - \frac{k(k+1)(2k+1)}{6}$$

$$= \frac{k(k+1)}{2}\left[\frac{k(k+1)}{2} - \frac{2k+1}{6}\right] = \frac{k(k+1)(3k+2)(k-1)}{12} \quad \Rightarrow$$

$$\mathrm{E}[r_{11}r_{12}] = \frac{1}{k(k-1)}\sum_{u\neq v}^{k} uv = \frac{(k+1)(3k+2)}{12} \quad \Rightarrow$$

$$\mathrm{Cov}(r_{11}, r_{12}) = \mathrm{E}[r_{11}r_{12}] - \mathrm{E}[r_{11}]\mathrm{E}[r_{12}] = \frac{(k+1)(3k+2)}{12} - \left(\frac{k+1}{2}\right)^2$$

$$= \frac{k+1}{12}\big[3k+2-3(k+1)\big] = -\frac{k+1}{12} \qquad (6.10)$$

It follows that

$$\operatorname{Var}(Q_1) = \operatorname{Var}\left(\sum_{u=1}^{k} u r_{1u}\right) = \sum_{u=1}^{k} u^2 \operatorname{Var}(r_{1u}) + \sum_{u \neq v}^{k} uv \operatorname{Cov}(r_{1u}, r_{1v})$$

$$= \operatorname{Var}(r_{11}) \sum_{u=1}^{k} u^2 + \operatorname{Cov}(r_{11}, r_{12}) \sum_{u \neq v}^{k} uv$$

$$= \frac{(k+1)(k-1)}{12} \cdot \frac{k(k+1)(2k+1)}{6} - \frac{k+1}{12} \cdot \frac{k(k+1)(3k+2)(k-1)}{12}$$

$$= \frac{k(k+1)^2(k-1)}{12}\left[\frac{2k+1}{6} - \frac{3k+2}{12}\right]$$

$$= \frac{k(k+1)^2(k-1)}{12}\left[\frac{4k+2-3k-2}{12}\right] = \frac{k^2(k+1)^2(k-1)}{144} \qquad (6.11)$$

Consequently,

$$\operatorname{Var}_0(L) = n \operatorname{Var}(Q_1) = \frac{nk^2(k+1)^2(k-1)}{144} \qquad (6.12)$$

Approximate rejection rule: Reject H_0 at level α to conclude $\tau_1 \le \cdots \le \tau_k$ if

$$L^* = \frac{L - \mathrm{E}_0[L]}{\sqrt{\mathrm{Var}_0(L)}} = 3\frac{4L - nk(k+1)^2}{k(k+1)\sqrt{n(k-1)}} \ge z_\alpha$$

Ties: If there are ties within a block, assign the average block rank to each tied value. Then the rejection rule $L \ge l_\alpha$ is valid approximately, and $L^* \ge z_\alpha$ can be used as a conservative rule, since ties and average ranks reduce the variance.

Example 6.5 Refer to Example 7.2 of the textbook (page 306). Table 7.5 shows the data (ranks) on Strength Index of Cotton from 5 treatments and 3 blocks:

	Treatments (Potash lb/acre)				
Blocks	144	108	72	54	36
1	7.46 (2)	7.17 (1)	7.76 (4)	8.14 (5)	7.63 (3)
2	7.68 (2)	7.57 (1)	7.73 (3)	8.15 (5)	8.00 (4)
3	7.21 (1)	7.80 (3)	7.74 (2)	7.87 (4)	7.93 (5)
	$R_1 = 5$	$R_2 = 5$	$R_3 = 9$	$R_4 = 14$	$R_5 = 12$

Thus

$$L = R_1 + 2R_2 + 3R_3 + 4R_4 + 5R_5 = 5 + 2(5) + 3(9) + 4(14) + 5(12) = 158$$

By R, $\Pr(L \geq 155) = 0.01$. Hence the p-value is

$$\Pr(L \geq 158) < \Pr(L \geq 155) = 0.01$$

This shows very strong evidence for $\tau_1 \leq \tau_2 \leq \tau_3 \leq \tau_4 \leq \tau_5$, with at least one strict inequality. Since the potash level is decreasing from treatment level 1 to level 5, the test results strongly support the trend of decreasing breaking strength with increasing level of potash.

If we use the large-sample approximation, then by (6.8) and (6.12),

$$E_0[L] = \frac{3(5)(5+1)^2}{4} = 135 \quad \text{and} \quad \mathrm{Var}_0(L) = \frac{3 \times 5^2 (5+1)^2 (5-1)}{144} = 75 \Rightarrow$$

$$L^* = \frac{158 - 135}{\sqrt{75}} = 2.66 > 2.33 = z_{0.01} \;\Rightarrow \text{Reject } H_0 \text{ at the 1\% level}$$

This leads to the same conclusion as that based on L.

6.2 Multiple comparisons

Two-sided multiple comparisons

Let $R_1, \ldots, R_k$ be defined in (6.2), and r_α satisfy

$$\Pr\left(|R_u - R_v| < r_\alpha, 1 \le u < v \le k\right) = 1 - \alpha \quad \text{under } H_0 : \tau_1 = \cdots = \tau_k$$

The Wilcoxon-Nemenyi-Macdonald-Thompson two-sided all-treatment multiple comparison procedure is defined as follows. For each pair (τ_u, τ_v) with $u < v$:

$$\text{Decide } \tau_u \ne \tau_v \text{ if } |R_u - R_v| \ge r_\alpha; \quad \text{otherwise accept } \tau_u = \tau_v. \tag{6.13}$$

Comment 26 on page 319 of the textbook discusses how to find r_α and presents an example with $k = 4$ and $n = 2$. It can also be found by R program.

Large-sample approximation

When n is large, r_α can be approximated by $q_\alpha \sqrt{nk(k+1)/12}$, where q_α is given by (5.18) and can be calculated by R program.

Ties: (6.13) is valid approximately if the average block rank is used on ties.

Example 6.6 In Example 6.3, $k = 3$, $n = 22$, $R_1 = 53$, $R_2 = 47$ and $R_3 = 32$. Use R to get $r_{0.0087} = 20$. Thus following (6.13), at a target $\alpha = 0.01$ and an actual $\alpha = 0.0087$, we decide $\tau_u \neq \tau_v$ if $|R_u - R_v| \geq 20$; otherwise accept $\tau_u = \tau_v$:

- $|R_1 - R_2| = |53 - 47| = 6 < 20 \;\Rightarrow\;$ Accept $\tau_1 = \tau_2$
- $|R_1 - R_3| = |53 - 32| = 21 > 20 \;\Rightarrow\;$ Decide $\tau_1 \neq \tau_3$
- $|R_2 - R_3| = |47 - 32| = 15 < 20 \;\Rightarrow\;$ Accept $\tau_2 = \tau_3$

If we use $q_{0.01} = 4.121$ (by R) to approximate $r_{0.01}$, then

$$r_{0.01} \approx q_{0.01}\sqrt{\frac{22(3)(3+1)}{12}} = 4.121\sqrt{22} = 19.3 \;\Rightarrow\; \text{same results as above}$$

We should not use $\tau_1 = \tau_2$ and $\tau_2 = \tau_3$ to reach $\tau_1 = \tau_2 = \tau_3$, contradicting $\tau_1 \neq \tau_3$. The appropriate interpretations are: at $\alpha = 1\%$,

- the difference between treatments 1 and 3 is significant;
- the difference between treatments 1 and 2, or 2 and 3, is insignificant.

One-sided treatments-versus-control multiple comparisons

Let $R_1, \ldots, R_k$ be defined in (6.2), and r_α^* satisfies

$$\Pr\left(R_u - R_1 < r_\alpha^*, u = 2, \ldots, k\right) = 1 - \alpha \text{ under } H_0.$$

Then the *Nemenyi-Wilcoxon-Wilcox-Miller* one-sided treatments-versus-control multiple comparison procedure is stated as follows. For $u = 2, \ldots, k$,

$$\text{Decide } \tau_u > \tau_1 \text{ if } R_u - R_1 \geq r_\alpha^*; \quad \text{otherwise accept } \tau_u = \tau_1. \tag{6.14}$$

Comment 35 on page 325 of the textbook explains how to obtain r_α^*, and shows an example with $n = 3$ and $k = 3$.

Large-sample approximation: For large n, r_α^* can be approximated by

$$r_\alpha^* \approx m_{\alpha,1/2}^* \sqrt{\frac{nk(k+1)}{6}}, \text{ where } m_{\alpha,1/2}^* \text{ is given by (5.19) with } \rho = \frac{1}{2}.$$

See Example 7.4 of the textbook (page 323) for an illustration of the procedure.

6.3 Contrast estimation

As in Section 5, simple contrasts are $\Delta_{uv} = \tau_u - \tau_v$ and the contrast θ is

$$\theta = \sum_{i=1}^{k} a_i \tau_i = \sum_{i=1}^{k} \sum_{j=1}^{k} d_{ij} \Delta_{ij} \quad \text{with} \quad \sum_{i=1}^{k} a_i = 0 \quad \text{and} \quad d_{ij} = \frac{a_i}{k} \tag{6.15}$$

Estimators of contrasts: For $u, v \in \{1, \ldots, k\}$, let $D_i^{uv} = X_{iu} - X_{iv}$, $i = 1, \ldots, n$, and

$$Z_{uv} = \text{median}\{D_i^{uv}, i = 1, \ldots, n\}, \quad u, v \in \{1, \ldots, k\}.$$

It is obvious that $Z_{uv} = -Z_{vu}$ and $Z_{uu} = 0$. Define

$$Z_{u\cdot} = \frac{1}{k} \sum_{v=1}^{k} Z_{uv} = \frac{1}{k} \sum_{v \neq u}^{k} Z_{uv}, \quad u = 1, \ldots, k. \tag{6.16}$$

Then $\widetilde{\Delta}_{uv} = Z_{u\cdot} - Z_{v\cdot}$ is an estimator of Δ_{uv}, and an estimator of θ is given by

$$\tilde{\theta} = \sum_{u=1}^{k} a_u Z_{u\cdot} = \sum_{u=1}^{k} \sum_{v=1}^{k} d_{uv} \widetilde{\Delta}_{uv} \tag{6.17}$$

Example 6.7 For the data in Example 6.3 (Example 7.1 of the textbook), the differences $D_i^{uv} = X_{iu} - X_{iv}$ are provided in Table 7.11 (page 330). From these differences, the medians of $\{D_1^{uv},\ldots,D_{22}^{uv}\}$ for $u,v \in \{1,2,3\}$ are found to be

$Z_{12} = 0.05,\ Z_{13} = 0.125,\ Z_{23} = 0.10 \ \Rightarrow\ Z_{21} = -0.05,\ Z_{31} = -0.125,\ Z_{32} = -0.10$

It then follows from (6.16) that

$$Z_{1.} = \frac{Z_{12} + Z_{13}}{3} = \frac{0.05 + 0.125}{3} = 0.058,$$

$$Z_{2.} = \frac{Z_{21} + Z_{23}}{3} = \frac{-0.05 + 0.10}{3} = 0.017,$$

$$Z_{3.} = \frac{Z_{31} + Z_{32}}{3} = \frac{-0.125 - 0.10}{3} = -0.075.$$

Thus by (6.17) with $a_1 = 1,\ a_2 = 0,\ a_3 = -1$, the contrast $\theta = \tau_1 - \tau_3$ is estimated by $\tilde{\theta} = Z_{1.} - Z_{3.} = 0.058 - (-0.075) = 0.133$.

6.4 Incomplete block design

Balanced incomplete block design

- Refer to each treatment-block combination as a *cell*, and let c_{ij} denote the number of observations in the (i, j)-cell for block i and treatment j. In the complete block design under Assumption 6.1, $c_{ij} = 1$ for all (i, j)-cells.
- In practice, however, some cell may be empty, which may be due to missing data, constraints of the experiment, or some other reasons (like saving costs). Block data with some cells empty ($c_{ij} = 0$) are said to be *incomplete*.
- Consider the two-way layout model with $c_{ij} \in \{0,1\}$ for each (i, j)-cell. If
  - each block contains an equal number s $(< k)$ of treatments;
  - each treatment is observed in an equal number p of blocks; and
  - each pair of treatments appears in an equal number λ of blocks,

  then the model is called a *Balanced Incomplete Block Design* (*BIBD*).

Restrictions for BIBD

In a Balanced Incomplete Block Design (BIBD) with k treatments and n blocks, the total sample size is $N = ns = kp$, where

- s is the number of observed treatments in each block,
- p is the number of blocks with observed treatments.

Furthermore, there are $k(k-1)/2$ pairs of treatments, and each pair appears in λ blocks. Hence the total number of observed treatment pairs is $\lambda k(k-1)/2$.

On the other hand, there are $s(s-1)/2$ observed treatment pairs in each block, so that the total number of observed treatment pairs in all n blocks is $ns(s-1)/2$.

Consequently, since $ns = kp$, a BIBD must satisfy

$$\frac{\lambda k(k-1)}{2} = \frac{ns(s-1)}{2} = \frac{pk(s-1)}{2}, \quad \text{or equivalently,} \quad \lambda(k-1) = p(s-1)$$

Thus BIBD is under the restrictions $ns = pk$ and $p(s-1) = \lambda(k-1)$.

Example 6.8 The following table shows $c_{ij} = 1$ or 0 in a BIBD with $k = 5$, $s = 3$, $n = 10$, $p = 6$, $\lambda = 3$, and the total sample size $N = ns = pk = 30$:

Blocks ($n = 10$)	Treatments ($k = 5$)				
	1	2	3	4	5
1	1	1	0	1	0
2	1	0	0	1	1
3	0	1	1	0	1
4	0	0	1	1	1
5	0	1	0	1	1
6	1	0	1	1	0
7	1	1	1	0	0
8	1	0	1	0	1
9	1	1	0	0	1
10	0	1	1	1	0

It satisfies $p(s-1) = 6(3-1) = 12 = 3(5-1) = \lambda(k-1)$.

A test for general alternatives in BIBD

Hypotheses: $H_0 : \tau_1 = \cdots = \tau_k$ against $H_1 : \tau_1, \ldots, \tau_k$ are not all equal.

Test statistic: Let r_{ij} be the rank of X_{ij} within block i, with $r_{ij} = 0$ if $c_{ij} = 0$, and R_j as in (6.2). Then the *Durbin-Skillings-Mack test* statistic D is defined by

$$D = \frac{12}{\lambda k(s+1)} \sum_{j=1}^{k} \left(R_j - \frac{p(s+1)}{2} \right)^2 = \frac{12}{\lambda k(s+1)} \sum_{j=1}^{k} R_j^2 - \frac{3(s+1)p^2}{\lambda}, \qquad (6.18)$$

where

$$\frac{p(s+1)}{2} = \frac{p}{s} \sum_{j=1}^{s} j = \frac{n}{k} \sum_{j=1}^{s} j = \frac{1}{k} \sum_{i=1}^{n} \sum_{j=1}^{k} r_{ij} I_{\{c_{ij}=1\}} = \frac{1}{k} \sum_{j=1}^{k} R_j$$

Rejection rule: Reject H_0 at level α if $D \geq d_{\alpha,s}$, where $\Pr(D \geq d_{\alpha,s}) = \alpha$ under H_0. Comment 49 on page 336 of the textbook explains how to obtain $d_{\alpha,s}$.

Approximate rejection rule: Reject H_0 at level α if $D \geq \chi^2_{k-1,\alpha}$.

Ties: If there are ties, assign average block ranks to tied values within each block. Then the above rejection rules are valid approximately.

Example 6.9 The table below presents the data in a BIBD for toxic dosages required to kill 95% of the insects exposed to 7 chemicals A – G (treatments).

	Chemical						
Day	A	B	C	D	E	F	G
1	0.465(3)	0.343(1)	—	0.396(2)	—	—	—
2	0.602(1)	—	0.873(3)	—	0.634(2)	—	—
3	—	—	0.875(3)	0.325(1)	—	—	0.330(2)
4	0.423(1)	—	—	—	—	0.987(3)	0.426(2)
5	—	0.652(1)	1.142(3)	—	—	0.989(2)	—
6	—	0.536(3)	—	—	0.409(2)	—	0.309(1)
7	—	—	—	0.609(2)	0.417(1)	0.931(3)	—
	$R_1 = 5$	$R_5 = 5$	$R_3 = 9$	$R_4 = 5$	$R_5 = 5$	$R_6 = 8$	$R_7 = 5$

Tests to collect the data were run over 7 days (blocks), but only 3 chemicals can be tested each day. This BIBD has $k = 7,\ s = 3,\ n = 7,\ p = 3,\ \lambda = 1$. By (6.18),

$$D = \frac{12}{\lambda k(s+1)} \sum_{j=1}^{k} R_j^2 - \frac{3(s+1)p^2}{\lambda} = \frac{12}{7(4)}\left(5 \times 5^2 + 9^2 + 8^2\right) - \frac{3(4)3^2}{1} = 7.7143$$

By R, the critical point at $\alpha = 0.25$ is $d_{0.2305,3} = 8.5714$. Hence the p-value to test $H_0 : \tau_1 = \cdots = \tau_7$ is $\Pr(D \geq 7.7143) \geq \Pr(D \geq 8.5714) = 0.2305$.

The large-sample approximation of the p-value is

$$\Pr\left(\chi^2_{k-1} \geq 0.7143\right) = \Pr\left(\chi^2_6 \geq 0.7143\right) = 0.2598$$

Thus H_0 is accepted by both exact and approximate rejection rules at the 20% level. This result shows lack of evidence to claim a significant difference between the toxicities of the seven chemicals.

Two-sided multiple comparisons for BIBD

Let q_α be given by (5.18). The Skillings-Mack two-sided all-treatment multiple comparison procedure for BIBD is: for each pair (τ_u, τ_v) with $u < v$,

$$\text{Decide } \tau_u \neq \tau_v \text{ if } |R_u - R_v| \geq q_\alpha \sqrt{\frac{(s+1)(ps-p+\lambda)}{12}};$$

$$\text{Otherwise accept } \tau_u = \tau_v. \tag{6.19}$$

Example 6.9 (continued) Use R to find $q_{0.2} = 3.39$. Then calculate

$$q_{0.2}\sqrt{\frac{(s+1)(ps-p+\lambda)}{12}} = 3.39\sqrt{\frac{(3+1)(3\times 3-3+1)}{12}} = 5.18$$

From the table in Example 6.9, we can see that

$$\max_{1\le u<v\le 7} |R_u - R_v| = |R_1 - R_3| = 9-5 = 4$$

Hence $|R_u - R_v| \le 4 < 5.18$ for all $1 \le u < v \le 7$.

Consequently, the multiple comparison procedure in (6.19) accepts $\tau_u = \tau_v$ for all $1 \le u < v \le 7$, which is equivalent to $\tau_1 = \cdots = \tau_7$.

This result is consistent with the test result in Example 6.9, where $H_0 : \tau_1 = \cdots = \tau_7$ is accepted at the 20% level of significance.

In practice, multiple comparisons are usually not required if the test for general alternatives accepts the null hypothesis of no difference between the effects of all treatments under consideration.

Arbitrary incomplete block design

We now consider arbitrary empty cells with $c_{ij} = 0$ occurring in any way.

- Each nonempty (i, j)-cell is still assumed to have $c_{ij} = 1$ observation.
- Let s_i denote the number of nonempty cells in block i, $s_i \le k$, $i = 1, \ldots, n$. If $s_i < k$ for some $i \in \{1, \ldots, n\}$, then the block data are incomplete. When the data do not meet the condition for BIBD, they are said to be *unbalanced*.
- If $s_i = 1$, we remove block i from the analysis. The number of blocks with $s_i \ge 2$ is still denoted by n.
- Define the ranks within block i by

$$r_{ij} = \begin{cases} \text{rank of } X_{ij} \text{ among } s_i \text{ observations in block } i \text{ if } c_{ij} = 1, \\ (s_i + 1)/2 = \text{average rank in block } i \text{ if } c_{ij} = 0. \end{cases} \tag{6.20}$$

  Thus $r_{ij} \in \{1, 2, \ldots, s_i\}$ for $c_{ij} = 1$ and $r_{ij} = (s_i + 1)/2$ is fixed for $c_{ij} = 0$ in each block $i \in \{1, \ldots, n\}$.

Remark 6.1 We defined $r_{ij}=0$ for $c_{ij}=0$ in BIBD. If we follow (6.20) to define $r_{ij}=(s+1)/2$ for $c_{ij}=0$ in BIBD, the test statistic D in (6.18) is not affected.

To see this, let $r_{ij}=a$ for $c_{ij}=0$ with any $a\in\mathbb{R}$, and

$$R_j(a)=\sum_{i=1}^{n} r_{ij}=\sum_{i=1}^{n} r_{ij}I_{\{c_{ij}=1\}}+(n-p)a=R_j(0)+(n-p)a,\quad j=1,\dots,k,$$

Then the average of $R_j(a)$ over k treatments is given by (as $kp=ns$)

$$\bar{R}(a)=\frac{1}{k}\sum_{j=1}^{k}R_j(a)=\frac{1}{k}\sum_{j=1}^{k}\sum_{i=1}^{n}r_{ij}=\frac{1}{k}\sum_{i=1}^{n}\sum_{j=1}^{k}r_{ij}=\frac{1}{k}\sum_{i=1}^{n}[1+2+\cdots+s+(k-s)a]$$

$$=\frac{n}{k}\left[\frac{s(s+1)}{2}+(k-s)a\right]=\frac{p(s+1)}{2}+\left(n-\frac{ns}{k}\right)a=\bar{R}(0)+(n-p)a$$

$$\Rightarrow\ R_j(a)-\bar{R}(a)=R_j(0)+(n-p)a-\bar{R}(0)-(n-p)a=R_j(0)-\bar{R}(0)$$

Thus the test statistic D in (6.18) is unaffected by any $r_{ij}=a\in\mathbb{R}$ for $c_{ij}=0$.

For unbalanced incomplete data, however, r_{ij} must be defined by (6.20).

Test for general alternatives with arbitrary incomplete block data

Hypotheses: $H_0 : \tau_1 = \cdots = \tau_k$ against $H_1 : \tau_1, \ldots, \tau_k$ are not all equal.

To obtain the test statistics, let r_{ij} be defined in (6.20) and

$$A_j = \sum_{i=1}^{n} \sqrt{\frac{12}{s_i + 1}} \left(r_{ij} - \frac{s_i + 1}{2} \right), \ j = 1, \ldots, k; \ \ \mathbf{A} = \begin{bmatrix} A_1 \\ \vdots \\ A_{k-1} \end{bmatrix} \begin{pmatrix} \text{a column} \\ \text{vector} \end{pmatrix} \qquad (6.21)$$

Note that

$$\sum_{j=1}^{k} \left(r_{ij} - \frac{s_i + 1}{2} \right) = \sum_{j: c_{ij} = 1} \left(r_{ij} - \frac{s_i + 1}{2} \right) = \sum_{j: c_{ij} = 1} r_{ij} - \frac{s_i (s_i + 1)}{2} = 0 \ \Rightarrow$$

$$\sum_{j=1}^{k} A_j = \sum_{j=1}^{k} \sum_{i=1}^{n} \sqrt{\frac{12}{s_i + 1}} \left(r_{ij} - \frac{s_i + 1}{2} \right) = \sum_{i=1}^{n} \sqrt{\frac{12}{s_i + 1}} \sum_{j=1}^{k} \left(r_{ij} - \frac{s_i + 1}{2} \right) = 0 \ \Rightarrow$$

$$A_k = -A_1 - \cdots - A_{k-1}$$

Hence we exclude A_k from vector **A** in (6.21) to avoid redundancy.

Variance matrix of A

To get the variance matrix Σ_0 of **A** under H_0, define for $q \neq t \in \{1,\ldots,k\}$

$$\lambda_{qt} = \lambda_{tq} = \sum_{i=1}^{n} I_{\{c_{iq}=c_{it}=1\}} = \begin{Bmatrix} \text{number of blocks with both} \\ \text{treatments } t \text{ and } q \text{ present} \end{Bmatrix} \tag{6.22}$$

$$\sigma_{qt} = -\lambda_{qt} \text{ if } 1 \leq t \neq q \leq k-1; \quad \sigma_{qq} = \sum_{t \neq q}^{k} \lambda_{qt},\ q = 1,\ldots,k-1. \tag{6.23}$$

By (6.20), $\Pr(r_{ij} = u) = 1/s_i$ for $u = 1,\ldots,s_i$ (assuming no ties) under H_0 if $c_{ij} = 1$, and $r_{ij} = (s_i + 1)/2$ is constant if $c_{ij} = 0$. Hence by (6.9) with s_i in place of k,

$$\mathrm{Var}(r_{ij}) = \frac{(s_i+1)(s_i-1)}{12} I_{\{c_{ij}=1\}}$$

Similarly, $\mathrm{Cov}(r_{iq}, r_{it}) = 0$ if $c_{iq} = 0$ or $c_{it} = 0$ and by (6.10) with s_i in place of k,

$$\mathrm{Cov}(r_{iq}, r_{it}) = -\frac{s_i+1}{12} I_{\{c_{iq}=c_{it}=1\}} \text{ for } q \neq t$$

Then by the definition of $A_1,\ldots,A_k$ in (6.21),

$$\operatorname{Var}(A_q)=\sum_{i=1}^{n}\frac{12}{s_i+1}\operatorname{Var}(r_{iq})=\sum_{i=1}^{n}\frac{12}{s_i+1}\cdot\frac{(s_i+1)(s_i-1)}{12}I_{\{c_{iq}=1\}}=\sum_{i=1}^{n}(s_i-1)I_{\{c_{iq}=1\}}$$

$$=\sum_{i=1}^{n}\left(\sum_{t=1}^{k}I_{\{c_{it}=1\}}-1\right)I_{\{c_{iq}=1\}}=\sum_{i=1}^{n}\left(\sum_{t=1}^{k}I_{\{c_{it}=1\}}-I_{\{c_{iq}=1\}}\right)I_{\{c_{iq}=1\}}$$

$$=\sum_{i=1}^{n}\left(\sum_{t\neq q}^{k}I_{\{c_{it}=1\}}\right)I_{\{c_{iq}=1\}}=\sum_{t\neq q}^{k}\sum_{i=1}^{n}I_{\{c_{it}=c_{iq}=1\}}=\sum_{t\neq q}^{k}\lambda_{qt}=\sigma_{qq}\tag{6.24}$$

for $q=1,\ldots,k$. Similarly,

$$\operatorname{Cov}(A_q,A_t)=\sum_{i=1}^{n}\sum_{j=1}^{n}\sqrt{\frac{12}{s_i+1}}\sqrt{\frac{12}{s_j+1}}\operatorname{Cov}(r_{iq},r_{jt})=\sum_{i=1}^{n}\frac{12}{s_i+1}\operatorname{Cov}(r_{iq},r_{it})I_{\{c_{iq}=c_{it}=1\}}$$

$$=\sum_{i=1}^{n}\frac{12}{s_i+1}\left(-\frac{s_i+1}{12}\right)I_{\{c_{iq}=c_{it}=1\}}=-\sum_{i=1}^{n}I_{\{c_{iq}=c_{it}=1\}}=-\lambda_{qt}=\sigma_{qt}\tag{6.25}$$

for $1\le q\neq t\le k$.

It follows from (6.24) – (6.25) that the variance matrix of $\mathbf{A} = [A_1 \quad \cdots \quad A_{k-1}]^\mathsf{T}$ is

$$\Sigma_0 = (\sigma_{qt})_{(k-1)\times(k-1)} = \begin{bmatrix} \sigma_{11} & -\lambda_{12} & \cdots & -\lambda_{1,k-1} \\ -\lambda_{21} & \sigma_{22} & \cdots & -\lambda_{2,k-1} \\ \vdots & \vdots & \ddots & \vdots \\ -\lambda_{k-1,1} & -\lambda_{k-1,2} & \cdots & \sigma_{k-1,k-1} \end{bmatrix} \tag{6.26}$$

Test statistic: If the matrix Σ_0 in (6.26) is invertible, then the *Skillings-Mack statistic* for general alternatives is defined by

$$SM = \mathbf{A}^\mathsf{T}\Sigma_0^{-1}\mathbf{A}, \tag{6.27}$$

where $\mathbf{A}^\mathsf{T}$ is the transpose of $\mathbf{A}$ (a row vector).

If Σ_0 is not invertible, then replace Σ_0^{-1} in (6.27) by the generalized inverse Σ_0^- of Σ_0 such that $\Sigma_0\Sigma_0^-\Sigma_0 = \Sigma_0$.

When the data satisfy BIBD, the SM in (6.27) reduces to the test statistic D in (6.18) (see Appendix).

Rejection rule: Reject H_0 at level α if $SM \geq sm_\alpha$, where sm_α is a value of SM such that $\Pr(SM \geq sm_\alpha) = \alpha$.

Comment 64 on page 350 of the textbook explains how to find sm_α.

Large-sample approximation: If the sample size is large, then under H_0, the vector **A** has approximately a multivariate normal distribution with mean 0 and variance matrix Σ_0. Assume $\lambda_{qt} > 0$ for all $1 \leq q \neq t \leq k$. Then

$$SM \sim \chi^2_{k-1} \text{ approximately for large } n.$$

Approximate rejection rule: Reject H_0 at level α if $SM \geq \chi^2_{k-1,\alpha}$.

Ties: If there are ties within a block, assign average ranks to tied values. Then the above rejection rules have level α approximately.

Comment 66 on page 350 of the textbook discusses how to get level α exactly conditional on ties.

Example 6.10 Consider the following data X_{ij} (r_{ij}) with one empty cell.

	Treatments		
Blocks	R	A	N
1	3 (1)	5 (2)	15 (3)
2	1 (1)	3 (2)	18 (3)
3	5 (2)	4 (1)	21 (3)
4	2 (1)	– (1.5)	6 (2)
5	0 (1)	2 (2)	17 (3)
6	0 (1)	2 (2)	10 (3)
7	0 (1)	3 (2)	8 (3)
8	0 (1)	2 (2)	13 (3)

$k = 3$, $s_i = 3 \Rightarrow (s_i + 1)/2 = 2$ for $1 \le i\ (\ne 4) \le 8$, and $s_4 = 2 \Rightarrow (s_4 + 1)/2 = 1.5$

$$A_1 = \sqrt{\frac{12}{3+1}}(6+2-7\times 2) + \sqrt{\frac{12}{2+1}}(1-1.5) = \sqrt{3}(-6) + \sqrt{4}(-0.5) = -11.392$$

$$A_2 = \sqrt{3}(6\times 2+1-14) + \sqrt{4}(1.5-1.5) = -1.732$$

Hence $\mathbf{A}^{\mathsf{T}} = [A_1 \;\; A_2] = [-11.392 \quad -1.732]$.

By (6.22) – (6.23), $\lambda_{12} = 7$ (no block 4), $\lambda_{13} = 8$ (all blocks), $\lambda_{23} = 7$ (no block 4)

$$\sigma_{12} = \sigma_{21} = -\lambda_{12} = -7, \quad \sigma_{11} = \lambda_{12} + \lambda_{13} = 7 + 8 = 15, \quad \sigma_{22} = \lambda_{21} + \lambda_{23} = 7 + 7 = 14$$

$$\Rightarrow \Sigma_0 = \begin{bmatrix} 15 & -7 \\ -7 & 14 \end{bmatrix} \Rightarrow \Sigma_0^{-1} = \frac{1}{15 \times 14 - 7^2} \begin{bmatrix} 14 & 7 \\ 7 & 15 \end{bmatrix} = 0.01 \begin{bmatrix} 8.70 & 4.35 \\ 4.35 & 9.32 \end{bmatrix} \Rightarrow$$

$$SM = \mathbf{A}^\mathsf{T} \Sigma_0^{-1} \mathbf{A} = 0.01 [-11.392 \quad -1.732] \begin{bmatrix} 8.70 & 4.35 \\ 4.35 & 9.32 \end{bmatrix} \begin{bmatrix} -11.392 \\ -1.732 \end{bmatrix} = 13.287$$

By R program, $sm_{0.0098} = 8.528$. Hence

$$SM = 13.287 > 8.528 \Rightarrow \text{ Reject } H_0 \text{ at the 1\% level}$$

Or approximately, $SM = 13.287 > 9.210 = \chi^2_{2,0.01} \Rightarrow$ Reject H_0 at the 1% level.

Thus there is very strong evidence that the 3 treatments have difference effects.

Refer to Example 7.8 of the textbook (from page 346) for the meanings of the data and the practical interpretation of the test results.

6.5 Block design with replications

- In a general setting of a two-way layout, the number c_{ij} of observations in (i, j)-cell can be any nonnegative integer, and differ between cells.
- The random variables in (i, j)-cell are denoted by $X_{ijq},\ q = 1, \ldots, c_{ij}$.
- In addition to Assumption 6.1, $\{X_{ijq}, q = 1, \ldots, c_{ij}\}$ are assumed to be i.i.d. with cdf F_{ij} in any (i, j)-cell with $c_{ij} > 1$.
- Multiple observations in a cell are referred to as *replications*.
- We consider the special case with common $c_{ij} = c > 1$ for all (i, j)-cell. Then the total number of observations is

$$N = \sum_{i=1}^{n} \sum_{j=1}^{k} c_{ij} = nkc$$

- Order the values $\{X_{ijq}, q = 1, \ldots, c, j = 1, \ldots, k\}$ in block i in ascending order. Let r_{ijq} denote the rank of X_{ijq} among in block i.

Test for general alternatives with replications

Hypotheses: $H_0 : \tau_1 = \cdots = \tau_k$ against $H_1 : \tau_1, \ldots, \tau_k$ are not all equal.

Test statistic: The *Mack-Skillings statistic* for equal replications is defined by

$$MS = \frac{12}{k(N+n)} \sum_{j=1}^{k} \left(S_j - \frac{N+n}{2} \right)^2 = \frac{12}{k(N+n)} \sum_{j=1}^{k} S_j^2 - 3(N+n), \qquad (6.28)$$

where S_j is the sum of average cell ranks in treatment $j \in \{1, \ldots, k\}$:

$$S_j = \frac{1}{c} \sum_{i=1}^{n} \sum_{q=1}^{c} r_{ijq} \quad \text{and} \quad \frac{1}{k} \sum_{j=1}^{k} S_j = \frac{1}{kc} \sum_{j=1}^{k} \sum_{i=1}^{n} \sum_{q=1}^{c} r_{ijq} = \frac{n(kc+1)}{2} = \frac{N+n}{2} \qquad (6.29)$$

Rejection rule: Reject H_0 at level α if $MS \geq ms_\alpha$, where $\Pr(MS \geq ms_\alpha) = \alpha$. Comment 73 on page 359 of the textbook explains how to find ms_α.

Large-sample approximation: Reject H_0 at level α if $MS \geq \chi^2_{k-1,\alpha}$.

Ties: Average ranks are assigned to tied values within each block.

Example 6.11 Table 7.20 of the textbook (page 356) shows the data below (see Example 7.9 of the textbook for more details about the data):

	Block		
Treatment	1	2	3
1	7.58 (3)	11.63 (7)	15.00 (2)
	7.87 (8)	11.87 (11)	15.92 (9)
	7.71 (6)	11.40 (3)	15.58 (4)
2	8.00 (9.5)	12.20 (12)	16.60 (12)
	8.27 (12)	11.70 (8.5)	16.40 (11)
	8.00 (9.5)	11.80 (10)	15.90 (7)
3	7.60 (4)	11.04 (2)	15.87 (6)
	7.30 (1)	11.50 (5.5)	15.91 (8)
	7.82 (7)	11.49 (4)	16.28 (10)
4	8.03 (11)	11.50 (5.5)	15.10 (3)
	7.35 (2)	10.10 (1)	14.80 (1)
	7.66 (5)	11.70 (8.5)	15.70 (5)

The table shows X_{ijq} and their ranks (r_{ijq}) with $n = 3$, $k = 4$ and $c = 3$. Note that the treatments and blocks are arranged differently from the other examples.

From the ranks provided in the above table, use (6.29) to calculate

$$S_1 = (3+8+6+7+11+3+2+9+4)/3 = 17.67$$

$$S_2 = (9.5+12+9.5+12+8.5+10+12+11+7)/3 = 30.5$$

$$S_3 = (4+1+7+2+5.5+4+6+8+10)/3 = 15.83$$

$$S_4 = (11+2+5+5.5+1+8.5+3+1+5)/3 = 14$$

Since $n = 3$, $k = 4$, $c = 3$ and so $N = nkc = 36$, it follows from (6.28) that

$$MS = \frac{12}{4(36+3)}\left(17.67^2 + 30.5^2 + 15.83^2 + 14^2\right) - 3(36+3) = 12.93$$

By R, $ms_{0.0098} = 10.54$. Since $MS = 12.93 > 10.54 = ms_{0.0098}$, H_0 is rejected at the 1% level. Alternatively, $MS = 12.93 > 11.345 = \chi^2_{3,0.01} = \chi^2_{k-1,0.01}$, so that the large sample approximation leads to the same result.

Thus there is very strong evidence to support significant differences between the effects of the four treatments.

Two-sided multiple comparisons with equal replications

Let $S_1,\ldots,S_k$ be defined in (6.29) and q_α be given by (5.18). The Mack-Skillings two-sided all-treatment multiple comparison procedure is as follows:

$$\text{Decide } \tau_u \neq \tau_v \text{ if } |S_u - S_v| \geq q_\alpha \sqrt{\frac{k(N+n)}{12}}; \quad \text{otherwise accept } \tau_u = \tau_v. \quad (6.30)$$

Example 6.12 Refer to Example 6.11. For multiple comparisons of pairwise differences in treatments, let $\alpha = 0.025$ and find $q_{0.025} = 3.985$ by R. Hence by the procedure in (6.30), for $1 \leq u \neq v \leq 4$,

$$\tau_u \neq \tau_v \text{ if } |S_u - S_v| \geq 3.985\sqrt{\frac{4(36+3)}{12}} = 14.37; \text{ otherwise accept } \tau_u = \tau_v$$

From $S_1 = 17.67$, $S_2 = 30.5$, $S_3 = 15.83$ and $S_4 = 14$ in Example 6.11, calculate

$$|S_1 - S_2| = |17.67 - 30.5| = 12.83 < 14.37 \;\Rightarrow\; \tau_1 = \tau_2$$

Similarly, we can find $\tau_1 = \tau_3$, $\tau_1 = \tau_4$, $\tau_1 = \tau_3$, $\tau_2 \neq \tau_3$, $\tau_2 \neq \tau_4$ and $\tau_3 = \tau_4$.