STA 104 Applied Nonparametric Statistics

Chapter 5: Two-Way Layout Problems: Nonparametric Two-Way Analysis of Variance

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4. Two-Sided All-Treatments Multiple Comparisons for General Alternative in a Randomized Block Design with Equal Number of Replications Per treatment-Block Combination

Mack-Skillings test for General Alternatives in a Randomized Block Design with Equal Number of Replications Per treatment-Block Combination

It is often the case in two-way layout settings that we have more than one observation for some of the treatment-block combinations.

These multiple observations in a given cell are referred to as replications for that treatment-block combination.

Here we focus on the setting where we have a common, equal number $c > 1$ of replications for every treatment-block combination.

Setting

The data consist of $N = \sum_{i=1}^{n} \sum_{j=1}^{k} c = nkc$ observations, with $c > 1$ observations from the combination of the i th block with the j th treatment (i.e., the (i, j) th cell), for $i = 1, \ldots, n$ and $j = 1, \ldots, k$

	Treatments			
Blocks	1	2	$\ldots$	k
1	X_{111}	X_{121}	$\ldots$	X_{1k1}
	$\vdots$	$\vdots$	$\ldots$	$\vdots$
	X_{11c}	X_{12c}	$\ldots$	X_{1kc}
2	X_{211}	X_{221}	$\ldots$	X_{2k1}
	$\vdots$	$\vdots$	$\ldots$	$\vdots$
	X_{21c}	X_{22c}	$\ldots$	X_{2kc}
	$\vdots$	$\vdots$	$\vdots$	$\vdots$
n	X_{n11}	X_{n21}	$\ldots$	X_{nk1}
	$\vdots$	$\vdots$	$\ldots$	$\vdots$
	X_{n1c}	X_{n2c}	$\ldots$	X_{nkc}

Hypothesis

H_0 : $\underbrace{\tau_1 = \ldots = \tau_k}$

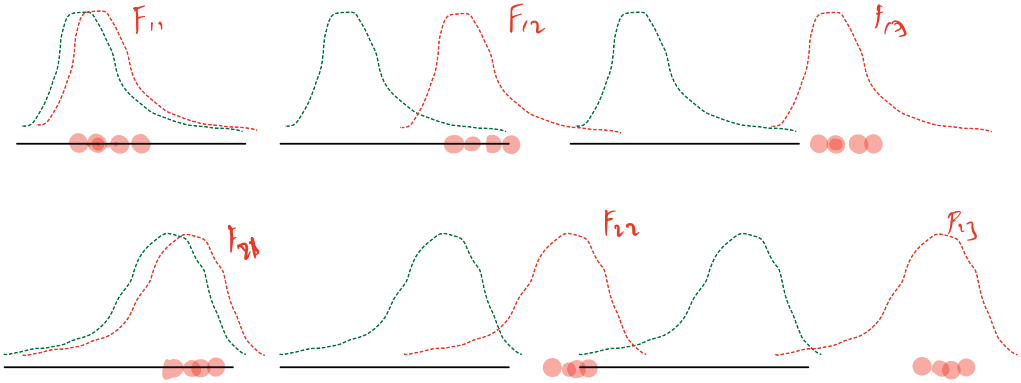
$F_{i1},\ldots,F_{ik}$ within block i are the same; that is, $F_{i1} \equiv F_{i2} \equiv \cdots \equiv F_{ik} \equiv F_i$, for each fixed $i=1,\ldots,n$

H_1 : $\underbrace{\tau_1 \ldots \tau_k \text{ not all equal}}$

at least two of the treatment effects are not equal

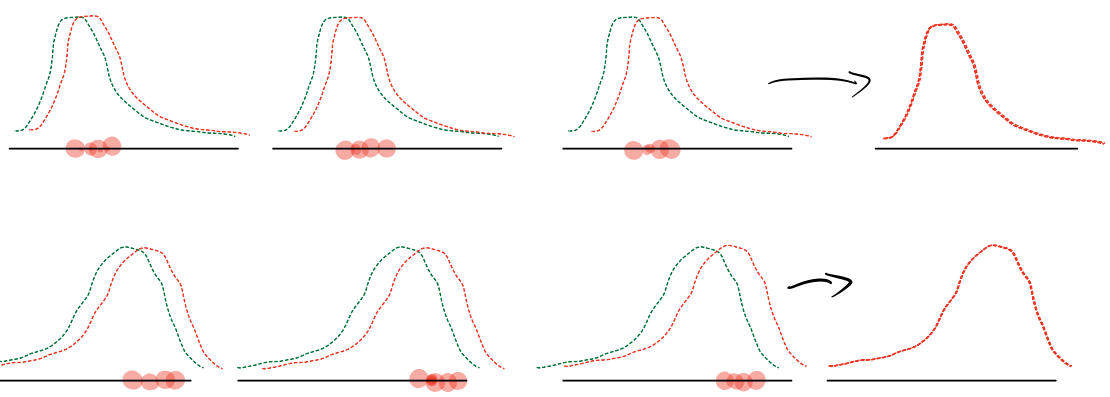
if H_0: $\tau_1 = \dots = \tau_K$ are all equal is True:

Blocks	Treatments					
	1	$\tau_1 = 0.5$	2	$\tau_2 = 5$ ...	K	$\tau_K = 10$
1 β_1	F_{11}		F_{12}		F_{13}	
2 β_2	F_{21}		F_{22}		F_{23}	



if H_0: $\tau_1 = \tau_2 = \dots = \tau_K$;

Blocks	Treatments					
	1	τ_1	2	τ_2 ...	K	τ_K
1 β_1						
2 β_2						



Motivation

Mack-Skillings idea (Friedman-type):

$\Rightarrow$ first order the kc observations from least to greatest separately within each of the n blocks

$\Rightarrow$ Let r_{ijq} denote the within block rank of X_{ijq} (the q th replication from the j th treatment in the i th block) among the kc total observations in the i th block and set

$$S_j = \sum_{i=1}^{n} \left[\sum_{q=1}^{c} r_{ijq}/c \right], \qquad \text{for } j = 1, \ldots, k$$

Thus, S_j is the sum (across blocks) of the cellwise averages of the within-blocks ranks assigned to the c observations from treatment j, for $j = 1, \ldots, k$.

$\Rightarrow$ The Mack-Skillings statistic for equal replications [2]

Common value of S_j

$$MS = \left[\frac{12}{k(N+n)}\right] \sum_{j=1}^{k} \left[S_j - \frac{N+n}{2}\right]^2$$

$$= \left[\frac{12}{k(N+n)}\right] \left\{\sum_{j=1}^{k} S_j^2\right\} - 3(N+n)$$

where $\frac{N+n}{2}$ is expected sum (across blocks) of the cellwise averages for each of the k treatments when H_0 is true; that is, $(N+n)/2$ is the expected value of S_j, for each $j = 1, \ldots, k$, when the null hypothesis H_0 is true.

[2] Special Case of $c = 1$: When we have a single observation for every treatment-block combination (i.e., $c = 1$), we are dealing with data from a complete randomized block design. In this setting, the Mack-Skillings statistic is equivalent to the Friedman statistic. Thus, the Mack-Skillings test represent natural extensions of the Friedman test, to the case of an equal number $c > 1$ of replications per cell.

$\Rightarrow$ Since MS is a constant times a sum of squared differences between the observed treatment sums of cellwise average ranks, S_j, and their common null expected value

- small values of MS represent agreement with H_0
- When the τ 's are not all equal, we would expect a portion of the associated treatment average ranks to differ from their common null expectation , with some tending to be smaller and some larger. The net result would be a large value of MS. This naturally suggests rejecting H_0 in favor of H_1 for large values of MS.

Derivation of null distribution using permutation

When H_0 is true, all possible $[(ck)!]^n$ permutations of the within-blocks ranks are equally likely. Thus, to obtain the exact null distribution of MS, we compute its value for each of these $[(ck)!]^n$ block rank configurations and then tabulate the collected outcomes. [3]

$c = 2 \quad k = 3 \quad n = 3$:

$k \times c = 6 \Rightarrow$ for each block: $6!$

$n = 3$ blocks

$\Rightarrow (6!)^3 \approx$ large

$\Rightarrow$ not ideal to practice

[3] he number $[(ck)!]^n$ of configurations for which we need to compute the value of MS can get large rather quickly, as either k or c is moderately increased.

Large sample approximation of null distribution

Define the centered treatment sums of cellwise average ranks
$S_j^* = S_j - E_0\left(S_j\right) = S_j - (N+n)/2$, for $j = 1, \ldots, k$

$\Rightarrow$ each S_j is an average

$\Rightarrow$ properly standardized version of the vector $\left(S_1^*, \ldots, S_{k-1}^*\right)$ has an asymptotic (nc tending to infinity) $(k-1)$-variate normal distribution when the null hypothesis H_0 is true.

Since the test statistic MS is a quadratic form of $\left(S_1^*, \ldots, S_{k-1}^*\right)$, therefore, quite natural that MS has an asymptotic (nc tending to infinity) chi-square distribution with $k-1$ degrees of freedom.

$$MS \sim \chi^2_{k-1}$$

Procedure

Permutation

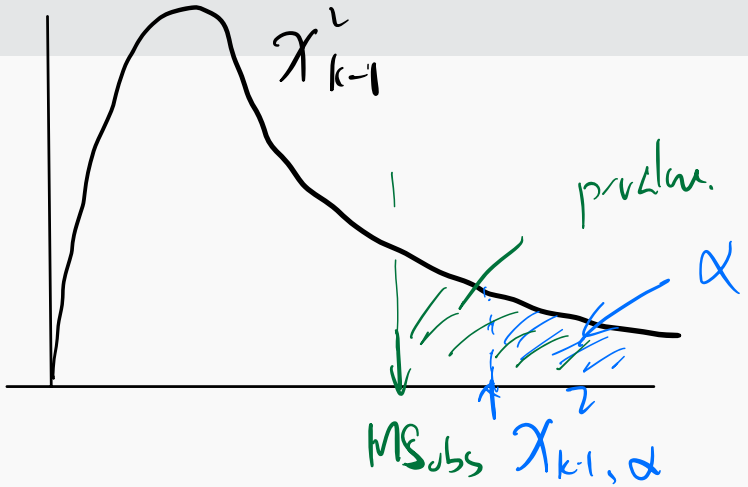
Reject H_0 if $MS \geq ms_\alpha$, otherwise do not reject

where ms_α is the upper α percentile point of the permutation distribution.

Large-sample approximation

Reject H_0 if $MS \geq \chi^2_{k-1,\alpha}$, otherwise do not reject

where $\chi^2_{k-1,\alpha}$ is the upper α percentile point of a chi-square distribution with k-1 degrees of freedom.



Example:Determination of Niacin in Bran Flakes

In a study to investigate the precision and homogeneity of a procedure for assessing the amount of niacin in bran flakes, Campbell and Pelletier (1962) prepared homogenized samples of bran flakes enriched with 0,4 , or 8mg niacin per 100 g of cereal. Portions of the homogenized samples were sent to different laboratories, which were asked to carry out the specified procedure for each of three separate samples. The resulting data (in milligrams per 100 g bran flakes) for a subset (4 out of 12) of the laboratories included in the study are presented.

Laboratory	Amount of niacin enrichment (milligrams per 100 g bran flakes) 0	4	8
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	7.95(9)	12.20(12)	16.60(12)
	8.27(12)	11.6(8)	16.40(11)
	8.05(10)	11.80(10)	15.90(7)
3	7.60(4)	11.04(2)	15.87(6)
	7.30(1)	11.45(5)	15.91(8)
	7.82(7)	11.49(4)	16.28(10)
4	8.03(11)	11.50(6)	15.10(3)
	7.35(2)	10.10(1)	14.80(1)
	7.66(5)	11.70(9)	15.70(5)

Of primary interest here is the precision of the laboratory procedure for determining niacin content in bran flakes. The actual amount of niacin enrichment in the prepared bran flakes serves only as a "nuisance" blocking factor in our evaluation of the consistency of the results across the four laboratories.

Hence, we have data from a two-way layout with $k = 4$ treatments (laboratories), $n = 3$ blocks (amounts of niacin enrichment), and $c = 3$ replications (individual bran flake samples) per laboratory/enrichment combination.

$$S_1 = \frac{3+8+6+7+11+3+2+9+4}{3} = 17.67,$$

$$S_2 = \frac{9+12+10+12+8+10+12+11+7}{3} = 30.33,$$

$$S_3 = \frac{4+1+7+2+5+4+6+8+10}{3} = 15.67,$$

$$S_4 = \frac{11+2+5+6+1+8.5+3+1+5}{3} = 14.17$$

$$\Rightarrow MS = \left[\frac{12}{4(36+3)}\right]\{1678.476\} - 3(36+3)$$

$$= 12.11$$

Large-sample p-value:

```
> pchisq(12.11,df=3,lower.tail = F)
[1] 0.007015691
```

We can reject H_0 at the $\alpha = .05$ level, providing rather strong evidence that the studied process for assessing niacin content in bran flakes does not produce consistent results across a variety of laboratories and is therefore not reliable as an evaluative procedure.

```
library(NSM3)
pMackSkil(x=c(7.58, 11.63, 15.00,
              7.87, 11.87, 15.92,
              7.71, 11.40, 15.58,
              7.95, 12.20, 16.60,
              8.27, 11.6, 16.40,
              8.05, 11.80, 15.90,
              7.60, 11.04, 15.87,
              7.30, 11.45, 15.91,
              7.82, 11.49, 16.28,
              8.03, 11.50, 15.10,
              7.35, 10.10, 14.80,
              7.66, 11.70, 15.70),
          b=rep(c(0,4,8),12),
          trt=c(rep(1,9),rep(2,9),rep(3,9),rep(4,9)),
          method="Asymptotic")
```