

STA 104 Applied Nonparametric Statistics

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

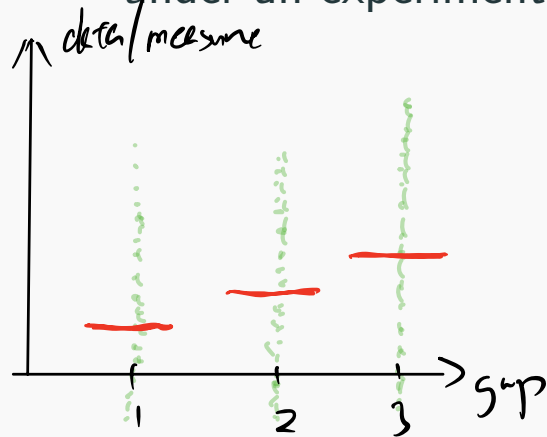
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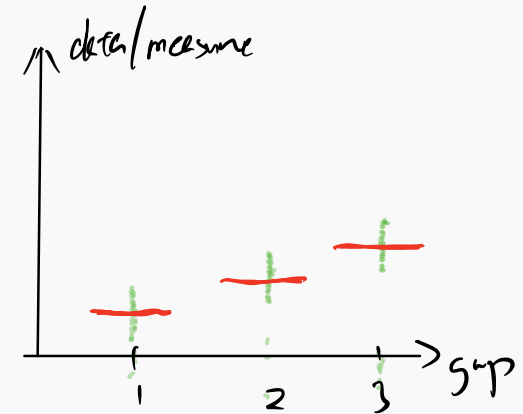
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The procedures of this chapter are designed for statistical analyses of data collected under an experimental design involving two factors, each at two or more levels.



Blocks	Treatments			
	1	2	...	k
1	X_{111}	X_{121}	...	X_{1k1}
	\vdots	\vdots	...	\vdots
	$X_{11c_{11}}$	$X_{12c_{12}}$...	$X_{1kc_{1k}}$
2	X_{211}	X_{221}	...	X_{2k1}
	\vdots	\vdots	...	\vdots
	$X_{21c_{21}}$	$X_{22c_{22}}$...	$X_{2kc_{2k}}$
	\vdots	\vdots	\vdots	\vdots
n	X_{n11}	X_{n21}	...	X_{nk1}
	\vdots	\vdots	...	\vdots
	$X_{n1c_{n1}}$	$X_{n2c_{n2}}$...	$X_{nkc_{nk}}$



~~X~~ $\begin{matrix} \boxed{i} & \boxed{j} & \boxed{k} \\ \uparrow & \uparrow & \nwarrow \end{matrix}$
 block treatment
 $i=1..n \quad j=1..k$

observation $l: 1..C_{ij}$

Design Rationale.

The n blocks in this basic two-way layout design represent an effort to reduce experimental errors and prevent misleading comparisons of "apples and oranges."

= natural variation = residuals

Our primary interest is in the relative location effects (medians) of the different levels of one of these factors, hereafter called the **treatment factor**, within the various levels of the second factor, hereafter called the **blocking factor**.

This blocking factor is associated quite commonly with the experimental design where subjects are first divided into more homogeneous subgroups (called **blocks**) and then randomly assigned to the various treatment levels within these blocks.

Design Rationale.

Such a design is called a randomized block design.

As a special case, when there is only one observation per treatment-block combination, it is called a randomized complete block design.

We will refer to the k levels of a treatment as the k treatments.

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

- For each treatment-block combination $i \in \{1, \dots, n\}$ and $j \in \{1, \dots, k\}$, the c_{ij} observations are a random sample from a continuous distribution with distribution function F_{ij} .
- The N observations are mutually independent.
- The distribution functions F_{ij} are connected through the relationship

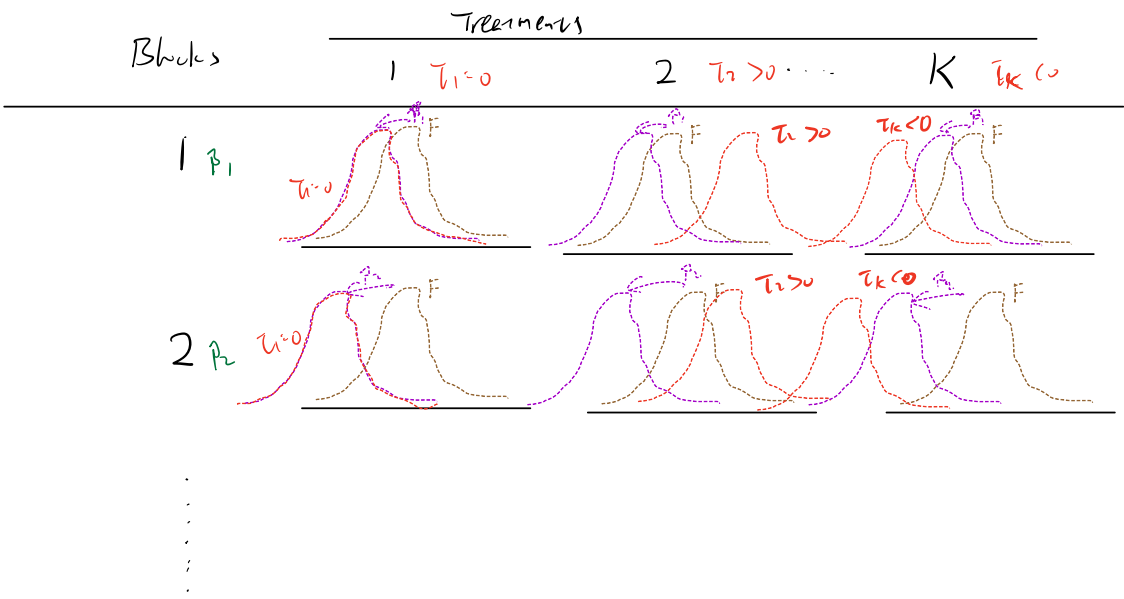
$$F_{ij}(t) = F(t - \beta_i - \tau_j), -\infty < t < \infty,$$

for $i = 1, \dots, n$ and $j = 1, \dots, k$, where F is a distribution function for a continuous distribution with unknown median θ ,

β_i is the unknown additive effect contributed by block i , and

τ_j is the unknown additive treatment effect contributed by the j th treatment.

Blocks	Treatments			
	1	2	...	k
1	X_{111}	X_{121}	...	X_{1k1}
	\vdots	\vdots	...	\vdots
	$X_{11c_{11}}$	$X_{12c_{12}}$...	$X_{1kc_{1k}}$
2	X_{211}	X_{221}	...	X_{2k1}
	\vdots	\vdots	...	\vdots
	$X_{21c_{21}}$	$X_{22c_{22}}$...	$X_{2kc_{2k}}$
\vdots	\vdots	\vdots	\vdots	\vdots
	\vdots	\vdots	\vdots	\vdots
	\vdots	\vdots	\vdots	\vdots
n	X_{n11}	X_{n21}	...	X_{nk1}
	\vdots	\vdots	...	\vdots
	$X_{n1c_{n1}}$	$X_{n2c_{n2}}$...	$X_{nkc_{nk}}$



This is the usual Two-Way Analysis of Variance (ANOVA), commonly associated with normal assumptions and theory:

$$X_{ijt} = \theta + \beta_i + \tau_j + e_{ijt}, \quad i = 1, \dots, n; \quad j = 1, \dots, k; \quad t = 1, \dots, c_{ij}$$

where

if no block: $\tau_j + e_{ijt}$: one-way ANOVA
 residual / error term

- θ is the overall median,
- τ_j is the treatment j effect,
- β_i is the block i effect,
- residuals e_{ijt} 's: random sample from a continuous distribution with median 0 .
 (Under the additional assumption of normality, the medians θ and 0 are, of course, also the respective means.)

Friedman test for General Alternatives in a Randomized Complete Block Design

Setting

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

Blocks	Treatments			
	1	2	...	k
1	X_{11}	X_{12}	...	X_{1k}
2	X_{21}	X_{22}	...	X_{2k}
	\vdots	\vdots	\vdots	\vdots
n	X_{n1}	X_{n2}	...	X_{nk}

X_{ij}
↑
Block ←
treatment

Hypothesis

$H_0 :$

$$\underbrace{\tau_1 = \dots = \tau_k}$$

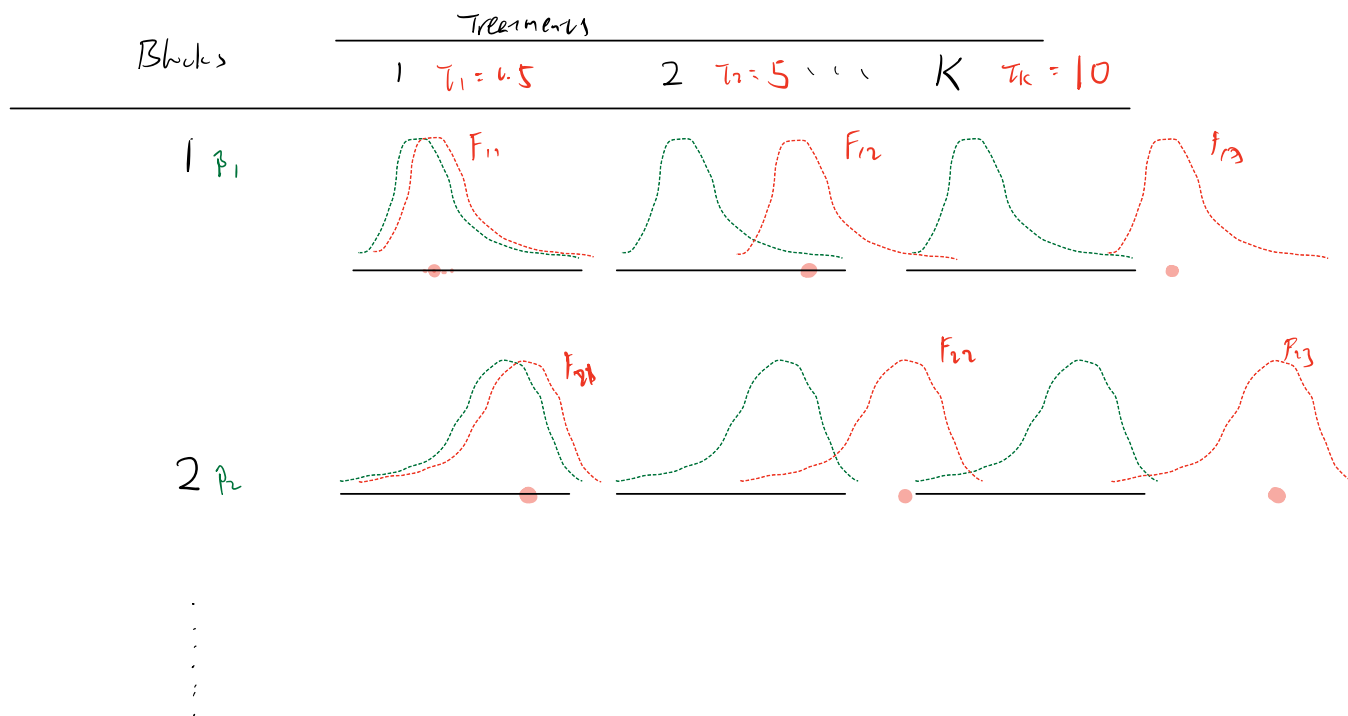
F_{i1}, \dots, F_{ik} within block i are the same; that is, $F_{i1} \equiv F_{i2} \equiv \dots \equiv F_{ik} \equiv F_i$, for each fixed $i=1, \dots, n$

$H_1 :$

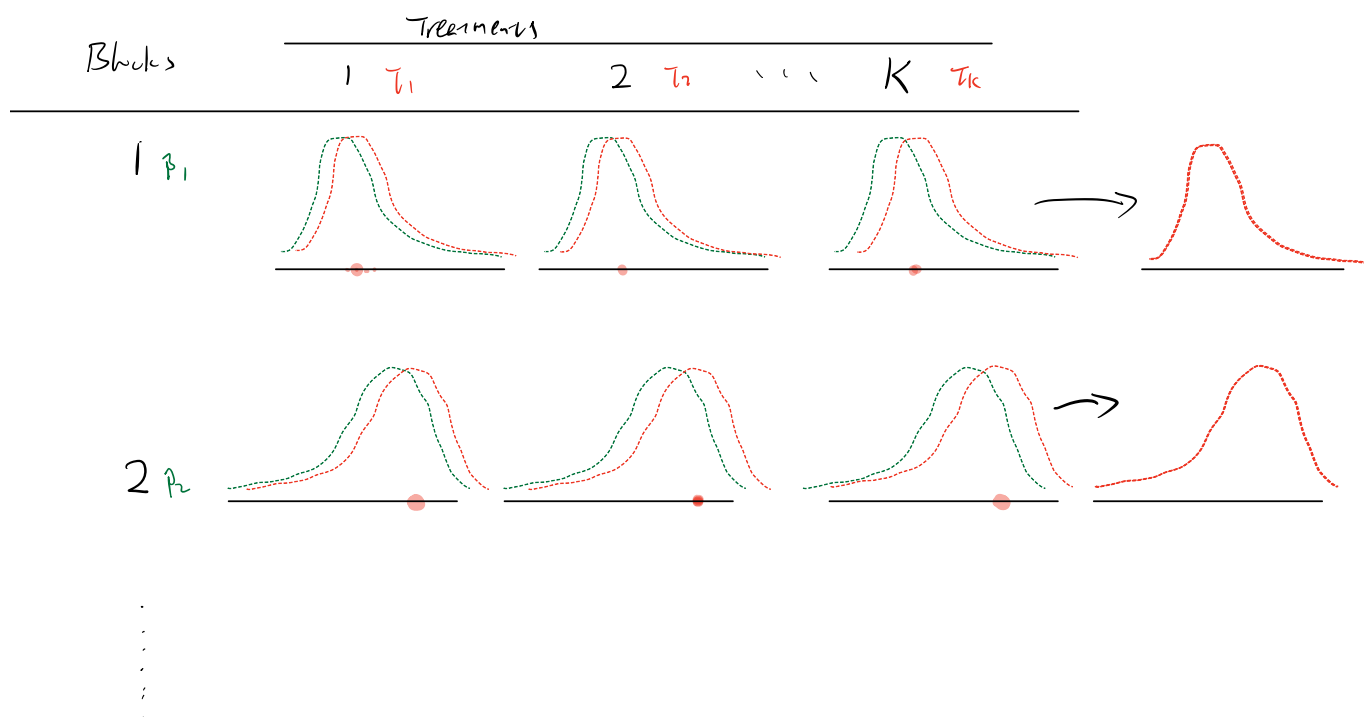
$\underbrace{\tau_1 \dots \tau_k \text{ not all equal}}$

at least two of the treatment effects are not equal

if $H_0: \tau_1 = \tau_2 = \dots = \tau_K \Rightarrow \text{True}$:



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



Motivation

Friedman (1937) idea: within-block rank sum

⇒ first order the k observations from least to greatest separately within each of the n blocks

⇒ Let r_{ij} denote the rank of X_{ij} in the joint ranking of the observations X_{i1}, \dots, X_{ik} in the i th block and set

$$R_j = \sum_{i=1}^n r_{ij} \quad \text{and} \quad R_{.j} = \frac{R_j}{n}.$$

Handwritten notes:
- Under R_j : \uparrow $\text{trt } j$
- Under the summation: $\text{sum of ranks associated with trt } j \text{ across blocks } i=1 \dots n$
- Above $R_{.j}$: \nwarrow $\text{average across blocks}$

Thus, for example, R_2 is the sum (over the n blocks) of the within-blocks ranks received by the treatment 2 observations and $R_{.2}$ is the average within-blocks rank for these same observations.

$$\boxed{1} \quad \boxed{2} \quad \dots \quad \boxed{k}$$

$$\frac{1}{k} \quad \frac{1}{k} \quad \dots \quad \frac{1}{k} \quad \sim \quad \frac{1}{k} (1 + 2 + \dots + k)$$

If null is true:

$$E_0(r_{ij}) = \frac{k+1}{2},$$

the average rank being assigned separately in each of the blocks. Thus, we have

$$E_0(R_{.j}) = E_0\left(\frac{1}{n}R_j\right) = \frac{1}{n}E_0\left(\sum_{i=1}^n r_{ij}\right) = \frac{1}{n}\sum_{i=1}^n E_0(r_{ij})$$

$$= \frac{n(k+1)}{2n} = \frac{k+1}{2}, \quad \text{for } j = 1, \dots, k,$$

“common value” if H_0 is true

and we would expect the $R_{.j}$'s to be close to $(k+1)/2$ when H_0 is true.

⇒ The Friedman statistic S^1 is then given by

~ similar to KW test

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

- small values of S 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, $(k+1)/2$, with some tending to be smaller and some larger. The net result (after squaring the observed differences to obtain the $[R_j - (k+1)/2]^2$ terms) would be a large value of S . This naturally suggests rejecting H_0 in favor of H_1 for large values of S .

¹The Friedman S statistic also arises naturally if we apply the usual two-way layout \mathcal{F} statistic to the ranks instead of the actual observations. Then S may be written as $S = [12/k(k+1)]$ SST, where SST is the treatment sum of squares applied to the ranks.

Derivation of null distribution using permutation

When H_0 is true, all possible $(k!)^n$ rank configurations for the r_{ij} 's are equally likely.

$$k=3. \quad n=3 \Rightarrow 9 \text{ obs}$$

$$3! \times 3! \times 3! = 6 \times 6 \times 6 = 216$$

$$k=4 \quad n=5$$

$$(4!)^5 = 24^5 \approx \text{huge} \dots$$

\Rightarrow impossible to do ...

Large sample approximation of null distribution

Let $T_j = R_{.j} - E_0(R_{.j}) = R_{.j} - (k + 1)/2$, for $j = 1, \dots, k$

\Rightarrow each $R_j = \sum_{i=1}^n r_{ij}/n$ is an average

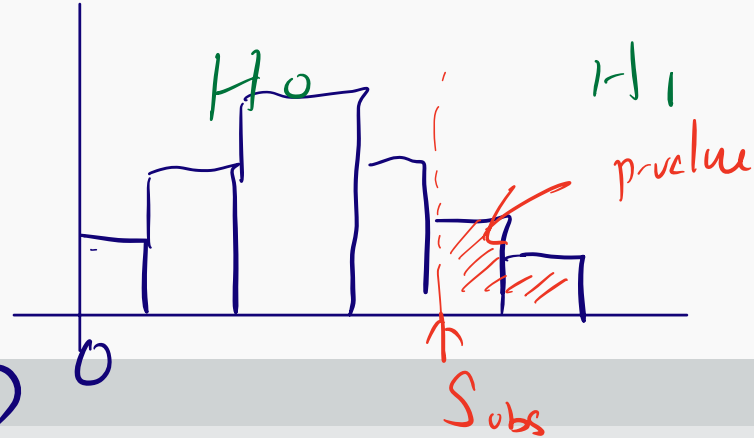
\Rightarrow properly standardized version of the vector $\mathbf{T}^* = (T_1, \dots, T_{k-1})$ has an asymptotic (n tending to infinity) $(k - 1)$ -variate normal distribution when the null hypothesis H_0 is true.

Since the test statistic S is a quadratic form of (T_1, \dots, T_{k-1}) , therefore, quite natural that S has an asymptotic (n tending to infinity) chi-square distribution with $k - 1$ degrees of freedom.

$$S \sim \chi_{k-1}^2$$

df: k-1

Procedure



Permutation (no preferential)

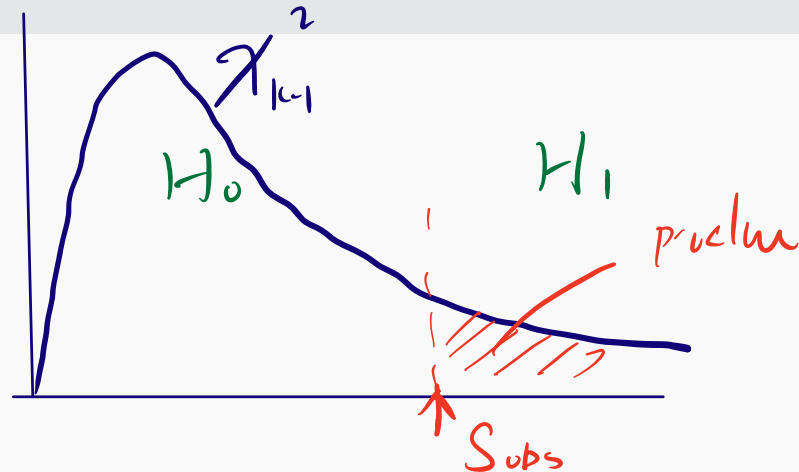
Reject H_0 if $S \geq s_\alpha$, otherwise do not reject

where s_α is the upper α percentile of the permutation null distribution.

Large-sample approximation

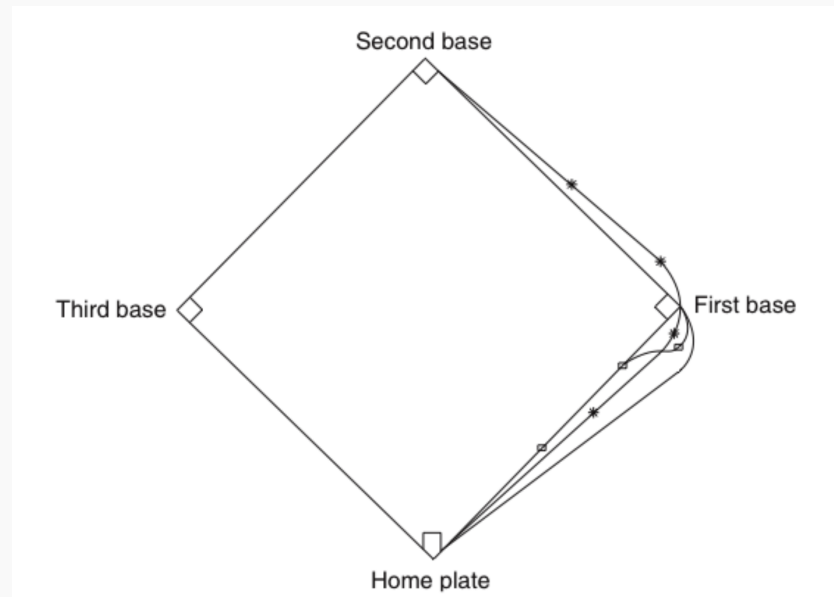
Reject H_0 if $S \geq \chi^2_{k-1, \alpha}$, otherwise do not reject

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



Example: Rounding First Base

Woodward (1970) in a study to determine which, if any, of three methods of rounding first base is best, in the sense that it minimizes, on the average, the time to reach second base. The three methods are "round out," "narrow angle," and "wide angle".



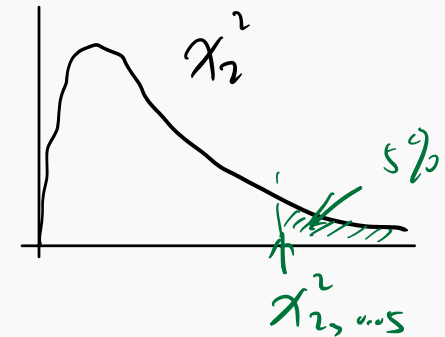
¹⁸
~~Twenty-two~~ baseball players participated in the study, and each of them ran from home plate to second base six times. Using a randomized order, these six trials per player were evenly divided (two each) among the three methods (round out, narrow angle, and wide angle). The entries are average times of the two runs per method. The within-blocks (players) ranks and the treatment (running method) rank sums (R_1 , R_2 , and R_3) are provided.

Players	Methods		
	Round out	Narrow angle	Wide Angle
1	5.40(1)	5.50(2)	5.55(3)
2	5.85(3)	5.70(1)	5.75(2)
3	5.20(1)	5.60(3)	5.50(2)
4	5.55(3)	5.50(2)	5.40(1)
5	5.90(3)	5.85(2)	5.70(1)
6	5.45(1)	5.55(2)	5.60(3)
7	5.45(2)	5.50(3)	5.35(1)
8	5.25(3)	5.15(2)	5.00(1)
9	5.85(3)	5.80(2)	5.70(1)
10	5.25(3)	5.20(2)	5.10(1)
11	5.65(3)	5.55(2)	5.45(1)
12	5.60(3)	5.35(1)	5.45(2)
13	5.05(3)	5.00(2)	4.95(1)
14	5.45(1)	5.55(3)	5.50(2)
15	5.45(1)	5.50(2)	5.55(3)
16	5.50(3)	5.45(2)	5.25(1)
17	5.65(3)	5.60(2)	5.40(1)
18	5.70(3)	5.65(2)	5.55(1)
	$R_1 = 43$	$R_2 = 37$	$R_3 = 28$

$$H_0: \tau_1 = \tau_2 = \tau_3$$

$$H_1: \tau_1, \tau_2, \tau_3 \text{ not all same}$$

$$\begin{aligned}
 S &= \frac{12}{nk(k+1)} \sum_{j=1}^k R_j^2 - 3n(k+1) \\
 &= \frac{12}{18 \times 3(4)} (43^2 + 37^2 + 28^2) - 3 \times 18(4) \\
 &= 6.33
 \end{aligned}$$



For the large-sample approximation, we compare the value of S to the chi-square distribution with $k - 1 = 2$ degrees of freedom.

```
> pchisq(6.33,df=2,lower.tail = F)
[1] 0.04221414
```

Hence, there is strong evidence here to reject the hypothesis that the methods are equivalent with respect to time to reach second base.

Check with built-in function: Agreed!

```
> RoundingTimes <- matrix(c(5.40, 5.50, 5.55,
+                           5.85, 5.70, 5.75,
+                           5.20, 5.60, 5.50,
+                           5.55, 5.50, 5.40,
+                           5.90, 5.85, 5.70,
+                           5.45, 5.55, 5.60,
+                           5.45, 5.50, 5.35,
+                           5.25, 5.15, 5.00,
+                           5.85, 5.80, 5.70,
+                           5.25, 5.20, 5.10,
+                           5.65, 5.55, 5.45,
+                           5.60, 5.35, 5.45,
+                           5.05, 5.00, 4.95,
+                           5.45, 5.55, 5.50,
+                           5.45, 5.50, 5.55,
+                           5.50, 5.45, 5.25,
+                           5.65, 5.60, 5.40,
+                           5.70, 5.65, 5.55),
+                          nrow = 18,
+                          byrow = TRUE,
+                          dimnames = list(1 : 18, c("Round Out", "Narrow Angle", "Wide Angle")))
>
> friedman.test(RoundingTimes)

Friedman rank sum test

data: RoundingTimes
Friedman chi-squared = 6.3333, df = 2, p-value =
0.04214
```