ORIGIN ≡ 1

Friedman Two-Way Analysis of Variance by Ranks Test

The Friedman Two-Way ANOVA by Ranks Test is the non-parametric analog to the One-Way Repeated Measures ANOVA design, or Randomized block ANOVA design. Both are Model III (Mixed Model) ANOVA in which treatments (A) are a fixed factor and individuals or block (B) are a random factor. The object here is to compare observations exactly matched across treatment classes for replicate individuals.

Data Structure:

k groups (treatments) exactly matched within individuals (objects). Typically, the order in which specific treatments are presented to individuals is randomized and exactly matched over the n replicates.

Let index i,j indicate the ith column (treatment class) and jth row (object). $X_{i,j}$ represents the rank or average rank of the treatment for each individual.

Friedman's Two-Way ANOVA by Ranks					
Individuals	Treatment Classes:				
(Replicates)	#1	#2	#3	…	#k
1					
2					
3					
…					
n	n	n	n		n
means:	X1bar	X2bar	X3bar	…	Xkbar

Assumptions:

- **The n Individuals or blocks represent a random sample.**
- **Underlying distribution of observations in treatment cells are continuous.**
- **Observations are of at least ordinal scale.**

Hypotheses:

H_0: Δ= 0   < No population differences in treatment

H_1: Δ ≠ 0   < Two Sided Test

Criterion for Approximation:

- **IF $n_i \geq 8$ THEN Approximation Applies OTHERWISE the test is conservative.**

Rank Data and Sum:

Zar Example 12.5:

a := 3

b := 5

i := 1 .. a

	tr1	Rtr1	tr2	Rtr2	tr3	Rtr3	
1	8.25	1	11.25	3	10.75	2	
2	11	1	12.5	3	11.75	2	
3	10.25	1	12	3	11.25	2	
4	9.5	2	9.75	3	9	1	
5	8.75	1	11	3	10	2	
	47.75		56.5		52.75		sum
		6		15		9	rank sum
		1.2		3		1.8	mean rank

$R := \begin{pmatrix} 6 \\ 15 \\ 9 \end{pmatrix}$ < rank sums
                from chart >

- **n = number of individuals (i.e., blocks), k = number of treatment classes**
- **Assign Data for treatment class to Ranks considering each individual (block) at a time. In the case of ties, t observations in a rank are assigned the appropriate average rank.**
- **Compute the Rank Sum (R_i) for each treatment class i.**

Test Statistic:

$$\chi r := \frac{12}{b \cdot a \cdot (a + 1)} \cdot \left[\sum_i \left(R_i \right)^2 \right] - 3 \cdot b \cdot (a + 1) \qquad\qquad \chi r = 8.4$$

< where R_i are the Rank sums for each treatment class i

IF no ties, THEN: $\chi := \chi r$ < uncorrected statistic

OTHERWISE:

correction factor for ties   > $$CF := 1 - \frac{\sum_{k=1}^{g} t_k}{b \cdot \left(a^3 - a \right)}$$

< t represent the number of observations that are tied in each tied group 1 to g

$$\chi rc := \frac{\chi r}{CF}$$

$\chi := \chi rc$ < corrected statistic

$\chi := \chi r$ $\chi = 8.4$ < no ties in this example

$$F_F := \frac{(b - 1) \cdot \chi r}{b \cdot (a - 1) - \chi r} \qquad\qquad F_F = 21$$

< alternative "generally preferred statistic" Zar Eq. 12.45 p. 279

Sampling Distribution of the Test Statistics χ & F_F:

If Assumptions hold and H_0 is true, then χ ~Friedman χ_r^2 table Zar 2010 Appendix B14

If Assumptions hold, H_0 is true, and Normal Approximation then $\chi \sim \chi^2_{(a-1)}$ or $F_F \sim F_{(a-1,(a-1)(b-1))}$

Critical Value of the Test:

$\alpha := 0.05$ < Probability of Type I error must be explicitly set

$C\chi 2r := 6.400$ < from Zar 2010 Table B14

$C\chi 2 := \text{qchisq}(1 - \alpha, a - 1)$ $C\chi 2 = 5.9915$ < χ^2 approximation when b>14 at α=0.05 or b>22 at α=0.01

$C_F := \text{qF}\left[1 - \alpha, a - 1, (a - 1) \cdot (b - 1) \right]$ $C_F = 4.459$ < using F_F statistic above

Decision Rules:

IF $\chi > C\chi 2r$ THEN REJECT H_0, OTHERWISE ACCEPT H_0 (exact table)

IF $\chi > C\chi 2$ THEN REJECT H_0, OTHERWISE ACCEPT H_0 (χ^2 approximation)

IF $F_F > C_F$ THEN REJECT H_0, OTHERWISE ACCEPT H_0 (alternative F_F statistic)

Probability Value:

$P\chi 2 := \left(1 - \text{pchisq}(\chi, a - 1) \right)$ $P\chi 2 = 0.015$

$P_F := 2 \cdot \left[1 - \text{pF}\left[F_F, a - 1, (a - 1) \cdot (b - 1) \right] \right]$ $P_F = 0.0013$

$a = 3$

$b = 5$

Prototype in R:

```
#FRIEDMAN'S TEST
#ZAR EXAMPLE 12.5
ZAR=read.table("c:/DATA/Biostatistics/ZarEX12.5R.txt")
ZAR
attach(ZAR)
X=eff
g=treatment
b=block

friedman.test(X,g,b)
```

```
        Friedman rank sum test

data:  X, g and b
Friedman chi-squared = 8.4, df = 2, p-value = 0.01500
```