

ORIGIN ≡ 1

### Kruskal-Wallis Test

The Kruskal-Wallis is a non-parametric analog to the One-Way ANOVA F-Test of means. It is useful when the k samples appear not to come from underlying Normal Distributions, or when variance in the different samples are of greatly different magnitudes (non-homogeneous). As with other rank-based tests, it does not have as much power as the fully parametric tests, but nevertheless enjoys wide use. Note that when the number of samples k=2, this test is identical to the Mann-Whitney Test.

#### Data Structure:

k groups with not necessarily the same numbers of observations and different means.

Let index i,j indicate the ith column (treatment class) and jth row (object).

One-Way ANOVA					
	Treatment Classes:				
Objects (Replicates)	#1	#2	#3	...	#k
1					
2					
3					
...					
n	n1	n2	n3		nk
means:	X1bar	X2bar	X3bar	...	Xkbar

#### Assumptions:

- Observations in each class(block) are a random sample.
- Observations in each block are independent of observations in other class.
- Underlying distribution of observations in each cell are continuous.
- Measurement scale is at least ordinal.

#### Zar Example 10.10

#### Hypotheses:

$H_0: \Delta = 0$  < No population differences

$H_1: \Delta \neq 0$  < Two Sided Test

	number	loc	rank	RankSum
4	8.2	1	10	
3	9.6	1	12	
5	10.2	1	13	
2	12.1	1	14	
1	14	1	15	64
7	5.1	2	2	
8	5.5	2	4	
10	6.3	2	6	
9	6.6	2	7	
6	8.4	2	11	30
14	4.1	3	1	
15	5.4	3	3	
13	5.8	3	5	
11	6.9	3	8	
12	7.3	3	9	26

#### Criterion for Normal Approximation:

IF  $n_i \geq 5$  THEN Normal Approximation Applies

OTHERWISE use Special Tables e.g. Rosner Table 15 p. 844

**Normal Approximation:**

**Rank Data and Sum:**

- Pool the data over all treatment classes - Total sample size  $N = \sum n_i$
- Assign Data to Ranks. 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  $i$ .

$N := 15$	$k := 3$
$R_1 := 64$	$n_1 := 5$
$R_2 := 30$	$n_2 := 5$
$R_3 := 26$	$n_3 := 5$

**Test Statistic:**

$i := 1..3$

$$H_s := \frac{12}{N \cdot (N + 1)} \cdot \sum_i \frac{(R_i)^2}{n_i} - 3 \cdot (N + 1) \quad < \text{where } R_i \text{ are the Rank sums for each treatment class } i$$

$H_s = 8.72$

**IF no ties, THEN:**  $H := H_s$  **< no correction factor in this case...**

**OTHERWISE:**

$m := 0$

$$\text{correction factor } > \quad \Omega := 1 - \frac{\sum_{j=1}^m [(t_j)^3 - t_j]}{N^3 - N} \quad < t \text{ represent the number of observations that are tied in groups 1 to } g$$

$H_x := \frac{H_s}{\Omega}$  **< Corrected Test Statistic**

**Sampling Distribution of the Test Statistic H:**

If Assumptions hold,  $H_0$  is true, and assuming Normal Approximation then  $H \sim \chi^2_{(k-1)}$

**Critical Value of the Test:**

**< Probability of Type I Error must be explicitly set**

$\alpha := 0.05$

$C := qchisq(1 - \alpha, k - 1)$   $C = 5.9915$  **< Normal approximation** **< Note: df = (k-1)**

$C := 5.780$  **< Critical Value from Zar Appendix B-13**

**Decision Rule:**

**IF  $H > C$  THEN REJECT  $H_0$  OTHERWISE ACCEPT  $H_0$**

$H = 8.72$

**Probability Value:**

$P := (1 - pchisq(H, k - 1))$   $P = 0.0128$  **< Normal approximation**

**Zar Example 10.11****Hypotheses:** $H_0: \Delta = 0$  < No population differences $H_1: \Delta \neq 0$  < **Two Sided Test**

pH	pond	rank	RankSum	n
7.68	1	1		
7.69	1	2		
7.7	1	3.5		
7.7	1	3.5		
7.72	1	8		
7.73	1	10		
7.73	1	10		
7.76	1	17	55	8
7.71	2	6		
7.73	2	10		
7.74	2	13.5		
7.74	2	13.5		
7.78	2	20		
7.78	2	20		
7.8	2	23.5		
7.81	2	26	132.5	8
7.74	3	13.5		
7.75	3	16		
7.77	3	18		
7.78	3	20		
7.8	3	23.5		
7.81	3	26		
7.84	3	28	145	7
7.71	4	6		
7.71	4	6		
7.74	4	13.5		
7.79	4	22		
7.81	4	26		
7.85	4	29		
7.87	4	30		
7.91	4	31	163.5	8

**Criterion for Normal Approximation:**- IF  $n_i \geq 5$  THEN Normal Approximation Applies

OTHERWISE use Special Tables e.g. Rosner Table 15 p. 844

**Normal Approximation:**

**Rank Data and Sum:**

- Pool the data over all treatment classes - Total sample size  $N = \sum n_i$
- Assign Data to Ranks. 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  $i$ .

$k := 4$

$$R := \begin{pmatrix} 55 \\ 132.5 \\ 145 \\ 163.5 \end{pmatrix} \quad n := \begin{pmatrix} 8 \\ 8 \\ 7 \\ 8 \end{pmatrix} \quad N := \sum n \quad N = 31$$

**Test Statistic:**

$i := 1 \dots k$

$$H_s := \frac{12}{N \cdot (N + 1)} \cdot \sum_i \frac{(R_i)^2}{n_i} - 3 \cdot (N + 1) \quad \text{< where } R_i \text{ are the Rank sums for each treatment class } i$$

$H_s = 11.8761$

**IF no ties, THEN:**  $H_x := H_s$  < no correction factor..

**OTHERWISE:**

$m := 7$

$$t := \begin{pmatrix} 2 \\ 3 \\ 3 \\ 4 \\ 3 \\ 2 \\ 3 \end{pmatrix} \quad \text{< } t \text{ represent the number of tied observations in each of the } m \text{ groups of tied ranks}$$

correction factor >  $\Omega := 1 - \frac{\sum_{j=1}^m [(t_j)^3 - t_j]}{N^3 - N} \quad \Omega = 0.9944$

$H := \frac{H_s}{\Omega} \quad H = 11.9435$  < Corrected Test Statistic in this case

**Distribution of the Test Statistic H:**

If  $H_0$  is true and assuming Normal Approximation then  $H \sim \chi^2_{(k-1)}$

**Critical Value of the Test:**

< Probability of Type I Error must be explicitly set

$\alpha := 0.05$

$C := qchisq(1 - \alpha, k - 1) \quad C = 7.8147$  < Normal approximation < Note: df = (k-1)

**Decision Rule:**

**IF  $H > C$  THEN REJECT  $H_0$  OTHERWISE ACCEPT  $H_0$**

**Probability Value:**

$P := (1 - \text{pchisq}(H, k - 1))$        $P = 0.0076$       **< Normal approximation**

**Prototype in R:**

```
#KRUSKAL-WALLIS TEST  
#ZAR EXAMPLE 10.10  
ZAR=read.table("c:/DATA/Biostatistics/ZarEX10.10R.txt")  
ZAR  
attach(ZAR)  
kruskal.test(number,loc)
```

Kruskal-Wallis rank sum test

data: number and loc  
Kruskal-Wallis chi-squared = 8.72, df = 2, p-value = 0.01278

```
#ZAR EXAMPLE 10.11  
ZAR=read.table("c:/DATA/Biostatistics/ZarEX10.11R.txt")  
ZAR  
attach(ZAR)  
kruskal.test(pH,pond)
```

Kruskal-Wallis rank sum test

data: pH and pond  
Kruskal-Wallis chi-squared = 11.9435, df = 3, p-value = 0.007579