ORIGIN ≡ 1

Cochran's Q Test for for nominal scale data in
Randomized Blocks or Repeated Measures Designs

Cochran's Q Test is a non-parametric analog to the Repeated Measures ANOVA design, or Randomized Block ANOVA design. Both designs are Model III (Mixed Model) ANOVA in which treatments (A) are a fixed factor and individuals or blocks (B) are a random factor. As with Friedman's Test, the object is to compare observations exactly matched across treatment classes for replicate individuals or blocks. However, the data in this case are dichotomous nominal classes that may be arbitrarily labeled "0" or "1". If the number of treatment classes (a) = 2, this test is identical to McNemar's Test except for the latter's correction for continuity.

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 outcome of thetreatment for each individual in terms of only zero or one.

Cochran's Q Test for Nominal data					
	Treatment Classes:				
Individuals (Replicates)	**#1**	**#2**	**#3**	**…**	**#k**
1	"0" or "1"	"0" or "1"	"0" or "1"		"0" or "1"
2	"0" or "1"	"0" or "1"	"0" or "1"		"0" or "1"
3	"0" or "1"	"0" or "1"	"0" or "1"		"0" or "1"
…	"0" or "1"	"0" or "1"	"0" or "1"		"0" or "1"
n	**n**	**n**	**n**		**n**
means:	**X1bar**	**X2bar**	**X3bar**	**…**	**Xkbar**

Assumptions:

- The n Individuals or blocks represent a random sample.
- Observations are nominal scale.

Zar Example 12.6:

Hypotheses:

H_0: Δ = 0   < No population differences in treatment
H_1: Δ ≠ 0   < **Two Sided Test**

	lilo	liti	dklo	dkst	none	Totals
1	0	0	0	1	0	1
2	1	1	1	1	1	
3	0	0	0	1	1	2
4	1	1	0	1	0	3
5	0	1	1	1	1	4
6	0	1	0	0	1	2
7	0	0	1	1	1	3
8	0	0	1	1	0	2
totals	1	3	3	6	4	

Criterion for Approximation:

where: a = number of treatment classes
           b = number of individuals or individuals (blocks)

IF a > 3 and b·a > 23 THEN Approximation holds, OTHERWISE use special tables.

a := 5
             < approximation holds
b := 7

^ one discards individuals (blocks) with all "0" or all "1"
   - One block deleted here.

Group and Block Counts:

$$G := \begin{pmatrix} 1 \\ 3 \\ 3 \\ 6 \\ 4 \end{pmatrix}$$ **< group counts**

$$B := \begin{pmatrix} 1 \\ 2 \\ 3 \\ 4 \\ 2 \\ 3 \\ 2 \end{pmatrix}$$ **< block counts**

Test Statistic:

$a = 5$

$b = 7$

$$Q := \frac{(a-1) \cdot \left[\sum\limits_{i=1}^{a} \left(G_i\right)^2 - \frac{\left(\sum\limits_{i=1}^{a} G_i\right)^2}{a} \right]}{\sum\limits_{j=1}^{b} B_j - \frac{\sum\limits_{j=1}^{b} \left(B_j\right)^2}{a}}$$

$Q = 6.9474$

Sampling Distribution of the Test Statistic Q:

If Assumptions hold, H_0 is true, and given approximation above, then $Q \sim \chi^2_{(a-1)}$

Critical Value of the Test:

$\alpha := 0.05$ **< type I error rate must be set**

$C := qchisq(1 - \alpha, a - 1)$ $C = 9.4877$

Decision Rule:

IF Q > C THEN REJECT H_0, OTHERWISE ACCEPT H_0

Probability Value:

$P := (1 - pchisq(Q, a - 1))$ $P = 0.1387$

Prototype in R:

```
#COCHRAN'S Q TEST
#ZAR EXAMPLE 12.6
ZAR=read.table("c:/DATA/Biostatistics/ZarEX12.6R.txt")
ZAR
attach(ZAR)
X=score
tr=treatment
b=block
?mantelhaen.test

mantelhaen.test(X,tr,b)
```

                         Cochran-Mantel-Haenszel test

                    data: X and tr and b
                    Cochran-Mantel-Haenszel M^2 = 6.9474, df = 4, p-value = 0.1387

Note: this test is called the "Cochran-Mantel-Haenszel" Test in R.