Biostatistics 470

 $ORIGIN \equiv 1$

McNemar's Test for Paired Data

This test employs a 2X2 contingency table in which pairs of observations such as in treatments of "before" versus "after" observations are exactly paired for individuals within a study. Analogy with the paired t-test situation is evident, although here each variable involves categorical (nominal) data classes.

Assumptions:

- Paired exactly matched observations are made.
- X & Y refer to paired dependent observations

Model:

Interpret diagonal cells of paired observations as:

- concordant - in agreement in result between X & Y

- discordant not in agreement in result in two types:
 Type A (+,-) and Type B (-,+) definition arbitrary
- Let p be the probability of the Type A discordant result

Construct Contingency Tables of Concordant and Discordant cells:

- Tabulate paired O_{ii} for each cell
- Calculate n_D = total number of discordant pairs
- Calculate n_A = number of Type A discordant pairs

n := 50	
$n_A := 5$	< discordant cases (it doesn't matter
n _B := 11	which is assigned n _A vs n _B)
$n_{D} := 5 + 11$	$n_D = 16$ < total discordant cases

Hypotheses:

H₀: p = 1/2 < Discordant Type A and Type B results are equally probable There is no difference between treatments or between "before" and "after"

 $H_1: p \Leftrightarrow 1/2 < Two sided test$

Criterion for Normal Approximation:

- IF number of discordant pairs $n_D \geq 20$ THEN Normal approximation may be used OTHERWISE use Exact Test

 $n_D = 16$ < exact test is called for

Normal Approximation:

Test Statistic:

$$\chi := \frac{\left(n_{\rm A} - n_{\rm B}\right)^2}{n_{\rm D}} \qquad \qquad \chi = 2.25$$

Paired Conti		
Concordant	Discordant Type A	X=1
Discordant Type B	Concordant	X=2
Y=1	Y=2	Grand Total

1

	Lo		
Loc B	relief	norelief	total
relief	12	5	17
norelief	11	22	33
total	23	27	50

Zar Example 24.23

Test Statistic (Corrected for Continuity):

$$\chi_{\rm C} \coloneqq \frac{\left(\left| n_{\rm A} - \frac{n_{\rm D}}{2} \right| - \frac{1}{2} \right)^2}{\left(\frac{n_{\rm D}}{4} \right)} \qquad \qquad \chi_{\rm C} = 1.5625$$

Sampling Distribution of χ and χ_C :

If Assumptions hold and $H^{}_0$ is true then χ and $\chi^{}_C \sim \!\! \chi^2_{(1)}$

Critical Value of the Test:

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

 $CV := qchisq(1 - \alpha, 1)$ CV = 3.8415

Decision Rule:

IF χ > CV THEN REJECT H ₀ , OTHERWISE	ACCEPT H ₀
IF $\chi_{C} > CV$ THEN REJECT H ₀ , OTHERWISE	ACCEPT H ₀

Probability Value:

$P_{\chi} := (1 - pchisq(\chi, 1))$	$P_{\chi} = 0.133614$
$P_{C} := (1 - pchisq(\chi_{C}, 1))$	$P_{C} = 0.2113$

Exact Test:

Probability Values:

IF
$$\mathbf{n}_{A} < \mathbf{n}_{D}/2$$
:
 $P_{A} := 2 \cdot \sum_{k=0}^{n_{A}} \operatorname{combin}(n_{D}, k) \cdot \left(\frac{1}{2}\right)^{n_{D}}$
 $P_{A} = 0.210114$

 h this case applies
IF $\mathbf{n}_{A} > \mathbf{n}_{D}/2$:
 $P_{B} := 2 \cdot \sum_{k=n_{A}}^{n_{D}} \operatorname{combin}(n_{D}, k) \cdot \left(\frac{1}{2}\right)^{n_{D}}$
 $P_{B} = 1.923187$
IF $\mathbf{n}_{A} = \mathbf{n}_{D}/2$:
 $P_{C} := 1$

Prototype in R:

```
#McNEMAR'S TEST
#ZAR EXAMPLE 24.23 2x2 CASE
```

```
X=matrix(c(12,5,11,22),nrow=2,byrow=T)
X
```

mcnemar.test(X,correct=F) #without continuity correction

McNemar's Chi-squared test

data: X McNemar's chi-squared = 2.25, df = 1, p-value = 0.1336

mcnemar.test(X,correct=T) #with continuity correction

McNemar's Chi-squared test with continuity correction

data: X McNemar's chi-squared = 1.5625, df = 1, p-value = 0.2113

^ Note: it's clear from the values reported that R's mcnemar.test() uses the Normal Approximation.

Extension to Higher-Order Tables:

McNemar's test may be extended to 3X3 or higher square tables by expanding the test statistic to include the sum of values obtained from all possible pairs of 2X2 tables. If necessary, the number of all possible 2X2 tables may be calculated by using combinations.

Assumptions:

- Paired exactly matched observations are made.
- X & Y refer to paired dependent observations

Model:

Interpret diagonal cells of paired observations as:

- concordant in agreement in result between X & Y
- discordant not in agreement in result in two types:
 - Type A (+,-) and Type B (-,+) definition arbitrary
- Let p be the probability of the Type A discordant result

Construct Contingency Tables of Concordant and Discordant cells:

- Tabulate paired O_{ii} for each cell
- Calculate n_D = total number of discordant pairs
- Calculate n_A = number of Type A discordant pairs

$$n_A := \begin{pmatrix} 20\\ 7\\ 2 \end{pmatrix}$$
 < discordant A cases

< Note: it doesn't matter which is assigned $n_A vs n_B$

$$n_{\rm B} := \begin{pmatrix} 15\\5\\3 \end{pmatrix} < \text{discordant B cases}$$
$$n_{\rm D} := \begin{pmatrix} 20+15\\7+5\\2+3 \end{pmatrix} \qquad n_{\rm D} = \begin{pmatrix} 35\\12\\5 \end{pmatrix}$$

< number of rows

	Fath			
Son's Religion	protestent	catholic	jewish	total
protestant	173	20	7	200
catholic	15	51	2	68
jewish	5	3	24	268
total	193	74	33	300

Hypotheses:

r := 3

H₀: p = 1/2 < Discordant Type A and Type B results are equally probable There is no difference between treatments or between "before" and "after"

 $H_1: p \Leftrightarrow 1/2 < Two sided test$

Criterion for Normal Approximation:

- IF number of discordant pairs $n_D \geq 20$ THEN Normal approximation may be used OTHERWISE use Exact Test

 $n_{D} = \begin{pmatrix} 35\\12\\5 \end{pmatrix}$

< Normal Approximation is sufficient

Normal Approximation:

Test Statistic:

i := 1..3 $\chi := \sum_{i} \frac{\left(n_{A_{i}} - n_{B_{i}}\right)^{2}}{n_{D_{i}}}$ $\chi = 1.24762$

Sampling Distribution of χ:

If Assumptions hold and H_0 is true then χ and $\chi_C \sim \chi^2_{(r(r-1)/2)}$ where r is the number of rows

Critical Value of the Test:

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

$$df := \frac{r \cdot (r-1)}{2} \qquad df = 3$$

 $CV := qchisq(1 - \alpha, df)$ CV = 7.8147

Decision Rule:

IF $\chi > CV$ THEN REJECT H₀, OTHERWISE ACCEPT H₀

Probability Value:

 $P_{\chi} := (1 - pchisq(\chi, df))$ $P_{\chi} = 0.741607$

Prototype in R:

```
#ZAR EXAMPLE 24.26 3x3 CASE
Y=matrix(c(173,20,7,15,51,2,5,3,24),nrow=3,byrow=T)
Y
```

mcnemar.test(Y,correct=F)

McNemar's Chi-squared test

data: Y McNemar's chi-squared = 1.2476, df = 3, p-value = 0.7416