McNemar's test

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In statistics, **McNemar's test** is a non-parametric method used on nominal data. It is applied to 2 × 2 contingency tables with a dichotomous trait, with matched pairs of subjects, to determine whether the row and column marginal frequencies are equal ("marginal homogeneity"). It is named after Quinn McNemar, who introduced it in 1947[1]. A celebrated application of the test in genetics is the Transmission disequilibrium test for detecting genetic linkage.[2]

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Definition [edit]

The test is applied to a 2 × 2 contingency table, which tabulates the outcomes of two tests on a sample of *n* subjects, as follows.

	Test 2 positive	Test 2 negative	Row total
Test 1 positive	*a*	*b*	*a* + *b*
Test 1 negative	*c*	*d*	*c* + *d*
Column total	*a* + *c*	*b* + *d*	*n*

The null hypothesis of marginal homogeneity states that the two marginal totals for each outcome are the same, i.e. $a + b = a + c$ and $c + d = b + d$. Thus the null hypothesis is that $b = c$.[1]

The McNemar test statistic with a continuity correction is given by:[3]

$$\chi^2 = \frac{(|b - c| - 1)^2}{b + c}.$$

Under the null hypothesis, with a sufficiently large number of discordants, χ^2 has a chi-squared distribution with 1 degree of freedom. If *b* and/or *c* are small ($b + c < 20$) then χ^2 is not approximated by the chi-square distribution and a sign test should be used instead.[*citation needed*]

If the χ^2 result is significant, this provides sufficienct evidence to reject the null hypothesis, in favour of the alternative hypothesis that $b \neq c$, which would mean that the marginal proportions are significantly different from each other.

Example [edit]

In the following example, a researcher attempts to determine if a drug has an effect on a particular disease. Counts of individuals are given in the table, with the diagnosis (disease: *present* or *absent*) before treatment given in the rows, and the diagnosis after treatment in the columns. The test requires the same subjects to be included in the before- and after measurements (matched pairs).

	After: present	**After:** absent	Row total
Before: present	101	121	222
Before: absent	59	33	92
Column total	160	154	314

In this example, the null hypothesis of "marginal homogeneity" would mean there was no effect of the treatment. From the above data, the McNemar test statistic

$$\chi^2 = \frac{(|121 - 59| - 1)^2}{121 + 59}$$

has the value 20.67, which is extremely unlikely from the distribution implied by the null hypothesis. Thus the test provides strong evidence to reject the null hypothesis of no treatment effect.

Discussion [edit]

An interesting observation when interpreting McNemar's test is that the elements of the main diagonal contribute no information whatsoever to the decision if (in the above example) pre- or post-treatment condition is more favourable.[*citation needed*]

An extension of McNemar's test exists in situations where independence does not necessarily hold between the pairs; instead, there are clusters of paired data where the pairs in a cluster may not be independent, but independence holds between different clusters.[*citation needed*] An example is analyzing the effectiveness of a dental procedure; in this case, a pair corresponds to the treatment of an individual tooth in patients who might have multiple teeth treated; the effectiveness of treatment of two teeth in the same patient is not likely to be independent, but the treatment of two teeth in different patients is more likely to be independent.[4]

Related tests [edit]

- The Cochran test is a generalization that allows for more than two row and/or column categories.
- The Liddell's exact test is an exact alternative to McNemar's test.[5][6]
- The Stuart-Maxwell's test is different generalization of the McNemar test, used for testing marginal homogeneity in a square table with more than two rows/columns.[7]
- The Bhapkar's test (1966) is a more powerful alternative to the Stuart-Maxwell test.[8]

See also [edit]

- Pearson's chi-square test

References [edit]

1. ^ a b McNemar, Quinn (1947-06-18). "Note on the sampling error of the difference between correlated proportions or percentages". *Psychometrika* **12** (2): 153–157. doi:10.1007/BF02295996.
2. ^ Spielman RS, McGinnis RE, Ewens WJ (Mar 1993). "Transmission test for linkage disequilibrium: the insulin gene region and insulin-dependent diabetes mellitus (IDDM)" . *Am J Hum Genet.* **52** (3): 506–16. PMID 8447318.
3. ^ Fleiss, J. L. (1981). *Statistical methods for rates and proportions* (2nd ed.). New York: John Wiley. p. 114. ISBN 0-471-06428-9.
4. ^ Durkalski, V.L.; Palesch, Y.Y.; Lipsitz, S.R.; Rust, P.F. (2003), "Analysis of clustered matched-pair data", *Statistics in medicine* **22** (15), retrieved 2009-04-01
5. ^ http://www.jstor.org/stable/2988087
6. ^ http://rimarcik.com/en/navigator/z-nominal.html
7. ^ Sun, Xuezheng; Yang, Zhao (2008). "Generalized McNemar's Test for Homogeneity of the Marginal Distributions". SAS Global Forum.
8. ^ http://www.john-uebersax.com/stat/mcnemar.htm#bhapkar

- Sheskin, David (2004). "Test 20, the McNemar Test". *Handbook of parametric and nonparametric statistical procedures*. CRC Press. pp. 1193. ISBN 1584884401.

External links [edit]

- Vassar College's McNemar 2×2 Grid
- McNemar Tests of Marginal Homogeneity

Categories: Statistical tests | Categorical data | Non-parametric statistics