Alternative Approaches to the Analysis of Multidimensional Contingency Tables

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Abstract

The practical analyses of interactions between categorical variables in various areas (such as public opinion research or marketing research) are often only applications of chi-square tests in two-way contingency tables. However, in many situations it is impossible to use large-sample approximations to sampling distributions when their adequacy can be in doubt. It is known, that these approximations may be very poor when the contingency table contains very small expected frequencies. However, recent work has shown that these approximations can be very poor when the contingency table contains both small and large expected frequencies. Of course, the rule of thumb of a minimum expected frequency is not met either in the case of sparse table. The article deals with alternative approaches to the data analysis in such cases. It points out other possibilities and shows that thanks to the development of computer technology exact methods previously only difficult usable are available for this purpose.

Keywords	*JEL code*
Contingency tables, categorical data analysis, exact inference about associations	*C39*

INTRODUCTION

Using data drawn from the population concerned via certain form of random sampling, the statistical inference makes propositions about this population, about its underlying probability model. Categorical variables have a measurement scale consisting of a small set of discrete categories. The discrete probability distributions (particularly binomial, multinomial and Poisson ones) have then the key importance for statistical inference in categorical data analysis. Given a sufficiently large sample size, the discrete distributions of test statistics converge to normal distribution or chi-square one. It is known, that the sample size must be large enough to use the continuous approximations.

When the assumptions of the asymptotic method cannot be met and the validity of the corresponding large sample theory is doubtful, the results can be unreliable. Sometimes the data file can be small, sparse, unbalanced. However, recent work has shown that these approximations may not be optimal even in cases of a relatively large sample size. In all such cases procedures based on exact distribution of the test statistics should be applied.

The distribution of discrete test statistics under the independence hypothesis can be obtained by calculating all its possible values under rearrangements of data. The statistical methodology underlying these

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exact tests (also called permutation tests or randomization tests) exists already some time and is included into numerous statistical papers, monographs and textbooks. R. A. Fisher is known to be "a father" of exact methods for small samples: his well-known example with milk in tea for 2 × 2 contingency tables is mentioned in almost every statistical resource in this area.

Fisher's exact approach is conditional. To conduct exact inference about an association, or about the odds ratio in 2 × 2 table, the conditional distribution of one cell frequency given the sample size and the corresponding marginal totals is considered. The use of this conditional approach is still intensively discussed, particularly when both types of marginal totals in the table are not fixed naturally. However, it can be said that Fisher's approach dominates. In addition, it can be relatively easily expanded for larger tables, which is questionable for other proposed methods.

The computational demands of exact methods, especially in larger tables, can be severe, since all the outcomes that could occur must be enumerated to compute the *P*-value of an exact test. The actually observed data are compared to what might have been observed. Mehta and Patel (1996) present for example, that the set of all possible 5 × 6 contingency tables with relatively small marginal frequencies ($n = 34$) contains 1.6 billion tables. Thus practical applications of exact methods had to wait for development of computers and especially for new, fast and efficient computational algorithms.

According to Mehta and Patel, the *P*-value for independence tests in two-way contingency tables can be computed quickly only if min (r, c) ≤ 3, r is number of rows and c is number of columns in the table, and the sample size is relatively small. In larger tables the computational algorithm can take even many hours. In such case any repeated sampling *(resampling)* method can provide an estimate very close to the exact result.

The resampling methods do not enumerate all possible outcomes, but a random sample of them. The estimate of the *P*-value is usually obtained as a proportion of these replicates that produce a test statistic greater or equal that calculated for the actual data in the number of all replicated samples. Thus the *P*-value estimate is unbiased, the standard error is also available and so the confidence interval can be assembled. In the case of large number of replications, the width of this interval can be very small (the accuracy from 10 000 random permutations is not more than 0.01). This type of resampling method is known as Monte Carlo or approximate permutation test.

1   TWO-DIMENSIONAL CONTINGENCY TABLES

Consider now a data sample of size *n*; the data are cross-classified into a contingency table with *r* rows and *c* columns. Most often the hypothesis of interest is whether an association exists between the two classifications in the table. To test the hypothesis of independence between two categorical variables, Pearson and likelihood-ratio chi-squared tests are well-known. The test statistics:

$$\chi^2 = \sum_i \sum_j \frac{(n_{ij} - m_{ij})^2}{m_{ij}}, \tag{1}$$

and

$$G^2 = -2 \sum_i \sum_j n_{ij} \ln \frac{n_{ij}}{m_{ij}}, \; i = 1, 2 \ldots, r; j = 1, 2 \ldots, c, \tag{2}$$

where n_{ij} denotes observed frequencies and m_{ij} estimated expected frequencies, $m_{ij} = n_{i+}n_{+j} / n$, have the same limiting null chi-squared distribution with $df = (r - 1)(c - 1)$ and are asymptotically equivalent. The adequacy of the chi-squared distribution depends both on the sample size and on the number of cells in the table. The condition of a minimum expected count of 1 and no more than 20 % of m_{ij} less than 5 is commonly used (in the 2 × 2 table, the expected frequencies should exceed 10).

However, the approximations can be poor in sparse tables, in tables with both small and large expected frequencies. Other findings concerning the quality of approximations can be found in many works; they are summarized for example in Agresti (2002): first of all, the statistic χ^2 is preferable than G^2 in sparser tables and in case of smaller n. When the sample size requirements for the chi-square tests are not met, Fisher's exact test is an alternative.

This test of independence in the 2×2 table assumes fixed row and column marginal frequencies. Then n_{11} (for example), which determines all other three cell counts, can be used as a test statistic. It follows the hypergeometric distribution and so the exact test P-value can be calculated. This P-value is the sum of hypergeometric probabilities for tables at least as favorable to the null hypothesis as the observed table. To order the tables according to this "favorableness", different criteria can be used: larger n_{11}, or larger odds ratio $\theta = n_{11} n_{22} / n_{12} n_{21}$, or larger Pearson statistic χ^2 (different criteria can lead to different P-values). Because of distribution discreteness, the test is highly conservative for small samples. Some authors then recommend involving in the test P-value only half probability for the observed table (so called *mid-P-value* — Agresti, 2002).

Freeman and Halton generalized the Fisher's test for the $r \times c$ contingency table. When the row totals n_{i+}, $i = 1, 2 \ldots, r$, and the column totals n_{+j}, $j = 1, 2 \ldots, c$, in the table are fixed, the simultaneous distribution of the set of n_{ij}, $i = 1, 2 \ldots, r - 1$ and $j = 1, 2 \ldots, c - 1$, is multiple hypergeometric. The test P-value includes the probability of tables with the given margins that are at least as favorable to the null hypothesis as the observed table. To order the tables, Pearson statistic is usually used; otherwise, when the classification variables are ordinal, for example the gamma statistic can be used for this purpose.

To analyze complicated associations in multidimensional contingency tables, the log-linear model as a generalized linear model using the log link function can be also useful. For the two-dimensional $r \times c$ contingency table, the *saturated* loglinear model (when $m_{ij} = n_{ij}$) has the form:

$$\ln m_{ij} = \lambda + \lambda_i^X + \lambda_j^Y + \lambda_{ij}^{XY}. \tag{3}$$

Here λ is a cell effect, λ_i^X are row effects, λ_j^Y are column effects and λ_{ij}^{XY} are association parameters that reflect deviations from independence. In the simplest case of the 2×2 table, when we consider dummy indicators with $\lambda_2^X = \lambda_2^Y = \lambda_{12}^{XY} = \lambda_{21}^{XY} = \lambda_{22}^{XY} = 0$, then:

$$\lambda_{11}^{XY} = \ln\theta = \ln \frac{n_{11} n_{22}}{n_{12} n_{21}}, \tag{4}$$

here θ denotes the odds ratio. Thus, the independence hypothesis for model (3) in 2×2 contingency tables can be written as $\lambda_{11}^{XY} = \ln\theta = 0$, or $\theta = 1$, or $\ln m_{ij} = \lambda + \lambda_i^X + \lambda_j^Y$ (the *tested* model).

In the $r \times c$ table, when we consider dummy indicators again and set:

$$\lambda_r^X = \lambda_c^Y = \lambda_{1c}^{XY} = \lambda_{2c}^{XY} = \ldots = \lambda_{r1}^{XY} = \lambda_{r2}^{XY} = \ldots \lambda_{rc}^{XY} = 0, \text{ then}$$

$$\lambda_{ij}^{XY} = \ln\theta_{ij} = \ln \frac{n_{ij} n_{rc}}{n_{ic} n_{rj}}, \tag{5}$$

$$i = 1, 2\ldots, r - 1; j = 1, 2\ldots, c - 1.$$

Test of independence states $\lambda_{ij}^{XY} = \ln\theta_{ij} = 0$ for these $(r - 1)(c - 1)$ association parameters.

2 MULTIDIMENSIONAL CONTINGENCY TABLES

The associations between variables in multidimensional contingency tables can be very complicated. The influence of other variables on an association can be confounding. The model can be qualified as very useful particularly in such situation.

In the case of three variables, the loglinear model can be written as:

$$\ln m_{ijk} = \lambda + \lambda_i^X + \lambda_j^Y + \lambda_k^Z + \lambda_{ij}^{XY} + \lambda_{ik}^{XZ} + \lambda_{jk}^{YZ} + \lambda_{ijk}^{XYZ},$$ (6)

$i = 1, 2\ldots, r; j = 1, 2\ldots, c; k = 1, 2 \ldots, s$ (s denotes the number of layers — or strata — in the table).

The model includes two-factor parameters $\lambda_{ij}^{XY}, \lambda_{ik}^{XZ}, \lambda_{jk}^{YZ}$ to describe the *conditional* association for each pair of variables given the third variable. In the $r \times c \times s$ table, when we consider dummy indicators, in general there are $(r-1)(c-1)$ non-null parameters λ_{ij}^{XY}, $(r-1)(s-1)$ non-null parameters λ_{ik}^{XZ}, $(c-1)(s-1)$ non-null parameters λ_{jk}^{YZ} and $(r-1)(c-1)(s-1)$ non-null parameters λ_{ijk}^{XYZ}. It represents $(r-1)(c-1)$ odds ratios (5) at each level of variable Z, $(r-1)(s-1)$ odds ratios at each level of variable Y and $(c-1)(s-1)$ odds ratios at each level of variable X. The three-factor interactions λ_{ijk}^{XYZ} then describe how the odds ratio between two variables changes across categories of the third variable. Any model not having the three-factor interaction term has a homogenous association for each pair of variables (see Agresti, 1999).

When the loglinear model includes all lower-order terms composed from variables contained in a high-order model term, the model is called hierarchical. For example, the hierarchical model with λ_{ij}^{XY} terms includes λ_i^X, λ_j^Y, the hierarchical model without λ_{ijk}^{XYZ} includes all two-factor parameters etc. The established symbols usually used for hierarchical loglinear models list the highest-order terms for each variable. Thus, the model with all the two-factor parameters but without three-factor parameters has a symbol (*XY, XZ, YZ*), the model with three-factor parameters a symbol (*XYZ*) etc.

The statistic G^2 written in (2) for a two-dimensional table is a special case of the likelihood-ratio statistic called *deviance*. In general, the deviance compares the maximum of the log likelihood for a tested model and the maximum achievable log likelihood for the most general model with the perfect fit of cell frequencies — saturated model. Simpler models have larger deviances, more complicated models smaller deviances. As can be shown, the likelihood statistic comparing the two models is simply the difference between their deviances. This statistic has also approximately chi-square distribution with degrees of freedom equal to the difference between the numbers of parameters in the two compared models.

Thus, the tests about conditional associations can be based on the comparison of the loglinear models without and with relevant parameters. For example, the hypothesis of the conditional independence between X and Y can be tested by:

$$G^2(XZ, YZ) - G^2(XY, XZ, YZ),$$ (7)

where $G^2(XZ, YZ)$ is the deviance of the model without tested parameters (here λ_{ij}^{XY}) and $G^2(XY, XZ, YZ)$ is the deviance of the model with these parameters. The difference between the numbers of parameters, $(r-1)(c-1)$ in this example, determines the parameter of chi-square distribution of the test statistic. According to Agresti (2002), for given n and a number of cells in the contingency table, chi-squared approximation is better for tests with smaller *df*. Of course, conditions of chi-square approximation should be met. The extension of the loglinear model for more than three classifications is straightforward.

Cochran-Mantel-Haenszel approach is an alternative to the above procedure. The conditional distribution of a cell frequency given the sample size and the corresponding marginal totals (the hypergeometric distribution) is considered in this method.

In the 2×2 table, Mantel-Haenszel (MH) statistic, so-called randomization chi-square statistic Q,

$$Q = \frac{(n_{11} - m_{11})^2}{v_{11}}, \; m_{11} = \frac{n_{1+}n_{+1}}{n}, \; v_{11} = \frac{n_{1+}n_{2+}n_{+1}n_{+2}}{n^2(n-1)} \, ,$$ (8)

has an asymptotic chi-square distribution with one degree of freedom. Then, in a set of s contingency tables 2×2 arising by sorting data by other variable (or by an combination of other variables), the MH statistic Q_{MH},

$$Q_{MH} = \frac{\left(\sum_k n_{11k} - \sum_k m_{11k}\right)^2}{\sum_k v_{11k}}, \tag{9}$$

$$m_{11k} = \frac{n_{1+k} n_{+1k}}{n_k}, \ v_{11k} = \frac{n_{1+k} n_{2+k} n_{+1k} n_{+2k}}{n_k^2 (n_k - 1)}, \ k = 1, 2 \ldots, s,$$

has approximately chi-square distribution with one degree of freedom when overall sample sizes are large (individual cell counts and table sizes may be relatively small).

According to Stokes, Davis and Koch (1995), Mantel and Fleiss proposed a criterion to determine whether the chi-square approximation is appropriate for the MH statistic (9):

$$\min \left\{ \left[\sum_k m_{11k} - \sum_k L_k \right], \left[\sum_k U_k - \sum_k m_{11k} \right] \right\}, \tag{10}$$

where $L_k = \max(0, n_{1+k} - n_{+2k})$, $U_k = \min(n_{+1k}, n_{1+k})$.

It should be noted, that W. Cochran proposed a statistic similar to (9), but he used the unconditional approach: he treated the rows in the table as independent binomials with corresponding variance. The difference of both approaches is small, (n_k^3 in the denominator of v_{11k}). Because of their basic similarity, the approach is usually referred to as Cochran-Mantel-Haenszel (CMH) approach. The continuity correction (−0.5) is sometimes used in the numerator of the CMH statistics (see Stokes, Davis, Koch, 1995).

For a tree-dimensional contingency table, or in the set of s contingency tables $r \times c$, denote as:

$$\mathbf{n}_k^T = [n_{11k}, n_{12k}, \ldots, n_{1,c-1,k} \ldots, n_{21k}, n_{22k}, \ldots, n_{2,c-1,k}, \ldots, n_{r-1,c-1,k}], k = 1, 2 \ldots, s,$$

the vector of $(r - 1)(c - 1)$ simultaneous frequencies in all s strata, denote as:

$$\mathbf{m}_k^T = [m_{11k}, m_{12k}, \ldots, m_{1,c-1,k} \ldots, m_{21k}, m_{22k}, \ldots, m_{2,c-1,k}, \ldots, m_{r-1,c-1,k}], k = 1, 2 \ldots, s,$$

$$m_{ijk} = n_{i+k} n_{+jk} / n_{++k}, \ i = 1, 2, \ldots, r - 1, \ j = 1, 2, \ldots, c - 1,$$

the vector of corresponding expected frequencies and denote as $\mathbf{C}_k$ the covariance matrix with elements:

$$C(n_{ijk}, n_{i'j'k}) = \frac{n_{i+k}(\delta_{ii'} n_{++k} - n_{i'+k}) n_{+jk}(\delta_{jj'} n_{++k} - n_{j'+k})}{n_{++k}^2 (n_{++k} - 1)},$$

where for $i = i' \ \delta_{ii'} = 1$, for $i \neq i' \ \delta_{ii'} = 0$
$\qquad j = j' \ \delta_{jj'} = 1$, for $j \neq j' \ \delta_{jj'} = 0$.

The MH statistic $Q_{MH} (YX.Z)$ can be then written (according to Pecáková, 2011 for example) as:

$$Q_{MH}(YX.Z) = (\mathbf{n} - \mathbf{m})^T \mathbf{C}^{-1} (\mathbf{n} - \mathbf{m}), \tag{11}$$

$$\mathbf{n} = \sum_k \mathbf{n}_k, \ \mathbf{m} = \sum_k \mathbf{m}_k, \ \mathbf{C} = \sum_k \mathbf{C}_k.$$

The distribution of this statistic is chi-square with $df = (r - 1)(c - 1)$. Sample size requirements are yet based on total frequencies, summed across tables, rather than individual cell quantities. However, the MH (CMH) test has low power in the case of associations of opposite patterns in various strata. (To test these circumstances, Breslow-Day test was developed; if it is insignificant, then MH test can be used successfully — see Pecáková, 2002).

Violations of the conditions of approximate methods in the multidimensional table can be very often expected, particularly when the number of classifications and also the number of categories of variables is large and the sample size disregards this fact. For use of the approximation strategy, the number of variables reduction can arise from combining of more classi-fications. For example, instead of two variables sex and age (with categories younger — older) we can use only one variable with four categories: younger male, younger female, older male, older female.

This is also the way how to test some parameters of loglinear models for multidimensional tables. Some methods of their exact testing are actually special cases of one's developed for a two-way table. The comparison of two hierarchical loglinear models, (X, YZ) and (XYZ) for example, actually represents a test of independence for a two-way $r \times cs$ table; the model (X, Y, Z) against (X, YZ) can be used to test the independence of Y and Z in the two-way table, etc. However, the exact algorithms are not still available for some types of loglinear models parameters, or there is not available their computational form for the use of Monte Carlo method.

3 ANALYSES

3.1 Analysis 1[2]

At first, consider data from Pecáková (2011) in the Table 1. Here X represents the variable Age (three age groups: until 35 years, 36–50 years, above 50 years), Y is the variable Sex and Z represents the variable Willingness (a willingness to switch to a new soft drink brand with categories: yes, no). The sample size n is 230.

Table 1 Willingness to switch to a new soft drink brand							
Age	**Bellow 35**		**36–50**		**Above 50**		
Sex	Female	Male	Female	Male	Female	Male	**Total**
Yes	45	28	3	24	3	21	124
No	25	5	14	25	14	23	106
Total	70	33	17	49	17	44	230

Source: Pecáková (2011)

Two-way analysis:

Willingness is associated with Age. The *P*-values of both chi-square tests are 0.000. However, Willingness is not associated with Sex. The *P*-values are 0.178. The expected values in the table are quite large, the chi-squared approximations are possible. For comparison, the *P*-value of the exact test is 0.187.

As we can see in the Table 1, some cell frequencies in the subtables acquired according to the levels of the variable Age are small. The conditions of chi-squared approximations are not met everywhere. The exact *P*-values of Fisher's test of association between Willingness and Sex in different age groups are consecutively 0.038, 0.043 and 0.042. Thus, the variables Willingness and Sex are associated in the subtables. Thus, the results of both analyses are in conflict. Is the influence of the variable Age confounding?

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[2] All the calculations were accomplished by using SPSS 18.0 and SAS Enterprise Guide 4.1; α = 0.05.

Three-way analysis:

The difference between the deviances for the loglinear models without and with the association parameter is 15.314 (*P*-value = 0.000) and the association of the variables Willingness and Sex is confirmed.

MH statistic on the value of 12.856 (or CMH statistic on the value of 14.158) exposes the association of Willingness and Sex (the *P*-value the test is 0.000). The procedure is suitable; Breslow-Day test of odd ratio homogeneity is insignificant.

3.2 Analysis 2

Now consider data in the Table 2. The variables are the same like in the Table 1. The sample size is small, $n = 72$.

Age	Bellow 35		36–50		Above 50		
Sex	Female	Male	Female	Male	Female	Male	Total
Yes	9	2	2	11	0	10	34
No	6	7	7	5	5	8	38
Total	15	9	9	16	5	18	72

Table 2 Willingness to switch to a new soft drink brand

Source: Own construction

Two-way analysis:

The table is sparse. The Willingness is not associated with Age (the *P*-values of the chi-square tests are about 0.830) and it is not associated with Sex again (the *P*-values of the chi-square test are about 0.195; the chi-squared approximations are possible, but the asymptotic tests are somewhat liberal: the *P*-value of the exact test is 0.234).

In all the subtables, only the exact test can be used. The exact *P*-values of Fisher's test of association between Willingness and Sex in different age groups are consecutively 0.105, 0.041 and 0.046. The sample sizes are quite small, so the exact tests are somewhat conservative now.

Three-way analysis:

The test of the three-factor interaction in the loglinear model is significant *P*-value 0.003): the odds ratio between two variables changes across categories of the third variable. However, further increase in deviance in the test of association between Willingness and Sex is not significant (however, chi-square approximation can be doubtful in this analysis).

The previous result is evident from the MH approach again: the MH statistic of 1.255 (or CMH statistic 1.962) is not significant in this case. According to the criterion (10), the chi-square approximation is appropriate for this test:

$$\sum_k L_k = 2 + 0 + 0 = 2,$$

$$\sum_k U_k = 11 + 9 + 5 = 25,$$

$$\sum_k m_{11k} = 6.9 + 4.7 + 2.2 = 13.8,$$

$$\min\{[13.8 - 2], [25 - 13.8]\} > 5.$$

However, the power of the test is small because of result of Breslow-Day test (*P*-value is 0.003).

3.3   Analysis 3

The data file[3] comes from a survey sampling of the interest in getting work in the EU. The file was used in Pecáková (2010). We examine associations between the variable Interest (the interest in getting work in EU) with values:

1 = "yes, will definitely or probably try",
2 = "would be interested if offered a job",
3 = "no, probably or definitely will not be interested",

the variable Income (the ordinal variable with seven income groups) and the variable Age (four age groups). The sample size is 1 203, but there are missing values in the sample. The disposable sample size for examined three variables is 862.

Two-way analysis:
In the 3 × 7 table for the variables Interest and Income there are no cells with expected frequencies less than 5. The variables Interest and Income are nearly associated; the *P*-values of the asymptotic tests are about 0.06.

The subtables in the classification according to the age groups are very sparse. To calculate the exact tests, Monte Carlo method with 10 000 samples was applied. The results of the exact tests are 0.251, 0.763, 0.047 and 0.752. Only in the third group are variables associated, the results of both analyses disagree, the marginal association might be only apparent.

Three-way analysis:
The test of the three-factor interaction in the loglinear model is not significant again; the *P*-value is 0.125; the chi-square approximation can be doubtful in this analysis again.

CMH statistic on the value of 17 851 is not significant (*P*-value = 0.120). However, it should be noted that marginal frequencies are not all sufficiently large and the chi-square approximation might be in question. The sample size is not very large for the tests in multidimensional classification.

CONCLUSION

Sorting data by multiple categorical variables almost always causes a problem of vacant and few occupied fields in the table. In such a case, the conditions for the use of approximate methods are not met. It is necessary to take into account this fact when considering the sample size.

Small, sparse or unbalanced data sets limit the usability of tests on the loglinear model parameters in the analysis of multidimensional contingency tables. The use of MH (CMH) strategy is potential. The distribution of MH (or CMH) statistic depends on marginal frequencies, not on cell frequencies in single sub-tables; the sub-tables can be relatively sparse.

The exact procedures should be used in the case of violation of the conditions of approximate methods. Computers and statistical software have recently enabled the use of some exact procedures to analyze multidimensional tables (SPSS or SAS for example). Some methods of exact testing of loglinear models parameters are actually special cases of one's developed for a two-way table. However, the exact algorithms are not still available for some types of loglinear models parameters. In addition, the exact methods are computationally very demanding and standard statistical software may fail. The solution may involve the use a resampling algorithm, such as Monte Carlo.

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[3]   The data provided the Czech Public Opinion Research Centre (CVVM) in 2006 for a students' school-leaving work.

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