

Analyzing asymmetry of two-wave two-variable panel data with generalized correspondence analysis and loglinear models.

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Abstract

In this paper it is our objective to give a graphical display of the asymmetry of a square contingency table formed by two variables measured at two time points. This is done by making combined use of generalized correspondence analysis and loglinear symmetry models. The residuals of loglinear symmetry models have various forms of asymmetry in it. These residuals are submitted to a skewsymmetric form of generalized correspondence analysis. In this way a graphical display of asymmetry is obtained.

1. Introduction

This paper discusses the analysis of so-called two-wave two-variable data, i.e. two variables measured at two time points, with correspondence analysis and loglinear analysis, both techniques for analyzing categorical data.

An example of a two-wave two-variable table is taken from Plewis (1985) (see table 1). In this example mental health (with categories good, moderate and poor) and loneliness (with categories absent and present) are measured at two occasions. In fact we have a four-way table, and table 1 shows this table in two-way form: the state of persons at time 1 is coded in the rows, and the state of persons at time 2 is coded in the columns. Many questions can be answered from these data, for example, in what way do persons change generally, does loneliness influence mental health or the other way around, and so on. In this paper we will concentrate on *asymmetry* in these data, i.e. we concentrate on the fact that the number of persons changing from joint state X at time 1 to joint state Y at time 2 is not the same as the number of persons changing from joint state Y to joint state X.

Table 1. Mental health (A_1 and A_2) and loneliness (B_1 and B_2) interactively coded at two time points with marginal frequencies.

label	A_1	B_1	A_2						margin
			good		moderate		poor		
			B_2 abs	B_2 pres	B_2 abs	B_2 pres	B_2 abs	B_2 pres	
R11	good	abs	34	3	13	1	2	0	53
R12	good	pres	7	1	2	1	1	3	15
R21	mod.	abs	13	3	12	4	6	2	40
R22	mod.	pres	4	3	2	2	1	1	13
R31	poor	abs	7	2	6	0	11	7	33
R32	poor	pres	1	2	3	9	8	12	35
margin			66	14	38	17	29	25	

We will analyze these data using a combined approach of both correspondence analysis and loglinear analysis. Loglinear analysis (LLA) is a technique for analyzing categorical data with which diverse hypotheses about the relation between variables can be verified. Various loglinear models for two-wave two-variable panel data are known from the literature (see Hagenars, 1986; Plewis, 1985; see Groenen, 1988, for an overview). Correspondence analysis (CA) is another technique for analyzing categorical data. LLA and CA are closely related in the sense that CA can be interpreted as a method that decomposes the residuals from loglinear models (see van der Heijden et al., 1989, for an overview). In this paper we will use the two techniques jointly in the following way: we use loglinear models to obtain different forms of symmetry in

the data. Then generalized CA (GCA) is used to analyze the residuals from these models. In this way GCA provides us a graphical representations of the asymmetry. We start now with a short introduction to CA, LLA and GCA, and discuss whether ordinary CA can help us to interpret the asymmetry of two-wave two-variable data.

2. Correspondence analysis and loglinear analysis

Correspondence analysis will be discussed here only briefly. For more details we refer to Benzécri et al. (1973), Gifi (1981) and Greenacre (1984). CA gives a multi-dimensional representation of the dependence of the row and column variable of a two-way contingency table. The representation is formed by assigning scores to row and column categories. Let us define matrix \mathbf{P} as a two-way contingency table with proportions p_{ij} , where $p_{++} = 1$, \mathbf{D}_r as a diagonal matrix with marginal row proportions p_{i+} , \mathbf{D}_c as a diagonal matrix with marginal proportions p_{+j} and \mathbf{E} as the matrix with the independent proportions $e_{ij} = p_{i+}p_{+j}$. The decomposition provided by CA is

$$\mathbf{P} = \mathbf{E} + \mathbf{D}_r \mathbf{R} \mathbf{A} \mathbf{C}' \mathbf{D}_c = \mathbf{D}_r (\mathbf{t} \mathbf{t}' + \mathbf{R} \mathbf{A} \mathbf{C}') \mathbf{D}_c \quad (1)$$

where \mathbf{R} are the row scores normalized so that $\mathbf{R} \mathbf{D}_r \mathbf{R}' = \mathbf{I}$, \mathbf{C} are the column scores normalized so that $\mathbf{C} \mathbf{D}_c \mathbf{C}' = \mathbf{I}$, \mathbf{A} is a diagonal matrix with the singular values and \mathbf{t} is a vector of ones of appropriate length. So (1) shows that CA can be interpreted as the decomposition of the departure from independence of matrix \mathbf{P} .

Let us, for example, analyze table 1 with CA. The first and second dimensions of row and column scores are graphically presented in figure 1. In the sequel we will give the singular values and the proportion explained chi square distances. Plots are made with coordinates $\mathbf{R} \mathbf{A}$ and $\mathbf{C} \mathbf{A}$ so that the Euclidean distances are equal to chi-square distances. The first and second dimension have a singular values .591 (73%) and .274 (16%), respectively. We see in figure 1

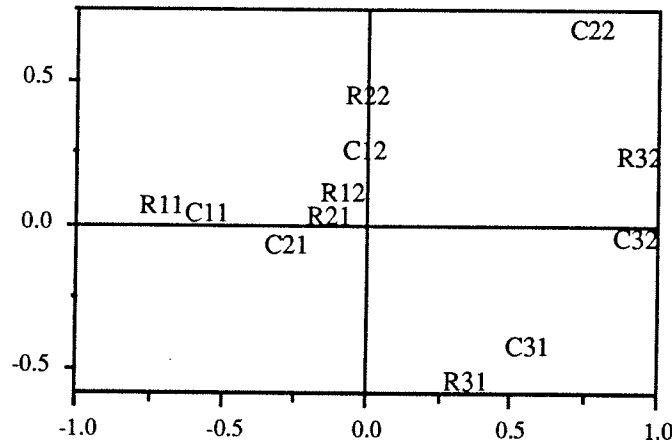


Figure 1. Dimension one and two of CA on table 1. Row points are labeled with R, column points with C.

that having good mental health and not being lonely at t_1 (R11) and t_2 (C11) have a higher proportion than expected. In the same way having poor mental health and being lonely at t_1 (R32) and t_2 (C32) also have a higher proportion than expected. Furthermore, we see that R11 and C11 are opposed to R32 and C32 in the first dimension. This leads us to the most important characteristic of this dimension, being that feeling alright (R11) at t_1 is followed more often than average by feeling alright at t_2 (C11) than by feeling bad (C32) at t_2 . Feeling badly at t_1 (R32) is followed more than expected by feeling badly at t_2 (C32) than by feeling alright (C11). The second dimension shows analogously that a moderate mental health and feeling lonely at t_1 (R22) is not changed at t_2 (C22) more than expected and people having a poor mental health without feeling lonely at t_1 (R31) remain the same more than expected at t_2 (C31).

Loglinear analysis is a technique used for analyzing contingency tables. Only a brief explanation of LLA is given so that the reader is able to understand the next sections. For more details we

refer to Bishop, Fienberg and Holland (1975). LLA decomposes the logarithm of probabilities in an ANOVA like way. For a two-way table this gives:

$$\log \pi_{ij} = u + u_{1(i)} + u_{2(j)} + u_{12(ij)} \quad (2)$$

In this decomposition there is one parameter for the mean, two sets of parameters for the margins and one set of parameters for the first order interactions. The parameters sum to zero for each index. Equation (2) is generalized to higher-way tables in a straightforward way.

In LLA one usually specifies a model with restrictions on the parameters. For (2) a well-known example is the independence model, for which $u_{12(ij)} = 0$. Once this model is specified, ML-estimates of the expected frequencies are calculated and the differences between the expected and observed frequencies are evaluated with the Pearson's goodness-of-fit statistic $\chi^2 (= \sum (\text{observed} - \text{expected})^2 / \text{expected})$ or the likelihood-ratio chi-squared test $L^2 (= 2 \sum (\text{observed}) \log (\text{observed}/\text{expected}))$. Both statistics are asymptotically chi-square distributed when the model is true and the data stem from a (product-)multinomial or a Poisson distribution. The number of degrees of freedom equals the number of cells minus the number of fitted parameters.

For our purpose it is important to know that ML estimates of loglinear models have the property that observed marginal proportions are equal to expected marginal proportions, for example, for the independence model $p_{i+} = \pi_{i+}$ and $p_{+j} = \pi_{+j}$. For this reason loglinear models are often denoted by the margins that are fitted to the expected proportions, for example, the independence model can be denoted as [1][2].

CA and LLA are closely related in the sense that CA decomposes the departure from the loglinear independence model (for other relations, see Goodman, 1986). In Van der Heijden and de Leeuw (1985) it was shown that this relation also holds for higher-way table. For example, they showed that CA of table 1 decomposes the departure from loglinear model $[A_1B_1][A_2B_2]$, because estimates of expected proportions π_{ijkl} are $\pi_{ijkl} = p_{ij++}p_{++kl}$. These values are also equal to the values in E.

Van der Heijden and de Leeuw (1985) also show how a generalization of CA can be used for the decomposition of other loglinear models. The generalization is due to Escofier (1983). The decomposition of generalized correspondence analysis (GCA) is:

$$P = Q + S_r R \Lambda C' S_c \quad (3)$$

where R , C and Λ have the same form as in (1), S_r and S_c are diagonal matrices with weights and P and Q are matrices of the same size. Note that S_r , S_c , P and Q do not have the same relation as D_r , D_c , P and E have in ordinary correspondence analysis (1). In this paper we will have P to be the observed proportions (as in (1)) and take for Q the estimates of an other model than the independence model.

The study of asymmetry in table 1 with ordinary CA will be very difficult, because the asymmetry is partly reflected by the margins and CA decomposes the departure from the margins. The asymmetry in table 1 that is not due to the margins is not necessarily displayed optimally in the first few dimensions by ordinary CA. Our objective is showing the asymmetry by making use of GCA. What we are going to do is this. We are going to decompose residuals from loglinear symmetry models with GCA. These residuals consist of asymmetry only. Thus we use loglinear models to filter the data.

3. Loglinear models for symmetry in two-wave two-variable data

For ordinary two-wave one-variable data symmetry models are well known (Bishop, Fienberg and Holland, 1975). However, with two-wave two-variable data symmetry models are more complicated. The ordinary symmetry model assumes that the marginal proportions have not changed. Therefore, asymmetry (i.e. the residuals from the symmetry model) may be due to differences between marginal proportions. Duncan (1979) and Hagenars (1985) have discussed symmetry models for two-wave two-variable data that do take into account differences between corresponding marginal row and column proportions. We can distinguish

three kind of differences between the marginal proportions of t_1 and t_2 of table 1:

1. the marginal proportions of A at t_1 can be different from the marginal proportions at t_2 ,
2. the marginal proportions of B at t_1 can be different from the marginal proportions at t_2 ,
3. the interaction of A and B at t_1 can be different from the interaction at t_2 .

Making use of these three kind of differences four symmetry models can be formulated. The first model is the ordinary symmetry model. The ML-estimates $\hat{\Pi}$ of the two-wave two-variable counterpart of the symmetry model can easily be found by computing:

$$\hat{\pi}_{ijkl} = \hat{\pi}_{klij} = (p_{ijkl} + p_{klij})/2 \quad (4)$$

The associated χ^2 and L^2 of the symmetry model have $IJ(IJ-1)/2$ degrees of freedom. This model states that the probability to go from joint state (i, j) at t_1 to joint state (k, l) at t_2 is the same as the probability to go from (k, l) at t_1 to (i, j) at t_2 . The marginal probabilities of rows are equal to those of the columns. To put it in another way, the above mentioned three types of differences are all absent. Model (4) is the symmetry model for two-way tables.

An easy procedure to fit symmetry with computer packages like SPSS^x or BMDP is an four-way extension of the two-way procedure of Bishop et al. (1975). Construct a five-way table of order $(I \times J \times I \times J \times 2)$ with the four-way table P in the first layer of the fifth variable and the transposed table P' in the second layer (see Hagenars, 1985). Fitting loglinear model $[A_1B_1A_2B_2]$ on this new five-way table will also give the estimates of the symmetry model. Every cell of the original table is estimated twice (namely in the first and in the second layer), so the chi-square and L^2 have to be divided by two. The number of degrees of freedom must be calculated as indicated above.

The next symmetry model is model (4) allowing for A_1A_2 asymmetry. This model is the symmetry model taking taking difference 1 into account. So the marginal proportions of variable B and the relation between A and B are supposed not to change in time. The estimates of this model can be found by fitting on top of model (4):

$$\hat{\pi}_{i+++} = p_{i+++} \quad \text{and} \quad \hat{\pi}_{++k+} = p_{++k+} \quad (5)$$

Now an extra $I-1$ parameters are needed for fitting the marginal proportions of variable A_1 and A_2 separately. Consequently the associated degrees of freedom decrease to $(IJ(IJ-1)/2)-(I-1)$. If we define our fifth variable in the fitting procedure to be C then fitting $[A_1B_1A_2B_2][A_1C][A_2C]$ in the five-way table yields the estimates of this model.

The third model is a even less restrictive model of the symmetry model. This model relaxes not only the equality restrictions on the marginal proportions of A, but also those of B. The model can be computed by fitting on top of model (5):

$$\hat{\pi}_{+j++} = p_{+j++} \quad \text{and} \quad \hat{\pi}_{+++l} = p_{+++l} \quad (6)$$

Another $J-1$ parameters are needed to lift the equality constraints on the marginal frequencies of B_1 and B_2 . Consequently the associated chi-square test has $(IJ(IJ-1)/2)-(I-1)-(J-1)$ degrees of freedom. The estimates of this model are found by fitting $[A_1B_1A_2B_2][A_1C][A_2C][B_1C][B_2C]$ in the five-way table.

The last model is the quasi-symmetry model for the two-wave two-variable contingency table, which can be found by fitting on top of model (6):

$$\hat{\pi}_{\substack{ij \\ \cancel{kl}++}} = p_{\substack{ij \\ \cancel{kl}++}} \quad \text{and} \quad \hat{\pi}_{\substack{++ \\ \cancel{kl}}} = p_{\substack{++ \\ \cancel{kl}}} \quad (7)$$

This model permits all three kinds of differences mentioned above. Model (7) differs from model (6) in that the interactions of variable A and B are allowed to be different at t_1 and t_2 . An additional $(I-1)(J-1)$ parameters are needed for loosening the equality constraints on the marginal proportions of A_1B_1 and A_2B_2 . The associated chi-square test has $(IJ-1)(IJ-2)/2$ degrees of freedom. This model totally reconstructs the margins of table 1. Fitting model (9) comes to the same as fitting the quasi-symmetry model for two-wave one-variable tables (Causinus, 1965). Model (7) can be estimated by fitting $[A_1B_1A_2B_2][A_1B_1C][A_2B_2C]$ in our five-way table.

The symmetry models above are nested and the difference between the various symmetry models can therefore be tested. One such test is the conditional test between the ordinary

symmetry model (4) and the quasi symmetry model (7) for marginal homogeneity. This test tells us whether the marginal row frequencies of table 1 are different from the marginal column frequencies or not. A conditional test of model (5) and model (7) can tell us whether there are changes in marginal frequencies of B and AB or not. Differences in marginal frequencies of variable A_1 and A_2 are allowed. A conditional test of model (6) and model (7) gives the answer to the question whether the interaction A_1B_1 equals A_2B_2 or not. Table 2 gives the results of a sequence of the four nested models and conditional tests for the example given in table 1. We may conclude that the three types of changes mentioned in the beginning of this section are not significant.

Table 2. Results for model (4) to model (7) and the conditional tests for table 1.

Model	L^2	df	p	χ^2
4. Symmetry	19.38	15	>.10	17.24
5. Symmetry and A_1A_2 asymmetry	14.20	13	>.25	12.93
6. Symmetry and A_1A_2 and B_1B_2 asymmetry	13.29	12	>.25	12.05
7. Quasi-symmetry	12.13	10	>.25	11.10
8. Marginal homogeneity (4) - (7)	7.25	5	>.25	
9. (5) - (7)	2.07	3	>.50	
10. (6) - (7)	1.16	2	>.50	

We have discussed some symmetry models that allow for asymmetry due to differences in marginal frequencies. The residuals of these models contain both asymmetry due to changes in marginal frequencies and asymmetry not due to changes in marginal frequencies. Using these four models we can filter the residuals of symmetry for the asymmetry due to changes in marginal frequencies.

4. A skewsymmetric generalization of CA

The residuals of the four symmetry models can be analyzed with GCA. For all models these residuals have the special property that the residuals are skewsymmetric, i.e. a residual $n_{ijkl} = (p_{ijkl} - \hat{\pi}_{ijkl})$ above the diagonal equals $-n_{klij} = -(p_{klij} - \hat{\pi}_{klij})$ below the diagonal. This can be seen from the fit procedure used above, i.e. construct a five-way table \mathbf{Z} with elements $z_{ijk11} = p_{ijkl}$ and $z_{ijk12} = p_{klij}$. In all four models z_{ijk1+} is fitted and the maximum likelihood estimate \hat{z}_{ijk1+} equals $z_{ijk1+} = p_{ijkl} + p_{klij} = \hat{\pi}_{ijkl} + \hat{\pi}_{klij}$. From the right most equation one easily derives that $(p_{ijkl} - \hat{\pi}_{ijkl}) = -(p_{klij} - \hat{\pi}_{klij})$ which proves that the residual matrix \mathbf{N} is skewsymmetric. Gower (1977; see also Constantine & Gower, 1978) showed that the singular value decomposition of a skewsymmetric matrix \mathbf{N} has the following form:

$$\mathbf{N} = \mathbf{K}\mathbf{\Lambda}\mathbf{L}' = \mathbf{K}\mathbf{\Lambda}\mathbf{J}\mathbf{K}' \quad (8)$$

where $\mathbf{K}'\mathbf{K} = \mathbf{I} = \mathbf{L}'\mathbf{L}$, $\mathbf{\Lambda}$ is a diagonal matrix with singular values, ordered in pairs $\lambda_1, \lambda_1, \lambda_2, \lambda_2$, and so on. Matrix \mathbf{J} is a block diagonal matrix with blocks $\begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$. If the number of rows is odd, the last singular value and the last diagonal element of \mathbf{J} equal 0. A plot of the row scores \mathbf{K} and column scores \mathbf{KJ} for paired dimensions shows us that the configuration of column points is merely a rotation of 90° of the configuration of row points. Because the singular values are paired the decomposition is not unique (Constantine and Gower, 1982). This means that the paired dimensions of row and column scores may be rotated. A more simple plot is obtained by showing only the row points and by giving the direction of rotation. This is illustrated in figure 2, where 2 row and 2 column points are plotted. Gower (1977) shows that for figure 2 element n_{12} and $-n_{21}$ are approximated by twice the *area* of the triangle of the origin, R1 and R2. Figure 2 shows that the value n_{12} is positive since R1 and C2 have an angle smaller than 90 degrees, and n_{21} is negative since the angle is larger than 90 degrees. So we can also plot only R1 and R2 and indicate that the direction of rotation is counter-clockwise, showing that value n_{12} is positive. Here we see that rotation of paired dimension does not change the area.

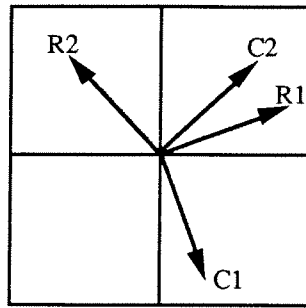


Figure 2. An example of two row points and two column points of a correspondence analysis solution of residuals of a symmetric matrix.

In Van der Heijden (1987) the properties of skewsymmetric matrices above was used to propose a skewsymmetric generalization of CA in the following way:

$$P = \Pi + DRAJR'D \tag{9}$$

where Π is the matrix with expected proportions of a symmetry model, R are the row scores, Λ is a diagonal matrix with singular values and D are weights equal to $(p_{ij++} + p_{++kl})/2$. The weights are used to scale the residuals, just as in ordinary CA. The row and column weights are identical in order to retain the skewsymmetric properties of the singular value decomposition above. We are going to use (9) to decompose the residuals from models (4) to (7). For these applications figure 2 can be interpreted as that joint state 1 is followed more by joint state 2 than vice versa.

Models (4), (5) and (6) may not fit because of two types of asymmetry: asymmetry due to differences in the margins and asymmetry not due to the margins. Residuals of model (7) only contain asymmetry not due to the margins. Decomposing the residuals of model (4) with (9) shows symmetry due to differences in marginal proportions of A_1B_1 and A_2B_2 . So the margins can differ due to asymmetry of A_1 and A_2 , B_1 and B_2 , and A_1B_1 and A_2B_2 . The residuals of model (5) have asymmetry controlled for changes in marginal proportions of variable A. Asymmetry due to marginal differences of B_1 and B_2 and marginal differences of A_1B_1 and A_2B_2 are still present, but the marginal differences of A_1 and A_2 are not present. During the interpretation of the GCA decomposition one has to be careful not to derive conclusions which refer to the marginal proportions of variable A_1 and A_2 , because these effects have been filtered out of the solution. The same can be told for the residuals of model (6). Now the GCA solution shows asymmetry controlled for differences in marginal proportions of A_1 and A_2 and of B_1 and B_2 . The solution still shows the marginal differences of A_1B_1 and A_2B_2 . Here one should be careful not to interpret the solution in terms of differences in marginal frequencies of variable A and of variable B. The residuals of model (7) only have the asymmetric effects controlled for differences in the interaction of A_1B_1 and A_2B_2 , so the GCA solution shows only asymmetry that is not due to marginal differences.

Example

GCA will be performed on residuals of the four models. Taking the χ^2 values in table 2 seriously would stop us from a residual analysis. Nevertheless, for purpose of illustration we will analyze the residuals with the method above.

GCA on residuals of the first model can be interpreted by looking at the plot of the first two dimensions of the row scores. Figure 3.a displays these first two dimensions of the CA solution with singular values .217, which explain 86% of the inertia.

The points for absence of loneliness (R11, R21 and R31) have small residuals; they are near to the origin and do not contribute much to the solution. Going clockwise from R32 to R22 the figure shows us that if people are lonely, a poor mental health (R22) is followed more by a moderate mental health (R32) than vice versa. This is the most important characteristic of the solution, because the area of the origin, R32 and R22 is the largest area. If people are lonely, a moderate mental health (R22) is more often followed by a good one (R12) than vice versa. There are roughly as many people (who are lonely and) who have a poor mental health at time point one (R32) and a good one at time point two (R12) as people who decline from good mental

health to a poor one, since the area spanned by R32, R12 and the origin is practically zero. This can easily be checked in table 1 by comparing the corresponding frequencies (2 and 3).

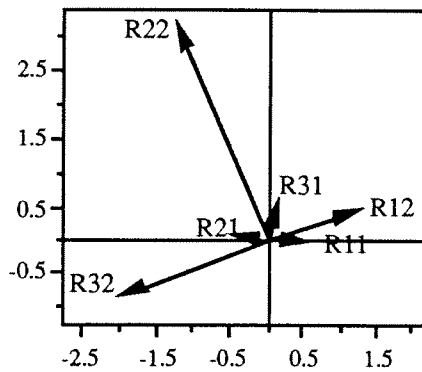


Figure 3.a GCA on residuals of model (4)

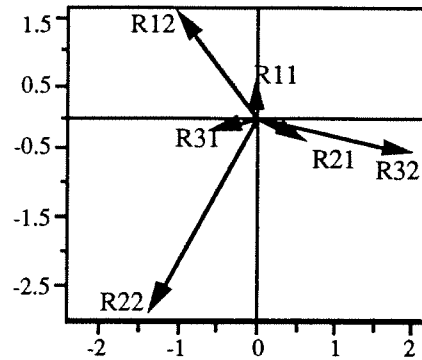


Figure 3.b GCA on residuals of model (5)

Model (5) is the symmetry model corrected for asymmetry due to the margins of A. The residuals of this model therefore contain asymmetry due to margins of B, due to interaction differences of AB and asymmetry not due to margins. Figure 3.b shows the CA solution on residuals of model (5). In the plot we see that again only the points referring to 'loneliness present' (R12, R22 and R32) contribute much to the CA solution. The solution in two dimensions, with singular values .164, is still very acceptable because 75% of the inertia is shown.

Considering only people who feel lonely, the plot shows us, going clockwise, that good mental health (R12) is followed more often by a bad one (R32) than vice versa. This effect is not very strong because the area spanned by R12, R32 and the origin is small. On the other hand, just as we have seen in figure 3.a, bad mental health (R32) is more followed by moderate mental health (R22) than the other way around and moderate mental health (R22) is more followed by good mental health (R12) than vice versa. This solution compared with the previous one shows us that taking asymmetry due to differences in marginal proportions of mental health into account there is some asymmetry between R12 and R32: for lonely people a good mental health is followed more often by a bad one.

The last two solutions, GCA on residuals of model (6) and (7), are very similar to figure 3.b and does not give us new information.

The residual analysis we propose will be more helpful when dealing with variables that have many categories. The symmetry models will tend not to fit adequately and our skewsymmetric generalization of CA can be of great help for analyzing the residuals.

5. Conclusion and discussion

The decomposition of the residuals of model (4), (5), (6) and (7) is a powerful tool with which one investigates the asymmetry in the data between two time points while suppressing the effects due to specific marginal proportions. Our method can be particularly helpful when dealing with variables with many categories. This method can be used for graphically displaying asymmetry of the data, when there is a need to suppress differences in margins between two time points. When, for example, CA on residuals of the symmetry model is completely dominated by very different marginal frequencies of A_1 and A_2 , then it is advised to use the residuals of the second model. Now the solution will be more easy to interpret because the marginal effects of the first variable have been filtered out of the solution.

Models (4), (5), (6) and (7) can also be extended in a straightforward way to two-wave multi-variable contingency tables. Then various symmetry models can be formulated allowing for asymmetry due to differences in main effects (like model (5) and (6)), asymmetry due to differences in first order interactions (like model (7)) and asymmetry due to differences in higher order interactions. For reasons of simplicity we have discussed two-wave two-variable contingency tables only.

We conclude that GCA on the residuals of these symmetry models gives us an interesting graphical display of asymmetry in the data. The interpretation is made in a straightforward way

in terms of joint-category X at t_1 which is followed more by joint-category Y at t_2 than the other way around. Therefore residual analysis of loglinear symmetry models using GCA provides an attractive instrument for analyzing two-wave two-variable data.

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