QUASI-EXPERIMENTAL DESIGN: FURTHER EXPLORATIONS

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Campbell (1965) has loosely defined quasi-experimental design as the application of the experimental mode of analysis to behavioral science situations which do not meet complete requirements of classical experimental control or design. He has focused primarily on inference problems associated with nonrandom assignment of experimental units to treatments. Other examinations of the quasi-experimental paradigm in the behavioral sciences have taken the form of analytic concern with relaxation of constraints in classical design models, and augmentation of common analyses to assay or compensate for deviations from classical assumptions. Such research has resulted in some interesting information about the relations between experimental classificatory models and the factor analytic models more commonly used by social scientist. For example, Gollob (1968) has presented a method of examing data which is based on a two-way (mixed) analysis of variance model in order to account for correlated error. The usual analytic procedure is augmented by a principal components representation of matrix of interaction parameters. Bock and Bargmann (1966) have conducted research which is based on systematic variation of the general factor analysis model. Structural characteristics of some models are related to the usual experimental designs. Maximum likelihood rather than least squares techniques are used to estimate parameters in this case, however.

In this paper, we shall limit consideration to deriving a general relation between a mixed classificatory model with fewer constraints and a restricted factor analytic model. Demonstration and evaluation of the model usage is based on simulated data.

Consider now the situation characterized by the following attributes: (a) A mixed analysis of variance model is with random main effect hypothesized, but alternative models (with fewer classical restrictions) are plausible; (b) Primary interest lies in the random main effects and interactions, rather than in the fixed effects.

These conditions are rather common in psychological and educational research. Students are frequently the random effect, and treatments or blocking attributes can be interpreted as the fixed effects. Insofar as fixed effect scales are arbitrary in the social sciences, there is often little justification for examining absolute values of scale scores. Rather, the interaction of student and score are most informative to the investigator.

The classical model and assumptions are given in equation (1) of the Appendix: a three-way ANOV representation with a random main effect. Sources of variance involving the random effects and random interactions can be examined conveniently by obtaining a covariance matrix in which the summation is taken over the random effect (subscript i). Assuming that the sample is large and using the assumptions indicated, the expected covariances can be condensed to expression (5). Multipliers of the variance terms are Kronecker deltas.

If the fixed effect scales are arbitrary, one can equate the averages to some constant value so that fixed main effects and the fixed interaction are unaffected by the procedure. One can show that adjustment of the observed scores, Y_{ijk} to y_{ijk}, does not alter expected values of the covariances (Stanley, 1961).

Suppose we now relax the assumption of unit weighting of each random effect in this model. Instead, the factors can be weighted differentially, depending on the specific jk combination (7). It is not unreasonable to conjecture that the weights attached to effects are a function of a specific treatment-block combination, for example. If the classical assumptions are true, the A_{jk}, B_{jk}, C_{jk} can be interpreted as the variance components associated with random effects. When parameters are dependent on jk, the squared estimates provide something <u>like</u> variance components within a jk combination.

Given this last equation, the substitutions indicated in equation (8) are made in order to conform to common factor analysis model notation. The expectation of the dispersion matrix under this model is given in equation (11), and matrix definitions are given in Appendix II for the case of j=1,2,3, k=I,II,III.

This is of the form of the usual factor analytic model considered by Lawley(1940) and others. It is restricted in the sense that certain factor structure and factor correlation matrix elements are constrained by the investigator to be zero, and the others are free and must be estimated.

Note that the dimensions and attributes of the factor structure and factor correlation matrix are a function of the original experimental design. In order to assure a meaningful solution, one must attend to the uniqueness of the hypothesized factor structure. Anderson and Rubin (1956) and Koopmans and Riersol (1950) provide sufficient conditions for indentification (up to rotation) of the solution. For parsimonious data description and for easy interpretation of results, the correlations among the factors (X_i, X_{ij},X_{ik}) are usually assumed to be zero. In this orthogonal case, the <u>phi</u> matrix is an identity and the factor structure given is unique.

Estimation of Parameters

The maximum likelihood estimates of free parameters in the restricted factor analysis model can be obtained by using an extension of Lawley's (1940) method. Joreskog and Gruvaeus (1967) provide detailed description of the procedure, and an excellent computer program for its implementation. One can impose on the hypothesized factor structure and on the factor correlation matrix <u>a priori</u> constraints that certain parameters are exactly equal to zero. This restricted maximum likelihood factor analysis (RMLFA) allows the investigator to make a large sample, Chi-square test for goodness of fit of the model to the data.

The procedure recommended by Joreskog (1967) for evaluation of goodness of fit is a sequential one. After successively altering the factor structure hypothesized, one accepts the solution having the best fit at the probability level specified. Since the tests are conditonal, one knows only that the probability of the accepted structure being different from the true structure is less than or equal to the specified significance level. Joreskog further suggest random division of the sample into halves, using one half to generate a final hypothesis of interest in a sequential manner, and the other half to test the hypothesis. His recommendations refer largely to testing hypotheses about the number of factors in the unrestricted (i.e., no fixed elements) factor analytic model. Lacking information to the contrary, we shall assume that much the same procedure is appropriate in making sequential decisions about modification of the restricted model.

Simulation of Data

In order to assess the utility of the model and of the sequential procedure described earlier, a pilot Monte Carlo study was initiated. The four basic factor structures considered are provided in Table 1; attention is restricted to orthogonal structures only.

Random floating point numbers, distributed NID (0,1) were generated and used as the independent variates (i.e., factor scores) in the factor analytic model. Sample size is restricted to be 200, and number generation was accomplished using a computer program (Control Data 3600) developed by Wolfe (1968). Two samples, each consisting of 200 units, comprise the validation sample (for a test of the final hypothesis). Linear functions of the random variables were computed on the basis of population factor loadings indicated in the matrices of Table 1 and the model (8) given in the Appendix. Variance-covariables were derived from the resulting sample observations.

The generated independent random variables conform closely to normal curve frequencies. Chi-square tests of hypotheses that the variance-covariance matrix for the independent varialbes is a sample from a population whose covariance matix is a diagonal results in acceptance of the null hypothesis. The hypothesis of independence among the observations (i.e., the linear combinations) is rejected for each generated matrix.

The form of the population factor structure for synthesis of samples conforms to requirements for uniqueness of the solution (Joreskog and Gruvaeus, 1967). Magnitudes of the factor loadings, and generated correlations are similar to those commonly obtained in analyses of psychological data. Structures 1 and 4 were chosen because they are suggestive of the experimental design situation characterized by homogeneity of error variance and additivity of effects. Structures 2 and 3 are minor variations on this model.

Results

Models which are successively hypothesized to fit the data are represented by factor patterns given in Table 2. Each pattern matrix corresponds to a hypothesized factor structure, with 1's representing free parameters which must be estimated, and 0's representing the elements which are restricted to be zero. For the first factor structure, four models were hypothesized, the last one (D) being the true model. Five models were each hypothesized to fit the data generated on the basis fo structures 2,3, and 4. The last model (E) in each case is the true one. The models increase in complexity to simulate the investigatior's objective to obtain parsimony in description.

Several attributes of any intermediate (false) solution warrant attention. Changes in successive hypothesized factor structures can be made conditional on such characteristics, in order to achieve a better fit of the model to data. Boruch and Wolins (in press) and Joreskog (1967) supply detailed information, including examples, on some of the following criteria.

Boundary problems occur when estimates of parameters fall at or outside the region of allowable values. Such improper solutions may be acceptable (Joreskog, 1967). The solution is not a maximum likelihood solution, since partial derivatives at the solution defined by parameter estimates are not all zero.

The size and significance of the Chi-square statistic, associated with maximum likelihood factor analysis, is an appropriate index of the goodness of fit in the confirmatory sense. The magnitude of the statistic, when used in successive exploratory tests of hypotheses, is a convenient index for examining the goodness of fit. In making comparisons of successive solutions in which degrees of freedom differ the computed Chi-square, divided by degrees of freedom, may be useful. The division allows examination of mean square residuals adjusted for degrees of freedom.

If multiple independent samples are available and hypothesized factor structures are planned in advance, then the ratios of independent Chi-squares, divided by degrees of freedom, can be examined.

Other devices for summarizing the results of particular analysis are commonly used: examination of residual correlations, of consistency of an estimated factor correlation matrix (in the oblique solution). For restricted solutions considered here, near zero estimates of parameters are also of interest.

Consider now the summary data provided in Table 3. Boundary problems are designated in the third column of the chart. In three instances (all similar factor structures), the limiting value of specific error variances was met. The hypothesized model was rejected on this basis. If the boundary condition is ignored, the magnitude of the Chi-square would lead to acceptance of the model.

The Chi-square tests for false models lead appropriately to rejection of the hypothesis in all cases except IV (Model D), while the confirmatory sample test (ICV) leads to a marginal rejection. The ratio of the Chi-square for models C and D to their respective degrees of freedom is not enlightening. The adjustment for degrees of freedom fails to show which model might be more acceptable in an umambiguous way.

The rejection of true models in independent tests appears to occur more frequently than one would expect (1 CV-Model D, 2 CV-Model E). A Type I error also occurs for the solution 2V-Model E. The rejections are marginal, but suggest that the probability of a Type I error may be larger than advertized. A tendency toward rejection of true solutions is part of the anecdotal rather than the systematic information in unrestricted factor analysis studies based on limited samples. These results imply that a similar problem affects tests on restricted models.

Examination of the estimated factor Loading for each solution reveals values near zero for each false hypothetical model. The values occur frequently for situations in which parameters are hypothesized but the true factor structure does not contain the elements.

The ratio of Chi-square statistic appears to be useful for interpretation of results. In general, the ratio decreases as the hypothesized models are successively changed to conform more closely to the true structure of the data. In the case of a comparison of Models B and C conditional on the factor structurel, for example, this is the case. Without rather well defined, systematic methods of successive testing, however, this index of fit is not likely to be very useful.

The ratios of successive Chi-square divided by their respective degrees of freedom are not appropriate for evaluation with respect to significance levels, since the successive Chi-square values are not independent. The ratios, however, are indicative of the magnitude of improvement in fitting two successive models. Of course, the more drastic changes in hypothesized factor structure are associated with the larger ratios.

This cursory examination is informative in only a suggestive way. Although the notion of exploratory and confirmatory factor analytic techniques appears to be appropriate for an experimental design-like situation as described earlier, the actual results achieved in this small situation are a bit dubious. There is some evidence to suggest that the probability of accepting a true solution is somewhat larger than the tabulated likelihoods, at least for the structures considered.

If one has no plan for sustematic alteration of hypothesized models, it is unlikely that successive tests to the true model will be as straightforward as the procedures demonstrated here. With some such system and the use of the Chi-square and Chi-square/degree of freedom ratio, some reasonable results can be achieved.

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TABLE 1

Population Factor Structures

(1)

700
700
700
700
700
700
700
700
700

(2)

70	00	00	50	00	00
70	00	00	00	40	00
70	00	00	00	00	65
00	44	00	50	00	00
00	44	00	00	40	00
00	44	00	00	00	65
00	00	55	50	00	00
00	00	55	00	40	00
00	00	55	00	00	65

(3)

77	00	00	58	00	00
66	00	00	00	32	00
71	00	00	00	00	62
00	45	00	50	00	00
00	49	00	00	40	00
00	44	00	00	00	65
00	00	58	44	00	00
00	00	61	00	44	00
00	00	47	00	00	70

(4)

70	00	00	50	00	00
70	00	00	00	50	00
70	00	00	00	00	50
00	50	00	50	00	00
00	50	00	00	50	00
00	50	00	00	00	50
00	00	70	50	00	00
00	00	70	00	50	00
00	00	70	00	00	50

TABLE 2

Factor Patterns for Sequential Testing of Models

For Factor Structure (1):

A

1	0	0
1	0	0
1	0	0
0	1	0
0	1	0
0	1	0
0	0	1
0	0	1
0	0	1

B

1	0	0	1
1	0	0	0
1	0	0	0
0	1	0	1
0	1	0	0
0	1	0	0
0	0	1	1
0	0	1	0
0	0	1	0

C

1	1	0	0
1	1	0	0
1	1	0	0
1	0	1	0
1	0	1	0
1	0	1	0
1	0	0	1
1	0	0	1
1	0	0	1

D

1
1
1
1
1
1
1
1
1

For Factor Structures (2), (3), and (4):

A

1	0	0
1	0	0
1	0	0
0	1	0
0	1	0
0	1	0
0	0	1
0	0	1
0	0	1

B

1	0	0	1
1	0	0	0
1	0	0	0
0	1	0	1
0	1	0	0
0	1	0	0
0	0	1	1
0	0	1	0
0	0	1	0

C

1	0	0	1	0
1	0	0	0	1
1	0	0	0	0
0	1	0	1	0
0	1	0	0	1
0	1	0	0	0
0	0	1	1	0
0	0	1	0	1
0	0	1	0	0

D

1	1	0	0	1	0	0
1	1	0	0	0	1	0
1	1	0	0	0	0	1
1	0	1	0	1	0	0
1	0	1	0	0	1	0
1	0	1	0	0	0	1
1	0	0	1	1	0	0
1	0	0	1	0	1	0
1	0	0	1	0	0	1

E

1	0	0	1	0	0
1	0	0	0	1	0
1	0	0	0	0	1
0	1	0	1	0	0
0	1	0	0	1	0
0	1	0	0	0	1
0	0	1	1	0	0
0	0	1	0	1	0
0	0	1	0	0	1

Appendix I

$$Y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + \ell_{ijk} \quad (1)$$

where

$i = 1,2,3, \ldots, N$ $\qquad \ell_{ijk} \sim NID(0,\sigma_\varepsilon^2)$

$j = 1,2,3, \ldots, b$ $\qquad \alpha_i \sim NID(0,\sigma_\alpha^2)$

$k = 1,2,3, \ldots, c$ $\qquad [(\alpha\beta)_{ij} \sim NID(0,\sigma_{\alpha\beta}^2)]$

$[(\alpha\gamma)_{ik} \sim NID(0,\sigma_{\alpha\gamma}^2)]$.

$$\operatorname*{Cov}_i(Y_{ijk},Y_{ij'k'}) = E\{(Y_{ijk} - E(Y_{.jk}))(Y_{ij'k'} - E(Y_{.j'k'}))\} \quad . \quad (2)$$

where

$E(\alpha_i) = 0$ $\qquad E(\sum_i(\alpha\beta)_{ij}) = 0 \quad (3)$

$E(\beta_j) = \beta_j$ $\qquad E(\sum_i(\alpha\gamma)_{ik} = 0$.

$E(\gamma_k) = \gamma_k$

$E((\beta\gamma)_{jk}) = (\beta\gamma)_{jk}$

$E(\sum_i \varepsilon_{ijk}) = 0$.

$$E\{(Y_{ijk}-E(Y_{.jk}))(Y_{ij'k'} - E(Y_{.j'k'}))\} \quad (4)$$

$$= E\{(\alpha_i + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + \varepsilon_{ijk})(\alpha_i + (\alpha\beta)_{ij'} + (\alpha\gamma)_{ij'} + \varepsilon_{ij'k'})\}$$

$$\operatorname*{Cov}_i(Y_{ijk},Y_{ij'k'}) = \sigma_\alpha^2 + \delta_{jj'}\sigma_{\alpha\beta}^2 + \delta_{kk'}\sigma_{\alpha\gamma}^2 + \delta_{jj'}\delta_{kk'}\sigma_\varepsilon^2 \quad . \quad (5)$$

$$y_{ijk} = \alpha_i + \alpha\beta_{jk} + \alpha\gamma_{jk} + \varepsilon_{ijk} \quad . \quad (6)$$

$$y_{ijk} = A_{jk}\alpha_i + B_{jk}(\alpha\beta)_{ij} + C_{jk}(\alpha\gamma)_{ik} + \varepsilon_{ijk} \quad (7)$$

A_{jk} , B_{jk} , C_{jk} are parameters where

$$\varepsilon_{ijk} \sim NID(0,\sigma^2_{\varepsilon jk})$$

$$\alpha_i \sim NID(0,1)$$

$$(\alpha\beta)_{ij} \ , \ (\alpha\gamma)_{ik} \sim N(0,1) \quad .$$

$$y_{i(jk)} = A_{jk}X_i + B_{jk}X_{ij} + C_{jk}X_{ik} + \varepsilon_{i(jk)} \quad . \tag{8}$$

$$\rho_{jk,j'k'} = E\{(y_{ijk} - E(y_{.jk}))(y_{ij'k'} - E(y_{.j'k'}))\} \quad .$$

$$\underset{i}{Cov}(y_{ijk},y_{ij'k'}) = E\{(y_{ijk})(y_{ij'k'})\} \tag{9}$$

$$= E\{(A_{jk}\alpha_i + B_{jk}(\alpha\beta)_{ij} + C_{jk}(\alpha\gamma)_{ik} + \varepsilon_{ijk})$$

$$(A_{j'k'}\alpha_i + B_{j'k'}(\alpha\beta)_{ij'} + C_{j'k'}(\alpha\gamma)_{ik'} + \varepsilon_{ij'k'})\}$$

$$= A_{jk}A_{j'k'} + B_{jk}B_{j'k'}\rho^{BB}_{jj'} + B_{jk}C_{j'k'}\rho^{BC}_{jk'}$$

$$+ B_{j'k'}C_{jk}\rho^{C\,B}_{j'k'} + C_{jk}C_{j'k'}\rho^{CC}_{kk'} + \rho_{e_{jk}e_{j'k'}} \tag{10}$$

where $\rho^{BB}_{jj'}$ is, for example, the correlation between $(\alpha\beta)_{ij}$ and $(\alpha\beta)_{i\,j'}$.

$$\underset{i}{Cov}(y_{ijk},y_{ijk}) = \Sigma = \Lambda\Phi\Lambda' + \Psi \tag{11}$$

$$\Lambda = \begin{bmatrix} A_{II} & B_{II} & 0 & 0 & C_{II} & 0 & 0 \\ A_{21} & 0 & B_{21} & 0 & C_{21} & 0 & 0 \\ A_{31} & 0 & 0 & B_{31} & C_{31} & 0 & 0 \\ A_{1II} & B_{1II} & 0 & 0 & 0 & C_{1II} & 0 \\ A_{2II} & 0 & B_{2II} & 0 & 0 & C_{2II} & 0 \\ A_{3III} & 0 & 0 & B_{3II} & 0 & C_{3II} & 0 \\ A_{1III} & B_{1III} & 0 & 0 & 0 & 0 & C_{1III} \\ A_{2III} & 0 & B_{2III} & 0 & 0 & 0 & C_{2III} \\ A_{3III} & 0 & 0 & B_{3III} & 0 & 0 & C_{3III} \end{bmatrix}$$

ψ = Diagonal matrix with non-zero entries of $\sigma^2_{\varepsilon jk}$