

Psychometrika

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ANNOUNCEMENTS

CALL FOR PAPERS

2003 ANNUAL MEETING OF THE PSYCHOMETRIC SOCIETY

JULY 7–10, 2003

SARDINIA, ITALY

The 2003 Annual Meeting of the Psychometric Society will be held in Sardinia, Italy.

Persons wishing to present talks or to organize symposia should send titles and abstracts of no more than 200 words. Submissions will be accepted on the Psychometric Society website at <http://www.psychometricsociety.org>. An online submission form will be provided, followed by an e-mail link for sending the abstract as a Microsoft Word or WordPerfect file to the Psychometric Society central office. References should not be included with abstracts.

Submissions must include the following information for each author: name, institutional affiliation, mailing address, and e-mail address.

Persons organizing symposia are requested to start as soon as possible and to keep the Program Chair informed about the progress. For papers with multiple authors, please indicate who will present the talk.

Each person is permitted to present at most one contributed paper. This restriction does not prevent an invited speaker or a symposium speaker from also presenting one contributed paper, nor does it limit the number of papers on which one can be listed as a co-author.

The on-line submission form will prompt you to classify your talk into one of the following areas: (AAP) Applications, (BSI) Bayesian Statistical Inference, (CDA) Categorical Data Analysis, (CTT) Classical Test Theory, (CCC) Classification/Clustering/Correspondence Analysis, (EDA) Exploratory Data Analysis, (FAC) Factor Analysis, (GRM) Graphical Models, (IRT) Item Response Theory, (GLM) Generalized Linear Models, (LDA) Longitudinal Data Analysis, (MDS) Multidimensional Scaling, (MVA) Multivariate Analysis, (ODS) Optimal/Dual Scaling, (SEM) Structural Equation Modeling, (VCA) Variance Components Analysis, (OTR) Others (please specify).

The time for a contributed paper is 20 minutes for presentation and 5 minutes for discussion.

The deadline for abstract submission is March 1, 2003.

You will be notified by March 31st whether your presentation is accepted.

For questions about submissions, e-mail Wanda Baker: wkbaker@uncg.edu.

For other questions, e-mail the Program Chair, Jacqueline Meulman: meulman@fsw.leidenuniv.nl.

More details about the meeting will be posted on the Society's website: <http://www.psychometricsociety.org>.

PSYCHOMETRIC SOCIETY DISSERTATION PRIZE

The purpose of this award is to recognize the best Ph.D. thesis that was accepted at a university during the past year, written in any field covered by the journal *Psychometrika*. Submitted theses will be evaluated by a panel of three judges appointed by the President of the Psychometric Society; their decision will be final. Judging will be on the basis of the level of originality in the ideas and techniques, the possible applications and their treatment, and potential impact. The panel may arrive at the conclusion that none of the submitted theses merits the award.

The award consists of a certificate, a monetary prize of \$500, and a free one-year membership in the Psychometric Society. The winner will be invited to present a summary of their thesis at the 2003 Annual Meeting of the Society to be held in Sardinia, Italy, during July 7–10. A stipend of up to \$1,000 will be given to defray expenses to attend the meeting and registration fees will be paid. The winner will also be encouraged to submit a paper based on the thesis to *Psychometrika*. If accepted for publication, the paper will be identified as being based on the thesis that won the Psychometric Society Dissertation Prize; the names of the university and the thesis supervisor will also be clearly indicated. The thesis supervisor may be co-author of the paper.

Please send four copies of the thesis with a cover letter from the thesis supervisor indicating why the thesis is suitable as an entry in the competition to:

Dr. Terry Ackerman
University of North Carolina-Greensboro
207 Curry Building
Greensboro, NC 27402-6171 U.S.A.

Entries must be received by **December 20, 2002**. Official confirmation that the thesis has been accepted in the prior year must be provided. If the original thesis is not in English a summary paper in English must accompany it. Any questions concerning the prize should be directed to Dr. Ackerman (e-mail: taackerm@uncg.edu).

MANUSCRIPTS RECENTLY ACCEPTED FOR PUBLICATION

Listed in the Order They will be Published

Tests of Homogeneity of Means and Covariance Matrices for Multivariate Incomplete Data

Kevin H. Kim and Peter M. Bentler

Testing Unidimensionality in Polytomous Rasch Models

Karl Bang Christensen, Jakob Bue Bjorner, Svend Kreiner, and Jørgen Holm Petersen

A MCMC-METHOD FOR MODELS WITH CONTINUOUS LATENT RESPONSES

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This paper introduces a new technique for estimating the parameters of models with continuous latent data. Using the Rasch model as an example, it is shown that existing Bayesian techniques for parameter estimation, such as the Gibbs sampler, are not always easy to implement. Then, a new sampling-based Bayesian technique, called the DA-T-Gibbs sampler, is introduced. The DA-T-Gibbs sampler relies on the particular latent data structure of latent response models to simplify the computations involved in parameter estimation.

Key words: MCMC methods, Gibbs sampling.

This paper introduces a new technique for estimating the parameters of a particular class of models that involves latent data. These latent data are called latent responses (Maris, 1995), and they are related to the observed data in a particular way. Specifically, the observed data are the result of a mapping that takes continuous latent data as its argument. An example of a simple mapping of this kind is dichotomisation. Dichotomisation is used in the derivation of Thurstone's (1927) model of comparative judgment.

In the first section, a new method for parameter estimation, called the DA-T-Gibbs sampler, is introduced. We use the Rasch model (Rasch, 1980) as an example throughout the first section. The Rasch model probably is the simplest psychometric model that can be written as a model with continuous latent responses, as is required by our method. In the second section, we show that the DA-T-Gibbs sampler not only applies to the Rasch model but can be used with a whole range of psychometric models. In the third section, a simulation study is described in which some of the properties of the DA-T-Gibbs sampler are evaluated.

1. A New MCMC-method for the Rasch Model

In this section, we introduce a new Markov chain Monte Carlo (MCMC) method for models with continuous latent data. To streamline the presentation of this new method, a simple model is used as an example, namely the Rasch model. It should be clear that the Rasch model does not require a new method of parameter estimation, because there already exist excellent estimation procedures for this model (see Molenaar, 1995, for an overview).

The section begins with a short review of the Rasch model. After this, the components of our method are introduced one at a time. First, the Gibbs sampler (Geman & Geman, 1984) is introduced. Second, the principle of data augmentation (DA) (Tanner, 1996) is introduced,

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TRANSFORMING THREE-WAY ARRAYS TO MAXIMAL SIMPLICITY

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Transforming the core array in Tucker three-way component analysis to simplicity is an intriguing way of revealing structures in between standard Tucker three-way PCA, where the core array is unconstrained, and CANDECOMP/PARAFAC, where the core array has a generalized diagonal form. For certain classes of arrays, transformations to simplicity, that is, transformations that produce a large number of zeros, can be obtained explicitly by solving sets of linear equations. The present paper extends these results. First, a method is offered to simplify $J \times J \times 2$ arrays. Next, it is shown that the transformation that simplifies an $I \times J \times K$ array can be used to also simplify the (complementary) arrays of order $(JK - I) \times J \times K$, of order $I \times (IK - J) \times K$ and of order $I \times J \times (IJ - K)$. Finally, the question of what constitutes the maximal simplicity for arrays (the maximal number of zero elements) will be considered. It is shown that cases of extreme simplicity, considered in the past, are, in fact, cases of maximal simplicity.

Key words: three-way PCA, core array, simplicity.

Tucker 3-analysis (Tucker, 1966) is a three-way generalisation of PCA based on the following approximate factorisation of the data array

$$x_{ijk} \approx \sum_{p=1}^P \sum_{q=1}^Q \sum_{r=1}^R a_{ip} b_{jq} c_{kr} g_{pqr},$$

where x_{ijk} is the value of unit i on variable j at occasion k , a_{ip} is an element of an $I \times P$ component matrix \mathbf{A} for individuals, b_{jq} is an element of a $J \times Q$ component matrix \mathbf{B} for variables, c_{kr} an element of a $K \times R$ component matrix \mathbf{C} for occasions, and g_{pqr} is an element of a so-called three-way *core* array \mathbf{G} of order $P \times Q \times R$, containing weights for the joint impact of any triple of components from \mathbf{A} , \mathbf{B} and \mathbf{C} . The parameters are usually estimated by minimising the sum of squared residuals for fixed numbers of components in each mode (Kroonenberg & de Leeuw, 1980).

It is well-known that the parameters of the Tucker-3 model are not uniquely determined. In particular, the core array can be transformed in three directions. For instance, a $3 \times 3 \times 2$ core array containing two slabs or slices \mathbf{G}_1 and \mathbf{G}_2 can be replaced by an array with slices $\mathbf{SG}_1\mathbf{T}$ and $\mathbf{SG}_2\mathbf{T}$, respectively, for any pair of nonsingular 3×3 matrices \mathbf{S} and \mathbf{T} . In addition, there is the possibility of transforming the array in the third direction by so-called slabmixing. That is, when \mathbf{U} is any nonsingular 2×2 matrix, we may also transform $\mathbf{SG}_1\mathbf{T}$ and $\mathbf{SG}_2\mathbf{T}$ into $\mathbf{G}_1^* = u_{11}\mathbf{SG}_1\mathbf{T} + u_{21}\mathbf{SG}_2\mathbf{T}$ and $\mathbf{G}_2^* = u_{12}\mathbf{SG}_1\mathbf{T} + u_{22}\mathbf{SG}_2\mathbf{T}$, respectively. In general, the slabs $\mathbf{G}_1, \dots, \mathbf{G}_R$, of any core array can be transformed to $\mathbf{G}_1^*, \dots, \mathbf{G}_R^*$ by means of the *Tucker transformation*

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LOCALLY DEPENDENT LATENT TRAIT MODEL AND THE DUTCH IDENTITY REVISITED

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In this paper, we propose a class of locally dependent latent trait models for responses to psychological and educational tests. Typically, item response models treat an individual's multiple response to stimuli as conditional independent given the individual's latent trait. In this paper, instead the focus is on models based on a family of conditional distributions, or kernel, that describes joint multiple item responses as a function of student latent trait, not assuming conditional independence. Specifically, we examine a hybrid kernel which comprises a component for one-way item response functions and a component for conditional associations between items given latent traits. The class of models allows the extension of item response theory to cover some new and innovative applications in psychological and educational research. An EM algorithm for marginal maximum likelihood of the hybrid kernel model is proposed. Furthermore, we delineate the relationship of the class of locally dependent models and the log-linear model by revisiting the Dutch identity (Holland, 1990).

Key words: hybrid kernel, EM algorithm, generalized log-linear model, reproducibility.

Introduction

The generalizing and extending of item response theory (IRT) have led to a wide range of exciting psychometric applications that go beyond the scope of conventional latent trait theory. The broadening of the scope of IRT can be viewed as a reaction to the tension between the rather restrictive assumptions of the basic IRT model and the appearance of new, innovative methods in both educational assessment and psychological testing for complex cognitive and psychological outcomes. These newer methods often measure more granular structures of response patterns. There have been many attempts to solve practical and challenging psychological and educational measurement problems by either generalizing IRT or relaxing some of its stringent assumptions. Examples of generalizing IRT (without relaxing its basic assumptions) include multivariate IRT (Andersen, 1980; Embretson, 1984; Stout, 1990), models that integrate auxiliary information concerning items (Mislevy, 1996), and models that integrate collateral information about the examinee (Mislevy & Sheehan, 1989). Examples of relaxing IRT restrictions include componential cognitive models (Embretson, 1984, 1985), locally dependent models (Fischer & Formann, 1982), conjunctive and serial processing models (Jannanore, 1986), local dependence modeled via conditional covariance function (Douglas, Kim, Habing, & Gao, 1998; Habing, 1998), random-effect item-clustering models (Bradlow, Wainer, & Wang, 1999), the Bahadur model (Ip, 2000), and hierarchical model using simultaneous estimation methods (Scott & Ip, 2002). Finally, examples of using other strategies to manage possible violations of IRT assumptions include item bundle (Rosenbaum, 1988) and testlet (Wainer & Kiely, 1987).

The purpose of this paper is to present an analysis of the structure of a class of locally dependent (LD) latent trait models. Central to the inferential concept in IRT is the local independence (LI) assumption. Stated generally, LI asserts that items are homogeneous, conditional on latent traits. That is, "structure" exists between, but not within, subsets of items referenced to a common set (one or more) of latent traits θ . For a two-item test with responses Y_i , $i = 1, 2$, LI

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HYPERGEOMETRIC FAMILY AND ITEM OVERLAP RATES IN COMPUTERIZED ADAPTIVE TESTING

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A computerized adaptive test (CAT) is usually administered to small groups of examinees at frequent time intervals. It is often the case that examinees who take the test earlier share information with examinees who will take the test later, thus increasing the risk that many items may become known. Item overlap rate for a group of examinees refers to the number of overlapping items encountered by these examinees divided by the test length. For a specific item pool, different item selection algorithms may yield different item overlap rates. An important issue in designing a good CAT item selection algorithm is to keep item overlap rate below a preset level. In doing so, it is important to investigate what the lowest rate could be for all possible item selection algorithms. In this paper we rigorously prove that if every item has an equal possibility to be selected from the pool in a fixed-length CAT, the number of overlapping items among any α randomly sampled examinees follows the hypergeometric distribution family for $\alpha \geq 1$. Thus, the expected values of the number of overlapping items among any randomly sampled α examinees can be calculated precisely. These values may serve as benchmarks in controlling item overlap rates for fixed-length adaptive tests.

Key words: computerized adaptive testing, hypergeometric distribution, item exposure rate, item selection, stratification, Simpson-Hetter method, item overlap rate, test security.

1. Introduction

Computerized adaptive testing (CAT) has become a popular mode of assessment in educational testing. Examples of large scale CATs include the Graduate Record Examinations (GRE), the Graduate Management Admission Test (GMAT), and the National Council License Examination for Nurses. A CAT differs profoundly from a paper-and-pencil test. In the former, different examinees are tested with different sets of items that are selected sequentially from a large item pool to fit examinee's trait level. In the latter, all examinees are given an identical set of items. Lord (1970), who called a CAT a tailored test, argued that tailoring items to the trait has an advantage over not tailoring because an examinee is measured most effectively when the test items are neither too difficult nor too easy. Wainer (1990) also noted that the basic notion of an adaptive test is to mimic automatically what a wise examiner would do. In doing so, certain types of items tend to be always selected, and many items are not selected at all, thereby making item exposure rates quite uneven. Since CATs are usually administered to small groups of examinees at frequent time intervals, examinees who take tests earlier may share information with examinees who will take tests later, increasing the risk that many items may become known. Therefore, item exposure must be controlled.

Item exposure control has been a major concern in the development and implementation of CATs. However, unlike many other aspects in CAT, there is a lack of theoretical developments in limiting item exposure. Way (1998) pointed out that there is no common understanding as yet

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TESTING THE SIGNIFICANCE OF THE SUCCESSIVE COMPONENTS IN REDUNDANCY ANALYSIS

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In this paper we study the interrelationships between two sets of data measured on the same subjects via redundancy analysis. We consider redundancy analysis from an inferential point of view. Under the hypothesis of multinormality, tests of significance are obtained for each successive redundancy component so that only the significant factors are retained for prediction purposes. An example illustrates the method.

Key words: redundancy analysis, significant factors, tests of significance, canonical correlation, multivariate linear regression.

1. Introduction

Canonical correlation analysis is a sequential procedure which consists of extracting linear functions (canonical factors) from two sets of variables simultaneously in order to maximize the correlation between these factors. It is a symmetric analysis in the sense that it does not distinguish between dependent variables and independent variables (predictors). It thus cannot account for the proportion of explained variance of dependent variables. In fact, canonical correlation analysis is not meant for prediction purposes.

When it is necessary to investigate the prediction of a set Y of variables from a set X of predictors, one usually uses the redundancy index introduced by Stewart and Love (1968) and later generalized by Gleason (1976). It is equal to the fraction of the total variance in the Y set which is accounted for by the linear prediction of Y by factors of X and thus measures the degree to which the set X can predict the set of dependent variables.

Using this measure of redundancy, van den Wollenberg (1977) introduced the method of redundancy analysis which consists of extracting factors from the X set which maximize redundancy between the two sets of variables. Redundancy analysis is seen to be a compromise between canonical correlation analysis and multivariate regression. It is also equivalent to principal component analysis with respect to a set of instrumental variables (see, for instance, Rao, 1964; or Bry, 1996).

The following authors have also considered redundancy analysis either to study their properties, to clarify its relationships to canonical correlation analysis or to multivariate regression, or to suggest some extensions of the method: Fornell (1979), Johansson (1981), DeSarbo (1981), Muller (1981), Tyler (1982), Dawson-Saunders and Tatsuoka (1983), Israëls (1984), van de Geer (1984) and Buzas, Fornell, & Byong-Duk Rhee, (1989).

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INFLUENCE ANALYSIS OF RANKING DATA

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This paper develops diagnostic measures to identify those observations in Thurstonian models for ranking data which unduly influence parameter estimates that are obtained by the partition maximum likelihood approach of Chan and Bentler (1998). Diagnostic measures are constructed by employing the local influence approach that uses geometric techniques to assess the effect of small perturbations on a postulated statistical model. Very little additional effort is required to compute the proposed diagnostic measures, because all of the necessary building blocks are readily available after a usual fit of the model.

Key words: ranking data, partition maximum likelihood estimation, local influence, diagnostic measure.

1. Introduction

Ranking data, also known as ordinal ipsative data, are obtained when subjects are asked to rank p objects from 1 (least preferred) to p (most preferred). One popular approach to analyzing such data is to operate on the assumption that judgments are based on a set of subjective values associated with the p different objects, and that the set of subjective values is distributed as multivariate normal (see, e.g., Böckenholt, 1992; Chan & Bentler, 1998; Thurstone, 1927). Procedures have been proposed to estimate the model and, in particular, the procedure suggested by Chan and Bentler (1998) employing the Partition Maximum Likelihood (PML) approach is computationally efficient. Although estimates produced by this procedure are in general consistent, unreliable estimates arise when there exist several observations in the data set influencing the estimation in a disproportionate way. Therefore, it is of interest to locate these observations. In effect, the identification and accommodation of influential observations has long been an important topic in various statistical analyses (see, e.g., Andersen, 1992; Cook, 1977; Poon & Poon, 2002; Poon, Wang & Lee, 1999; Tanaka, Watadani & Moon, 1991; Thomas & Cook, 1990; Yuan & Bentler, 2001; Yuan, Chan & Bentler, 2000). However, it has received very little attention in the analysis of ranking data.

In this article, we develop diagnostic measures for the identification of influential observations in the analysis of ranking data. The estimation method of Chan and Bentler (1998) is employed to analyze the multivariate normal model, and the local influence approach proposed by Cook (1986) is utilized to develop diagnostic measures. The local influence approach uses techniques of differential geometry to assess the influence of local perturbation on a postulated statistical model, and various influence measures can be constructed by introducing relevant perturbations to the model. The diagnostic measures thus developed can handle joint influences, and their computations require very little additional effort after a usual fit of the model.

In the next section, the multivariate normal model for analyzing ranking data is presented. The Maximum Likelihood (ML) estimation method is given in section 3, in which the basic principles of the local influence approach are also introduced. Section 4 summarizes the computational efficient estimation procedure suggested by Chan and Bentler (1998) and develops diagnostic measures for identifying influential observations to accompany this procedure. Sec-

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ON UNIQUENESS IN CANDECOMP/PARAFAC

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One of the basic issues in the analysis of three-way arrays by CANDECOMP/PARAFAC (CP) has been the question of uniqueness of the decomposition. Kruskal (1977) has proved that uniqueness is guaranteed when the sum of the k -ranks of the three component matrices involved is at least twice the rank of the solution plus 2. Since then, little has been achieved that might further qualify Kruskal's sufficient condition. Attempts to prove that it is also necessary for uniqueness (except for rank 1 or 2) have failed, but counterexamples to necessity have not been detected. The present paper gives a method for generating the class of all solutions (or at least a subset of that class), given a CP solution that satisfies certain conditions. This offers the possibility to examine uniqueness for a great variety of specific CP solutions. It will be shown that Kruskal's condition is necessary and sufficient when the rank of the solution is three, but that uniqueness may hold even if the condition is not satisfied, when the rank is four or higher.

Key words: Candecomp, Parafac, uniqueness, three-way arrays.

Let \mathbf{X} be a three-way data array of order $I \times J \times K$, containing K frontal slices $\mathbf{X}_1, \dots, \mathbf{X}_K$ of order $I \times J$. CANDECOMP/PARAFAC (CP), see Carroll and Chang (1970) and Harshman (1970), in R dimensions decomposes the slices as

$$\mathbf{X}_k = \mathbf{A}\mathbf{C}_k\mathbf{B}' + \mathbf{E}_k, \quad (1)$$

where \mathbf{A} is an $I \times R$ matrix, \mathbf{B} is a $J \times R$ matrix, \mathbf{C}_k is a diagonal matrix, containing the elements of row k of a $K \times R$ matrix \mathbf{C} , $k = 1, \dots, K$, and \mathbf{E}_k is a matrix of residuals. The decomposition is fully symmetric in \mathbf{A} , \mathbf{B} , and \mathbf{C} . That is, they may switch places in (1) if we switch the modes of the array and residual array accordingly.

Suppose there exists an alternative solution of the form

$$\mathbf{X}_k = \mathbf{G}\mathbf{D}_k\mathbf{H}' + \mathbf{E}_k \quad (2)$$

with \mathbf{G} and \mathbf{H} of the same order as \mathbf{A} and \mathbf{B} , respectively, and \mathbf{D}_k diagonal, containing the elements of row k of a $K \times R$ matrix \mathbf{D} , $k = 1, \dots, K$. A solution for CP is said to be *unique* when, for every other solution of the form (2), $\mathbf{G} = \mathbf{A}\Pi\Lambda_1$, $\mathbf{H} = \mathbf{B}\Pi\Lambda_2$, and $\mathbf{D} = \mathbf{C}\Pi\Lambda_3$, for some permutation matrix Π and diagonal matrices Λ_1 , Λ_2 , and Λ_3 , with $\Lambda_1\Lambda_2\Lambda_3 = \mathbf{I}_R$. It is obvious that the residuals play no role at all, in the present context. They will be ignored in the sequel. As a matter of convenience, we shall consider them to vanish, which means that \mathbf{X}_k does not denote a slice of the original array, but merely the CP fitted part of it.

This paper is concerned with conditions for uniqueness of CP decompositions. Kruskal (1977) has shown that uniqueness holds under relatively mild conditions, to be discussed shortly. These conditions are necessary and sufficient for uniqueness when $R = 2$, but they are not necessary when $R = 1$. It has long been conjectured that these conditions are generally necessary

The authors are obliged to Henk Kiers for commenting on a previous draft, and to Tom Snijders for suggesting a proof mentioned in the appendix.

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LATENT CHANGE CLASSES IN DICHOTOMOUS DATA

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Changes in dichotomous data caused by treatments can be analyzed by means of the so-called linear logistic model with relaxed assumptions (LLRA). The LLRA does not require observable criteria representing a single underlying latent trait, but it postulates the generalizability of the treatment effects over criteria and subjects. To test this latter crucial assumption, the mixture LLRA was proposed that allows directly unobservable types of subjects to have different treatment effects. As the earlier methods for estimating the parameters of the mixture LLRA have specific drawbacks, a further method based on the conditional maximum likelihood principle will be presented here. In contrast to the earlier conditional methods, it uses all of the dichotomous change data while having fewer parameters. Further, its goodness-of-fit tests become more sensitive to a falsely specified number of change-types even though the treatment effects are biased. For typically occurring small to moderate sample sizes, however, parametric bootstrapping of the distributions of the fit statistics is recommended for performing hypotheses tests. Finally, three applications of the new method to empirical data are described: first, about the effect of the so-called Trager psychophysical integration, second, about the effect of autogenic therapy on patients with psychosomatic symptoms, and, third, about the effect of religious education on the attitude towards sects.

Key words: latent heterogeneity, linear logistic models, local stochastic independence, mixture binomial, (parametric) bootstrapping, panel data, treatment effect.

1. Introduction

Formann (1994) described four approaches for measuring change in latent subgroups using dichotomous panel data observed before and after the treatment(s): the unconditional, two variants of the conditional, and the semiparametric maximum likelihood (ML) method. These mixture approaches generalized the linear logistic model with relaxed assumptions (LLRA; Fischer, 1972, 1983, 1989) in such a way that linear logistic latent class analysis (LOGLCA) was immediately applicable. Under the unconditional ML approach, both the structural (fixed effects) change parameters as well as the incidental (random effects) subject parameters (more precisely, their means) were estimated jointly. Under the semiparametric approach, the distributions of the subject parameters were approximated semiparametrically while estimating the change parameters according to the ML principle. Both approaches used the complete response vectors observed per person at both points in time. In contrast to this, both conditional ML approaches considered the change data, under the full-information approach all of the vectors of trichotomous change data (positive change, negative change, no change), under the partial-information approach only those complete vectors of dichotomous change data (positive change, negative change) where no single entries were missing (no change). For details, see Formann (1994, p. 1029).

Some simulation studies made it clear that, apart from their common need for very large samples, all four methods proposed have disadvantages in performance as regards estimating the parameters or in power against falsely specified numbers of change-types. The unconditional and conditional ML methods have been shown to be inferior to the semiparametric ML method, provided that the number of support points is appropriately chosen. But this number—reflecting the sample's heterogeneity—is unknown from the beginning and thus has to be determined dur-

The mixture LLRA is implemented in the menu-driven program MIXLLRA which can be obtained from Ivo Ponocny via e-mail (ivo.ponocny@univie.ac.at).

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A BRANCH-AND-BOUND ALGORITHM FOR FITTING ANTI-ROBINSON STRUCTURES TO SYMMETRIC DISSIMILARITY MATRICES

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The seriation of proximity matrices is an important problem in combinatorial data analysis and can be conducted using a variety of objective criteria. Some of the most popular criteria for evaluating an ordering of objects are based on (anti-) Robinson forms, which reflect the pattern of elements within each row and/or column of the reordered matrix when moving away from the main diagonal. This paper presents a branch-and-bound algorithm that can be used to seriate a symmetric dissimilarity matrix by identifying a reordering of rows and columns of the matrix optimizing an anti-Robinson criterion. Computational results are provided for several proximity matrices from the literature using four different anti-Robinson criteria. The results suggest that with respect to computational efficiency, the branch-and-bound algorithm is generally competitive with dynamic programming. Further, because it requires much less storage than dynamic programming, the branch-and-bound algorithm can provide guaranteed optimal solutions for matrices that are too large for dynamic programming implementations.

Key words: combinatorial optimization, branch and bound, seriation, anti-Robinson form.

1. Introduction

The seriation and unidimensional scaling of a set of n objects, $S = \{o_1, o_2, \dots, o_n\}$, is an important combinatorial problem in quantitative psychology. In many cases, information about the relationships among the objects in S is represented in the form of an $n \times n$ proximity matrix. The seriation of large matrices ($n > 25$) typically requires the use of heuristic solution procedures that provide good (but not necessarily globally optimal) solutions. Perhaps the most common type of local-search operation deployed in heuristic procedures for seriation and unidimensional scaling is based on the pairwise interchange of objects in the sequence (Baker & Hubert, 1977; Groenen, 1993). Hubert and Arabie (1994) suggested using object block reversals and object insertions as additional local-search strategies. An integrated local-search process consisting of pairwise interchange, object block reversals, and object insertions has proven effective for several problems related to seriation and unidimensional scaling (Brusco & Stahl, 2000; Hubert & Arabie, 1994; Hubert, Arabie, & Meulman 1997).

Despite the reliance on heuristic procedures for large-scale seriation and unidimensional scaling tasks, considerable attention has also focused on the development of optimal procedures. As recently observed by Hubert, Arabie, and Meulman (2001), optimal solution procedures can successfully be applied to problems that are nontrivial in size. These procedures also facilitate the development of heuristic solution methods by providing benchmarks. Perhaps the most widely used optimal solution procedure for seriation and unidimensional scaling is dynamic programming, which has been successfully applied to a number of problems including the seriation of asymmetric matrices (Brusco & Stahl, 2001; Hubert & Golledge, 1981; Lawler 1964) and least-squares unidimensional scaling (Hubert & Arabie, 1986; Hubert et al., 2001). Hubert et al. (2001) have recently documented many combinatorial data analysis problems that can be modeled using the dynamic programming paradigm, and also have made software programs available for such problems. For seriation and unidimensional scaling of proximity matrices on a modestly

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