



Chapter 5

Conclusions

5.1 Introduction

In the previous chapters we have developed convergent algorithms for the estimation of the parameters corresponding to the MATCHALS models (1.8) through (1.12) given in Chapter 1. These models are designed to investigate the relationships between n sets of configurations containing the coordinates of the same p stimuli, and are offered as an alternative for the PINDIS models of Lingoes and Borg (1978). Each one of the MATCHALS algorithms is capable of handling m -dimensional complete as well as incomplete configurations and, unlike the PINDIS models and algorithms, nowhere is any transformation parameter being 'borrowed' from another model, except as initial estimate.

The MATCHALS models and algorithms also confront us with new problems and questions, some of which have already been mentioned, and others that we will discuss in this final chapter. First, however, we will summarize the most important conclusions of Chapters 2, 3, and 4. In section 5.2 an overview is given of the main properties of the MATCHALS algorithms. In section 5.3 we recapitulate the uniqueness properties of the MATCHALS models, and in section 5.4 we summarize the results concerning the decompositions of the sums of squares associated with the different models. The last two sections of this chapter are devoted to topics that we have not discussed so far: the statistical aspects of the models (section 5.5), and the possibility of using the models as a form of confirmatory scaling (section 5.6).

5.2 The MATCHALS algorithms

The algorithm for the estimation of the unknown parameters in the GPA model is by far the fastest of the five algorithms presented in this book. In general, it takes only a few iterations to converge, even when a strict convergence criterion is used. This algorithm iterates over two sets of parameters only: the rotation matrices and the scaling factors. Although it can not be proved that the GPA algorithm always converges to a global optimum, it seems to do so in practice.

The algorithms presented for the dimension weighting models consume considerably more CPU-time than the GPA algorithm. The number of iterations required to reach convergence is (much) larger, and within each iteration three sets of

parameters have to be estimated in the DIMFREE algorithm, while the DIMIDIO algorithm iterates over only two sets of parameters. For the estimation of a new centroid configuration in each iteration of the DIMFREE algorithm, it makes quite a difference whether the configurations are complete or not. In the case of incomplete configurations the Moore-Penrose inverse of m matrices of order $(p \times p)$ must be calculated (where m is the number of dimensions and p the number of stimuli), while the nonmissing case only requires the computation of the proper inverse of one $(m \times m)$ diagonal matrix. In DIMIDIO the difference in CPU-time between complete and incomplete configurations with respect to the estimation of an optimal centroid configuration is even more dramatic. Without missing data, we only need to determine the proper inverse of one matrix of order $(m \times m)$, while the calculation of the Moore-Penrose inverse of a full $(pm \times pm)$ matrix is required in the case of incomplete configurations. The latter case may even prove to become impractical for large p and m . Although the DIMFREE and DIMIDIO algorithms must converge, it can not be guaranteed that they will always converge to a global minimum. However, in the case of constructed data sets with known perfect solutions we have found that they did recover the perfect solution.

The algorithms for the estimation of the unknown transformation parameters of the stimulus weighting models are also much more expensive than the GPA algorithm. A most serious disadvantage of the stimulus weighting algorithms is that they seem to converge to local minima very easily.

5.3 Uniqueness properties of the MATCHALS models

The solution of the GPA model is unique up to a simultaneous rotation of the complete solution. We have used this indeterminacy to rotate the solution to the principal components of the optimal centroid or group configuration. But any other set of dimensions in the GPA group configuration can be chosen for interpretational purposes. In GPA, the centroid configuration is always a column-centered matrix.

The latter property of the GPA group configuration is shared by the DIMFREE group configuration. In addition, the DIMFREE group configuration has an important property that is lacking in the GPA model: its axes are unique, because it is this set of axes that is differentially weighted. Therefore, what counts in the interpretation of the

DIMFREE solution is the ordering of the stimuli on these optimally oriented dimensions of the group configuration. Although the axes are unique, the *variances* of the coordinates of the stimuli on these axes are not. We have used this freedom to unit normalize the columns of the centroid configuration, yielding a DIMFREE solution that is unique up to reflections and permutations of the m dimensions (cf., section 3.3.7 of Chapter 3).

The centroid configuration in the DIMIDIO model is, again, columnwise centered, but its columns may be replaced by arbitrarily weighted linear combinations of these same columns. This indeterminacy can be used to replace the 'raw' centroid configuration by an orthonormal basis, yielding a DIMIDIO group configuration that is columnwise orthonormal. This procedure results in unique dimension weights and rotation matrices for the individual configurations, and reduces the previous indeterminacy to a mere rotational indeterminacy (cf., section 3.4.6 of Chapter 3). Since the centroid configuration is rotated idiosyncratically before its dimensions are weighted, the interpretation in DIMIDIO should focus on the idiosyncratic axes of the group configuration.

In contrast with the GPA, DIMFREE, and DIMIDIO models the group configuration obtained in the STIMFREE model will usually not be a column-centered matrix. The *angles* between the vectors generated by connecting the stimulus points in the group configuration with the origin are unique in STIMFREE. Only the lengths of the latter vectors are not determined uniquely. Because this greatly facilitates the interpretation of the stimulus weights, we have used this indeterminacy to unit normalize the rows of the centroid configuration. As a result, the end points of the stimulus vectors all lie on the unit (hyper)sphere (cf., section 4.3.7 in Chapter 4). About the properties of the STIMIDIO model we can be very brief: the STIMIDIO solution is *not* unique (cf., section 4.4.7).

5.4 Analyses of variation

In each of the five MATCHALS models the total sum of squares of the individual configurations (SS_{total}) can be partitioned in two parts: the variation accounted for by the model (SS_{fit}), and the residual variation (SS_{residual}). Since the configurations are always normalized such that their total variation equals n , that is, the number of

Table 5.1 Overview of the possible partitionings of SS_{tot} , SS_{fit} , and SS_{res} with respect to individual configurations, stimuli, and dimensions in the five MATCHALS models.

models	by configuration	by stimulus	by dimension
GPA	no	yes	yes
DIMFREE	yes	no	yes
DIMIDIO	yes	no	yes
STIMFREE	yes	no	yes
STIMIDIO	yes	no	yes

configurations, the partitioning takes the following form: $n = SS_{\text{fit}} + SS_{\text{res}}$. Hence, for all models $(1/n)SS_{\text{fit}}$ is a measure of total fit.

In Table 5.1 we have summarized for the five models whether SS_{total} , SS_{fit} , and SS_{residual} can each be further partitioned with respect to individual configurations, stimuli and dimensions. As the table shows, the GPA model is the only model where the sums of squares can not be partitioned with respect to individual configurations (cf., section 2.5 of Chapter 2). In the remaining models the contribution of each configuration to the solution can be assessed unambiguously. Moreover, the measure of configuration fit that we derived in the dimension and stimulus weighting models can be shown to be equal to the squared correlation between the elements of the optimally transformed individual configuration and the elements of the optimally weighted centroid configuration. For the stimuli the situation is completely reversed: the GPA model is the only model where SS_{tot} , SS_{fit} , and SS_{res} can be further partitioned with respect to the individual stimuli. Finally, a partition with respect to the separate dimensions can be performed in all five models.

5.5 Statistical aspects

Although measures of total fit are available for all five models, as well as measures of configuration fit for the dimension and stimulus weighting models, an important question remains. For what value of the total fit can we state that a model fits the data well? And, perhaps even more importantly, how small must the value of the fit be

before we decide to reject a particular model? One way to answer these questions, of course, is to design statistical tests. However, as yet no statistical sampling theory has been developed, and no tests are available to determine whether the values of the measures of total and configuration fit are significant or not.

A more feasible approach is to provide baselines against which to evaluate the measures of fit. This typically calls for Monte Carlo studies such as have been performed for the PINDIS models by Langeheine (1982). Baselines can be obtained by generating random configurations using varying numbers of configurations, stimuli, dimensions, and missing rows in the configurations, and then analyzing these data sets with MATCHALS.

Such studies are especially necessary for the dimension and stimulus weighting models proposed in this book. Since new centroid configurations are being estimated in these models, and because we provide better algorithms, it can be expected that, all other things being equal, the values of the measures of fit for these models on random data will be (much) higher than those found by Langeheine.

Some insight in the meaning of the fit values can be gained by comparing the number of parameters estimated in each model with the degrees of freedom of the total sum of squares. An overview of these figures is given in Table 5.2, where n , p , and m are the number of configurations, stimuli, and dimensions, and p_j denotes the number of non-missing rows of configuration X_j . As the table shows, the number of parameters estimated in the GPA, DIMFREE, and DIMIDIO models does not depend on the number of missing rows in the configurations. Therefore, if we analyse a data

Table 5.2 Numbers of free parameters in the MATCHALS models.

model	df of SS_{tot}	estimated parameters	total number of estimated parameters
GPA	$m \sum_{j=1}^n (p_j - 1)$	R_j 's, s_j 's, Z	$n \binom{m}{2} + (n - 1) + m(p - 1)$
DIMFREE	$m \sum_{j=1}^n (p_j - 1)$	Q_j 's, W_j 's, Y	$n \binom{m}{2} + nm + m(p - 1)$
DIMIDIO	$m \sum_{j=1}^n (p_j - 1)$	Q_j 's, W_j 's, Y , S_j 's	$n \binom{m}{2} + nm + m(p - 1) + n \binom{m}{2}$
STIMFREE	$m \sum_{j=1}^n (p_j - 1)$	T_j 's, V_j 's, Y	$n \binom{m}{2} + \sum_{j=1}^n p_j + mp$
STIMIDIO	$m \sum_{j=1}^n (p_j - 1)$	T_j 's, V_j 's, Y , h_j 's	$n \binom{m}{2} + \sum_{j=1}^n p_j + mp + nm$

set only containing complete configurations with GPA, DIMFREE or DIMIDIO, and then re-analyse the same data set treating some rows as missing, the fit of the latter solution will always be better than the fit of the solution for the complete configurations. It is important to keep in mind, however, that such an improvement in fit is only due to the fact that the same number of parameters has been estimated for a smaller number of stimulus points.

It also follows from Table 5.2 that, if we are dealing with four complete configurations of eight stimuli in three dimensions, for example, the total sum of squares has 84 degrees of freedom, while a total number of 36, 45, 57, 64, and 76 parameters is estimated in the GPA, DIMFREE, DIMIDIO, STIMFREE, and STIMIDIO models, respectively. Hence, with four configurations containing eight stimuli the ratio between the total number of estimated parameters and the degrees of freedom of the total sum of squares is quite lop-sided: the DIMFREE model already consumes more than half of the degrees of freedom.

However, the larger the number of stimuli and configurations, the better the ratio becomes. With fifteen complete three-dimensional configurations containing information about 20 stimuli, for instance, the degrees of freedom of SS_{tot} are 855, while a total number of 116, 147, 192, 405, and 450 parameters is consumed by the GPA, DIMFREE, DIMIDIO, STIMFREE, and STIMIDIO models, respectively. Therefore, it can be expected that for fifteen configurations containing 20 stimuli the fit for random data will be much smaller than for four configurations containing information about eight stimuli (although the STIMIDIO model still consumes more than half of the degrees of freedom of the total sum of squares).

But baselines are badly needed, and Monte Carlo studies will have to be performed to be able to decide to what extent a MATCHALS solution is capitalizing on chance. As long as these baselines are not available, however, the following procedure can be used to investigate the significance of the match found for a given set of configurations. Re-analyse the given data set a number of times (say k times) after a separate random permutation of the rows of each configuration, and calculate the mean and standard deviation of the observed fits, including the fit for the original data set. Then compute the t ratio for the latter fit, and check whether the t value is significant beyond the level of some a priori chosen probability α . If so, this is a strong indication that the match is not merely due to chance.

5.6 Confirmatory versus exploratory analysis

In the PINDIS computer program of Lingoes and Borg an option is available allowing the user to input an externally derived centroid configuration. Such a configuration may be self-designed and based on theoretical grounds (a circumplex, for example), or the result of a previous MDS or other analysis. If this option is chosen in the PINDIS program, all PINDIS models of Lingoes and Borg are fitted on this fixed external centroid configuration. This procedure makes it possible to investigate the match between the (optimally transformed) individual configurations and the 'hypothesis' or 'target' (i.e., the given centroid configuration) that one had in mind, and can in this sense be regarded as a form of confirmatory data analysis.

It is worth mentioning that we have also developed convergent alternating least squares algorithms that fit the GPA model and the dimension and stimulus weighting models given a fixed external centroid configuration. These algorithms have, again, been designed to handle m-dimensional as well as incomplete individual configurations. Since the default option in PINDIS already uses the centroid configuration obtained in GPA as fixed group configuration in the dimension and stimulus weighting models (cf., section 1.2 of Chapter 1), our algorithms for performing confirmatory analyses according to the latter four models are, in fact, improved and generalized versions of the algorithms proposed by Lingoes and Borg.

Appendix

An APL prototype version of the MATCHALS program in which all the algorithms presented in this book have been implemented can be obtained from the author at the following address:

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