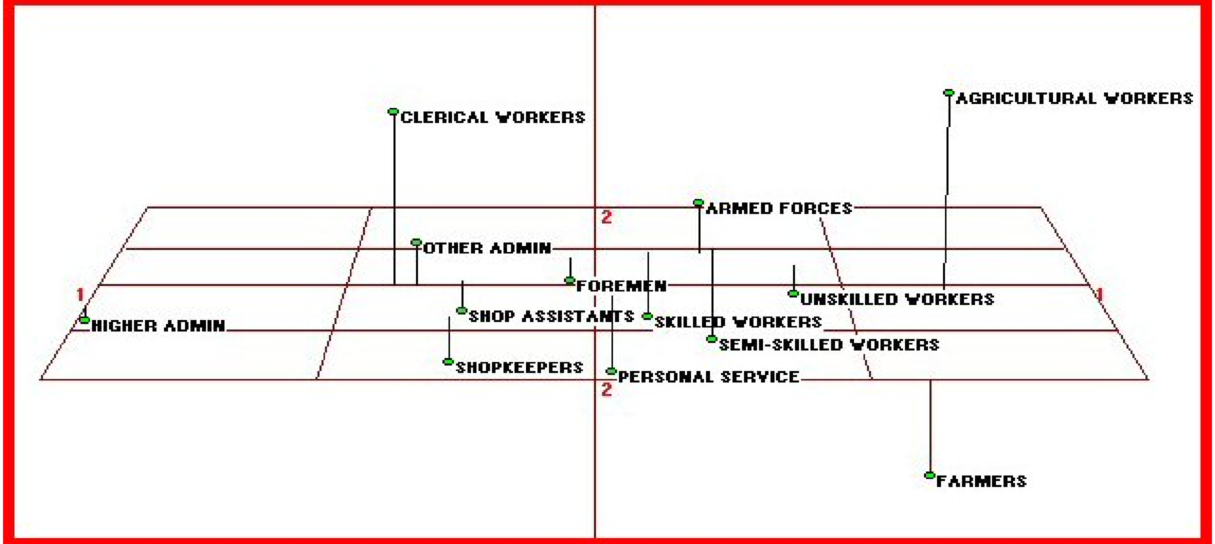
THE NewMDSX SERIES OF MULTIDIMENSIONAL SCALING PROGRAMS

USERS' MANUAL

FOR WINDOWS 9x / NT / 2000/XP

NewMDSX



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Background

The original MDS(X) Project was funded (1974-1982) by the U.K. Social Science Research Council in conjunction with the Program Library Unit of the University of Edinburgh. It grew out of the frustration of a research group at Edinburgh University trying to work out the similarities and differences in programs coming from different sources – particularly Bell Laboratories and University of Michigan (Guttman-Lingoes). The project was designed to:

- Collect MDS and related programs in common use or of particular interest
- rewrite the source-code up to Fortran77 specifications
- replace the common subroutines by numerically efficient versions
- provide a common instruction set for running programs
- produce a utility for producing measures from raw data for input into (any) multidimensional scaling programs.

For many years, a mainframe version was widely available, and maintained until recently by Manchester Information and Associated Services [http://www.mimas.ac.uk/]. Until recently its main use has been on PCs operating under MD-DOS. This manual describes a new version for use with Windows 9x, NT, 2000, and XP.

The Windows version now includes programs for Correspondence Analysis (CORRESP) , analysis of sorting data (MDSORT), and principal components analysis (PRINCOMP), in addition to the routines originally available in MDS(X).

For information about MDS(X) on MAC machines contact Wolfgang Otto: [wotto@sozpsy.unizh.ch]. He has also operated NewMDSX for Windows successfully using the MAC PC emulator.

A version of NewMDSX for Linux is in preparation.

The NEWMDS Project has a number of SPONSORS and COUNTRY REPRESENTATIVES in addition to the Core Project Team.

1. SPONSORS
<LIST TO FOLLOW>
2. COUNTRY REPRESENTATIVES
<LIST TO FOLLOW>
3. NEWMDSX PROJECT TEAM

Professor A. P. M. Coxon (University of Edinburgh)	apm.coxon@ed.ac.uk
Dr A.P.Brier	a.p.brier@boltblue.com
Professor C.L. Jones (University of Toronto)	cjones@chass.utoronto.ca
Mr D.T. Muxworthy (University of Edinburgh)	dtm@holyrood.ed.ac.uk
Mr W. Otto (University of Zurich)	wotto@sozpsy.unizh.ch
Dr S.K. Tagg (Strathclyde University)	s.k.tagg@strath.ac.uk
Dr. Wijbrandt H. van Schuur (University of Groningen)	h.van.schuur@ppsw.rug.nl
Dr Nico Tiliopoulos (Queen Margaret University College, Edinburgh)	n.tiliopoulos@ed.ac.ak

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All enquiries about NewMDSX should be directed to enquiries@newmdsx.com

The NewMDSX Home Page is at http://www.newMDSX.com

INTRODUCTION

Why scale to begin with ?

The purpose of scaling is to obtain a quantitative representation of a set of data.

How is such a representation obtained ? The basic idea is that much data can be thought of as giving information about how similar or dissimilar things are to each other. Scaling models then take this idea seriously, and represent the objects as points in space. In this space, the more similar objects are, the closer they lie to each other. The pattern of points which most accurately represent the information in the data is referred to as 'the solution' or 'final configuration'. Some common uses of MDS are:-

1. to measure an attitude, attribute or variable. e.g. the subjective loudness of a series of tones, the degree of ethnocentrism, the intensity of a particular sexual orientation, preference for a range of educational policies, the utility of a set of goods, the prestige of a group of occupations.

2. to portray complex data in a simpler manner. e.g. to represent the relationships between a set of objects in an easily assimilable, usually spatial, form.

3. to infer latent dimensions or processes. e.g. to identify the factors involved in peoples' judgements of the desirability of types of housing, or the most likely historical sequence of a set of graves, or how subjects' overall judgements of similarity relate to the known properties of the objects concerned.

DATA THEORY AND MEASUREMENT

The main impetus towards developing MDS models came from the wish to develop distance models as a paradigm for the measurement and analysis of psychological and social science data, and to build such models without being committed to the strong distributional or measurement assumptions usually made. This so-called "non-metric" orientation has been associated above all with Clyde Coombs (1964) who pioneered much early non-metric MDS modelling, and whose viewpoint might be summarised in the following propositions:

i) Assumptions about the "level of measurement" of one's data, and assumptions involved in the scaling models used to analyse data, commit one to substantive hypotheses about human behaviour.

ii) It is better to err on the side of conservatism in attributing metric properties to social science data, and to use weaker measurement structures to represent them.

iii) Because most social science data have been elicited in non-experimental settings, and often refer to diversified or non-

> homogeneous populations, it is well to be especially sensitive to individual or group differences, which may be crucial to the interpretation of the processes generating the data, but which are typically "washed out" in the usual aggregation procedures.

Coombs' initial work lay in the analysis of preferential data and he evolved a distance model for their analysis. This model, which he termed "Unfolding Analysis" was especially sensitive to individual differences. The failure to develop a workable algorithm for fallible data meant that Unfolding Analysis was of little interest to the practising scientist, however attractive it was, or sensitive it was to representing individual differences. A tractable algorithm in fact awaited the development of multi-dimensional scaling procedures, which were equally committed to making use only of ordinal information to obtain a metric solution to the data.

NON-METRIC MDS: THE BASIC MODEL

Developments in non-metric MDS procedures and models represent one of the most significant methodological advances of the last forty years. Stated simply, their purpose seems very pedestrian – namely to relax the assumption of linearity usually made about the kind of function linking the dissimilarities (the data) and the distances in the solution. In this sense, it could be seen as analogous to the shift of interest to non-parametric statistics. The greatest pay-off from the use of non-metric MDS is that the same basic algorithm is easily extended to very different types of data, to different models (other than just the distance model) and it is readily applied in a wide variety of situations and in disciplines as diverse as archaeology and electronics as well as the usual social science applications. Moreover, unlike conventional multivariate models, assumptions about distributions rarely need to be made and the procedures in no way depend upon the particular measures of similarity used. For example, frequencies, probabilities, ratings, co-occurrences are quite as appropriate as measures of similarity as are composite indices like coefficients of correlation, covariance, association and overlap. Perhaps most importantly, however, non-metric MDS solutions are "order-invariant". That is to say that only the ordinal content of the data is made use of in obtaining a solution, so that any set of data with the same ordering of (dis)similarities will generate the same metric solution.[1]

The basic rationale of non-metric MDS is well discussed in Shepard (1962). He begins by considering the difficulty of achieving numerical representation when only a ranking of the objects is known. This stems from the fact that points representing the objects can be moved very extensively (i.e. can take on a large range of numerical values), whilst still satisfying such ordinal constraints. However, once the representation must in addition satisfy "ordered metric" constraints (i.e. once the data contain, in addition, information on the order of the inter point distances) the range of possible numerical values is greatly reduced:

> "if non-metric constraints are imposed in sufficient number they begin to act like metric constraints ... As the points are forced to satisfy more and more Inequalities on the inter-point distances ... the Spacing tightens up until any but very small Perturbations of the points will usually isolate one or more of the inequalities" (ibid. 288).

The notion that order relations on distances impose very severe constraints on the uniqueness of numerical representation is now commonplace, but its convincing demonstration awaited the development of an iterative algorithm to implement the set of constraints obtained from the data. The basic rationale for this non-metric MDS algorithm is given by Kruskal (1964) and this has formed the basis for almost all subsequent work in this area.[2]

2.1 The empirical data are interpreted as follows

i) There is a set C of objects (often termed stimuli), and these objects will be represented as points in a multidimensional space. Significant information about the relations between the objects is contained in some empirical measure of dis/similarity, linking pairs of objects. Only the (possibly weak) ordering of these dissimilarity coefficients

$$\delta(c_i , c_j) = \delta_{ij}$$

will be preserved in obtaining the solution.

In common terminology, the measures input to MDS are termed "proximities" or "dis/similarities". This usage emphasizes the fact that such measures may be EITHER similarities OR dissimilarities; the only difference is that dissimilarities will be positively related to the distances of the solution whereas similarities will be related negatively to the distances of the solution. Thus if similarity measures (such as correlations, co-occurrences as well as actual similarity ratings)are input then the higher the similarity of two objects, the closer they will be made to be in the solution space, whereas if a dissimilarity measure (such as the Index of Dissimilarity, Euclidean distance or dissimilarity ratings)is input, the higher the dissimilarity of two objects, the more distant they will be made to be in the solution space. Users should be especially careful to check which of the two types their data measure is, as this is one of the most common mistakes made in MDS runs, and even if such a mistake is made, a program will still run to completion, giving high-stress "inverted", meaningless solutions.
Because input measures are most commonly similarities, this is usually the default value in programs. However, in explaining MDS, it is often simpler to talk of data as dissimilarities, because they are semantically analogous to the distances of the Distance model.

ii) The solution, or configuration of points x_{ia} (corresponding to the coordinate of each point c_i on dimension a) is embedded in a r-dimensional metric space, and a distance function

$$d(c_i , c_j) = d_{ij}$$

is defined on this space. For simplicity, this distance is assumed to be Euclidean.

ii) The goal of any non-metric MDS procedure (at least for a distance model) is to find a set of points (X) in a space of minimum dimensionality such that the dissimilarities (data) are a monotone (ordinal) function of the distances, i.e. that whenever

$$\delta_{ij} < \delta_{kl}$$

then

$$d_{ij} \leq d_{kl} \quad \text{(Kruskal's Weak Monotonicity Criterion)}$$

> A configuration in r-space which satisfies this criterion is a r-dimensional solution for the data.

Shepard (1962) first developed an algorithm to obtain such a solution as a two step iterative process consisting of:
(i) determining the metric configuration that best reproduced the data, and (ii) emphasising or "flattening" the resulting configuration into as few dimensions as possible. Besides proving the viability of this approach, he also showed that it was possible to recover the *specific form* of the monotone function specified in the model. Thus, so long as the δ_{ij} are any monotone function of the "genuine" distances, the plot of δ_{ij} by the recovered distances will reveal the form of that transformation. *Non-metric* MDS can incorporate any monotone function linking the δ_{ij} and d_{ij}.

Kruskal (1964), starting from Shepard's work, defined non-metric MDS as follows:

> "We view multidimensional scaling as a problem of *statistical fitting* – the dissimilarities are given and we wish to find the configuration whose distances fit them best."

This he did by explicitly introducing a "badness of fit" quantity to be minimized in the iterative process, namely STRESS, which is a normalized residual sum of squares from monotone regression (see Carroll and Kruskal 1969).

$$S_i = \frac{[\ \Sigma_{i<j}\ (d_{ij} - \hat{}d_{ij})^2\ ]^{½}}{\Sigma_{i<j}\ d^2_{ij}}$$

and he introduced the new fitting quantities $\hat{}d_{ij}$ (known variously as "pseudo distances", "disparities" or "discrepancies"), which are the least-squares fit to the distances (d_{ij}) and are as close as possible to being in the same order as the data. (These quantities incidentally avoid performing arithmetic on the data quantities (δ_{ij}) which is *ex hypothesi* excluded by the non-metric approach). These d_{ij} are obtained by a technique known as monotone or isotonic regression (see *ibid*, 126).

The iterative procedure developed by Kruskal basically proceeds as follows:

i) *an initial configuration* in a user-determined dimensionality is produced.[3]

ii) *the configuration is normalised.*

iii) pairwise distances between the points in this space are then calculated.

iv} *monotone regression*: The distances are fitted by a best fitting monotone function, giving a set of "disparities".

v) *the stress* (badness of fit) of the current configuration is calculated from the distances and disparities.

vi) if stress is acceptably low, the final configuration and summary data are output. Alternatively:

vii) a correction factor is next calculated to move the configuration in the direction of lower stress. This moves the points in the direction giving a new configuration which has greater conformity with the data (i.e. to a configuration of lower stress).

viii) If the gradient is zero, then a (possibly local) minimum has been reached in the sense that any further gradual change in the configuration will increase stress.

This basic algorithm of Kruskal's, often referred to as M-D-SCAL, differs slightly from the approach implemented by MINISSA in the NewMDSX series: Roskam's approach in MINISSA is to manipulate simultaneously the disparities and the distances. This is discussed at greater length in the documentation of MINISSA. This process of minimization using negative gradients has now been replaced by more efficient methods in many programs.

EXTENSIONS OF THE NONMETRIC MULTIDIMENSIONAL DISTANCE MODEL

MDS procedures can be differentiated by three criteria:

the form of the data to be analysed;

the model which specifies the precise way in which the data are represented in the space; and

the transformation or function which is assumed to relate the original data to the solution. (This third criterion is often referred to as the 'level of measurement'). Thus the basic non-metric model, which may be considered as a paradigm, provides for:

(DATA)

(1) the internal analysis of a
(2) square
(3) symmetric
(4) two-way data matrix by a

(MODEL)

(5) Euclidean
(6) distance model, involving

(FUNCTION)

(7) a monotonic transformation of the data.

The restrictions implied by each emphasized qualifier in the previous Sentence have been successively relaxed allowing the extension of MDS to a very wide class of models for very different types of data: examples of each generalisation are given below:

3.1 Internal vs. External analysis

The basic MDS algorithm generates a configuration of points purely in accordance with the ordinal information in the data, i.e. the result is defined "internally" by the data matrix.

In some cases, however, the positions of the stimuli may be already known or assumed, and in this case so-called “external” analysis is performed, using additional external data information (often called “properties” and fitting the new properties within this frame. A particularly important example occurs in preference mapping where a set of preference judgements (external properties) are related to a known configuration of stimulus points (see PREFMAP).

3.2 Various matrices

A very useful generalisation is the extension to conditional similarity data, where data are treated as comparable only within rows (or only within columns). Data relating two distinct sets of objects (e.g. subjects and stimuli) thus become analysable in the MDS framework. The most common example of this type is preference data (e.g. where a set of subjects judges, say, a set of alternative political policies in terms of their desirability). The most obvious benefit of this extension is that it provides a tractable method of analysis for unfolding models.

Briefly, the Unfolding Model seeks mapping in the same space of a set of points representing stimuli (usually the objects of choice or preference) and a distinct set of points representing the subjects (each point representing the most preferred or ‘ideal’ location of the subject concerned. In the resulting configuration, therefore, a more-preferred stimulus is closer to the subject’s ‘ideal’ point than a less-preferred point, and hence an individual’s preference order represents the rank order of that distance between his/her (fixed) ideal point and the locations of the set of stimuli.

It is a relatively simple matter to adapt the non-metric MDS algorithm to deal with such data and produce procedures for ‘multidimensional unfolding analysis’ where the final configuration represents a mapping of both ‘subject’ and ‘object’ points into a multidimensional space. (For a fuller discussion see MINIRSA).

A parallel move away from the paradigm case involves the analysis of square but asymmetric data matrices, such as might for instance be obtained from a sociometric experiment in which each of a set of subjects is asked to rank or rate the other members of the set in terms of, say, friendship. In this case the same set may be mapped twice, first as a set of judges and secondly as stimuli. A possibility of external preference analysis is given in the present series by the PREMAP program (q.v.).

NewMDSX also includes programs specifically written for thye direct analysis of special types of data, such as free-sortings (MDSORT), triadic judgments (TRISOSCAL), as well as frequency Tables (CONJOINT, CORRESP) and Profiles(PARAMAP).

3.3 Extensions from the Euclidean distance model

A Euclidean distance (d_{jk}) is defined as:

$$d_{jk} = \left[\sum_{a} | x_{ja} - x_{ka} |^{2} \right] \tfrac{1}{2}$$

where x_{ja} is the co-ordinate of point j on the a’th distance.

To date, the vast majority of MDS studies have used the Euclidean distance model, whether through convenience, beliefs about its robustness, or attachment to its substantive implications (Shepard 1969, Sherman 1970). Euclidean distance is, however, a special case of a more general family of Minkowski metrics, defined as:

$$d_{jk} = \left[\sum_{a} | x_{ja} - x_{ka} |^{r} \right] 1/r$$

where the so-called Minkowski parameter r can lie between 1 and infinity.

A good deal of psychological research (Attneave 1950) shows that when dimensions of judgement are few and sufficiently salient or recognisable, the 'city-block' metric (r = 1) provides a better explanation of, and fit to, judgemental data. By contrast, the 'dominance metric' (r = infinity), where the largest single dimensional difference dominates all others, should fit a good many complex stimuli. Arnold (1971) provides an interesting test of the behavioural assumptions of different metrics on the ratings of similarities between pairs of words drawn from distinct word-classes. The possibility of varying the Minkowski parameter is allowed inMRSCAL (q.v.) and MINISSA (City Block and Euclidean only).

Lingoes (1972) and others have also developed non-metric analogues of factor analysis. Once again, the purpose is to provide a lowest-stress fit to a monotone transform of the symmetric data matrix of (dis)similarities. An example of a metric factor analysis (or vector) model is the MDPREF model, where, as in the distance model, stimuli are represented as points in a multidimensional space, but a subject's preferences are represented in this space as a vector or line oriented to the region of his/her greatest preference. The order of projections of stimuli points on this line represents the subject's order of preference.

A further instance of the generalisability of the non-metric MDS algorithm is its extension to an additive model, which regards the data as some additive combination of factors rather than of the complex distance function. This additive model is a special case of conjoint models implemented by the CONJOINT program (q.v.) and in effect provides a non-metric version of analysis of variance.

3.4 Metric and non-metric approaches

Historically, the first MDS models were designed to preserve metric information in the data and assumed that the empirical (dis)similarities were some linear function of the model distances. The main metric program of the present set differs, however, in many ways from 'classic' metric MDS. As we have seen, the more recent approach used ordinal information, and hence the much broader class of monotonic functions is available. In MDS procedures, this distinction has basically been implemented by the form of regression used – usually linear regression of data upon distances in the metric case, and monotonic regression in the non-metric case.

This class has been extended to allow Kruskal's suggestion that multivariate linear regression or polynomial regression (of higher than linear degree) be exploited in some circumstances (Kruskal 1969), and secondly Shepard and Carroll's (1966) Parametric mapping model PARAMAP, which seeks to maximise an index of continuity which assures that the function will be at least locally monotone.

3.5 Three-way scaling

Perhaps the most far-reaching development in multidimensional scaling has been the extension to 3- or higher-way data matrices. To call a data matrix 'two-way' is in fact to say nothing more than that it is a matrix, i.e. it is composed of some measure between two sets of objects which, as we have seen, may or may not be identical. If the data are, say, adjudged dissimilarities on a set of stimuli by one individual at one time then the solution is simple. But in the case of a matrix of similarity judgements elicited from a number of subjects (usually, though not necessarily, individuals)[4] the third 'way' is the 'stack' of these two-way matrices. The basis of the problem is that if data from a number of subjects are aggregated before analysis, there is no way of knowing whether important and systematic differences exist in subjects' judgements, and hence whether the aggregate solution represents anything but a statistical artefact. Conversely, however, even if a solution is obtained from each subject individually, there is no obvious way in which the degree of commonality between subjects' 'cognitive maps' can be assessed. One attractive conceptualisation of the problem by Horan (1969) suggests that a "Normal Attribute Space" be defined as the union of all dimensions used by subjects. This space, which is called the "Group Stimulus Space" in the INDSCAL program will usually be of high dimensionality (since it may very well include purely idiosyncratic dimensions) has the advantage that every subject is using some subset of the dimensions. Carroll and Chang (1970) in their classic paper on three-way scaling go on to suggest that, rather than subjects' use of dimensions being 'all or nothing', they rather attach weights (representing differential salience or importance) to them. Thus, when an individual's set of weights are applied to the Group Stimulus Space, the effect is to differentially stretch or contract the dimensions and yield an idiosyncratic, transformed, configuration of points (the so-called "Private Space"). This general approach and specific method are more fully discussed in the section on INDSCAL.

Notes

1. See Lingoes (1966) and Sibson (1972) for an extended discussion of these points.

2. See Shepard (1962), Guttman (1965), Lingoes and Roskam (1971) for basic contributions to the development of the algorithm. The technical issues involved will only be touched on here, but are fully discussed in Lingoes and Roskam, and in Green and Rao (1971). The most robust and near-optimal algorithms are represented by the Guttman-Lingoes-Roskam series (Lingoes and Roskam 1971 In the NewMDSX series, the program implemented is MINISSA (v.i.).

3. Kruskal initially recommended the generation of a random or arbitrary starting configuration. It has subsequently been shown that this will considerably increase the probability of a process finishing in a local minimum. A "quasi-non-metric" initial configuration defined by Guttman-Lingoes or Torgerson is greatly preferable. See Lingoes and Roskam (1971).

4. Subjects may be not only individuals but "pseudo-subjects" groups, distinct times, places, replications, or, indeed, in an interesting application, scaling solutions obtained from different MDS programs (see Green 1972).

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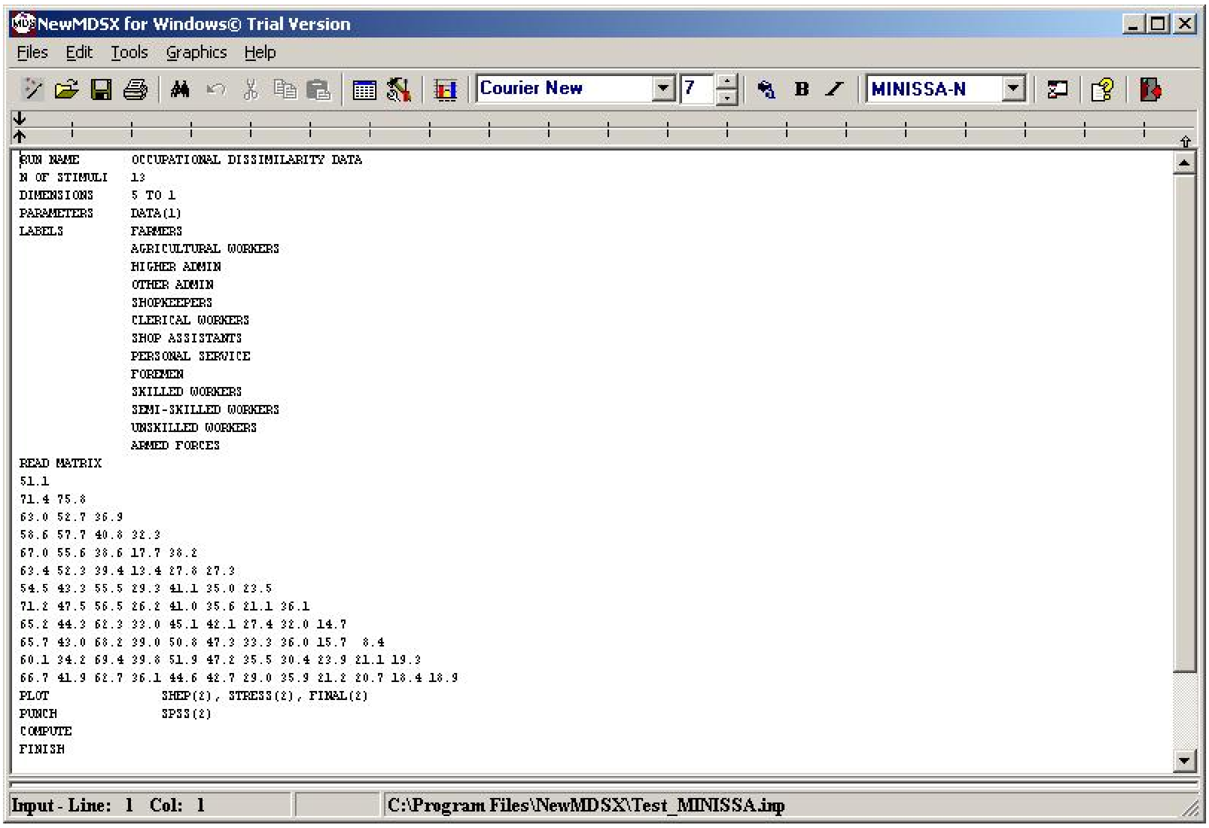
HOW TO USE NewMDSX FOR WINDOWS

1.1 Overview

The main Editor/Interface appears automatically when the program is loaded, and is used to control the creation and editing of files and the execution of the various NewMDSX procedures. It consists of two resizeable panels, the upper for input and the lower(closed in the following)for output files.



```
RUN NAME        OCCUPATIONAL DISSIMILARITY DATA
N OF STIMULI    13
DIMENSIONS      5 TO 1
PARAMETERS      DATA(1)
LABELS          FARMERS
                AGRICULTURAL WORKERS
                HIGHER ADMIN
                OTHER ADMIN
                SHOPKEEPERS
                CLERICAL WORKERS
                SHOP ASSISTANTS
                PERSONAL SERVICE
                FOREMEN
                SKILLED WORKERS
                SEMI-SKILLED WORKERS
                UNSKILLED WORKERS
                ARMED FORCES
READ MATRIX
51.1
71.4 75.8
63.0 52.7 36.9
58.6 57.7 40.8 32.3
67.0 55.6 38.6 17.7 38.2
63.4 52.3 39.4 13.4 27.8 27.3
54.5 43.3 55.5 29.3 41.1 35.0 23.5
71.2 47.5 56.5 26.2 41.0 35.6 21.1 36.1
65.2 44.3 62.3 33.0 45.1 42.1 27.4 32.0 14.7
65.7 43.0 68.2 39.0 50.8 47.3 33.3 36.0 15.7  8.4
60.1 34.2 69.4 39.8 51.9 47.2 35.5 30.4 23.9 21.1 19.3
66.7 41.9 62.7 36.1 44.6 42.7 29.0 35.9 21.2 20.7 18.4 18.9
PLOT                SHEP(2), STRESS(2), FINAL(2)
PUNCH               SPSS(2)
COMPUTE
FINISH
```

Input - Line: 1 Col: 1

C:\Program Files\NewMDSX\Test_MINISSA.inp

Before selecting an input file or entering new data, the name of the NewMDSX program to be used must first be selected in the pull-down window to the right of the toolbar. In the above illustration, this is MINISSA.

A number of demonstration input (_*.inp_) files for the various NewMDSX procedures are automatically installed with the program. These can be loaded from the **File** menu or by using the open file button on the toolbar, after first selecting the name of an NewMDSX procedure from the pull-down menu to the right of the toolbar. In the above illustration, the file *Test_MINISSA.inp* has been selected. Besides offering to open or save files, the **File** menu also allows you to **Reopen** files you have recently used, without having to search for them again. Clicking on the Run button on the toolbar will execute the procedure selected in the pull-down menu, taking as input the file currently displayed in the editor window.

The main window also serves as a fully-functional text editor, with the ability to change font types, sizes and colours, to search for strings in the file displayed, edit, annotate and save input and output files associated with the various NewMDSX procedures. When images have been saved, it can also be used to amend them, to outline and label features of interest as required.

Clicking on the Data Entry button (or the **Tools**|**Data entry** menu item) calls the WOMBATS routine (Work Out Measures Before Attempting To Scale). This generates matrices of a wide variety of measures of (dis)similarity which can be stored for use by NewMDSX procedures or by other programs.

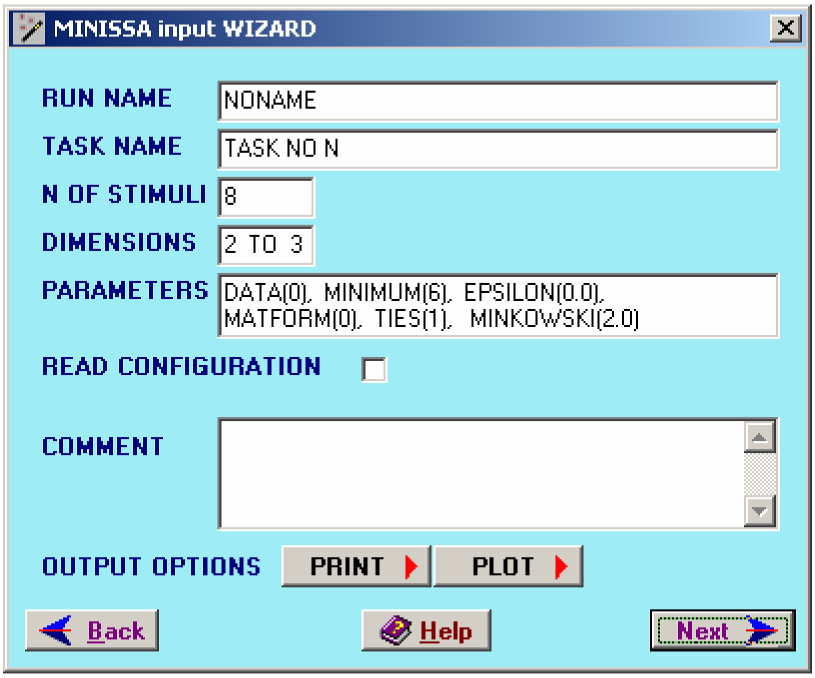
Use the adjacent button (or **Tools**|**Matrix conversion**) to call a utility to convert between different matrix formats.

New input files to the selected NewMDSX procedure can be created most conveniently with the help of the corresponding Input Wizard. This also offers a facility for data input in spreadsheet form, according to the parameters which the user has selected, and automatically initiate the corresponding analysis, displaying the results in the main window.

Clicking on the Graphics button when output from one of the NewMDSX procedures is displayed will open a graphic display of the configuration or diagram following the current cursor position (see below, 1.4.).

1.2. Data entry

When using the input Wizard to create an input file for one of the NewMDSX routines, simply follow the prompts for the necessary commands, as they appear in the Wizard's opening window, in the following example creating an input file to MINISSA:



MINISSA input WIZARD

RUN NAME: NONAME

TASK NAME: TASK NO N

N OF STIMULI: 8

DIMENSIONS: 2 TO 3

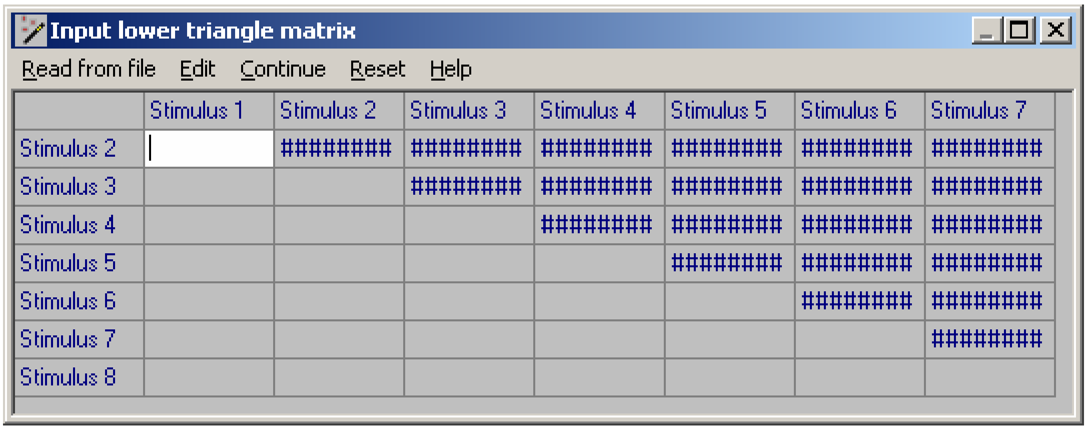
PARAMETERS: DATA(0), MINIMUM(6), EPSILON(0.0), MATFORM(0), TIES(1), MINKOWSKI(2.0)

READ CONFIGURATION □

COMMENT

The data to be analysed are entered into the following spreadsheet, displayed after clicking on the button marked **Next** in the above window. This will invite a rectangular or lower-triangular data matrix of the dimensions specified by the user, according to the requirements of the procedure currently selected and the value of the **DATA TYPE** parameter.

Note that it is also possible to enter your own row and column names in the spreadsheet, to help identify the stimuli in the output. This simply adds an appropriate **LABELS** specification (see p. 24) to the input file created by the input Wizard.



	Stimulus 1	Stimulus 2	Stimulus 3	Stimulus 4	Stimulus 5	Stimulus 6	Stimulus 7
Stimulus 2		########	########	########	########	########	########
Stimulus 3			########	########	########	########	########
Stimulus 4				########	########	########	########
Stimulus 5					########	########	########
Stimulus 6						########	########
Stimulus 7							########
Stimulus 8							

After positioning the spreadsheet cursor in an appropriate starting location, you may also click on **Read from file** to load data in the appropriate order from a free format plain text file, which may have been exported directly from another program or created by cutting and pasting from a file in another format. Alternatively, click on **Edit** to paste data direct from the Windows clipboard. If the first line of data to be read, or pasted, in this way contains a series of variable labels,

for example:

```
   VAR1 VAR2 VAR3 VAR4 VAR5
   99.0 51.1 71.4 63.0 58.6
   51.1 99.0 75.8 52.7 52.7
   71.4 75.8 99.0 36.9 40.8
   63.0 52.7 36.9 99.0 32.3
   58.6 57.7 40.8 32.3 99.0
```

where a symmetric matrix of similarity values is headed by simple variable names, these will be inserted in the spreadsheet in the appropriate locations.

For PINDIS (see pp124ff), which allows the input of labelled configurations, the format is as follows:

```
   VAR1 -0.1358  0.2993 -0.7294
   VAR2  0.2229 -0.6381  0.5729
   VAR3  0.2679 -0.7446 -0.3938
   VAR4 -1.1287  0.2396  0.2875
   VAR5  0.7737  0.8437  0.2628
```

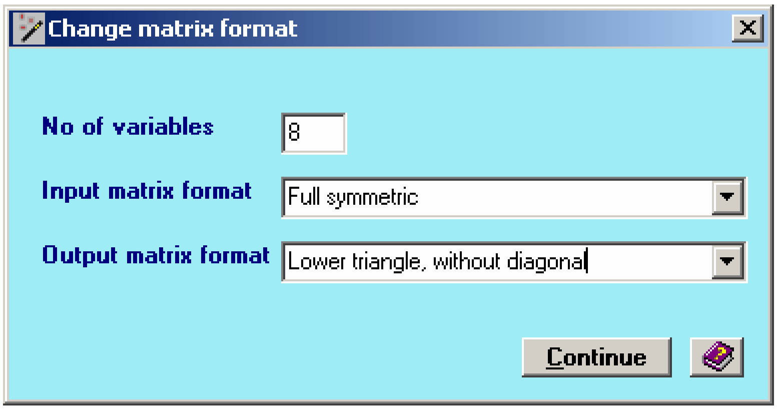
These are the techniques to use to speed up importing and exporting data to and from NewMDSX. It is worth spending some time looking at them, in conjunction with the demonstration data provided with each routine, before attempting to enter your own data for analysis.

Finally, click on **Continue** to close the spreadsheet window and create the corresponding input file.

It is, of course, also always possible to use the main editor/interface to directly enter or modify input files as required.

1.3 Matrix conversion

A utility has been included in NewMDSX for Windows to facilitate conversion between the matrix formats commonly encountered in importing from and exporting to other programs, as well as between routines in NewMDSX.

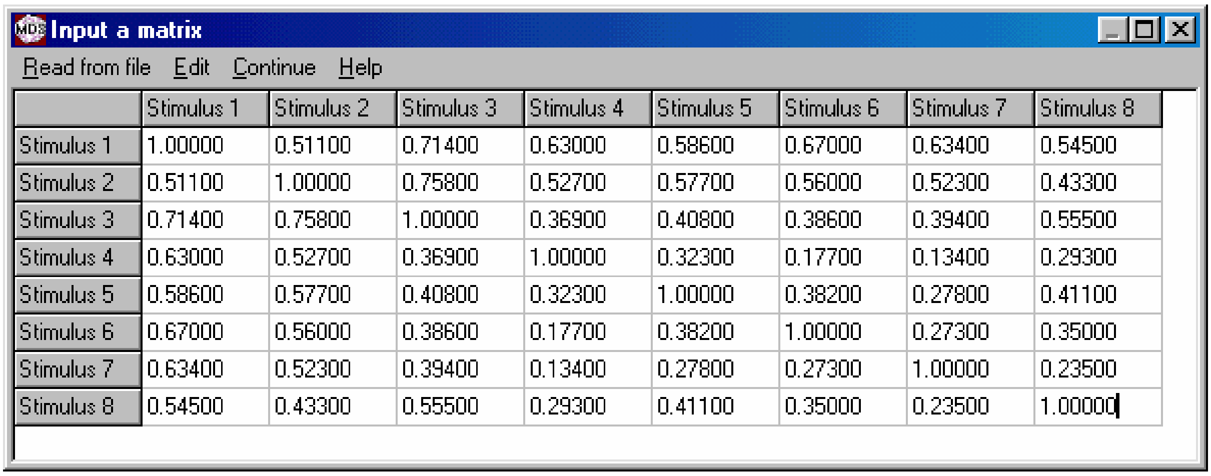


No of variables: 8

Input matrix format: Full symmetric

Output matrix format: Lower triangle, without diagonal

Clicking on **Continue** in the window shown above opens a spreadsheet window to create the input matrix, which may have been exported from another program and saved in a free format text file, or may have been placed in the Windows clipboard ready to be copied into the spreadsheet displayed:



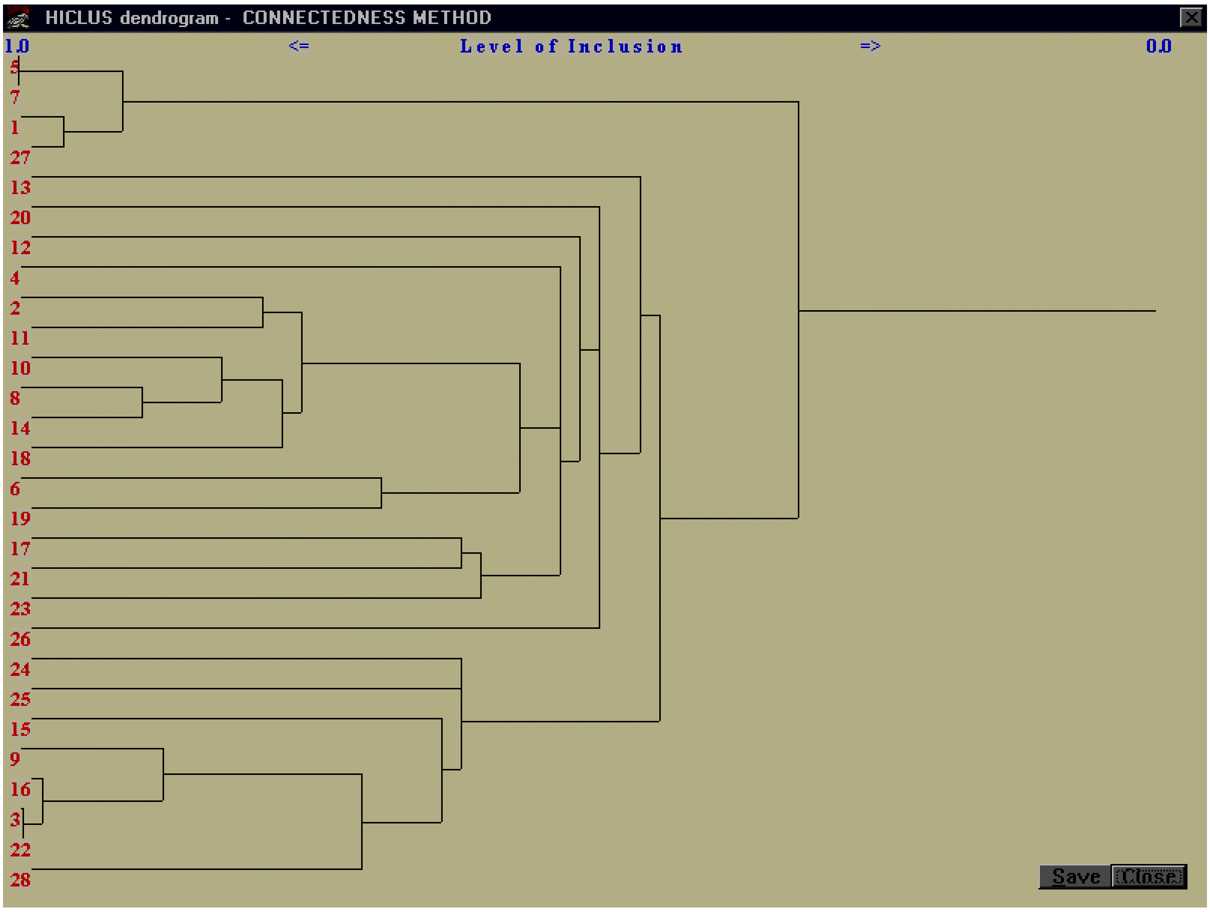
	Stimulus 1	Stimulus 2	Stimulus 3	Stimulus 4	Stimulus 5	Stimulus 6	Stimulus 7	Stimulus 8
Stimulus 1	1.00000	0.51100	0.71400	0.63000	0.58600	0.67000	0.63400	0.54500
Stimulus 2	0.51100	1.00000	0.75800	0.52700	0.57700	0.56000	0.52300	0.43300
Stimulus 3	0.71400	0.75800	1.00000	0.36900	0.40800	0.38600	0.39400	0.55500
Stimulus 4	0.63000	0.52700	0.36900	1.00000	0.32300	0.17700	0.13400	0.29300
Stimulus 5	0.58600	0.57700	0.40800	0.32300	1.00000	0.38200	0.27800	0.41100
Stimulus 6	0.67000	0.56000	0.38600	0.17700	0.38200	1.00000	0.27300	0.35000
Stimulus 7	0.63400	0.52300	0.39400	0.13400	0.27800	0.27300	1.00000	0.23500
Stimulus 8	0.54500	0.43300	0.55500	0.29300	0.41100	0.35000	0.23500	1.00000

Click on **Read from file** to load numerical data from a text file, or on **Edit**, to paste data direct from the Windows clipboard. Click on **Continue** to close the spreadsheet window and display the resulting matrix in the input window, from where it can be saved or copied for further use.

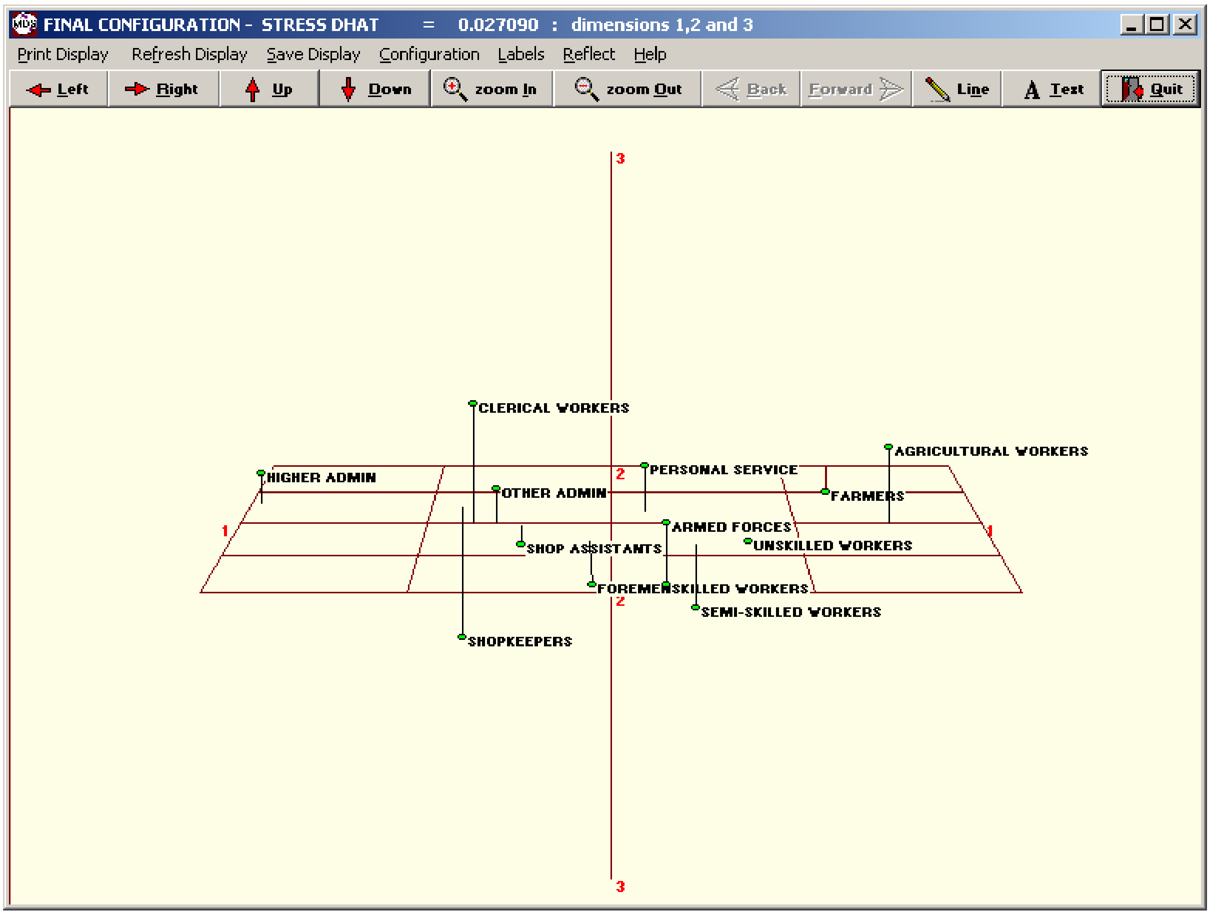
1.4. Graphics

When a NewMDSX procedure has been executed and the results are displayed in the output window, clicking on the **Graphics** option invokes a graphic display of the first suitable data configuration or diagram which the program can locate in the listing following the current position of the editor cursor.

1.4.1 When the results of a HICLUS cluster analysis are displayed in the editor window, this will show the cluster diagram (if any), immediately following the current cursor position, as a graphic dendrogram:



1.4.2 When the results of the other NewMDSX procedures are displayed in the editor window, clicking on the Graphics button will show the configuration (if any) for which the data are listed following the current cursor position, in the form of a pseudo-3-dimensional display, as follows. Alternatively, click on the Graphics button when the cursor is inside one of the 'line-printer' output plots.



This display can be manipulated as follows:

- click on the buttons on the toolbar, or use the short-cut keys indicated to rotate, zoom, or reflect the display. Click on any point to highlight its label.

- **Back** and **Forward** change the combinations of dimensions displayed if the configuration selected in fact contains more than three dimensions

- click on the axis end points to see the effect of incremental clockwise rotations of the configuration with respect to the selected axis (the numerical keys 1, 2, and 3 have the same result). Use Configuration to keep track of this process and save rotated configurations if required. Use the menu item **Reflect** to see the result of reflecting the display about the vertical or horizontal axes. To see reflection about dimension 2, first rotate the display to two dimensions only.

- hold down the **right mouse button** with the pointer on the display, move the pointer to another position and release the mouse button again, to drag the display to a different location in the window.

- Click on the menu item **Labels** to adjust the maximum number of characters, the font and character size displayed in point labels.

Clicking **Draw** allows you to draw on the display with the **mouse**, to highlight features of interest. **Lines** enables you to draw straight lines, from a point where the **mouse button** is depressed to a point where it it liftes again. Clicking **Text** causes a box to appear to enter text. On closing this box, move the **mouse** to the position required and press a **mouse button** to add the text to the image displayed. The image as amended must then be **saved** immediately on completion, as the additions will be lost when the display is further changed. Click on **Refresh Display** to clear and return to the original image.

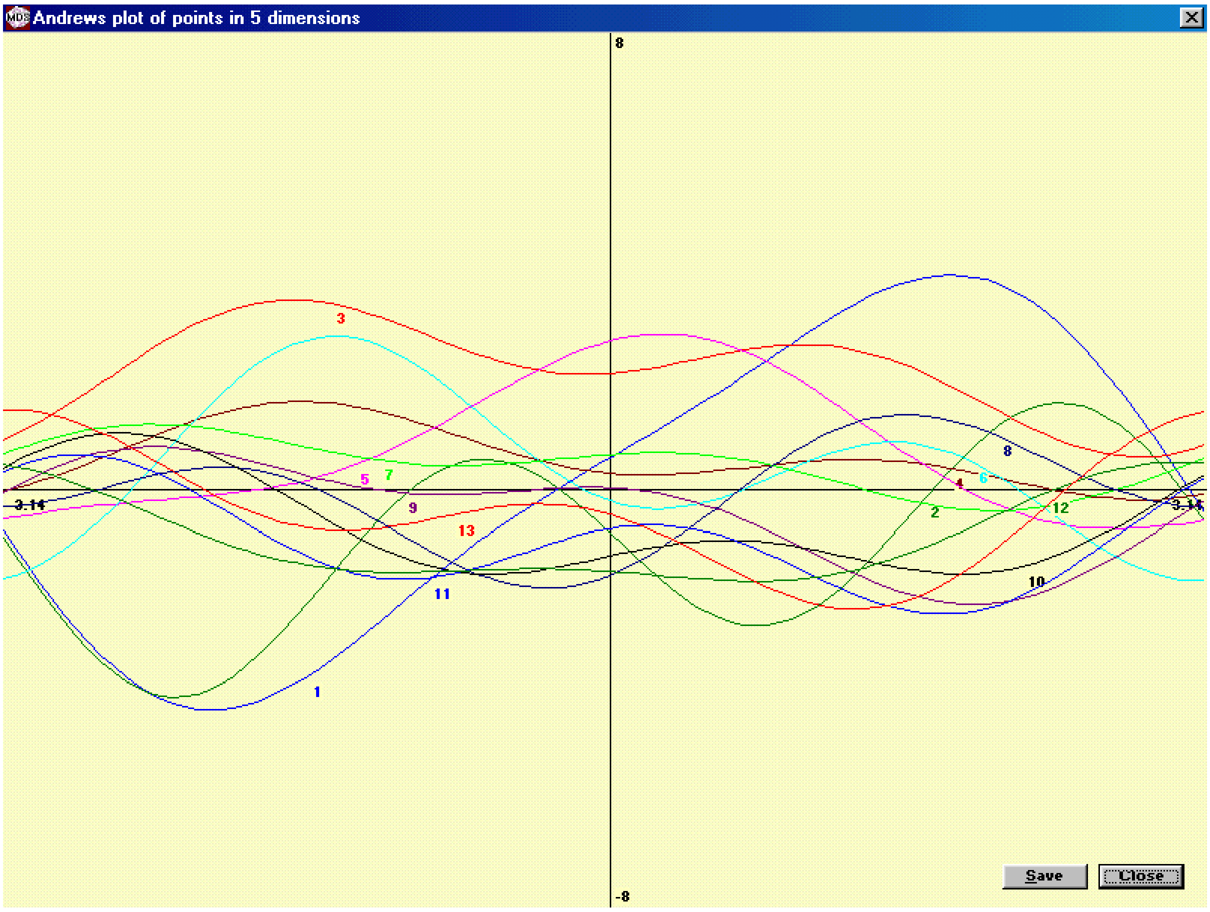
1.4.3 For graphical display of higher-dimensional configurations, Andrews plots are offered as an alternative to a series of pseudo-3-dimensional displays.

If the data are k-dimensional, each point **x'** = $(x_1, x_2, \ldots, x_k)$ defines a function

$$f\mathbf{x}(t) = x_1/\mathrm{sqrt}(2) + x_2.\sin(t)+x_3.\cos(t)+x_4.\sin(2t)+x_5.\cos(2t)+ \ . \ . \ .$$

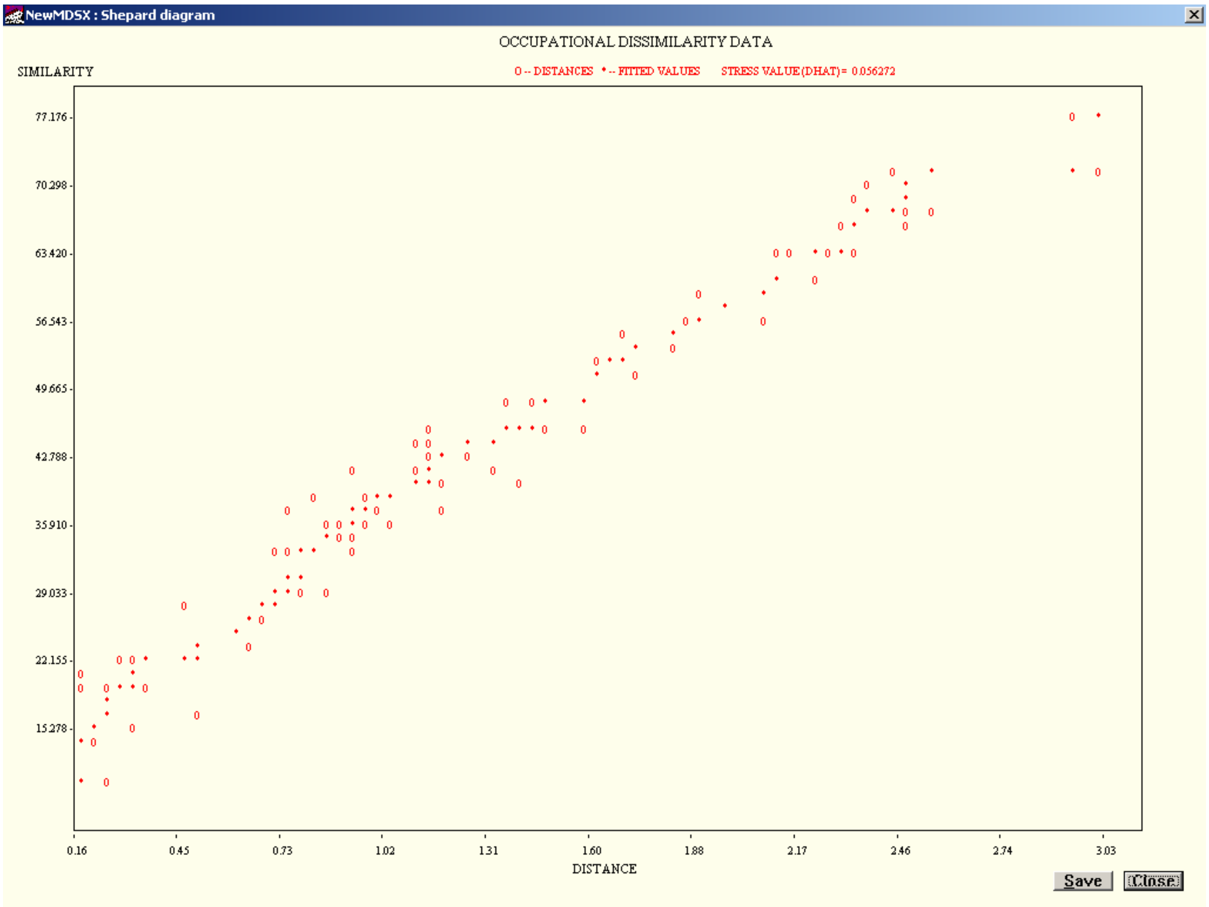
which is plotted over the range $-\pi < t < \pi$.

In these plots, points in a higher-dimensional configuration which are close together in Euclidean space are represented by functions which remain close together for all values of *t*. Outlying values on the other hand lead to a peak in the corresponding function for some *t*. This form of plot is useful to summarise higher-dimensional data when the number of individual stimuli in the MDS analysis remains relatively small, say less than 10. The plots become confusing, however, for larger numbers of stimuli/variables.



See D.F.Andrews, "Plots of high-dimensional data" Biometrics,28, 1972, pp. 125-136, for a full discussion of this plotting technique in the interpretation of data.

1.4.4. The output from most NewMDSX procedures includes Shepard diagrams, relating values fitted by scaling to the original data. Placing the editor cursor in front of the words 'SHEPARD PLOT' (or 'CORRELATION', in the case of output from PROFIT, will open a graphic display of the diagram which follows.



Click on the **Save** button in each of these displays to save them in a graphics file for later reference. Alternatively, you may use ALT+PrtScr to save the display to the Windows Clipboard for inclusion in other documents.

Click on the **Close** button in the display window to close it and return to the main NewMDSX window.

1.5. THE NewMDSX COMMAND LANGUAGE

The NewMDSX procedures themselves employ a set of commands similar to, though not identical with, those originally used in SPSS. Program-specific parameters are set with the command PARAMETERS. (Consult the documentation for the individual procedures for full details of their particular commands and PARAMETERS).

All commands in NewMDSX may be entered in UPPER or lower case letters and in free format. Spaces are ignored except in keywords, which must be typed in full. All input is expected to be in free format, separated only by spaces. In certain instances, where data are taken from other sources, it may not be possible to read them correctly in free format. In such cases *a fixed format for the data can be specified, using the Fortran-style INPUT FORMAT statement (several of the example data sets supplied with the program illustrate how this is done).*

The output commands PRINT, PLOT and PUNCH are retained in their original form, for compatibility with earlier versions of MDS(X) although they now have different functions. PRINTed and PLOTted output now all appears in the main output file generated by a NewMDSX procedure, while PUNCHed output is placed in a secondary output file and may be saved for separate use, as required.

1.5.1 FORMAT OF COMMANDS

A command has two distinct parts:

i) the command word itself, and

ii) an operand (or parameters) field which follows the command word, separated by any number of spaces.

The operand field may be blank for some commands.

The command word

All commands in NewMDSX may be entered in upper or lower case letters, but the spelling (and any spaces in the command) must conform to the specifications in section 1.5.2.

The operand field

The operand (or parameters) field may also be in upper or lower case characters, and must follow the command word, separated from it by an arbitrary number of spaces. All spaces in the operand are ignored except in the spelling of keywords, which must be typed in full.

Commands must occupy one and only one line of input except for the PARAMETERS command, COMMENT, LABELS and the three output option commands PRINT,
PLOT and PUNCH which may continue for as many lines as necessary, in free format.

Generally, there is no fixed order of precedence of commands. However, all data definition instructions (N OF SUBJECTS, N OF STIMULI, PARAMETERS, etc.) must precede READ MATRIX. For compatibility with earlier versions of MDS(X), each READ MATRIX or READ CONFIG command may be preceded by an INPUT FORMAT specification, if one is used, although by default all data will be assumed to be in free format, with the values separated by spaces. It is therefore only necessary to consider using a fixed INPUT FORMAT specification when the data for some reason will not be correctly interpreted in this way.

It should also be noted that the PRINT, PLOT and PUNCH commands must precede the COMPUTE command.

All commands are echoed in the output and all errors (up to the specified ERROR LIMIT) are flagged. If an error has occurred then the remaining input will be scanned for errors.

1.5.2 NewMDSX COMMANDS (obligatory commands are marked with an asterisk for ease of reference)

1. The RUN NAME

```
------------------------------------------------------------------------

      RUN NAME        any descriptive title for the run
------------------------------------------------------------------------
      Function  :  Provides a name for the run
```

Status : Optional

2. The TASK NAME

```
TASK NAME      any descriptive title for a subtask
```

Function : Provides a name for the task (Useful in runs where more than one task is performed)
Status : Optional
Notes : On encountering a second (and subsequent) TASK NAME, PARAMETERS will resume their default values.

3. The COMMENT command

```
COMMENT           any comments
```

Function : Allows the user to insert comments and notes at any point in the run. Comments may be continued on subsequent lines in free format.
Status : Optional

4. The LABELS command

```
LABELS         plus a series of variable labels, on successive
               lines, beginning with the one containing the command
```

Function : Available in most procedures to allow the association of labels to assist in identification of variables in tables and plots.
Status : Optional

5. The PRINT DATA command

```
PRINT DATA        (YES)
                  (or )
                  (NO )
```

Function : Allows the user to have any input data echoed in output. Can be useful if the system appears to be misreading your data.
Status : Optional
Notes : PRINT DATA is initially set to NO and will remain in force until the end of the run or another PRINT DATA is encountered.

*6. The # OF SUBJECTS instruction

```
----------------------------------------------------------------------
      #  OF SUBJECTS   number of subjects in the analysis:  must
           or          be an integer value
      NO OF SUBJECTS
           or
      N  OF SUBJECTS
----------------------------------------------------------------------
```

Function : Provides the system with the number of subjects
in the analysis.
Status : Obligatory for most procedures
Notes : Not applicable to some procedures: see the
relevant program documentation.
CORRESP uses N OF ROWS

*7. The # OF STIMULI instruction

```
----------------------------------------------------------------------
      #  OF STIMULI    number of stimuli in the analysis:  must
           or          be an integer value
      N0 OF STIMULI
           or
      N  OF STIMULI
----------------------------------------------------------------------
```

Function : Provides the system with the number of stimuli
in the analysis
Status : Obligatory for most procedures
Notes : Not applicable to some procedures: see the
relevant program documentation.
CORRESP uses N OF COLUMNS

*8. The DIMENSIONS instruction

```
-----------------------------------------------------------------------

      DIMENSIONS        <number>
                     <number list>         Not possible for all procedures:
                     <number> TO <number>   consult program documentation
-----------------------------------------------------------------------------
```

Function : Sets the dimensionalities for the analysis
Status : Obligatory
Notes : Solutions are usually computed from the highest
dimensionality down to the lowest, whatever the
order specified in the command.

9. The PARAMETERS command

```
-----------------------------------------------------------------------------

      PARAMETERS        keyword (value), keyword (value) etc.

-----------------------------------------------------------------------------
```

Function : Allows the user to set program parameters to
control the analysis
Status : Optional
Notes : See the relevant program documentation for full
details of keywords and values.

10. The ITERATIONS instruction

```
----------------------------------------------------------------------

      ITERATIONS       maximum number of iterations to be performed
```

Function : Sets the maximum number of iterations to be
performed in the analysis
Status : Optional
Notes : Applicable only to those procedures which employ
an iterative procedure. A maximum of 100 iterations
will be assumed if this instruction is not used.

11. The INPUT FORMAT instruction

INPUT FORMAT   a FORTRAN format descriptor enclosed in brackets
(excluding the word FORMAT)

Function : Describes the data to be read in
Status : Optional; free format input is assumed if not used.
Notes : This is included for the sake of completeness. Most
users will probably be content to use free format input.
The format, if specified, must be suitable for reading
real numbers. Please consult the relevant program
documentation.
If in doubt, consult a FORTRAN programmer.

12. The READ MATRIX command

READ MATRIX   blank

Function : Instructs the system to begin reading the data
matrix (or matrices) from the selected INPUT
MEDIUM (according to INPUT FORMAT, if used).
Status : Obligatory
Notes : READ MATRIX may be preceded by an INPUT FORMAT
Command, and where applicable # OF SUBJECTS and
# OF STIMULI instructions. See relevant program
documentation for the type of matrix expected.
The data matrix must immediately follow
the READ MATRIX instruction.

13. The READ CONFIGURATI0N command

READ CONFIG   blank

Function : Instructs the system to read in an initial
configuration rather than generating its own.
Use of this option can often cut the time taken
to reach the solution.
Status : Optional
Notes : READ CONFIG, if used, may be preceded by its
own INPUT FORMAT instruction if free format input
is not satisfactory and, where applicable,
# OF SUBJECTS, # OF STIMULI, and DIMENSIONS
instructions.
See the relevant program documentation for the type
of matrix expected.

```
                  The configuration must immediately follow the
                  READ CONFIG instruction.
```

*14. The COMPUTE command

```
     COMPUTE           blank
```

```
      Function :  Instructs the system to start the computation
      Status   :  Obligatory
      Notes    :  COMPUTE must be preceded by READ MATRIX.
```

15. The PRINT, PLOT and PUNCH commands

```
      PRINT              ALL
       or
      PL0T               ALLBUT
       or
      PUNCH              EXCEPT
                       <matrix name (dimensions)>
                       <matrix list>
                       <null>
```

```
      Function :  Allows user control over the amount of output generated
      Status   :  Optional
      Notes    :  These are retained for in their original form for
                  compatibility with earlier versions of MDS(X). PRINTed
                  and PLOTted selections appear in the main output file,
                  and PUNCHed selections in a secondary output file.
                  For convenience, specifying a PLOT option will
                  automatically also PRINT the corresponding values in
                  tabular form in the output file.
                  See the relevant program documentation for details of
                  options available in each procedure.
```

16. The ERROR LIMIT instruction

```
    ERROR LIMIT       <number>
```

```
      Function :  Sets the number of errors to be encountered in
                reading the input file before processing ceases
      Status   :  Optional
      Notes    :  The default value allows for 20 errors.
```

17. The FINISH command

```
     FINISH
```

```
      Function :  Terminates the run
      Status   :  Obligatory (must be the last command in the run
                  instructions)
```

2. CANDECOMP (CANonical DECOMPosition)

2.1 OVERVIEW

Concisely: CANDECOMP (CANonical DEC0MPosition) provides internal analysis of a 3- to 7-way data matrix of (dis)similarity matrices, by a weighted scalar product distance model using a linear transformation of the data.

Following the categorisation developed by Carroll and Arabie (1979) the program may be described as:

Data:	Three- to seven-way	Model:	Generalised Scalar products
	Two- to seven-mode		Two to seven sets of points
	Polyadic		Internal or External
	Linear		
	Complete		

2.1.1 ORIGIN, VERSIONS AND ACRONYMS

The present CANDECOMP program performs the analysis described in Carroll and Chang (1970) as “Canonical decomposition of N-way matrices”. The original INDSCAL program performed both this N-way analysis and contained as a special case, the 3-way, 2-mode analysis which became known as the INDSCAL model. These two are now separated, and the 3-way 2-mode model is implemented by INDSCAL-S. The CANDECOMP program is adapted from the original Bell Laboratories(1971) INDSCAL program.

2.1.2 CANDECOMP IN BRIEF

CANDECOMP takes as input a table of data values with between three and seven "ways". In the solution, each of these ways is represented by a configuration of points representing the elements of that particular way in a space of chosen dimensionality. Each data value is regarded as being the scalar product between the relevant elements. The program assumes that the data are at the interval level of measurement.

2.1.3 RELATION OF CANDECOMP TO OTHER NewMDSX PROGRAMS

CANDECOMP may be used to perform individual differences analysis if there are more than three ways (e.g. if the study involves replications).

The present program is a modified version of Carroll and Chang's original INDSCAL program. The so-called INDIFF option in that program (i.e. the special case when there were three ways and two modes in the data) became generally known, rather confusingly, as the INDSCAL model or, simply, "individual differences scaling". This INDIFF option now forms the INDSCAL-S program in the NewMDSX series, while CANDECOMP provides the full range of options available in Carroll and Chang's original program.

2.2. DESCRIPTION OF INPUT

2.2.1 DATA

There are two basic forms of data input to CANDECOMP, which we will refer to as being applicable to

     1. an "extended INDSCAL" analysis
and 2. the CANDECOMP analysis proper.

What we call the 'extended INDSCAL' analysis refers to the case Where two of the ways of the matrix refer to the same set of objects, that is, one of the matrices is square and the row- and column-elements refer to the same set of objects. These objects will be represented by only one configuration in the output. By contrast all the ways of the CANDECOMP analysis are regarded as distinct.

2.2.1.1 The extended INDSCAL analysis

Users who wish to analyse three-way, two-mode data are referred to the INDSCAL-S program.

In an INDSCAL analysis of this sort we have a set of matrices obtained from a set of subjects. Each matrix is a matrix (dis)similarity coefficients of some sort between a set of stimuli. There will thus obviously be as many matrices as there are subjects and each matrix will have as many rows as there are stimuli. The INDSCAL model analyses the way in which the subjects differentially perceive the stimuli. Suppose that we are interested in extending this analysis to take account of the effect of other factors. We might, for instance, replicate a study, use different forms of data collection, split subjects into some rational groupings etc. etc., and wish to use the INDSCAL model to analyse the effects of these factors by the same model as we used to investigate the subjects in the original analysis.

If the user is analysing data of this type, then the parameter SET MATRICES should be given the value 1 in the PARAMETERS command. This tells the program that two of the ways of the matrix - those corresponding to the stimuli - are identical and should be set equal (see 2.2). The DATA TYPE parameter should also be given a suitable value. Users should read 2.1.3 for a description of the use of the SIZES parameter.

2.2.1.2 The CANDECOMP analysis

As we have noted, this 'extended INDSCAL' analysis is a special case of the general CANDECOMP analysis where two of the ways are identical. We now consider the general case, where all the ways are considered distinct. (They need not, of course, actually be distinct sets of entities, they will merely be regarded as such by the program and be given a separate set of weights).

Consider the typical case where a set of subjects has given numerical ratings to a set of stimuli on a number of criteria. Since the procedure is linear, the use of rankings is not recommended. The data consist of a set of matrices, one for each criterion, each of which contains as many rows as there are subjects and as many columns as there are stimuli. If such a study was replicated after a period of time, thus forming a fourth way, then the resulting data constitute another block of such matrices.

The default parameter values allow for this analysis.

2.2.1.3 The presentation of data to CANDECOMP

Data are read by the READ matrix command in free format, or using an associated INPUT FORMAT specification if preferred. The dimensions of the input matrix are given to the program by means of the SIZES command which is peculiar to CANDECOMP. This replaces the N OF SUBJECTS, N OF STIMULI commands which are not recognised by this program. SIZES takes as operand up to seven numbers, separated by commas each of which is the number of objects in one of the ways of the matrix. There are as many numbers as there are ways in the data.

2.2.1.3.1 The order of the SIZES command

NOTE: ***The order in which the ways are entered in SIZES is crucial.***

The number of columns in the data matrix should be specified as the third number in the SIZES specification.

The number of rows in the basic matrix should be the second number on the command.

The number of matrices in the third way is the first number.

The number of elements in the fourth, fifth, sixth and seventh ways is given by the fourth, fifth, sixth and seventh numbers respectively.

In the case of the extended INDSCAL analysis, the first and second ways are identical, thus the second and third numbers in the SIZES specification must be equal.

2.2.1.3.1.1 Example

suppose we are interested in assessing the sound-quality of stereo amplifiers[*], and that we have ten different makes of equipment. We gather together say twenty listeners and proceed in the following way. A tape containing extracts of different types of music and speech is played to the listeners using each of the amplifiers in turn. Before each of the amplifiers is used the tape is played through a 'reference' machine. The listeners are asked to assess each of the sets on, say, five criteria (e.g. distortion, frequency response and channel separation.)

This assessment is done on a nine-point scale in comparison with the reference set which is scored as an arbitrary 5, Thus, so far we have a three-way data matrix, listeners x amplifiers x criteria. Since it is possible that some of the criteria may be influenced by the characteristics of, say, the speakers used in the reproduction of the tape, a further way might be added by playing the tape through each amplifier, say, four times, each time through a different set of speakers. Replications in say, three rooms of different acoustic properties might constitute a fifth way, and if we were foolhardy and/or rich enough to repeat the whole procedure, without serious revolt from the listeners, we might add a sixth way. Thus we have 20 listeners, 10 sets, 5 criteria, 4 speakers, 3 rooms and 2 replications.

Arranging the data so that the sets (in which we are primarily interested form the rows of the matrix (see 2.2)) our data look like this.

Each matrix has ten rows and five columns, this being the set of ratings given to each of the sets on each of the criteria by one of the listeners and there will be twenty such matrices corresponding to

[*] Thanks are due to S.P. Thomas and Q. Deane of the Consumers Association for suggesting this application and describing the basic form of the experiment.

the twenty listeners. (i.e. (20 x 10) = 200 lines in all, since the matrices follow each other without break). There will then be another three such blocks of 200 lines (making four blocks, 800 lines in all) corresponding to the different speaker types. Each of the three rooms will have provided 800 lines in this way, making 2400 lines and since there are two replications there will be in all 4800 lines, each of five columns in the data matrix. The SIZES specification corresponding to this matrix would be

```
          SIZES          20, 10, 5, 4, 3, 2
```

2.2.2. THE MODEL

The CANDECOMP program generates one configuration for each way of the analysis and the number of points in each configuration will be the number of elements in the corresponding way of the matrix. In the extended INDSCAL analysis however (i.e. when SET MATRICES (1)) matrices two and three - those corresponding to the second and third numbers in SIZES - are set equal when the algorithm has converged. One more iteration is then performed and only one configuration then produced for this way of the data (see INDSCAL-S).

The axes of the solution space are identical in each configuration and the solution should be interpreted in relation to these axes which it has usually been found, yield readily to substantive interpretation. Each configuration then reflects the differential importance of the properties represented by the axes in the following way. Each point in each configuration is properly considered as the terminus of a vector drawn from the origin of the space and for each vector the ratio between its coordinate on axis a and on axis b reflects the differential importance of the properties represented by those axes in the judgement of that subject and analysis should focus on this patterning.

All the configuration are normed so that the sum of squares of the coordinates on each axis is unity except for matrix 1. This means that strictly speaking the patterning of weights (coordinates) is comparable across 'ways'. It is not, however, clear how this is to be interpreted in the general case. The first matrix, being un-normed, will tend to show greater dispersion among the vectors and it is recommended that the 'way' in which the user wishes to concentrate forms the first way of the data. (i.e. the second element in the SIZES specification).

2.2.2.1. The algorithm

1. The input data matrices are converted into matrices of scalar products.
2. The scalar products between the elements in the input configuration input by the user or generated by the program are calculated to serve as initial estimates of the solution.
3. Each scalar product is assumed to be the result of the vector multiplication of as many vector coordinates as there are ways in the data matrix. At each iteration, all but one of these is held constant while the remaining parameter (coordinate) is estimated (the alternating strategy, akin to Alternating Least Squares).
4. When this process has converged, the two matrices referring to the symmetric matrix are set equal (if SET MATRICES (1)), the appropriate normalisation performed (see 2.3.1) and the solution output.

2.2.3 FURTHER FEATURES

2.2.3.1 Normalisation options

Two different questions of normalisation arise: over the input data and over the solution.

2.2.3.1.1 Normalisation of the data input

If the program is being used to perform a higher-way INDSCAL analysis, then the input matrices are normalised so that the influence of each subject is equalised in the analysis before the data are converted to scalar products. When a set of covariances or correlations are input the program does not convert to scalar products (since both covariances and correlations are scalar products) and, in the case of correlations, neither does it normalise. It is therefore important that data of this type be announced to the program by means of the relevant DATA TYPE parameter value.

In the case of the general CANDECOMP analysis the data are not normalised and differences in magnitude between subjects' judgements will affect the analysis. It is recommended, however, that the data for a CANDECOMP analysis be centred before the analysis proceeds both to provide a common origin for the various 'ways' and to eliminate consensual effects which often overwhelm fine structural detail.

2.2.3.1.2 Normalisation of the solution

Each of the configurations except that referring to the subjects of the solution is normalised as noted above (2.2). It is therefore recommended that the way in which the user wishes more variation to be concentrated form the first way (rows) of the input matrix.

It should, however, be noted that differences in the magnitude of scales needed by different subjects will affect the length of the vectors (the distance of a particular point from the origin) in this space and it is more than ever important to concentrate on the ratio between the coordinates on the respective axes.

2.2.3.2 Initial configuration

An initial configuration, which provides the initial estimates for the iterative procedure, is normally generated by the program from a pseudo-random distribution. CANDECOMP is prone to suboptimal solutions and users are recommended to make a number of runs with different starting configurations. A series of similar (preferably identical) solutions will usually indicate that a global minimum has been found.

2.2.3.2.1 Initial configuration for the extended INDSCAL option

If the CANDECOMP program is being used to perform the extended INDSCAL analysis (i.e. SET MATRICES(1)) then the user may choose to input an initial configuration of the points represented by the symmetric matrix (the stimulus matrix). This may be an a priori guess at the solution or the result of a MINISSA analysis in which the averaged judgements have been analysed. In this case the configuration is input after the READ CONFIG command. It consists of the coordinates of the stimulus points in the maximum dimensionality requested. These are read according to the associated INPUT FORMAT specification, if used. Otherwise data are assumed to be in free format.

2.2.3.3 External analysis

Users may wish to use CANDECOMP to perform an "external" INDSCAL analysis by holding constant a known configuration and estimating the configurations of subjects etc. This may be done only if SET MATRICES(1). A configuration is input by the user as described above and the FIX POINTS parameter is set to 1 in the PARAMETERS statement. The program will then estimate only the remaining matrices.

2.3. INPUT COMMANDS

Keyword	Operand	Function
SIZES	up to seven numbers, separated by commas	specify the numbers of objects in each of the ways of the matrix.There must be as many numbers as there are ways in the data.
DIMENSIONS	\<number\> \<number list\> \<number\> TO \<number\>	The number of dimensions to be listed and plotted in detail
READ MATRIX		Start reading input data, according to DATA TYPE
COMPUTE		Start computation
FINISH		Final statement in the run

2.3.1 LIST OF PARAMETERS

The following values may be set, following the keyword PARAMETERS

Keyword	Default	Function
DATA TYPE	0	0: An N-way table is input. 1: Lower triangle similarity matrix. 2: Lower triangle dissimilarity matrix. 3: Lower triangle matrix of distances. 4: Lower triangle correlation matrix. 5: Lower triangle covariance matrix. 6: Full symmetric similarity matrix. 7: Full symmetric dissimilarity matrix.
RANDOM	12345	(Any positive integer) Seed for pseudo-random number generator.
SET MATRICES	0	0: The CANDECOMP analysis is performed. 1: The performed extended INDSCAL analysis is performed (matrix 2 and 3 are set equal.
FIX POINTS	0	0: Iterate and solve for all matrices. 1: One matrix is held constant (external analysis).
CRITERION	0.005	(values between 0 and 1) Sets improvement level for terminating iterations.
CENTRE	0	0: No action. 1: If an N-way table is input (DATA TYPE (0)) it will be centred by subtracting the 'row means' in each of the N-ways (see section 2.3.1).

2.3.2 NOTES

1. The control statement SIZES is obligatory for CANDECOMP.

```
                   (N )    (SUBJECTS)
2.   The commands  (# ) OF (        ) are not valid with CANDECOMP.
                   (NO)    (STIMULI )
```

3. When DATA TYPE takes values 1 through 5 no diagonal is input. For values 6 and 7 the diagonals are input but ignored.

4. In the parameters SET MATRICES and FIX POINTS the spaces are significant characters.

5. Program Limits

Maximum no. of dimensions	=	10
Maximum no. of elements per way	=	100
Way 1 x Way 2 x Way 3		< 1800

The general format for PRINTing, PLOTting and PUNCHing options is as follows. n denotes the number of ways in the analysis ($3 < n < 7$), m the number of modes ($2 < m < 7$).

2.3.3.1 PRINT options

Option	Form	Description
INITIAL	n matrices will be listed.	The initial estimates of the configurations are listed. Each matrix contains the coordinates of the points on the required dimension. If the user has input an initial configuration, then the second two matrices will be identical.
FINAL	m matrices	The solution configurations are listed. Each matrix contains the coordinates of the relevant number of points on the axes of the space. These are followed by the correlations between each subject's data and solution The matrix of cross-products between the dimensions is listed.
HISTORY		The overall correlation at each iteration is listed. The unnormalised matrices at convergence are also listed (there will be n of these).

By default only the FINAL matrices and the overall correlation at convergence are listed.

2.3.3.2 PLOT options

Option	Description
INITIAL	The initial configuration may be plotted as r(r-1)/2 plots only if one has been input by the user.
CORRELATIONS	The overall correlation at each iteration is plotted in the form of a histogram.
WAY1 WAY2 WAY3 WAY4 WAY5 WAY6 WAY7	r(r-1)/2 plots are produced for each way specified.

2.4. EXAMPLE

```
    RUN NAME             EXAMPLE FROM SEC. 2.1
    TASK NAME            LISTENING TESTS AD NAUSEAM
    DIMENSIONS           4 TO 2
    SIZES                20,10,5,4,3,2
    PRINT DATA           YES
    READ MATRIX
       <all the data follow here>
    COMPUTE
    PRINT                ALL
    FINISH
```

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APPENDIX

No other known programs perform the CANDECOMP type of analysis, though it is akin to both the PARAFAC model and Tucker’s 3-mode Factor Analysis. See also P.M.Kroonenberg’s three-mode web site at http://www.leidenuniv.nl/fsw/three-mode/index.html.

3. CONJOINT (unidimensional CONJOINT measurement)

Concisely: CONJOINT (unidimensional CONJOINT measurement) analyses
DATA: data in the form of a rectangular N-way array of integers
TRANSFORM: using a monotonic transformation of the data
MODEL: by means of any of a family of simple composition functions

Being a conjoint measurement model, CONJOINT is not easily or helpfully described in terms of the Carroll and Arabie classification.

3.1.1 ORIGIN, VERSIONS AND ACRONYMS OF CONJOINT

CONJOINT is a product of the Nijmegen stable (Roskam 1974), previously known as UNICON (Unidimensional Conjoint Analysis), and is a general version of the earlier ADDIT program, which in turn developed from the Guttman-Lingoes CM (for conjoint measurement) programs (see Lingoes, 1967, 1968; also Lingoes, 1978).

3.1.2 BRIEF DESCRIPTION OF CONJOINT

The CONJOINT program provides the common analysis which takes a dependent variable and a set of independent variables and then estimates for a given simple composition function, that monotone transformation which will best fit that function. By a 'simple composition function' we mean an expression linking the independent variables by means of the operators +, - and x.

The most common application of CONJOINT is to use the additive (+) model, when the model becomes identical to Kruskal's MONANOVA (Monotonic Analysis of Variance) <ref>. Several applications have shown that by employing a monotonic transformation, interactions shown by the linear ANOVA model can be eliminated and hence shown to be artefacts of the level of measurement chosen.

The program implements the conjoint measurement models developed by Luce and others <Krantz et al 1971 & other refs> as a form of fundamental measurement.

3.1.3 RELATION TO OTHER NewMDSX PROCEDURES

CONJOINT, like HICLUS (q.v) is unusual in the NewMDSX series in that it does not seek representation of the data in terms of distance, but rather seeks that monotone transformation of the data which best accords with the form of the model specified.Moreover, it is inherently uni-variate in the sense that each way is represented as a unidimensional variable.

3.2. DESCRIPTION OF THE PROGRAM

3.2.1 DATA

The user must supply two things for a run of CONJOINT:

i) the data
ii) the form of the composition model

and the program then estimates the best fit to the model by monotonically transforming the data.

The data are presented to the program as a rectangular N-way array of integers, whose "facets" or "ways" (these terms are used interchangeably) will be the number of categories contained in each of the variables.

3.2.1.1 Example

Suppose a researcher is investigating the determinants of support for the Official Irish Republican Army, (measured, say, in terms of a Likert rating scale), and also has information on the gender, Left-Right political allegiance, and religious affiliation of his subjects:

Let

Q represent the dependent variable (in this case, Attitude to the Official IRA)

and

$$\left.\begin{array}{l} A \\ \\ B \\ \\ C \end{array}\right\} \text{represent the independent variables (or "facets")} \quad \left\{\begin{array}{lcl} \text{Sex} & = & \{\text{Male, Female}\} \\ \\ \text{Politics} & = & \{\text{Left, Centre, Right}\} \\ \\ \text{Religion} & = & \{\text{Catholic, Anglican,} \\ & & \text{Protestant, Other}\} \end{array}\right.$$

In this case the data for input to CONJOINT will consist of a 3-way ("cube") of data whose characteristic entry δ_{jkl} gives the average attitude scale value for the subjects who are in the jth category of Sex, the *k*th category of Politics and the *l*th category of Religion:

e.g

δ_{111} contains the average attitude score for those who are Male (j = 1), Left (k = 1) and Catholic (l = 1)

The cube will consist of four matrices, (one for each denomination) each with three rows and two columns (NB. not two rows and three columns), corresponding to the facets of religion, politics and sex respectively. (For details of input format see Section 3.3.2).

3.2.1.2 The form of the composition function

The user is also asked to supply the form of the composition function postulated to underlie the data. In the case of the above example, an additive composition function might be chosen, where dependent score (Attitude to the IRA) is considered to be a monotonically rescaled, additive composition of the three facets of Sex, Politics and Religion, i.e:

$$q_{jkl} \underline{\approx} m(a_j + b_k + c_l)$$

Here $\underline{\approx}$ stands for a least-squares fit and 'm' is a monotone function.

Any more complex model which can be expressed by means of a combination of addition, subtraction and multiplication of the facets is acceptable to the program. Bracketing is allowed subject to the restriction that a multiplication may not be followed directly by a left parenthesis. (This problem may usually be overcome by permuting the facets).

3.2.1.2.1 The input of composition functions

The user must specify two things:

i) the form of the model

ii) the number of categories in the facets

3.2.1.2.1.1 The coding of models

CONJOINT makes use of a control statement peculiar to it for the coding of the model. The command is MODEL and it contains in the parameter field a specification in ordinary notation of the model to be fitted. For example, for the study with three facets mentioned above, we might use the simple additive model. In this case the command would be

```
          MODEL           A + B + C
```

Spaces in the parameter field are not significant, and no INPUT FORMAT is required. It may be the case that one facet is a subset of another (or indeed may be identical). In this case the name of the first facet can be repeated. Thus for a study for three facets when the third is a subset of the second and the model is multiplicative, then

```
          MODEL           A * B * B
```

Note that the asterisk (*) is used to denote multiplication when encoding a model.

3.2.1.2.1.2 The coding of categories

The numbers of categories in each of the facets (and thus the dimensions of the input array) are given by the parameter A-FACET, B-FACET, C-FACET, D-FACET and E-FACET in the PARAMETERS command. No more than five facets are allowed. The argument to each of these parameters is the number of categories in each of the facets, thus in our example (2.1.1) above:

```
      PARAMETERS     A-FACET(2), B-FACET(3), C-FACET(4)
```

Note that the hyphen is a significant character and the shortening of B-FACET to its significant length.

If sub-setting is involved, then A-FACET refers to the first facet, B-FACET to the second etc., regardless of the actual names given in the MODEL specification.

For example, consider the example given above where

```
         MODEL      A * B * B
```

where the third facet is a subset of B, and suppose further that A consists of three categories, B of ten and the 'subset' is a recoding of the ten categories into two.

The PARAMETERS command in this case would then be

```
       PARAMETERS    A-FACET(2), B-FACET(10), C-FACET(2)
```

3.2.2 THE MODEL

The program finds that monotone transformation of the data (δ) which is as close as possible (in a least squares sense) to a set of values (d) which conform to the requirements of the composition function specified. This is analogous in the basic model of MDS to the set of fitting values which approximate the actual distances in the solution space.

3.2.2.1 The Algorithm

1. A set of initial estimates of the independent variables is generated by a pseudo-random number device.

2. These are combined in the manner specified by the MODEL statement.

3. Fitting values are calculated.

4. The measure of departure in the trial solution from monotonicity (STRESS) is calculated.

5. A number of tests are performed: e.g.

   Is the STRESS sufficiently low ?
   Has the improvement in STRESS in the last iteration been so small as to be not worth proceeding ?
   Has a maximum number of iterations been performed ?

   If the answer to any of these is YES, then the current estimates are output as solution.

6. The direction in which each value has to be moved to bring it into closer accordance with the fitting values and the approximate magnitude of the move are calculated.

7. The values are moved in accordance with the information calculated in 6 and the program returns to step 2.

3.2.3 FURTHER OPTIONS

3.2.3.1 Missing data

The program allows the user to specify, by means of the MISSING DATA parameter a code which instructs the program to ignore that entry in its calculation of STRESS. This may also help the user in coding of fractional replications (v.i.).

3.2.3.2 Ties in the data

Two ways of treating tied data values are recognised in the CONJOINT program: the so-called primary and secondary approaches. The user is given the option by means of the TIES parameter in the PARAMETERS command.

3.2.3.2.1 The primary approach (TIES(1))

In the primary approach, ties in the data are broken in the fitting values, if, in so doing, STRESS is made less. This option places little or no importance on the appearance of ties.

3.2.3.2.2 The secondary approach (TIES(2))

By contrast, the secondary approach regards the information on ties as important and requires that tied data values are fit by equal fitting values.

3.2.3.3 Levels of measurement in the data

CONJOINT treats each facet as being a nominal scale, and estimates an interval level weight for each category of each facet. If the categories happen to be ordered (say, High, Medium and Low Status) there is nothing in the procedure which will guarantee the category weights will be similarly ordered.

3.2.3.4 Replications

Users may wish to analyse by the same model a number of replications of the same study. Such a study is signalled to the program by means of the REPLICATIONS parameter. This parameter sets the number of sets of data not the number of replications, i.e. if you have an original study and two follow-ups then the correct coding is REPLICATIONS (3).

If a replicatory study provides data on only a subset of the original variables, then it is suggested that the study be coded as a replication with MISSING DATA values inserted at the appropriate places in the data matrix.

In the case of replica studies the program will obviously estimate only one set of averaged fitting values but as many sets of distinct fitting values as there are data sets.

3.2.3.5 The CRITERION parameter

At step 5 of the algorithm the program calculates the improvement in STRESS between the values of this iteration and those at the previous one. If this improvement is less than the value specified on the CRITERION parameter then the process is stopped and the current values output as solution.

It is recommended that in exploratory studies or when a number of models is being tested on a set of data that this value be increased in order to save on machine time.

3.2.3.6 Local minima

The program begins the iterative process by assigning to each of the parameters a randomly-generated value. The starting 'seed' for the random number generator is specified as RANDOM in the PARAMETERS command. The values so produced are statistically random, in the sense that each value has a known and equal probability of occurrence. They are not, however, random inasmuch as the same series of numbers will emerge from the same starting value.

The procedure minimises STRESS by manipulating these initial, pseudo-random numbers. It has been noted (Roskam, 1969) that random starts are prone to the problem of local minima. A local minimum occurs when, although in the 'local' environment STRESS is at a minimum, inasmuch as to change any of the values only slightly, would be to increase its value, there nevertheless exists a set of numbers outside of that 'local environment' which generate a lower 'globally' minimum STRESS value.

It is suggested that the user make a number of runs using the same data but using different starting values. This is done automatically within one run of CONJOINT by means of the keyword RESTARTS in the PARAMETERS command. The number specified by this parameter should be the number of different starts required.

The appearance of a number of highly similar (or identical) solutions is inductive proof of a global minimum.

3.3. INPUT COMMANDS

Keyword		Function
MODEL	letters for each facet in the data with operators + or *	specifies the form of the composition function postulated to underly the data. See the detailed description above.
READ MATRIX		read the data according to the facets

	specified
COMPUTE	start computation
FINISH	final statement in the run

3.3.1 LIST OF PARAMETERS

The following values may be specified following the keyword PARAMETERS

Keyword	Default Value	Function
TIES	1	1: Primary approach 2: Secondary approach
REPLICATIONS	1	Sets number of data-sets for replicated studies.
RANDOM	12345	Seed for pseudo-random-number generator
MISSING	0	Sets value to be regarded as missing datum.
RESTARTS	1	Sets number of times the program will restart analysis using different random starts.
A-FACET B-FACET C-FACET D-FACET E-FACET	1	Sets the number of categories in each facet.
CRITERION	0.00001	Sets stopping value for stress.

3.3.2 NOTES

1. The control statement MODEL is obligatory for CONJOINT.

2. The following commands are not valid:

```
READ CONFIG
LABELS
ITERATIONS
#  ⎫
N  ⎬  OF STIMULI
No ⎭
#  ⎫
N  ⎬ OF SUBJECTS
No ⎭
```

3. The program accepts as input integer (I-type) variables. An INPUT FORMAT specification, if used, should take account of this and should read one row of the data.
4. The data for CONJOINT are input as a rectangular array of integers in which the first facet is that associated with the fastest-running subscript. Consider first the two-facet case. If facet A has 5 categories and facet B has three then the input array will have five columns and three rows. (NOT five rows and three columns). If a third facet C were added, which had two categories, then two such 3 x 5 arrays would be input (six rows in all, each of five columns). A fourth facet with four categories would result in four such blocks, i.e. twenty four rows in all. The data follow without separation.

3.3.3 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of CONJOINT the options are as follows:

3.3.3.1 PRINT options

Option	Description
TABLES	Two matrices are listed: 1. the matrix of fitting-values 2. the solution matrix. Both will, of course, be of the same order as the input data.
HISTORY	An extended history of the iterative process. For details see Appendix 3.
SOLUTION	

By default, only the SOLUTION will be listed, along with the final STRESS value.

14.3.3.2 PLOT options

Option	Description
STRESS	A Histogram of STRESS at each iteration is produced.
SHEPARD	A Shepard diagram plotting data against solution is plotted and the fitting values indicated.
RESIDUALS	A histogram of residual values with both natural and logarithmic values is produced.

A Shepard diagram is produced by default.

3.3.3.3 PUNCH options

Option	Description
SPSS	The following values are output. I, J, K, L, M (being indices of the five possible facets) DATA, FITTING, SOLUTION, RESIDUALS, being the corresponding values in a fixed format.
FINAL	The solution is saved.
STRESS	A listing of STRESS values at each iteration is produced in a fixed format.

By default, no secondary output is produced.

3.3.4 PROGRAM LIMITS

Maximum number of facets = 5.
Maximum number of categories = not specified.
Maximum(number of elements x number of replications) = 2500
Maximum number of scale values = 500.

3.4. EXAMPLE

```
   RUN NAME                  FERTILITY BY PRESENT HUSBAND'S ORIGIN & STATUS
   TASK NAME                 * * * TWO WAYS DISTINCT * * *
   COMMENT                   DATA FROM HOPE 1972, TABLE 1.
   INPUT FORMAT              (4I5)
   PRINT DATA                YES
   MODEL                     A + B
   PARAMETERS                A-FACET(4), B-FACET(4), CRIT(0.005), TIES(2)
   PRINT                     HISTORY
   PLOT                      SHEPARD, RESIDUALS
   READ MATRIX
    1.74 1.79 1.96 2.00
```

```
 2.05 2.14 2.51 2.97
 1.87 2.01 2.67 3.69
 2.40 3.20 3.22 3.68
COMPUTE
FINISH
```

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APPENDIX 1: RELATION OF CONJOINT TO OTHER PROGRAMS NOT IN NewMDSX

The additive option in CONJOINT is exactly analogous to the ADDIT program which in turn derives from the MONANOVA (monotonic analysis of variance) procedure of Kruskal (see above).

APPENDIX 2: OUTPUT FROM CONJOINT

The output of CONJOINT consists of two parts: each part is preceded by a program identification heading, and printing of the problem TITLE and the measurement MODEL as it was specified by the user at input.

The first part of the output, consists of a summary or extensive history of the iterations, depending upon the PRINT option chosen.

The second part of the output contains the scaling solution, the values of $z_{jk\,..}$ and the values of $\hat{z}_{jk\,...}$

1. Following the printing of the problem TITLE, the MODEL is printed in the form of a sequence A B C D E referring to the facets of the design, each letter preceded by the algebraic operation. For instance, when the model is $z_{jk} = (a_j - b_k) \times c$ and the facets are defined as being different from each other, the program will print:

```
MODEL  ( +A - B ) x C
```

2. Next, the program will print which facets are identical, if any. For instance, when $z_{jk} = a_j\ b_k + a$, the program will print:

```
MODEL  ( +A ) x  B - C          C = A
```

Note the introduction of parenthesis and of + r symbol, which is redundant in this example.

3. After this, the program will write the scaling SOLUTION with the following form:

S O L U T I O N

A a_1 a_2 a_3 a_4 a_5 a_6 a_7 a_8 a_9 a_{10} a_{11} a_{12} a_{13} etc.

B b_1 b_2 b_3 b_4 b_5 b_6 b_7 b_8 b_9 b_{10} etc.

C c_1 c_2 c_3 etc

etc. etc.

Note that identical values will be printed when facets are identical. So, if for instance, facets B and A are the same, the program will write B followed by the same values as it printed with A.

4. Next, the program prints a table of ZHAT values. These values

$(\hat{z}_{jk\,..(h)})$ match the values $z_{jk\,..} = f(a_j, b_k, c, ..)$ in the least

squares sense and are weakly monotonic with the data.

Each entry in this table consists of

x j k .... $\hat{z}_{jk\,..(h)}$

where x is a consecutive number, indexing the elements in this table, and j,k, ,.. refer to the levels or categories of the facets A,B,C,.. The entries in this table appear in the order of replications, that is:

first appear $z_{lk..(1)}$ (j=1,..., k=1,....; =1,...; etc) then all $z_{jk..(2)}$'
etc.

Within each replication, the entries appear in increasing order of $r_{jk..(h)}$'
which is also the non-decreasing order of $\hat{z}_{jk...(h)}$

Missing data are omitted in this table' So, x runs up to the total number of elements actually present in the data. (Since this table is ordered according to the ordinal information in the data, the user can also use it to check for any errors in his input).

Following this table, the program prints the numbers of distinct values

in the data, the number of distinct values in ZHAT (= $\hat{z}_{jk...(h)}$) and

the number of distinct values in Z (= $z_{jk..(h)}$). This count goes

through all replications, bypassing missing data elements. Ideally, there should be no ties in Z; when there are, this means degeneracy of the solution (except in those cases where the model calls for equal values, e.g. $z_{jk} = z_{kj} = a_j + a_k$); in other words, the number of distinct

values in Z should be equal to the number of elements in Q=AxBxCx.. (except of course when some elements from Q are absent in all replications).

When the secondary approach to ties is used, tied data will be tied in ZHAT, and should be also in Z if the stress is low. In general, the number of distinct elements in ZHAT wiil be less than the number of distinct elements in the data, and the more so when the stress is high. In the output, the number of distinct elements is labelled: NUMBER OF EQUIVALENCE CLASSES.

5.   Finally, the program prints a matrix of Z. Unlike the table of ZHAT, whose entries are different for each replication, the elements in Z are the same for all replications, and the matrix of Z is of course printed only once. The order in which the elements of Z are printed is the same as the input order of the data.
The category labels A1, A2, A3, etc. are printed at the top line.
At the right of each line, the pertinent indices of other facets are printed, headed by 'B', 'C' etc. at the top line.

For instance:

A1	A2	A3	B	C
z_{111}	z_{211}	z_{311}	1	1
z_{121}	z_{221}	z_{321}	2	1
z_{112}	z_{212}	z_{312}	1	2
z_{122}	z_{222}	z_{322}	2	2

6.   Output items 1 through 5 are repeated for every problem submitted to the program.

4. CORRESP (CORRESPondence analysis)

4.1. OVERVIEW

Concisely: CORRESP provides internal analysis of two-way or multi-way data of a variety of kinds, and represents them as two sets of "points" ("row" points and "column points") in the same space. It can be classified as follows:

DATA: N-way, n-mode Table

TRANSFORMATION: Linear

MODEL: Chi-square distance

Simple correspondence analysis has typically been applied to represent row and column categories of a two-way contingency table in a two dimensional map. But the same procedure can be applied, at least descriptively, to any matrix which can plausibly be regarded as consisting of 'pseudo-frequencies'.

It can also be applied descriptively to non-frequency data such as rankings or profiles, or data representing the intensity of responses to stimuli, or any of a variety of indices of proximity.

4.1.1 ORIGINS, VERSIONS AND ACRONYMS

Correspondence analysis is a translation of the French 'analyse des correspondances', developed by Benzécri et al.(1973) and made popular by its adoption by Pierre Bourdieu in **Distinction** (1979). It was then by no means a new technique, having been described and differently named and applied in a number of unrelated fields, since Hirschfield(1935). It is closely related to canonical correlation and discriminant analysis and has been called, among other names, the method of reciprocal averages, and dual scaling, as well as ***l'analyse factorielle des correspondances***. Correspondence analysis is also one way of implementing ***unfolding*** as introduced by Coombs(1964). Not only have different names been used for the same techniques in different fields. It is also not always realized that different computational procedures lead to the same results. Developed by the Gifi group in the Department of Data Theory at the University of Leiden for use with relatively large and sparse matrices representing multi-way categorical data, the HOMALS procedure (Analysis of homogeneity by alternating least squares) available with SPSS uses an iterative procedure to achieve the equivalent of multiple correspondence analysis. (see Van de Geer (1993) Vol.2, Ch.2). CORRESP directly calculates the singular value decomposition by finding the eigenvalues and eigenvectors of the matrix of cross-products of the input data matrix, after it has been normalized by dividing each row entry by the square root of the product of the corresponding row and column totals. In this it is markedly similar to PRINCOMP, and especially to MDPREF and differs from the latter only in the pre-treatment of the data and the form of normalisation (See, in particular, Weller and Romney(1990)).

The first paper containing a fully worked-out numerical example corresponding to current definitions is by R.A.Fisher(1940). Canonical analysis in its classical form is traced to two articles by Hotelling (1935, 1936) using Lagrange multipliers and eigen-analysis. Psychological literature most frequently refers to the "Eckart-Young decomposition theorem", from an early paper (1936) that clarified how a matrix could be decomposed into its basic structure of rows and columns.

4.1.2 FURTHER SPECIFICATION

The CORRESP program provides internal analysis of categorical data which can be input as a series of rows, representing individual subjects or observations with their values according to a series of column categories.

The classical application is to a two-way, 2-mode contingency table, where the frequencies represent the numbers of observations classified according to two sets of categories. In this case, and where data can properly regarded as frequencies of a similar kind (and expected frequencies are not too small) it is possible to apply the chi-squared statistic to test the significance of the canonical dimensions extracted. Application to other kinds of data can be only descriptive and exploratory.

Input of multi-way indicator matrices, or Burt matrices (obtained by multiplying an indicator matrix by its transpose) is one form of multiple correspondence analysis, as is Guttman scaling. Stacking of a series of two-way tables is another. See the Appendix, below, for further details.

Correspondence analysis is increasingly popular in analyzing Contingency Tables and in exploring the relationships between frequencies of artefacts found at different archaeological sites or levels of excavation ('seriation'), and of animals or plants and habitats ('gradient analysis').

4.1.3 RELATION OF CORRESP TO OTHER PROCEDURES IN NewMDSX

CORRESP uses a direct singular value decomposition of pre-standardized data to produce canonical scores for rows and columns which can be plotted as points in the same space. MDPREF also represents row and column variables in the same space, but instead fits the row variables as vectors to the configuration derived from the column variables. For this reason, MDPREF is sometimes referred to as a "vector" model and CORRESP as a "point" model. CORRESP examines only interactive factors by neglecting the magnitude effect after decomposition, but so can MDPREF when treating data as row-conditional. The main reason for MDPREF projecting one set of points onto a unit circle/sphere, however, is to remove them from the location of the set; to facilitate projection interpretation and to discourage inter-set point distance interpretation, which is otherwise tempting when using correspondence analysis.

If separate PRINcipal COMPonents analyses are performed on the row and column correlation matrices of data which have also been standardized by rows and columns, these produce equivalent sets of results.

If the preference data are expressed as quasi-frequencies that may be seen as the quantity of choice received by each column item, MDPREF for column standardized and double-centred data provides similar results to those obtained by CORRESP and PRINCOMP.

4.2. DESCRIPTION

4.2.1 INPUT DATA

CORRESP accepts as input data a set of frequencies forming a rectangular matrix. This can be a simple two-way contingency table of categorical data, or more generally an indicator matrix of rows representing subjects and columns representing presence and absence of a series of binary attributes for each subject. The indicator matrix can be condensed by adding together identical rows, and will produce the same scores for equivalent data.

When using correspondence analysis descriptively for data other than strict frequencies, there are five restrictions to be observed. For some, CORRESP will report an error if they are violated; for others, it is up to the user to examine the data to avoid misinterpretation.

1. Inferential tests such as Chi-square are not valid for non-frequencies (or when expected frequencies are too small).

2. The data must be in the form of 'similarities', i.e. if they are ranks, they should be ordered from highest to lowest preference (compare DATA TYPE(4)for MDPREF). If the data are distances, they should be reflected by subtraction from a number larger than the largest distance, so that they can be regarded as similarities.

3. When analysing symmetric square matrices, it is essential that the diagonal from top left to bottom right contain large positive values (see the Appendix below for an example using stacked matrices.

4. All values in the matrix must be positive, or the results will not be valid.

5. In the analysis of sparse matrices, consider the possibility that the data may contain disjoint sets, which should be separated prior to analysis. It may also be necessary to submit the data to a succession of analyses, if interpretation is hindered by the presence of obvious outliers, which should be removed before contining. When deleting outliers, it is important to remember this may require deletion of both rows and columns, according to the type of matrix.

4.2.2 THE MODEL

4.2.2.1 Description of the Algorithm

1. The input matrix is first normalized by dividing each row entry by the square root of the product of the corresponding row and column totals.

2. The cross-products matrix of the columns of the resulting matrix **A** is formed.

3. The next step finds the basic structure of **A**, producing summary row and column vectors (**U** and **V**) and a diagonal matrix of singular values **d** corresponding to the columns of **A**, so that **A** = **Ud**(**V**T). The matrices **U** and **V** are the eigenvectors of the matrices of column (or row) cross-products of **A**, and the **d** values are related to the corresponding eigenvalues (**d**=sqrt(**D***(*n*-1)), where **D** is the diagonal of eigenvalues and *n* is the number of rows in **A**).

4. The canonical or ‘optimal’ scores are calculated for the number of dimensions requested. These form the configuration output and plotted as the solution.

4.2.2.2 Interpretation of the solution

The default **CORRESP** output indicates the number of non-negative eigenvalues of the matrix of cross-products of the normalized input matrix. This indicates the rank of the matrix, irrespective of the number of dimensions the user has requested to be output. They may be inspected in full by including the **PRINT** option **ROOTS**. The largest root will always be first and the others will follow in decreasing order. Some may be very small. An appropriate dimensionality may be chosen by means of the familiar scree-test.

The basic structure (singular value decomposition) of the matrix is always listed in full. The singular value (otherwise known as latent or characteristic root or eigenvalue) corresponding to the first, or 'trivial' dimension is always 1.0 and is disregarded, while the remainder are termed the 'inertia'. Their relative magnitude gives an indication of the amount of variation in the data accounted for by the corresponding dimension. Where appropriate, reference can be made to the chi-squared contributions of each dimension of 'inertia' and to the overall chi-squared value for the analysis.

To assist interpretation of the dimensions, the contributions of the individual row and column points to 'inertia' are listed, followed by the corresponding canonical, or 'optimal', scores, which are conventionally plotted in reporting the results of correspondence analysis. In the graphic displays of these results, note that an additional menu item **Vectors** enables you optionally to represent the rows of the table as vectors, if preferred.

The identification of 'outliers' amongst the subjects by visual inspection is straightforward. It may help to clarify the plotted solution if these are removed, before repeated the analysis. Note that in removing an outlier, it is necessary to delete both the row and column of the input indicator matrix.

4.3. INPUT COMMANDS

CORRESP requires an input matrix of r rows and c columns, where r may be equal to c. The optional LABELS command allows the column and row categories to be identified as appropriate; the first 6 characters of these input values appear in the graphic plots which can be requested in NewMDSX for Windows.

The DIMENSIONS command is used here only to limit the number of dimensions for which details are listed in the output. There is no PARAMETERS instruction for CORRESP.

Keyword		Function
N OF COLUMNS	c	Number of columns in the input matrix
N OF ROWS	r	Number of rows in the input matrix
DIMENSIONS	n	Number of dimensions to list and plot in detail.
LABELS	followed by a series of labels (<= 65 char) each on a separate line	Identify the column and labels, in order, from right to left and top down.
READ MATRIX		Start reading input data
COMPUTE		Start computation
FINISH		Final statement in the run

4.3.1 NOTES

1. N OF COLUMNS,
   N OF ROWS and
   DIMENSIONS are obligatory.

2. READ CONFIG is not valid with CORRESP.
3. LABELS are optional.

4.3.2 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of CORRESP, the options are as follows:

4.3.2.1 PRINT options

Option	Form	Description
FIRST	r x c	The input matrix, rows by columns
CROSS-PRODUCTS	r x r, c x c	Cross-products of the rows and columns of the normalized input matrix.
CORRELATIONS	r x r, c x c	The correlation matrices of rows and columns of the normalized input matrix.
ROOTS		The eigenvalues of the cross-products of the normalized input matrix.
FINAL		All of the output described above, in the chosen dimensionality.
CHISQUARE		The total chisquared value, with degrees of freedom, and the contributions of the individual factors of "inertia".

By default the FINAL output is produced.

4.3.2.2 PLOT options

Option	Description
ROWS	The n(n-1)/2 plots of the canonical ("optimal") row scores in the chosen dimensionality.
COLUMNS	The n(n-1)/2 plots of the canonical ("optimal") column scores in the chosen dimensionality.
JOINT	Both the above.
ROOTS	A scree diagram of the latent roots.

By default, the first two dimensions of the joint space only are plotted.

4.3.2.3 PUNCH options (to secondary output file)

No secondary output file is produced by CORRESP

4.3.3 PROGRAM LIMITS

Maximum no. of rows	=	100
Maximum no. of columns	=	60

4.4. EXAMPLES

4.4.1 EXAMPLE OF A SIMPLE RUN

```
RUN NAME  CORRESPONDENCE ANALYSIS EXAMPLE - Weller & Romney(1990) p.60
COMMENT   1660 subjects are classified by parental socio-economic
          status (columns) and categories of mental health (rows).
          Data from Srole et al. (1962).
N OF COLUMNS    4
N OF ROWS       3
LABELS     A+B
           C+D
           E
           F
           WELL
           MILD+MODERATE
           IMPAIRED
PRINT FIRST FINAL CHISQ
```

```
DIMENSIONS      2
READ MATRIX
 121 129  36  21
 300 388 151 125
  86 154  78  71
COMPUTE
FINISH
```

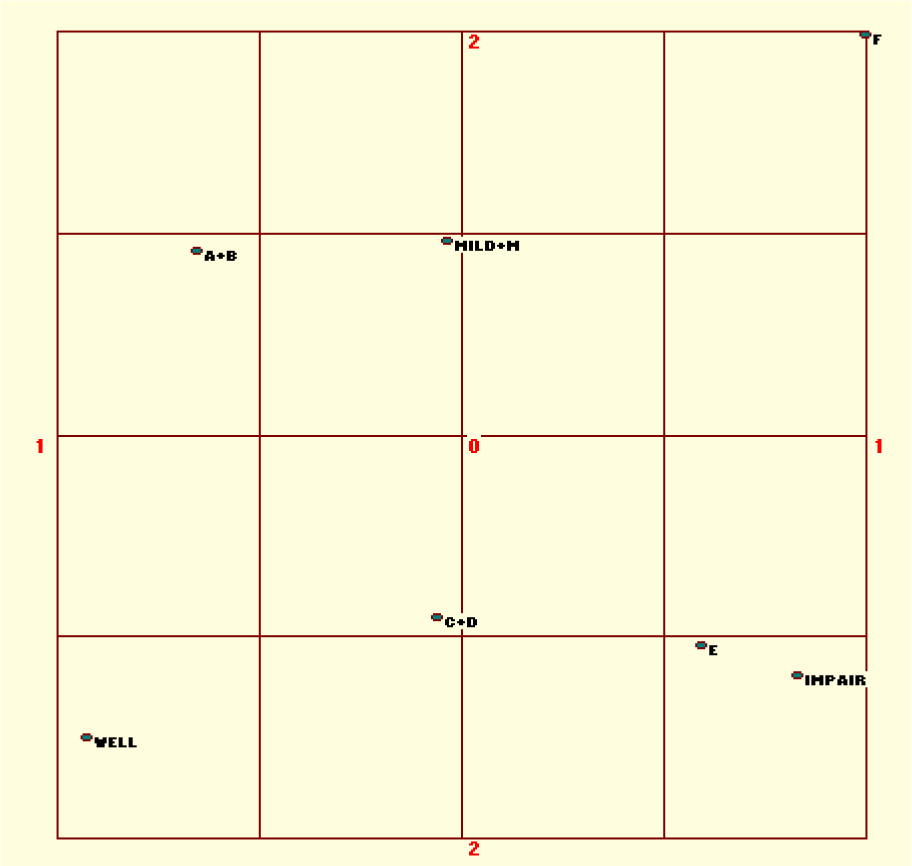
......

produces the following output

```
 NORMALIZED INPUT MATRIX (A)
 ROWS        COLUMNS
         1          2          3          4
   1     0.3067     0.2842     0.1262     0.0814
   2     0.4291     0.4824     0.2988     0.2733
   3     0.1937     0.3014     0.2429     0.2444


 THE CROSS-PRODUCTS MATRIX HAS 3 EIGENVALUES GREATER THAN ZERO

 CORRESPONDENCE ANALYSIS EXAMPLE - WELLER & ROMNEY(1990) P.60
 TASK NUMBER  1
 ROOTS OF THE CROSS-PRODUCTS MATRIX

 **** SOLUTION IN  2 DIMENSIONS ****
 EXPLAINED VARIANCE = 100.00%

 BASIC STRUCTURE (SINGULAR VALUE DECOMPOSITION)

 ROW VECTORS (U MATRIX)
         1          2          3
   1     0.4300    -0.7017    -0.5680
   2     0.7621    -0.0552     0.6452
   3     0.4841     0.7103    -0.5110


 COLUMN VECTORS (V MATRIX)
         1          2          3
   1     0.5526    -0.6378     0.4449
   2     0.6358    -0.0754    -0.5119
   3     0.3995     0.4247    -0.3735
   4     0.3616     0.6381     0.6329


 SINGULAR VALUES - DIMENSIONS
         0          1          2
        1.0000     0.1589     0.0083

 PROPORTION OF TOTAL VARIANCE
        0.9753     0.0246     0.0001     TOTAL   1.0000

 EXPLAINED "INERTIA"
                   0.9973     0.0027     TOTAL   1.0000

 CHI-SQUARED       41.9222     0.1136
 CONTRIBUTIONS
 TOTAL CHI-SQUARED=    42.0358  (DF=  6)

 CANONICAL ("OPTIMAL") SCORES
 ROWS       DIMENSIONS
         1          2
   1  WELL
```

```
        -1.6317    -1.3209
   2  MILD+MODERATE
        -0.0725     0.8466
   3  IMPAIRED
         1.4674    -1.0556

 CANONICAL ("OPTIMAL") SCORES
 COLUMNS    DIMENSIONS
           1          2
   1  A+B
        -1.1541     0.8050
   2  C+D
        -0.1185    -0.8052
   3  E
         1.0631    -0.9347
   4  F
         1.7647     1.7504
```

The canonical scores are plotted as follows, showing the relationship between patients' parents' social class categories and diagonses of the severity of mental illness:

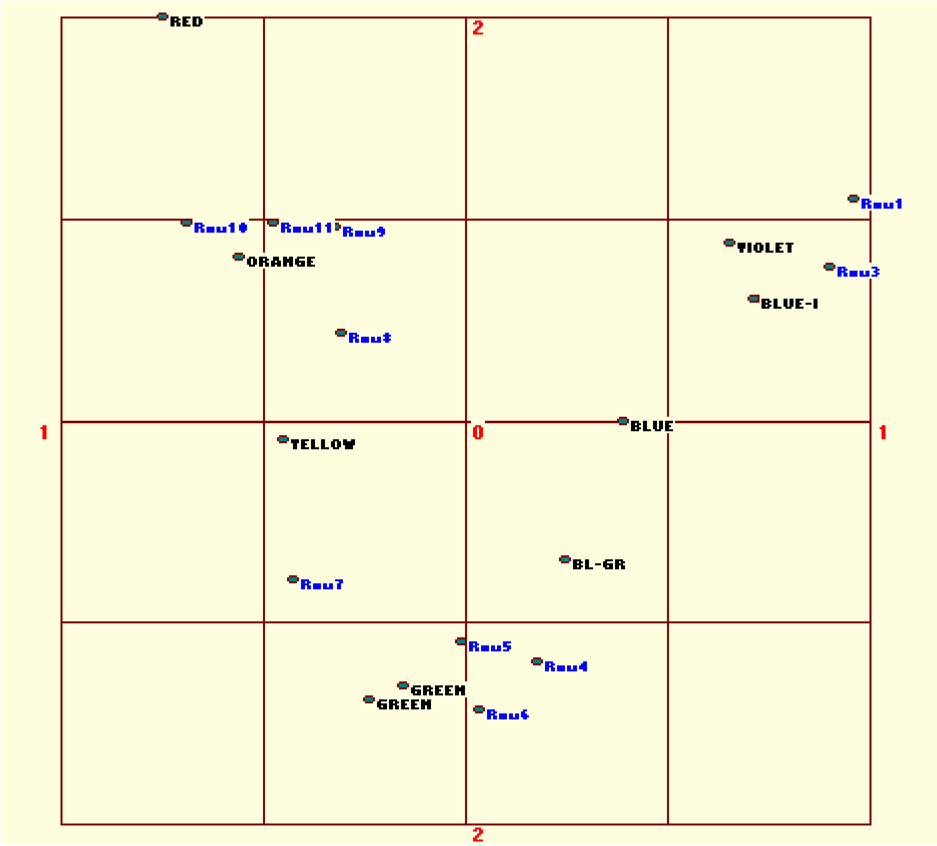


4.4.2 EXAMPLE 2 : REACTIONS TO STIMULI

```
RUN NAME  Marks's receptor cone colour sensitivity data
COMMENT  CA analysis, as discussed in Weller & Romney, Metric
```

```
         Scaling, pp.9ff. The values represent the amount of
         light absorbed by each type of receptor cone in goldfish.
         Rows are eye receptor cones 1-11,
         columns are light stimuli.
LABELS Green
       Yellow
       Red
       Blue-I
       Bl-Gr
       Blue
       Green
       Orange
       Violet
N OF ROWS      11
N OF COLUMNS    9
DIMENSIONS      2
READ MATRIX
  12.0   0.0   0.0 153.0  57.0  89.0   4.0   0.0 147.0
  32.0  23.0   0.0 154.0  75.0 110.0  24.0  17.0 153.0
  14.0   0.0   0.0 152.0 100.0 125.0   0.0   0.0 145.0
 154.0  93.0   0.0 101.0 140.0 122.0 153.0  44.0  99.0
 152.0 116.0  26.0  85.0 127.0 103.0 148.0  75.0  46.0
 151.0 109.0   0.0  78.0 121.0  85.0 174.0  57.0  73.0
  97.0 137.0  45.0   2.0  52.0  46.0 106.0  92.0  14.0
  84.0 151.0 120.0  65.0  73.0  77.0 102.0 154.0  44.0
  86.0 139.0 146.0  59.0  52.0  58.0  79.0 163.0  87.0
  55.0 120.0 132.0   0.0  39.0  40.0  62.0 147.0   0.0
  56.0 136.0 111.0  27.0  24.0  23.0  72.0 144.0  60.0
PLOT        JOINT
COMPUTE
FINISH
```

The resulting plotted values show the sensitivity of the different receptor cones to the different colours. The stimuli are located in a horseshoe shape according to the wavelength of light involved (the row label Row2 is overwritten by stimulus label BLUE-I):

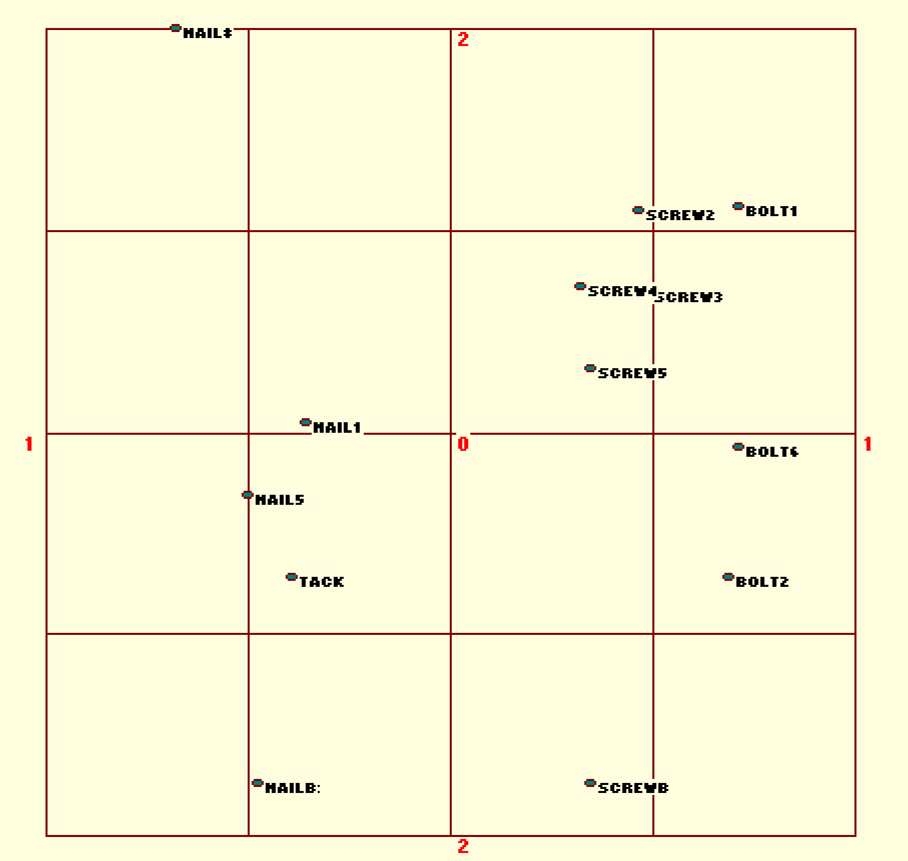


4.4.3 AN EXAMPLE OF MULTIPLE CORRESPONDENCE ANALYSIS

The data used here are for "Hartigans Hardware" from GIFI(1990),pp.128ff. A series of items are coded according to characteristics of their shape, length, whether they are threaded, etc. and presented in a full indicator matrix. The columns are a series of 0,1 codes for presence/absence of the recorded characteristics and the rows represent the objects.

```
RUN NAME  Hartigans Hardware example
TASK NAME Outlier Object 10 removed
N OF COLUMNS   18
N OF ROWS      23
DIMENSIONS     2
LABELS  THREADN
THREADY
FLAT
CONE
ROUND
.....
.....
BOLT6
TACK1
TACK2
NAILB
SCREWB
READ MATRIX
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0
 1.0 0.0 0.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 1.0 0.0
 1.0 0.0 0.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0
 1.0 0.0 0.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 0.0 0.0 1.0 1.0 0.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 0.0 0.0 1.0 1.0 0.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0
 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 0.0 0.0 1.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 0.0 0.0 1.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 0.0 0.0 1.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0
 0.0 1.0 0.0 0.0 0.0 0.0 1.0 1.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0
 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0
 0.0 1.0 0.0 1.0 0.0 0.0 0.0 1.0 0.0 0.0 1.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0
PRINT       FINAL
PLOT        ROWS JOINT
COMPUTE
FINISH
```

The resulting plot of the rows scores clearly recovers the classification of the items, identified by descriptive names:



APPENDIX : FORMS OF DATA INPUT FOR CORRESPONDENCE ANALYSIS

It is often helpful to represent categorical data in the form of an 'indicator' matrix. In general, for a variable z_j with k_j categories, the indicator matrix is a table with k_j columns and n rows, where n is the number of objects. The cells of the matrix $\mathbf{G_j}$ contain a 1 if the column category applies to the row object, and a zero if it does not. In each row, therefore, there is only one element 1, and the rest are all zero (assuming the categories are exhaustive and mutually exclusive). A matrix of this kind is called a *complete indicator matrix*.

Indicator matrices $\mathbf{G_j}$ can be combined in a *super indicator matrix* **G**, with n rows and $\sum k_j$ columns. As each row of $\mathbf{G_j}$ contains only one element 1, the rows of **G** will add up to the number of variables. Matrices of this kind containing categories for three or more variables provide a means of presenting data for multiple correspondence analysis, as in the third example above.

If the transpose of an indicator matrix **G** is multiplied by the original indicator matrix, the resultant symmetric matrix, with rows and columns corresponding to the column categories, in correspondence analysis is sometimes called a *Burt matrix*. On the diagonal of this matrix are a series of two-by-two matrices with counts of the 'presence' of an item in the upper left corner and its 'absence' in the lower right corner, the other elements being zero. This kind of matrix offers another alternative in generalizing correspondence analysis to multi-way data.

The first example shown above inputs a simple contingency table for correspondence analysis. This could instead have been arranged into a very large binary ('indicator') matrix of 1660 rows, each representing a subject, and seven columns, three representing the categories of the row variables and four those of the row variables.

It is frequently the case that a number of rows of the complete indicator matrix are identical, representing observed items with identical profiles in terms of the column categories. Nishisato and Sheu (1980) have shown that the results are equivalent if it is condensed by adding together any identical rows. For the data of the first example above, this would yield the following matrix:

Row categories			Column categories			
1	2	3	1	2	3	4
121	0	0	121	0	0	0
0	300	0	300	0	0	0
0	0	86	86	0	0	0
129	0	0	0	129	0	0
0	388	0	0	388	0	0
0	0	154	0	154	0	0
36	0	0	0	0	36	0
0	151	0	0	0	151	0
0	0	78	0	0	78	0
21	0	0	0	0	0	21
0	125	0	0	0	0	125
0	0	71	0	0	0	71

Readers may verify that this produces the same optimal scores. (see Weller & Romney, p.67).

As a final example, Weller and Romney demonstrate multiple comparisons using "stacked" matrices. They combine together, vertically, a series of symmetric tables of judged similarities between English kinship terms, drawn from different sources, from which the following is an extract (the rows and columns of each table represent the terms "Grandfather", "Grandson", "Father", "Son", "Brother", "Uncle", "Nephew", and "Cousin"):

GrFa	GrSo	Fa	So	Br	Un	Ne	Co
6.00	4.10	4.00	1.43	1.00	1.56	0.81	0.62
4.10	6.00	1.62	3.17	1.55	0.77	1.68	1.10
4.00	1.62	6.00	3.80	2.32	1.95	0.61	0.55
1.43	3.17	3.80	6.00	3.68	0.63	1.23	1.43
1.00	1.55	2.32	3.68	6.00	1.61	1.56	1.75
1.56	0.77	1.95	0.63	1.61	6.00	3.71	3.48
0.81	1.68	0.61	1.23	1.56	3.71	6.00	4.24
0.62	1.10	0.55	1.43	1.75	3.48	4.24	6.00
....							
6.00	4.25	4.50	2.31	1.01	0.92	0.31	0.27
4.25	6.00	1.88	4.04	1.36	0.20	1.38	0.81
4.50	1.88	6.00	4.02	2.31	2.13	0.26	0.25
2.31	4.04	4.02	6.00	3.01	0.32	1.02	0.75
1.01	1.36	2.31	3.01	6.00	2.47	1.63	1.75
0.92	0.20	2.13	0.32	2.47	6.00	4.27	3.86
0.31	1.38	0.26	1.02	1.63	4.27	6.00	4.71
0.27	0.81	0.25	0.75	1.75	3.86	4.71	6.00

The value 6.0 has been placed on the diagonal of each matrix as this was the largest possible similarity score in the data, and has been used to represent identity.

A correspondence analysis of the combined table provides a visual representation of the similarities among the different kin terms and the different data sources simultaneously.

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5. HICLUS (HIerarchical CLUStering)

5.1 OVERVIEW

Concisely: HICLUS (HIerarchical CLUStering) provides internal analysis of two-way one-mode (dis)similarity data by means of a hierarchical clustering scheme using a monotonic transformation of the data.

DATA: 2-way, 1-mode dis/similarity matrix

TRANSFORM: Monotonic

MODEL: Ultra-metric distance

Since HICLUS does not employ a spatial representation, the Carroll-Arabie (1979) classification is not useful in describing the program.

Unlike most other programs in NewMDSX, HICLUS is not an iterative algorithm. Nor is it strictly speaking a monotonic transform. It is the HICLUS representation of the solution-- a “stacked” series of increasingly fine partitions -- that remains invariant under monotonic transformation and not (for instance) the dendogram solution.

5.1.1 ORIGIN, VERSIONS AND ACRONYMS

HICLUS was originally programmed by Johnson (1967) following work by Ward (1963). The present program is based on the original Bell Laboratories version of the program.

5.1.2 HICLUS IN BRIEF

The method of hierarchical clustering implemented in HICLUS is often used as an alternative or as a supplementary technique to the basic model of MDS and takes the same form of data.

The matrix of (dis)similarities between a set of objects is used to define a set of non-overlapping clusters such that the more similar objects are joined together before less similar objects. The scheme consists of a series of clustering (levels). In the initial level each object forms a cluster, whilst at the highest level all the objects form a single cluster. In a hierarchical clustering scheme (HCS) there are exactly (p-1) levels where there are p objects.

The clustering scheme is hierarchical in the sense that once two objects have been joined together at a lower level of the scheme, they may not be split at a higher level.

5.1.3 RELATION OF HICLUS TO OTHER PROCEDURES IN NewMDSX

HICLUS is commonly used as an interpretative aid in analysing configurations of points resulting from MDS analyses.

5.2. DESCRIPTION

5.2.1 DATA

HICLUS expects data in the form of a lower triangle matrix of (dis)similarity measures between a set of objects (stimuli). Any of the types of data suitable for input to MINISSA are suitable (q.v.)'

It is often tempting to submit to HICLUS the solution distances from (say) a MINISSA run. This is not recommended since a MINISSA solution will be globally stable, but locally unstable in the following sense. The location of the stimulus points in the space is not uniquely defined, since each may be moved within a fixed region without affecting the goodness-of-fit. It is precisely the small distances affected by such movements which are crucial in the early stages of the HICLUS analysis. Users are therefore advised to submit the original data to HICLUS.

5.2.2 THE MODEL

A hierarchical clustering scheme (HCS) consists of a set of clusterings of a set of objects at increasing levels of generality. At the lowest level, each object is considered a separate cluster. At the next level the two most similar objects are merged to form a cluster. At each subsequent stage either the most similar individual objects remaining are joined together to form a new cluster or an object (or indeed cluster) is joined to the cluster to which it is most similar. At the highest level objects fall into one large, undifferentiated cluster.

5.2.2.0.1 A simple example

```
                             Objects:
                      C   B   E   D   F   A
          Level:  0   .   .   .   .   .   .
                  1   .   XXXXX   .   .   .
                  2   .   XXXXX   .   XXXXX
                  3   XXXXXXXXX   .   XXXXX
                  4   XXXXXXXXX   XXXXXXXXX
                  5   XXXXXXXXXXXXXXXXXXXXX
```

In this example, B and E are merged at level 1, F and A are merged at level 2, C is merged with the cluster (B,E) at level 3, D is merged with (F,A) at level 4, and finally (C,B,E) and (D,F,A) are merged into a single cluster at the fifth level.

Notice that once an object has been assigned to a cluster it may not "leave" that cluster. This is the defining characteristic of a hierarchical scheme.

The crucial question when defining a HCS is one which asks how we are to calculate the (dis)similarity between an object and an existing cluster.

Consider three objects, a, b and c. If b and c have been joined to form a cluster (b,c) then the question arises, how are we to find the dissimilarity of a to (b,c). We might take it to be equal to the dissimilarity between a and b or to that between a and c or some average of the two. Since we are committed to using only the ordinal information in the data we disregard the averaging approach and are left in the general case, where a cluster may consist of more than two objects, with two options, which mark the full range of possible options in defining "the" distance between a cluster and another point: choosing the minimum distance, and the maximum distance. Clearly, any aggregate measure for defining "the" distance, such as the mean , the median or the mode will lie between these extremes.

5.2.2.0.2 The "minimum" method

Also known as the "connectedness" or "single-link" method, this approach defines the dissimilarity between a point and a cluster as the smallest of the dissimilarities between the external point and the constituent points in the cluster. This method tends to join single points to existing clusters ("chaining") and schemes resulting from it are often not easily
amenable to substantive interpretation. The "level" value in this approach gives the length of the longest chain joining any two points in the cluster. This approach is chosen by specifying METHOD(1) in the PARAMETERS statement.

5.2.2.0.3 The "maximum" method

Also known as the 'diameter' or 'complete link' method, this approach defines the dissimilarity between a point and a cluster to be the largest (maximum) of the dissimilarities between it and the points constituting
the cluster. In this case the " level" gives the size of the diameter of the largest at that level. This method is chosen by specifying METHOD(2) in the PARAMETERS. The default option METHOD(3) allows for both methods to be used sequentially.

With perfect data, both methods will give rise to the sameclustering.

5.2.2.1 The Algorithm

At each level:

1. The smallest dissimilarity (greatest similarity) coefficient in the data matrix is identified.

2. The row- and column-element corresponding to this coefficient are then merged to form a cluster (i.e. one row and one column are effectively removed from the matrix).

3. The (dis)similarity coefficients between the new cluster and each of the remaining elements (points or clusters) are calculated according to the METHOD chosen.

4. The matrix is reduced by one row and column and the program returns to step 1.

5. When all the points are thus merged the solution is output in the form of a histogram (the so-called Hierarchical Clustering Scheme).

5.3. INPUT COMMANDS

Keyword		Function
N OF STIMULI	<integer>	The number of variables in input matrix.
LABELS	followed by a series of labels (<= 65 char) each on a separate line	Identify the variables in plotting dendrograms. Labels should contain text characters only, without punctuation.
READ MATRIX		read the data according to the DATA TYPE specified
COMPUTE		start computation
FINISH		final statement in the run

5.3.1 LIST OF PARAMETERS

The following values may be specified, following the keyword PARAMETERS

Keyword	Default	Function
DATA TYPE	0	0: The data are similarities - input is lower triangle without diagonal
		1: The data are dissimilarities - input lower triangle without diagonal
		2: The data are similarities - input is full symmetric matrix
		3: The data are dissimilarities - input full symmetric matrix
METHODS	3	1: Only the minimum method is used.
		2: Only the maximum method is used.
		3: Both methods are used (independently).

5.3.2 NOTES

1. The following commands are not valid with HICLUS.

```
 ( #  )
 ( N  ) OF SUBJECTS
 ( NO )
DIMENSIONS
ITERATIONS
PLOT
PUNCH
```

2.

```
 ( #  )              may be replaced with  ( #  )
 ( N  ) OF STIMULI                         ( N  ) OF POINTS
 ( NO )                                    ( NO )
```

3. The input should be specified as floating-point (F type) numbers and should be presented as a lower-triangle matrix without diagonal.

5.3.3 PROGRAM LIMITS

Maximum number of stimuli = 80

5.3.4 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of HICLUS the options are as follows:

5.3.4.1 PRINT options

Option	Description
HISTORY	A detailed history of the clustering is produced.

5.3.4.2 PLOT and PUNCH options

There are no plotting or secondary output options in HICLUS.

5.4. EXAMPLE

```
  RUN NAME           HICLUS TEST DATA
  N OF POINTS       10
  INPUT FORMAT      (10F4.0)
  PARAMETERS        DATA TYPE(1), METHODS(2)
  READ MATRIX
     <data>
  COMPUTE
  FINISH
```

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APPENDIX : RELATION OF HICLUS TO PROGRAMS NOT IN NewMDSX

For a full range of options regarding hierarchical and other clustering schemes, users are referred to the CLUSTAN package.

6. INDSCAL-S (INDividual Differences SCALing)

6.1. OVERVIEW

Concisely: INDSCAL-S (INDividual Differences SCALing: Symmetric or short version) provides internal analysis of a three-way data matrix consisting of a set of (dis)similarity matrices, by a weighted distance model using a linear transformation of the data.

Following the categorisation developed by Carroll & Arabie (1979)
the program may be described as:

DATA: Three-way, two mode dis/similarities or correlations

TRANSFORMATION: Linear

MODEL Weighted Euclidean Distance or Scalar Products

6.1.1 ORIGIN, VERSIONS AND ACRONYMS

INDSCAL was developed by J.D. Carroll and J.J. Chang of Bell Telephone Laboratories. The original INDSCAL program performed two types of analysis: INDIFF, which is the most commonly used part of the program and often referred to simply as INDSCAL, and CANDECOMP. It is this former analysis (the INDIFF option) which comprises the present program (INDSCAL-

S). The CANDECOMP option appears as a separate program within NewMDSX. The present program is specially adapted from the 1972 version of INDSCAL.

A quasi non-metric INDSCAL known as N-INDSCAL exists but is known to be unstable.

In what follows we shall follow the convention of referring to the model as INDSCAL and this program as INDSCAL-S.

6.1.2 INDSCAL IN BRIEF

INDSCAL was originally developed to explain the relationship between subjects' differential cognition of a set of stimuli. Suppose that there are N subjects and p stimuli. The program takes as input a set of N matrices each of which is a square symmetric matrix (of order p) of (dis)similarity judgments/measures between the p stimuli.

The model explains differences between subjects' cognitions by a variant of the distance model. The stimuli are thought of as points positioned in a 'group' or 'master' space. This space is perceived differentially by the subjects in that each of them affords a different salience or weight to each of the dimensions of the space. In the graphic displays of these results, note that an additional menu item **Vectors** enables you optionally to plot the subjects as vectors, if preferred. The trans-formation which is assumed to take the data into the solution is a linear one.

6.1.3 RELATION TO OTHER NewMDSX PROGRAMS

INDSCAL is a special case of CANDECOMP where the second and third 'way' of the data matrix are identical. In the Carroll-Wish terminology INDSCAL is three way, two mode; CANDECOMP three way, three mode (actually N-way, N-mode where $3 \leq N \leq 7$).

INDSCAL can also be thought of as a generalisation (to a third Way) of the metric distance program MRSCAL.

The INDSCAL model is also analogous to P1 (the dimensionally-weighted distance model) of the PINDIS hierarchy of models. However, the input data are quite different, as INDSCAL takes original measures of dis/similarity and PINDIS takes the co-ordinates of a set of previously scaled solutions)

6.2. DESCRIPTION

6.2.1 DATA

Imagine that a group of subjects is asked to assess the dissimilarity between a set of objects. It is inevitable that these judgments will differ. The problem then arises of the relationship between the sets of judgments. The INDSCAL model assumes that subjects can be thought of as systematically distorting a shared space in arriving at their judgments and it seeks to reconstruct both the individual private (distorted) spaces and the aggregate "group" space.

There is no reason why the judgments of (dis)similarity should come from "real" individuals. They may be different occasions, methods, places, groups etc., in which case they are often referred to as 'pseudo-subjects'.

The mode of distortion which the INDSCAL model proposes is this. The basic, shared configuration (known as the Group Space in INDSCAL) has a given number of fixed dimensions. In making their dissimilarity estimates different subjects are thought of as attaching different salience or importance to different dimensions. Thus, for instance, in judging the differences between two houses an architect might primarily distinguish between them in terms of style, whereas a prospective buyer might attach relatively little weight to that aspect but a great deal to the difference in price.

6.2.1.1 Example

Suppose we were interested in how people perceive the distances between 6 different areas of a city, and asked them to give their estimates of the distance between each of the pairs of areas (fifteen in all). These estimates we collect into three lower-triangle matrices as follows:

```
3.6                           Subject 1
6.7  9.2
7.0  3.1  3.1
6.0  4.1  3.0  3.1
4.1  5.0  3.6  6.7  4
5.7                           Subject 2
7.3  9.4
7.1  3.3  4.3
6.0  4.2  4.2  3.3
5.7  6.4  4.6  7.3  4
7.3                           Subject 3
9.0 12.0
9.9  4.3  3.3
8.4  5.7  3.0  4.3
4.2  5.8  4.1  9.0  5.6
```

The fifteen judgments of each subject are collected into the lower triangle of a square symmetric matrix which would be submitted to INDSCAL-S as shown in section 4.4.1

6.2.2 MODEL AND ALGORITHM

The INDSCAL model interprets 'individual differences' in terms of subjects applying individual sets of weights to the dimension of a common 'group' or 'master' space. Hence the main output of an INDSCAL analysis is a 'Group Space' in which the stimuli (in our example, the area locations) are located as points. The configuration of stimuli in this Group Space is in effect a compromise between different individuals' configurations, and it may conceivably describe the configuration of no single individual (i.e. one that weights the dimensions equally).

Complementing the Group Space is a 'Subject Space'. This space has the same dimensions as the Group Space but in it each individual (or data-source)is represented as a vector, whose end-point is located by the set of co-ordinates which are the values of the numerical 'weights' which he assigns to each dimension. These individual weights or saliences are solved for by the program and
are its next most important output.

Thus the subject whose individual cognition corresponds exactly with the "group space configuration" - if that subject exists - would be situated in a two-space on a line at 45 between the axes, whereas someone who paid no attention to one of the axes would be situated at zero on that axis.

Having obtained the 'Group Space' and an individual's set of weights, it is often useful to take the Group Space Configuration of stimuli points and transform it into that individual's 'Private Space'. A Private Space is simply the Group Space with its dimensions stretched or contracted by the square-root of the weights which that subject has assigned to them.

6.2.2.1.1 Some properties of the INDSCAL model

It should be noted that INDSCAL produces a unique orientation of the axes of the Group Space, in the sense that any rotation will destroy the optimality of the solution and will change the values of the subject weights. Moreover, the distances in the Group Space are weighted Euclidean, whereas those in the private spaces are simple Euclidean. Because of this, it is not legitimate to rotate the axes of a Group Space to a more 'meaningful' orientation, as is commonly done both in factor analysis and in the basic multidimensional scaling model. It has generally been found that the recovered dimensions yield readily to interpretation.

Secondly, each point in the Subject Space should be interpreted as a vector drawn from the origin. The length of this vector is roughly interpretable as the proportion of the variance in that subject's data accounted for by the INDSCAL solution. All subjects whose weights are in the same ratio will have vectors oriented in the same direction. Consequently, the appropriate measure for comparing subjects' weights is the angle of separation between their vectors and not the simple distance between them. For this reason, clustering procedures which depend on distance should not be used to analyse the Subject Space.

6.2.2.2 The Algorithm

1. The program begins by converting each subject's dissimilarities into estimates of Euclidean distances by estimating the additive constant (see Torgerson 1958; Kruskal 1972).

2. These distance estimates are then double-centred to form a scalar-product matrix.

3. These scalar-products may be considered as the product of three numbers. The first of these will come to be considered as the subject weight. The other two give at this stage two distinct estimates of the value of the stimulus co-ordinates.

4. An initial configuration is input by the user or generated by the program (see 6.2.3.3).

5. The scalar-products between the points in this configuration are calculated and serve as an initial estimate of the solution parameters.

6. For each scalar-product at each iteration a pair of these three numbers is held constant in turn and the value of the other is estimated.

7. When maximum conformity to the data is reached by this iterative process, the two estimates of the stimulus coordinates are set equal and one more iteration is performed.

8. The matrices are normalised and output as solution.

6.2.3 FURTHER OPTIONS

6.2.3.1 Data

Consider again the example given above (section 6.2.1.1). In it we had three subjects judging six stimuli. Thus each subject generates a lower triangle matrix of five rows if the diagonals are omitted. These are input to the program after the READ MATRIX command sequentially, i.e. the matrix of subject I is followed by that of subject II which is followed by that of subject III, without break, fifteen lines in all.

The program will also analyse other types of data including correlation or covariance matrices. In this case the 'stimuli' will be the variables which are correlated and the 'subjects' perhaps replicative studies.

At the beginning of an INDSCAL analysis each input matrix of similarities, dissimilarities, or distances is converted into a matrix of scalar products. To equalize each subject's influence on the analysis these data are normalized by scaling each scalar products matrix so that its sum of squares equals one. Data input as covariances or correlations are not converted to scalar products and are not normalized in this way, thus it is essential to signal this type of input by means of the DATA TYPE parameter (see Section 6.3).

6.2.3.2 Number of dimensions

Some experimentation is generally needed to determine how many dimensions are appropriate for a given set of data. This involves analysing the data in spaces of different dimensionality. For each space of r dimensions the program uses as a starting configuration the solution in (r + 1) dimensions less the dimension accounting for the least variance. Usually between two and four dimensional solutions will be adequate for any reasonable data set.

6.2.3.3 Starting configuration

The analysis begins with an initial configuration of stimulus points. This may be supplied by the user and read under a READ CONFIG command. This configuration should contain stimuli coordinates in the maximum dimensionality required.

Alternatively the program can generate a configuration either by a method similar to that used in IDIOSCAL or by picking pseudo-random numbers from a rectangular distribution. If the value of the parameter RANDOM is 0 then the IDIOSCAL procedure is used otherwise the value is used as a seed to generate the random numbers. Since sub-optimal solutions are not uncommon with this method users are strongly recommended to make several runs with different starting configurations. A series of similar (or identical) solutions may be taken to indicate that a true 'global' solution has been found.

Alternatively, the user may wish to overcome this particular difficulty by submitting, as an initial configuration one obtained from, say, a MINISSA run in which the averaged judgements have been analysed. This method will also reduce the amount of machine time taken to reach a solution.

6.2.3.4 External analysis

On occasion a user may wish to determine only subject weights for some previously determined stimulus configuration, such as a previous INDSCAL solution, or, some known configuration (as in our notional example the actual geographical location of the city areas). This option requires that an input configuration be supplied under the READ CONFIG command. The full set of data should be read in under the READ MATRIX command but FIX POINTS should be set to 1 in the PARAMETERS command and the program will then solve only for the subject weights.

6.2.3.4.1 Large data sets

The FIX POINTS option is particularly useful when the user has more data than the program is capable of handling (see 3.2). The user can use the configuration obtained either from a MINISSA analysis of averaged judgments or from an INDSCAL analysis of some random or judiciously selected subset of subjects and fit to it any number of subjects' weights.

6.2.3.5 The SOLUTIONS parameters

The axes of the solution correspond to the major direction of variation in the subjects' data. They will not usually correspond to the principal axes of the configuration, in which, the coordinates on the axes are uncorrelated. In the INDSCAL solutions, by contrast, the coordinates will usually be correlated and these correlations are output as the scalar-products matrix for the stimulus configuration. A similar scalar-products matrix is output for the subject space. In this however, it is a dispersion matrix whose diagonal entries are variances, representing the degree to which subject variation is concentrated in that dimension, and whose off-diagonal entries represent the co-variation between dimensions in the subject weights.

If the user wishes to constrain the solution as closely as possible to orthogonality (i.e. in the sense that the correlation between the coordinates is zero) then the parameter SOLUTIONS should be set to 1 in the PARAMETERS command. Users are warned that this will necessarily produce a suboptimal solution.

6.2.3.6 Negative weights in INDSCAL solutions

There is no interpretation of a negative subject weight in an INDSCAL solution. Nevertheless, from time to time negative values do occur in the subject matrix. If these are close to zero, then the occurrence is likely to be due to rounding error and should be regarded as zero in interpreting the solutions. Large negative values on the other hand suggest a more substantial error or that the model is not appropriate to the data.

6.2.3.7 Individual correlations as a measure of goodness-of-fit

Being a 'metric' procedure the index of goodness-of-fit of model to data is the correlation between the scalar products formed from the subject's data and those implied by the model. The program outputs a correlation coefficient for each subject and also the average correlation for all subjects and a root-mean-square coefficient which indicates the proportion of variance explained.

6.2.3.8 The stopping criterion

At step 7 of the algorithm the improvement in correlation is computed. If this is less than the value specified on the CRITERION parameter in the PARAMETERS command, then the iterations are ended. Users should make this value larger if they wish to essay a number of exploratory analyses or to test a number of starting configurations.

6.3. INPUT COMMANDS

Keyword		Function
N OF STIMULI	n	Number of stimuli for analysis
N OF SUBJECTS	m	Number of subjects for which data are to be input
DIMENSIONS	[number]	

	[number list] [number] TO [number]	Dimensions for analysis
LABELS	followed by a series of labels (<= 65 characters), each on a separate line	Optionally identify the stimuli in the output
READ CONFIG	n x max.dimensions Matrix	Read optional initial configuration
READ MATRIX	m x n matrix	Read the data according to the DATA TYPE
COMPUTE		Start computation
FINISH		Last statement in run

6.3.1 LIST OF PARAMETERS

The following values may be specified following the keyword PARAMETERS

Keyword	Default Value	Function
SOLUTIONS	0	0: Compute all dimensions simultaneously 1: Compute separate one dimensional solutions.
FIX POINTS	0	0: Iterate and solve for all matrices. 1: Solve for subject weights only
RANDOM	0	Random number seed for generating the initial configuration. (Used when the user does not provide the initial configuration by use of READ CONFIG) 0: IDIOSCAL starting configuration
DATA TYPE	1	1: Lower half similarity matrix (without diagonals) 2: Lower half dissimilarity matrix (without diagonals) 3: Lower half Euclidean distances (without diagonals) 4: Lower half correlation (without diagonals). 5: Lower half covariance matrix (without diagonals). 6: Full symmetric similarity matrix (diagonals ignored). 7: Full symmetric dissimilarity matrix (diagonals ignored).
CRITERION	0.005	Sets criterion value for termination of iterations.
MATFORM	0	0: Input configuration saved Stimuli(rows) by dimensions (columns). 1: Input configuration saved dimensions (rows) by stimuli (columns). Only valid with READ CONFIG.

6.3.2 NOTES

1. Program limits

Maximum number of dimensions	=	5
Maximum number of stimuli	=	30
Maximum number of subjects	=	60
N OF SUBJECTS x (N OF STIMULI)	=	18000
max (N OF SUBJECTS, N OF STIMULI) x maximum no. of dimensions x 3	=	2500

2. Labels should contain text characters only, without punctuation.
3. The program expects input in the form of real (F-type numbers), and an INPUT FORMAT, if it is necessary to use one should allow for this. The INPUT FORMAT specification, if used, should read the longest line of the input matrices.

6.3.3 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of INDSCAL, the available options are as follows:

6.3.3.1. PRINT options (to main output file)

Option	Form	Description
INITIAL	N x r p x r p x r	Three matrices are listed: 1. the initial estimates of the subject weights 2. & 3. separate estimates of the stimulus configuration.
FINAL	N x r p x r N r x r	Two matrices are listed being the matrix of subject weights and the coordinates of the group space. These are followed by the correlation between each subject's data and solution and the matrix of cross-products between the dimensions.
HISTORY		An iteration by iteration history of the overall correlation. (The final (3) matrices at convergence are also listed)
SUMMARY		Summary of results produced at end of each analysis.

By default only the solution matrices and the final overall correlation are listed.

6.3.3.2 PLOT options (to main output file)

Option	Description
INITIAL	The initial configuration may be plotted only if one is input by the user.
CORRELATIONS	The correlations at each iteration are plotted.
GROUP	Up to r(r-1)/2 plots of the p stimulus points.
SUBJECTS	Up to r(r-1)/2 plots of the Subject Space

By default the Subject and Group Spaces will be plotted.

6.3.3.3 PUNCH options (to secondary output file)

Option	Description
FINAL	Outputs the final configuration and the subject correlations in the following order: - each subject is followed by the coordinates of its weight on each dimension; - each stimulus point is followed by its coordinates on each dimension.
CORRELATIONS	The overall correlation at each iteration is output in a fixed format.
SCALAR PRODUCTS	the scalar product matrix is output.

By default, no secondary output is produced.

6.4. EXAMPLE

```
   RUN NAME                    INDSCAL TEST DATA
   TASK NAME                   ...FROM EXAMPLE IN 2.1.1
   N OF SUBJECTS               3
   N OF STIMULI                6
   DIMENSIONS                  2
   PARAMETERS                  CORRELATIONS(1),RANDOM(34551)
   COMMENT                     THIS IS THE SET-UP FOR THE EXAMPLE
                               GIVEN.
                               NOTICE THE USE OF THE SHORTENED
                               PARAMETER
                               DESIGNATION AS IN 'DATA(2)'
   INPUT FORMAT                (5F3.0)
   READ MATRIX
    36
    23 92
    70 31 31
    60 41 30 31
    41 50 36 67 40
    57
    73 94
    71 33 43
    60 42 42 33
    57 64 46 73 40
    73
    90120
    99 43 33
    84 57 30 43
    42 58 41 90 56
   PRINT                       FINAL, HISTORY
   PLOT                        ALL
   COMPUTE
   FINISH
```

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7. MDPREF (MultiDimensional PREFerence Scaling)

7.1. OVERVIEW

Concisely: MDPREF (MultiDimensional PREFerence Scaling) provides internal analysis of two-way data of either a set of paired comparisons matrices or a rectangular, row-conditional matrix by means of a vector model, using a linear transformation of the data.

DATA: 2-way 2-mode dis/similarity or preference data (alternatively, a set of (0,1) dominance matrices of [pairwise preference)
TRANSFORMATION: Linear
MODEL: Scalar Products or Vector

In the terminology developed by Carroll and Arabie (1979) MDPREF may be described as:

Data:	Two mode	Model:	Scalar-product
	Two- or three-way		Two sets of "points"
	Interval level		One space
	Row-conditional		Internal
	Complete or incomplete		

7.1.1 ORIGINS, VERSIONS AND ACRONYMS

MDPREF is based on a model developed at Bell Laboratories by J.D. Carroll and J.J. Chang (see Carroll , 1973). In this paper they develop two types of solution, one iterative and the other analytical, making use of the Eckart-Young decomposition theorem (1936). The MDPREF program implements this latter type, since the solutions obtained were virtually identical. A quasi-non-metric version (N-MDPREF) has been developed, but is not currently available. The NewMDSX version of MDPREF additionally includes the option for the User to divide the subjects into groups,and perform an analysis of variance of the subject vectors (as directional statistics). This was programmed by Charles Jones.

7.1.2 FURTHER SPECIFICATION

The MDPREF program provides internal analysis of preference data. This involves a set of subjects making preference or any similar sort of judgment about a set of stimuli (objects). From the data the program positions the stimuli as points in a Euclidean space, and represents each subject by a vector or line directed towards the region where that subject's highest preference lies. In the case of perfect fit, the projections of the stimuli on this line correlate perfectly with the subject's preference scores.

7.1.3 RELATION OF MDPREF TO OTHER PROCEDURES IN NewMDSX

MDPREF analyses 'preference' data by means of a point vector or "ideal vector" model. Each subject or judge is represented in the space as a vector directed (which indicates the direction of increasing preference. The stimuli are represented as points in the same space, so that the projections of the stimuli onto a given subject's vector maximally reproduce his(her) preferences.

The same point vector model is implemented both in phase IV of PREFMAP and in PROFIT, although in these cases the scaling is 'external' in the sense that the configuration of stimulus points is known beforehand and the subjects are fitted into this space as vectors. In MDPREF by contrast both subject vectors and stimulus points are positioned simultaneously from the information in the data, a so-called 'internal' analysis. (Note however that PREFMAP phase IV does allow a quasi internal analysis q.v.)

CORRESP also uses a direct singular value decomposition of pre-transformed data to produce canonical scores for rows and columns which can be plotted as points in the same space. CORRESP examines only interactive factors by explicitly removing the magnitude effect prior to decomposition, but so can MDPREF when treating data as row-conditional. The difference between the two lies in the transformations applied to the data before processing, so that the results, while similar in appearance, are not the same.

The same data as used in MDPREF may also be internally scaled by the non-metric distance model ('unfolding analysis') implemented in NewMDSX as MINIRSA. In this case, both subjects and stimuli are represented as points in the same space.

7.2. DESCRIPTION

7.2.1 INPUT DATA

MDPREF accepts input data in either of two main forms: as a set of pair-comparisons matrices (see David (1963), Ross (1934)) or as a set of rankings or ratings forming a rectangular, so-called "first-score" matrix. Options within the program differ with different data input and the type of input is chosen by the DATA TYPE parameter in the PARAMETERS command. In the following the "first-score" input is dealt with in sections 7.2.1.1 and 7.2.1.1.1 and the method of pair-comparisons and its associated options in sections 7.2.1.2 to 7.2.1.2.1.1. Further options are discussed in section 7.2.3.

7.2.1.1 The first-score matrix (DATA TYPE 1-4)

Suppose a set of N subjects is asked to rank in order of, say, preference, or give a rating to the set of p stimuli. The resultant data forms a rectangular 'row-conditional' matrix with N rows (subjects) and p columns (stimuli), called the "first score matrix" in the program. Each row of the matrix represents the preference rank or score assigned by that subject to the stimuli.

Such a matrix can also be obtained by taking the pair comparison matrix for a given subject and summing each row. The resultant column of scores gives that subject's rank order of preference for the stimuli and these may be collected to form the "first-score matrix".

7.2.1.1.1 Ranks or Scores ?

Preference judgments may be represented for MDPREF (as in MINIRSA and other procedures) in four distinct ways. The major distinction is that between a rank and a score. If a subject is asked to write down in his order of preference for five stimuli, he might respond with:

ACDEB

*The program in fact converts pair-comparison input into "first-score" form in this way before proceeding with the analysis.

If these letters (or stimulus names) are given numeric values this becomes:

13452

This is the rank-ordering method (analogous to Coombs's I-scales) and means that stimulus 1 is preferred to 3 which is preferred to 4 etc.

Data may be input to MDPREF in this form by specifying DATA TYPE(1). In various data-collection techniques it may be that the ordering obtained begins with the least-preferred stimulus so that the previous example would in this case be written as: BEDCA, signifying that B is least preferred, followed by E, and so forth. If this is the case then the data should be specified as: DATA TYPE(2).

A different way of representing such data is by the 'score' method. In this method each column represents a particular stimulus and the entry in that column gives the score or rating of that stimulus (for that subject) in his 'scale of preference'. Thus, in our original example the I-scale ACDEB (where A is preferred to C, which is preferred to D etc.) would in this method be represented as follows:

	A	B	C	D	E
subject i	1	5	2	3	4

In this instance, the lowest number ('1') is used to denote the most preferred stimulus and the highest ('5') to represent the least preferred. This option is chosen by: DATA TYPE(3). Alternatively, the highest number might have been used to represent the most preferred stimulus and if this is so, DATA TYPE(4) should be specified.

(Although in illustrating the score method we have used the number 1 to 5, the data might equally well have been numerical ratings).

For an example see 5.2.1.2.1.1

Figure 1 provides a simple means of identifying the appropriate DATA TYPE value.

Figure 1.

```
                            Are the data      ----- Yes -----  DATA TYPE(O)
                           pair comparisons ?
                                 |
                                 No
                                 |
                            Are the data
                           ranks or scores?
                          /                \
                     ranks                  scores
                    /                              \
    Is the first                                      Does the highest
    stimulus the                                      value mean most
    most preferred?                                   preferred?
    /              \                                /            \
 yes                no                           yes             no
DATA TYPE (1)    DATA TYPE(2)                 DATA TYPE(3)   DATA TYPE(4)
```

7.2.1.2 The pair-comparisons matrices (DATA TYPE(0))

Suppose a subject is asked to consider all possible pairs of p stimuli and for each pair to indicate which stimulus (s)he prefers (or which stimulus possesses more of a given attribute). (S)he is asked to make p (p-1)/2 judgments of preference. (Since this increases approximately as p-squared, with a large number of stimuli this number of pairs becomes prohibitively large. Consequently, strategies exist to reduce the number of judgments (see 5.2.3.1)). The data thus obtained may be collected into a square, asymmetric matrix whose rows and columns each represent the p stimulus points, whose entries a_{ij} take the value 1 if the subject prefers stimulus i to stimulus j, and a_{ji} will normally be 0, meaning that the subject does not prefer stimulus j to stimulus i (but see 5.2.3.1). The subject may be allowed to express indifference between the stimuli, or leave blank a particular pair comparison. Allowance is made for these options in the program, and the relevant coding conventions are described in section 5.2.3.

If there are N subjects performing this test of preference, then there will be N such matrices. These are input to MDPREF by specifying in the PARAMETERS command the value DATA TYPE(0), which is the default value.

7.2.1.2.1 Coding of paired comparisons matrices

In the example above the entry '1' was taken to stand for preference by the particular subject for the row-stimulus over the column stimulus, and the value ' ' for its converse. Further values are required to represent indifference between stimuli and missing data. Since coding conventions vary, the program allows the users to specify their own. This is done by means of the command READ CODES (which has no operand field and if required may have associated with it its own INPUT FORMAT specification). READ CODES instructs the program to read in four values for the codes, the first of which will represent preference, the second its opposite ("anti-preference"), the third indifference and the fourth a missing data value.

7.2.1.2.1 Example

```
.
INPUT FORMAT        (4I2)
READ CODES
1 0 8 9
.
.
```

It will be noted that the codes must be specified as integer (I-type) variables. Thus our example has the program read

1 as the code for preference
0 as the code for "anti-preference"
8 as the code for indifference
9 as the code for a missing datum

Note also that even if, in a particular analysis, fewer than four codes are used, four values should nevertheless be specified and read under READ CODES.

The N paired-comparisons matrices are read by the READ MATRIX command, according to an optional INPUT FORMAT, if the data are not in free format. If used, this should specify the format of one row of the input matrices, and the individual matrices should follow each other without separation. (For example, see 5.5.1). Also note that if there are missing data then MISSING(1) should be specified in the PARAMETERS command.

7.2.1.3 Example of data types

When eliciting judgments by means of pair comparisons we need three things: (i) a set of subjects who will evaluate (ii) a set of stimuli (iii) on a given criterion.

Each subject vector will then represent the direction in which that subject sees the criterion increasing over the configuration of stimulus points. Suppose we were interested in the 'user-friendliness' of the accompanying documentation of various computer packages. We might ask Computing Centre advisers to fill in the following:

> ... Taking each pair in turn please indicate by ticking in the box provided, which of each pair of packages is more "user friendly" ...

SPSS	[ ]3	GENSTAT	[ ]1
GENSTAT	[ ]1	CLUSTAN	[ ]4
NewMDS(X)	[ ]2	SPSS	[ ]3
SAS	[ ]5	NewMDS(X)	[ ]5
....		....	

And we would go on to list (probably in random order) all twenty pairs of these five programs. For each adviser we would then construct a matrix similar to this:

Subject 32

	GENSTAT	NewMDSX	SPSS	CLUSTAN	GLIM
GENSTAT		1	1	1	1
NewMDSX	0		9	1	1
SPSS	0	9		1	8
CLUSTAN	0	0	0		1
GLIM	0	0	8	0	

This subject believes that GENSTAT is more 'user-friendly' than all the other packages, NewMDSX than CLUSTAN and GLIM, and CLUSTAN than GLIM. Furthermore,(s)he left the pair SPSS/NewMDSX blank (hence code 9) and decided that there was No difference between BMDP and CLUSTAN (code 8).

7.2.1.3.1 Data for 'First-score'

In the example above, five stimuli were presented in pairs, twenty in all. If we were concerned with more than that number of stimuli we might feel that the number of pairs was too large for the subject to manage without boredom, error or bloody mindedness taking its toll. We might then decide to abandon the pair comparison method (which is, of course, sensitive to intransitivities in a subject's data) and use instead a method of ranking or rating. For instance, we might ask:

> Please place the letters corresponding to the packages listed in the box provided so that the first letter represents the program which you feel to be most 'user-friendly' and the last the one you feel to be least 'user-friendly'.

A: GENSTAT
B: NewMDSX (Most) User-friendly (Least)
C: SPSS [ ][ ][ ][ ][ ][ ][ ]
D: CLUSTAN
E: GLIM
F:
G:

This method is obviously less time-consuming but less sensitive than the method of pair comparison. In this case we simply take each subject's list of letters (I-Scale) and collect them into instruction lines with the subject numbers:

```
 .
 .
S023    ABCDEFG
S024    GFEDCBA
S025    ACEGBDF
 .
 .
```

Here we would specify DATA TYPE(1) to MDPREF to denote the fact that our data are ranked (I-Scales) with the highest 'preference' first.

7.2.2 THE MODEL

The MDPREF model represents the preferences of a subject for a group of stimuli as a vector through the configuration of stimulus points. This vector indicates the direction in which his (her) preference increases over the space. Substantively this makes strong assumption about the nature of preference, in that the model implies an "ideal" point - i.e. a point of maximum preference - at infinity (which is similar to the classic econometric assumption of insatiability. In MDPREF, where the point of maximum preference is at infinity, the contours are perpendicular to the vector). There is no reason to cavil, for instance at the idea of seriousness (Coxon 1980) or, as in our earlier example, "user friendliness" increasing uniformly over the space.

MDPREF is a linear (or metric) procedure and the measure of goodness-of-fit of the model to the data is a product-moment correlation. Consider one subject vector passing through a configuration of stimulus points with the projections (perpendicular lines drawn from the points onto the vector). It is the values given to the points at which these perpendicular lines meet the vector which are maximally correlated with that subject's data. (This is guaranteed by the Eckart-Young decomposition).

The subject vectors are normalised (for convenience only) to the same length, i.e. so that their ends lie at a common distance from the origin of the space, forming a circle, sphere or hypersphere depending on the dimensionality chosen for analysis. Thus when a solution of more than 3 dimensions is represented as a set of 2-dimensional plots, some of the vectors will not, in fact, lie on the boundary circle since they will have been projected down from the higher dimensions. The length of the vector in the sub-space is related to the amount of variation in that subject's data explained by those two dimensions of the solution space. In the graphic displays of these results, an additional menu item **Vectors** enables you to plot or suppress the subject vectors if these are becoming too cluttered.

7.2.2.1 Description of the Algorithm

1. If the input is in the form of pair comparisons matrices, these are converted into a "first-score" matrix. Optionally, these may be centred and/or normalised.

2. The major and minor product-moment matrices are formed.

3. The inter-subject and inter-stimuli correlations are calculated.

4. The p-m matrices are factored by the Eckart-Young procedure to provide coordinates of the stimulus space and of the subject vector ends.

5. The first r columns of the relevant factor matrices are taken. These form the two configurations output as solution.

7.2.3 FURTHER OPTI0NS

7.2.3.1 Dimensionality

The program lists the latent roots of the matrices. The number of positive roots will be not greater than the number of stimuli or the number of subjects, whichever is the smaller. The magnitude of the roots gives an indication of the amount of variation in the data accounted for by that dimension. The largest root will always be first and the others will follow in decreasing order. Some may be zero. An appropriate dimensionality may be chosen by means of the familiar scree-test.

7.2.3.2. Normalising and Centring

With the data in the form of a first score matrix the user may choose how the matrix is to be centred and normalised using the parameters CENTRE and NORMALISE. The default for these parameters is 0 and means no action.

Other options allow various courses. CENT(1) instructs the program simply to subtract the row means. This will, in a rating exercise, remove any effect due to differences in the actual values used by particular subjects. NORM(1) allows the program not only to subtract the row means but also to take out any effect due to differences in the range or spread of scores involved by normalising each row by dividing it by its standard deviation.

CENT(2) and NORM(2) perform the same operation on the column elements, i.e. subtracting column means and column normalising respectively. This latter option has the effect of taking out the unanimity effect in subjects judgements and leaving only the significant differences in judgements (see Forgas (1979)). CENT(3) instructs the program to double centre the matrix by subtracting both row and column means. NORM(3) does this, and normalises the entire matrix.

7.2.3.3 Weighting of pair comparison matrices

Since pair-wise judgements are often difficult to make, the user may sometimes wish to accord to each judgement a 'weight'. This might represent the degree of confidence which the subject attaches to his judgement, or perhaps the reliability which the researcher ascribes to each judgement.

If weights are input then there must be one weights matrix per subject. The weights matrix immediately follows its associated pair comparisons matrix. This may optionally be read according to a WEIGHTS FORMAT statement, which should be suitable for real (F-type) numbers.(For an example see Section 4.2.) If there is no WEIGHTS FORMAT provided, free format input is assumed.

7.2.3.3.1 The SAME PATTERN parameter

If, as often happens, there is more than one identical weights matrix, then the number of such matrices should be specified as the SAME PATTERN parameter. In this case, the weights matrix follows the first pair comparisons matrix and is read according to an optional WEIGHTS FORMAT statement, if it is not in free format. Those pair comparisons matrices having the same pattern of weights then follow each other without separation.

7.2.3.4 Blocking of pair-comparisons data

If the number of pair-comparisons judgements has been thought too great then the researcher may resort to the use of incomplete data, i.e. certain element-pairs may not be presented to the subjects (see Burton & Nerlove, 1971). The resulting data-matrix will have 'blocks' missing. If one of these strategies is used and the data are arranged in blocks then BLOCK(1) must be specified in the PARAMETERS command so that allowance can be made in the calculation of row- and column-sums.

7.2.3.5 Interpretation of the solution

The MDPREF program positions the N subject vectors and the p stimulus points in a space of user-specified dimensionality. Interpretation of the stimulus configuration should proceed as for any MDS configuration, although it should be borne in mind that since this is an interval scaling model, the stimulus points have been positioned to secure maximum agreement with the subject's vectors. Consequently, interpretation of the position of stimulus points should be made with regard to the principal direction(s) and spread of the subject vector ends.

The identification of 'outliers' amongst the subjects by visual inspection is straightforward.

7.2.3.5.1 ANOVA of Subject Vectors.

Often the subjects belong to a range of groups, and the User is interested in whether they differ from each other in terms of their subject vectors. If this is so, the user mustprovide a group-number identification AFTER the last value in each subject’s line. (These numbers need to be sequential and start with 1) and signify this by the presence of GROUPS(m) in the Parameter list (where m is the number of groups). Certain one-, two- and multi-sample tests for mean direction are available and give directional analogues to the analysis of variance. Appendix 2 gives a brief summary of statistics available in MDPREF and fuller description may be found in Pearson and Hartley (1972) and Mardia (1972). (See also Stephens (1962; 1969)).

7.3. INPUT PARAMETERS

MDPREF allows data to be input in two forms:

1. A "first-score" matrix in which case an N x p matrix is input.

2. A set of pair comparisons matrices in which case there will be N matrices, each p x p.

Options available with each type of option differ. The type of input is chosen by the parameter:

DATA TYPE	Default	0: Data are in a pair-comparisons matrix. 1: Data are ranks (I-scales) of column indices in decreasing order of preference. 2: As 1 but in increasing order of preference. 3: Data are scores in order of column indices - high score means low preference. 4: As 3 but high scores mean high preference.

7.3.1 OPTIONS WITH THE FIRST SCORE MATRIX

Keyword Default Function

MATFORM	0	0: The matrix is saved subjects (rows) by stimuli (columns). 1: The matrix is saved stimuli (rows) by subjects (columns).
GROUPS	0	The number of groups present in an analysis of variance should be specified (See Appendix 2).
CENTRE	0	0: The data are not centred. 1: Row-means only are subtracted. 2: Column means only are subtracted. 3: Matrix is double centred.
NORMALISE	0	0: Matrix is not normalised. 1: Rows are centred and normalised. 2: Columns are centred and normalised. 3: Both rows and columns are centred and normalised.

7.3.2 OPTIONS WITH PAIRED COMPARISONS MATRICES

Keyword	Default	Function
SAME PATTERN	0	Sets the number of subjects whose pattern of missing data or weights matrices are the same.
WEIGHTS	0	0: No weights are input 1: Weights are input
BLOCK	0	0: The data are not arranged in blocks 1: The non-empty cells are arranged in blocks or are to be treated as such. (NOTE: Weights cannot be used with this option).
MISSING	0	0: There are no missing data 1: There are missing data in the matrix.

7.3.3 NOTES

1. READ CONFIG is not valid with MDPREF.

2. Note that even if only two or three codes are used in the paired comparisons matrices, the READ CODES command must specify four codes, which must be in the order specified.

7.3.4 PROGRAM LIMITS

Maximum number of stimuli	60
Maximum number of subjects	100
Maximum number of dimensions	8
Maximum number of groups	15

7.3.5 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of MDPREF, the options are as follows.

7.5.1 PRINT options

Option	Form	Description
FINAL	p x r N x r	The stimulus matrix followed by the subject matrix.
FIRST	N x p	The first-score matrix. (This is the input matrix after being modified i.e. centred/normalised). Means & standard deviations of subjects are listed.

CROSS-PRODUCTS		Four matrices are listed:
	N x N	1. the cross-product matrix (subjects)
	p x p	2. " " " " (stimuli)
	N x N	3. the correlation(PPM) matrix(subjects)
	p x p	4. " " " (stimuli)
SECOND	N x p	The second-score matrix.
ROOTS		The latent roots.
RESIDUALS	N x p	The first-score matrix less the second-score.
CORRELATIONS	N	The correlation for each subject Between the data and the stimulus projections is listed.

The default option allows for only the final configuration to be listed.

7.5.2 PLOT options

Option	Description
SUBJECTS	The n(n-1)/2 plots of the subject vectors in chosen dimensionalities.
STIMULI	The n(n-1)/2 plots of the stimulus points in the chosen dimensionalities.
JOINT	Both of the above.
SHEPARD	In this case simply the first-score plotted against the second-score.
ROOTS	A scree diagram.
RESIDUALS	Histogram of residual values
GROUPS	A plot showing the average vector of the groups (if chosen).

The default options allow for the first two dimensions of the joint space in each dimensionality only to be plotted.

7.3.5.3 PUNCH options

Option	Description
SUBJECT SPACE	The final configuration of subjects is saved.
STIMULUS SPACE	The final configuration of stimuli is saved.

By default, no secondary output is produced.

7.4. EXAMPLES

7.4.1 EXAMPLE OF A SIMPLE RUN

```
RUN NAME           TEST RUN OF MDPREF
TASK NAME          FIRST SCORE OPTION
N OF SUBJECTS      20
N OF STIMULI       16
DIMENSIONS         2,3
PARAMETERS         DATA TYPE(1), NORMALIZE(1)
COMMENT            *****
                   THE PARAMETERS STATEMENT SPECIFIES FIRST SCORE
                   MATRIX AS INPUT. THIS MATRIX IS TO BE
                   NORMALISED BY ROW
                   *****
READ MATRIX
   <the 20x16 first score matrix follows here in free format>
PRINT             CROSS-PRODUCTS(2), SECOND(2,3)
COMPUTE
```

```
  TASK NAME         PAIRED COMPARISONS OPTION
  N OF SUBJECTS     20
  N OF STIMULI      10
  DIMENSIONS        2
  READ CODES
  1 0 8 9
  COMMENT
                     ... WHEREAS THIS ONE REFERS TO THE INPUT MATRICES
                     NO PARAMETERS STATEMENT IS INSERTED AS
                     ALL DEFAULT OPTIONS ARE ASSUMED
  PLOT               SHEPARD, RESIDUALS
  READ MATRIX
     <20 square matrices, each of order 10 follow here>
  COMPUTE
  FINISH
```

7.4.2 EXAMPLE OF A RUN WITH WEIGHTS ADDED

```
  RUN NAME             MORE MDPREF TEST DATA
  TASK NAME            ... THIS TIME WITH WEIGHTS
  N OF SUBJECTS        10
  N OF STIMULI         5
  DIMENSIONS           2,3
  PARAMETERS           WEIGHTS (1)
  COMMENT              default DATA TYPE(0)

  READ CODES
  1 0 8 9
  WEIGHTS FORMAT       (5F2.0)
  COMMENT              *****
                       WE NOW INPUT FOR EACH OF THE 10
                       SUBJECTS A P-C MATRIX AND A WEIGHTS
                       MATRIX WITHOUT SEPARATION. NOTE THE
                       USE OF AN OPTIONAL WEIGHTS FORMAT.IN
                       THIS CASE IT COULD EQUALLY WELL HAVE
                       BEEN OMITTED.
                       *****
  READ MATRIX
  9 1 1 1 1
  0 9 1 1 1
  0 0 9 1 1            PAIRED COMPARISONS
  0 0 0 9 1
  0 0 0 0 9
   0 2 1 9 4
   3 0 3 6 2
   8 5 0 3 1              WEIGHTS
   4 8 2 0 9
   3 4 5 8 0
    <here, without break, follow 9 other such pairs of matrices>
  PLOT                 SHEPARD  (2)
  COMPUTE
  FINISH
```

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APPENDIX 1 : THE RELATION OF MDPREF TO PROGRAMS NOT IN NewMDSX

MDPREF is analogous to the INGRID program widely used in the analysis of repertory grids (Slater, 1960). The use of various MDS(X) programs in this type of analysis is described in detail by Tagg (1980); see also Forgas (1979). A similar model is used by Tucker; see Tucker (1955; 1960). A MDPREF-like model is not included in either ALSCAL or the G-L series but an approximation is implemented by the Takane-Young-de Leeuw program PRINCIPALS (see Takane et al, 1975).

APPENDIX 2: STATISTICS FOR DIRECTIONAL DATA

A2.1 Definitions

We shall be concerned with differences and similarities between subjects' preferences, i.e. between the vectors. A sample of vectors may be thought of as drawn from a population whose overall direction is the polar vector. The average direction for the sample set of vectors is called the modal vector. The vector sum of a set of vectors is a resultant vector and its sum of squares its length (R).

A2.2 Measures of distribution

It is clear that the greater the length of the resultant vector, the more agreement exists in the sample.

The probability density of distribution of vectors around the polar vector is given by kappa, high values of which imply a concentrated symmetrical distribution of vectors around the polar, while a zero value gives a uniform distribution around the circle or sphere.

Kappa may be estimated from sample data by

$$K = N-1 / N-R$$

where N is the total number of vectors (and also, obviously, the sum of the lengths of N unit vectors) and R the length of the resultant. Note, however, that this approximation is only accurate when R/N > 0.7 (i.e. kappa > 3.3).

A2.3 Tests of significance

A directional analogy to one-way analysis of variance is an approximate test for comparison of polar vectors from two or more samples. The parameter 2K(N-R) is distributed approximately as chi-square with 2(N-1) degrees of freedom.

It is possible, arguing from the analogy with analysis of variance, to partition the chi-square for the concentration of vectors from two independent samples about a common estimated mean vector. The overall X<s2>s is the sum of the components from (a) the concentration of vectors in each sample about their mean vectors, and (b) the concentration of the two estimated mean vectors.

An approximation to the F-test compares 'between-group' and 'within group' components. With S samples an F-distribution is approximated by

$$U = \frac{(N-S)\ \left(\sum_i R_i - R\right)}{(S-1)\ \left(N - \sum_i R_i\right)}$$

In the three-dimensional (spherical) case this statistic has (2S-2) and (2N-25) degrees of freedom in the numerator and denominator respectively. In the circular (two-dimensional) case these values are respectively (S-1) and (N-S).

The statistical theory which would allow us to proceed to a two-way analysis of variance has not been developed.

A2.4 Input parameters for statistics

statistics are only available with the 'first-score' option. If the user wishes to use the program to perform the one way analysis (s)he should specify the number of groups on the GROUPS parameter in the PARAMETERS statement. Each row of the matrix (i.e. each subject) should then be assigned to a group. This is done by appending to each row the number of the group to which that subject is assigned. With free-format input, the group number is simply added to the end of the corresponding row of the matrix, separated by a space. The INPUT FORMAT specification, if used, should be amended to read this number as an integer (I-type) value.

8. MDSORT (Multidimensional Scaling for SORTing data)

8.1 OVERVIEW

MDSORT expects as input a matrix consisting of a set of N row vectors, one for each respondent i, arrayed so that each column refers to a given object j and where the entry $f(i,j)$ consists of the category/group number in which the object is located by respondent i. The only restriction is that each stimulus/object must be assigned to one and only one category. The model implemented in MDSORT is designed specifically for the direct analysis of free-sorting data, and was developed to generate a joint representation of objects and subjects' categories, which simultaneously scales and represents the sorting data.
DATA: 2-way 2-mode data matrix of subjects' stimulus allocation to own category („pile-sort")
TRANSFORMATION: Linear
MODEL: Scalar Product

8.2 DESCRIPTION

See Coxon (1999) for a full description of the Sorting method and its applications.The basic operation of sorting consists of subjects allocating a set of objects into categories of their own choosing. The researcher usually defines a common set of "objects" (stimuli, statements, names, artefacts, pictures) and then asks typically asks each of the n subjects to sort the p objects into a subject-chosen number (c) of groups/categories. The mathematical representation of the sorting is:

the partition of a set of p elements into a number (c) of *cells.*

The most important characteristic of a partition is that the categories of a subject's sorting must be mutually exclusive and exhaustive, i.e. each object must be sorted into one, and only one, category. This allows an object to be put into a category by itself, but it explicitly disallows overlapping categories. Sorting data are therefore, at least initially, at the nominal level of measurement.

Takane's (1980) model takes the data as a matrix **F** consisting of a set of N row vectors, one for each respondent i, arrayed so that each column refers to a given object/stimulus j, and the entry $f(i,j)$ consists of the category/group number in which the object is located by subject i. The categories are in a sequential (but arbitrary) numbering, and respondents may employ differing numbers of categories in sorting the set of stimuli.

That is:

$$\mathbf{F} = [f_{ij}], \qquad (i = 1,...,N; \;\; j = 1,...,p)$$

where the value of cell f_{ij} is the category number, say k, in which object j occurs in i's sorting.

The **F** data matrix is then expanded into a set of individual matrices $\mathbf{G_k}$ each of which is of size p rows and q categories, where q may differ from subject to subject in free-sorting :

$$\mathbf{G_k} = [\; g_{jq}^{\;k} \;] \qquad (i = 1,...,N; \; j = 1,...,p; \; q = \#ci \;)$$

Where

g_{jq}^{k} = 1, 0: 1 if object *j* occurs in subject *i*'s *q*th category;
0 otherwise.

Takane (1980) proceeds directly to a joint scaling by decomposing the data matrix. The major feature of the model is that a decomposition is sought which simultaneously seeks to locate both the object point locations and the category centroids for each subject - this being the degree of individual difference allowed in this model, which thus allows the subjects to be represented by a series of category centroids, rather than by a single ideal point.

The intention is to obtain a configuration of stimulus/object points in such a way that the sum of squared inter-category distances (averaged over subjects) is maximized under suitable normalization restrictions. MDSORT determines a matrix **X** of coordinates of the *n* objects in a minimal, user-chosen dimensionality, *r*. The squared distances between category centroids are related by definition to the trace of the product-moment of **X**, which is determined so that tr(**X'BX**)} is maximized, where **B** is the mean of the sums of the subject-specific similarity matrices:

$$\mathbf{B} = \frac{1}{\mathrm{N}} \overset{N}{\underset{k=1}{3}} \Pi\ \mathbf{G}_k$$

The subject-specific matrix $\Pi\ \mathbf{G}_k$, thus plays an important role in understanding this process, and is related to the data matrix $\mathbf{G}_k$ as follows:

$$\Pi\ \mathbf{G}_k = \mathbf{G}_k(\mathbf{G}_k{}'\mathbf{G}_k)^{-1}\mathbf{G}_k{}'$$

The (*k,j*) element of ($\mathbf{G}_k\mathbf{G}_k{}'$)is 1 when objects *j* and *k* are sorted into the same group and is 0 otherwise. The$(\mathbf{G}_k{}'\mathbf{G}_k)^{-1}$ matrix scales nonzero elements of $\mathbf{G}_k\mathbf{G}_k{}'$ by the size of categories, so that the similarity between two objects sorted into the same group is inversely related to the size of the category. The values output for the matrix **B** are therefore also related to the sizes of the sorted categories, corresponding to the assumption of Burton's (1975) weighted similarity measure G. The raw co-occurrences may also be output, and may be submitted for comparison to other scaling routines within ***NewMDSX.***

With the addition of the restriction for the multidimensional case that **X'X** = **I**, the required maximum of tr(**X'BX**) is the matrix of normalized eigenvectors of **B** corresponding to its *r* dominant eigenvalues and satisfying the centering requirement by excluding the constant eigenvector. Once **X** has been obtained in this way, category centroids for each subject can be derived from it, in combination with and based on its relationship to the original input data matrix.

Takane himself points out that however desirable it may be to link the scaling and representation of the data (e.g. by seeking to reproduce aspects of subjects' behaviour in making a sorting), this is not actually achieved in the model (nor, it should be added, in any similar model). The MDSORT model maximizes the average sum of squared distances – a useful technical requirement – but it is hardly likely that subjects themselves form their categories so that the sum of the intercategory distances is a maximum.

8.3.1 INPUT COMMANDS

DIMENSIONS n Integer
This restricts the output to the first n principal components, in diminishing order of significance.

N OF STIMULI n Integer
The number of objects/stimuli sorted, corresponding to the number of columns in the input data matrix.

N OF SUBJECTS n Integer
The number of subjects for which sortings are Available, corresponding to the number of rows in the input matrix.

READ DATA
precedes the input data matrix. By default input is assumed to be in free format. If an INPUT FORMAT command is used, it must be specified to read a line of integer values corresponding to the N OF STIMULI.

LABELS followed by a series of labels (<= 65 characters), each on a separate line
optionally identify the stimuli in the output. Labels should contain text characters only, without punctuation.

8.3.2 OUTPUT

8.3.2.1 PRINT options (to main output file)

Option	Description
SIMILARITIES	Outputs the matrix **B** of similarities between the stimuli derived from the input data.
CLUSTERS	Outputs the set of individual cluster centroids corresponding to these overall similarities.
CO-OCCURRENCES	Outputs the matrix of raw co-occurrences in categories of the stimuli.

8.3.2.2 PLOT options (to main output file)

Option	Description
STIMULI	Plots the stimulus configuration, representing the number of normalized principal components specified by the DIMENSIONS statement.
CLUSTERS	Plots the set of cluster centroid configurations For the individual subjects. If the N OF SUBJECTS is more than a small number, this option may produce a rather large output file.

NOTES
1. READ DATA, N OF STIMULI and N OF SUBJECTS are obligatory in MDSORT.
2. No secondary output file is produced.
3. No PARAMETERS are used by MDSORT.
4. Program limits: STIMULI - 200
   DIMENSIONS – 8

8.4 EXAMPLE

```
RUN NAME    COMPARISONS OF A SERIES OF COMPOSERS
```

```
N OF STIMULI  16
N OF SUBJECTS 19
DIMENSIONS    2
PLOT  STIMULI
PRINT SIMILARITIES CLUSTERS
READ DATA
 1 1 2 3 4 4 2 5 6 7 7 7 6 6 8 8
 1 1 2 2 2 3 2 4 4 5 5 5 4 4 3 3
 1 1 2 3 3 2 6 4 4 5 5 1 4 4 7 4
 1 1 2 3 3 4 2 5 5 1 6 7 5 5 7 5
 1 1 2 3 2 3 5 6 5 6 6 4 6 6 4 4
 1 1 2 3 4 4 2 5 5 6 6 1 5 5 7 7
 1 1 1 3 3 3 1 2 2 3 3 2 2 2 2 2
 1 1 2 3 4 4 2 5 5 6 6 3 5 5 7 7
 1 1 2 2 2 2 2 3 3 1 2 2 3 3 3 3
 3 1 2 4 4 4 1 5 1 6 6 3 5 3 7 5
 1 1 2 3 4 4 2 3 5 6 6 7 5 5 4 4
 3 3 4 5 4 4 1 6 6 2 2 2 6 6 2 6
 4 4 5 6 3 6 3 2 1 5 6 6 1 2 6 2
 3 3 4 4 4 5 4 1 2 5 5 3 2 2 2 5
 3 3 4 5 5 4 6 1 2 4 4 6 2 1 5 1
 3 3 4 4 4 5 4 6 6 7 7 1 6 1 2 1
 3 3 4 5 6 7 1 1 1 7 7 7 1 1 2 1
 3 3 4 5 4 6 4 1 1 6 6 3 1 1 2 1
 3 3 4 5 5 5 6 7 7 8 8 8 1 1 2 2
COMPUTE
FINISH


OUTPUT
........

 SIMILARITY MATRIX DERIVED FROM THE DATA

            1        2        3        4        5        6        7        8
            9       10       11       12       13       14       15       16

  1     0.425    0.408    0.013    0.000    0.000    0.000    0.013    0.000
        0.000    0.035    0.000    0.088    0.000    0.018    0.000    0.000
  2     0.408    0.425    0.013    0.000    0.000    0.000    0.031    0.000
        0.018    0.035    0.000    0.070    0.000    0.000    0.000    0.000

........

 16     0.000    0.000    0.000    0.000    0.013    0.044    0.009    0.120
        0.067    0.013    0.013    0.043    0.085    0.120    0.170    0.304


 EIGENVALUES, CHI SQUARES AND THE CORRESPONDING D.F.


        1        0.847   -109.682       113
        2        0.639    -59.682       111
        3        0.566    -48.871       109
        4        0.503    -40.910       107
        5        0.401    -29.964       105
        6        0.378    -27.771       103
        7        0.343    -24.602       101
        8        0.328    -23.245        99
        9        0.248    -16.654        97
       10        0.216    -14.224        95
       11        0.201    -13.108        93
       12        0.176    -11.339        91
       13        0.142     -8.982        89
       14        0.125     -7.834        87
       15        0.097     -5.961        85
       16        0.000     -0.000        83


 STIMULUS COORDINATES

                    1       2

   CONTRIBUTION   0.162   0.123

       1 (1)      0.622  -0.200
       2 (2)      0.620  -0.195
       3 (3)     -0.065   0.172
       4 (4)     -0.145  -0.072
       5 (5)     -0.151  -0.068
       6 (6)     -0.129   0.030
       7 (7)     -0.029   0.224
       8 (8)     -0.174  -0.264
       9 (9)     -0.145  -0.217
      10 (A)      0.050   0.471
      11 (B)     -0.010   0.509
      12 (C)      0.148   0.301
      13 (D)     -0.168  -0.248
      14 (E)     -0.140  -0.229
      15 (F)     -0.131  -0.051
      16 (G)     -0.152  -0.163

.......

CLUSTER CENTROIDS FOR EACH SUBJECT

      SUBJECT=  1

          1 (1)           0.621  -0.197
          2 (2)          -0.047   0.198
          3 (3)          -0.145  -0.072
          4 (4)          -0.140  -0.019
          5 (5)          -0.174  -0.264
          6 (6)          -0.151  -0.231
          7 (7)           0.063   0.427
          8 (8)          -0.142  -0.107

      SUBJECT=  2

          1 (1)           0.621  -0.197
          2 (2)          -0.097   0.064
          3 (3)          -0.137  -0.062
          4 (4)          -0.157  -0.239
          5 (5)           0.063   0.427

.......

      SUBJECT= 19

          1 (1)          -0.154  -0.238
          2 (2)          -0.142  -0.107
          3 (3)           0.621  -0.197
          4 (4)          -0.065   0.172
          5 (5)          -0.141  -0.037
          6 (6)          -0.029   0.224
          7 (7)          -0.160  -0.240
          8 (8)           0.063   0.427

.......
```

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9. MINIRSA (MINI Rectangular Smallest Space Analysis)

9.1. OVERVIEW

Concisely: MINIRSA (MINI Rectangular Smallest Space Analysis, or non-metric Multidimensional Unfolding Analysis)
provides internal analysis of two-way data in a row-conditional format of a (dis)similarity measure by a Euclidean distance model using a monotonic transformation of the data.

DATA: 2-way, 2-mode row-conditional preference or dis/similarity data
TRANSFORMATION: monotonic

Following the terminology developed by Carroll and Arabie (1979) MINIRSA may be described as:

Data: Two-mode
Two-way
Ordinal
Row conditional
Complete or incomplete
One replication

Model: Euclidean distance incorporating
Two sets of points in
One space
The solution is internal

9.1.1 ORIGIN, VERSIONS AND ACRONYMS

The MINIRSA program included in the NewMDSX series is adapted from Roskam's 1973 release.

9.1.2 BRIEF DESCRIPTION OF MINIRSA

MINIRSA performs a non-metric multidimensional unfolding analysis. Consider a set of subjects and a set of stimuli where the subjects indicate their preferences for the stimuli (the judgements need not be of preference; any asymmetric relation is acceptable). The aim of the program is to position both stimuli of subjects as points in a space of minimum dimensionality so that, for each subject, the rank order of the distances from his or her point of maximum preference in the space (the "ideal point") to the stimuli matches the subject's preference ordering as closely as possible.

9.1.3 RELATION OF MINIRSA TO OTHER PROCEDURES IN NewMDSX

MINIRSA analyses preference data by means of an 'ideal point' or 'point-point' model. That is to say that each subject, or "judge" is represented in the solution space as a point positioned at his(her) point of maximum preference. The stimuli are also positioned as points in the same space so that the nearer a point lies to a given subject's ideal point the greater is that subject's preference for it.

(By contrast the MDPREF program implements a 'point-vector' model, where the subjects are represented in the solution space as vectors: i.e. directions of increasing preference (which is formally equivalent to having an ideal point at infinity).

MINIRSA is also equivalent to the third phase of PREFMAP except in so far as MINIRSA provides an <u>internal</u> analysis, that is to say that both subject and stimulus points are simultaneously positioned to satisfy the data, whereas in PREFMAP phase 3 the subject points are inserted into a pre-existing configuration of stimulus points. (Note, however, that PREFMAP also provides for a quasi-internal analysis q.v.).

9.2. DESCRIPTION OF THE PROGRAM

9.2.1 DATA

MINIRSA takes data in a 'row-conditional' format. In the simplest case, a group of N subjects might be asked to rank in order of preference a set of p stimuli. The judgement may, of course, be a ranking (or rating) in terms of any suitable criterion of which preference is the intuitively most obvious example.

The data matrix, then, consists of N rows each of which reflects a particular subject's order of preference for the stimuli. There are p columns. The various p ways in which these may be presented are detailed below (9.2.1.1).

MINIRSA does not accept paired-comparisons data as such but will take the row sums of such matrices (see MDPREF, Section 7.2.1.2).

9.2.1.1 Ranks or Scores

Preference judgements may be represented for MINIRSA (as in MDPREF and other procedures) in four distinct ways. The major distinction is that between a rank and a score. If a subject is asked to write down in his order of preference for five stimuli, he might respond with:

ACDEB

If these letters (or stimulus names) are given numeric values this becomes:

13452

This is the rank-ordering method (analogous to Coombs's I-scales) and means that stimulus 1 is preferred to 3 which is preferred to 4 etc.

Data may be input to MINIRSA in this form by specifying DATA TYPE(1). In various data-collection techniques it may be that the ordering obtained begins with the least-preferred stimulus so that the previous example would in this case be written as: BEDCA, signifying that B is least preferred, followed by E, and so forth. If this is the case then the data should be specified as: DATA TYPE(2).

A different way of representing such data is by the 'score' method. In this method each column represents a particular stimulus and the entry in that column gives the score or rating of that stimulus (for that subject) in his 'scale of preference'. Thus, in our original example the I-scale ACDEB (where A is preferred to C, which is preferred to D etc.) would in this method be represented as follows:

		A	B	C	D	E
subject	i	1	5	2	3	4

In this instance, the lowest number ('1') is used to denote the most preferred stimulus and the highest ('5') to represent the least preferred. This option is chosen by: DATA TYPE(3). Alternatively, the highest number might have been used to represent the most preferred stimulus and if this is so, DATA TYPE(4) should be specified.

(Although in illustrating the score method we have used the number 1 to 5, the data might equally well have been numerical ratings).

Figure 1 provides a simple means of identifying the appropriate DATA TYPE value.

Figure 1

```
                         Are the data
                       ranks or scores ?
                     /                   \
                ranks                     scores
                /                              \
      Is the first                         Does the highest
      stimulus the                          value mean most
     most preferred ?                        preferred ?
     /               \                       /             \
   yes                no                   yes              no
    |                  |                    |                |
DATA TYPE(0)       DATA TYPE(1)         DATA TYPE(2)    DATA TYPE(3)
```

9.2.2 THE MODEL

Coombs (1964) developed the notion of unidimensional unfolding in which a set of stimuli were so placed along the continuum (the "J(“joint”)-scale") that a subject might be thought of as being located at one point (our 'ideal point') in such a way that his or her preference for the stimuli decreased the further away from the ideal point a given stimulus is situated. If the J-scale is folded at the ideal point, this then forms the subject’s I (for “individual”) scale. The point of Unfolding analysis is to take a set of individual I-scales and unfold them into a joint scale. In this simple 1-space the fact that the distance from the subject's ideal point to stimulus a was greater than the distance from the ideal point to stimulus b implied that the subject preferred stimulus b to stimulus a. (For a more detailed overview see Appendix 3). The generalisation to spaces of higher dimensionality is intuitively obvious though computationally complex. MINIRSA is the program which performs non-metric multidimensional unfolding in the NewMDSX library.

MINIRSA takes data of the form described and seeks to position both sets of objects - subjects and stimuli - as points in a space of minimum dimensionality. The subjects are positioned at their points of maximum preference: their 'ideal points'. For each subject the distances to the stimuli will reflect the order of preference as revealed by the data: the most preferred stimulus will be the nearest stimulus point to a subject's ideal point, the least-preferred, the farthest away.

Strictly speaking, this will hold only if the data are 'perfect' (i.e. fit the given dimensionality) and for all but minimal STRESS values, some inversions will occur.

It is instructive to consider the contours enclosing areas of equal preference. In MINIRSA these will describe circles around each of the subject points (as contrasted, for instance, with PREFMAP phases I, II, where the contours are ellipses and MDPREF and PREFMAP IV where the "contours" are straight lines perpendicular to the subject's vector).

9.2.2.1 The Algorithm

1. If the user does not provide one, the program generates an initial stimulus configuration (see Appendix 2.5) in which the subjects are initially placed between their two most preferred stimuli.

2. The configuration is normalised.

3. The distances in the configuration (between each subject and the stimuli) are calculated.

4. The fitting values are next calculated following Kruskal's method of monotone regression.

5. STRESS2 is calculated (n.b. NOT STRESS1; see below)
6. If STRESS2 has reached zero or an acceptable minimum then the configuration is output as solution. If not, then

7. For each point on each dimension both the direction in which it should move so that STRESS2 is minimized and the optimal size of that move (the 'step-size') are calculated.

8. The configuration is moved in accordance with (7) and the program returns to step 2.

9. The solution is rotated to principal axes. (A translation of the origin is also allowed).

9.2.2.1.1 MINIRSA and MINISSA

The MINIRSA algorithm differs from the basic MINISSA algorithm on two major counts.

9.2.2.1.1.1 The monotonicity requirement

Since at step 5 Kruskal's method of calculating the fitting values is used, the program only enforces the requirement of weak monotonicity on the fitting value. Specifically, this means that different data values may be fit by the same fitting values.

9.2.2.1.1.2 STRESS

The input data to MINIRSA is considered to be 'row-conditional' (i.e. no comparability is assumed between subjects' rankings). Thus it is inappropriate to calculate STRESS according to the simple STRESS$_1$ formula, but rather a form of STRESS$_2$ is calculated. For each distinct ranking ("I-scale"), the STRESS$_2$ value is first calculated: (STRESS$_2$ is used in preference to STRESS$_1$ in order to prevent the occurrence of degenerate solutions, with fitting values all having the same value). The overall STRESS$_2$ value is then defined as a weighted average of the individual STRESS values.

9.2.3 FURTHER FEATURES

9.2.3.1 Missing Data

MINIRSA allows for missing data. The value to be regarded as indicating a missing value should be specified in the PARAMETERS statement by means of the MISSING parameter: e.g. if 9 is the code for a missing datum then MISSING(9) is appropriate.

9.3. INPUT PARAMETERS

9.3.1 LIST OF PARAMETERS

Keyword	Default Value	
DATA TYPE	1	1: Data are ranks (I-scales) of column indices in decreasing order of preference. 2: As 1 but in increasing order of preference. 3: Data are scores in order of column

		indices - high score means low preference 4: As 3 but high scores mean high preference
MINIMUM ITERATIONS	6	Sets the minimum number of iterations to be to be performed before convergence test.
MISSING DATA	0	Sets the data value which is to be regarded as missing data.
MATFORM	0	NOTE: only relevant when 'READ CONFIG' is used. 0: The input configuration is saved subjects and stimuli (rows) by dimensions (columns). Subjects are saved before stimuli. 1: The input configuration is saved dimensions (rows) by subjects and stimuli (columns).

9.3.2 NOTES

```
    ( #  )                             ( #  )
1.  ( N  ) OF SUBJECTS may be replaced by ( N  ) OF ROWS.
    ( No )                             ( No )
    ( #  )                             ( #  }
2.  ( N  ) OF STIMULI may be replaced by  ( N  ) OF COLUMNS
    ( No )                             ( No )
```

3. See section 6.2.3.2 for details of frequency counts.

9.3.3 PROGRAM LIMITATIONS

Maximum number of subjects	=	100
Maximum number of stimuli	=	60
Maximum number of dimensions	=	5

9.3.4 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of MINIRSA the particular options are as follows.

9.3.4.1 PRINT options (to the main output file)

Keyword	Form	Description
INITIAL	N x r p x r	Two matrices are produced being the coordinates of the subject points and the stimulus points in the required dimensions.
FINAL	N x r p x r	Similarly, two solution matrices are listed.
DISTANCES	N x N p x p N x p	Three matrices are listed: 1.The distances between the subject points. 2.The distances between the stimulus points. 3.The distances between the subjects and the stimuli.
FITTING	N x p	The matrix of disparities (DHAT's).
RESIDUALS	N x p	The matrix of residuals is listed.
HISTORY		This keyword generates an extremely detailed history of the iterative process. Users are warned that this option generates a large amount of output.

By default only the final configurations and the final STRESS value are listed.

9.3.4.2 PLOT options (to the main output file)

Keyword	Description
SUBJECTS	A plot of the subject points only

is produced.

STIMULI — A plot of the stimulus points only is produced.

JOINT — The configuration of subject and stimulus points is plotted.

SHEPARD — The Shepard diagram is produced

STRESS — A histogram of STRESS values at each iteration is produced.

POINT — The contribution of each subject to the overall STRESS value is plotted.

RESIDUALS — A histogram of residual values is produced.

By default a Shepard diagram and the joint space only are plotted.

9.3.4.2 PUNCH options (to a secondary output file)

Keyword — Description

SPSS — A file suitable for input to SPSS is produced. The following values appear:

```
I      :  the subject index no.
IFR    :  no. of repeat orderings.
0      :  the stimulus index no.
INPUT  :  the datum corresponding to I,J.
FITTING:  the corresponding DHAT value.
DIST   :  the solution distance between I & J.

RESID  :  the corresponding residual value.
```

The format of the file is (4I4,3F10.4)???.

STRESS — The STRESS values at each iteration are output in a fixed format.

FINAL — A file of the final configuration is produced.

9.4. EXAMPLE

```
  RUN NAME              MINIRSA TEST DATA
                        46 I-SCALES FROM 5 CONVEX STIMULI
  ITERATIONS            80
  DIMENSIONS            2
  N OF SUBJECTS         46
  N OF STIMULI          5
  PRINT                 DISTANCES, RESIDUALS
  PLOT                  POINT
  READ MATRIX
    <data follow here>
  COMPUTE
  FINISH
```

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APPENDIX 1: RELATION OF MINIRSA T0 OTHER PROGRAMS NOT IN NewMDSX

Internal multidimensional unfolding analysis, implemented by MINI-RSA, is also implemented by the SSAR-II program in the Guttman-Lingoes series and in Young and Lewyckyj's ALSCAL IN SPSS-4 package (with parameters set so that the measurement level is ordinal and the data type is rectangular and row-conditional).

More general variants are also possible in these packages. The Guttman-Lingoes programs permit other types of conditionality (see Lingoes 1972, pp 57-59) and ALSCAL IN SPSS-4 allows other levels of measurement (see Young and Lewyckyj 1979, p 23).

10. MINISSA (Michigan-Israel-Nijmegen Integrated Smallest Space Analysis)

OVERVIEW

Concisely: MINISSA (Michigan-Israel-Nijmegen Integrated Smallest Space Analysis) provides internal analysis of a two-way symmetric matrix of (dis)similarities by means of an Euclidean distance model using a monotone transformation of the data.

DATA: 2-way, 1-mode dis/similarity measures
TRANSFORMATION: Monotonic
MODEL: Euclidean distance

Following the categorisation developed by Carroll and Arabie (1979) the program may be fully described as:

Data:		Model:	
	One mode		Minkowski metric (restricted)
	Two-way		One set of points
	Dyadic		One space
	Ordinal		Internal
	Unconditional		
	Complete		
	One replication		

10.1.1 ORIGIN AND VERSIONS OF MINISSA

NewMDSX for Windows offers MINISSA(N), a fast, efficient version of the basic Guttman-Lingoes MINI-SSA program with a limited number of user options. This version emanates from Nijmegen and is part of Roskam's KUNST library of MDS programs. In particular, MINISSA(N) embodies the changes and improvements outlined in his classic monograph (Lingoes and Roskam 1973)integrating the Bell and Michigan traditions of basic non-metric scaling.

MINISSA(M), based upon the original SSA program in the Michigan (Guttman-Lingoes) series, contains a large number of user options, and is less easy to use than MINISSA(N). It was referred to as SSA(M) in the original MDS(X) series.

10.1.2 BRIEF DESCRIPTION OF MINISSA

MINISSA performs what is known as the basic non-metric model of MDS by taking (the lower triangle of) a square symmetric matrix whose elements are to be transformed to give the distances of the solution. This transformation will preserve the rank order of the input data. The model is formally equivalent to that developed by Kruskal (1964) although MINISSA uses a hybrid computational approach to the minimization problem, involving techniques originated by both Kruskal and Guttman. This approach is efficient and succeeds better than other programs in avoiding suboptimal solutions (Lingoes and Roskam 1973).

10.1.3 RELATION TO OTHER PROCEDURES IN NewMDSX

The MINISSA method and algorithm also forms the basis of MRSCAL. In MRSCAL it is assumed that there is a linear or power relation between the data and the solution distances output from MINISSA may be used as input for PINDIS.

10.2. DESCRIPTION OF THE PROGRAM

10.2.1 DATA

MINISSA accepts as input either the lower triangle (without diagonal) or a full square symmetric data matrix. Each entry of this input matrix is a measure of (dis)similarity between the row-element and the column element. Commonly these are pair-wise ratings of similarity, but any symmetric measure may be used (including correlations, covariances if they are non-negative) and co-occurrences.

The aim of the algorithm is to position the elements as points in a space of minimum dimensionality so that a measure of departure from perfect fit between the (monotonically) rescaled data and the distances of the solution (STRESS) is minimised. Perfect fit occurs if a monotone transformation of the data can be found which forms a set of actual distances.

10.2.1.1 Example

Benjamin(1958) collected data on the social mobility of some 2600 subjects using thirteen occupational categories. Macdonald, used the index devised by Blau and Duncan (1967, p.43) to measure the dissimilarity in mobility between occupational groups. (For a fuller description of this index see section 2.3.3.4 of the Users' Guide). The measure, writes Macdonald (1972, pp.213-14) may be interpreted as "the percentage of the sons of (group) A that would have to be reallocated jobwise for the sons of A to match the sons of B". He assembles the index values into a lower diagonal matrix, and these are included in the example described in section 4. The scaling solution is discussed at length in Macdonald's article.

10.2.2 THE ALGORITHM

1. An initial configuration is input by the user, or one is generated by the program (see 7.2.3.2 below).

2. This configuration is normalised (see 7.2.2.2 below).

3. The distances between the points are calculated according to the Minkowski metric chosen (see 7.2.3.3 below).

4. The disparities or fitting-values are calculated (see 7.2.2.1).

5. STRESS, the index of badness-of-fit between the disparities and the distances, is calculated.

6. A number of tests are performed to determine whether the iterative process should continue, e.g.

   Is STRESS sufficiently low ?

   Has the improvement of STRESS over the last few iterations been so small as to be not worth continuing ?

   Has a specified maximum number of iterations been performed ?

   If the answer to any of these is YES, then the configuration is output as solution. If not, then

7. For each point on each dimension the direction in which it would have to move for STRESS to be minimized is calculated as is the optimal size of the move (the 'step-size').

8. The configuration is moved in accordance with 7 and the program returns to step 2.

10.2.2.1 Minimization, fitting values

In MINISSA there are two methods of finding the minimum STRESS value. These are known in Guttman's (1968) terminology as soft and hard squeeze methods. The program begins by using the soft squeeze which minimizes raw STRESS and when this has reached a minimum switches to the hard squeeze and minimizes STRESS1. By convention different fitting values (step 4) are used in the different phases.

10.2.2.1.1 Soft squeeze

Soft squeeze derives from a technique of Guttman's (1968). It is particularly efficient at quickly reducing STRESS. Fitting values are calculated using a procedure known as rank-image permutation. These fitting values are known as d^* (DSTARS) and have the property of being strongly monotone with the data. That is to say that unequal data values must be matched with unequal fitting values (formally if $\delta_{ij} > \delta_{kl}$ then $d^*_{ij} > d^*_{kl}$).

10.2.2.1.2 Hard squeeze

When a minimum has been reached using the soft squeeze the program switches to the so-called hard squeeze, which is a simpler, more well-behaved method. Fitting values are now calculated using a procedure known as monotone (or isotonic) regression and are known as $\hat{d}$ (DHATS). These have the property of being weakly monotone with the data in that unequal data may be matched with equal fitting values if in so doing STRESS is reduced (formally, if $\delta_{ij} > \delta_{kl}$ then $\hat{d}_{ij} \geq \hat{d}_{kl}$).

To summarise:

	SOFT SQUEEZE (initial method)	HARD SQUEEZE (second method)
Minimizes:	Raw Stress	$STRESS_1$
Using:	d^* (DSTAR)	$\hat{d}$ (DHAT)
Relation to data:	strongly monotone	weakly monotone

Users who wish to vary the combination of fitting values with methods are referred to SSA(M).

10.2.2.2 STRESS and normalization

In the so-called 'soft-squeeze' the program minimizes raw STRESS (otherwise known as raw phi, or $STRESS_0$) which is simply the sum of the squared differences between the distances in the configuration and the DSTAR's, i.e. $\Sigma_{ij} (d_{ij} - d^*_{ij})^2$. Since this index might be minimized by successive scaling down of the overall size of the configuration, the configuration is normalised after each iteration.

In the so-called 'hard-squeeze' however, $STRESS_1$ is calculated and minimized. $STRESS_1$ is simply a normalized form of raw STRESS, the normalizing factor being the sum of the squared distances in the configuration. This removes the dependence of the original index on the size of the configuration. Values for STRESS of both flavours are output by the program.

10.2.2.2.1 Step-size and angle factor

At step 7, the algorithm computes the direction in which each point should be moved in order to reduce STRESS. This is done by calculating the partial derivation of STRESS with respect to each point - the negative gradient. It is also important however correctly to compute the optimal amount of movement in that direction. This is the so-called 'step-size'. This step-size may be changed at each iteration. These changes are monitored by the 'angle factor', which is in effect the cosine of the angle between successive gradients, i.e. the correlation between them. This ensures that, as the program moves towards convergence, and the gradient becomes less steep the step-size will decrease, so as to minimize the possibility of overshooting a minimum STRESS value. MINISSA prints out at termination the final angle factor. At this stage the value ought to be very small. If it is large, then more iterations should be attempted.

10.2.3 FURTHER OPTIONS IN MINISSA

10.2.3.1 Ties in the data

It is possible to treat ties in the data in two ways when calculating STRESS. These are known as the primary and secondary approaches and are chosen by the user, by means of TIES on the PARAMETERS command.

10.2.3.1.1 The primary approach (TIES (1))

The primary approach allows that if two data elements are equal then the assigned fitting values may be unequal The tie is broken if, in so doing, STRESS is reduced. Substantively this approach regards ties in the data as relatively unimportant. It is, of course, possible for the program to capitalise on this approach to produce a 'good', though degenerate configuration. If data contain a lot of ties and the program is using the primary approach then long horizontal lines will appear in the Shepard diagram. A number of such horizontal lines is a sign of possible degeneracy in the solution.

10.2.3.1.2 The secondary approach (TIES (2))

On the other hand, the secondary approach regards the equality of data elements as important information and requires that the fitting values be equal for equal data. This constraint is more stringent than the primary approach and will normally result in higher STRESS values.

10.2.3.1.3 The parameter EPSILON

A further approach to tied data is given by means of EPSILON on the PARAMETERS command. Each pair of data values will be compared and, if the difference between them is less than this value they will be regarded as tied. This approach is recommended if the user wishes to place little emphasis on the smaller variations in the data.

For a full description of options regarding ties and the preservation of order information, see the Users' Guide section 3.2.3. The user wishing to combine a particular approach to ties with a particular type of fitting value is referred to the options available in SSA(M) mentioned in the Appendix below.

10.2.3.2 The initial configuration

The values of a 'good' starting point for the iterative process include saving on machine time and avoidance of local minima. Two options exist within MINISSA for the choice of initial configuration:

The user may supply a starting configuration. This may be a guess at the solution, an a priori configuration or a solution to a previous metric scaling. The matrix of coordinates is preceded by a READ CONFIG command, which may if necessary have associated with it an optional INPUT FORMAT specification to read real (F-type) values. The configuration may be input either stimuli (rows) by dimensions (columns) or dimensions (rows) by stimuli (columns). (In this latter case, the parameter MATFORM should be given the value (1) in the PARAMETERS command).

Alternatively, the program will generate a starting configuration with desirable numerical properties. This configuration is the usual one in the Guttman-Lingoes-Roskam MINI programs and uses only the ordinal properties of the data. It has been found to be particularly useful in avoiding problems with local minima. Further details justifying this choice of initial configuration will be found in Lingoes and Roskam (1973, pp.17-19), and Roskam (1975, pp.37-44).

10.2.3.3 Distances in the configuration

The user may choose how the distances between the points in the configuration are to be computed by the MINKOWSKI parameter. The default of 2.0 gives the ordinary Euclidean metric and 1.0 gives a 'city-block' metric but any positive number may be used. It is however unwise to use large values as there is then a risk of overflow.

10.2.3.4 The final configuration

When the iterative process is terminated, the current configuration is output as the solution. If the metric is Euclidean (i.e. MINKOWSKI(2)) then the configuration is rotated to principal axes. It should be noted that these axes are arbitrary from the point of view of interpretation, but have certain desirable geometric properties. In particular the coordinates of the points on the axes are uncorrelated. Furthermore it is often helpful in deciding on the 'correct' dimensionality of the solution to notice how much variation is associated with each axis. This variation is given in the output by the value SIGMA which is the standard deviation of the coordinates on each axis.

10.2.3.5 STRESS and dimensionality

The estimation of the appropriate dimensionality of an MDS solution is central to the analysis. Three methods are commonly used with MINISSA in addition to that involving SIGMA alluded to above.

The first guideline (attributed to Forrest Young) asserts that the ratio between the number of data elements and the number of latent parameters (i.e. coordinates) should be at least two. This compression ratio should serve as a useful guide when choosing the dimensionalities for a run of the program.

The second is a heuristic device analogous to the familiar "scree test" of factor analysis. STRESS should decrease with increasing dimensionality until in n-2 dimensions a perfect (though trivial) fit will be achieved. If a graph is drawn of STRESS against dimensionality it is a common occurrence to find an 'elbow' - a sharp decrease in STRESS between dimensions occurring at some relatively low dimensionality. At this value, to add dimensions will not significantly improve the fit of data to solution so it is reasonable to attempt interpretation of this solution.

If however 10 and 60 points are being used and the dimensionality is less than or equal to 5 the program will print a value of STRESS$_1$ based on an approximation to random data as detailed in Spence (1979).

10.2.3.6 Local minima

For a given set of data each configuration will have an associated STRESS value. The MINISSA procedure finds the 'best' configuration, by finding the partial derivatives of STRESS (with respect to the coordinates). It is possible that a given STRESS value, although locally the minimum attainable, may not be the real 'global' minimum.

As mentioned earlier both a good initial configuration and a hybrid algorithm (such as MINISSA) tend to decrease the possibility of local minima occurring. Relatively high STRESS values may be a sign of local minima as would a decrease in STRESS in decreasing dimensionality. If the user suspects local minima, then it is suggested (s)he try a number of different starting configurations.

10.3. INPUT PARAMETERS

All parameter keywords may be shortened to the first four letters. All subsequent mis-spellings are ignored.

10.3.1 LIST OF PARAMETERS

Keyword	Default Value	Function
DATA TYPE	0	0: The data are similarities (high values mean high similarities between points) - input is lower triangle matrix without diagonal 1: The data are dissimilarities (high values mean high dissimilarities between points) - input is lower triangle without diagonal 2: The data are similarities - input is full symmetric matrix 3: The data are dissimilarities - input is full symmetric matrix
MINIMUM ITERATIONS	6	Sets the minimum number of iterations to be performed before the convergence test.
EPSILON	0.0	Data are to be considered tied if difference between them is less than EPSILON.
MATFORM	0	(Only relevant when 'READ CONFIG' is used). 0: The input configuration is saved stimuli (rows) by dimensions (columns). 1: The input configuration is saved dimensions (rows) by stimuli (columns).
TIES	1	1: Primary approach to ties in the data. 2: Secondary approach to ties in the data.
MINKOWSKI	2.0	1: Distances in the configuration are measured by 'city-block' metric. 2: Distances are measured by a Euclidean metric. Any positive number may be used.

10.3.2 NOTES

```
    ( #  )                             ( #  )
1.  ( N  ) OF STIMULI may be replaced by  ( N  ) OF POINTS
    ( NO )                             ( NO )
```

```
2.  ( #  )
    ( N  ) OF SUBJECTS  is not valid.
    ( NO )
```

3. LABELS followed by a series of labels (<= 65 characters), each on a separate line, optionally identify the stimuli in the output. Labels should contain text characters only, without punctuation.

4. Note that the program expects real (F-type) numbers. The data should be input as the lower half of a matrix without diagonal. The INPUT FORMAT statement, if used, should read the longest row of this matrix (i.e. n-1 values when there are n stimuli).

5. Note that MINISSA expects (dis)similarities and is not intended to work with negative values.

6. Program limits:

```
      Maximum number of stimuli     =  80
      Maximum number of dimensions  =   8
```

10.3.3 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of MINISSA, the available options are as follows:

10.3.3.1 PRINT options (to the main output file)

Option	Form	Description
INITIAL	p x r matrix	Initial configuration, either generated by the program or input by the user (p = no. of stimuli).
FINAL	p x r matrix	Final configuration, rotated to principal components.
DISTANCES	lower triangular, with diagonal	Solution distances between points, calculated according to MINKOWSKI parameter.
FITTING	lower triangular, with diagonal	Fitting values: the disparities (DHAT) values.
RESIDUALS	lower triangular, with diagonal	The difference between the distances and the disparities.
HISTORY		An iteration by iteration history of STRESS and values.

By default only the final configuration and the final STRESS values are listed.

10.3.3.2 PLOT options (to the main output file)

Option	Description
INITIAL	Up to r(r-1)/2 plots of the initial configuration. (r = no. of dimensions).
FINAL	Up to r(r-1)/2 plots of final configuration (r = no. of dimensions).
SHEPARD	The Shepard diagram of distances plotted against data. Fitting values are shown by *, actual data/distance pairs by 0.
STRESS	Plot of STRESS values by iteration, with a final plot of stress by the number of dimensions.

POINT	Histogram of point contributions to STRESS.
RESIDUALS	Histogram of residual values.

By default, the Shepard diagram and the final configuration will be plotted. Configuration plots are calibrated both from 0 to 100 and from 0 to the maximum coordinate value.

10.3.3.3 PUNCH options (secondary output file)

Option	Description
SPSS	Outputs I (Row index), J (Column index) and corresponding DATA, DISPARITIES, DISTANCES, RESIDUALS values in the format:(2I3,4F12.0).
FINAL	Outputs final configuration as stimuli(row) by dimension(column) matrix. Each row is prefaced by the stimulus number. Format: (I4, rF10.0) where r is the number of dimensions.
STRESS	Outputs STRESS value by iteration.

By default, no secondary output is produced.

10.4. EXAMPLE

```
   RUN NAME             8 POINT ZERO STRESS DATA
   TASK NAME            AS MADE FAMOUS BY USERS GUIDE
   N OF STIMULI         8
   DIMENSIONS           2
   INPUT FORMAT         (7F4.0)
   PARAMETERS           TIES(2), DATA(1)
   READ MATRIX
     <data>
   PRINT                 ALL
   PLOT                  SHEP(2)
   COMPUTE
   FINISH

  RUN NAME               OCCUPATIONAL DISSIMILARITY DATA
  TASK NAME              AS IN SEC. 2.1.1
  N OF STIMULI           13
  DIMENSIONS             5 TO 1
  PARAMETERS             DATA(1)
  INPUT FORMAT           (12F5.0)
  LABELS                 FARMERS
                         AGRICULTURAL WORKERS
                         HIGHER ADMIN ETC
                         OTHER ADMIN ETC
                         SHOPKEEPERS
                         CLERICAL WORKERS
                         SHOP ASSISTANTS
                         PERSONAL SERVICE
                         FOREMEN
                         SKILLED WORKERS
                         SEMI-SKILLED WORKERS
                         UNSKILLED WORKERS
                         ARMED FORCES
   READ MATRIX
   51.1
   71.4  75.8
   63.0  52.7  36.9
   58.6  57.7  40.8  32.3
   67.0  55.6  38.6  17.7  38.2
   63.4  52.3  39.4  13.4  27.8  27.3
   54.5  43.3  55.5  29.3  41.1  35.0  23.5
   71.2  47.5  56.5  26.2  41.0  35.6  21.1  36.1
   65.2  44.3  62.3  33.0  45.1  42.1  27.4  32.0  14.7
   65.7  43.0  68.2  39.0  50.8  47.3  33.3  36.0  15.7   8.4
   60.1  34.2  69.4  39.8  51.9  47.2  35.5  30.4  23.9  21.1  19.3
   66.7  41.9  62.7  36.1  44.6  42.7  29.0  35.9  21.2  20.7  18.4  18.9
   PLOT                                   SHEP(2)
   COMPUTE
   FINISH
```

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APPENDIX : RELATION OF MINISSA TO OTHER PROGRAMS

The MINISSA program merges the two main traditions of basic non metric MDS: the Shepard-Kruskal approach (using monotone regression, weak monotonicity and minimising STRESS) and the Guttman-Lingoes approach (using rank images, strong monotonicity and minimising raw STRESS). The former was implemented in the original MDSCAL program, and the latter in the Guttman-Lingoes SSA-1 program. Both of these programs are now outdated and have been withdrawn.

The basic model is now implemented as the default option by a number of general purpose programs: KYST (the successor to MDSCAL), TORSCA (for Torgerson Scaling) and ALSCAL-4 (the successor to POLYCON). The chief advantages of MINISSA are its small size and speed of computation and its resistance to suboptimal solutions.

11. MRSCAL (MetRic SCALing)

11.1. OVERVIEW

Concisely: MRSCAL (MetRic SCALing) provides internal analysis of a two-way data matrix by means of a Minkowski distance model using either a linear or a logarithmic transformation of the data.

DATA: 2-way, 1-mode dissimilarity measure
TRANSFORMATION: Linear or Logarithmic transform
MODEL: Minkowski distance model

Following the categorisation developed by Carroll and Arabie (1979) MRSCAL may be described as:

Data:	One mode	Model:	Minkowski metric
	Two-way		One set of points
	Dyadic		One space
	Unconditional		Internal
	Complete		
	One replication		

11.1.1 ORIGIN AND VERSIONS OF MRSCAL

The MRSCAL program is the basic metric distance scaling program in Roskam's MINI series. The MRSCAL program in the NewMDSX series is based upon the 1971 and KUNST (1977) versions.

11.1.2 BRIEF DESCRIPTION OF MRSCAL

The MRSCAL algorithm is a metric counterpart to MINISSA. Its aim is to position a set of stimulus objects as a set of points in a space of minimum dimensionality in much the same way as MINISSA, except that the distances in this space will be a linear (or optionally a logarithmic) function of the dissimilarities between the stimuli. In this it has obvious similarities to 'classic' MDS (Richardson 1938, Young and Householder 1938) and to the linear (metric) scaling procedure developed by Messick and Abelson (1956) and made more widely known by Torgerson (1958). The MRSCAL algorithm however, utilises the iterative procedures which Guttman, Lingoes and Roskam (1971) developed and also allows the user additional options, both in the manner by which the distances in the solution space are measured (see Section 2.2.2) and in the form of the transformation function linking data to distances in the solution (see Section 2.2.4) which make it both more general and more robust than the original procedures.

11.1.3 RELATION OF MRSCAL TO OTHER PROCEDURES IN NewMDSX

MRSCAL is an exact metric counterpart to MINISSA, differing from it in that it restricts the field of possible transformation of the data to linear (or power) ones.

Output from MRSCAL may be input to PINDIS.

11.2. DESCRIPTION

MRSCAL accepts as input the lower triangle (without diagonal) or a square symmetric data matrix. Each entry of this matrix will be a measure of the (dis)similarity between the row-element and the column element. If the linear transformation option is chosen it should be borne in mind that product moment correlations and covariances may not be acceptable in that they are only monotonically (and not linearly) related to distance.

The aim of the algorithm is to position these elements as points in a space of minimum dimensionality such that a STRESS-like measure of departure from perfect fit (Guttman’s coefficient of alienation) between the (linearly) rescaled data and the distances in the solution is minimised. A perfect fit occurs if a linear (or logarithmic) transformation of the data is found which is a set of actual distances.

11.2.1.1 Example

Benjamin (1958) collected data on the social mobility of some 2600 subjects using thirteen occupational categories. Macdonald, who investigated the notion of social distance, uses the Dissimilarity Index devised by Blau and Duncan (1967, p.43) to measure the dissimilarity in mobility between occupational groups. (For a fuller description of this index see section 2.3.3.4 of the Users' Guide). The measure, writes Macdonald (1972, pp. 213-14) may be interpreted as "the percentage of the sons of (group) A that would have to be reallocated jobwise for the sons of A to match the sons of B". He assembles the index values into a lower diagonal matrix, and these are included in the examples described in section 4. The scaling solution is discussed at length in Macdonald's article.

11.2.2 THE ALGORITHM

The program proceeds as follows.

1. An initial configuration is input (or one may be generated by the program (see 2.2.1 below)).

2. The configuration is normalised.

3. The inter-point distances are calculated according to the Minkowski metric chosen by the user (see 2.2.2 below).

4. A set of fitting quantities are computed that are

   i) a linear (or power) transformation of the data; and

   ii) a least-squares best-fit to the distances.

5. The coefficient of alienation between the fitting-quantities and the distances is computed.

6. A number of tests is performed to determine whether the iterative process should continue; e.g. Is STRESS sufficiently low? Has the improvement in STRESS over the last few iterations been great enough to warrant continuing ? Has a specified maximum number of iterations been performed ?
7. If not, then the gradient is computed. This gives for each point on each dimension the direction in which that point should be moved on that dimension in order that STRESS be minimized.

8. If the gradient is zero then the configuration is output as solution.

9. If not, then the points are moved in accordance with (7) and the program returns to step 2.

11.2.2.1 Initial configuration

The user may provide a starting configuration by means of the Command READ CONFIG, with an associated INPUT FORMAT specification if the data are not in free format. In this case a coordinate for each point on each dimension is input. This may be done either by stimuli (rows) by dimensions (columns) or dimensions(rows) by stimuli (columns).
In this latter case the parameter MATFORM should be given the value 1

in the PARAMETERS command.

If this is not done, however, then the program constructs an initial configuration from the original data by the Lingoes-Roskam procedure which, as has often been shown, is a good initial approximation of a solution and also has certain desirable geometrical properties.

11.2.2.2 Distances in the configuration

The user may choose the way in which the distance between the points in the configuration is measured by means of the MINKOWSKI parameter. The default value 2 provides for the ordinary Euclidean metric where the distances between two points will be the length of the line joining them. The user may specify any value for the parameter. Commonly used values, however, include 1, the so-called 'city-block' or 'taxi-cab' metric where the distance between the two points is the sum of the differences between their co-ordinates on the axes of the space, and infinity (in MRSCAL approximated by a large number (>25)) the so-called 'dominance' metric when the largest difference on any one axis will eventually come to dominate all others. (Users are warned that high values of MINKOWSKI are liable to produce program failure due to overflow).

11.2.2.3 STRESS and the coefficient of alienation

The family of STRESS formulae for the MINI series is based on the sum of the squared differences between the fitting-values and the distances. In MRSCAL, since the fitting-values are at interval level, a product-moment form is applicable, represented by MU which is the correlation between the distances and the fitting-values, and is hence a measure of goodness of fit. In addition, a related badness of fit measure very similar to STRESS is calculated, known as the coefficient of alienation, K. The two measures used in MRSCAL are related by:

$$K = (1-MU^2)$$

11.2.2.3.1 Angle factor and step-size

At step 7, the algorithm computes the direction in which each point should be moved in order to reduce STRESS. This is done by calculating the partial derivative of STRESS with respect to each point - the negative gradient. It is also important, however correctly, to compute the optimal amount of movement in that direction. This is the so-called 'step-size'. This step-size may be changed at each iteration. These changes are monitored by the 'angle factor', which is in effect the cosine of the angle between successive gradients, i.e. the correlation between them. This ensures that, as the program moves towards convergence, and the gradient becomes less steep the step-size will decrease, so as to minimize the possibility of overshooting a minimum STRESS value. MRSCAL prints out at termination the final angle factor. At this stage the value ought to be very small if it is large, then more iterations should be attempted.

11.2.2.4 Linear and logarithmic transformations

The most common use of MRSCAL is to find a linear transformation of the data which best fits a configuration of points in the chosen dimensionality. The program will also, however, perform an analysis using logarithmic transformations of the data values. In this case the Shepard diagram will show a smooth exponential curve. The user must specify which transformation is required. If no PARAMETERS statement is read and/or no specification of the transformation made, then no analysis will be performed.

11.2.3 FURTHER FEATURES

11.2.3.1 The CRITERION parameter

In step 6 of the algorithm a number of stopping tests are performed. One of these involves calculating the improvement in fit between the present and the previous iteration. If the improvement is less than the value given by CRITERION in the PARAMETERS statement, then the process is terminated and the current configuration is output as solution. A large value for CRITERION will have the effect of stopping the iterative process earlier than would otherwise be the case. This allows the user to make more "cheaply" a number of exploratory analyses.

11.2.3.2 The final configuration

When the iterative process is terminated, the current configuration is output as the solution. If the metric is Euclidean (i.e. MINKOWSKI (2)) then the configuration is rotated to principal axes. It should be noted that these axes are arbitrary from the point of view of interpretation, but have certain desirable geometric properties. In particular the coordinates of the points on the axes are uncorrelated. Furthermore it is often helpful in deciding on the 'correct' dimensionality of the solution to notice how much variation is associated with each axis. This variation is given in the output by the value SIGMA which is the standard deviation of the coordinates on each axis.

11.2.3.3 Dimensionality

As a general rule solutions should be computed in a number of dimensionalities. Since a perfect fit will be obtained in n-2 dimensions the trial dimensionalities should always be in dimensionalities less the n-3. As a guide to the choice of trial dimensionalities it is recommended that the product of stimuli x dimensions should be less than half the number of data elements (Young's index of data compression).

A further method is one superficially similar to the 'scree' test of factor analysis. This involves examining the plot of stress by dimensionality. Since MU is a measure of goodness of fit the plot will show an ascending function and the elbow test for appropriate dimensionality may be performed. The 'appropriate' dimensionality, i.e. one of which interpretation may be attempted, is that at which the graph shows an 'elbow', i.e. where the addition of extra dimensions is otiose.

11.3. INPUT PARAMETERS

11.3.1 LIST OF PARAMETERS

Keyword	Default Value	Function
DATA TYPE	0	0: The data are similarities (high values mean high similarities between points) – input is lower triangle matrix without diagonal
		1: The data are dissimilarities (high values mean high dissimilarities between points) – input is lower triangle without diagonal
		2: The data are similarities – input is full symmetric matrix
		3: The data are dissimilarities – input is full symmetric matrix
LINEAR TRANSFORMATION	0	0: Linear transformation is not performed
		1: Linear transformation is performed.
LOG TRANSFORMATION	0	0: Logarithmic transformation is not performed

		1: Logarithmic transformation is performed.
CRITERION	0.00001	Sets the criterion value for terminating the iterations.
MINKOWSKI	2	Sets the Minkowski metric for the analysis.
MATFORM	0	(RELEVANT ONLY WHEN 'READ CONFIG' IS USED) 0: The input configuration is saved: stimuli(rows) by dimensions(columns) 1: The input configuration is saved: dimensions(rows) by stimuli(columns)

N.B. Either LINEAR TRANSFORMATION or LOG TRANSFORMATION must be specified

11.3.2 NOTES

```
   ( #  )
1. ( N  ) OF SUBJECTS is not valid with MRSCAL.
   ( NO )

   ( #  )                               ( #  )
2. ( N  )   OF STIMULI may be replaced by ( N  ) OF POINTS
   ( NO )                               ( NO )
```

3. LABELS followed by a series of labels (<= 65 characters), each on a separate line, optionally identify the stimuli in the output. Labels should contain text characters only, without punctuation.

4. a) The program expects input to be in the form of the lower triangle of a matrix of real (F-type) numbers, or a full square matrix, with diagonal.

   b) The INPUT FORMAT, if used, should read the longest, i.e. last, row of this matrix.

5. Maximum no. of stimuli = 80
   Maximum no. of dimensions = 8

11.3.3 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of MRSCAL, the available options are as follows:

11.3.3.1 PRINT options (to the main output file)

Option	Form	Description
INITIAL	p x r matrix	Initial configuration, either generated by the program or listed by the user (p = no. of stimuli, r = no. of dimensions).
FINAL	p x r matrix	Final configuration, rotated to Principal components.
DISTANCES	lower triangular, with diagonal	Solution distances between points, calculated according to MINKOWSKI parameter.
FITTING	lower triangular, with diagonal	Fitting values: the disparities (DHAT) values.

RESIDUALS	lower triangular, with diagonal	The difference between the distances and the disparities.

By default only the final configuration and the final STRESS values are listed.

11.3.3.2 PLOT options (to the main output file)

Option	Description
INITIAL	Up to r(r-1)/2 plots of the initial configuration. (r = no. of dimensions).
FINAL	Up to r(r-1)/2 plots of final configuration (r = no. of dimensions).
SHEPARD	The Shepard diagram of distances plotted against data. Fitting values are shown by *, actual data/distance pairs by 0.
STRESS	Plot of STRESS by iteration.
POINT	Histogram of point contributions to STRESS.
RESIDUALS	Histogram of residual values (logged).

By default, only the Shepard diagram and the final configuration will be plotted. Configuration plots are calibrated both from 0 to 100 and from 0 to the maximum coordinate value.

11.3.3.3 PUNCH options (to secondary output file)

Option	Description
SPSS	Outputs I (Row index), J (Column index) and corresponding DATA, DISPARITIES, DISTANCES, RESIDUALS values in the format: (2I4, 4F10.0).
FINAL	Outputs final configuration as stimulus (row) by dimension (column) matrix. Each row is prefaced y the stimulus number. Format: (I4,rF9.6) where r is the number of dimensions.
STRESS	Outputs STRESS value by iteration.

By default, none of these options is produced.

11.4.   EXAMPLE

```
   RUN NAME            8 POINT ZERO STRESS DATA
   TASK NAME           AS MADE FAMOUS BY USERS' GUIDE
   N OF STIMULI        8
   DIMENSIONS          2
   INPUT FORMAT        (7F4.0)
   PARAMETERS          LINE(1), DATA(1)
   READ MATRIX
     <data>
   PRINT                ALL
   PLOT                 SHEP (2)
   COMPUTE
   FINISH
```

APPENDIX : RELATION OF MRSCAL TO SIMILAR PROGRAMS OUTSIDE NewMDSX

The earliest work in MDS assumed that the data dissimilarities were direct estimates of Euclidean distances, and solved for the coordinates of the space that generated them. This so-called "classic MDS" thus assumes the distances are at the ratio level of measurement. Later developments (Messick and Abelson, 1956) assumed that the data were "relative" distances - i.e. a linear function of the solution distances, thus implying interval level of measurement - and therefore had to solve additionally for the "additive constant" necessary to turn the data into distance estimates. A surprisingly robust procedure for implementing such "linear" or metric scaling is described in detail in Torgerson (1958).

Similar procedures to those provided by MRSCAL are implemented in the following package and programs:

(1) KYST (the successor to the original general purpose package known as MDSCAL) provides options for specifying linear and power transformations relating data to the solution distances, and thus implement linear and logarithmic scaling respectively.

(2) ALSCAL-4 (the successor to POLYCON and TORSCA) also allows the user to specify ratio or interval levels of measurement, which also implement classical and linear scaling respectively. There is an additional facility for the user to specify a polynomial in degree 1 to 4 as the nearest equivalent to a logarithmic transformation.

12. PARAMAP (PARAmetric MAPping)

12.1. OVERVIEW

Concisely: PARAMAP (PARAmetric MAPping) provides internal analysis of either a matrix (of co-ordinates or profiles) or a square symmetric matrix of (dis)similarity coefficients by means of a distance model which maximises continuity or local monotonicity.

DATA: either 2-way, 1-mode dissimilarities, or 2-way 2-mode data (profiles or co-ordinates)
TRANSFORMATION: Continuity (local monotonicity) or smoothness (kappa coefficient)
MODEL: Euclidean distance
(n.b. only one set of points – usually the row elements) is represented.

Alternatively, using the categorisation developed by Carroll and Arabie (1979) PARAMAP may be described as:

Data:	One-mode (possibly two-mode)	Model:	Distance
	Two-way		One set of points
	Interval or ratio		One space

12.1.1 ORIGIN, VERSIONS AND ACRONYMS

The PARAMAP procedure was developed by Shepard and Carroll and is documented in Shepard and Carroll (1966). The present program is based on the original program.

12.1.2 PARAMAP IN BRIEF

PARAMAP takes as input either a rectangular matrix of profile data, or a symmetric matrix of distances or covariances/correlations. The program derives distances from the various inputs which are considered as ratio quantities and as existing in a space of high dimensionality. These data the program seeks to represent in a space of lower (user-specified) dimensionality so that the function relating the two sets of distances is as smooth (continuous) as possible. It can be shown that the criterion used to maximise smoothness also accurately represents small distances, and hence preserves 'local' information in the data and may be regarded as implementing local monotonicity.

12.1.3 RELATION OF PARAMAP TO OTHER NewMDSX PROCEDURES

PARAMAP will take as data the distance matrix output from other scaling procedures, such as MINISSA, MRSCAL etc. It may also be used to analyse data of the same form as input to PREFMAP or MDPREF except that, since the data are used to compute a matrix of distances the data must be at least at the interval level of measurement. In the case of rectangular data input, only the 'stimulus' points are represented in the space by this program.

12.2. DESCRIPTION

12.2.1 DATA

Data may be input to PARAMAP in two basic forms
1. as a matrix of distances
or 2. as a matrix of coordinates (or 'profile' data).

The type of data input is described by DATA TYPE in the PARAMETERS command.

12.2.1.1 Data on the form of distances

The PARAMAP model actually operates on squared distances so data may be input to the program either as a matrix of distances between points or as a matrix of squared distances between points. Since the program simply squares the original distances and then proceeds there is no particular advantage in using one form rather than another. If distances are input then DATA TYPE (4) is appropriate, for squared distances DATA TYPE (2). The data are read by the READ MATRIX command, according to its associated INPUT FORMAT specification, if the data are not in free format, and consist of a lower-triangular matrix without diagonal. Distance matrices output by such procedures as MINISSA, MRSCAL, MVNDS, HICLUS, TRISOSCAL are suitable for analysis by PARAMAP, but INDSCAL solutions are not amenable to PARAMAP analysis.

12.2.1.1.1 Covariance/correlation data

Data in the form of a covariance matrix may also be input to the program by specifying DATA TYPE (1). These are considered as being the scalar products between vectors in a space. The implied (squared) distances are calculated directly from these scalar-products by means of the cosine rule. Since the operation of this rule requires that the length of the vectors must be known, the diagonal of the matrix must also be input (the diagonal elements, the variances, consist of the squared vector lengths).

This is not the case with a correlation matrix since the vectors are normalised to unit length, thus it is important to distinguish between input of correlation and covariance matrices. A correlation matrix may be input by specifying DATA TYPE (3), in which case the diagonal elements of the matrix should not be input.

12.2.1.2 Matrices of coordinates

The default option DATA TYPE (0) allows the user to input a matrix of coordinates for p points in r dimensions. This is again converted by the program to a set of (squared) distances before proceeding. The input matrix might be an actual matrix of coordinates or profile data for N subjects on p variables. If this is the case, since these are treated as coordinates, there should be good grounds for regarding the data as being at least interval level. It is for this reason that 'preference data' are not normally analysed by this model.

12.2.2 THE MODEL

As has been noted, the PARAMAP program operates on a matrix of (squared) distances in a high-dimensional space. The basic model seeks a representation of this information in a space of lower dimensionality (user-specified) with as much of the 'local' information as possible in the data preserved. This is intuitively similar to the technique common in geography of representing information about distances on the sphere of the globe as a flat, two-dimensional conformal map. On the map, the local distances are 'true' reflections of the spherical distances but as the distances involve increase, so does the amount of distortion.

This is achieved by defining an index of continuity (Carroll and Chang, 1964; Shepard and Carroll, 1966) as a measure of departure from perfect representation. This measure K (KAPPA) in effect assigns a heavy weighting factor to the small distances in the configuration. This factor is increased as iterations continue so that even small discrepancies in the small distances are progressively more heavily penalised.

PARAMAP thus makes use of a criterion of local monotonicity, producing a configuration in which the smaller distances are faithfully represented and large distances distorted - quite unlike the case of say, a MINISSA solution in which the global structure is highly reliable and the local structure relatively unreliable. The ability to project down relatively high-dimensional configurations into much lower dimensionality (at the cost of sacrificing the faithful reproduction of high distances) is one of the main advantages of PARAMAP, and can often be used for precisely this reason.

The KAPPA index is minimized when the function relating the data to solution is as smooth as possible. Thus the Shepard diagram in PARAMAP is at least as important as the solution configuration, and will normally have a characteristically "fan-like" shape: small input distances are represented by small output distances, but as input distances become longer the corresponding output distances will take on an increasingly wide range of values. (Alterations in the exponent values of KAPPA will affect this shape considerably).

12.2.2.1 The Algorithm

1. The data are normalised if appropriate and the matrix of squared inter-point distances is computed.

2. If one is not input by the user the program generates an initial configuration.

3. The index of continuity between data-derived distances (Step 1) and the solution distances is computed.
4. A number of tests is performed to determine whether the degree of fit is acceptable or whether a minimum has been reached. If so, then the configuration is output as solution.
5. If fit is unsatisfactory then the direction of movement for each point on each dimension is calculated as is the optimum amount of such movement.

6. The configuration is moved in accordance with (5) and the program returns to Step 3.

12.2.3 FURTHER FEATURES

12.2.3.1 The weighting factors

The generalised index of continuity, κ^* (KAPPA STAR) contains three factors A, B and C which control the weighting assigned to various elements in the formula. The basis of the index of continuity is the sum of the ratios of the data distances to the solution distances. This sum is normalised by the sum of the solution distances. Each of these elements is weighted by being raised to a specific power. These powers are the values A, B and C. A is the exponent associated with the data distances, B with the solution distances and C with the normalising factor. There are two constraints on the possible values of A, B and C. The first is that C must be negative, and the second that B + C - A should equal zero if similarity transformations are required, as will normally be the case. The default options allow for the values A(1), B(2), C(-1) as recommended by Shepard and Carroll (1966), which reduces the general index κ^* to the index κ (as used in PROFIT q.v.). Users may wish to vary these values. The crucial consideration would seem to be the ratio between the weights assigned to the data values and to the solution values (A and B respectively). In general, B should be greater than or equal to A.

12.2.3.2 The CRITERION parameter

At step 4 of the algorithm PARAMAP performs a number of tests to determine whether the iterative process should proceed. One of these is to decide whether the index of continuity has reached a minimum value.

This value is set by the user by means of the CRITERION parameter. The default value CRITERION (0) asks the program to try for a perfectly smooth functional relationship between data and solution. It is, of course, likely that the process will terminate before KAPPA reaches zero if a minimum is found. The user may specify non-negative values of CRITERION, reasonably between 0.05 and 0.1 in order to make exploratory analyses of a data set.

12.2.3.3 Normalisation

If a rectangular matrix is input, the user may choose to normalise the matrix before the distances are computed. There are three options. If the distances are to be calculated from the matrix without normalisation then NORMALISE(0), the default option is appropriate. If the rows of the matrix are to be normalised, then NORMALISE(1) should be specified in the PARAMETERS command. Alternatively, the column effects may be removed by specification of NORMALISE(2).

Normalisation has the effect of removing the influence of both the spread and absolute magnitude of the data scores on the resulting distances.

12.2.3.4 The initial configuration

The user may choose to input an initial configuration of points which represent a guess at the possible solution configuration. In this case a configuration containing the stimulus points in the required dimensionalities are input. Two points should be noted. First, a configuration must be input with stimuli as rows and dimensions as columns. Secondly, if solutions are to be obtained in more than one dimensionality then a configuration for each dimensionality should be input. These should be read under the READ CONFIG command. The configurations should follow each other without break. The lowest dimensionality should come first and an INPUT FORMAT specification, if the data are not in free format, should be suitable for reading one row of the longest matrix (i e. the highest dimensionality). Such a course may decrease the amount of time taken to reach a solution.

Otherwise (at step 2 of the algorithm) the program will generate a random configuration of points to provide the starting configuration. Different starting configurations should be tried if relatively high values of KAPPA occur. This is done by specifying in the PARAMETERS command different values for RANDOM, since the process is random only insofar as the values generated are taken from a rectangular distribution. Each "seed" will, however, generate the same configuration.

12.3. PARAMETERS

12.3.1 LIST OF PARAMETERS

Keyword	Default Value	Function
DATA TYPE	0	0: Input matrix is a rectangular matrix of stimulus coordinates. 1: Input matrix is lower-triangle covariance matrix with diagonal. 2: Input matrix is a lower triangle matrix of squared inter-point distances without diagonal. 3: Input matrix is lower triangle matrix of correlation coefficients without diagonal. 4: Input matrix is lower triangle matrix of inter-point distances without diagonal.
MATFORM	0	Relevant only when DATA TYPE(0) is specified. 0: The input matrix is saved stimuli (rows) by dimensions (columns). 1: The input matrix is saved

			dimensions(rows) by stimuli(columns).
NORMALISE	1	0:	No normalisation
		1:	The X matrix is normalised on the last iteration.
RANDOM	12345		Enter any odd five digit integer. Sets the random number generator seed value.
A	1		Small 'a' of the KAPPA formula.
B	2		Small 'b' of the KAPPA formula.
C	-1		Small 'c' of the KAPPA formula.
CRITERION	0		Sets the criterion value for the terminating value for KAPPA.

12.3.2 NOTES

1. What we refer to as stimuli in the list of parameters are the entities actually represented in the configuration, and it is the number of these entities which is given by N OF STIMULI.

2. The number of dimensions on which the stimuli are measured is given to the program by the N OF SUBJECTS command.

3. Program Limits

Maximum number of stimuli	= 100
Maximum number of subjects (data dimensions)	= 60
Maximum number of dimensions (solution dimensions)	= 5

12.3.3 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of PARAMAP the particular options are as follows.

12.3.3.1 PRINT options

Option	Form	Description
INITIAL	p x r	The coordinates at the initial configuration are listed.
FINAL	p x r	The coordinates of the stimuli in the solution configuration are listed.
DISTANCES	lower triangle	The squared distances in the solution are listed.
HISTORY		An iteration-by-iteration history of the algorithm is listed.

By default the initial and final configurations and the final value of KAPPA are listed.

12.3.3.2 PLOT options

Option	Description
INITIAL	The initial configuration is plotted. r(r-1)/2 two-way plots are produced.
FINAL	The solution configuration in the form of r(r-1)/2 plots is produced.
FUNCTIONS	r^2 plots of the functions required to translate the r dimensions at x into the r dimensions of Y.
SHEPARD	A plot of the initial distances against the fitted values is produced.

KAPPA A histogram showing the value of KAPPA at each iteration is produced.

By default only the FINAL configuration is plotted.

12.3.3.3 PUNCH options (to a secondary output file)

Option Description

SPSS The following are output in a fixed format
I = stimulus index
J = subject index
DATA = corresponding (squared) data distance
DISTANCE = corresponding (squared) solution distance
RESIDUAL = corresponding residual value

FINAL The coordinates of the stimuli in the final configuration are output in a fixed format.

KAPPA The values for KAPPA at each iteration are output.

By default, no secondary output is produced.

12.4. EXAMPLE

```
    RUN NAME          UNBENDING THE HORSESHOE
    TASK NAME         FROM USERS' GUIDE AND COXON & JONES 1980
    N OF SUBJECTS     2
    N OF STIMULI      16
    DIMENSIONS        1
    PARAMETERS        MATF(0)
    INPUT FORMAT      (4X, 2F8.5)
    READ MATRIX
         <data>
    COMPUTE
    FINISH
```

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APPENDIX :

PARAMAP is the only program in the scaling area to perform such scaling, although it is formally equivalent to conformal mapping procedures used in geography etc.

13. PINDIS (Procrustean INdividual DIfferences Scaling)

13.1. OVERVIEW

Concisely: PINDIS (Procrustean INdividual DIfferences Scaling) Is a hierarchy of six models which provides an internal analysis of a set of configurations by a Procrustean fitting model which uses a similarity transformation of the data.

DATA: 2-way 2mode data (configurations of p stimuli in r dimensions)
TRANSFORMATION: depends on model number. P0 (basic model) performs similarity transforms to put configurations into maximum conformity. Other models employ “impermissible” transforms, which do not preserve original relative distance information.
MODEL: P1 and P2 are weighted distance models (P2 with idiosyncratic rotation) akin to INDSCAL and IDIOSCAL;
P3 and P4 are vector models (with idiosyncratic origins)
P5 is a hybrid distance-vector model. (see below)

Alternatively, following the categorisation suggested by Carroll and Arabie (1979) the program may be described as follows:

Data: A set of configurations:
Three-way
Three-mode
Non-symmetric
Dyadic
Ratio level of measurement
Matrix conditional
Incomplete (missing dimensional co-ordinates)
One replication

Model:
P0: Similarity
P1: Dimensional weighting
P2: Dimensional weighting and rotation
P3: Perspective (vector)
P4: Perspective and translation
P5: Double weighted
Two spaces
Internal/External

13.1.1 ORIGIN, VERSIONS AND ACRONYMS

PINDIS was developed by Lingoes and Borg at the University of Michigan. A number of early versions of the program exist. The present program was adapted from the 1975 version which is documented in Borg (1977).

13.1.2 PINDIS IN BRIEF

PINDIS provides means of dealing with the question of individual differences. It takes as input a set of configurations obtained from previous scaling analyses. From these it derives a 'centroid configuration' which is an optimal fit to the input configurations by means of “permissible” (relative-distance preserving) operations on the input configurations. These operations are: differential rotation, reflection and re-scaling. .

13.1.3 THE RELATION OF PINDIS TO OTHER PROCEDURES IN NewMDSX

PINDIS differs from all other procedures in the NewMDSX library in accepting configurations as data. However, most of the models have affinities with other programs:

P0 Procrustean rotation is not related to any other NewMDSX program.

P1 and P2 are distance models.

P1 (Dimension weighting) is very similar to INDSCAL in permitting individual weighting of fixed dimensions.

The parallels are discussed in Borg and Lingoes (1978).

P2 (Rotated and weighted distance) is very similar to the Carroll and Chang's IDIOSCAL model in permitting individual rotation of the dimensions followed by differential weighting of the dimensions.

P3 and P4 are weighted vector models.

P5 is a double weighting (dimensional and vector weighting) model.

P3 to P5 do not have a parallel in any other program in NewMDSX.

13.2. DESCRIPTION

13.2.1 DATA

The PINDIS program takes as its input data a number of configurations. These will normally be the result of some previous scaling analysis, although any technique giving dimensional output is suitable. The number of points in each of the configurations should be the same although the dimensionalities of the spaces may differ.

The intuitively most apparent form of the data might be a three-way analysis where each configuration results from the scaling of a given individual's judgements of a set of stimuli.

The maximum number of dimensions in any one configuration is given in the DIMENSIONS statement, the number of configurations by N OF SUBJECTS. The number of points in the configuration is given on by N OF STIMULI and the data are read by the READ CONFIGS command. These may be input either stimuli (rows) by dimensions (columns) or vice versa (in which case MATFORM(1) should be specified in the PARAMETERS command). If the data are not in free format, an INPUT FORMAT specification should be provided to read the longest row of the configurations.

13.2.2 THE MODEL

PINDIS stands for Procrustean INdividual DIfferences Scaling, and consists of a set of six models for dealing with the question of how different configurations are to be related to each other. In psychological terms, the general assumption is that each subject is systematically distorting a common, shared structure. The configuration obtained from a given individual is thought of as being a systematic distortion of a "master" configuration, the 'group space', and the program seeks both to derive this 'group space' and to relate the given configuration to it. The program contains six models which define different modes of (successively more complex) distortions. It will be seen that it is quite possible that different subjects will be best fit by different models. The first main output of PINDIS is an estimate of this shared aggregate group space or centroid configuration as it is known in the program. This is normally generated by the program from the input configurations in the manner described below but it is possible to input a fixed reference configuration and then use PINDIS for an external analysis (see 13.2.3.1).

13.2.2.1 The basic model (P0): Similarity transformation (Unit weighting)

The basic "model" of the PINDIS is simple Procrustean fitting and depends on the fact that MDS solutions are unique up to translation, rotation and reflection and uniform stretching or shrinking rescaling of axes. This is simply to say that in a configuration from, say, MINISSA, the significant information is contained in the relative distances between the stimulus and, in particular:

1. that the position of the origin is arbitrary and may be moved (translated) without destroying any of the significant information in the solution. (This is not the case for factor analytic solutions (see 13.2.3)).

2. that the axes of the configuration are in an arbitrary, though possibly convenient, position and may be (rigidly) rotated without destroying the salient information in the solution.

3. that a configuration may be reflected without loss of information. Intuitively this means that a configuration may come out of an analysis "back-to-front". Geometrically reflection is merely a special case of rotation.

4. that the actual numbers assigned to the distances are not significant information but may be made uniformly bigger or smaller at will. Intuitively, this means that the actual configuration may be enlarged or reduced so long as this process is uniform.

These operations, translation, rotation (with which we include reflection) and rescaling (uniform stretching etc.) comprise a similarity transformation and are known in the model as the "permissible transformations" in that changing a configuration by any (or all) of them gives a configuration which contains neither more nor less information than the original in terms of relative distances.

The program's first step is to take each pair of configurations in turn and, by applying the permissible similarity transformations, move them into maximum conformity with each other. Having done this, the program has effectively eliminated any differences in the configurations due to the conventions of the program producing them and has left the substantive differences - the differences due to random error and differential cognition. The centroid configuration is formed simply by taking the average position of each point over all the configurations. The model at this stage implies that in reporting their perceptions, subjects make no systematic distortions to the group space (the centroid).

The communality of each configuration to the centroid is then calculated. This may be regarded as the proportion of variance (r^2) in that particular configuration which is explained by the centroid.

The higher order models allow that subjects may systematically distort this centroid configuration. It is the mode of distortion which differs in these models.

13.2.2.2 In dimensional weighting the mode of distortion is analogous to that of the INDSCAL model in that subjects, in arriving at their perceptual spaces, are thought of as applying differential weights to the dimensions of the group space (the centroid). Substantively this amounts to saying that subjects will attach greater salience to certain (fixed) aspects of the difference between stimuli than to others, or that they will be prone to make finer distinctions on some criteria over others.

The user may choose whether these differential weights are to be applied to the centroid obtained at P0 or whether this configuration is to be rotated to some optimal position before the weights are applied. The default option allows for this latter course and may be expected to result in substantively more interpretable solutions. If, however, the user wishes to fix the centroid after P0, or has input a hypothesis configuration with 'meaningful' axes, then ROTATE(0) should be specified in the PARAMETERS statement.

The communality of the centroid to each of the input matrices is then calculated. This and the similar values obtained from higher models should be compared to the value from P0 which is treated as the baseline from which the more complex models are assessed. Final choice of the preferred explanatory model is made on the basis of the increase in the fitting value (r^2) which takes into account the fact that at each stage the number of free parameters increases dramatically.

13.2.2.3 Dimensional salience with idiosyncratic orientation (P2)

In this model each subject is thought of as distorting the centroid by first rotating the axes of the configuration to his/her own preferred orientation and then applying differential weights to these new axes. (It should be noted that if ROTATE(0) has been specified then this solution will be identical to P1).

The substantive interpretation of the model is that subjects are not only affording differential salience to the same criteria but also using different criteria.

In models P1 and P2 the mode of distortion which took the centroid into the subject configurations was essentially a dimensional weighting. In models P3 and P4 the distortions are applied directly to the actual stimulus points, which are considered as vectors from the origin of the space.

13.2.2.4 Perspective model with fixed origin (vector weighting) (P3)

Let us remind ourselves that the aim of the PINDIS procedure is to get the points of the centroid configuration (the group space) as close as possible to each of the individual input configurations in turn. This model seeks to do this by differentially stretching or shrinking each stimulus vector drawn from the origin of the space. What does this mean? Essentially the process may be conceived of in this way. Take a subject configuration and plot it on top of the centroid so that the origin and axes coincide. Now draw a line to connect the origin with a particular stimulus point in the centroid configuration and produce it beyond both the point and the origin. The point on this line which is nearest to the corresponding point in the subject configuration is the point we are looking for.

The substantive justification for this model relies on the axes and origin of the space being interpretable/meaningful and asserts that the significant information in the configuration is the balance (actually the ratio) between the coordinates on the constituent axes. It is sometimes called the "unscrambling" model since a weight applied to a stimulus vector moves the position of that stimulus in the space.

13.2.2.5 The perspective model with idiosyncratic origin (P4)

Although the actual orientations of the axes of the configuration do not affect the direction of the stimulus vector, the position of the origin is crucial. The idiosyncratic vector model additionally allows the subjects to move the origin of the centroid space to an idiosyncratic position before the vector weighting operations are performed.

If the centroid configuration has a rational origin and it does not make sense to shift it about in this manner, then the user should specify TRANSLATE(0) in the PARAMETERS command (see also 13.2.3).

13.2.2.6 The double weighted (dimension and vector weighting) model (P5)

This model allows both dimensional and vector weighting simultaneously. Although the number of free parameters in this model is large, it has been found that the goodness-of-fit of this particular model is often surprisingly low. This may indicate that the geometrical processes which define it have little psychological rationale (it is largely within the psychological field that it has been tried) though other substantive applications may find one.

The double weighting solution may be suppressed by specifying SUPPRESS(1) in the PARAMETERS command.

13.2.2.7 Some general points

For each of the models the program calculates the communality between the centroid (or alternatively hypothesis configuration if one has been supplied) and each of the subject configurations. Choice of a particular model should be made by comparing this value for each subject for each model against the communality at PO. Some improvement should manifest itself as the number of free parameters increases. If a higher level model has virtually the same communality (for a given subject) as a lower one then obviously parsimony suggests that the lower one be preferred.

The number of parameters estimated in each model in finding a given subject configuration is a function of the dimensionality of the configuration (r) and the number of stimulus points (p).

P0 = 0	(simply permissible transformations)
P1 = r	(dimension weights)
P2 = r r (r(r-1)/2)	(dimension weights and pair-wise rotation certificate)
P3 = p	(stimulus vector weights)
P4 = p + r	(stimulus vector weights and r-dimensional origin)
P5 = p + (p + r)	(dimension weights, stimulus vector weights and origin).

The models thus form a semi-lattice:

```
(distance)          (vector)
    P2       P5        P4

    P1                 P3

             P0
        (similarity)
```

13.2.3 FURTHER FEATURES

13.2.3.1 External analysis

The user may wish to use the PINDIS program to effect an external analysis by inputting, as well as the subject configurations, a fixed hypothesis configuration, which may be an a priori arrangement of points or the result of a previous MDS or other dimensional analysis. This configuration is input to the program by means of the READ HYPOTHESIS command which is peculiar to PINDIS, if necessary with its own associated INPUT FORMAT specification. This configuration will form the centroid at PO and will be rotated, weighted, etc., in the other models and users are urged to pay particular attention to the values given to the ROTATE (see 13.2.2.2 and 13.2.2.3) TRANSLATE (see 13.2.2.5) and ORIGIN (see below) parameters to ensure that they do not violate the logic of the configuration.

13.2.3.2 The use of the ORIGIN parameter

We note at 13.2.2.4 the importance of the position of the origin of the space in the weighted vector models. One way of making substantive sense of vector weighting is by moving the origin to a substantively meaningful position rather than at an arbitrary centroid and considering each of the other points as directions of distinction from that point. Consider this hypothetical example. Suppose we were interested in the perceptions of political parties. We might take the configurations belonging to members of a particular party and place the origin of the space at the point representing that party. The distance to the other party points (the length of the stimulus vectors) is then proportional to the perceived difference between the party of affiliation and the others but the direction will also have significance in representing the mode of difference (say right vs. left, populist vs. elitist). It may very well be the case that there is virtual consensus over the modes of difference, i.e. the ways in which the parties differ but disagreement over how different they are. Some right wing Conservatives may, for instance, be very anxious to dissociate themselves from the UK Independence Party and while acknowledging the fact that the U.K.I.P. is more right-wing, will insist on the difference between the Front and the Tories being made as large as between, say, the Tories and the Labour party. Other members of the Conservative party, of a more moderate bent, might be less neurotic about admitting the similarity between the two. In this case, the weighted vector model provides a feasible model of the differences between the two groups. The user may use this option by specifying the number of the point to be regarded as the origin as the argument to the ORIGIN parameter.

TESTS OF SIGNIFICANCE

Langeheine (1980) has provided Tables of Significance for the PINDIS fit measures, based upon extensive simulation studies.

13.3. PARAMETERS

13.3.1 LIST OF PARAMETERS

Keyword	Default	Description
SUPPRESS	1	0: Double-weighted solution (P5) is performed. 1: Double-weighted solution (P5) is suppressed.
ROTATE	1	0: Idiosyncratic rotations of the centroid are not allowed, i.e. P2 is not performed. 1: Idiosyncratic rotations are allowed.
TRANSLATE	0	0: No translation of the origin allowed i.e. P4 is not performed. 1: Translation of origin to an idiosyncratic position is allowed.
ORIGIN	0	0: The origin is situated at the centroid of the space <any positive integer> gives the number of the point to be regarded as the origin.
MATFORM	0	0: The input configurations are input stimuli(rows) by dimensions(columns) 1: The input configurations are input dimensions(rows) by stimuli(columns)

13.3.2 NOTES

1. READ CONFIGS is obligatory in PINDIS.

2. READ MATRIX is not valid with PINDIS.

3. LABELS followed by a series of labels (<= 65 characters), each on a separate line, optionally identify the stimuli in the output. Labels should contain text characters only, without punctuation.

4. Maximum number of dimensions = 6
   Maximum number of stimuli = 50
   Maximum number of configurations = 50

13.3.3 PRINT PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. The particular options for PINDIS are as follows:

13.3.3.1 PRINT options

Option	Form	Description
CENTROID	p x r	The centroid configuration is listed at each phase.
SUBJECTS	N(p x r)	The subject matrices are listed at each phase.

Both of these are produced by default.

13.3.3.2 PLOT options

Option	Description
CENTROID	The centroid configuration is plotted at each phase.
SUBJECTS	The subject configurations at each phase are plotted.

Both configurations are plotted by default.

13.3.3.3 PUNCH options

Option	Description
CENTROID	The coordinates of the centroid configuration are output.

By default, no secondary output file is produced.

13.4. EXAMPLE

```
 RUN NAME              RUN OF TEST DATA FOR PINDIS
 PRINT DATA            YES
  NO OF SUBJECTS        5
 NO OF STIMULI         16
 DIMENSIONS            3
 COMMENT               FIVE CONFIGURATIONS ARE TO BE INPUT.
                       EACH HAS SIXTEEN POINTS IN THREE DIMENSIONS
 PLOT                  ALL
 COMMENT               ALL PARAMETERS WILL ASSUME DEFAULT VALUES
 READ HYPOTHESIS
    <the hypothesis (target) matrix follows here>
 READ CONFIGS
    -0.283    -0.899    -0.049
    -0.348    -0.827     0.099
     .....     .....     .....
    -0.930     0.400     0.020
    -0.870     0.500     0.190
COMPUTE
FINISH
```

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RELATION OF PINDIS TO OTHER PROGRAMS

Within NewMDSX, P1 is akin to INDSCAL.
MATCHALS (Commandeur 19XX) is similar to the PINDIS hierarchy.

15. PRINCOMP (Principal Components)

15.1 OVERVIEW

PRINCOMP expects as input a matrix of correlations or covariances. It is included here to allow comparison with the dimensions identified by non-metric MDS procedures for the same data. For convenience, input matrices may be in any of the formats used elsewhere in NewMDSX. An error is reported if the input matrix is not one of correlations or covariances, i.e. if, for any **i, j**, $(x_{ij})^2 > (x_{ii} . x_{jj})$.

15.2 DESCRIPTION

DATA: 2-way, 1-mode matrix of scalar products (covariances, correlations)
TRANSFORMATION: Linear
MODEL: Scalar-products

Principal components is a mathematical technique, with no underlying statistical model, which is frequently used to identify a limited number of orthogonal linear combinations of the original p variables

$$y_i = a_{i1} x_1 + a_{i2} x_2 + ... + a_{iq} x_q, \quad q \le p$$

that can be used to summarise the data, while losing as little information as possible. Technically, it simply produces an orthogonal rotation of the input matrix to its principal axes, or eigenvectors, arranged in diminishing order of size.

By default, PRINCOMP will list all **n** eigenvalues (latent roots) and principal components (eigenvectors) of a matrix of **n** variables, in descending order of their contribution to the total variance of the original matrix. The first principal component is therefore the linear combination which accounts for the largest possible proportion of the overall variance, often interpeted as a kind of general factor providing the greatest discrimination between the individual observed data values. This however is not always the one that is of greatest interest to the investigator, it is the second or subsequent components that give an indication of the structure of relationships between the variables.

Components are reported with the vectors normalized to their corresponding eigenvalues, rather than unity, so that they are analogous to factor loadings. When they arise from a correlation matrix, they may be interpreted as correlations between the components and the original variables.

In many sets of multivariate data the variables will be measured in different units and are standardised before analysis. This is equivalent to extracting the principal components as eigenvectors of the matrix of correlations, rather than of the covariance matrix. Note that the eigenvalues and principal components of these matrices are not generally the same, and that choosing to analyse a matrix of correlations is equivalent to deciding to consider all of the variables to be equally important.

The number of principal components to be listed may be restricted to the number given in in the DIMENSIONS statement. The size of the input matrix is given by N OF STIMULI and the matrix is read by the READ MATRIX command. The format of the input matrix is given by the parameter DATA TYPE in the PARAMETERS command. If an INPUT FORMAT specification is used, it should read the longest row of the type of matrix to be input. By default, however, free format input is assumed.

15.3 INPUT PARAMETERS

15.3.1 PARAMETERS

Keyword	Default	Description
DATA TYPE	1	1: Lower triangular matrix without diagonal 2: Lower triangular matrix with diagonal 3: Upper triangular matrix without diagonal 4: Upper triangular matrix with diagonal 5: Full symmetric matrix.

15.3.2 PLOT options (to main output file)

Option	Description
COMPONENTS	Plots the principal components. If a parameter is added, this specifies the number of normalized principal components to be plotted. (Plotting all components is liable to generate a rather large output file.)
ROOTS	Produces a 'scree plot' of the latent roots against the principal components.

NOTES

1. The READ MATRIX command is obligatory in PRINCOMP.
2. LABELS followed by a series of labels (<= 65 characters), each on a separate line, optionally identify the stimuli in the output. Labels should contain text characters only, without punctuation.
3. There are no PRINT options as such in PRINCOMP. By default, the eigenvalues (or latent roots) of the input matrix are listed in descending order, together with the corresponding eigenvectors, or principal components, and the proportions of the total variance accounted for by each.
4. No secondary output file is produced by PRINCOMP.
5. Program limit - 80 stimuli

15.4 EXAMPLE

```
RUN NAME   A CORRELATION MATRIX TO DEMONSTRATE PRINCOMP
N OF STIMULI    6
DIMENSIONS      6
PARAMETERS DATA TYPE(1)
READ MATRIX
0.54
0.34 0.65
0.37 0.65 0.84
0.36 0.59 0.67 0.80
0.62 0.49 0.43 0.42 0.55
PLOT  COMPONENTS(2) ROOTS
COMPUTE
FINISH
```

```
OUTPUT
.........
A CORRELATION MATRIX TO DEMONSTRATE PRINCOMP

EIGENVALUES
        1          2          3          4          5          6
     3.80526    0.99117    0.49642    0.30970    0.28669    0.11076


PRINCIPAL COMPONENTS NORMALIZED TO EIGENVALUES
           1          2          3          4          5          6
   1    -0.6434     0.6552    -0.2264     0.2943    -0.1311     0.0411
   2    -0.8256     0.0364    -0.4114    -0.3824    -0.0371    -0.0133
   3    -0.8439    -0.3519    -0.0913     0.1493     0.3306     0.1554
   4    -0.8774    -0.3691     0.0008     0.1723    -0.0528    -0.2479
   5    -0.8478    -0.2221     0.3217    -0.0528    -0.3262     0.1383
   6    -0.7134     0.5011     0.4050    -0.1486     0.2228    -0.0649

        % TOTAL VARIANCE
        63.4210    16.5194     8.2737     5.1617     4.7782     1.8460

........
```

References

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16. PROFIT (PROperty FITting)

16.1 OVERVIEW

Concisely: PROFIT (PROperty FITting) provides external analysis of a configuration by a set of properties (ratings or rankings in row-conditional format) by a scalar products (vector) model using either a linear or "smoothness" transformation of the data.
DATA: external mapping of 2-way 2-mode matrix of "properties" into user-provided configuration of the same points
TRANSFORMATION: Linear and/or continuity (kappa)
MODEL: Scalar-products or vector

According to the categories developed by Carroll and Arabie (1979) PROFIT may be described as:

Data:	Two-mode	Model:	Scalar-product
	Two-way		Two set of points
	Asymmetric		One space
	Dyadic		External
	Ordinal or Interval/Ratio		
	Row-conditional		
	Complete		

16.1.1 ORIGINS, VERSIONS AND ACRONYMS

PROFIT was developed by J.D. Carroll and J.J. Chang at Bell Laboratories and originally documented in Chang and Carroll (1968).

16.1.2 PROFIT IN BRIEF

PROFIT takes as input both a configuration of stimulus points and a set of rankings or ratings of the same set of stimuli. These rankings and ratings are usually estimates of different properties of the stimuli. The program locates each property as a vector through the configuration of points, so that it indicates the direction over the space in which the property is increasing. The fitting is accomplished by maximising the correlation between the original property values and the projection of the stimuli onto the vector. This correlation may be either linear or non-linear (continuity).

16.1.3 RELATION OF PROFIT TO OTHER PROCEDURES IN THE NewMDSX SERIES

1. PROFIT using the linear option is formally identical to Phase 4 (vector model) of the preference mapping program PREFMAP, also using the linear option. (Note that PREFMAP phase IV may also be used with a quasi-non-metric option, providing a form of ordinal property fitting).

2. An internal form of the point-vector model (i.e. where the input configuration is not fixed but is generated from the data) is available in MDPREF.

3. An option within PARAMAP allows a rectangular or row-conditional (two-way, two mode) array of data to be input for internal analysis using a continuity (kappa) transformation between the data and the solution. But only the stimuli are represented in the solution.

16.2. DESCRIPTION OF THE PROGRAM

16.2.1 DATA

There are two parts to the input data for PROFIT.

16.2.1.1 The configuration

The configuration consists of the coordinates for a set of objects (stimuli) on a number of dimensions. This may be an a priori configuration (Coxon, 1974) or one resulting from another multidimensional scaling analysis, or, indeed, from a factor analysis. The configuration is input to the program by means of the READ CONFIG Command, with its associated INPUT FORMAT specification, if used, and may be presented either stimuli (rows) by dimensions (columns) or dimensions (rows) by stimuli (columns). In this latter case the parameter MATFORM should be given the value 1. Since the configuration is not substantially altered by the PROFIT algorithm, analysis can only take place in a given dimensionality and attempts to specify more than one value in the DIMENSIONS command will cause an error.

16.2.1.2 The properties

Each of the "properties" which PROFIT will seek to represent as vectors in the configuration, is a set of values which distinguish the stimuli on a particular criterion. These may be physical values (as in the following example) or subjective evaluations of the stimuli on criteria other than that or those used to generate the original configuration. For instance, a simple use of the program might be to map into a MINISSA representation of the perceived similarities between a set of stimuli, information about the subjects' preferences of the same stimuli.

16.2.1.2.1 Input of properties

Each property consists of a set of values, one for each stimulus in the configuration. All properties must be in the same format and unless the data can be read in free format this is given by the INPUT FORMAT specification which precedes the READ MATRIX command which reads the properties. Each property is preceded, however, by a separate input statement containing a label, which is listed in the output.

16.2.1.3 Example

To illustrate the use of the PROFIT program we take the configuration reported by Wish (Wish et al, 1972). In their study individuals (subjects) gave ratings on a scale of the degree of similarity between pairs of nations (stimuli). The averaged ratings were used to obtain a four-dimensional MDS solution where a larger distance between a pair of points in this space indicates a greater dissimilarity between the nations concerned. After visual inspection of the plots the authors interpreted the dimensions as shown in figure la and lb.

We may wish to concentrate on the following properties of the nations concerned:

1) Gross National Product per Capita, 1965
2) Total Population, 1965
3) Population Growth Rate, Total Time Span (1950-1965)
4) Ethno-linguistic Fractionalization
5) Soviet Aid per Capita, 1954/5 - 1965
6) Total U.S. Economic and Military Aid per Capita (1958-1965)

These aggregate data were obtained under the direction of Taylor (Taylor et al, 1973) and the list could be expanded to contain as many of the 300 and more variables which they report for each country. The set up for two properties of this example is given in section 16.4.

16.2.2 THE MODEL

PROFIT seeks to represent the properties as vectors over the configuration of points. The analysis is external in as much as the configuration is regarded as being fixed: the stimulus points cannot be moved to make the fit of the vectors better (other than to centre the space round its centroid).

A fitted vector is regarded as indicating the direction in which the given property is increasing. This implies theoretically that preference increases continually, never reaching a maximum (corresponding to the economic concept of insatiability).

The property values are then correlated with the projections of the stimuli onto the vector in the following way. The vector is drawn through the origin of the space. (This is for convenience only. In fact, any vector parallel to this will give an identical result, since it is only the projections which are significant.) The perpendicular projections from the origin to the bases of the projections calculated. It is this final set of measurements (the distances from the origin to the projections) which is correlated with the original property values and it is this correlation which is the index of goodness-of-fit between data and solution. Two options are available to the user in calculating this correlation. The program will either calculate and maximise the (linear) product-moment correlation between data and solution or a (non-linear) "smoothness" or "continuity" measure (or, indeed, both). These are chosen by means of the REGRESSION parameter.

Despite its name, the non-linear procedure does not fit curves rather than straight lines into the space. Rather, the function which links the data (property values) to the solution (point projections) is not constrained to being linear and may instead be drawn from the wider class of non-linear functions. In PROFIT, the particular index of non-linear badness-of-fit is KAPPA, which ensures local monotonicity. This means that in the Shepard diagram the function plot might be upwardly monotone in the lower range and downwardly monotone in the upper range, since it is the variations between data values adjacent (or close) to each other which are crucial in calculating the index: Kappa maintains only the smoothness or continuity of the function between adjacent values (hence "local" monotonicity). In the algorithm this is done by giving adjacent (or close) data values a heavy weight. The user is given the option of varying this weight to give varying importance to different aspects of the data (see below).

16.2.2.1 The Algorithm

Since the linear and non-linear procedures differ from each other quite considerably, we discuss them here separately.

16.2.2.1.1 The linear procedure

1. The columns of the configuration are normalised.

2. The XMAT matrix is computed.

For each property in turn:

3. The direction cosines of the vectors are computed.

4. The projections of the points onto the vectors are computed.

5. The correlation between the projections and the property values is computed.

6. The cosines corresponding to the angles between each pair of vectors are computed.

7. The configuration and vector-ends are plotted using both normalised and original coordinates.

16.2.2.1.2 The non-linear procedure

1. The configuration is normalised.

For each property:

2. KAPPA and ZSQ measures of alienation and correlation respectively are computed.

3. The cosines of the angles between the vectors and the original axes are calculated.

4. The projections of the points onto the vectors are calculated.

When all properties have been thus treated:

5. The cosine of the angle between each pair of vectors is calculated.

6. The configuration of points and vectors is plotted in original and normalised co-ordinates.

16.2.3 FURTHER OPTIONS

16.2.3.1 Linear vs. non-linear regression

Because the results of non-linear analysis are more difficult to evaluate, it is often tempting to start with the more familiar linear regression. The linear procedure is however merely a special case of the non-linear and, since usually we do not possess prior information on the form of the relation expected between property values and stimulus projections, the more general non-linear analysis may be preferred as an exploratory technique.

The PROFIT program always reports the product-moment correlation coefficient. It is quite possible that a relatively low value for the non-linear continuity measure KAPPA, and a high value for the (linear) correlation coefficient will be found. This would indicate that the relation is indeed linear and PROFIT should then be run with the linear option in order to test this assumption and provide the information on the (linearly) best fitting property vector.

16.2.3.2 Non-linear measures of goodness-of-fit

In the case of linear property fitting, the product moment correlation is a suitable measure of goodness-of-fit between the data and the solution. In the non-linear case no such familiar index is available. Rather, an index KAPPA (κ), which is a badness-of-fit measure, is minimized. Intuitively this measure is minimized whenever the form of the function relating the data to the solution becomes smoother or more continuous locally, whatever its actual overall shape may be. Thus it may be considered as an index of 'local' monotonicity.

16.2.3.2.1 The use of the weight parameter

Carroll defined the general index of non-linear correlation Kappa (κ) between an independent variable p and a dependent x as:

$$\kappa = \frac{1}{S^2} \sum_{i \neq j} w_{ij} (x_i - x_j)^2$$

Where

$$w_{ij} = f (|p_i - p_j|)$$

and f is a monotone decreasing function,

and $$S^2 = \frac{1}{N} \sum_{i} (x_i - \bar{x})^2$$

In PROFIT the independent p corresponds to one property and the dependent x to the projections of the points on to the vector. PROFIT seeks to minimize κ.

The weighting function plays a crucial role in the definition of Kappa. This function can take on three different values and each value defines a different "flavour" of κ. The choice of flavour depends crucially on the characteristics of the property values.

16.2.3.2.1.1 When WEIGHT (0)

This is the general definition of non-linear correlation and no restrictions are placed on the data. Therefore, this index can always be applied to examine the extent to which the property values (data) and the projections of the stimulus points (solution) are related by a smooth or continuous function.

16.2.3.2.1.2 When WEIGHT (1)

In this case, it is assumed that the property values are equally spaced. So the level of measurement of the properties is in effect taken to be ordinal if the order is specified with equal intervals. To do this any equally spaced values may be chosen, such as 1, 2, 3,...N or 5, 10, 15,...5N.

There is no restriction on the characteristics of the stimulus configuration when using this option. This option limits the calculation of Kappa to adjacent points. In this case, κ becomes equivalent to Von Neumann's η (Eta, the ratio of the mean square successive difference) as defined in Von Neumann (1941). See below (16.2.3.2.2.2) for the use of BCO in conjunction with this option.

16.2.3.2.1.3 When WEIGHT (2)

If the property values tend to be highly clustered into two or more groups of values, then the PROFIT program can be used to determine whether this is also the case for the projections of the stimuli on the fitted vector. To do this we must choose the property values in such a way that it becomes possible to discriminate the clusters. Ordinal level of measurement is sufficient, provided the property values are equally spaced. By defining the maximum distance between two points which are to be taken as falling in the same grouping, the program then selects the clusters. This maximum distance is set using the BCO parameter (see 2.3.2.2.3 below).

The weight factor will now have the effect of restricting attention to property distances which are close to each other (in effect, in the same grouping) and ignoring values outside the BCO value. In this case, κ can be shown to be the equivalent of the "correlation ratio" (Carroll 1964, see also Nie et al, 1975).

16.2.3.2.2 The use of the BCO parameter

This parameter has a different use and meaning when used in conjunction with different WEIGHT options:

16.2.3.2.2.1 When WEIGHT = 0

In the general case a value of 0 for BCO (the default) will make the weighting function be undefined for equal property values. If there are equal property values and BCO(0) the program will terminate. Thus this option in effect assumes that there are no ties between the property values. If ties do occur among your property values then a small value of BCO (say .001) should be used. This will allow calculation of the weight factor even when the property values are equal. A large value for BCO has the effect of allowing Kappa to decrease indefinitely and is not recommended.

16.2.3.2.2.2 When WEIGHT (1)

When Von Neumann's η is approximated, then the value of the BCO parameter has a more simple explanation than in the previous case. Now BCO simply gives the size of the equal intervals. Note that if WEIGHT(1), which is the default value, then BCO(0) has no meaning and some other value must be specified.

16.2.3.2.2.3 When WEIGHT (2)

In this case the BCO parameter gives the maximum distance allowed between points in the hypothetical clusters described above in 2.3.2.1.3. Again in this case, the default value BCO (0) has no meaning, and must be over-ridden by some other value.

16.3. INPUT PARAMETERS

16.3.1 LIST OF PARAMETERS

Keyword	Default Value	Function
REGRESSION	1	1: Linear regression only will be performed. 2: Non-linear regression. 3: Both regressions will be performed (independently).
MATFORM	0	0: The input configuration is saved stimuli (rows) by dimensions (columns). 1: The input configuration is saved dimensions (rows) by stimuli (columns).
WEIGHT	0	(See Section 16.2.3.2). 0: Carroll's index of continuity. 1: Von Neumann's ratio of the mean square successive difference. 2: the "correlation ratio".
BCO	0	(See Section 16.2.3.2).

16.3.2 NOTES

1. # OF PROPERTIES may be used in PROFIT in place of # OF SUBJECTS.

2. READ CONFIG is obligatory.

3. LABELS followed by a series of labels (<= 65 characters), each on a separate line, optionally identify the stimuli in the output. Labels should contain text characters only, without punctuation.

4. Since the non-linear option involves calculation of large powers of the data values, exponent overflow may occur. In this case

the data values should be made smaller. This might be done by changing the format statement so as to divide the values by, say, 100.

5. PROGRAM LIMITS

Maximum dimensionality:	10
Maximum number of points:	60
Maximum number of properties:	20

16.3.3 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of PROFIT, the available options are as follows:

16.3.4.1 PRINT options

The PRINT DATA command will echo both the input stimulus configuration and the property values.

Keyword	Form	Description
INITIAL	p x r	The matrix of stimulus points as normalised by the program. This will differ in linear and non-linear approaches.
CORRELATIONS (Default)	1 x N	The following are listed: 1(a) the correlations for each property (linear regression). (b) the eigenroots associated with each vector (non-linear regression).
PROPERTIES		The following are listed:
	N x r	1. The direction cosines between each of the fitted vectors and each dimension in the normalised space.
	N x r	2. The direction cosines between each vector and each dimension of the original space.
	N x N	3. The cosines of the angles between the vectors.
RESIDUALS		A table of residuals is listed i.e. obtained distances - original distances.

16.3.4.2 PLOT OPTIONS

INITIAL	The stimulus configuration plotted in pairs of dimensions with both original and normalised co-ordinates marked (up to r(r-) 2 plots).
FINAL	Both stimulus points and property vectors plotted together original and normalised co-ordinates (up to r(r-1)2 plots).
SHEPARD	N plots of original property values against projections on fitted vectors giving the shape of the linking function.
RESIDUALS	Histogram of residual values.

By default only the first two dimensions of the joint space are plotted.

16.3.4.3 PUNCH options

Option	Description
SPSS	This command produces a file containing the following variables: I property

j stimulus
DATA original value on property i of stimulus j
FITTED projection on fitted vector
RESID difference between original and fitted values.

SOLUTION Two matrices are saved:
i) the matrix of stimulus points as normalised, and
ii) the matrix of direction cosines for the fitted vectors.

16.4. EXAMPLE

```
  RUN NAME             PROFIT TEST DATA
  N OF STIMULI         21
  N OF PROPERTIES      2
  DIMENSIONS           4
  PARAMETERS           REGRESSION(3), BCO(.OOl)
  COMMENT               * * * *
                       NOTICE THAT BOTH LINEAR AND NON-LINEAR OPTIONS
                       ARE TO BE USED AND THAT THE SMALL VALUE IS
                       GIVEN TO BCO BECAUSE THERE ARE TIES IN THE DATA
                       (SEE SECTION 2.3.2.2.1)
                       * * * *
 INPUT FORMAT          (4F4.3)
 COMMENT               * * * *
                       THE ABOVE FORMAT STATEMENT REFERS TO THE
                       CONFIGURATION TO FOLLOW ...
                       * * * *
 READ CONFIG
   <here follows the configuration in four dimensions>
 INPUT FORMAT          (11F5.0)
 COMMENT               * * * *
                       ... WHILE THE ABOVE FORMAT REFERS TO
                       THE PROPERTIES
                       * * * *
READ MATRIX
POPULATION GROWTH RATE 1950-1965
1.60 0.50 1.10 1.10 4.70 1.10 2.40 0.80 0.80 3.10 3.40
1.70 2.00 2.10 1.40 2.50 1.50 2.20 1.20 1.60 1.60
ETHNO-LINGUISTIC FRACTIONALISATION
505 325 026 261 199 015 877 099 436 071 305
694 886 764 657 044 118 038 754 028 666
PLOT                  SHEPARD
COMPUTE
FINISH
```

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APPENDIX : RELATION OF PROFIT TO OTHER PROGRAMS OUTSIDE THE NewMDSX SERIES

No programs outside the NewMDSX series (and the corresponding Bell Laboratories versions) implement a continuity or "smoothness" scaling transformation, and therefore no parallel programs exist for the non-linear version of PROFIT.

The linear version of PROFIT can be thought of as a linear multiple regression program: predicting property values from a linear combination of dimensional co-ordinates of the stimuli involved. Strictly speaking, any multiple regression program can therefore be used to implement linear PROFIT.

A number of MDS programs outside the NewMDSX series have the capability of external scaling with linear (metric) or ordinal (non-metric) transformation functions. (Guttman-Lingoes SSA-1; KYST; ALSCAL in SPSS) - but only for an ideal point (distance) model. However, none of these allow the possibility of using a vector (scalar products) model. Currently the only accessible equivalent of linear PROFIT occurs in the PRINCIPALS model in the Young - de Leeuw - Takane ALSCAL series.

17. TRISOSCAL (TRIadic Similarities Ordinal SCALing)

17.1. OVERVIEW

Concisely: TRISOSCAL (TRIadic Similarities Ordinal SCALing) provides internal analysis of:

DATA: a set of triadic (dis)similarity measures
TRANSFORMATION: using a local or global monotonicity transform
MODEL: Minkowski distance model

Alternatively, following the categorisation developed by Carroll and Arabie (1979) TRISOSCAL may be described as follows:

Data:	One-mode	Model:	Minkowski distance
	Polyadic (triadic)		One set of points
	Ordinal		One space
	Triad-conditional		Internal
	Incomplete		
	Replications allowed		

17.1.1 ORIGIN, VERSIONS AND ACRONYMS

The present program is a revised version of the TRISOSCAL program developed by M.J. Prentice at the University of Edinburgh, which was in turn developed as a generalisation of MINITRI, a program in E.E. Roskam's (University of Nijmegen) MINI series. The original Roskam MINITRI approach is included in the present version as an option (see below).

17.1.2 TRISOSCAL IN BRIEF

In a triadic comparison exercise, subjects are presented with sets of 3 objects drawn from a larger collection and asked to judge the relative (dis)similarity of the objects involved. Two alternative methods of triadic data collection are catered for in this program (which is unique to the NewMDSX series). Given a triad of objects (A,B,C), the subject may be asked:

1. which pair is the most dis/similar
2. which pair is the most dis/similar, and which pair is the least dis/similar.

The TRISOSCAL program
seeks to represent these dissimilarities as distances between the objects, considered as points in a space of minimum dimensionality. The data are considered to be at the ordinal level.

17.2. DESCRIPTION

17.2.1 DATA

The fourth quadrant of Coombs's (1964) fourfold typology of data concerns distance information on pairs of pairs. The most obvious method of obtaining directly such data is the so-called method of tetrads in which the subject is presented with all possible combinations of four objects and asked: "which is the most similar/dissimilar pair ?" This method has the disadvantage of requiring a very large number of judgements even on fairly small sets of stimuli. The method of triads while eliciting information on pairs of objects in systematic relation to other objects in the set reduces considerably the number of judgements required of a subject.

17.2.1.1 The method of triads

The method of triads consists in presenting the subject with all possible triads (but see 2.3.3). (S)He is asked to consider the three possible pairs formed by the triad ABC, namely (A,B), (B,C) and (A,C) and to state either "which is the most similar pair of these three ?"

or

"which is the most similar pair and which the
least similar pair of these three ?"

The first method yields only a partial ordering on each triad in that we know only that, for any triad A, B, C, that (A,B) is more similar than (B,C) and than (A,C). The latter case, by contrast, produces a strict ordering since if the subject chooses (A,B) as the most similar and (B,C) as the least similar, then the order of the three pairs in terms of similarity is necessarily (A,B) (A,C) (B,C).

If the first method has been used in obtaining the data then the user should specify ORDER(0)in the PARAMETERS command. If the method producing a strict ordering has been used then ORDER(1) should be specified.

13.2.1.1.1 Presentation of the data

The number of objects to be positioned as points in the space is specified in the N OF STIMULI command, the number of actual triads is presented to the program in the N OF TRIADS specification.

Each object is labelled by a number and thus each triad consists of three numbers, say (5, 2, 4) which are interpreted in the following way.

17.2.1.1.1.1 When ORDER (0)

The pair which is chosen as the most similar is designated by the first pair of numbers of the three. Thus in our example the pair (5,2) is that chosen.

If the subject has been asked which pair is the most dissimilar then the pair chosen should again be the pair defined by the first two numbers, but in this case the parameter DATA TYPE should be given the value 1 in the PARAMETERS command.

17.2.1.1.1.2 When ORDER (1)

When the subject has been asked to choose both the most similar and the least similar pair, then the triad is interpreted in the following way.

The first pair of numbers defines the pair chosen as the most similar. The pair consisting of the first and last number is that chosen as the least similar. The pair consisting of the second and third numbers is thus the "middle" pair. Thus for the triad 5,2,4 the pair (5,2) is the most similar, the pair (2,4) the next most similar and the pair (5,4) the least similar.

By specifying DATA TYPE (1) in the PARAMETERS command the data are interpreted as dissimilarities rather than similarities. The default DATA TYPE (0) regards the data as similarities as described above.

17.2.2 THE MODEL

Roskam (1970) has shown that the common procedure of aggregating triadic data by a simple vote-count procedure (counting the number of times that pair *jk* is judged more similar than pair *lm*) not only obscures but can positively distort the order information in the data, especially when not all triads are presented. Rather than the simple vote-count, he suggests that each point *j* be assigned a sub-matrix, whose row- and column-elements correspond to pairs in which *j* occurs. Within these it is possible to use the vote-count method. Each of these matrices is represented as a row of a new rectangular asymmetric matrix whose row-elements correspond to the objects and whose column-elements, although labelled as objects, refer to the pair formed by the column-element with the particular row-element.

This matrix forms the basis of the analysis but is treated in two different ways by two differing STRESS approaches (v.i.). The "local" approach treats the matrix as row-conditional while the "global" approach does not enforce this conditionality.

17.2.2.1 The Algorithm

1. An initial configuration is generated or one is supplied by the user (see 17.2.3.2).

2. The distances in the configuration are calculated according to the Minkowski metric chosen (see 17.2.3.1).

3. The fitting values are calculated (see 17.2.2.2).

4. STRESS is calculated according to the option chosen (see 17.2.2.2).
5. A number of tests are performed: e.g.
   Has STRESS reached an acceptable minimum ?
   Has a specified number of iterations been performed ?
   Has the improvement in STRESS over the last few iterations been too small to warrant continuing ?

   If the answer to any of these is YES then the current configuration is output as solution. If not, then:-

6. The direction in which each point should move in order that STRESS should decrease as well as the estimated optimum size of that movement are calculated.

7. The configuration is moved in accordance with 6 and the program returns to stage 2 above.

17.2.2.2 Fitting-values and STRESS

At each iteration a set of fitting values is calculated which are constrained to being in the same order as the dissimilarities implied in the data. These fitting values are used to calculate the value of STRESS which is an index of how well the particular configuration matches the data. Two methods are available within TRISOSCAL for making this calculation - Roskam's "local" approach and Prentice's "global" approach.

17.2.2.2.1 The "Local" approach

This is the approach used exclusively in the original Roskam MINITRI program. Fitting values are assigned to pairs of points (stimuli) so that the order of the fitting-values matches the order of dissimilarities within each triad. Each inversion of that order will lead to an increase in the value of STRESS. In this method no account is taken of inversions of order occurring between triads. Consequently, the same datum (pair) can be fitted by different fitting values in different triads.

17.2.2.2.2 The "Global" approach

Consider the following two triads: (ABC) and (BCD). In the "local" approach the program is free to assign to the one pair (B,C) which occurs in both triads two distinct fitting values without affecting the value of STRESS. The "global" approach forces the program to assign the same fitting value. This has the effect of requiring that the order of fitting values be kept across the whole set of stimuli. This is the option of choice when the data refer to one individual’s set of triadic data. This option is chosen by specifying STRESS(1) in the PARAMETERS command.

Since the "global" approach obviously imposes far greater constraints on the solution than the "local" approach, the values of STRESS obtained will be considerably higher. The "local" procedure ignores transitivity between triads and thus it is often advisable to use this option if the data have been collected from a large number of subjects.

Examples of the use of both options are found in Coxon & Jones (1979), and where data from single individuals are scaled separately, it is often useful to use PINDIS (P0, P1) to combine the configurations

17.2.3 FURTHER FEATURES

17.2.3.1 Distances in the configuration

The user may choose the way in which the distance between the points in the configuration is measured by means of the MINKOWSKI parameter. The default value 2 provides for the ordinary Euclidean metric where the distances between two points will be the length of the line joining them. The user may specify any value for the parameter. Commonly used values, however, include 1, the so-called 'city-block' or 'taxi-cab' metric where the distance between the two points is the sum of the differences between their co-ordinates on the axes of the space, and infinity (in TRISOSCAL approximated by a large number (>25)) the so-called 'dominance' metric when the largest difference on any one axis will eventually come to dominate all others. (Users are warned that high MINKOWSKI values are liable to produce program failure due to numerical overflow).

17.2.3.2 The initial configuration

It is not possible to generate an initial configuration directly from the triadic data. However, as a vote count matrix is formed (section 17.2.2) this is used to generate an initial configuration in the same way as the Guttman-Lingoes-Roskam MINI programs. This configuration uses only the ordinal properties of the vote count matrix and has certain desirable properties such as avoiding local minima.

If the user wishes to supply an initial configuration then this is input via the READ CONFIG command and, if the data are not in free format, an associated INPUT FORMAT specification. The configuration must be in the maximum dimensionality to be used in the solution. The parameter MATFORM is used to specify how the input configuration is entered and is detailed in section 17.3.1.

17.2.3.3 Balanced incomplete block designs

Even with the method of triads the number of judgements required of subjects, increasing with the cube of the number of stimuli, rapidly becomes unmanageable. Balanced incomplete block designs are designs which reduce this number, while ensuring that certain desirable conditions (such as ensuring that every possible triad is presented at least once) are met. These are described in Burton and Nerlove (1976).

17.3. INPUT PARAMETERS

17.3.1 LIST OF PARAMETERS

Keyword	Default Value	Function
DATA TYPE	0	0: Input data are similarities 1: Input data are dissimilarities.
MINKOWSKI	2.0	(Any positive number) sets the Minkowski parameter for determination of distances in the configuration.

ORDER	0	0: Partial order is input 1: Pull order is input (section 17.2.1)
STRESS	0	0: STRESS calculated using "local" approach. 1: STRESS calculated using "global" approach (see 17.2.2.2).

17.3.2 NOTES

1. The N OF TRIADS statement, having the same form as N OF STIMULI, is mandatory in TRISOSCAL.

2. N OF TRIADS may be replaced by N OF SUBJECTS.

3. Program Limits:

Maximum number of stimuli allowed by the program is	50
Maximum number of triads allowed by the program is	3333
Maximum number of dimensions =	8

17.3.3 PRINT, PLOT AND PUNCH OPTIONS

The general format for PRINTing, PLOTting and PUNCHing output is described in the Overview. In the case of TRISOSCAL, the available options are as follows:

17.3.3.1 PRINT options

Option	Form	Description
INITIAL	p x r	The co-ordinates of the points in the initial configuration are listed.
FINAL	p x r	The solution matrix, the co-ordinates of the stimulus points in the final configuration are listed.
DISTANCES	p x p (lower triangle only)	The matrix of inter-point distances in the final configuration is listed.
FITTING	p x p (lower triangle only)	The matrix of fitting values is listed.
RESIDUALS	p x p (lower triangle only)	The matrix of residuals (distances-fitting values) is listed.
HISTORY		A detailed history of the iterative process is listed.
COUNT	p x p (lower triangle only)	The vote-count matrix as derived from the triadic comparisons is listed.
GRADIENT	p x r	The matrix at gradients as applied to the final configuration is listed.

By default only the final configuration is listed.

17.3.3.2 PLOT options

Option	Description
INITIAL	The initial configuration is plotted as r(r-1)/2 two-way plots.
FINAL	The solution is plotted as r(r-1)/2 two-way plots.
SHEPARD	The Shepard diagram of data against distances is plotted.

POINT — A histogram of the contribution to STRESS of each point is plotted.

RESIDUALS — A histogram of residual values is produced.

STRESS — A histogram of the STRESS values at each iteration is produced.

By default only the Shepard diagram and the FINAL configuration are plotted.

17.3.3.3 PUNCH options (to an optional secondary data file)

Option — Description

FINAL — The solution configuration is output, indexed in a fixed format.

SPSS — The following are output in a fixed format:
I = row index
J = column index
VOTE = entry in vote-count matrix
Corresponding to I,J
DIST = the corresponding distance
FITTING = the corresponding fitting value
RESID = the corresponding residual value

STRESS — An iteration by iteration history of STRESS values is saved in a fixed format.

17.4. EXAMPLE

```
   RUN NAME           SOME DATA FOR TRISOSCAL
   N OF STIMULI       10
   N OF TRIADS        120
   DIMENSIONS         2 TO 3
   PARAMETERS         MINKOW(1), ORDER(1), STRESS(1)
   READ MATRIX
     <data follow here>
   PRINT               COUNT
   PLOT                SHEPARD, POINT(3)
   COMPUTE
   FINISH
```

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APPENDIX :

There are no other programs widely available for the analysis of triadic data.

18. WOMBATS: Work Out Measures Before Attempting to Scale

18.1 Overview

Concisely: WOMBATS (Work Out Measures Before Attempting To Scale), does just what its acronym says and computes from a rectangular data matrix one or more (dis)similarity measures suitable for input to other NewMDSX procedures.

18.1.1 WOMBATS in brief

The WOMBATS program is in effect a utility which takes as input a rectangular matrix either of raw data, and computes a measure of (dis)similarity between each pair of variables in the matrix. These measures are output in a format suitable for input either to other NewMDSX procedures or to other programs. This output format is chosen by the user.

18.2. DESCRIPTION OF THE PROGRAM

The following section describes briefly those aspects of the program pertinent to its use. The measures calculated in WOMBATS are those detailed in chapter 2 of `The User's Guide' (Coxon 1982). For a fuller discussion, see that reference.

Section 2.1 describes the type of data suitable for input, and its presentation to the program and section 2.2 the range of measures available. Section 2.3 describes further options including those for outputting the results.

18.2.1 Data

The basic form of input data for the WOMBATS program is a rectangular matrix in which the rows represent cases (or subjects) and the columns, variables (or stimuli). This may be a matrix of 'raw' data as collected by the user or exported from EXCEL, SPSS or a similar program.

The number of rows in the matrix is specified by the user in the N OF CASES command or, (alternatively, in N OF SUBJECTS). The number of columns fields is given by either N OF VARIABLES or N OF STIMULI. (In these commands 'N' may of course be replaced by either 'NO' or '#'.) The data are read by the program when it encounters a READ MATRIX command, and the INPUT FORMAT specification, if used, should describe one row of the data matrix. Otherwise, data values are be entered in free format, separated by spaces.

If the data to be input are for some reason in a matrix where the rows represent variables and the columns cases, then the user should specify MATFORM(O) in the PARAMETERS command.

The chosen measures are calculated between the entities designated as variables (so-called R-analysis). This will be the case whatever value is taken by the parameter MATFORM. If the user wishes measures to be calculated between cases rather than between variables (Q-analysis), see section 2.3.1 below.

N.B. The program expects data to be input as real numbers. The INPUT FORMAT statement, if used, must therefore be specified to read F - type numbers, even if the numbers do not contain a decimal point.

18.2.1.1 Levels of Measurement

The user must specify, for each of the variables in the analysis, the level of measurement at which it is assumed to be. Five levels are recognised by the program. The recognised levels are ratio, interval, ordinal, nominal and dichotomous. If a particular variable is not explicitly assigned to a particular level by the user, then the program assigns it by default to the ordinal level of measurement.

Each of the measures in the program assumes that the variables on which it is operating have the properties of a particular level of measurement. If an attempt is made to compute a measure which assumes a level of measurement higher than that at which the variables have been declared to lie, the program will fail with an error message. No restriction is placed, obviously, on the attempt to calculate measures which assume levels lower than those declared.

The user signals the measurement level of the variables to the program by means of the LEVELS command, peculiar to the WOMBATS program. This consists of the command LEVELS, and one or more of the keywords RATIO, INTERVAL, NOMINAL, DICHOTOMOUS or ORDINAL. (Obviously, since the program defaults to ordinal, there is no need actually to specify variables associated with this last keyword). In parentheses following each keyword used are listed the variables which are to be assumed to be at that level of measurement. In these parentheses, ALL and TO are recognized. The following are valid examples of a LEVELS declaration.

```
      LEVELS            INTERVAL (1, 2, 5, 7,), NOMINAL (3, 4, 6, 8)
      LEVELS            RATIO (ALL)
      LEVELS            NOMINAL (1 TO 4), INTERVAL (7 TO 11)
```

In the last example, variables 5 and 6 are presumed by default to be at the ordinal level.

18.2.1.2 Missing Data

Variables that include missing data are a problem. The user may specify, for each variable in which there are missing data, one code which the program will read as specifying a missing datum. Users will note however that an attempt to calculate certain measures between variables will fail if missing data are present. The measures for which this is the case are indicated in the discussion of the available measures in section 18.2.2.1.

The user signals the occurrence of missing data by means of the MISSING statement. This consists of the command MISSING followed by the value(s) to be regarded as signifying missing data. In parentheses following each missing data value is a list of the variables for which that value represents a missing datum. In these parentheses the forms ALL and TO are recognised. The following are valid examples of a MISSING declaration.

```
      MISSING           -9.(1, 2, 7, 9),  99.(3, 4, 6, 8)
      MISSING           0. (ALL)
      MISSING           .1(1 TO 7), -.1(8 TO 16)
```

18.2.2 ANALYSIS

The aim of the WOMBATS program is to calculate for each pair of variables in the analysis a measure of the (dis)similarity between them. Having described the data to the program, the user must then choose the measure to be calculated. WOMBATS currently offers 26 different measures.

The required measures are chosen by means of the MEASURES command. This contains the keyword MEASURES followed by one only of the keywords referring to the available measures described below. Only one measure is computed in each TASK of the run. If more than one measure is required on the same set of data, then a separate TASK NAME is necessary.

18.2.2.1 Available measures

It is convenient to consider the available measures in WOMBATS under their respective assumed levels of measurement.

18.2.2.1.1 Dichotomous measures

Sixteen measures of agreement between dichotomous variables are included in WOMBATS. These correspond to those described in `The User's Guide to MDS' pp.24-27. Missing data are allowed in all these measures.

In this section, the following notation will be crucial. Consider two dichotomous variables which we will assume to measure whether the objects under consideration do or do not possess a particular attribute. The co-occurrence(or frequency) matrix of these two variables looks as follows.

		Variable 1	
		1/Yes	0/No
Variable 2	1/Yes	a	b
	0/No	c	d

The cell `a' is the number of times that the attributes 1 and 2 co-occur, `b', the number of times attribute 2 is present when attribute 1 is not, `c' is the number of times attribute 1 is present and 2 is not and `d' is the number of objects possessing neither attribute 1 nor attribute 2. All the measures of agreement to be considered in this section result from the combination of these quantities in some way.

The measures available for the comparison of dichotomous variables are denoted by the `keywords' D1, D2, ..., D16 and it is these `keywords' that appear in the MEASURES command

For example, the command

```
      MEASURES                D15
```

will select Yule's Q as the measure to be calculated

Before choosing a dichotomous measure, users should consider:

- whether they wish "co-absences" (cell d) to feature in the assessment of similarity, and
- whether they wish the measure to have Euclidean properties. Gower and Legendre(1986) prove that if a similarity measure has non-negative values and the self-similarity s_{ii} is 1, then the dissimilarity matrix with entries $\delta_{ij} = \sqrt{(1-s_{ij})}$ is Euclidean.

Note that any similarity measure can be converted into a dissimilarity measure by a related transformation:

$\delta_{ij} = (1-s_{ij})$ if the similarity measure takes values between 0 and 1,

or $\delta_{ij} = (\max-s_{ij})$ where max is the value of the greatest similarity.

D1 and D2 are undoubtedly the simplest and most commonly-used of these measures.

Each dichotomous measure is now considered:

Command MEASURES D1
Type Similarity measure
Range low = 0, high = 1

Name Jaccard's coefficient

Formula $\frac{a}{(a+b+c)}$

Description Excludes `d'. Represents the probability of a pair of objects exhibiting both of a pair of attributes when only those objects exhibiting one or other are considered. It is possible that a division by zero may occur in the calculation of this measure.

Command MEASURES D2
Type Similarity measure
Range low = 0, high = 1
Formula

$$\frac{a}{(a+b+c+d)}$$

Name Russell and Rao's measure

Description: Represents the probability of a pair of objects in a pre-selected set exhibiting both of a pair of attributes.

Command MEASURES D3
Type Similarity measure
Range low = 0, high = 1
Name Sokal's measure

$$\frac{(a + d)}{(a + b + c = d)}$$

Formula

Description Includes `d' in numerator and denominator. Represents the probability of a matching of two attributes.

Command MEASURES D4

Type Similarity measure

Range low = 0, high = 1

Formula

$$\frac{2a}{(2a+b+c)}$$

Name Dice's measure

Description Gives the positive matches `a' twice as much importance as anything else. Excludes entirely the mismatches. It is thus possible that a division by zero may occur in the calculation of this measure.

Command MEASURES D5

Type Similarity measure

Range low = 0, high = 1

Formula

$$\frac{2(a+d)}{(2(a+d)+b+c)}$$

Name no name

Description Includes `d' in both numerator and denominator. The matches (a and d) are given twice as much weight as the mismatches.

Command MEASURES D6

Type Similarity measure

Range low = 0, high = 1

Formula

$$\frac{a}{(a+2(b+c)}$$

Name no name

Description Excludes `d' entirely. The matches (b and c) are accorded twice as much weight as the matches. It is possible that a division by zero may occur in the calculation of this measure.

Command MEASURES D7

Type Similarity measure

Range low = 0, high = 1

Name Rogers and Tanimoto's measure

$$\frac{(a+d)}{(a+d+2(b+c)}$$

Formula

Description Includes `d' in numerator and denominator. The mismatches (b and c) are accorded twice as much weight as the matches.

Command	MEASURES	D8
Type	Similarity measure	
Range	low = 0, high = a + b + c + c + d - 1	
Name	Kulczynski's measure	

$$\frac{a}{b+c}$$

Formula

Description Excludes `d' entirely. This measure is the simple ratio of the positive matches (a) to the mismatches (cf. D9). it is possible that a division by zero could occur in the calculation of this measure and an undefined statistic occur. The maximum value otherwise is as stated.

Command MEASURES D9
Type Similarity measure (Sokal & Sneath)
Range low = 0, high = a + b + c + d - 1
Formula

$$\frac{(a+d)}{(b+c)}$$

Name no name
Description This measure is the simple ratio of all matches (positive and negative) to the mismatches (cf D8). The statistic may be undefined, due to a zero divisor. The maximum finite value is as stated.

Command MEASURES D10
Type Similarity measure
Range low = 0, high = 1
Name Kulczynski's measure

$$\frac{1}{2}(\frac{a}{a+c}+\frac{a}{a+b})$$

Formula
Description Excludes `d' entirely. This measure is a weighted average of the matches to one or other of the mismatches. This statistic may be undefined.

Command MEASURES D11
Type Similarity measure
Range low = 0, high = 1
Formula

$$\frac{1}{4}(\frac{a}{a+c}+\frac{a}{a+b}+\frac{d}{b+d}+\frac{d}{c+d})$$

Name no name
Description Includes `d' in numerator and denominator. This is the analogue of D10 with mismatches included.

Command MEASURES D12
Type Similarity measure
Range low = 0, high = 1
Formula

$$\frac{a}{\sqrt{\langle (a+c)(a+b) \rangle}}$$

Name Ochiai's measure
Description Excludes `d' from numerator. It uses the geometric mean of the marginals as a denominator. This statistic may have a zero divisor.

Command MEASURES D13
Type Similarity measure
Range low = 0, high = 1
Formula

$$\frac{ad}{\sqrt{\langle (a+c)(a+b)(b+d)(c+d)\rangle}}$$

Name no name
Description Includes `d' in numerator and denominator. It uses the geometric mean of the marginals as a denominator and will return a value of 0 iff either a or d is empty.

Command MEASURES D14
Type Similarity measure
Range low = -1, high = +1
Formula

$$\frac{(a+d)-(b+c)}{(a+b+c+d)}$$

Name Hamann's coefficient
Description Simply the difference between the matches and the mismatches as a proportion of the total number of entries. A value of 0 indicates an equal number of matches to mismatches. Some thought should be given to the interpretation of any negative coefficients before scaling the results.

Command MEASURES D15
Type Similarity measure
Range low = -1, high = +1
Formula

$$\frac{(ad)-(bc)}{(ad+bc)}$$

Name Yule's Q
Description This is the original measure of dichotomous agreement, designed to be analogous to the product-moment correlation. A value of 0 indicates statistical independence. Some thought should be given to the interpretation of any negative coefficients before scaling the results. This statistic may be undefined.

Command MEASURES D16
Type Similarity measure
Range low = -1, high = +1
Formula

$$\frac{(ad-bc)}{\sqrt{\langle (a+c)(a+b)(b+d)(c+d)\rangle}}$$

Name Pearson's Phi

Description

A value of 0 indicates statistical independence. Some thought should be given to the interpretation of any negative coefficients before scaling the results. The statistic may be undefined if any one cell is empty.

18.2.2.1.2 Nominal measures

Five measures are available in WOMBATS for the measurement of nominal agreement between variables. Four of these are based on the familiar chi-square statistic. The other is the Index of Dissimilarity.

18.2.2.1.2.1 Chi-square based measures

The following procedure is used to evaluate the chi-square statistic that forms the basis of four of the available measures.

Consider two variables x and y. We form the table whose row elements are the values taken by (or the categories of) the variable x and whose column elements are the values (categories) taken by variable y. (Obviously, since this is a nominal measure, these values have no numerical significance). The entries of this table are the number of cases which take on particular combinations of values of x and y i.e. the number of cases that fall into the particular combinations of categories.

The value of the chi-square statistic is calculated by comparing the actual distribution of these values in the cells of the table to that distribution which would be expected by chance (statistical independence occurs when $p(i,j) = p(i) \times p(j)$) . Thus, the higher the value of the statistic, the more the actual distribution diverges from the chance or expected one (0).

In the case of there being missing data in the original matrix, then the whole row or column corresponding to that value is deleted. Caution should be exercised if there are many missing data and particularly if these are unequally distributed around the variables since the value of the statistic is dependent on the number of values it considers and strictly speaking chi-square measures based on largely different numbers of cases are not comparable.

The other measures in this section seek to overcome the dependence of chi-square on the number of cases by norming it. The norming factor differs for each statistic.

The following notation will be used in discussing nominal measures:

N	will indicate the number of cases
r	will stand for the number of rows in the matrix i.e. the number of categories (values) taken by variable x and
c	will stand for the number of columns i.e. the number of categories in variable y.

Name	Chi - square
Command	MEASURES CHISQUARE
Type	Similarity measure
Range	low = 0, high = N x min(r,c)
Comment	A value of 0 indicates statistical independence. The maximum value is dependent on the value of N.

Name	Phi
Command	MEASURES PHI
Type	similarity measure
Range	low = 0, high = ≤(min(r,c)-1)
Comment	The phi coefficient is chi-square normed to be independent of N. Reaches a maximum for 2 x 2 tables in which case it reduces to the product-moment correlation.

It may, however, exceed 1 when the minimum of r and c is greater than 2.

Name	Cramer's V
Command	MEASURES CRAMER
Type	similarity measure
Range	low = 0, high = 1
Comment	Cramer's coefficient is chi-square normed to be independent of N and of the number of r and c. Reaches a maximum for non-square tables.

Name	Pearson's Contingency coefficient C
Command	MEASURES PEARSON
Type	similarity measure
Range	low = 0, high = 1
Comment	Pearson's coefficient is chi-square normed to be independent of N, originally developed as a measure for contingency tables. Cannot reach its maximum of 1 for non-square tables.

18.2.2.1.2.2 The index of dissimilarity

The remaining statistic in this section is the index of dissimilarity. In the case of the chi-square measures, the implicit comparison is between the actual (bi-variate) distribution and the expected (chance) one. In the case of the index it is two (univariate) distributions that are compared.

Consider again the table that is formed by cross-tabulating the values of variable x and those of variable y. If the two variables had identical distributions then all the off-diagonal cells would be empty. The index of dissimilarity is simply the proportion of cases that appear in these off-diagonal cells and may be thought of as the proportion of changes needed to change the one distribution into the other. The index does not require equal numbers of values in the variables.

Name	Index of dissimilarity
Command	MEASURES ID
Type	dissimilarity
Range	low = 0, high = 100

18.2.2.1.2 Ordinal level measures

At present, there are three measures of ordinal agreement in WOMBATS, all related to the basic tau (τ) measure of Kendall (19..). τ_b, τ_c and Goodman and Kruskal's gamma (γ). There are two important distinctions in considering these measures. First, we need to know if they measure weak or strong monotonic agreement between the variables and secondly how they treat tied values in them. This second distinction can be crucial since much ordinal level data, being composed of a relatively small number of categories, will contain a large proportion of tied data values.

Consider a two-way table between ordinal variables x and y. For any pair of individuals ***i,j*** , one of the following five conditions will hold:

a) Concordant (C): where X and Y order the individuals in the same way (if ***i*** is higher(lower) on X, the ***j*** is higher(lower) on Y)

b) Discordant (D): where X and Y order the individuals in opposite ways
c) Tied on X (T_x)
d) Tied on Y (T_y)
e) Tied on both X and Y (T_{xy})

The numerator of all the ordinal measures here considered is the difference between numbers of concordant and discordant pairs. They differ in the form the denominator takes.

Name Goodman and Kruskal's gamma (γ)
Command MEASURES GAMMA
Type similarity measure
Range low = -1, high = +1
Formula

$$\gamma = (C-D)/(C+D)$$

Comment Measures the weak monotonic agreement between the variables, taking the ratio of the difference between concordant and discordant pairs to their sum. It thus ignores the ties completely. For this reason it is possible that the value be undefined (i.e. there may be no cases). If there are no ties then the index reduces to Yule's Q (D15). Some thought should be given to the interpretation of the negative values before the results are scaled.

Name Kendall's tau-b (τ_b)
Command MEASURES TAUB
Type similarity measure
Formula

$$\tau_b = (C-D) \;/\; \{\sqrt{(C+D+T_y)}.\sqrt{(C+D+T_x)}\}$$

Range low = -1, high = +1

Comment Measures strong monotonic agreement in the variables, relating the difference between concordant and discordant pairs of the geometric mean of the quantities arrived at by adding in the ties to the denominator. This should be used only for square tables.

Name Kendall's tau-c (τ_c)
Command MEASURES TAUC
Type similarity measure
Formula (corrects for non-square tables)

Range low = -1, high = +1

Comment In the formula, m stands for the lesser of the number of rows and columns in the original matrix. The statistic may be used for non-square tables and reduces, in the case of square ones to tau-b.

18.2.2.1.4 Interval level measures

The interval level measures currently available in WOMBATS are product-moment measures (covariance and the product-moment correlation) and Euclidean distance.

Consider the conventional scatter-plot of, a number of cases measured on two variables. These cases may be represented as points in a space, the two dimensions of which are the variables concerned. (The statement holds for more than two variables, of course.) The Euclidean distance between the cases is the straight line distance between the points which represent them. The correlation between each pair of points is simply the cosine of the angle between the two vectors drawn from the origin to the points concerned and the covariance is that same cosine multiplied by the length of the vectors.

Command	MEASURES DISTANCE
Type	dissimilarity
Range	low = 0, high = maximum variance in the variables
Comments	If the ranges of the variables involved are markedly different, then some attempt at rescaling (i.e. normalisation) should be made so that differences in a highly valued variable do not swamp out differences in one of humbler dimensions. Does not take into account the extent to which the variables are correlated. (A measure which does so is Mahalanobis 1936, qv.)

Command	MEASURES COVARIANCE
Type	similarity
Range	low = 0, high = highest variance
Comments	The interpretation given to the negative values should be carefully thought out before scaling.

Command	MEASURES CORRELATION
Type	similarity
Range	low = 0, high = 1
Comments	The negative values may need to be given some thought before the results of this calculation are scaled.

18.2.3 FURTHER OPTIONS

18.2.3.1 Measures between cases

It may be that the user wishes to have the measures calculated between the cases (subjects, individuals) in the analysis rather than the variables. This is accomplished simply by specifying in the PARAMETERS command, the keyword ANALYSIS, followed in brackets by the figure 1.

This command has the effect of calculating the measures between the entities designated as cases and is independent of the MATFORM parameter.

18.2.3.2 Multiple analyses

Only one measure may be calculated at each TASK NAME. In order to calculate more than one measure on the same data at one time, more than one TASK NAME should be contained in one RUN. The TASK NAME command also resets PARAMETERS values to their original (default) values and it is necessary to reset these on subsequent runs, as required.

18.3. OUTPUT OPTIONS

The measures are output by default as a lower triangular matrix suitable for input to other procedures in the NewMDSX library. There is no need to signal this output with a command. Other options are available which match different conventions in other programs (see below) and in this case it is necessary to specify the output format for the measures.

18.3.1 Secondary output

If an OUTPUT FORMAT statement is included, specifying a valid FORTRAN format in brackets, this will be used to save the matrix in an optional secondary output file. By default, there is no secondary output.

18.3.2 Alternative output forms

By request, measures may be output as an upper triangular or as full (symmetric) matrix. This is accomplished by use of the keyword OUTPUT in the PARAMETERS command:

- The default specification OUTPUT(1) gives a lower triangle without diagonal, and
- OUTPUT(2) a lower triangle with digonal, and
- OUTPUT(3) a full matrix.

This parameter does not affect the operation of the OUTPUT FORMAT command, if used.

18.3 Examples

```
RUN NAME            WOMBATS TEST PROG
TASK NAME           CORRELATION TEST
NO OF STIMULI        4
NO OF SUBJECTS      15
LEVELS              INTERVAL  (1 TO 4)
OUTPUT FORMAT       (1X,3F13.7)
MISSING             2.(2 , 3)  3.( 4)
PARAMETERS          OUTPUT (1)
MEASURE             CORREL
READ MATRIX
 1. 1. 3. 4.
 1. 2. 3. 3.
 2. 4. 3. 3.
 4. 3. 3. 4.
 3. 2. 3. 2.
 4. 3. 3. 4.
 3. 3. 2. 1.
 1. 1. 4. 3.
 3. 4. 3. 1.
 3. 4. 2. 1.
 1. 2. 1. 1.
 3. 3. 4. 2.
 4. 3. 2. 1.
 1. 2. 1. 2.
 2. 3. 4. 1.
COMPUTE
TASK NAME           CUBE
NO OF STIMULI       8
NO OF SUBJECTS       3
LEVELS               INTERVAL (1 TO 8)
MEASURE              DISTANCE
READ MATRIX
 0. 0. 0. 0. 1. 1. 1. 1.
 1. 1. 0. 0. 1. 1. 0. 0.
 1. 0. 1. 0. 1. 0. 1. 0.
COMPUTE
TASK NAME            TAU AND SIMILAR
NO OF STIMULI         4
NO OF SUBJECTS       15
LEVELS               INTERVAL  (1 TO 4)
MISSING              2.(2 , 3)  3.( 4)
PARAMETERS           OUTPUT(1)
INPUT FORMAT          (8F3.0)
MEASURE                GAMMA
READ MATRIX
 1. 1. 3. 4.
 1. 2. 3. 3.
 2. 4. 3. 3.
 4. 3. 3. 4.
 3. 2. 3. 2.
 4. 3. 3. 4.
 3. 3. 2. 1.
 1. 1. 4. 3.
 3. 4. 3. 1.
 3. 4. 2. 1.
 1. 2. 1. 1.
 3. 3. 4. 2.
 4. 3. 2. 1.
 1. 2. 1. 2.
 2. 3. 4. 1.
COMPUTE
TASK NAME      INDEX OF DISSIMILARITY TEST
NO OF CASES      4
NO OF VARS       4
PARAMETERS     OUTPUT(5)
INPUT FORMAT     (4F3.0)
MEASURE         ID
READ MATRIX
 58 22 41 19
 30 38 14 23
 25 44 19 22
 07 51 12 51
COMPUTE
TASK NAME            PHI
NO OF STIMULI        4
NO OF SUBJECTS       15
LEVELS               INTERVAL  (1 TO 4)
MISSING              2.(1 , 3)  3.( 4)
PARAMETERS           OUTPUT(3)
INPUT FORMAT          (8F3.0)
MEASURE              PHI
READ MATRIX
 1. 1. 3. 4.
 1. 2. 3. 3.
 2. 4. 3. 3.
 4. 3. 3. 4.
 3. 2. 3. 2.
 4. 3. 3. 4.
 3. 3. 2. 1.
 1. 1. 4. 3.
 3. 4. 3. 1.
 3. 4. 2. 1.
 1. 2. 1. 1.
 3. 3. 4. 2.
 4. 3. 2. 1.
 1. 2. 1. 2.
 2. 3. 4. 1.
COMPUTE
FINISH
```

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