PROXSCAL

PROXSCAL is available in the Categories option.

```
PROXSCAL varlist

[/TABLE = {rowid BY columnid [BY sourceid]}]
          {sourceid                      }

[/SHAPE = [{LOWER**}]]
           {UPPER  }
           {BOTH   }

[/INITIAL = [{SIMPLEX**        }]]
             {TORGERSON        }
             {RANDOM[({1})]    }
                      {n}
             {[('file'|'dataset')] [varlist] }

[/WEIGHTS = varlist]

[/CONDITION = [{MATRIX**      }]]
              {UNCONDITIONAL }

[/TRANSFORMATION = [{RATIO**                          }]]
                    {INTERVAL                         }
                    {ORDINAL[({UNTIE   })]            }
                             {KEEPTIES}
                    {SPLINE [DEGREE = {2}] [INKNOT = {1}]}
                                      {n}           {n}

[/PROXIMITIES = [{DISSIMILARITIES**}]]
                 {SIMILARITIES     }

[/MODEL = [{IDENTITY**    }]]
           {WEIGHTED      }
           {GENERALIZED   }
           {REDUCED[({2})]}
                     {n}

[/RESTRICTIONS = {COORDINATES('file'|'dataset') [{ALL    }]                                  }]
                                        {varlist}
                 {VARIABLES('file'|'dataset') [{ALL    }][({INTERVAL                     })]}
                                      {varlist}   {NOMINAL                    }
                                                  {ORDINAL[({UNTIE   })]      }
                                                           {KEEPTIES}
                                                  {SPLINE[DEGREE={2}][INKNOT={1}]}
                                                                {n}         {n}

[/ACCELERATION = NONE]

[/CRITERIA = [DIMENSIONS({2**      })]
                         {min[,max]}
             [MAXITER({100**})]
                      {n    }
             [DIFFSTRESS({0.0001**})]
                         {value   }
             [MINSTRESS({0.0001**}) ]]
                        {value   }

[/PRINT = [NONE][INPUT][RANDOM][HISTORY][STRESS**][DECOMPOSITION]
          [COMMON**][DISTANCES][WEIGHTS**][INDIVIDUAL]
          [TRANSFORMATIONS][VARIABLES**][CORRELATIONS**]]

[/PLOT = [NONE][STRESS][COMMON**][WEIGHTS**][CORRELATIONS**]
         [INDIVIDUAL({varlist})]
                     {ALL    }
         [TRANSFORMATIONS({varlist}) [({varlist})[...]] ]
                          {ALL    }    {ALL    }
         [RESIDUALS({varlist}) [({varlist})[...]] ]
                    {ALL    }    {ALL    }
         [VARIABLES({varlist})]]
                    {ALL    }

[/OUTFILE = [COMMON('file'|'dataset')] [WEIGHTS('file'|'dataset')] [DISTANCES('file'|'dataset')]
            [TRANSFORMATIONS('file'|'dataset')] [VARIABLES('file'|'dataset')] ]

[/MATRIX = IN('file'|'dataset')]].
```

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** Default if the subcommand is omitted.

This command reads the active dataset and causes execution of any pending commands. See the topic "Command Order" on page 40 for more information.

Overview

PROXSCAL performs multidimensional scaling of proximity data to find a least-squares representation of the objects in a low-dimensional space. Individual differences models are allowed for multiple sources. A majorization algorithm guarantees monotone convergence for optionally transformed metric and nonmetric data under a variety of models and constraints.

Options

Data Input. You can read one or more square matrices of proximities that can either be symmetrical or asymmetrical. Alternatively, you can provide specifications with the TABLE subcommand for matrices with proximities in a stacked format. You can read proximity matrices created by PROXIMITIES and CLUSTER with the MATRIX subcommand. Additionally, you can read weights, initial configurations, fixed coordinates, and independent variables.

Methodological Assumptions. You can specify transformations considering all sources (unconditional) or separate transformations for each source (matrix-conditional) on the CONDITION subcommand. You can treat proximities as nonmetric (ordinal) or as metric (numerical or splines) using the TRANSFORMATION subcommand. Ordinal transformations can treat tied observations as tied (discrete) and untied (continuous). You can specify whether your proximities are similarities or dissimilarities on the PROXIMITIES subcommand.

Model Selection. You can specify multidimensional scaling models by selecting a combination of PROXSCAL subcommands, keywords, and criteria. The subcommand MODEL offers, besides the identity model, three individual differences models. You can specify other selections on the CRITERIA subcommand.

Constraints. You can specify fixed coordinates or independent variables to restrict the configuration(s) on the RESTRICTIONS subcommand. You can specify transformations (numerical, nominal, ordinal, and splines) for the independent variables on the same subcommand.

Output. You can produce output that includes the original and transformed proximities, history of iterations, common and individual configurations, individual space weights, distances, and decomposition of the stress. Plots can be produced of common and individual configurations, individual space weights, transformations, and residuals.

Basic Specification

The basic specification is PROXSCAL followed by a variable list. By default, PROXSCAL produces a two-dimensional metric Euclidean multidimensional scaling solution (identity model). Input is expected to contain one or more square matrices with proximities that are dissimilarities. The ratio transformation of the proximities is matrix-conditional. The analysis uses a simplex start as an initial configuration. By default, output includes fit and stress values, the coordinates of the common space, and a chart of the common space configuration.

Syntax Rules

- The number of dimensions (both minimum and maximum) may not exceed the number of proximities minus one.
- Dimensionality reduction is omitted if combined with multiple random starts.
- If there is only one source, then the model is always assumed to be identity.

Limitations

- PROXSCAL needs at least three objects, which means that at least three variables must be specified in the variable list. In the case of the TABLE subcommand, the minimum value for rowid and columnid must be at least three.
- PROXSCAL recognizes data weights created by the WEIGHT command but only in combination with the TABLE subcommand.
- Split-file has no implications for PROXSCAL.

Variable List Subcommand

The variable list identifies the columns in the proximity matrix or matrices that PROXSCAL reads. Each variable identifies one column of the proximity matrix, with each case in the active dataset representing one row, unless specified otherwise with the TABLE subcommand. In this case, the variable list identifies whole matrices or sources.

- Only numeric variables can be specified.
- The total number of cases must be divisible by the number of variables. This is not applicable when the TABLE subcommand is used.
- PROXSCAL reads data row by row; the columns are represented by the variables on the variable list. The order of the variables on the list is crucial.

Example

```
DATA LIST
  /object01 object02 object03 object04.


BEGIN DATA
  0 2 6 3
  2 0 5 4
  6 5 0 1
  3 4 1 0
END DATA.


PROXSCAL VARIABLES=object01 TO object04.
```

- This example specifies an analysis on a 4×4 proximity matrix.
- The total number of cases must be divisible by 4.

TABLE Subcommand

The TABLE subcommand specifies the row identifier rowid and the column identifier columnid. Using TABLE, the proximities of separate sources are given in separate variables on the PROXSCAL variable list.

In the same manner, sources are identified by sourceid. In combination with rowid and columnid, the proximities are stacked in one single variable, containing the proximities of all sources, where sources are distinguished by the values of sourceid.

Using sourceid as the only variable on the TABLE subcommand indicates the use of stacked matrices, where individual stacked matrices are recognized by different values of sourceid.

- Rowid, columnid, and sourceid should not be specified on the variable list.
- When specifying both upper- and lower-triangular parts of the matrix, the SHAPE subcommand will determine the handling of the data.
- If a cell's value is specified multiple times, the final specification is used.
- Rowid, columnid, and sourceid must appear in that order.
- Omitting sourceid causes PROXSCAL to use the sources specified on the PROXSCAL variable list. Each variable is assumed to contain the proximities of one source.

- Specifying multiple sources on the PROXSCAL variable list in conjunction with specifying rowid, columnid, and sourceid is not possible and causes PROXSCAL to ignore sourceid.

rowid. *Row identifying variable.* The values of this variable specify the row object of a proximity. The values must be integers between 1 and the number of objects, inclusive.

columnid. *Column identifying variable.* The values specify the column object of a proximity. The values must be integers between 1 and the number of objects, inclusive.

sourceid. *Source identifying variable.* The values specify the source number and must be integers between 1 and the number of sources, inclusive. The value labels of this variable are used to identify sources on other subcommands. These value labels must comply with variable name conventions. Omitting a value label causes PROXSCAL to use the default label *SRC_n*, where *n* is the number of the source.

Example

```
DATA LIST
  /r_id c_id men women.


BEGIN DATA
2 1 1.08 1.14
3 1 0.68 1.12
3 2 0.95 0.75
4 1 0.96 0.32
4 2 0.76 0.98
4 3 0.47 0.69
. . .... ....
.. .. .... ....
13 10 0.55 0.86
13 11 0.61 0.97
13 12 0.46 0.83
END DATA.


PROXSCAL men women
  /TABLE=r_id BY c_id
  /PLOT = INDIVIDUAL (women).
```

- PROXSCAL reads two proximity matrices (*men* and *women*), where the row objects are specified by *r_id* and the column objects by *c_id*.
- A chart of the individual space for *women* is plotted.

This is one way to proceed. Another way is to add the proximities of the additional source below the proximities of the first source and specify sourceid on the TABLE subcommand, containing values distinguishing the first and the additional source (see the next example).

Example

```
DATA LIST
  /r_id c_id s_id prox.


BEGIN DATA
2 1 1 1.08
3 1 1 0.68
3 2 1 0.95
4 1 1 0.96
4 2 1 0.76
4 3 1 0.47
. . . ....
.. .. . ....
13 10 1 0.55
13 11 1 0.61
13 12 1 0.46
2 1 2 1.14
3 1 2 1.12
3 2 2 0.75
4 1 2 0.32
4 2 2 0.98
4 3 2 0.69
. . . ....
.. .. . ....
```

```
13 10 2 0.86
13 11 2 0.97
13 12 2 0.83
END DATA.


VALUE LABELS s_id 1 'men' 2 'women'.


PROXSCAL prox
  /TABLE=r_id BY c_id BY s_id
  /PLOT = INDIVIDUAL (women).
```

- PROXSCAL reads two proximity matrices. The row objects are identified by *r_id* and the column objects, by *c_id*. The proximity matrices are gathered in one variable, *source01*, where each source is distinguished by a value of the source identifying variable *s_id*.
- A chart of the individual space for *women* is plotted.

Example

```
DATA LIST LIST
  /obj_1 obj_2 obj_3 obj_4 s_id


BEGIN DATA
0  0  0  0 1
1  0  0  0 1
2  3  0  0 1
4  5  6  0 1
7  0  0  0 2
0  0  0  0 2
8  9  0  0 2
12 11 12 0 2
END DATA.


VALUE LABELS s_id 1 'women' 2 'men'.


PROXSCAL obj_1 obj_2 obj_3 obj_4
  /TABLE = s_id
  /MODEL = WEIGHTED
  /PLOT = INDIVIDUAL (women).
```

- PROXSCAL reads two proximity matrices. The objects are given on the PROXSCAL variable list. Each source is distinguished by a value of the source identifying variable *s_id*, which is also used for labeling.
- A chart of the individual space for *women* is plotted.

SHAPE Subcommand

The SHAPE subcommand specifies the structure of the proximity matrix.

LOWER. *Lower-triangular data matrix.* For a lower-triangular matrix, PROXSCAL expects a square matrix of proximities of which the lower-triangular elements are used under the assumption that the full matrix is symmetric. The diagonal is ignored but must be included.

UPPER. *Upper-triangular data matrix.* For an upper-triangular matrix, PROXSCAL expects a square matrix of proximities of which the upper-triangular elements are used under the assumption that the full matrix is symmetric. The diagonal is ignored but must be included.

BOTH. *Full data matrix.* The values in the corresponding cells in the upper and lower triangles may be different. PROXSCAL reads the complete square matrix and, after obtaining symmetry, continues with the lower-triangular elements. The diagonal is ignored but must be included.

- System or other missing values on the (virtual) diagonal are ignored.

Example

```
PROXSCAL object01 TO object07
  /SHAPE=UPPER.
```

- PROXSCAL reads square matrices of seven columns per matrix of which the upper-triangular parts are used in computations.
- Although specified, the diagonal and lower-triangular part of the matrix are not used.

INITIAL Subcommand

INITIAL defines the initial or starting configuration of the common space for the analysis. When a reduction in dimensionality is specified on the CRITERIA subcommand, a derivation of coordinates in the higher dimensionality is used as a starting configuration in the lower dimensionality.

- You can specify one of the three keywords listed below.
- You can specify a variable list containing the initial configuration.

SIMPLEX. *Simplex start.* This specification is the default. PROXSCAL starts by placing the objects in the configuration all at the same distance of each other and taking one iteration to improve this high-dimensional configuration, followed by a dimension-reduction operation to obtain the user-provided maximum dimensionality specified in the CRITERIA subcommand with the keyword DIMENSIONS.

TORGERSON. *Torgerson start.* A classical scaling solution is used as initial configuration.

RANDOM. *(Multiple) random start.* You can specify the number of random starts (*n*). *n* is any positive integer. The random sequence can be controlled by the RANDOM SEED command and not by a subcommand within the PROXSCAL command. Each analysis starts with a different random configuration. In the output, all *n* final stress values are reported, as well as the initial seeds of each analysis (for reproduction purposes), followed by the full output of the analysis with the lowest stress value. The default number of random starts is 1. Reduction of dimensionality—that is, using a maximum dimensionality that is larger than the minimum dimensionality—is not allowed within this option and the minimum dimensionality is used, if reduction is specified anyway.

Instead of these keywords, a parenthesized IBM SPSS Statistics data file can be specified containing the coordinates of the initial configuration. If the variable list is omitted, the first MAXDIM variables are automatically selected, where MAXDIM is the maximum number of dimensions requested for the analysis on the CRITERIA subcommand. Only nonmissing values are allowed as initial coordinates.

Example

```
PROXSCAL object01 TO object17
  /INITIAL=RANDOM(100).
```

- This example performs 100 analyses each, starting with different random configurations. The results of the analysis with the lowest final stress are displayed in the output.

WEIGHTS Subcommand

The WEIGHTS subcommand specifies non-negative weights on the proximities included in the active dataset.

- The number and order of the variables in the variable list is important. The first variable on the WEIGHTS variable list corresponds to the first variable on the PROXSCAL variable list. This is repeated for all variables on the variable lists. Every proximity has its own weight. The number of variables on the WEIGHTS subcommand must therefore be equal to the number of variables on the PROXSCAL variable list.
- Negative weights are not allowed. If specified, a warning will be issued and the procedure will abort.

Example

```
DATA LIST FILE='cola.dat' FREE
  /object01 TO object14 weight01 TO weight14.


PROXSCAL object01 TO object14
  /WEIGHTS=weight01 TO weight14.
```

- In this example, the VARIABLES subcommand indicates that there are 14 columns per matrix of which the weights can be found in *weight01* to *weight14*.
- *weight01* contains the weights for *object01*, etc.

CONDITION Subcommand

CONDITION specifies how transformations among sources are compared. The TRANSFORMATION subcommand specifies the type of transformation.

MATRIX. *Matrix conditional.* Only the proximities within each source are compared with each other. This is the default.

UNCONDITIONAL. *Unconditional.* This specification is appropriate when the proximities in all sources can be compared with each other and result in a single transformation of all sources simultaneously.

- Note that if there is only one source, then MATRIX and UNCONDITIONAL give the same results.

Example

```
PROXSCAL object01 TO object15
  /CONDITION=UNCONDITIONAL
  /TRANSFORMATION=ORDINAL(UNTIE).
```

- In this example, the proximities are ordinally transformed, where tied proximities are allowed to be untied. The transformations are performed simultaneously over all possible sources.

TRANSFORMATION Subcommand

TRANSFORMATION offers four different options for optimal transformation of the original proximities. The resulting values are called transformed proximities. The distances between the objects in the configuration should match these transformed proximities as closely as possible.

RATIO. *No transformation.* Omitting the entire subcommand is equivalent to using this keyword. In both cases, the transformed proximities are proportional to the original proximities. This "transformation" is only allowed for positive dissimilarities. In all other cases, a warning is issued and the transformation is set to INTERVAL.

INTERVAL. *Numerical transformation.* In this case, the transformed proximities are proportional to the original proximities, including free estimation of the intercept. The inclusion of the intercept assures that all transformed proximities are positive.

ORDINAL. *Ordinal transformation.* The transformed proximities have the same order as the original proximities. In parentheses, the approach to tied proximities can be specified. Keeping tied proximities tied, also known as secondary approach to ties, is default. Specification may be implicit, ORDINAL, or explicit, ORDINAL(KEEPTIES). Allowing tied proximities to be untied, also known as the primary approach to ties, is specified as ORDINAL (UNTIE).

SPLINE. *Monotone spline transformation.* The transformed proximities are a smooth nondecreasing piecewise polynomial transformation of the original proximities of the chosen degree. The pieces are specified by the number and placement of the interior knots.

SPLINE Keyword

SPLINE has the following keywords:

DEGREE. *The degree of the polynomial.* If DEGREE is not specified, the degree is assumed to be 2. The range of DEGREE is between 1 and 3 (inclusive).

INKNOT. *The number of interior knots.* If INKNOT is not specified, the number of interior knots is assumed to be 1. The range of INKNOT is between 1 and the number of different proximities.

Example

```
PROXSCAL object01 TO object05
  /TRANSFORMATION=ORDINAL(UNTIE).
```

- In this example, the proximities are ordinally transformed, where tied proximities are allowed to be untied.
- The default conditionality (MATRIX) implies that the transformation is performed for each source separately.

PROXIMITIES Subcommand

The PROXIMITIES subcommand specifies the type of proximities used in the analysis. The term proximity is used for either similarity or dissimilarity data.

DISSIMILARITIES. *Dissimilarity data.* This specification is the default when PROXIMITIES is not specified. Small dissimilarities correspond to small distances, and large dissimilarities correspond to large distances.

SIMILARITIES. *Similarity data.* Small similarities correspond to large distances and large similarities correspond to small distances.

Example

```
PROXSCAL object01 TO object12
  /PROXIMITIES=SIMILARITIES.
```

- In this example, PROXSCAL expects the proximities to be similarities.

MODEL Subcommand

MODEL defines the scaling model for the analysis if more than one source is present. IDENTITY is the default model. The three other models are individual differences models.

IDENTITY. *Identity model.* All sources have the same configuration. This is the default model, and it is not an individual differences model.

WEIGHTED. *Weighted Euclidean model.* This model is an individual differences model and equivalent to the INDSCAL model in the ALSCAL procedure. Each source has an individual space, in which every dimension of the common space is weighted differentially.

GENERALIZED. *Generalized Euclidean model.* This model is equivalent to the GEMSCAL model in the ALSCAL procedure. Each source has an individual space that is equal to a rotation of the common space, followed by a differential weighting of the dimensions.

REDUCED. *Reduced rank model.* This model is similar to GENERALIZED, but the rank of the individual space is equal to n. This number is always smaller than the maximum number of dimensions and equal to or greater than 1. The default is 2.

- If IDENTITY is specified for only one source, this subcommand is silently ignored.
- If an individual differences model is specified for only one source, a warning is issued, and the model is set to IDENTITY.

Example

```
PROXSCAL object01 TO object07
  /MODEL=WEIGHTED.
```

- A weighted Euclidean model is fitted, but only when the number of cases in the active dataset is a multiple of 7, starting from 14 (14, 21, 28, and so on). Otherwise, there is only one source, and the model is set to IDENTITY.

RESTRICTIONS Subcommand

PROXSCAL provides two types of restrictions for the user to choose from. The first type fixes (some) coordinates in the configuration. The second type specifies that the common space is a weighted sum of independent variables.

COORDINATES. *Fixed coordinates.* A parenthesized IBM SPSS Statistics data filename must be specified containing the fixed coordinates for the common space. A variable list may be given, if some specific variables need to be selected from the external file. If the variable list is omitted, the procedure automatically selects the first MAXDIM variables in the external file, where MAXDIM is the maximum number of dimensions requested for the analysis on the CRITERIA subcommand. A missing value indicates that a coordinate on a dimension is free. The coordinates of objects with nonmissing values are kept fixed during the analysis. The number of cases for each variable must be equal to the number of objects.

VARIABLES. *Independent variables.* The common space is restricted to be a linear combination of the independent variables in the variable list. A parenthesized IBM SPSS Statistics data file must be specified containing the independent variables. If the variable list is omitted, the procedure automatically selects all variables in the external file. Instead of the variable list, the user may specify the keyword FIRST(n), where n is a positive integer, to select the first *n* variables in the external file. The number of cases for each variable must be equal to the number of objects. After the variable selection specification, we may provide a list of keywords (in number equal to the number of the independent variables) indicating the transformations for the independent variables.

VARIABLES Keyword

The following keywords may be specified:

INTERVAL. *Numerical transformation.* In this case, the transformed values of a variable are proportional to the original values of the variable, including free estimation of the intercept.

NOMINAL. *Nominal transformation.* The values are treated as unordered. The same values will obtain the same transformed values.

ORDINAL. *Ordinal transformation.* The values of the transformed variable have the same order as the values of the original variable. In parenthesis, the approach to tied values can be specified. Keeping tied values tied, also known as secondary approach to ties, is default. Specification may be implicit, ORDINAL, or explicit, ORDINAL(KEEPTIES). Allowing tied values to be untied, also known as the primary approach to ties, is specified as ORDINAL (UNTIE).

SPLINE. *Monotone spline transformation.* The transformed values of the variable are a smooth nondecreasing piecewise polynomial transformation of the original values of the chosen degree. The pieces are specified by the number and placement of the interior knots.

SPLINE Keyword

SPLINE has the following keywords:

DEGREE. *The degree of the polynomial.* If DEGREE is not specified, the degree is assumed to be 2. The range of DEGREE is between 1 and 3 (inclusive).

INKNOT. *The number of interior knots.* If INKNOT is not specified, the number of interior knots is assumed to be 1. The range of INKNOT is between 0 and the number of different values of the variable.

Example

```
PROXSCAL aunt TO uncle
  /RESTRICTIONS=VARIABLES(ivars.sav) degree generation gender
                         (ORDINAL ORDINAL NOMINAL).
```

- In this example, there are three independent variables specified: *degree*, *generation*, and *gender*.
- The variables are specified in the data file *ivars.sav*.
- On both *degree* and *generation*, ordinal transformations are allowed. By default, tied values in ordinal variables are kept tied. *Gender* is allowed to be nominally transformed.

ACCELERATION Subcommand

By default, a fast majorization method is used to minimize stress.

NONE. *The standard majorization update.* This turns off the fast method.

- If the subcommand RESTRICTION is used with fixed coordinates or independent variables, ACCELERATION=NONE is in effect.
- If an individual differences model is specified on the MODEL subcommand, ACCELERATION=NONE is in effect.

Example

```
PROXSCAL VARIABLES=object01 TO object12
  /ACCELERATION=NONE.
```

- Here, relaxed updates are switched off through the specification of the keyword NONE after ACCELERATION.

CRITERIA Subcommand

Use CRITERIA to set the dimensionality and criteria for terminating the algorithm, or minimization process. You can specify one or more of the following keywords:

DIMENSIONS. *Minimum and maximum number of dimensions.* By default, PROXSCAL computes a solution in two dimensions (min=2 and max=2). The minimum and maximum number of dimensions can be any integers inclusively between 1 and the number of objects minus 1, as long as the minimum is less than or equal to the maximum. PROXSCAL starts computing a solution in the largest dimensionality and reduces the dimensionality in steps, until the lowest dimensionality is reached. Specifying a single value represents both minimum and maximum number of dimensions, thus DIMENSIONS(4) is equivalent to DIMENSIONS(4,4).

MAXITER. *Maximum number of iterations.* By default, *n*=100, specifying the maximum number of iterations that is performed while one of the convergence criterion below (CONVERGENCE and STRESSMIN) is not yet reached. Decreasing this number might give less accurate results but will take less time. *N* must have a positive integer value.

DIFFSTRESS. *Convergence criterion.* PROXSCAL minimizes the goodness-of-fit index normalized raw stress. By default, PROXSCAL stops iterating when the difference in consecutive stress values is less than 0.0001 (*n*=0.0001). To obtain a more precise solution, you can specify a smaller value. The value specified must lie between 0.0 and 1.0, inclusively.

MINSTRESS. *Minimum stress value.* By default, PROXSCAL stops iterating when the stress value itself is small, that is, less than 0.0001 (*n*=0.0001). To obtain an even more precise solution, you can specify a smaller value. The value specified must lie between 0.0 and 1.0, inclusively.

Example

```
PROXSCAL VARIABLES=object01 TO object24
  /CRITERIA=DIMENSIONS(2,4) MAXITER(200) DIFFSTRESS(0.00001).
```

- The maximum number of dimensions equals 4 and the minimum number of dimensions equals 2. PROXSCAL computes a four-, three-, and two-dimensional solution, respectively.
- The maximum number of iteration is raised to 200.
- The convergence criterion is sharpened to 0.00001.

PRINT Subcommand

PRINT specifies the optional output. By default, PROXSCAL displays the stress and fit values for each analysis, the coordinates of the common space, and, with appropriate specification on corresponding subcommands, the individual space weights and transformed independent variables, corresponding regression weights, and correlations.

- Omitting the PRINT subcommand or specifying PRINT without keywords is equivalent to specifying COMMON, WEIGHTS, and VARIABLES.
- If a keyword(s) is specified, only the output for that particular keyword(s) is displayed.
- In the case of duplicate or contradicting keyword specification, the last keyword applies.
- Inapplicable keywords are silently ignored. That is, specifying a keyword for which no output is available (for example, specifying INDIVIDUAL with only one source) will silently ignore this keyword.

NONE. *No output.* Display only the normalized raw stress and corresponding fit values.

INPUT. *Input data.* The display includes the original proximities, and, if present, the data weights, the initial configuration, and the fixed coordinates or the independent variables.

RANDOM. *Multiple random starts.* Displays the random number seed and stress value of each random start.

HISTORY. *History of iterations.* Displays the history of iterations of the main algorithm.

STRESS. *Stress measures.* Displays different stress values. The table contains values for normalized raw stress, Stress-I, Stress-II, S-Stress, dispersion accounted for (D.A.F.), and Tucker's coefficient of congruence. This is specified by default.

DECOMPOSITION. *Decomposition of stress.* Displays an object and source decomposition of stress, including row and column totals.

COMMON. *Common space.* Displays the coordinates of the common space. This is specified by default.

DISTANCES. *Distances.* Displays the distances between the objects in the configuration.

WEIGHTS. *Individual space weights.* Displays the individual space weights, only if one of the individual differences models is specified on the MODEL subcommand. Depending on the model, the space weights are decomposed in rotation weights and dimension weights, which are also displayed. This is specified by default.

INDIVIDUAL. *Individual spaces.* The coordinates of the individual spaces are displayed, only if one of the individual differences models is specified on the MODEL subcommand.

TRANSFORMATION. *Transformed proximities.* Displays the transformed proximities between the objects in the configuration.

VARIABLES. *Independent variables.* If VARIABLES was specified on the RESTRICTIONS subcommand, this keyword triggers the display of the transformed independent variables and the corresponding regression weights. This is specified by default.

CORRELATIONS. *Correlations.* The correlations between the independent variables and the dimensions of the common space are displayed. This is specified by default.

Example

```
PROXSCAL VARIABLES=source01 TO source02
  /TABLE=row_id BY col_id
  /MODEL=WEIGHTED
  /PRINT=HISTORY COMMON STRESS.
```

- Here, a weighted Euclidean model is specified with two sources.
- The output consists of the history of iterations of the main algorithm, the coordinates of the common space, the individual space weights, and several measures of fit.

PLOT Subcommand

PLOT controls the display of plots. By default, PROXSCAL produces a scatterplot of object coordinates of the common space, the individual space weights, and the correlations between the independent variables (that is, equivalent to specifying COMMON, WEIGHTS, and CORRELATIONS).

- Specifying a keyword overrides the default output and only output is generated for that keyword.
- Duplicate keywords are silently ignored.
- In case of contradicting keywords, only the last keyword is considered.
- Inapplicable keywords (for example, stress with equal minimum and maximum number of dimensions on the CRITERIA subcommand) are silently ignored.
- Multiple variable lists are allowed for TRANSFORMATIONS and RESIDUALS. For each variable list, a separate plot will be displayed.

NONE. *No plots.* PROXSCAL does not produce any plots.

STRESS. *Stress plot.* A plot is produced of stress versus dimensions. This plot is only produced if the maximum number of dimensions is larger than the minimum number of dimensions.

COMMON. *Common space.* A scatterplot matrix of coordinates of the common space is displayed.

WEIGHTS. *Individual space weights.* A scatterplot is produced of the individual space weights. This is only possible if one of the individual differences models is specified on the MODEL subcommand. For the weighted Euclidean model, the weights are printed in plots with one dimension on each axis. For the generalized Euclidean model, one plot is produced per dimension, indicating both rotation and weighting of that dimension. The reduced rank model produces the same plot as the generalized Euclidean model does but reduces the number of dimensions for the individual spaces.

INDIVIDUAL. *Individual spaces.* For each source specified on the variable list, the coordinates of the individual spaces are displayed in scatterplot matrices. This is only possible if one of the individual differences models is specified on the MODEL subcommand.

TRANSFORMATIONS. *Transformation plots.* Plots are produced of the original proximities versus the transformed proximities. On the variable list, the sources can be specified of which the plot is to be produced.

RESIDUALS. *Residuals plots.* The transformed proximities versus the distances are plotted. On the variable list, the sources can be specified of which the plot is to be produced.

VARIABLES. *Independent variables.* Transformation plots are produced for the independent variables specified on the variable list.

CORRELATIONS. *Correlations.* A plot of correlations between the independent variables and the dimensions of the common space is displayed.

Example

```
PROXSCAL VARIABLES=source01 TO source02
  /TABLE=row_id BY col_id
  /MODEL=WEIGHTED
  /CRITERIA=DIMENSIONS(3)
  /PLOT=COMMON INDIVIDUAL(source02).
```

- Here, the syntax specifies a weighted Euclidean model with two sources in three dimensions.
- `COMMON` produces a scatterplot matrix defined by dimensions 1, 2, and 3.
- For the individual spaces, a scatterplot matrix with 3 dimensions is only produced for the individual space of *source02*.

OUTFILE Subcommand

`OUTFILE` saves coordinates of the common space, individual space weights, distances, transformed proximities, and transformed independent variables to an external IBM SPSS Statistics data file or previously declared dataset. The only specification required is a name for the output file.

COMMON. *Common space coordinates.* The coordinates of the common space are written to an external IBM SPSS Statistics data file or previously declared dataset. The columns (variables) represent the dimensions *DIM_1*, *DIM_2*, ..., *DIM_n* of the common space. The number of cases (rows) in the IBM SPSS Statistics data file equals the number of objects.

WEIGHTS. *Individual space weights.* The individual space weights are written to an external IBM SPSS Statistics data file or previously declared dataset. The columns represent the dimensions *DIM_1*, *DIM_2*, ..., *DIM_n* of the space weights. The number of cases depends on the individual differences model specified on the `MODEL` subcommand. The weighted Euclidean model uses diagonal weight matrices. Only the diagonals are written to file and the number of cases is equal to the number of dimensions. The generalized Euclidean model uses full-rank nonsingular weight matrices. The matrices are written to the data file row by row. The reduced rank model writes matrices to the data file in the same way as the generalized Euclidean model does but does not write the reduced part.

DISTANCES. *Distances.* The matrices containing the distances for each source are stacked beneath each other and written to an external IBM SPSS Statistics data file or previously declared dataset. The number of variables in the data file are equal to the number of objects (*OBJ_1*, *OBJ_2*, ..., *OBJ_n*) and the number of cases in the data file are equal to the number of objects times the number of sources.

TRANSFORMATION. *Transformed proximities.* The matrices containing the transformed proximities for each source are stacked beneath each other and written to an external IBM SPSS Statistics data file or previously declared dataset. The number of variables in the file are equal to the number of objects (*OBJ_1*, *OBJ_2*, ..., *OBJ_n*) and the number of cases in the data file are equal to the number of objects times the number of sources.

VARIABLES. *Independent variables.* The transformed independent variables are written to an external IBM SPSS Statistics data file or previously declared dataset. The variables are written to the columns (*VAR_1*, *VAR_2*, ..., *VAR_n*). The number of variables in the data file are equal to the number of independent variables and the number of cases are equal to the number of objects.

Example

```
PROXSCAL VARIABLES=source01 TO source04
  /TABLE=row_id BY col_id
  /OUTFILE=COMMON('/data/start.sav').
```

- Here, the coordinates of the common space are written to the IBM SPSS Statistics data file *start.sav*.
- Filenames should be enclosed in quotes and are stored in the working directory unless a path is included as part of the file specification. datasets are available during the current session but are not available in subsequent sessions unless you explicitly save them as data files.

MATRIX Subcommand

MATRIX reads matrix data files. It can read a matrix written by either PROXIMITIES or CLUSTER.

- The specification on MATRIX is the keyword IN and the matrix file in parentheses.
- Generally, data read by PROXSCAL are already in matrix form, whether in square format, or in stacked format using the TABLE subcommand.
- The proximity matrices PROXSCAL reads have ROWTYPE_ values of PROX.
- Using MATRIX=IN, PROXSCAL will ignore variables specified on the main variable list. All numerical variables from the matrix data file are processed.
- PROXSCAL ignores variables specified in the WEIGHTS subcommand in combination with the use of MATRIX=IN.
- With MATRIX=IN, only a source identifying variable can be specified on the TABLE subcommand. The sources are created as a result of a split file action.

IN('file'|'dataset'). *Read a matrix data file.* Specify a quoted file specification or previously declared dataset name, enclosed in parentheses. Data read through the MATRIX subcommand does not replace the active dataset.

Example

```
GET FILE = '/data/proxmtx.SAV'.


PROXSCAL
  /MATRIX=IN('/data/matrix.sav').
```

- MATRIX=IN specifies an external matrix data file called *matrix.sav*, of which all numerical variables are used for the current analysis.