KUNST

GRIDAN

Analysis of idiographic grid data

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1 General description

GRIDAN* analyses idiographic grid data, for instance resulting from applications of the self-confrontation method according to Hermans (1976). As its input GRIDAN expects one or more "tests" each consisting of a matrix of "profiles" (the rows) by "affects" (the columns). These data must be prepared in advance and stored in one or more files. GRIDAN analyses the tests one by one.

1.1 The basic data

In the self-confrontation method, the most important profiles refer to *value-areas*. A value-area is anything that is of immediate importance for the subject: a goal, a memory, a problem, a person and so on. As a part of the method, the subject constructs his private set of value-areas and attaches labels to them. As a rule, the total number of value-areas will be between 13 and 70.

In the second stage of the method the person is presented with a standard list of feelings (or affects); he or she is asked to indicate, by means of a number rating, for each feeling the extent to which he/she experiences this feeling in connection with each of the value labels. The list of scores for a value-area forms its profile. (The ratings range for example from 0 = *never*, 1 = *rarely*, 2 = *sometimes*, 3 = *rather often* and 4 = *often* to 5 = *very often*.) As an example Figure 1 might represent the strength of 16 feelings associated with the value-area "unwanted child". *Gridan* requires that the same set of affects is used over the tests in a single run of the program, but the profiles vary from test to test.

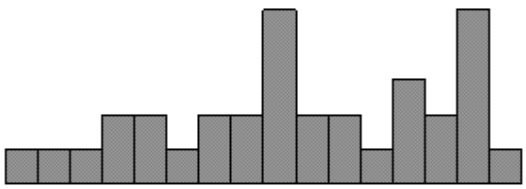

Figure 1: Graphical representation of a profile.

In addition to the ratings related to value-areas, there may be some overall profiles like generalized feelings ("how do you generally feel?") or ideal experience ("how would you like to feel?") and so-called *marker profiles*, to be explained later (see 1.4).

The program can also construct **sum-scales** by adding for each profile the scores on a subgroup of affects. These affects may have different weights in the addition. Any two sum-scales may be used to construct a **ratio-scale** assigning to each profile the ratio of the two sum-scale scores.

* This program (*Gridan*) replaces the older programs *Confron* and *Kungrid*, as it can produce the results of both programs.

1.2 Affects and scales

Gridan offers six predefined lists of affects and accompanying scales. These sets are commonly in use. However, the user is free to change these definitions or to construct any new set of affects and scales. The predefined lists are shown in Figure 2. The list with 30 affects is the original one mentioned in Hermans et al., 1985. The 16 and 28 affects lists are subsets from this 30 affects list as mentioned in Van Geel (2000, page 42). The 24 affects list is also mentioned in van Geel (2000, page 62). The list of 18 affects is borrowed from Hermans & Verstraeten (1980, page 92).

Of course, you can change the number of affects and their names as well as the scale definitions if you like. Since the settings of any analysis can be saved in a settings file, you can build your own collection of affect lists and scales.

16 Affects	**18 Affects**	**20 Affects**	**24 Affects**	**28 Affects**	**30 Affects**
Joy (PI) SelfEste(S) Happines(PI) Worry (NI) Strength(S) Enjoymen(PI) Caring (O) Love (O) Unhappin(NI) Tenderne(O) SelfConf(S) Intimacy(O) Desponde(NI) Pride (S) Disappoi(NI) InnrCalm(PI)	Joy (PI) Powerles(NI) Satisfac(PI) Irritati(NI) Contentm(PI) Worry (NI) Stress (NI) Success (PI) Belongin(PI) Insecure(NI) Disappoi(NI) Guilt (NI) At ease (PI) Loneline(NI) Warmth (PI) Trust (PI) FeelHurt(NI) Energy (PI)	Joy (PI) Usefulne(S) Together(O) Nervous (R) Worry (NI) Happines(PI) Belongin(O) Stress (R) SelfConf(S) Unhappin(NI) Enjoymen(PI) Restless(R) Anger (NI) SelfEste(S) Affectio(O) InnrCalm(PI) Developm(S) Sympathy(O) Jumpy (R) Disappoi(NI)	Joy (PI) SelfEste(S) Anxiety (NI) Happines(PI) Strength(S) Tenderne(O) Stress (NI) Enjoymen(PI) Caring (O) Love (O) SelfConf(S) Loneline(NI) Warmth (O) Trust (PI) Inferior(NI) Energy (PI) Security(PI) Anger (NI) Solidari(O) Pride (S) Intimacy(O) Disappoi(NI) InnrCalm(PI) Freedom (S)	Joy (PI) Powerles(NI) SelfEste(S) Anxiety (NI) Happines(PI) Worry (NI) Strength(S) Stress (NI) Enjoymen(PI) Caring (O) Love (O) SelfAlie(NI) Tenderne(O) Guilt (NI) Solidari(PI) SelfConf(S) Loneline(NI) Warmth (PI) Trust (PI) Inferior(NI) Intimacy(O) Security(PI) Anger (NI) Pride (S) Energy (PI) Disappoi(NI) InnrCalm(PI) Freedom (PI)	Joy (PI) Powerles(NI) SelfEste(S) Anxiety (NI) Happines(PI) Worry (NI) Strength(S) Stress (NI) Enjoymen(PI) Caring (O) Love (O) SelfAlie(NI) Unhappin Tenderne(O) Guilt (NI) Solidari(PI) SelfConf(S) Loneline(NI) Warmth (PI) Trust (PI) Inferior(NI) Intimacy(O) Security(PI) Anger (NI) Desponde Pride (S) Energy (PI) Disappoi(NI) InnrCalm(PI) Freedom (PI)
Scales: P= Positive N= Negative S= Self O= Other I= Involvem Quality= P/I	**Scales:** P= Positive N= Negative I= Involvem Quality= P/I	**Scales:** P= Positive N= Negative R= Restless S= Self O= Other I= Involvem Quality= P/I	**Scales:** P= Positive N= Negative S= Self O= Other I= Involvem Quality= P/I	**Scales:** P= Positive N= Negative S= Self O= Other I= Involvem Quality= P/I	**Scales:** P= Positive N= Negative S= Self O= Other I= Involvem Quality= P/I

Figure 2: Predefined sets of affects and scales.

1.3 The analysis

Gridan computes some descriptive statistics on these data, like the correlations between the value-areas, the correlations between the affects, sums over profiles, sums over affects and so on.

In addition to *correlations*, *Gridan* uses (Euclidean) *distances* to compare profiles. The interesting point is, that in the comparison of two profiles, distance is sensitive to differences in level (mean affect score of a profile), scatter (standard deviation of the affects within a profile) and shape (the rising and declining of the scores), whereas correlation is only sensitive to shape. The distances are standardized such that they can be compared over analyses, even if the range of the scores or the number of affects is different. To that goal, the raw distances are divided by the range of the scores times the square root of the number of affects (the affects constitute the dimensions in which the distances are computed).

Once the step being made from correlation to Euclidean distance, it is a small additional step to the representation of the data matrix in fewer dimensions than the number of affects. *Gridan* uses a principal components analysis on the affects in order to construct a representation in fewer dimensions. In a sample of 127 tests with real live data from the self-confrontation method, Van Geel and De Mey found that the representation in two dimensions maintained the original distances very well. The mean cophenetic coefficient (the correlation between the standardized distances in the 16 affect-dimensions and those from the two-dimensional representation) was 0.96 (Van Geel & De Mey 1996). Nevertheless, you may specify a higher dimensionality.

A well-known problem with principal component techniques is that they tend to represent larger distances better than small ones. Therefore, *Gridan* offers the opportunity to evaluate the quality of the representation by a scatter plot (a so-called Shepard plot) showing the original distances at the x-axis and the distances from the reduced space on the y-axis.

1.4 Active and passive profiles

In 1.1, we already mentioned the idea of overall profiles like generalized feelings or ideal experience. They represent profiles (data rows) that possibly must be treated in a special way. Therefore, their labels are marked by a **star** in their very first position and we call them *starred* profiles. The most important difference between starred and unstarred profiles is the role they play in the projection of the original data in a two- or more-dimensional space. This space will be based only on the unstarred profiles. The starred profiles will receive their positions in the space, but they have no influence on its construction. Therefore, starred profiles are also called *passive*, where the unstarred profiles are called *active*. This difference between starred (passive) and unstarred (active) profiles makes it possible to manipulate the construction of the space.

Now profiles can be divided into the following groups:

Value areas: the basic profiles in the self-confrontation method.

Overall profiles: special starred profiles, that are treated somewhat different, but, like value areas, are scored by the test subject.

Marker profiles: special starred profiles, designed to guide the representation in two- or more-dimensional space. These profiles are added by the researcher or counselor and usually represent extremely pure types. Van Geel for instance defines six marker profiles that form a hexagon in two-dimensional space. They have extremely high scores on some affect scales and extremely low scores on others.
For the set of 16-affects the hexagon markers are:
+HH (strength and unity): maximum scores on scales Positive, Self and Other and minimum score on Negative.
+S (autonomy and success): maximum scores on scales Positive and Self and minimum scores on Negative and Other.
-S (aggression and anger): maximum scores on scales Negative and Self and minimum scores on Positive and Other.
-LL (powerlessness and isolation): maximum score on scale Negative and minimum score on Positive, Self and Other.
-O (unfulfilled longing): maximum scores on scales Negative and Other, minimum scores on Self and Positive.
+O (unity and love): maximum scores on scales Positive and Other and minimum scores on Negative and Self.

Now at least four situations can be distinguished:

1. There are **no starred profiles**: all profiles are playing an active role in the definition of the space.

2. All **value-areas are starred**, but some **unstarred *marker* profiles** are added: The markers actively define the space and the value-areas are passively projected on it. The markers may be those defined by Van Geel's hexagon or any other set. The hexagon is based on theoretical considerations and backed by empirical research. Therefore, *Gridan* offers a special option to add these hexagon markers automatically to the data, provided that one of the six predefined affect sets is used. The hexagon markers will define the space together with any unstarred profiles that possibly are already in the input data.

3. All **value-areas are unstarred**, but some **starred marker profiles** are added: Now the space is defined by the value-areas and the markers are projected passively on it. The positions of the markers may be helpful in the interpretation of the space.

4. All **value-areas are unstarred** and some **unstarred marker profiles** are added: Now both value-areas and markers actively define the space, but if the markers have extreme scores, they may have a relatively strong impact on the final configuration.

Note that the choice between these four possibilities has to be made before you start *Gridan*, that is, when the data are prepared, with an exception for the automatically added hexagon.

Figure 3 shows part of a data file with the hexagon explicitly added. The sixteen affects list is used. Note that in real life the user never has to add these markers, when using a predefined affects list, since it is easier to let *Gridan* add them automatically.

Figure 4 shows the form of the hexagon.

```
                  Self      Worry    Enjo     Love     Tend     Inti     Pride   Innr
                  Este               ymen              erne     macy             Calm

              Joy      Happ     Stre     Cari     Unha     Self     Desp     Disa
                       ines     ngth     ng       ppin     Conf     onde     ppoi
             (P) (S) (P) (N) (S) (P) (O) (O) (N) (O) (S) (O) (N) (S) (N) (P)
```

Hexagon +HH:	5	5	5	0	5	5	5	5	0	5	5	5	0	5	0	5
Hexagon +S:	5	5	5	0	5	5	0	0	0	0	5	0	0	5	0	5
Hexagon -S:	0	5	0	5	5	0	0	0	5	0	5	0	5	5	5	0
Hexagon -LL:	0	0	0	5	0	0	0	0	5	0	0	0	5	0	5	0
Hexagon -O:	0	0	0	5	0	0	5	5	5	5	0	5	5	0	5	0
Hexagon +O:	5	0	5	0	0	5	5	5	0	5	0	5	0	0	0	5
*Unwanted child	0	0	0	1	1	0	1	1	4	1	1	0	2	1	4	0
*Creche terrible	0	0	0	4	1	1	0	1	5	0	0	0	3	1	4	0
*Missed father	0	0	0	4	0	0	0	0	4	3	0	1	3	2	5	0
	.....															
	.....															
*General feeling	3	3	2	4	3	3	2	3	4	1	2	2	2	3	3	1
*Ideal	3	3	2	4	3	3	2	3	4	1	2	2	2	3	3	1

Figure 3: Input file with active hexagon markers for the 16-affect list and some starred, passive profiles.

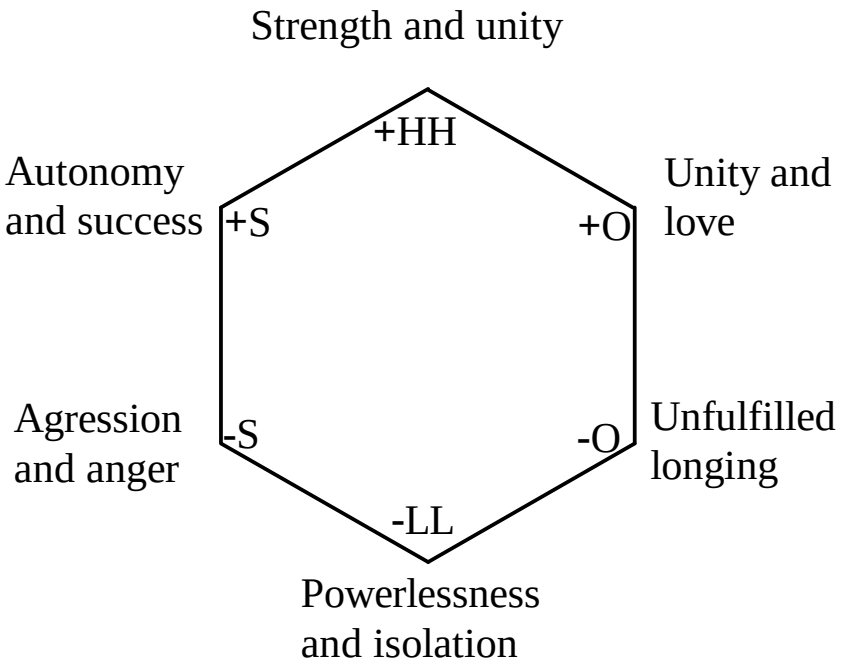

Figure 4: Form of the hexagon.

2 The data

The input for GRIDAN comes from one or more separate files, each containing the results of one or more “tests”. The files must be prepared in advance by a word processor or an editor of any kind and saved as “text only” (a flat ASCII file, as it is often called).

Each test contains one row for each profile (as in Figure 5). Such a row holds the scores that form the profile. In general, the scores will be something like ratings on a six points scale. Usually each row contains a label for the profile. That label may be 40 characters long or less. If it is longer than 8 characters, it still will be truncated to its first 8 characters at some places in the analysis report. 'Starred' profiles must contain an asterisk in their very first position.

```
....+....1....+....2....+....3....+....4....+....5....+....6....+..
Third child not wanted by husband  0 1 1 3 3 2 2 2 2 1 2 1 3 1 4 1
Object as marriage ran out         0 1 1 5 3 1 1 1 5 0 1 0 3 0 5 0
*Ideal                             3 3 2 4 3 3 2 3 4 1 2 2 2 3 3 1
```

Figure 5: Three lines in an input file with scores on 16 affects.

Each single profile (i.e. each row) is represented by one or more lines in the file, although it will seldom happen that you need more than one line per row. The exact structure of such a row must be given by the *data definition* menu (see 6.3).

If an input file contains more than one test, there are two ways to mark the boundaries between the tests.

1. the option *blanks*: tests are separated by a *blank* profile, that is, a profile with spaces in a specific area. The area is always 4 positions long and can be defined by the user. If the profiles contain more than one line, the blank area must be in the first line.

2. the test sizes: the user specifies the number of profiles in each of the tests of the *blank* profile.

Both the specification of the blank area and the definition of the test sizes take place during the interaction at the start of the program.

We strongly advise you to use one line per profile and to separate the scores within that line by spaces, commas or tabs. If a file contains more than one test, separate the tests by a single empty line. If you do so, the data definitions will turn out to be very simple.

Note that the labels of the profiles are stored with the data, but that the names of the affects have to be specified with the program options and therefore have to be the same for all tests in one program run.

3 Files

There are five file types that are important for this program:

data files:
The files that contain the data to be analyzed. One program run can analyze several files and each file can contain several tests.

settings files:
These files are used to save the options as they are specified by a user. A settings file contains all information about the analysis to be performed, including the description of the data, but not the data themselves. It is possible to have more than one settings file. By default, their extension is '`.setgri`'.

listing files:
A listing file contains the main results of an analysis in a nice layout for human readers. There will be one listing file for each data file. The name will borrow its first part from the data file and end on '`.LST`' (or on '`1.LST`', '`2.LST`', ... and so on). You can inspect it by any editor, but in order to have an orderly layout you must view it in a small non-proportional font like Courier New 9.

raw output files:
Depending on the chosen options, the program may produce one file with “raw” output for each input file. These raw files are meant to be input for other programs. Their names will take their first part from the data files and end with '`.OUT`' (or '`1.OUT`', '`2.OUT`', ... and so on).

plot files:
If the program produces any plots (graphical representations) the listing files will contain coarse versions of the plots, but the program will also produce a more refined bitmap for each plot. The names of these bitmap files will take their first part from the data files and on Windows machines they will end with '`.BMP`' (or '`1.BMP`', '`2.BMP`', ... and so on).

4 Installing the program on Windows

The installation of the program is very simple:

1. Copy the file *Gridan.exe* to any place on your hard disk. Optionally you may make shortcuts on the task bar and/or the desktop.

2. After the first time you have used the program, double click on the listing file. Windows will ask you to select the program to be used when opening the file. Select a simple text editor like NotePad or WordPad.

3. After the first time you have saved the program settings, double click on the settings file. Windows will ask you to select the program to be used when opening the file. Select the program *Gridan.exe* or any shortcut to it.

That is all: from now on, you can start the program by double clicking the exe-file, one of its shortcuts or a settings file.

5 Running the program

To run *Gridan* you must double click on its executable file (for Windows: *Gridan.exe*) or, if you have used the program before, on one of its settings files (for instance *Current.SetGri*). The first thing you will see then, is the main window of the program, as shown in Figure 6.

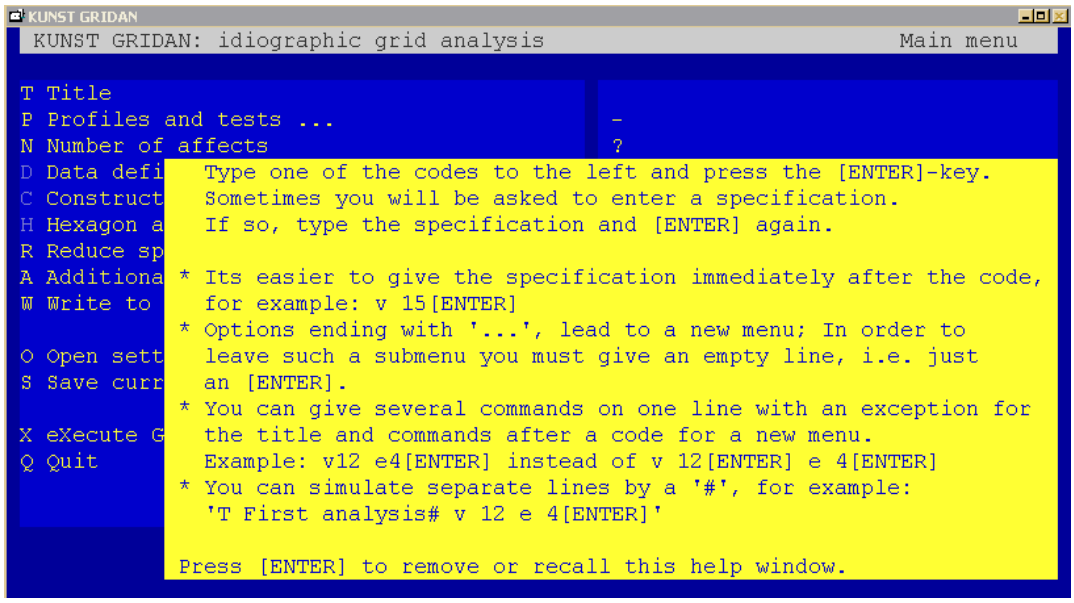

Figure 6: The main window.

On the screen the light part with the text '`Type one ...`' is a yellow text window. Windows like that contain hints and explanations. If you have read the text (or do not need it), you can press the Enter-key and the yellow window will vanish (see Figure 7).

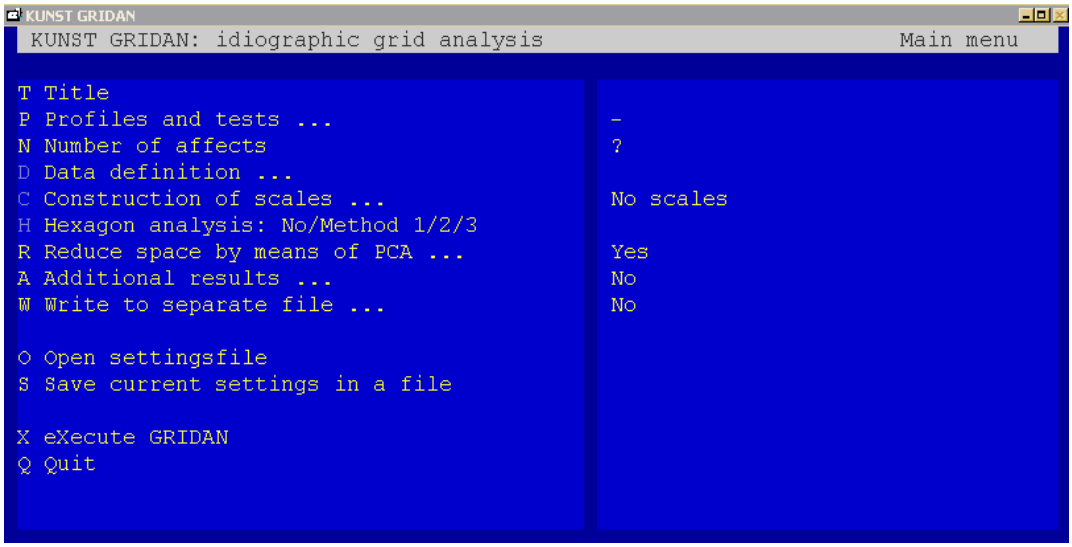

Figure 7: The main window without help-window.

Now you can see the entire main window. The left part is the *main* menu. It consists of a list of options, each preceded by a one-character code. To select an option, you must type the code, followed by the information you want to give and then the Enter-key. From now on, we will indicate the Enter-key as: Enter. You may for instance type: `T Analyzing first session`Enter to define the title that will appear as a header in the listing files. If you do not know what the meaning of an option is, you may just enter its code and Enter. There will appear a question on the screen and, if helpful, a yellow window to give you information. Press Enter to remove the yellow window and then give the specification belonging to the code, or ignore the yellow window and give the specification at once. **Do not repeat the code itself!**

The right part of the window gives a short review of the options as they are currently set. In the example of Figure 7, you can see the following:

- No title line is defined.
- Profiles and tests need not to be defined.
- The number of affects is not yet specified, but must be given.
- The data definitions cannot be chosen before the number of affects is known (although it is difficult to see in this print, the option character 'D' is gray).
- Scales cannot be defined before the number of affects is known (the character 'C' is gray too).
- A default hexagon cannot be used as long as the number of affects is unknown (the 'H' is gray).
- A principal components analysis will be performed.
- No additional results will be reported.
- No raw output file will be produced.

6 Menu options

6.1 The main menu

The *main* menu (see Figure 7) contains the following options:

`T Title`
This option allows you to specify a header to be used in the listing files.

`P Profiles and tests ...`
If you type `P`Enter the *main* menu will be replaced by the *profiles and tests* menu. This menu allows you to define the numbers of tests and the number of profiles in each test. It will be discussed in the next section.

`N Number of affects`
By this option you must specify the number of affects for all tests during this run. If you specify 16, 18, 20, 24, 28 or 30, the program will ask you if you want the predefined set with the specified number of affects. If you choose to do so, the set will be chosen, along with the corresponding scale definitions. You still have the possibility to add or remove affects or to modify the scale definitions.

`D Data definition ...`
If you type `D`Enter the *main* menu will be replaced by the *data definition* menu. This menu allows you to define the input data. It will be discussed in 6.3.

`C Construction of scales ...`
This option leads to a new menu that allows you to define scales, or to modify existing scale definitions. It will be treated in 6.4.

`H Hexagon analysis: No/1/2/3`
With this option you can specify whether the set of predefined hexagon marker profiles must be added to the data or not and which role the hexagon has to play. This option is only available if one of the predefined affect sets is chosen. Otherwise, you must define any marker profiles yourself by adding them to the input data.

Each time you type `H`Enter the choice circles through the series:
`No` → `1` → `2` → `3` → `No` →...

The meaning of the options is as follows:

- `No`: No hexagon will be added.
- `1`: The hexagon will be active; all user profiles will be passive, even if they are unstarred in the input file.
- `2`: The hexagon will be passive; the user profiles will be active if they are unstarred and passive otherwise.
- `3`: The hexagon will be active; the user profiles will be active if they are unstarred and passive otherwise.

If one of the options `1`, `2` or `3` is chosen, the option `P` is automatically set to `yes`, so a principal components analysis will be performed.

`P Principal components analysis`
If you type `P`Enter the *Principal components analysis* window will appear. Its options control the way the spatial representation is constructed. This menu will be discussed in 6.5.

`A Additional results ...`
This option leads to a new menu, that allows you to order additional information in the listing file. It will be treated in 6.6.

`W Write to separate file ...`
This option leads to a new menu that allows you to write several results to a “raw” text file. It will be discussed in 6.7.

`O Open settings file`
If you have ever saved the options for *Gridan* or if you received a settings file from someone else, you can retrieve the options from the settings file. If you type `O`Enter, a file-selector box will appear on the screen that allows you to select the settings file. By default settings files from *Gridan* have the extension '`.setgri`'. It may be handy to save your current settings before collecting new ones. The program may remind you of that. After you have collected information from a settings file, its name will be visible on the upper right part of the main window.

`S Save current settings`
If you want to save the options and specifications that you have made so far, you can enter `S`Enter. If you do so a file-selector box will appear that allows you to specify the place and the name of the file to which the settings must be written.

`X eXecute Gridan`
If you have specified all options you can type `X`Enter to start the computations. The program will check if all obligatory options are specified and if there are no inconsistencies. If everything is right, the computations will start. If the program has been correctly installed and runs without problems, it will, when it is finished, automatically open the last (or only) listing file it has made. If it fails to do so, you can open it yourself by any text editor like *WordPad*, *NotePad* or *Word*. In order to have a nicely outlined text, you must select a small non-proportional font like Courier New 9.

`Q Quit`
The option Q is a kind of emergency exit. If you choose it, *Gridan* will halt without performing any calculations and without producing any output files.

6.2 The profiles and tests menu

From the *main* menu, you may type the option `P`Enter to enter the *profiles and tests* menu. After you have filled out the options in this menu you must press Enter to return to the *main* menu.

If tests in your input file(s) are separated by empty lines and you want to analyze all tests, you can leave the options in this menu at their default values (see Figure 8), with a possible exception for the option `E`.

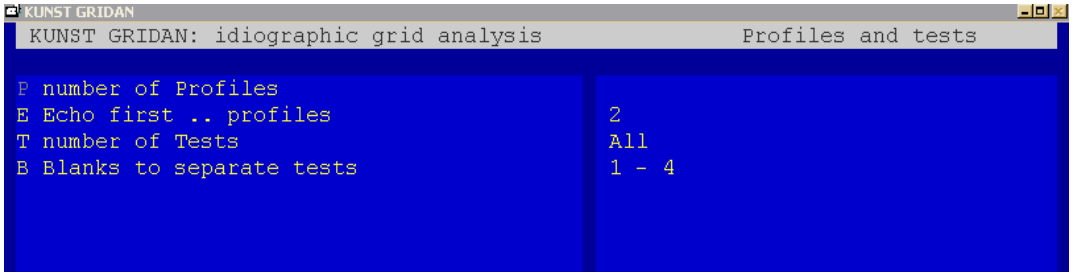

Figure 8: The profiles and tests menu.

In the *profiles and tests* menu the following options can be chosen:

`B Blanks to separate tests`
This option is the most likely one to mark the boundaries between tests within a file. If it is active, the program will recognize the boundaries between tests by an empty line, or, to be more precise, a profile with spaces in a specific field of its first line. The given number is the starting position of the field; its length is always 4.
If you are using fixed format input with more than one line per profile, the empty profile also must contain more lines.

`T number of Tests`
This option serves two purposes.

1. If a file contains more than one test and these tests are not separated by blank rows (see the option `Blanks`), you can specify the number of tests to be analyzed (this option) and thereafter the number of profiles in each of the subsequent tests (the option `P`). For example: `T 3`Enter`P 25 29 26`Enter. The latter method cannot be applied if there are several data files, unless the number of profiles per test is the same for all files.
2. Even if tests within a file are separated by blank rows, you may want to restrict the analyses to just a few tests at the beginning of the file.

`P number of Profiles`
This option can be used to define the numbers of profiles in subsequent tests. It makes only sense if the option `Blanks` is not used and the number of tests to be analyzed is specified. You may leave out the size of the last test; the program will assume that it runs until the end of the file.

If each input file contains only one test, you can specify '`P All`' to indicate that the file must be read from beginning to end and that the program must count the profiles itself.

`E Echo first ... profiles`
If you type `e ##`Enter the first ## profiles of each test will be shown in the listing file. This may help you to check if the input specifications are correct.

6.3 Definition of the data

From the *main* menu, you may type the option `D`Enter to enter the *data definitions* menu. After you have filled out the options in this menu you must press Enter to return to the *main* menu.

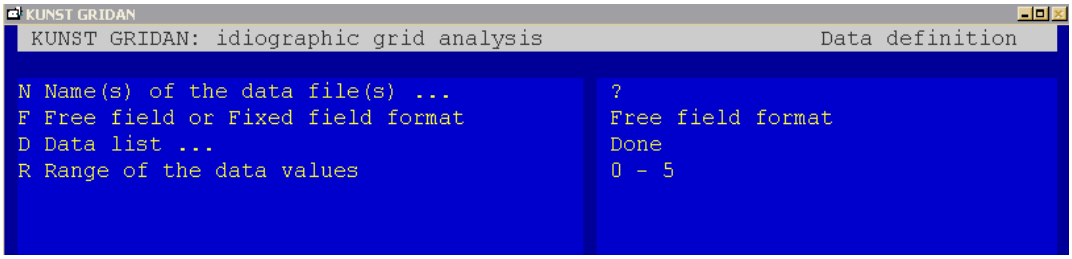

Figure 9: The data definition menu.

In the *data definition* menu (see Figure 9) the following options can be chosen:

`N Name(s) of the data file(s)`
If you choose this option a file-selector box will appear that enables you to select one or more data files.

`F Free field or Fixed field format`
This option defines where the values in a profile are to be found:

In a *free* format, the positions of the values may be different from row to row, although their order must be always the same. You can still choose whether line numbers are specified or not.
If the input file contains one single line per profile and the scores are separated by spaces, commas or tabs, you can select the free format option and skip the data list, with possibly one exception: by default the profile identification (the text identifying the profile) is taken from positions 1-8 of the input lines. If this identification is to be found elsewhere, you must use the data list to adjust its location.
Note that the distinction between active and passive profiles is based on the first position of this identification field.

In general, the use of free format is highly recommended since it is less sensitive to irregularities in the data or mistakes in the specifications.

In a *fixed* format, each profile consists of the same number of lines (most probably just one) and each value has a precisely defined position in that line. This format is especially useful if the values are typed one after the other without intervening spaces, tabs or commas. Each time you type `F`Enter the choice switches.

`D Data list ...`
If you choose this option, a new window will open with a layout that differs from the usual menu layout. Its layout depends on the chosen format type. Figure 10 shows a data list for fixed format data. Now you can type one of the indicated characters (`C`, `P`, `T`, `N`, `L`, `D`) followed by a sequence number or a range of sequence numbers and then followed by the corresponding information. The possibilities can best be clarified by some examples:

You type: `c1 5-7`Enter
Thereby you specify that the first **c**olumn (affect score) is in positions 5 through 7 (right adjusted).
From now on, you can leave out the code `C`; it will be assumed as long as you do not select another code.

You type: `2-4 11-16`Enter
This means that affects 2, 3 and 4 occupy positions 11 through 16, so affect 2 is in position 11-12, affect 3 is in positions 13-14 and affect 4 in positions 15-16.

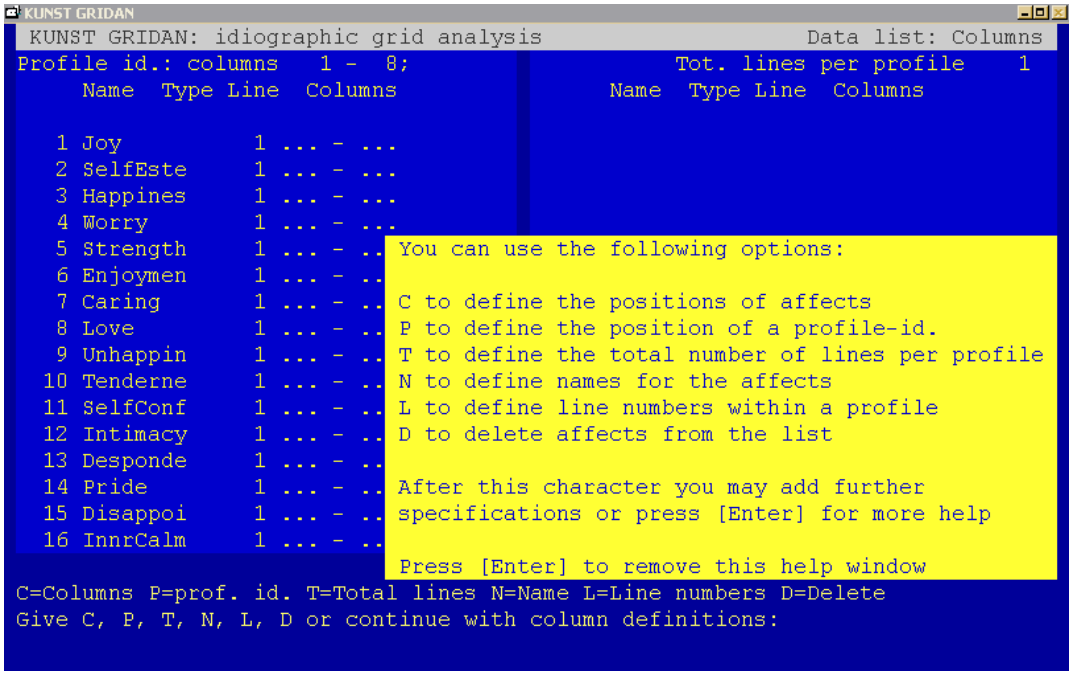

Figure 10: The data list for fixed format data.

You type: `5 18`Enter
This means that affect 5 occupies position 18.

You type: `L6 2`Enter
Now you have entered a different code. The code **L** indicates that you are defining line numbers. You specify that affect 6 is contained in the second line of a profile. Line numbers must be in ascending order. Therefore, the program will adjust the line numbers of affect 7 and higher to 2 if they are still 1. From now on, you may leave the code L out, until you switch to another code.

You type: `12-16 3`Enter
You specify that affects12 through 16 are contained in the third line of a profile.

You type: `N1 Pleasure`Enter
The code **N** indicates that you are specifying names. Affect 1 will receive the name '`Pleasure`'. Names will be truncated to 8 characters.

You type: `2-5 Esteem`Enter
Affects 2 through 5 will all be called '`Esteem`'!

You type: `6-12 Affect6`Enter
Affects 6 through 12 will be called '`Affect6`', '`Affect7`', ..., '`Affect12`'. As you see, if the name ends on a number, subsequent names will have their numbers adjusted.

You type: D5Enter
The option **D** allows you to remove an affect from the list. All sequence numbers and all other definitions will be adjusted accordingly. In this example, you remove the fifth affect. You can also specify a range of affect numbers, for instance 'D5-7', to remove the affects 5, 6 and 7.

You type: P1-8Enter
With the option **P** you define an area in the first line of each row that contains an alphanumerical profile label. These labels will be used in the listing file. Moreover the first character of this label defines whether a profile is active or passive: the labels of passive profiles start with an asterisk.

You type: T4Enter
If you don't use the option **T**, the program will assume that the number of lines for each profile is equal to the line number of the last affect in the data list. If there are more lines in a row, you must specify so by the option T. In this example, you specify that there are 4 lines in each profile.

You type: FEnter or BEnter
If there are more than 32 affects, they will not fit at once on the data list screen. Therefore, you have the possibility to scroll **f**orward and **b**ackward with the options F and B.

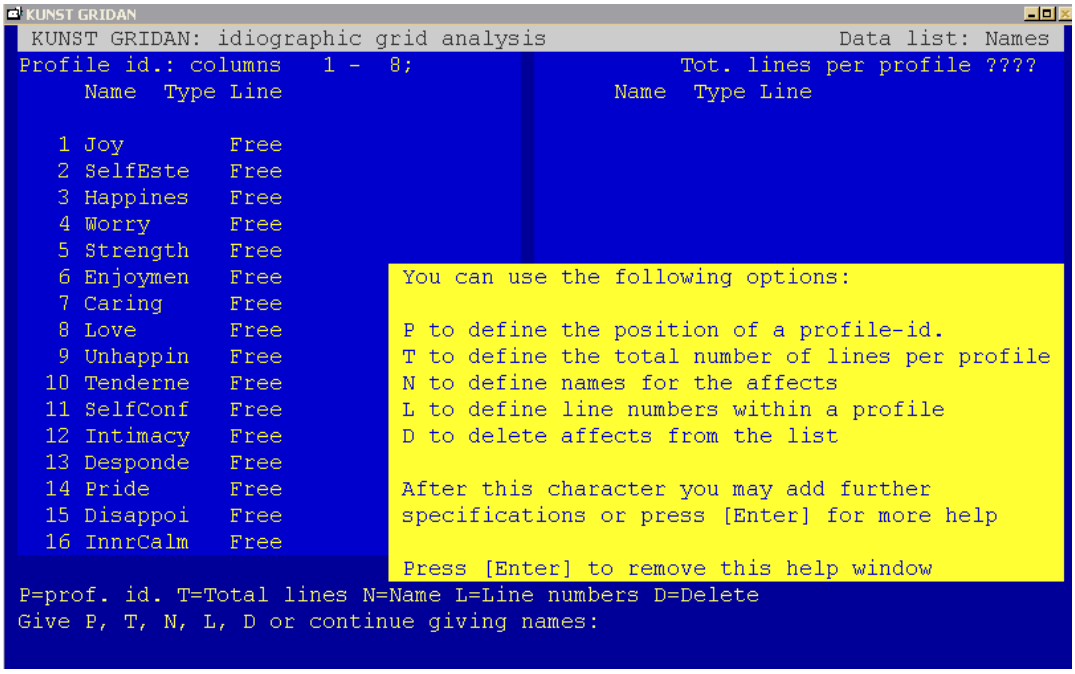

Figure 11: The data list for free format data.

If you use free format data (see Figure 11), you need none of the options in the data list, except possibly the option P to define the position of the profile labels. However, you may specify on which line of a profile each affect is recorded. So you can use the option L. The options P, T, N and D are also available. Their meaning and use are the same as with fixed format data (see above).

If you have finished the data list, you can go back to the *data* menu by entering an empty line (just Enter). If the yellow window is still visible, you must enter two empty lines (Enter Enter): one to remove the yellow window and one to return to the *data* menu.

`R Range of the data values`
By typing `R #1-#2`Enter or `R #1 #2`Enter you specify the minimum and maximum score (#1 and #2) a profile can assign to an affect. Values outside this boundaries will be replaced by the nearest of the two boundaries. This range also plays a role in the standardization of the distances between profiles: they will be divided by the range times the square root of the number of affects.

6.4 Construction and use of scales

In the *main* menu, typing cEnter leads to a submenu that handles scales. Before you define scales, make sure that the affects are defined properly.

When you chose a predefined set of affects, you will automatically receive a set of accompanying scales. An overview is given in 1.2. Figure 12 gives an example of the *scales* menu, using a predefined set of affects.

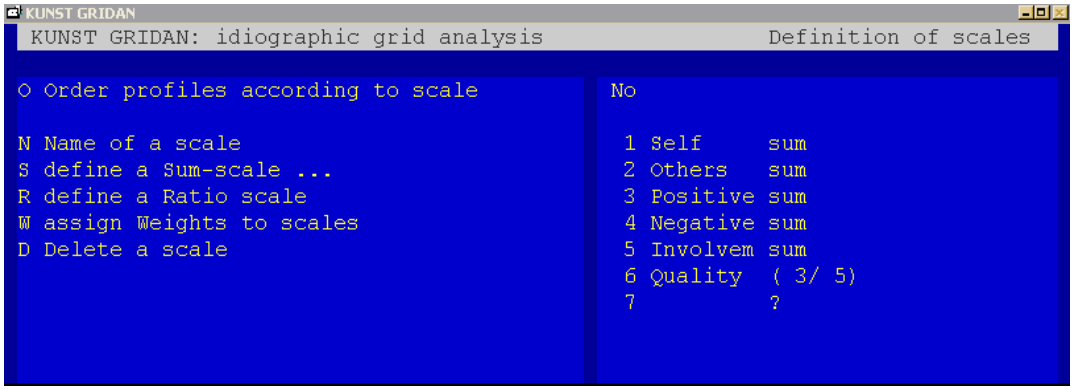

Figure 12: The scales menu.

On the right side of the screen, a list is given of the scales as they are defined so far. For each scale the list contains a sequence number, a name and a "type": `sum` or `ratio`.
The score of a profile on a sum-scale is the (weighted) sum of its scores on the affects in the scale.
The score of a profile on a ratio-scale is the ratio of its scores on the two sum-scales from which it is derived.
In Figure 12 five sum-scales (`Self, Others, Positive, Negative` and `Involvem`) and one ratio-scale (`Quality`) are defined. At the end of the list, there is an empty scale with a question mark as its type. There will always be such an empty scale unless the maximum number of scales (14) is reached. Use the sequence number of the empty scale to define a new one.

In this menu the following options can be chosen:

`O Order value-areas according to scale`
This option influences the order of the unstarred profiles at some places in the listing file: they will be sorted (in descending order) by their scores on the scale you point out here.

`N Name of a scale`
With this option you can name or rename a scale: just type `N` followed by a scale number and a name, like `N 5 Safety`Enter to give the fifth scale the name *Safety*.

`S define a Sum-scale`
Option `S` is used to define (or redefine) a sum-scale. When you type `S##`Enter, where ## is the number of a scale, the screen will display a list of all affects. If the scale already exists, the affects that are part of it are marked by an arrow as in Figure 13.

Figure 13: Definition of a sum-scale.

Now you can add or remove an affect by typing its number; if it was part of the scale, it will be removed (the arrow disappears); if it was not, it will be added (it gets an arrow).

You can also specify a range like `8-10`. If you do so, not all the affects in the range will switch: the first is switched, the others copy its new status. If the first affect of the range has an arrow, *all* affects in the range will end without arrows; if the first has no arrow, *all* affects in the range will get one.

You can leave the list of affects by entering an empty line (just Enter). If the yellow window is still visible, you must enter two empty lines (Enter Enter): one to remove the yellow window and one to return to the *scales* menu.

`R define a Ratio scale`

In the *scales* menu, the option `R` can be used to define a ratio-scale: type `R#1 #2 #3Enter` where #1 is the number of the ratio scale to be defined, #2 is the number of the numerator and #3 that of the denominator scale. You may also use "/" between #2 and #3. In Figure 12, you see that scale 6, called `Quality`, is defined as the ratio of scale 3 (`Positive`) and scale 5 (`Involvement`) (defined `as R 6 3/5`). Option `R` will be disabled if there are less than two sum-scales.

`W assign Weights to scale`

Option `W` allows you to assign weights to the elements of a scale. By default, all weights in a scale are equal to `1/n`, where `n` is the number of affects in the scale. Weights are useful if you want to combine subscales with different numbers of items in one overall scale. The weights can assure that the subscales have values in the same range. In such cases, it will be sufficient to weight each of the subscales with the product of the sizes of the other subscales.

Weights can also be used to change the direction of an affect: if the weight is negative, the affect score will be subtracted from the scale.

Of course weighting the numerator or the denominator of a ratio-scale influences the range of the ratio-scale. The option `E`Enter can be used to assure that the numerator and the denominator of a ratio-scale are in the same range of values, namely `1/n`, where `n` is the number of affects in the scale.

If you type `W ##`Enter, where ## is the number of a sum-scale, the screen will show a list of the affects in the scale and their current weights. You can change the weights only one by one (otherwise the program wouldn't see the difference between the dash used in a range and the sign of a negative weight). Figure 14 shows such a list.

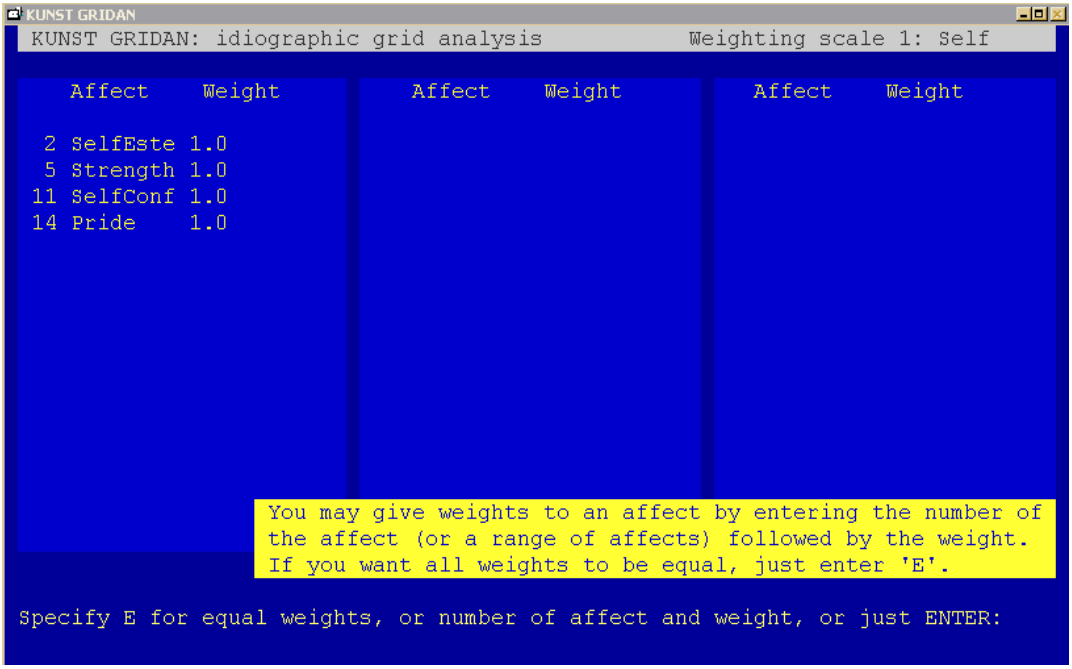

Figure 14: List of weights in a sum scale.

To change, for instance, the weight of the affect `Selfconf` to 2.5 one must type: `11 2.5`Enter. There is one way to change all weights at once: if you type only an **`E,`** the weights will be reset to their default value: `1/n`.

`D Delete a scale`
Within the *scales* menu, the option `D` can be used to delete a scale or a range of scales. Type `D #`Enter or `D #1-#2`Enter , where # is the sequence number of a scale and `#1-#2` a range of scale numbers. However, if a scale is part of a ratio scale, it cannot be removed before the ratio-scale is removed or redefined.

6.5 Principal components analysis

In the *main* menu, typing `P`Enter leads to a submenu that controls the principal components analysis (see Figure 15).

If the program tries to build a spatial representation of the profiles in a test, it interprets the `n` scores of the profiles on the affects as the coordinate points of the profiles in a `n`-dimensional space. Principal components analysis is a technique to find a projection of this configuration on a subspace with lesser dimensions, with a minimal loss of information about the distances between the profiles. As mentioned in section 1.3, Van Geel and De Mey found that the representation in two dimensions maintains the original distances very well. Especially this two-dimensional space offers the possibility to obtain an intuitive impression of a persons affect space and the place of his value areas in that space. The interpretation can be assisted by the addition of some prototypical marker profiles in the final representation.

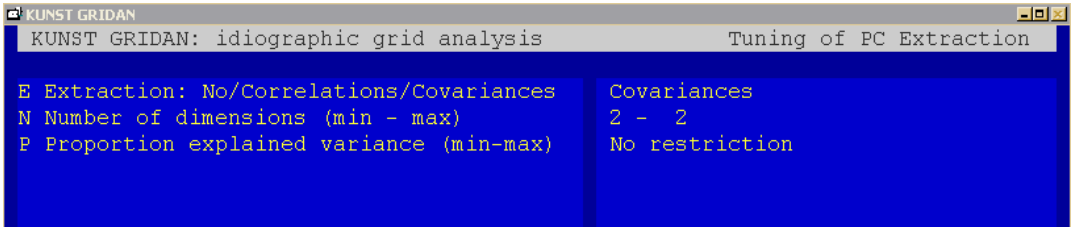

Figure 15: The tuning of the principal component analysis.

The *principal components analysis* menu offers the following options:

`E Extraction: No/Correlations/Covariances`
By typing `E`Enter you circle through these three possible options:

- `No`: do not perform a principal components analysis.
- `Correlations`: perform the analysis on the correlations of the affects.
- `Covariances`: perform the analysis on the covariances of the affects.

If you choose to perform the analysis, the most obvious choice is the covariance matrix, since it will produce the best reproduction of the original distances between the profiles. If the covariance matrix is used, affects with large variance will have more impact than those with small variance. If the correlation matrix is used however, all affects will be rescaled to the same variance, before the reduced space is computed.

p = proportion of variance explained	d = number of dimensions		
	d < minimum	min < d < max	d ≥ maximum
p < minimum	go on	go on	stop
minimum < p < maximum	go on	mean variance rule	stop
p > maximum	go on	stop	stop

Figure 16: Rules to determine the number of dimensions.

The other two options (`P` and `N`) control the number of dimensions to be extracted.

Extraction is performed dimension by dimension according to the following rules (as summarized in Figure 16):

- The extraction will never stop before the specified minimum number of dimensions is reached, unless all variance is completely explained.
- The extraction will always end if the specified maximum number of dimensions is reached.
- The extraction will not stop as long as the proportion of explained variance is less than the minimum, unless the maximum number of dimensions is reached.
- The extraction will stop as soon as the maximum proportion of explained variance is reached, unless the number of dimensions is still below the minimum.
- If the number of dimensions and the proportion of explained variance are both within their limits, the extraction stops as soon as a new dimension would explain less than the mean variance of the affects (if a covariance matrix is analyzed) or less then 1 (if a correlation matrix is analyzed).

`P Proportion explained variance (min-max)`
By typing `P #1-#2`Enter or `P #1 #2`Enter you specify the minimum and maximum proportion of variance to be explained. If you want to discard this criterion at all, type `P 1`Enter or `P 0`Enter.

`N Number of dimensions (min - max)`
By typing `N #1-#2`Enter or `N #1 #2`Enter you specify the minimum and maximum number of dimensions to be extracted. To define exactly the number of dimensions, you may give just one number, like `N 3`Enter. If you want to eliminate this criterion, type `N 0`Enter.

6.6 Additional results in the listing file

Entering `A`Enter in the *main* menu leads to the *additional results* menu (see Figure 17). The options in this menu offer the probability to get additional information in the listing file besides to what is given by default.

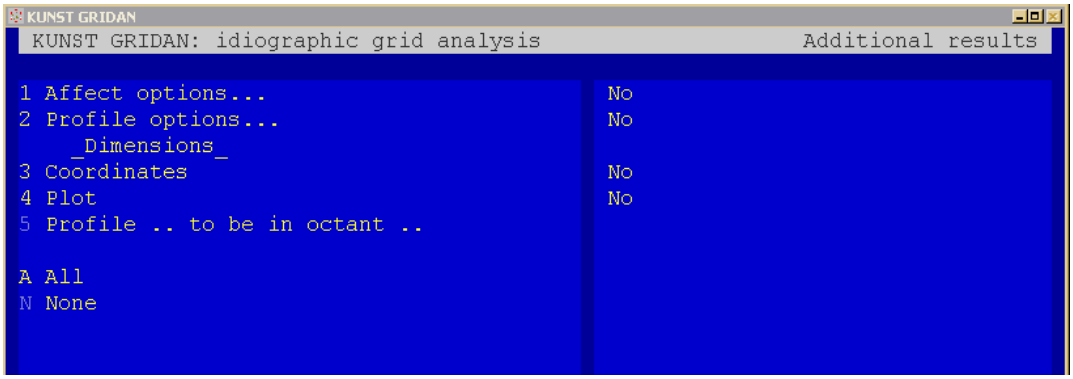

Figure 17: The additional results menu.

The menu contains the following options:

`1 Affect options ...`
`2 Profile options ...`
The options `1` and `2` lead to the *affect options* menu and the *profile options* menu. They will be discussed in 6.6.1 and 6.6.2.

`3 Coordinates`
By typing `3`Enter you switch the option from `yes` to `no` or the other way around. If it is `yes`, the listing file will contain the coordinates of the profiles in the reduced space. In order to maximize the similarity of the original distances of the active profiles to their distances in reduced space, the coordinates on a dimension are scaled such that the standard deviations are the square roots of the corresponding eigenvalues.

`4 Plot`
By typing `4`Enter you switch the option from `yes` to `no` or the other way around. If it is yes, the listing file will contain a plot of all profiles in the reduced space. If the number of dimensions is greater than 2, a separate plot will be shown for each pair of dimensions. In the listing file, these plots are rather coarse images, build as characters in a grid. More detailed pictures will be stored in separate bit map files.

`5 Profile .. to be in octant ..`
This option defines the orientation of the plots in case of a two-dimensional solution. First, you can point to a profile and then to an octant in the plane, in which that profile must be shown. The numbering of the octants in the plane is counter clockwise as shown in Figure 18.

Example: If you type `5 20 1`Enter, the plot will be rotated and possibly reflected such that the 20-th profile appears in the first octant.

`A All`
`N None`
If you type `A`Enter, options `1`, `2` , `3` and `4` will be switched to `yes` all together.
If you type `N`Enter, options `1`, `2` , `3` and `4` will be switched to `no` all together

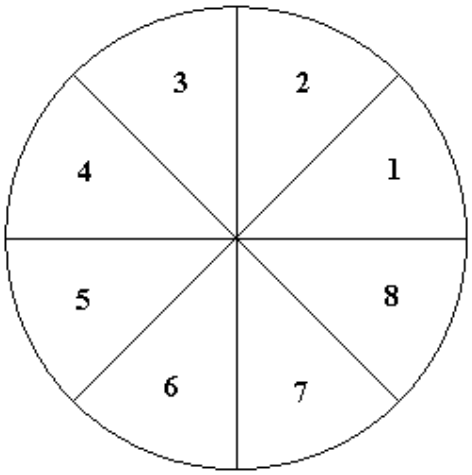

Figure 18: The octants in the plane.

6.6.1 Additional affect options

Typing `1Enter` in the *additional results* menu leads to the *affect options menu* (see Figure 19). By the options in this menu, you can order additional information on the affects.

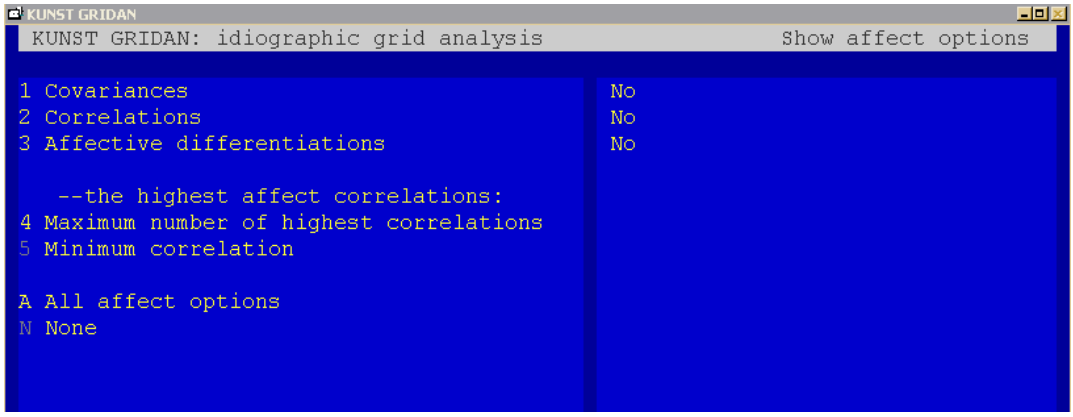

Figure 19: The affect options menu

The menu contains the following options:

`1 covariances`
By typing `1Enter` you can switch this option from `no` to `yes` and the other way around. If it is `yes,` the matrix of covariances between the affects will be shown in the listing file. They will be computed from the active (unstarred) profiles.

`2 correlations`
By typing `2Enter` you can switch this option from `no` to `yes` and the other way around. If it is `yes,` the matrix of correlations between the affects will be shown in the listing file. They will be computed from the active (unstarred) profiles.

`3 affective differentiations`
By typing 3Enter you can switch this option from `no` to `yes` and back. If it is `yes`, the program will compute the affective differentiation for each of the affects, that is the proportion of variance in the affect that cannot be explained by the other affects. The affective differentiation of an affect is the complement of the multiple correlation between that affect and all others. The affective differentiations are only computed if a principal components analysis is performed.

`4 maximum number of highest correlations`
`5 minimum correlation`
Options `4` and `5` can be used to obtain a list of pairs of affects ordered by the absolute values of their correlations, starting with the highest correlation and ending with the lowest.

If you type `4 ##1`Enter the list will be restricted to the first `##1` correlations with the highest absolute value. The default value for `##1` is 0, so no list will be given at all. Typing `5 ##2`Enter will restrict the list to those correlations that have absolute values above `##2`. If you type `A`Enter to select all options in the menu, `##1` will be set to 10 and `##2` to 0.4.

6.6.2 Additional profile options

Entering 2Enter in the *additional results* menu leads to the *profile options* menu (see Figure 20). By the options in this menu, you can order additional information on the profiles.

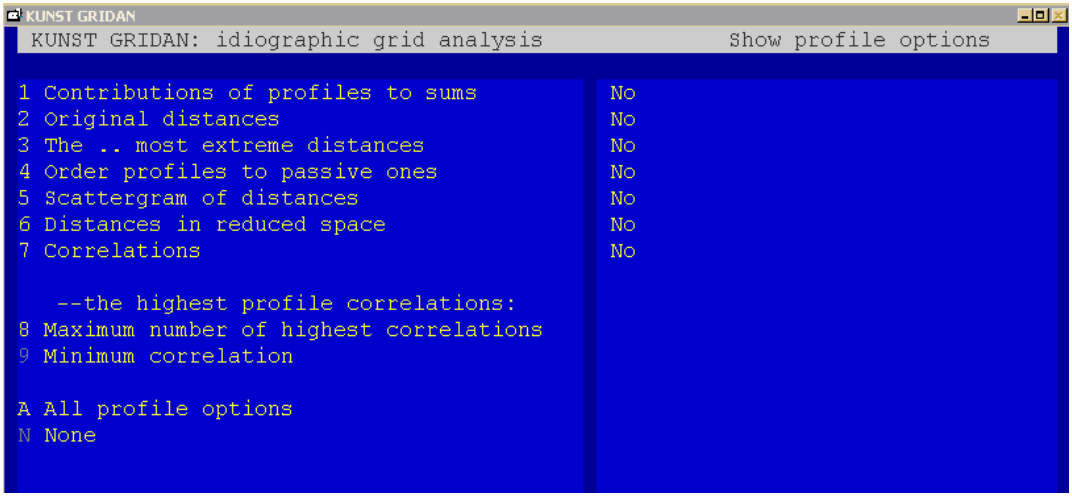

Figure 20: The profile options menu.

The menu contains the following options:

`1 contributions of profiles to sums`
You can switch this option from `yes` to `no` and back by typing 1Enter. If it is set to `yes`, the listing file will show for each affect the scores of the active profiles on it in descending order. Although this overview may be useful, you must realize that it takes a considerable amount of space in the listing file.

`2 original distances`
You can switch this option from `yes` to `no` and back by typing `2`Enter. If it is set to `yes`, the listing file will contain a matrix of standardized distances between the profiles in the original data file. The distance `d` between two profiles `x` and `y` in a space of `n` affects is defined as:

$$d(x,y) = \frac{1}{r}\sqrt{\sum_{i=1}^{n}(x_i - y_i)^2}$$, where r is a scaling value.

`3 the .. most extreme distances`
`If you type 3 ##`Enter the listing file will show the ## smallest and the ## largest standardized distances between the active profiles in the data. If you type `3 All`Enter, all distances between the active profiles will be shown, ordered from largest to smallest.

`4 order profiles to passive ones`
You can switch this option from `no` to `yes` and from `yes` to `no` by typing `4`Enter. If it is `yes`, the listing file will contain for each passive profile a list of all profiles, ordered by their distance to that passive profile. This option is restricted to the five first passive profiles that are encountered in the input data or added by the hexagon option.

`5 scattergram of distances`
You can switch this option from `no` to `yes` and back by typing `5`Enter. If it is `yes`, the listing file will show a scattergram of the distances between the profiles in the input file (on the x-axis) and the corresponding distances in the reduced space (on the y-axis). This so-called 'Shepard plot' gives an impression of the quality of the resemblance between the original data space and the reduced space. The closer this scattergram comes to a line, the better the distances in the reduced space represent the original distances.

Note: This option will not produce any results unless a principal components analysis is chosen also.

`6 distances in reduced space`
You can switch this option to `yes` or `no` by typing `6`Enter. If it is set to `yes`, the listing file will contain a matrix of distances between the profiles in the reduced space.
Note: this option will not produce any results unless a principal components analysis is chosen also.

`7 correlations`
You can switch this option from `yes` to `no` and back typing `7`Enter. If it is set to `yes`, the listing file will contain a matrix of correlations between the profiles.

`8 maximum number of highest correlations`
`9 minimum correlation`
Options `8` and `9` can be used to obtain an ordered list of pairs of profiles ordered by the absolute values of their correlations, starting with the highest correlation and ending with the lowest.
If you type `8 ##1`Enter the list will be restricted to the first `##1` correlations with the highest absolute value. The default value for ## is 0, so no list will be given at all.
Typing `9 ##2`Enter will restrict the list to those correlations that have absolute values above `##2`.

If you type A Enter to select all options in the menu, option 8 will be set to 10, option 9 to 0.4 and option 3 will receive the value 10.

6.7 Additional results in the raw output file

In the *main* menu the option W leads to the *write to separate file* menu as shown in Figure 21.

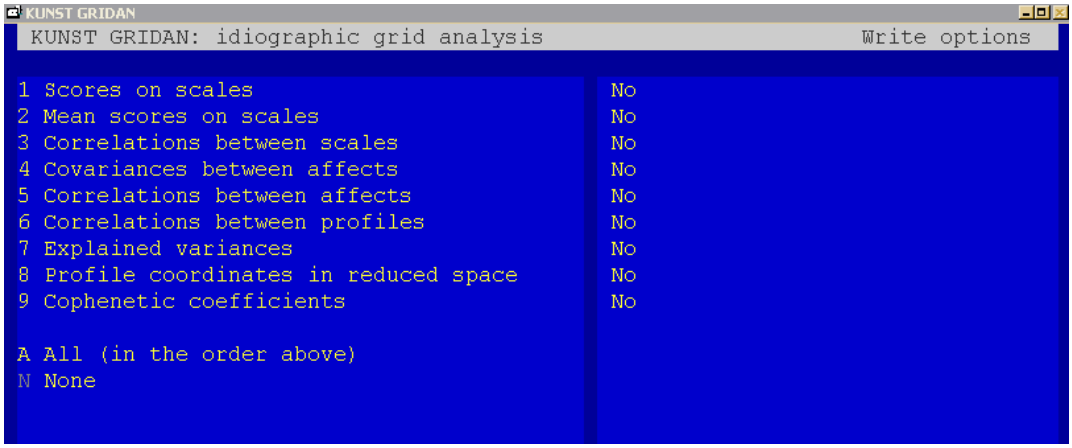

Figure 21: The Write-to-separate-file menu.

This menu contains a list of flags. If you type # Enter, where # is one of the options 1 through 9, the corresponding option switches from no to yes or back. The options all lead to output in a separate file without any layout. This output file makes it relatively easy for other programs to collect the information for their own use.

If any output option is chosen, a raw output file will be produced. If more than one kind of output is produced, the file will contain the results in the order as they are mentioned in the menu. In the output file a single labeling line will precede each option.

`1 scores on scales`
If this option is set to yes, the raw output file will contain the scores of all profiles on all scales. Note that, although you may have asked to order the profiles according to a scale (option O in the *scales* menu), here the profiles will be given in their original order.

`2 mean scores on scales`
If this option is set to yes, the raw output file will contain for each scale the mean score of the active (unstarred) profiles on the affects that constitute the scale.

`3 correlations between scales`
If this option is set to yes, the raw output file will contain a matrix of correlations between all scales, computed from the active profiles.

`4 covariances between affects`
If this option is set to yes, the raw output file will contain a matrix of covariances between the affects, computed from the active profiles.

`5 correlations between affects`
If this option is set to `yes`, the raw output file will contain a matrix of correlations between the affects, computed from the active profiles.

`6 correlations between value areas`
If this option is set to `yes`, the raw output file will contain a matrix of correlations between all profiles.

`7 explained variances`
If this option is set to `yes`, the raw output file will contain the proportion of affect variance explained by the dimensions in the reduced space, followed by the total available affect variance. This option applies only if a principal components analysis is performed.

`8 profile coordinates in reduced space`
If this option is set to `yes`, the raw output file will contain the coordinates of all profiles in the reduced space. This option applies only if a principal components analysis is performed.

`9 cophenetic coefficients`
If this option is set to `yes`, the raw output file will contain the cophenetic coefficients for the active profiles, the passive profiles and all profiles. The cophenetic coefficient is the correlation between the distances from the original data and those in the reduced space. This option applies only if a principal components analysis is performed.

7 Results

After execution of *Gridan*, you will find one or more new files in your working directory:

- the listing file (.lst)
- if you asked for additional output in a separate file (`W` in the *main* menu) the raw output file (.out)
- possibly some bit map files

7.1 Results in the listing file

The listing file will contain the main results for the tests in the corresponding data file. Its precise content depends on the specifications by the user and the input data. The lines in the listing have a length of 80 characters or less. View (and print) this file with a small non-proportional font like Courier New 9.

- The file starts with an overview of the options as they are chosen by the user.
- Then follow the results test by test.

Data descriptives:

- A list of the first profiles. The list is meant as a check on the data and the data format used. How many profiles are echoed, depends on the echo option in the *profiles and tests* menu (see 6.2).

```
2.1  Means and standard deviations of the profiles
_____________________________________________________


                                  Profile       Mean   Stand.Dev.

                      Unwanted child   1:      1.062     1.559
                 Creche was terrible   2:      1.250     2.812
                       Missed father   3:      1.375     3.109
          ..................................................
          ..................................................
                    *General feelings  23:      2.562     0.746
                      *Ideal feelings  24:      3.125     2.109
```

Figure 22: Means and standard deviations of the profiles.

- A list of the profiles with their means and standard deviations (the population formula: sd = $\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_i - x)^2}$ with x_i = the score on the i-th affect). Figure 22 shows an example.

```
2.2  Means and standard deviations of the affects
 ____________________________________________________

             Passive profiles are excluded from the computation.
             The affects are ordered by their mean.

                                    Affect       Mean   Stand.Dev.

                                Worry      4:      2.955     1.260
                                Unhappin   9:      2.909     1.240
                                Disappoi  15:      2.818     1.266
                                ..................................
                                ..................................
                                Tenderne  10:      1.591     1.302
                                Intimacy  12:      1.500     1.469
```

Figure 23: Means and standard deviations of the affects.

- A list of the affects with their means and standard deviations (again the population formula) based on the active profiles. Figure 23 shows an example.

```
2.3  Data from test 1
 ____________________

TOTAL*: Sum of all profiles.
TOTAL : Sum of the active profiles.

                 S   H       S   E           U   T   S   I   D       D   I
                 e   a       t   n           n   e   e   n   e       i   n
                 l   p       r   j   C       h   n   l   t   s       s   n
                 f   p   W   e   o   a       a   d   f   i   p   P   a   r
                 E   i   o   n   y   r   L   p   e   C   m   o   r   p   C
             J   s   n   r   g   m   i   o   p   r   n   a   n   i   p   a
             o   t   e   r   t   e   n   v   i   n   n   c   d   d   o   l
             y   e   s   y   h   n   g   e   n   e   f   y   e   e   i   m
-------------------------------------------------------------------------------
Unwanted:    0   0   0   1   1   0   1   1   4   1   1   0   2   1   4   0
Creche w:    0   0   0   4   1   1   0   1   5   0   0   0   3   1   4   0
Missed f:    0   0   0   4   0   0   0   0   4   3   0   1   3   2   5   0
.....................................
.....................................
*General:    3   3   2   4   3   3   2   3   4   1   2   2   2   3   3   1
*Ideal f:    4   4   4   1   4   5   2   5   1   4   2   4   1   4   1   4
-------------------------------------------------------------------------------
TOTAL*:     66.     59.     64.     41.     69.     41.     49.     66.
               63.     70.     67.     62.     40.     39.     57.     44.
TOTAL :     59.     53.     57.     37.     64.     37.     46.     62.
               56.     65.     59.     54.     35.     33.     50.     39.
```

Figure 24: The data matrix.

- The matrix of scores on the affects (see Figure 24), possibly ordered by the score on one selected scale (by use of option `O` in the *scales* menu). At the bottom of the matrix some aggregated information is displayed:
  Total*: for each affect the sum of the scores from all profiles including the passive ones.
  Total: for each affect the sum of the scores from the active profiles.

```
2.4  Contributions of active profiles to affect sums
 ____________________________________________________

             The affect sums are ordered from greatest to smallest.


 Sum 65.0 on affect 4 (Worry) is constructed as follows:


       Profile     Score      Profile     Score      Profile     Score
 ------------------------------------------------------------------------

      13 (Object a)   5 :     3 (Missed f)   4 :    22 (Jesus is)   2
      21 (Worry ab)   5 :    11 (Enjoyed )   3 :    18 (Discussi)   2
       4 (Strictly)   4 :    16 (Sleep mu)   3 :     6 (Fantasy )   1
       9 (Married )   4 :    12 (Third ch)   3 :    17 (Music an)   1
       2 (Creche w)   4 :     8 (Dental n)   3 :     1 (Unwanted)   1
      14 (Trimmed )   4 :    10 (Pregnanc)   3 :    19 (Religiou)   1
      15 (Find mys)   4 :     7 (Last cla)   2 :
      20 (Fundamen)   4 :     5 (Nature g)   2 :


 Sum 64.0 on affect 9 (Unhappin)is constructed as follows:
 ..........
 ..........
```

Figure 25: Contributions of active profiles to affect sums.

- Optionally (option 1 in the *additional profile options* menu) for each affect the list of the active profiles in descending order according to their scores on the affect. The affects themselves are ordered according to their sum score (based on the active profiles). Figure 25 gives an example.

```
2.5  Scores on scales
 ____________________

     Passive profiles are excluded from the computation of mean and alpha.

                              P      N      I
                              o      e      n      Q
                        O     s      g      v      u
                        t     i      a      o      a
                S       h     t      t      l      l
                e       e     i      i      v      i
                l       r     v      v      e      t
                f       s     e      e      m      y
 ------------------------------------------------------------
  1 Unwanted:   3.00   3.00   0.00  11.00  11.00   0.00
  2 Creche w:   2.00   1.00   1.00  16.00  17.00   0.06
  3 Missed f:   2.00   4.00   0.00  16.00  16.00   0.00
  ..............................
  ..............................
 23 *General:  11.00   8.00   9.00  13.00  22.00   0.41
 24 *Ideal f:  14.00  15.00  17.00   4.00  21.00   0.81
 ------------------------------------------------------------
       Alpha:   0.91   0.94   0.95   0.90   0.17    -
        Mean:   9.09   7.23   9.55  10.77  20.32   0.44
```

Figure 26: Scores of profiles on scales.

- The scores of the profiles on the scales (if there are any), the corresponding reliabilities (Cronbach's alpha) and the mean scores over the active profiles (see Figure 26). Since the self-confrontation method is not really a test, it is not quite appropriate to speak of reliability. In this context Cronbach's alpha is just one of many statistics available to measure the extent to which the affects in a scale measure one single underlying property. Low values of alpha may be a motive

to have a closer look at the correlations between the affects in the scale. Cronbach's alpha is not computed for ratio scales.

```
 2.6  Correlations between the scales
 ____________________________________

              Passive profiles are excluded from the computation.


              :    Self    Others  Positive Negative Involvem
              :     1        2        3        4        5
 -------------------------------------------------------------
 Others     2 :    0.671
 Positive   3 :    0.835    0.853
 Negative   4 :   -0.480   -0.606   -0.706
 Involvem   5 :    0.725    0.632    0.744   -0.053
 Quality    6 :    0.744    0.770    0.957   -0.844    0.553
-------------------------------------------------------------
              :     1        2        3        4        5
              :    Self    Others  Positive Negative Involvem
```

Figure 27: Correlations between the scales.

- the matrix of correlations between the scales (if there are scales). Figure 27 shows an example.

```
2.7  Covariances between the affects
 ___________________________________

              Passive profiles are excluded from the computation.


              :    Joy    SelfEste Happines  Worry   Strength Enjoymen  Caring
              :     1        2        3        4        5        6        7
 ------------------------------------------------------------------------------
 Joy        1 :    4.217
 SelfEste   2 :    2.674    2.339
 Happines   3 :    3.176    2.186    2.878
 .........................
 .........................
 ------------------------------------------------------------------------------
              :     1        2        3        4        5        6        7
              :    Joy    SelfEste Happines  Worry   Strength Enjoymen  Caring
```

Figure 28: Covariances between the affects.

```
2.8  Correlations between the affects
 ___________________________________

              Passive profiles are excluded from the computation.


              :    Joy    SelfEste Happines  Worry   Strength Enjoymen  Caring
              :     1        2        3        4        5        6        7
 ------------------------------------------------------------------------------
 SelfEste   2 :    0.851
 Happines   3 :    0.912    0.843
 Worry      4 :   -0.532   -0.294   -0.501
 .........................
 ------------------------------------------------------------------------------
              :     1        2        3        4        5        6        7
              :    Joy    SelfEste Happines  Worry   Strength Enjoymen  Caring
```

Figure 29: Correlations between the affects

- optionally (option 1 and 2 in the *additional affect options* menu) the covariances and the correlations between the affects (see Figure 28 and Figure 29). Passive profiles are excluded from the computation.

```
2.9  Highest correlations between affects
 ____________________________________________

 Restrictions:
   - at most 10 correlations
   - only correlations that exceed 0.4 in absolute value

             Affects                Correlation

 Happines   3  <->   6  Enjoymen :     0.933
      Joy   1  <->   6  Enjoymen :     0.916
      Joy   1  <->   3  Happines :     0.912
 Enjoymen   6  <->   8  Love     :     0.897
 Happines   3  <->   8  Love     :     0.892
     Love   8  <->  12  Intimacy :     0.870
 Tenderne  10  <->  12  Intimacy :     0.867
 SelfEste   2  <->  16  InnrCalm :     0.855
      Joy   1  <->   2  SelfEste :     0.851
      Joy   1  <->  15  Disappoi :    -0.844
```

Figure 30: Highest correlations between affects.

- optionally (depending on options 4 and 5 in the *additional affect options* menu) a list of pairs of affects ordered by the absolute values of their correlations and starting with the highest correlated pairs (see Figure 30).

```
2.10  Correlations between the profiles
 ____________________________________________



              :  Unwanted Creche w Missed f Strictly Nature g Fantasy Last cla
              :     1        2        3        4        5        6        7
 ------------------------------------------------------------------------------
 Creche w   2 :    0.828
 Missed f   3 :    0.784    0.835
 Strictly   4 :    0.824    0.952    0.820
 ........................
 ........................
 ------------------------------------------------------------------------------
              :     1        2        3        4        5        6        7
              :  Unwanted Creche w Missed f Strictly Nature g Fantasy Last cla
```

Figure 31: Correlations between the profiles.

- optionally (option 7 in the *additional profile options* menu) the correlations between the profiles (see Figure 31).

```
 2.11  Highest correlations between profiles
 ___________________________________________

 Restrictions:
   - at most 10 correlations
   - only correlations that exceed 0.4 in absolute value

                         Profiles                            Correlation

  Creche was terrible   2  <->   4  Strictly disciplined :     0.952
  Nature gave comfort   5  <->   6  Fantasy about gnomes :     0.937
 Strictly disciplined   4  <->  13  Object as marriage r :     0.924
  Creche was terrible   2  <->  13  Object as marriage r :     0.923
 Fantasy about gnomes   6  <->  17  Music and dancing ma :     0.897
 Pregnancies were hap  10  <->  11  Enjoyed the children :     0.885
  Nature gave comfort   5  <->  10  Pregnancies were hap :     0.879
 Strictly disciplined   4  <->  24  *Ideal feelings      :    -0.865
 Religious but not da  19  <->  24  *Ideal feelings      :     0.858
 Last class did me ri   7  <->   8  Dental nurse to plea :     0.856
```

Figure 32: Highest correlations between profiles.

- optionally (depending on options 8 and 9 in the *additional profile options* menu) a list of pairs of profiles ordered by the absolute values of their correlations and starting with the highest correlated pairs (see Figure 32).

```
2.12  The standardized distances between the profiles
 ____________________________________________________

 The raw distances divided by their theoretical maximum:  20.000

 The mean standardized distance between the active profiles is   0.378


             :  Unwanted Creche w Missed f Strictly Nature g Fantasy Last cla
             :     1        2        3        4        5        6        7
-------------------------------------------------------------------------------
Creche w   2 :    0.194
Missed f   3 :    0.229    0.200
Strictly   4 :    0.212    0.112    0.218
.............................
.............................
-------------------------------------------------------------------------------
             :     1        2        3        4        5        6        7
             :  Unwanted Creche w Missed f Strictly Nature g Fantasy Last cla
```

Figure 33: Standardized distances between profiles.

- the mean standardized distance between the active profiles. The standardization means that the distances are divided by the square root of the number of affects and by the range of the data (see Figure 33).
- optionally (option 2 in the *additional profile options* menu) the standardized distances between all profiles (see Figure 33).

2.13 The 10 largest distances between the active profiles

Profiles					Distance
Enjoyed the children	11	<->	4	Strictly disciplined :	0.7124
Religious but not da	19	<->	4	Strictly disciplined :	0.7124
Jesus is my confidan	22	<->	4	Strictly disciplined :	0.7000
Religious but not da	19	<->	3	Missed father :	0.6782
Enjoyed the children	11	<->	2	Creche was terrible :	0.6745
Jesus is my confidan	22	<->	3	Missed father :	0.6727
Enjoyed the children	11	<->	3	Missed father :	0.6708
Religious but not da	19	<->	2	Creche was terrible :	0.6708
Jesus is my confidan	22	<->	2	Creche was terrible :	0.6652
Discussing facts of	18	<->	4	Strictly disciplined :	0.6614

Figure 34: The 10 largest distances between the active profiles.

2.14 The 10 smallest distances between the active profiles

Profiles					Distance
Fantasy about gnomes	6	<->	5	Nature gave comfort :	0.1000
Dental nurse to plea	8	<->	7	Last class did me ri :	0.1000
Strictly disciplined	4	<->	2	Creche was terrible :	0.1118
Music and dancing ma	17	<->	6	Fantasy about gnomes :	0.1225
Enjoyed the children	11	<->	10	Pregnancies were hap :	0.1323
Music and dancing ma	17	<->	5	Nature gave comfort :	0.1414
Jesus is my confidan	22	<->	19	Religious but not da :	0.1500
Religious but not da	19	<->	18	Discussing facts of :	0.1581
Object as marriage r	13	<->	2	Creche was terrible :	0.1658
Object as marriage r	13	<->	4	Strictly disciplined :	0.1732

Figure 35: The 10 smallest distances between the active profiles.

- optionally (depending on option 3 in the *additional profile options* menu) a list of the largest and a list of the smallest distances between the active profiles (see Figure 34 and Figure 35).

```
2.15  Profiles ordered by standardized distances to passive profiles
 ____________________________________________________________________


 Distances to passive profile 23: *General feelings

                                        Profile      Distance

        Find myself by reading, listening   15 :     0.1581
             Married because of attention    9 :     0.1581
            Dental nurse to please father    8 :     0.1936
  ..................................................
  ..................................................
                           Missed father    3 :     0.4153
           Strictly disciplined by mother    4 :     0.4183



 Distances to passive profile 24: *Ideal feelings

                                        Profile      Distance

    Religious but not daring to surrender   19 :     0.1581
                     Jesus is my confidant   22 :     0.1658
                Discussing facts of life   18 :     0.2000
 ..................................................
  ..................................................
                       Creche was terrible    2 :     0.6928
           Strictly disciplined by mother    4 :     0.7399
```

Figure 36: Profiles ordered by standardized distances to passive profiles

- depending on option 4 in the *additional profile options* menu the profiles in order of their distance to the (first 5) passive (starred) profiles (see Figure 36).

Representation in reduced space:

Note that the extraction is based on the active profiles only!
Note also that all following items will not be produced when no principal components analysis is performed.

```
3.1  The affective differentiations   (unique proportion of the variance
 ___________________________________    of each affect)


       Affect    Differentiation

 Joy        1:     0.0324
 SelfEste   2:     0.0691
 Happines   3:     0.0511
 ..................
 ..................
```

Figure 36: The affective differentiations.

- optionally (depending on option 3 in the *additional affect options* menu) the affective differentiation coefficients. The affective differentiation of an affect is the proportion of variance in it, that cannot be explained by the other affects. (see figure 36).

```
3.2  The Principal Components Extraction
 ____________________________________________


 The number of dimensions will be determined by the following rule(s):
     - the number must be in the range 2 - 2

 The analysis is based on the covariance matrix of the 16 affects, using
 only the active profiles.

 Eigenvalues:     The eigenvalue of a dimension defines the amount of variance
                  accounted for by that dimension.

 Dimension    Eigenvalue

      1         22.3181
      2          2.7451


 Extraction ended because
    the maximum number of dimensions is reached.
```

Figure 37: The principal components analysis: the eigenvalues.

The following items pertaining to the principal components extraction are displayed:

- the eigenvalues. The eigenvalue of a dimension defines the amount of variance accounted for by that dimension. The total available variance is the sum of the variances of the affects or, if the principal components analysis is based on the correlations, the number of affects (see Figure 37).

```
Component matrix:  This matrix gives the covariances between the affects
                    and the unit scaled components.

 Affects are ordered by the dimension on which they load highest and by
 the loading itself. In each row, the highest loading is marked by an
 asterisk.

       Affect    Dimension

                :    1        2
 --------------------------------
 Joy         1 :  -1.9632*  0.0838
 Happines    3 :  -1.6293* -0.0396
 Enjoymen    6 :  -1.5665*  0.0259
 Love        8 :  -1.4163* -0.0911
 SelfEste    2 :  -1.3378* -0.5390
 Intimacy   12 :  -1.2593*  0.0818
 InnrCalm   16 :  -1.1401* -0.3938
 Pride      14 :  -1.0545* -0.4741
 Disappoi   15 :   1.0521* -0.5269
 Caring      7 :  -0.9597*  0.0788
 Tenderne   10 :  -0.9523*  0.3001
 Unhappin    9 :   0.7747* -0.5953
 Strength    5 :  -0.7720* -0.6166
 Worry       4 :   0.7315* -0.5867
 SelfConf   11 :  -0.6844* -0.3361
 Desponde   13 :   0.6540  -0.6963*
 --------------------------------
```

Figure 38: The component matrix.

- the component matrix. In case of an extraction on the covariances, this matrix contains the covariances between the affects and the unit scaled dimensions. In case of an extraction on the correlation matrix, it contains the correlations between the affects and the dimensions (see Figure 38).

```
Component matrix corrected for variances:
                 This matrix gives the correlations between the affects and
                 the components.

 To interpret a component in terms of affects, consider the affects that load
 high on that dimension in absolute value.
 Affects are ordered by the dimension on which they load highest and by
 the loading itself. In each row, the highest loading is marked by an
 asterisk.

       Affect    Dimension

                :    1        2
 ---------------------------------
 Happines   3 :  -0.9604* -0.0234
 Joy        1 :  -0.9560*  0.0408
 Enjoymen   6 :  -0.9425*  0.0156
 Love       8 :  -0.9261* -0.0596
 SelfEste   2 :  -0.8748* -0.3524
 InnrCalm  16 :  -0.8690* -0.3002
 Intimacy  12 :  -0.8570*  0.0556
 Disappoi  15 :   0.8309* -0.4161
 Pride     14 :  -0.7986* -0.3591
 Caring     7 :  -0.7863*  0.0646
 Tenderne  10 :  -0.7312*  0.2304
 SelfConf  11 :  -0.7044* -0.3459
 Strength   5 :  -0.6471* -0.5168
 Unhappin   9 :   0.6248* -0.4802
 Worry      4 :   0.5803* -0.4655
 Desponde  13 :   0.6037  -0.6427*
 ---------------------------------
```

Figure 39: The component matrix corrected for variances.

- in case of an extraction on the covariances: the component matrix corrected for variances. This matrix contains the correlations between the affects and the dimensions (see Figure 39), so they are helpful in the interpretation of the dimensions. In the example of Figure 39 for instance, the first dimension shows very strong negative correlations with the affects `Happines`, `Joy` and `Enjoymen`, so it may be interpreted as *Unhappiness*.

Communalities:
The communality of an affect is the part of its variance that is explained by the components.

The communality corrected for variance of an affect is the proportion of its variance that is explained by the components.

		Communality	Corrected Communality
Joy	1 :	3.8612	0.9156
SelfEste	2 :	2.0803	0.8894
Happines	3 :	2.6561	0.9229
Worry	4 :	0.8794	0.5535
Strength	5 :	0.9762	0.6857
Enjoymen	6 :	2.4545	0.8885
Caring	7 :	0.9272	0.6224
Love	8 :	2.0142	0.8612
Unhappin	9 :	0.9545	0.6210
Tenderne	10 :	0.9969	0.5877
SelfConf	11 :	0.5814	0.6157
Intimacy	12 :	1.5926	0.7376
Desponde	13 :	0.9126	0.7776
Pride	14 :	1.3368	0.7666
Disappoi	15 :	1.3845	0.8636
InnrCalm	16 :	1.4548	0.8453

Figure 40: The communalities, raw and corrected for variance

- the communalities of the affects. If the extraction is based on the correlation matrix, they are the proportions of explained variance. If the extraction is based on the covariance matrix, the communalities are the **portions** of explained variance. In this case, also the communalities corrected for variances (proportions of explained variance) are displayed (see Figure 40).

Overview of the variances of the affects:

		variance of affects	proportions
explained by component	1 :	22.318	0.706
explained by component	2 :	2.745	0.087
		---	---
total explained	:	25.063	0.793
unexplained	:	6.552	0.207
		---	---
total	:	31.616	1.000

Figure 41: Overview of the variances of the affects.

- an overview of the explained and unexplained affect variances (see Figure 41).

3.3 Raw least square weights (Bx)

Column i gives the weights needed to compute the position of the profiles on dimension i from the deviation scores X.
(A deviation score is the original score minus the affect mean over the active profiles.)
Geometrically: the coefficients to compute the projections of the profiles in the best fitting space from the deviation scores.
To use these weights on other deviation scores, they were divided by the maximum theoretical distance: 20.0

Affect		Dimension 1	2
Joy	1 :	-0.0208	0.0025
SelfEste	2 :	-0.0142	-0.0163
Happines	3 :	-0.0172	-0.0012
Worry	4 :	0.0077	-0.0177
Strength	5 :	-0.0082	-0.0186
Enjoymen	6 :	-0.0166	0.0008
Caring	7 :	-0.0102	0.0024
Love	8 :	-0.0150	-0.0027
Unhappin	9 :	0.0082	-0.0180
Tenderne	10 :	-0.0101	0.0091
SelfConf	11 :	-0.0072	-0.0101
Intimacy	12 :	-0.0133	0.0025
Desponde	13 :	0.0069	-0.0210
Pride	14 :	-0.0112	-0.0143
Disappoi	15 :	0.0111	-0.0159
InnrCalm	16 :	-0.0121	-0.0119

Figure 42: Raw least square weights of the affects.

3.4 Standardized least square weights (Bz)

Column i gives the weights needed to compute the position of the profiles on dimension i from the standardized scores Z.
(A standardized score is the original score minus the affect mean divided by its standard deviation; the mean and the standard deviation are computed from the active profiles.)
Geometrically: the coefficients to compute the standardized projections of the profiles in the best fitting space from the standardized scores.
To use these weights on other standardized deviation scores, they were divided by the maximum theoretical distance: 20.0

Affect		Dimension 1	2
Joy	1 :	-0.0427	0.0052
SelfEste	2 :	-0.0217	-0.0249
Happines	3 :	-0.0293	-0.0020
Worry	4 :	0.0098	-0.0223
Strength	5 :	-0.0097	-0.0222
Enjoymen	6 :	-0.0276	0.0013
Caring	7 :	-0.0124	0.0029
Love	8 :	-0.0229	-0.0042
Unhappin	9 :	0.0102	-0.0223
Tenderne	10 :	-0.0131	0.0118
SelfConf	11 :	-0.0070	-0.0099
Intimacy	12 :	-0.0196	0.0036
Desponde	13 :	0.0075	-0.0228
Pride	14 :	-0.0147	-0.0189
Disappoi	15 :	0.0141	-0.0201
InnrCalm	16 :	-0.0158	-0.0156

Figure 43: Standardized least square weights of the affects

- the raw and standardized least square weights, needed to compute the profile coordinates in reduced space. The raw weights can be applied to the deviation scores. A deviation score is the original score minus the affect mean over the active profiles. The standardized weights can be applied to the z-scores (the deviation scores divided by their standard deviations over the active profiles). See Figure 42 and Figure 43.

```
 3.5   Coordinates of the profiles in the reduced space
 ____________________________________________________

             The coordinates in the best fitting space using the raw least
             square weights Bx on the deviation scores.

                       Profile        Dimension
                                      1        2
            Unwanted child   1 :   0.2923   0.1027
         Creche was terrible   2 :   0.3416   0.0100
               Missed father   3 :   0.3295   0.0480
               ................................
               ................................
           *General feelings  23 :  -0.0094  -0.0619
             *Ideal feelings  24 :  -0.3314   0.0414
```

Figure 44: Overview of the variances of the affects.

- the profile coordinates in reduced space (see Figure 44).

```
3.6  Positions of profiles 1 to 24:
 ____________________________________

            The passive profiles are marked with '*'.

 Dimension  1 against  2.             Dimension       Scaling factor=100/0.381
                                          2
         -100   -80   -60   -40   -20     0    20    40    60    80   100
          ..+.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+.
      100 :                                ::                               :100
       96 :                                ::                               : 96
       91 :                                ::                               : 91
       86 :                                ::                               : 86
       81 :                                ::                               : 81
       77 :                                ::                               : 77
       72 :                                ::                               : 72
       67 :                                ::                               : 67
       62 :                                ::                               : 62
       58 :                                ::                               : 58
       53 :                                ::                               : 53
       48 :                                ::                               : 48
       43 :                                ::                               : 43
       39 :                     6          ::                               : 39
       34 :                                ::                               : 34
       29 :                                ::                               : 29
       24 :                   5            ::                         1     : 24
       20 :                  17            ::                               : 20
       15 :                                16                21             : 15
       10 :   *24*                         ::                          3    : 10
        5 :      22  10                     ::                               :  5
 Dim.  1  ::::::::::::::::::::::::::::7::::::::::::::12::::::::::::::2:::4:  0
       -5 :      11                      8::                               : -5
      -10 :                               ::                               :-10
      -15 :                              *23*                         13    :-15
      -20 :                               ::                  20           :-20
      -24 :             18                ::                               :-24
      -29 :                               ::                               :-29
      -34 :                        15     ::                               :-34
      -39 :                               ::                               :-39
      -43 :                               ::                               :-43
      -48 :                               ::                               :-48
      -53 :                               14                               :-53
      -58 :                               ::                               :-58
      -62 :                               ::                               :-62
      -67 :                               ::                               :-67
      -72 :                               ::                               :-72
      -77 :                               ::                               :-77
      -81 :                               ::                               :-81
      -86 :                               ::                               :-86
      -91 :                               ::                               :-91
      -96 :                               ::                               :-96
     -100 :                               ::                               -100
          ..+.....+.....+.....+.....+.....+.....+.....+.....+.....+.....+.
         -100   -80   -60   -40   -20     0    20    40    60    80   100

 Overlap:  +++    8    9  +++   11   19  +++

 A graphical representation of the plot of dimension  1 against dimension  2
 is given in file:
 exampleP.bmp
```

Figure 45: Plot of the profiles in the reduced space

- optionally plot(s) of the profiles in the reduced space (see Figure 45).

```
3.7  Fitting Measures
 ____________________

 1. The ratios of the lengths of the reproduced and the original profiles.
    Large values indicate good fit.
 2. The explained squared distances of the profiles (squared ratio).
    Large values indicate good fit.
 3. The unexplained squared distances of the profiles (1 - explained).
    Small values indicate good fit.

                                                    Explained   Unexplained
                            Profile       Ratio       sq.dist.      sq.dist.

                 Unwanted child   1:     0.9134        0.8343        0.1657
             Creche was terrible   2:     0.9681        0.9372        0.0628
                   Missed father   3:     0.8716        0.7597        0.2403
          ......................................................
          ......................................................
                *General feelings  23:     0.5439        0.2959        0.7041
                  *Ideal feelings  24:     0.9229        0.8517        0.1483


        Overall proportions of squared distances:        0.7934        0.2066

          Contribution of the 22 active profiles:        0.7320        0.1914
          Contribution of the 2 passive profiles:        0.0613        0.0153
```

Figure 46: `Fitting measures.`

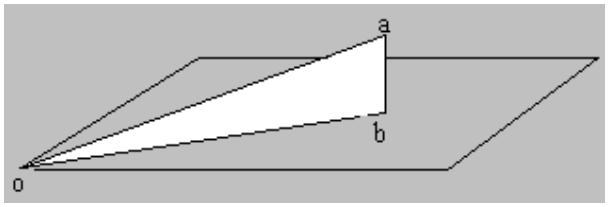

Figure 47: Geometrical representation of a `fitting measure`.

- some fitting measures: per profile:
  - F_1: The ratio of the lengths of the reproduced and the original profile. In Figure 47 the point `a` represents the original profile and the point `b` its projection on the spatial representation (the plane). The origin `o` is the point where all affects have their average score. The length of profile `a` is its distance to this point. The fitting measure F_1 is the ratio `ob/oa`. Its square can be interpreted as the proportion of the profile length that is retained by the spatial representation. A large value of F_1 indicates that the profile is well represented in the reduced space.
  - F_2: the 'explained' proportion of the squared length of the profile: the square of F_1. Again, large values indicate good fit.
  - F_3: The 'unexplained' proportion of the squared length of the profile: the squared length of the line `ab` divided by the squared length of the line `oa` or, to keep it simple, $1-F_2$. Small values indicate good fit.
  - F_4: The total proportion of explained lengths: the sum of the squared lengths `ob` in the reduced space divided by the sum of the squared lengths `oa` in the original space over all profiles. Large values indicate good overall fit.

```
 3.8  Standardized distances between profiles in best fitting space
 ____________________________________________________________________


 The mean standardized distance between the active profiles is   0.316


              :  Unwanted Creche w Missed f Strictly Nature g Fantasy  Last
              :     1        2        3        4        5        6        7
-------------------------------------------------------------------------------
Creche w   2 :    0.105
Missed f   3 :    0.066    0.040
Strictly   4 :    0.130    0.040    0.065
.....................................................
.....................................................
-------------------------------------------------------------------------------
              :     1        2        3        4        5        6        7
              :  Unwanted Creche w Missed f Strictly Nature g Fantasy  Last
```

Figure 48: Standardized distances between profiles in best fitting space.

- the mean standardized distance between the active profiles in reduced space (see Figure 48).
- optionally the standardized distances between the profiles in reduced space (depending on option 6 of the *additional profile options* menu) space (see Figure 48).

```
 3.9  The cophenetic coefficient:   (The correlation between the distances
 ________________________________    from the raw data and those in the
                                     best fitting space.)

 - For the 22 active profiles:     0.983
 - For the 2 passive profiles:     undefined; probably no variance.
 - For all profiles:               0.984
```

Figure 49: Cophenetic coefficients.

- the cophenetic coefficients. A cophenetic coefficient is the correlation between profile distances in the original data and those in the reduced space. Coefficients are given for the active profiles, the passive profiles and all profiles together (see Figure 49).
- optionally a Shepard diagram: a scattergram of the distances in the raw data and the corresponding distances in the reduced space (depending on option 5 in the *additional profile options* menu).

7.2 Results in the raw output file

If any "raw" output is asked (the option `W` in the *main* menu) it will be written to the raw output file.

All pieces of output are written in the same way. Each row consists of one or more lines. The first line contains an identifying text in the first eight positions, followed by seven numbers of ten positions (including 3 decimal digits). The first number starts at position nine. If there are more lines per row, the second and following lines start with eight spaces again followed by seven numbers starting at position nine. For all types of output, this form is applied to each row separately.

Figure 50 shows a part of an output file: the last part of the scores of the profiles on four scales (three sum-scales and a ratio) and the beginning of the correlations between the affects.

```
....+....1....+....2....+....3....+....4....+....
....
....
School      14.000    51.000    65.000     0.215
Mother      14.000    55.000    68.000     0.203
>> Correlations between the affects:
Joy         -0.337
Caring       0.261    -0.255
Anxiety     -0.556     0.531    -0.145
....
```

Figure 50: Part of the raw output file.

The output may consist of the following parts:

- scores of the profiles on the scales. Even when option `O` (in the *scales* menu) is chosen to order profiles according to some scale, the profiles are written in their original order.
- mean scores on the scales over the active profiles. It will have the same layout as the scores on the scales with the text "`ScalMean`" in the first eight columns.
- the correlations between the scales.
- the covariances between the affects.
- the correlations between the affects.
- the correlations between the profiles. Even when option `O` (in the *scales* menu) is chosen to order profiles according to some scale, the profiles are written in their original order.
- the variance parts explained by the reduced dimensions and the total available variance.
- the profile coordinates in reduced space.
- the cophenetic coefficients.

If any of these values cannot be computed a value of 9999.9999 will be reported, unless otherwise indicated in the listing file.

8 Literature

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9 Formulas

9.1 Cronbach's alpha

$$\alpha = \frac{a}{a-1}\left(1 - \frac{\sum_{i=1}^{a} \sigma_i^2 w_i^2}{\sigma_t^2}\right)$$

where a = the number of affects in the scale
σ^2_i = the variance of the i-th affect in the scale
w_i = the weight of the i-th affect in the scale
σ^2_t = the variance of the scale

9.2 The principal components analysis

n_a = number of active profiles
n_p = number of passive profiles
n = $n_a + n_p$: number of profiles
a = number of affects
f = number of dimensions in reduced space
r = $\sqrt{a}$ times the theoretical range of data (maximum - minimum)
X = data matrix; dimensions: $n \times a$
X_a = data matrix without the passive rows; dimensions: $n_a \times a$
U = matrix with value 1 in all its cells; dimensions: $n \times n_a$
M = $\frac{1}{n_a} UX_a$; cell (i,j) contains the mean of the j-th affect over the active profiles; all rows are equal; dimensions: $n \times a$
Y = X - M: deviation scores; from each cell (i,j) in X the mean score on the j-th affect over the active profiles is subtracted; dimensions: $n \times a$
Y_a = Y without the passive rows; dimensions: $n_a \times a$
C = $\frac{1}{n_a} Y_a' Y$: covariances between affects from the active profiles; dimensions: $a \times a$
S = diagonal matrix with standard deviations of affects; $S(i,i) = \sqrt{C_{ii}}$; dimensions: $a \times a$
R = correlation matrix from C; $R(i,j) = \frac{C_{i,j}}{S_i S_j}$
q_i = $\frac{C_{ii} - \frac{1}{B_{ii}}}{C_{ii}}$, with $B = C^{-1}$: the affective differentiation of the i-th affect; i.e. 1 minus the squared multiple correlation between the i-th affect and the other affects. If C is a singular matrix, all q_i are zero.

In case of an analysis on the covariance matrix C:

D = standardized distances between the rows of Y; $D(i,j) = \frac{1}{r}\sqrt{\sum_{k=1}^{a}\left(Y_{ik} - Y_{jk}\right)^2}$; dimensions: n × n

L = standardized lengths of the rows of Y; $L(i) = \frac{1}{r}\sqrt{\sum_{k=1}^{a} Y_i^2}$; dimensions: n

Λ = Diagonal matrix with the f largest eigenvalues from C; dimensions: f × f

V = matrix of eigenvectors corresponding to Λ; dimensions: a × f

A = $V\Lambda^{\frac{1}{2}}$: coordinates of the affects in reduced space; dimensions: a × f

A_s = $S^{-1}A$: coordinates of the affects in reduced space, corrected for variances; dimensions: a × f

P = $\frac{1}{r}YV$: standardized coordinates of profiles in reduced space; dimensions: n × f

D_r = standardized distances between the rows of P; $D_r(i,j) = \sqrt{\sum_{k=1}^{f}\left(P_{ik} - P_{jk}\right)^2}$; dimensions: n × n

L_r = standardized lengths of the rows of P; $L_r(i) = \sqrt{\sum_{k=1}^{f} P_i^2}$; dimensions: n

t = $\sum_{i=1}^{n} P_i^2$: sum of squared lengths of profiles in Y

F_1 = fitting measure 'ratio': $F_1(i) = \frac{L_{ri}}{L_i}$; dimension: n

F_2 = fitting measure: explained squared distances: $F_2(i) = F_1^2(i)$; dimension: n

F_3 = fitting measure: unexplained squared distances: $F_3(i) = 1\text{-}F_2(i)$; dimension: n

f_4 = fitting measure: overall proportion explained squared distance: $\frac{\sum_{i=1}^{n} L_{ri}^2}{\sum_{i=1}^{n} L_i^2}$

f_5 = $1\text{-}f_4$: fitting measure: unexplained squared distance

In case of an analysis on the correlation matrix R:

Z = YS^{-1}: standardized scores

D = standardized distances between the rows of Y; $D(i,j) = \frac{1}{r}\sqrt{\sum_{k=1}^{a}\left(Z_{ik} - Z_{jk}\right)^2}$; dimensions: n × n

L = standardized lengths of the rows of Z; $L(i) = \frac{1}{r}\sqrt{\sum_{k=1}^{a} Z_i^2}$; dimensions: n

Λ = Diagonal matrix with the f largest eigenvalues from R; dimensions: f × f

V = matrix of eigenvectors corresponding to Λ; dimensions: a × f

A = $V\Lambda^{\frac{1}{2}}$: coordinates of the affects in reduced space; dimensions: a × f

A_s = A: coordinates of the affects in reduced space, corrected for variances; dimensions: a × f

P = $\frac{1}{r}ZV$: standardized coordinates of profiles in reduced space; dimensions: n × f

D_r = standardized distances between the rows of P; $D_r(i,j) = \sqrt{\sum_{k=1}^{f} \left(P_{ik} - P_{jk}\right)^2}$; dimensions: $n \times n$

L_r = standardized lengths of the rows of P; $L_r(i) = \sqrt{\sum_{k=1}^{f} P_i^2}$; dimensions: n

t = $\sum_{i=1}^{n} P_i^2$: sum of squared lengths of profiles in Y

F_1 = fitting measure 'ratio': $F_1(i) = \frac{L_{ri}}{L_i}$; dimension: n

F_2 = fitting measure: explained squared distances: $F_2(i) = F_1^2(i)$; dimension: n

F_3 = fitting measure: unexplained squared distances: $F_3(i) = 1\text{-}F_2(i)$; dimension: n

f_4 = fitting measure: total explained squared distance: $\frac{\sum_{i=1}^{n} L_{ri}^2}{\sum_{i=1}^{n} L_i^2}$

f_5 = $1\text{-}f_4$: fitting measure: total unexplained squared distance

Content