Scientific Software International

Getting started with BILOG-MG

Introduction

To illustrate the use of the interface in creating syntax files, the data file **exampl01.dat** in the **examples** subfolder of the BILOG-MG installation folder is used. This problem is based on an example in Thissen, Steinberg & Wainer (1993).

In the late 1980s, R. Darrell Bock created a "College Level Spelling Test" comprising a sample of 100 words drawn from a large source list by simple random sampling. Data collected using that test are the basis for the empirical example in the paper "IRT Estimation of Domain Scores" (R.D. Bock, M.F. Zimowski, & D. Thissen, *Journal of Educational Measurement*, 1997, 34, 197-211). Parameter estimates for the 2PL IRT model for the 100-item test are tabulated in that paper. Bock created the script for conventional oral presentation of the test, and recorded the original reading of the script (by Monica Marie Bock) on reel-to-reel magnetic tape. Subsequent copies onto cassette tape were used by Jo Ann Mooney in the collection of data from around 1000 University of Kansas Undergraduates. We are using the file with 100 words (items) and 1000 records (examinees).

The words for the test were randomly selected from a popular wordbook for secretaries. Students were asked to write the words as used in a sentence on the tape recording. Responses were scored 1 if spelled correctly and 0 if spelled incorrectly. Because the items are scored 1,0, according to the defaults assumed by the program, an answer key is not required.

The purpose of this section is to give the new user a quick overview of the interface and the absolute minimum input needed to run the program. A few lines of the data in **exampl01.dat** are shown below:

```
 11 0000
 21 0001
 31 1000
 41 1001
 …
162 1111
```

The first three characters in each line represent the examinee identification field. This is followed by the responses to the four items in the test.

A first model: 2PL model for spelling data

As a first example, we wish to set up a simple 2-PL model for this data. To construct a command file, begin by selecting the **New** option from the **File** menu. The **Open** dialog box is now activated.
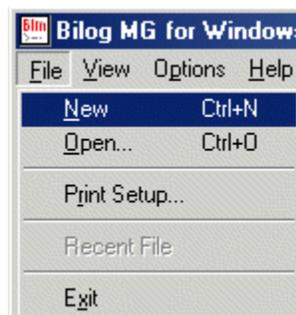
Assign a name, with the ***.blm** file extension, to the command file. In this case, the command file **first.blm** is created in the **examples** folder as shown below. Click **Open** when done to return to the main BILOG-MG window.
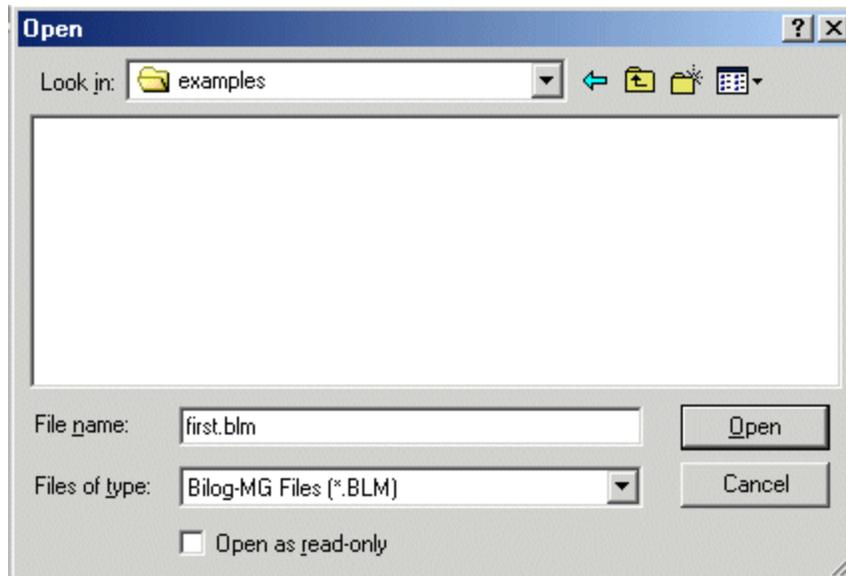
Note that a number of options have been added to the main menu bar of the BILOG-MG window. Of interest for this example are the **Setup**, **Data**, **Run** and **Output** options. The **Setup** menu is used to describe the model to be fitted to the data. As a first step, select the **General** option from this menu to access the **General** dialog box.
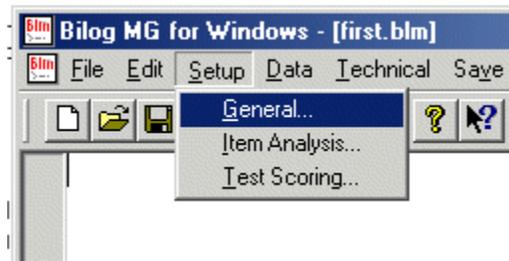
The **General** dialog box has four tabs, on which both required and optional keywords may be set. On the **Job Description** tab below, the number of items in the test is indicated as 4. The type of model is selected on the **Model** tab. As the default model fitted by BILOG-MG is a 2PL model, this tab is not used now. Click **OK** to return to the main window.

The next step in specifying the analysis is to assign the items to be calibrated to the test. To do this, select the **Item Analysis** option on the **Setup** menu to access the **Item Analysis** dialog box.

Change the default value of 1 under **Subtest Length** to 4 by clicking in this field and typing in "4". By default, all items will be analyzed, as indicated under the **Analyze this run** header. Click **OK** when done.

This completes the model specification. All that remains to be done is to provide information on the data. To do so, the **Data** menu is used. In this case, we have examinee data and thus the **Examinee Data** option is selected from the **Data** menu.
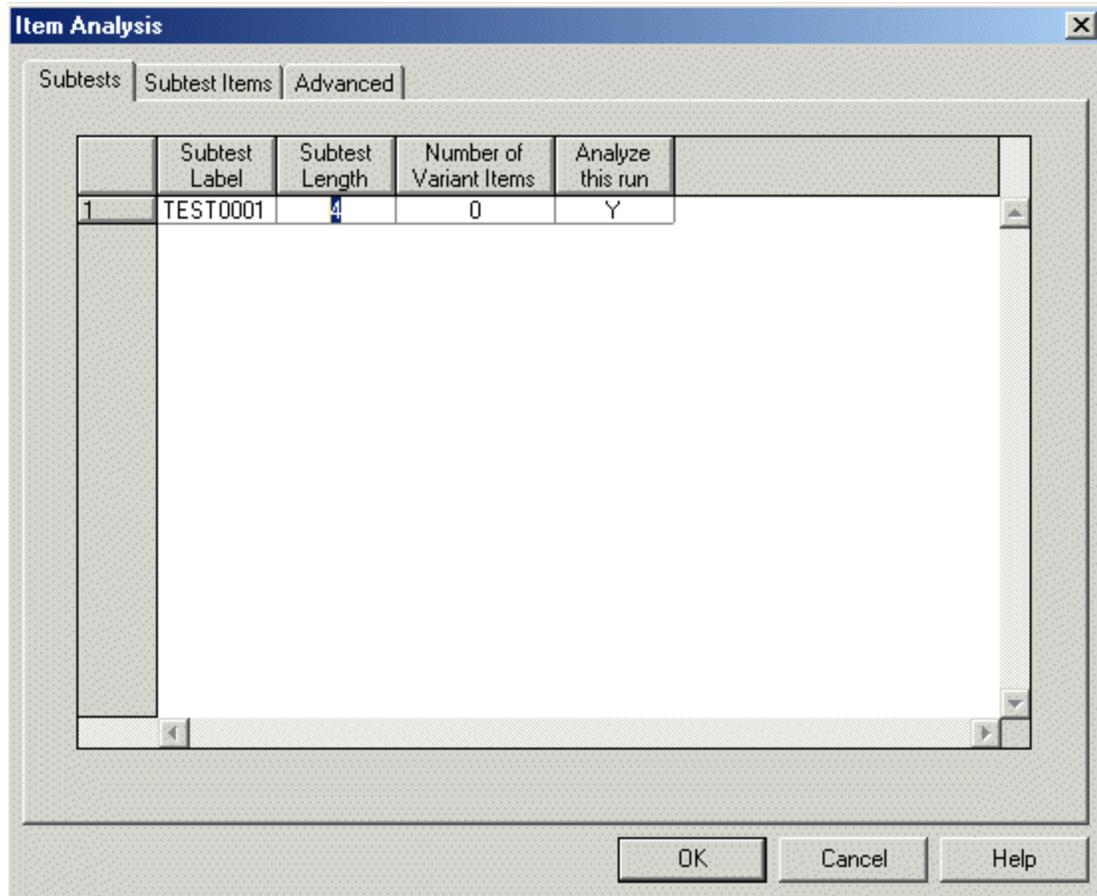
On the **Examinee Data** dialog box, enter the number of characters representing the examinee identification (in this case 3) in the **Number of Case ID Characters** field. By default, all data are used as shown below.

To provide information on the name and format of the data file, click the **Data File** tab.

❑ Use the **Browse** button to browse for the data file.
❑ Next, indicate that the data are in fixed format by clicking the **Read as Fixed-Column Records** radio button.
❑ Complete the table in the **Read as Fixed-Column Records** group box by clicking in the cell next to **Case ID** under the **First** header. Enter a "1" here to indicate that the examinee identification starts in column 1 of the data. Next, enter a "3" under the **Last** header to indicate the end of the examinee identification.
❑ Note that **Form Number**, **Group Number**, etc. is disabled due to the information we entered from the **Setup** menu. The only other fields to complete are the **Response String** fields.
❑ The response to the first item is in column 5 of the data, so a "5" is entered in the cell next to **Response String** under the **First** header. The response to the last item is in column 8, and an "8" is thus entered in the **Last** column.
❑ By default, BILOG-MG assumes that there is one line of data for each examinee, as indicated by the **Number of Data Record per Case** field. As this is the case for data in

exampl01.dat, no further information is required. Click the **Set Format** button to write the format statement (3A1,1X,4A1) to the **Format String** field. Click **OK** to return to the main BILOG-MG window.

Examinee Data
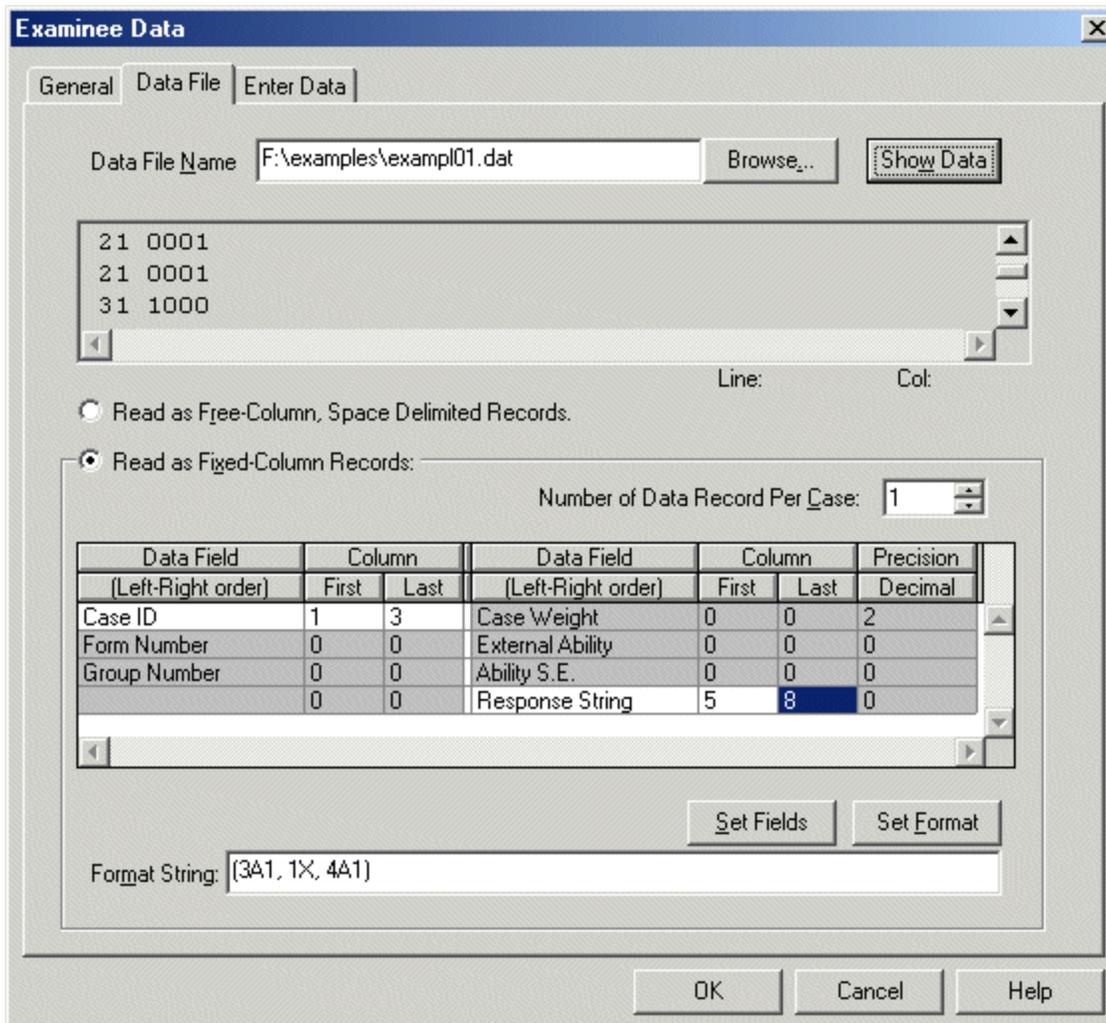
General | Data File | Enter Data

Data File Name: `F:\examples\exampl01.dat`   Browse...   Show Data

```
21 0001
21 0001
31 1000
```

Line: Col:

○ Read as Free-Column, Space Delimited Records.

⦿ Read as Fixed-Column Records:

Number of Data Record Per Case: 1

Data Field	Column		Data Field	Column		Precision
(Left-Right order)	First	Last	(Left-Right order)	First	Last	Decimal
Case ID	1	3	Case Weight	0	0	2
Form Number	0	0	External Ability	0	0	0
Group Number	0	0	Ability S.E.	0	0	0
	0	0	Response String	5	8	0

Set Fields   Set Format

Format String: `(3A1, 1X, 4A1)`

OK   Cancel   Help

Having completed the specification in terms of model and data, the command file is created by selecting the **Build Syntax** option from the **Run** menu. The syntax created by the program is now displayed in the main window, as shown below. Note that no options are given on the ITEMS and SCORE commands in this file, indicating that all program defaults will be used.

Save the completed syntax to file by selecting the **Save** option on the **File** menu.

The analysis is now performed by using some of the other options on the **Run** menu. Although the analysis can be done phase by phase (using the **Classical Statistics Only**, **Calibration Only**, and **Scoring Only** options) all three phases can be run in sequence by selecting the **Stats, Calibration and Scoring** option from this menu.
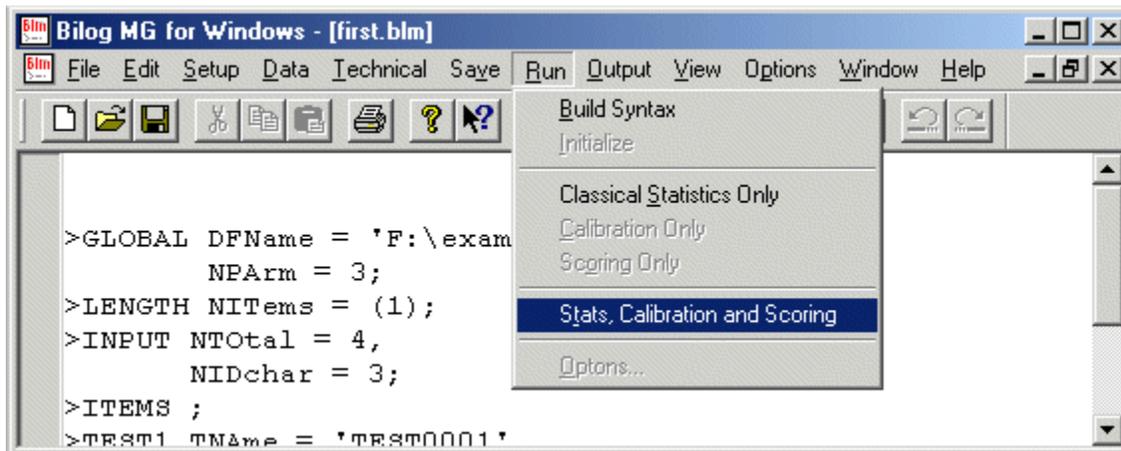
After successful completion of all three phases of the analysis, a message to this effect is displayed on the screen. If a problem was encountered during analysis, this message box will indicate that all phases were not completed successfully. Access the output from the analysis through the **Output** menu. Classical statistics are given in the ***.ph1** file.
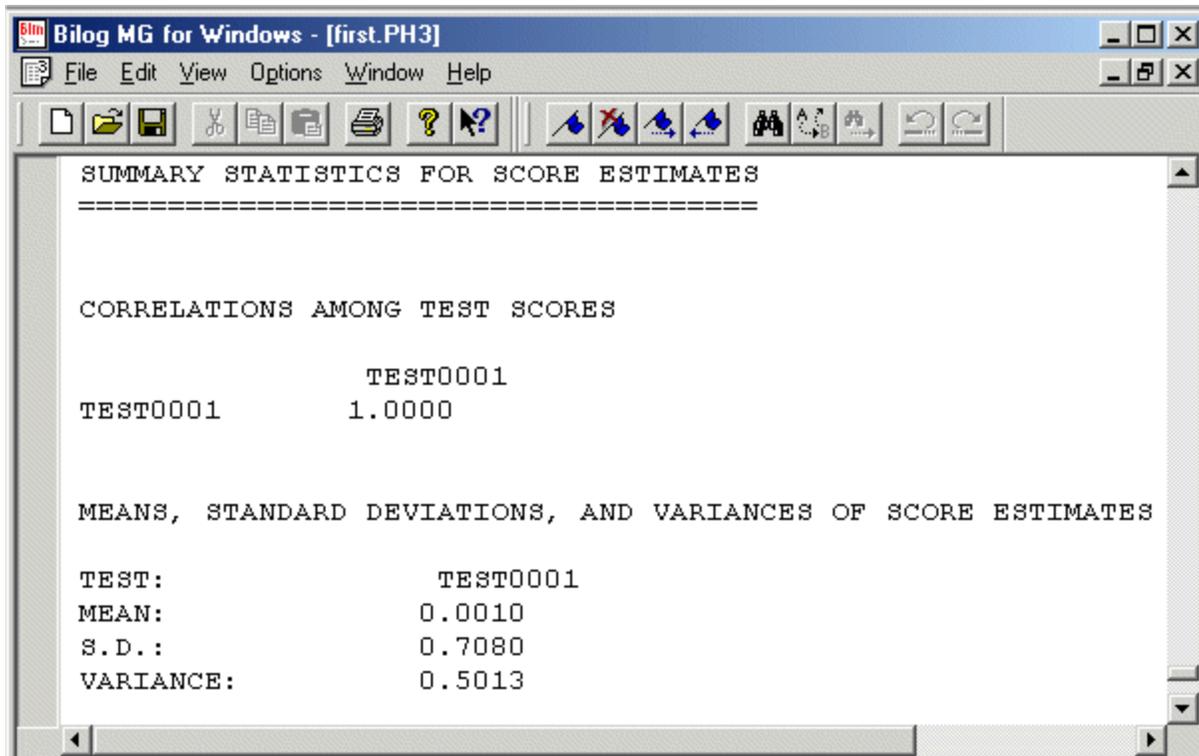
A section of this output file is shown below.

```
Bilog MG for Windows - [first.PH1]
 File  Edit  View  Options  Window  Help

'ATISTICS FOR SUBTEST TEST0001

                                                   ITEM*TEST CORRELATION
  NAME          #TRIED      #RIGHT    PCT    LOGIT/1.7   PEARSON   BISERIAL
  -------------------------------------------------------------------------
  ITEM0001      660.0       520.0     78.8    -0.77       0.236     0.333
  ITEM0002      660.0       411.0     62.3    -0.29       0.319     0.407
  ITEM0003      660.0       201.0     30.5     0.49       0.288     0.379
  ITEM0004      660.0       351.0     53.2    -0.07       0.322     0.405
  -------------------------------------------------------------------------
```

In the **first.ph2** file, the results of the item calibrations are given. The item parameter estimates for the four items in the test are shown below.

```
Bilog MG for Windows - [first.PH2]
 File  Edit  View  Options  Window  Help

  ITEM       INTERCEPT     SLOPE      THRESHOLD    LOADING     ASYMPTOTE
  -----------------------------------------------------------------------
  ITEM0001 |   0.757   |   0.661   |   -1.146   |   0.551   |    0.194
           |   0.126*  |   0.124*  |    0.265*  |   0.103*  |    0.087*
           |           |           |            |           |
  ITEM0002 |   0.145   |   1.032   |   -0.141   |   0.718   |    0.181
           |   0.170*  |   0.251*  |    0.181*  |   0.175*  |    0.078*
           |           |           |            |           |
  ITEM0003 |  -1.261   |   1.233   |    1.022   |   0.777   |    0.114
           |   0.454*  |   0.459*  |    0.135*  |   0.289*  |    0.039*
           |           |           |            |           |
  ITEM0004 |  -0.225   |   1.033   |    0.218   |   0.719   |    0.168
           |   0.210*  |   0.275*  |    0.170*  |   0.191*  |    0.069*
  -----------------------------------------------------------------------
```

Scoring results are given in the **first.ph3** file. The complete list of scores is printed to this file by default. A section of this output, showing summary statistics for the score estimates, is shown below.

```
SUMMARY STATISTICS FOR SCORE ESTIMATES
======================================



CORRELATIONS AMONG TEST SCORES

                      TEST0001
TEST0001         1.0000



MEANS, STANDARD DEVIATIONS, AND VARIANCES OF SCORE ESTIMATES

TEST:                 TEST0001
MEAN:                 0.0010
S.D.:                 0.7080
VARIANCE:             0.5013
```

A second model: DIF model for spelling data

The data analyzed in the previous example came from two groups of respondents. The groups in this example are the two sexes. The same four items are presented to both groups on a single test form. The group indicator is found in column 3 of the data records.

```
11 0000
21 0001
31 1000
41 1001
…
162 1111
```

The third column of the data contains either a 1 or a 2, indicating whether an examinee belonged to group 1 (male) or group 2 (female).

The previous single-group analysis for this group, contained in the command file **first.blm**, is modified to perform a DIF analysis for the two groups. As a first step, the **General** option on the **Setup** menu is used to indicate the presence of multiple groups.

On the **Job Description** tab of the **General** dialog box, change the **Number of Examinee Groups** from the default value of 1 to 2, as shown below.

In the case of a DIF model, a 1PL model is required. To change the model from the default 2PL model previously used, click the **Model** tab and check the **1-Parameter Logistic (1PL)** radio button in the **Response Model** group box.

To request a DIF model, click the **Differential Item Functioning (DIF)** radio button in the **Special Models** group box. By default, the first group will be used as reference group as indicated in the **Reference Group** field.

Once this is done, all necessary changes to the **General** dialog box have been made. Click **OK** to return to the main BILOG-MG window.
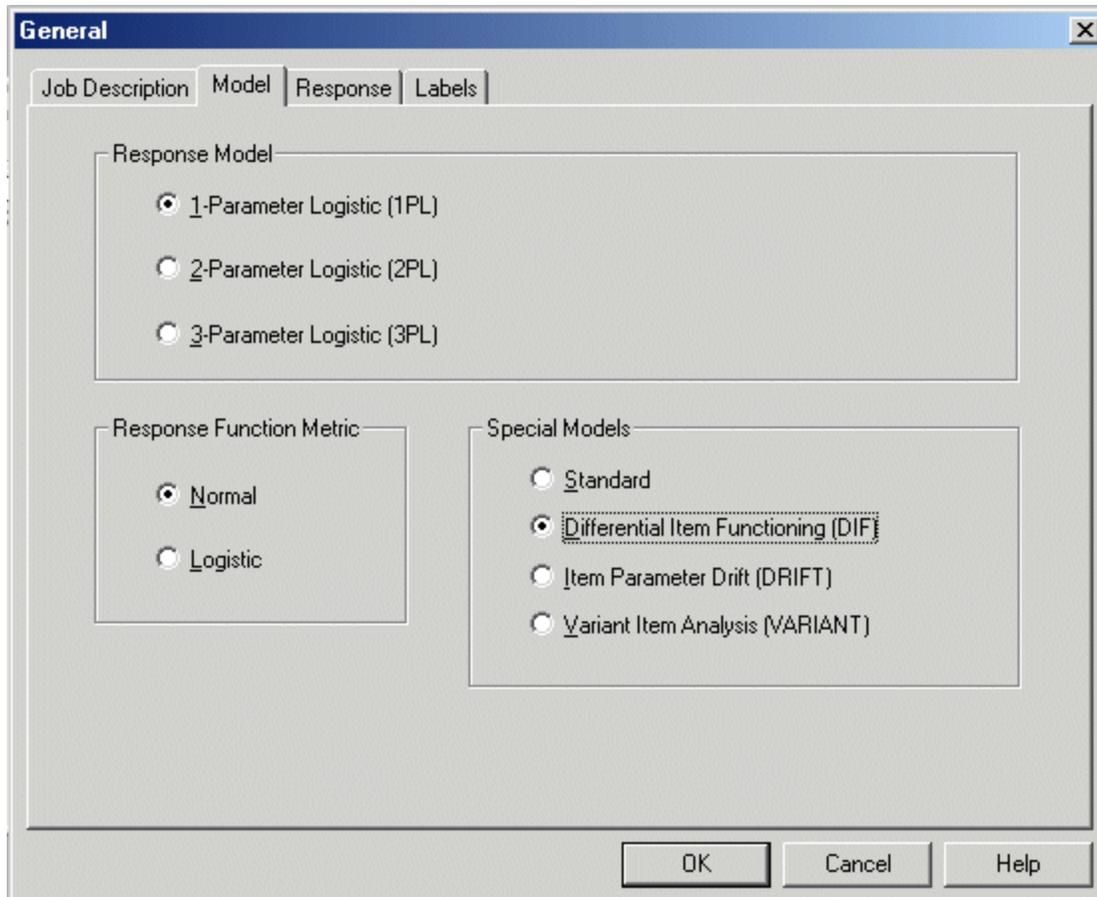
The allocation of items to be calibrated for each of the two groups is specified using the **Item Analysis** option of the **Setup** menu. Once this option is selected, the **Item Analysis** dialog box is displayed.

Leaving the **Subtests** tab as previously completed, click the **Group Items** tab. By default, all items will be selected for the first group. This is indicated by the display of the item names in a bold font in the first column of the table. To select all four items for the second group, click on ITEM0001 in the second column. While holding the Shift button on the keyboard down, click on ITEM0004. All four items are now highlighted. Click the **Select** button at the bottom left of the dialog box to select all items.

This completes the model specification. Click **OK** to return to the main window.
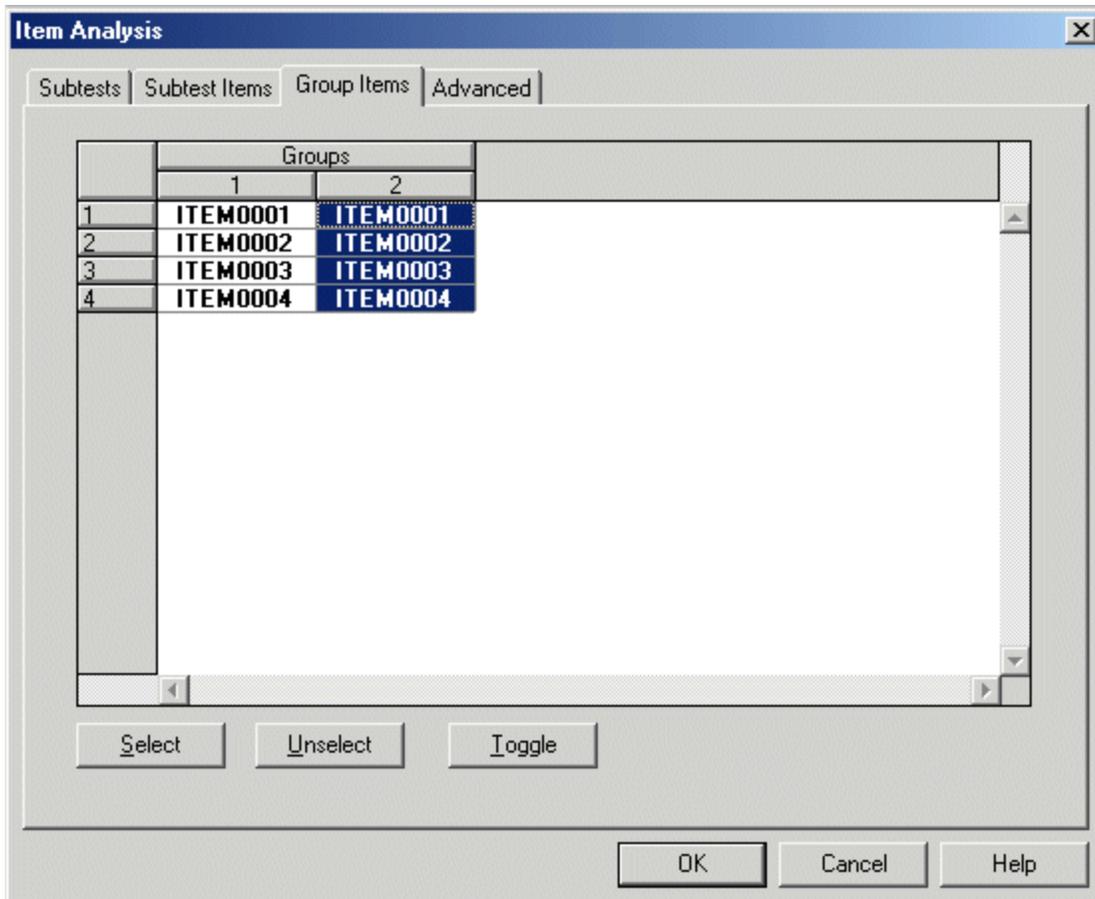
The only remaining task is to revise the reading of the data file so that the group identification field can be recognized and processed by the program. To do so, select the **Examinee Data** option from the **Data** menu.

On the **General** tab of the **Examinee Data** dialog box, the number of case identification characters is now decreased to 2, as shown below. (Recall that previously this field was set to 3: in effect, a combination of actual examinee ID and group ID was used to identify the cases in the previous example.)
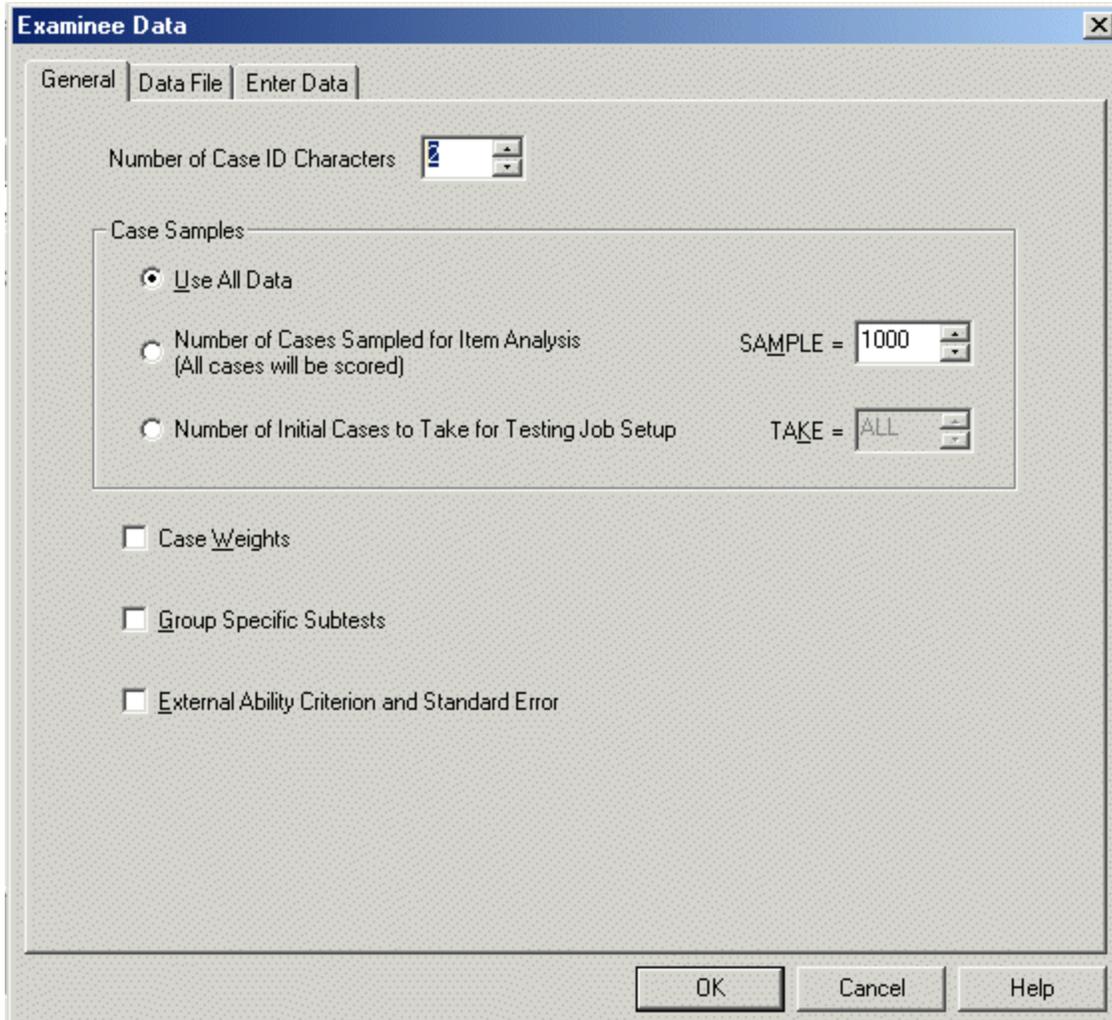
The format statement is now adjusted accordingly by changing the entries in the **Read as Fixed-Column Records** group box:

- ❑ The **Last** value for the **Case ID** is set to 2.
- ❑ The **Group Number** field, now enabled due to our selection of a multiple-group analysis from the **Setup** menu, is set to 3 under both the **First** and **Last** headers, as the group identification, given in column 3 of the data, is one character in length.
- ❑ Finally, these changes are made to the format statement by clicking the **Set Format** button. Note that the format statement now contains an additional "I1" indicating the group number in integer format.

This completes the syntax specification. Return to the main window by clicking the **OK** button.
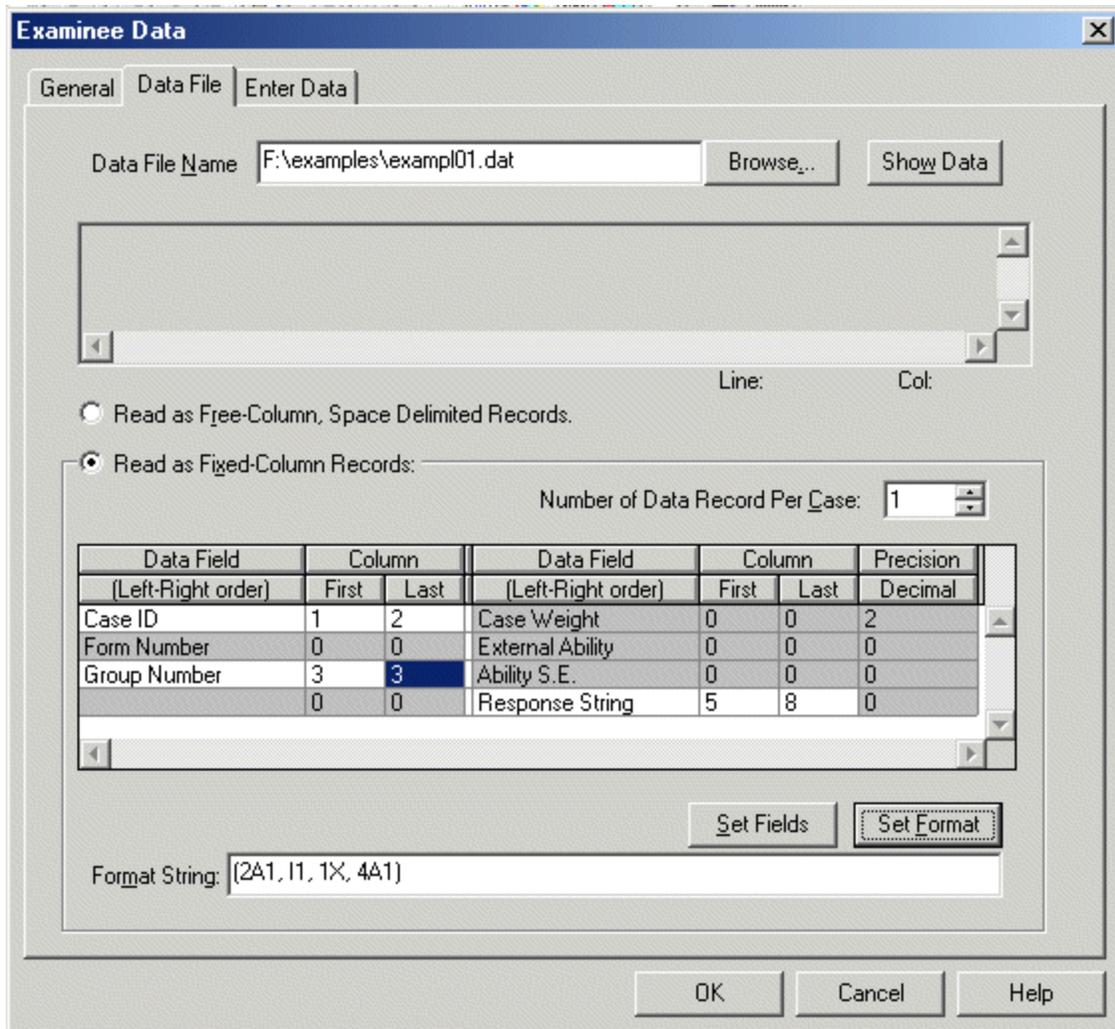
The revised command file is generated by selecting the **Build Syntax** option from the **Run** menu.
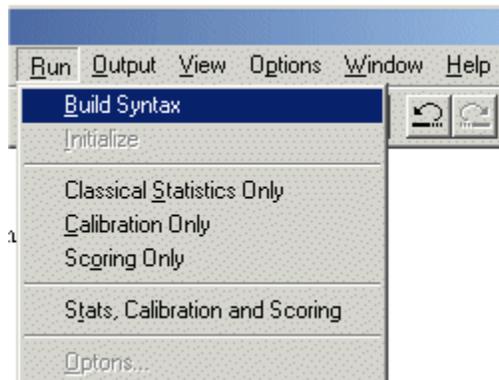
After generating the syntax, it is saved to file using the **Save As** option on the **File** menu. The revised syntax is saved in the file **second.blm** in the **examples** folder. Click the **Save** button after specifying a name for and path to the new command file.

When the syntax displayed in the main BILOG-MG window is compared to the first example, we note the addition of two GROUP commands and the NGROUP and DIF keywords on the INPUT command. The revised format statement is also included. The NPARM keyword on the GLOBAL command (not shown here) indicates that a 1-PL model is requested.

The three phases of the analysis can be run separately using the **Classical Statistics Only**, **Calibration Only**, and **Scoring Only** options on the **Run** menu. To run the phases sequentially, select the **Stats, Calibration, and Scoring** option from this menu.

Output for the analysis is accessed as before using the **Output** menu from the main menu bar.

In the partial output from the **second.ph1** file for this DIF analysis classical item statistics are provided by group. Similar statistics are also given for the combined group (not shown below).

```
Bilog MG for Windows - [second.PH1 *]
File  Edit  View  Options  Window  Help

ITEM STATISTICS FOR GROUP:   1     GROUP001
                                                    ITEM*TEST CC
ITEM    NAME        #TRIED      #RIGHT     PCT     LOGIT/1.7   PEARSON
-------------------------------------------------------------------
   1    ITEM0001    285.0       215.0     0.754     -0.66      0.243
   2    ITEM0002    285.0       181.0     0.635     -0.33      0.351
   3    ITEM0003    285.0        91.0     0.319      0.45      0.364
   4    ITEM0004    285.0       179.0     0.628     -0.31      0.360
-------------------------------------------------------------------


ITEM STATISTICS FOR GROUP:   2     GROUP002
                                                    ITEM*TEST CC
ITEM    NAME        #TRIED      #RIGHT     PCT     LOGIT/1.7   PEARSON
-------------------------------------------------------------------
   1    ITEM0001    375.0       305.0     0.813     -0.87      0.249
   2    ITEM0002    375.0       230.0     0.613     -0.27      0.293
   3    ITEM0003    375.0       110.0     0.293      0.52      0.227
   4    ITEM0004    375.0       172.0     0.459      0.10      0.303
-------------------------------------------------------------------
```

The Phase 2 output in the **second.ph2** file provides item parameter estimates, and DIF specific output as shown below.

```
Bilog MG for Windows - [second.PH2]
File  Edit  View  Options  Window  Help

MODEL FOR GROUP DIFFERENTIAL ITEM FUNCTIONING:
ADJUSTED THRESHOLD VALUES

   ITEM                GROUP
                     1              2
------------------------------------------
   ITEM0001 |   -1.139  |   -1.563
            |    0.128* |    0.127*
            |           |
   ITEM0002 |   -0.575  |   -0.609
            |    0.116* |    0.103*
            |           |
   ITEM0003 |    0.769  |    0.683
            |    0.083* |    0.109*
            |           |
   ITEM0004 |   -0.545  |   -0.002
            |    0.114* |    0.100*
------------------------------------------
```

Although the **second.ph3** file is created as shown below, no scoring is performed in the case of a DIF analysis.

```
*** LOGISTIC MODEL ITEM ANALYSER ***

*** PHASE 3 ***


****************************
            SCORING
****************************

*****THE DIF MODEL CANNOT BE SCORED*****
```