

# MCMC GGUM v1.2 User's Guide

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The MCMC GGUM computer program is developed to estimate the Generalized Graded Unfolding IRT Model (Roberts, Donoghue, & Laughlin, 2000). Different from the GGUM2000 (Roberts, 2001) and GGUM2004 (Roberts, Fang, Cui, & Wang, 2006), which are based on EM algorithm, the MCMC GGUM computer program employs the Metropolis-within-Gibbs algorithm (Casella & George, 1995; Chib & Greenberg, 1995; Gamerman, 1997; Gelman, Carlin, Stern, & Rubin, 2003; Gilks, Richardson, & Spiegelhalter, 1996; Hastings, 1970; Metropolis, Rosenbluth, Rosenbluth, Teller, & Teller, 1953; Tierney, 1994). The program estimates the item and person parameters simultaneously, and is capable of calibrating data sets with up to 10 response categories, and, theoretically, with no limit on the number of items and respondents. This program can also handle missing values in the data.

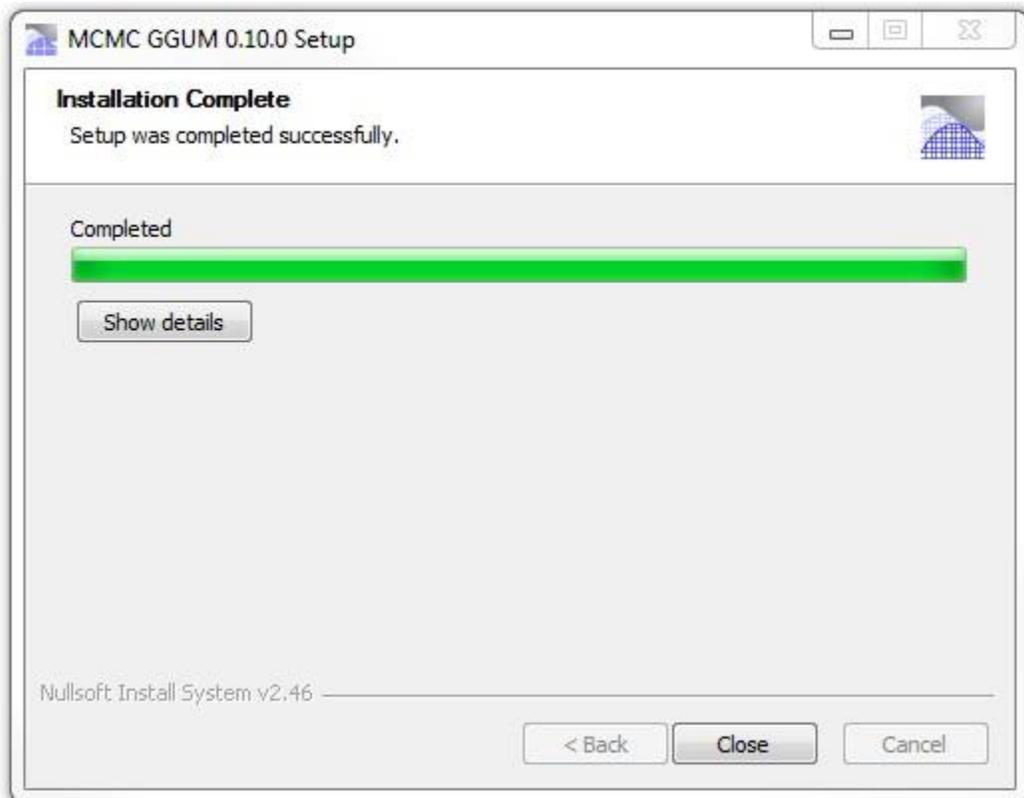
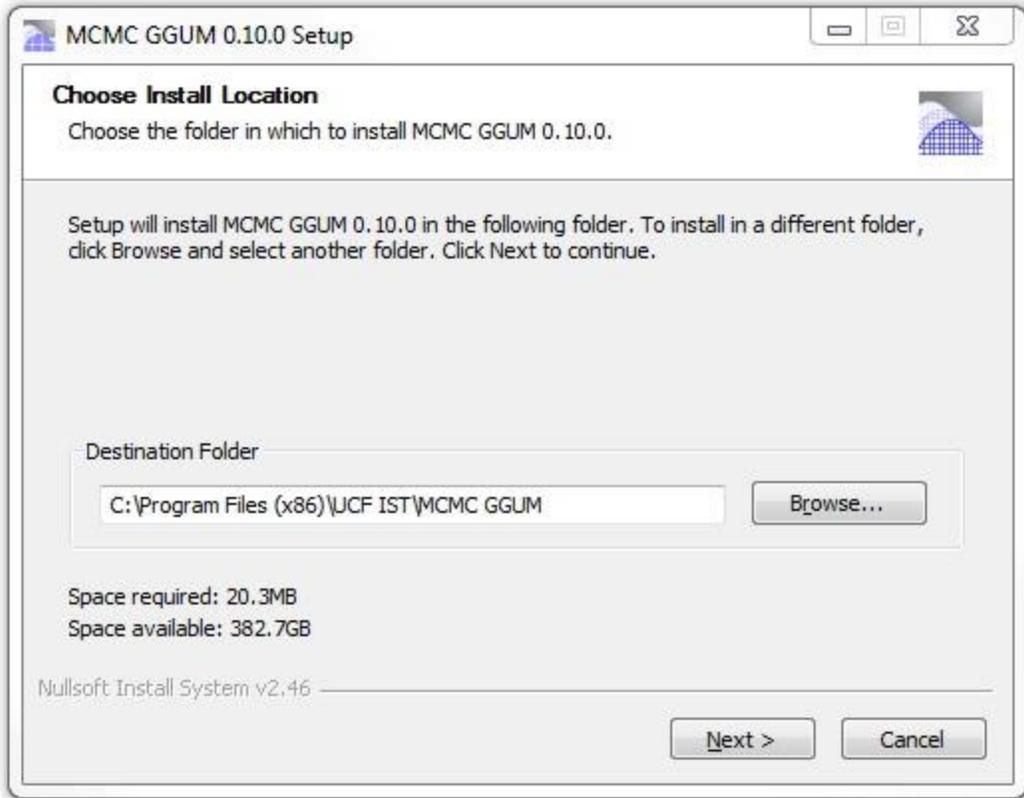
The MCMC GGUM program has a Windows based graphical user interface. This User's Guide is written to provide some basic guidelines on using the program.

### **Download and Installation**

The installer is available for free to download at <<http://psychology.cos.ucf.edu/snap>>. When it is properly downloaded, the file looks like the icon as follows on your desktop.



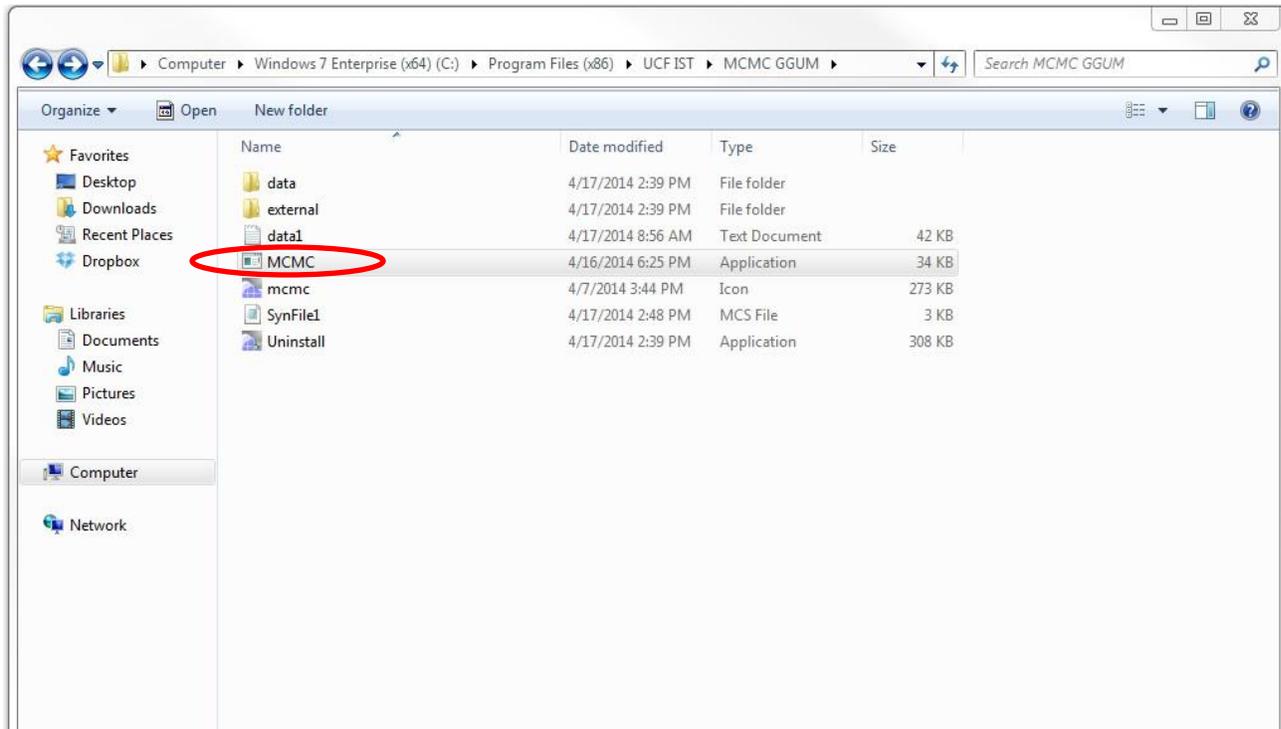
When double clicked to install, it may require the administrator privilege to proceed. The installation starts with the following interface, where you may change the destination folder for the installation. The default destination folder is shown in the following interface:



Then follow the instruction, and click “Next” to complete the installation. When the installation is completed, close the interface window. A shortcut of the application will be created on the desktop. Click the shortcut to open/execute the program.



The other way (also recommended) to open/execute the program is to find the MCMC file located in the installation folder, as circled in the figure below.



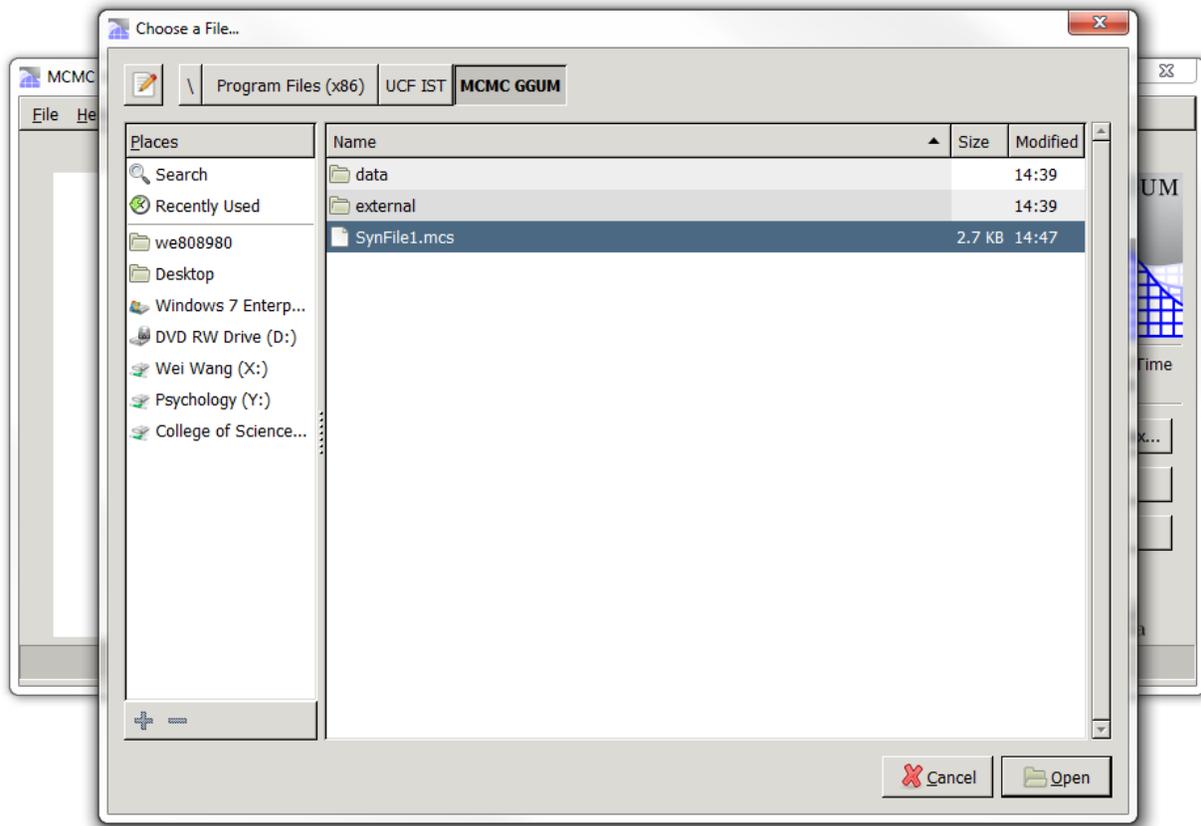
### Running the Program

To run the program properly, first, make sure that both the syntax file and the data file are located in the main folder of the installation folder. The details of a syntax file will be elaborated in the following section.

The following two figures show the Window interfaces of the MCMC GGUM Program. Click “Import Syntax” button on the right side to locate and import a syntax file. If a syntax file is properly written, no error message would appear, and you may click “Run” button to run the program.



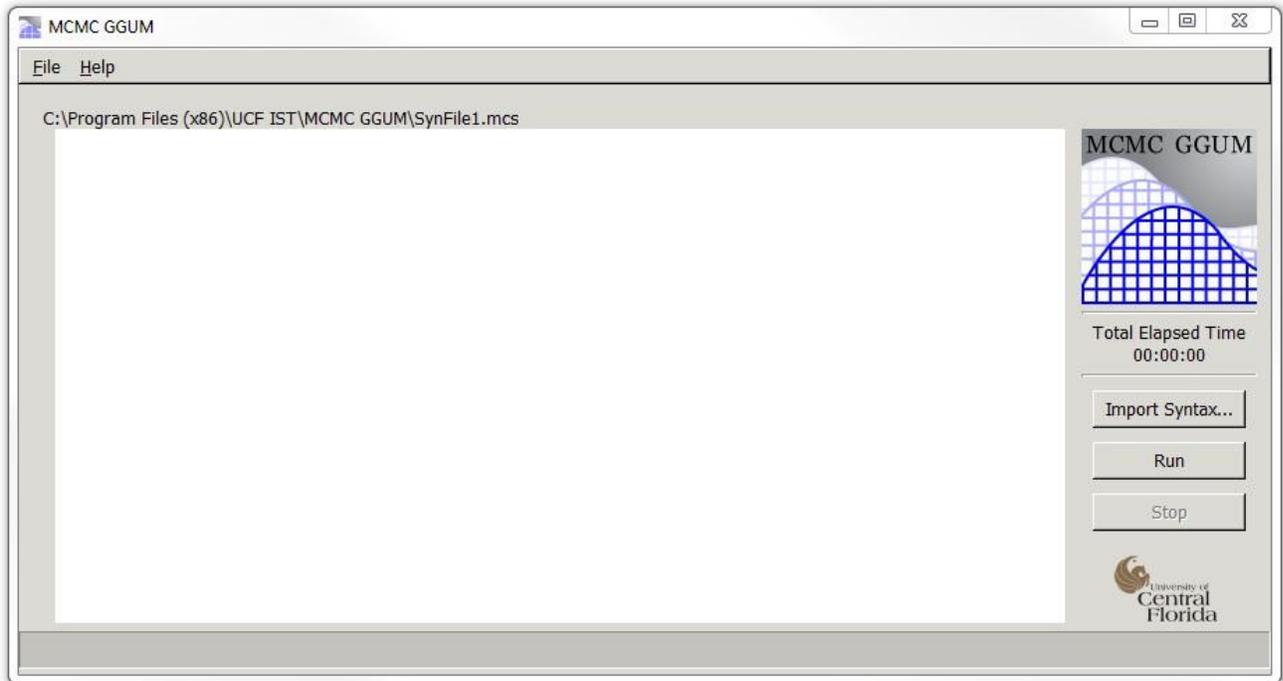
Clicking the Import Syntax button will open a new window shown below, which allows for a syntax file to be appropriately located. Once the designated syntax file is found and highlighted, click “Open” to close the new window and get the program ready to run.



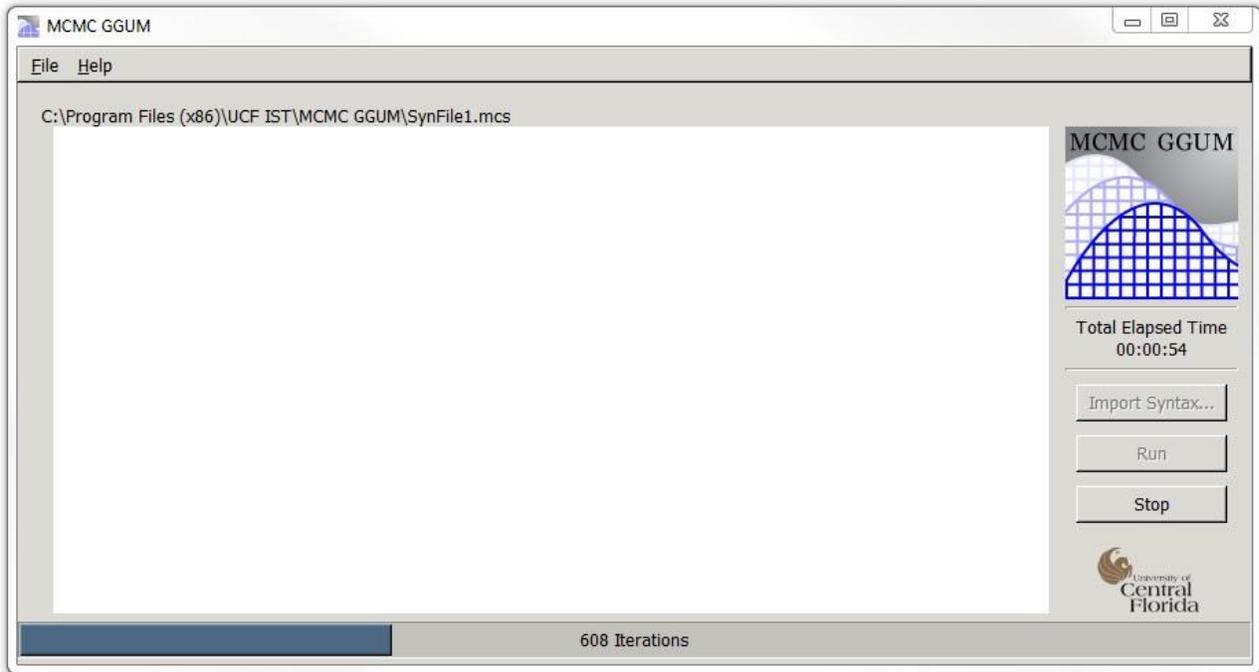
When a syntax file contains an error, an error message as below may appear. Common errors include a misspecification of data location or data information (e.g., numbers of rows and columns). Other common errors may be mismatched vectors for the parameters.



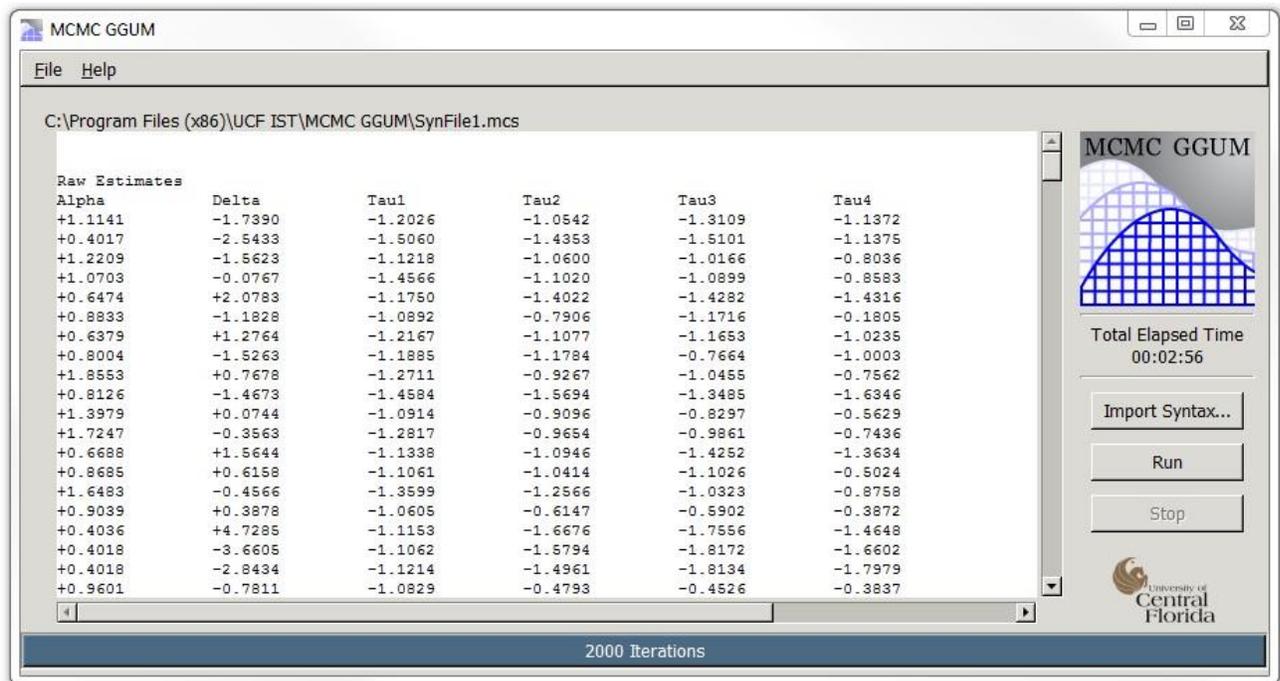
When a syntax file has no errors and is imported properly, the window interface displays the correct directory of the syntax file at the upper left corner of the window, as shown in the following figure. The program is ready to run.



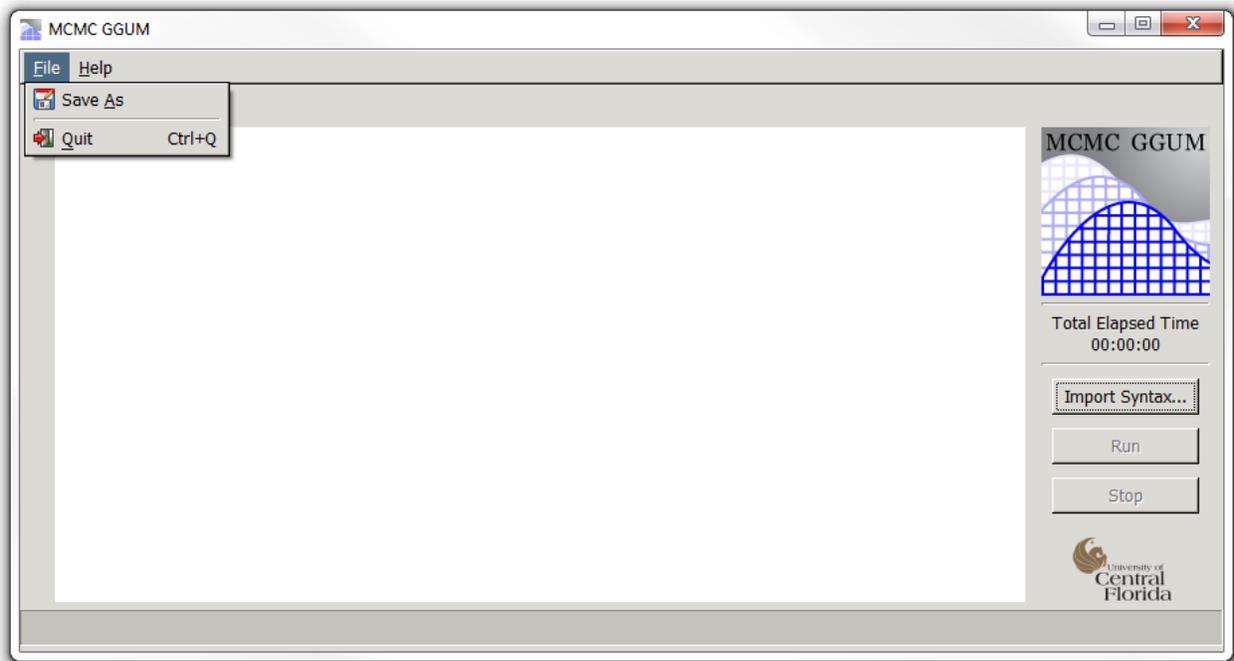
When the program is running, the time elapsed will be shown on the right side above the “Import Syntax” button and a blue progress bar presenting the completed iterations displays at the bottom of the interface, as shown in the following figure.



When the program finishes all the iterations, the parameter estimates and related output are displayed in the main window of the program as shown below. The output information will be discussed in a separate section.



There are two menus available at the upper-left corner of the window interface: **File** and **Help**. The drop-down list of File menu includes Save As and Quit. The Save As option is used to save the trace output for users interested in running further analyses. The Help menu provide brief “About” information regarding this computer program.



### Syntax File

A sample syntax file is provided with the installation of the program. Users only need to slightly modify the syntax entries in order to run the program. The sample syntax and its explanation are presented as follows.

```

SyntaxExample5c - Notepad
File Edit Format View Help
1000 # Number of Rows
20 # Number of Columns
ExampleData5c.txt # Input File
2000 # Number of Iterations
1000 # Number of Burn
5 # Number of Categories

# Ordering
8 10 6 2 20 3 17 4 16 18 11 13 9 12 1 14 15 5 7 19

# Convergence ratios
0.1 0.5

# a vectors
1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0

# d vectors
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
-6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0 -6.0
6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0 6.0

# tau 1 vectors
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
-2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0
-1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0 -1.0

# tau 2 vectors
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
-2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0

# tau 3 vectors
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
-2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0

# tau 4 vectors
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
-2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0

# initial delta values
-2.8 -2.5 -2.2 -1.9 -1.6 -1.3 -1.0 -0.7 -0.4 -0.1 0.1 0.4 0.7 1.0 1.3 1.6 1.9 2.2 2.5 2.8

# candidate theta
0.15

# candidate a
0.15

# candidate d
0.2

# candidate tau
0.2

```

The syntax file of this program can be opened with a .txt file. Comments are preceded by

“#”.

The first two rows of the syntax indicate the dimension information of a response data set: the **Number of Rows** (i.e., sample size) and **Number of Columns** (i.e., number of items). The third row of the Input File requires the directory of the data file. When the data file is located in the main installation folder as recommended, it simply enters the data file name (e.g., “data1.txt”). Otherwise, a full directory is required here (e.g., “/irt/work/Data/MCMC\_GGUM/data1.txt”).

The **Ordering row** enters the order of all the items. For the program to accurately produce estimates of both item and person parameters, it is advisable to provide the order information in the syntax. That is, before running the program, users need to *approximately identify* which items measure low, intermediate, and high latent trait. In other words, the program needs to approximately classify all the items into low, intermediate, and high categories. Previous research has shown that subject matter experts can fairly rate item locations (Stark, Chernyshenko, & Guenole, 2011). The ordering index in this row sorts out items from low to high on the measured latent trait based on approximate judgment. The ordering does not have to be accurate.

The **convergence ratios** setting use the first 10% and last 50% parts of a chain as default. The convergence test follows Geweke’s (1992) method: The test statistic is the difference between the two sample means (i.e., two parts of the chain, typically the first 10% and the last 50% of the chain after burn-in) divided by its estimated standard error. The standard error is estimated from the spectral density at zero and so takes into account any autocorrelation.

The four rows for all the vectors (i.e., *a* vector, *b* vector, *tau1* vector, etc.) represent the  $v$ ,  $\omega$ ,  $a$ ,  $b$  **four parameter** in the four-parameter beta distribution, denoted as in  $\text{Beta}(v, \omega, a, b)$ , where the interval  $[a, b]$  is the support area, and can be adjusted based on the ordering index. The variance of the four-parameter beta can also be modified based on the values of  $v$  and  $\omega$ , where larger values are associated with smaller variances. For example,  $\text{Beta}(12.66, 12.66, -5, 5)$  approximates

the standard normal distribution  $N(0, 1)$  very well, with the maximum difference between the two distributions merely about .005. And when  $\nu = \omega = 1$ , the Beta  $(1, 1, a, b)$  is a uniform distribution  $U(a, b)$  with the boundaries of  $a$  and  $b$ . Thus the normal distribution and uniform distribution are just special cases of the four-parameter beta distribution. In addition, the skewness of the four-parameter beta distribution is changeable based on the values of  $\nu$  and  $\omega$ : when  $\nu = \omega$ , the distribution is symmetric; when  $\nu > \omega$ , the distribution is left skewed, and when  $\nu < \omega$ , the distribution is right skewed. This flexibility is important for prior distributions in estimating ideal point model parameters.

**Initial delta values** feature allows users to specify starting values, which improves estimation accuracy with a relatively short chain.

Finally, the last four entries in the syntax file specify the **standard deviation** for sampling candidate values. A smaller value indicates a narrower bandwidth for searching a candidate value for a next iteration, which leads to a lower rejection rate and a higher acceptance rate. Hence the rejection rate can be adjusted by varying these values.

### **Summary/Checklist**

In order to run the software properly, we summarize the checklist for users to build your own syntax file. This may also be helpful with troubleshooting if you find the software doesn't run or the generated output doesn't make sense.

- (1) Make sure the data is properly formatted (e.g., starts with 0; -9 is used for missing values; three spaces per column, etc).
- (2) Check the numbers of rows (items), columns (examinees/respondents), data file name and directory, and number of categories.
- (3) Change the order index. The first number (e.g., 8) means that item (e.g., the 8<sup>th</sup> item) is the most negative on the latent trait continuum.

- (4) For the four-parameter beta vectors, first of all, the number of elements in each vector corresponds the number of items. If the data has ten items, each vector should consist of ten elements. Second, number of tau parameters corresponds the number of categories minus one, that is, if you estimate 4-category data, only three tau's (i.e., tau1, tau2, tau3) should be used, and if you estimate 6-category data, tau5 should be added, and so on.
- (5) Initial delta values should be given. The number of elements specified here also corresponds the number of items. And if the scale includes both negative and positive item, the initial values should start with a negative number. If the scale only includes positive items, the initial should start with 0 and make equal spaces (the upper boundary is 3.0). If it is the latter case, it is recommended changing -6 in the d vectors to 0.
- (6) The four candidate parameters determine the standard deviation to search for a candidate value throughout the chain moving. A small number means a narrow search range, resulting in a low rejection rate. So if you desire a large rejection rate, you may increase the candidate values.
- (7) If all the issues above have been checked and the software still has trouble, it is likely the problem of the data quality. It is possible that some respondents simply carelessly endorse one category of all the items (i.e., straight-column answers). Imagine that if we administer 20 extraversion tests, with some items high on extraversion and some low on extraversion (i.e., introversion), if a respondent straightly disagrees (or agrees) with all the 20 items, his/her response would have little information to estimate theta or item parameters. It is recommended that we remove cases that endorse with only

one and two categories. The following R script is used to identify and remove such responses. This procedure will be integrated in the software for the upgraded version.

```
library(gdata)
dt0<-as.matrix(read.table("DecemberRussianSDOClean2.txt"))#read dataset
dt0<- as.matrix(read.table("dataset0.txt")) # read in your data set
dim(dt0) ; head(dt0) # check if the data input is correct

temp <-rep(NA, nrow(dt0)) # to run frequency for each respondent
  for (k in 1:nrow(dt0)){
    a <-as.vector(dt0[k,])
    temp[k] <-length(table(a))
  }
temp
sort(temp) # to check if there are respondents who endorse as few as
#one or two categories
order(temp) # to identify who are the respondents endorsing
#only one or two categories

dt1 <-dt0[-c(61,151,155,148,223),]#remove those respondents and rewrite
# the data set(presumably you want to remove
#respondents numbers(61,151,155,148,223))
dim(dt1) # check if it is correct and how many respondents remain

write.fwf(as.data.frame(dt1), file="dataset1.txt", colnames=F,
width=rep(3,ncol(dt0)), sep="") # write the new data set file
```

## Output Files

The output of the program includes two files: the raw trace file, which can be saved by clicking the **Save As** option from the File drop-down menu; and the estimation output file, which is displayed in the main window of the computer program, and it can be copied and pasted in an Excel file.

The estimation output file presents information in the following order:

- (1) Item parameter estimates of the original order;
- (2) Item parameter estimates of the sorted order;
- (3) Item parameter estimation standard errors;
- (4) Rejection rates for all the item parameters;

- (5) Person (Theta) parameter estimates, including the initial values, estimated values, and standard errors.
- (6) Z-score of the convergence test with  $p$ -values in the parentheses.
- (7) Averaged Z-score of all the absolute Z-scores and its corresponding  $p$ -value in the parenthesis.

### **Additional Information**

The response data needs to start with 0. For example, for five-category response data, the data range from 0 to 4. The missing values in the response data should be denoted by -9.

Running time varies from computer to computer, and depends on the number of iterations, the number of items, and number of respondents, and also on the configuration of a computer. In our trial run with an Intel<sup>R</sup> i7-2620 laptop computer, it took about 30 minutes to run 20,000 iterations with a dataset of 20 items and 1000 respondents.

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