



## Training workshop May 2012

### Class 1 instructions: Latent trait models for single groups

The data for these exercises are taken from the latest (2008-9) wave of the European Values Survey:

*EVS (2011): European Values Study 2008: Integrated Dataset (EVS 2008). GESIS Data Archive, Cologne. ZA4800 Data file Version 3.0.0, [doi:10.4232/1.11004](https://doi.org/10.4232/1.11004)*  
<http://info1.gesis.org/dbksearch/sdesc2.asp?no=4800&db=e&doi=10.4232/1.11004>

We will focus on a set of items asking respondents how much confidence they have in a range of institutions. We focus on a subset of the items for the analyses here, but include the full list of items in the data set, so that you may explore models using other items if you wish. The institutions are:

Variable name	Description
church	church
army	armed forces
educ	education system
press	the press
tu	trade unions
police	the police
parlt	parliament
civil	civil service
welfare	social security system
eu	European Union
nato	NATO
un	United Nations
health	health care system
justice	justice system
company	major companies
environ	environmental organisations
party	political parties
govt	government

In the data set they are provided in two forms. Variable names followed by a '4' (e.g. church4) are items with 4-point scales (with coding reversed from the original) so that:

1	=	none at all
2	=	not very much
3	=	quite a lot
4	=	a great deal

Variable names followed by a '2' (e.g. church2) are binary items recoded from the originals so that:

0	=	none or not very much
1	=	quite a lot or a great deal.

## Brief introduction to Mplus and R functions

Here we provide a few notes to get you started. For more detailed instructions, please refer to our webpages at <http://stats.lse.ac.uk/lcat/?cat=14>.

First you need to start Mplus and set up R for the session. We will show you in the computer class how to do this.

In Mplus, click on the blank document icon. An input window will appear, with heading 'Mptext1'. This is where you would type the commands for the model you want to run. For these classes we suggest it is easier for you to use the pre-prepared input files provided. You are welcome to modify these if you wish to try alternative models. Locate and open the file for the first question, which is called **1trait\_binary\_gb.inp**. To run the model, click the 'RUN' icon on the menu bar. A new output window appears displaying the output (it is automatically given the same core document name as your input file). You can take a look at the output file, but in these sessions we will mostly read the results into R and view them from there, where the LCAT functions allow you to present them more flexibly, as well as to calculate extra fit statistics from them.

Now switch to R. Create this short-cut for use in reading in Mplus files, by typing something like the following in the Command window and hitting 'return':

```
sessionpath<-"c:/courses/LCATworkshop/inputs"
```

This defines 'sessionpath' as the path to folder that contains the input (and soon will also contain the output) files for the models we will run in these classes. Note that you may need to change the file path as appropriate for you, depending on where you have stored the inputs folder. It will become clear soon how this is a useful step.

As you read the results of this first model into R, define an object – essentially a space where all the work you do on a particular set of models will be stored. Let's call it "bin6gb" (the first set of models in these exercises all use the same six binary items for the same sample of British survey respondents). Next you type an arrow next to it, followed by the name of the function you are calling (`lcat`), followed by the name of the output file for the model (`1trait_binary_gb.out`), followed by the short cut (`sessionpath`) for its destination:

```
bin6gb<-lcat("1trait_binary_gb.out",sessionpath)
```

R will take a moment to process the results. You can now view them in a variety of ways, according to your interests. To see a summary of the results for all models in the object `bin6gb` (currently only one model), type:

```
bin6gb
```

To see the model results in probability scale, type:

```
print(bin6gb,1)
```

`print` is the command for these results, `bin6gb` is the name of the object (where you are beginning to store your results), and `1` means you are calling up the first element in that object – or the first model in the set of models you will run in session 1.

To view the results in the more standard logit scale, type the command below. `alt` is an argument in the function whose default is "False"; you don't need to type it unless you want to switch it to "True":

```
print(bin6gb,1,alt=T)
```

Now you have seen the parameter estimates in their two different formats, you might want to draw some plots of item characteristic curves (ICCs). But before you do that, you may find it convenient to be able to flip the direction of the latent trait around. It may be, for example, that your model is one in which low levels of the latent trait denote high trust, and high levels of the latent trait denote low trust. For reporting, it would be more intuitive if high levels of the latent trait denoted high levels of trust. You can use the command `reorder` to reverse the direction of the trait, if need be.

```
reorder(bin6gb,1,traits=-1)
```

So you identify the object for this session, then apply the command, and then specify the model output you want to change: `bin6gb` followed by `1` to indicate the first element or model in the list. Then `traits=-1` indicates that this trait is reversed in direction. After you apply the command you will see a notice in R telling you that this has been executed. Try viewing the results again (using the `print` command) to demonstrate to yourself that this has worked.

When you are ready to draw some ICCs, use the `plot` command, for example as follows:

```
plot(bin6gb,1,items=1:6,levels=2)
```

`plot` is the general command and `bin6gb,1` identifies the model you are inspecting. `items=1:6` means it will return a graph showing curves for all 6 items in your set. If you wanted to see the curves just for items 2 and 4 you could type `items=c(2,4)`. `levels=2` specifies the level of the variable. Since we are using binary items we have two levels, and level 2 is the higher one, i.e. the more trusting response (In Mplus the results are given with the items' coding beginning at 1, i.e. 1 and 2 for these variables, even though in the original data file they are coded 0 and 1).

If you would like to keep the resulting plot, the easiest way is to copy and paste it into a Word document, or similar. The same is true for the output given in the R Console. R will add output to the end of the window, but will overwrite plots.

You may now wish to move to the next model, which is very similar except that it uses polytomous versions of the items instead of binary versions. In Mplus, open the input file `1trait_nominal_gb.inp`. Run it, and read the results into Mplus but first create a new object for the new data:

```
poly6gb<-lcat("1trait_nominal_gb.out",sessionpath)
```

When you run the next model, `1trait_ordinal_gb.inp` (which also uses polytomous versions of the six variables), and read in the results you will need to add it to the object `poly6gb` with the command `addto=poly6gb` at the end of the line:

```
poly6gb<-lcat("1trait_ordinal_gb.out",sessionpath,addto=poly6gb)
```

Now you have two elements (or models) in the object `polytomous6gb`, so you will need to refer to this model as `poly6gb,2` when you call its results in R.

If you for example make a mistake with a model and want to replace it with a new version, add a comma and then `overwrite=T` to the command. This will overwrite the old element which has that name with the new one you are reading in (the old and new elements need to have the same name in order for one to be overwritten by the other).

A selection of suggested models and operations are listed below (the first one is again included as a summary), with very brief explanations. Do feel free to modify them if you wish, and do ask if you have any questions.

## 1. 1 latent trait; 1 group; 6 binary items

- Mplus input file: **1trait\_binary\_gb.inp**
- Model: 1 trait, 6 binary items (police2 parlt2 justice2 eu2 nato2 un2), 1 group = British sample ('gb')
- R command to read in the data and apply the LCAT function:  

```
bin6gb<-lcat("1trait_binary_gb.out",sessionpath)
```
- Viewing the results in two different formats:  

```
print(bin6gb,1)  
print(bin6gb,1,alt=T)
```
- Reversing the direction of the trait and checking the results:  

```
reorder(bin6gb,elements=1,traits=-1)  
print(bin6gb,1)
```
- Plotting ICCs for the higher level of response (trust quite a lot or a great deal) for items 1 to 6:  

```
plot(bin6gb,1,items=1:6,levels=2)
```

## 2. 1 latent trait; 1 group; 6 polytomous nominal items

- Mplus input file: **1trait\_nominal\_gb.inp**
- Model: 1 trait, 6 4-category items (police4 parlt4 justice4 eu4 nato4 un4) treated as nominal (unordered), 1 group = British respondents ('gb')
- R command to read in the data and apply the LCAT function; *defining a new object* since now we are analysing the 4-category versions of the variables:  

```
poly6gb<-lcat("1trait_nominal_gb.out",sessionpath)
```
- Viewing the results in two different formats:  

```
print(poly6gb,1)  
print(poly6gb,1,alt=T)
```
- Reversing the direction of the trait and checking the output:  

```
reorder(poly6gb,elements=1,traits=-1)  
print(poly6gb,1)
```
- Plotting ICCs for each response option separately, just for item 6 (i.e. un4):  

```
plot(poly6gb,1,items=6,levels=1:4)
```
- Plotting ICCs for each response option separately, just for item 1 (i.e. police4):  

```
plot(poly6gb,1,items=1,levels=1:4)
```
- Plotting ICCs for the lowest item response (i.e. "none at all"), just for items 1 and 6:  

```
plot(poly6gb,1,items=c(1,6),levels=1)
```
- Plotting ICCs for the two highest item responses (i.e. "quite a lot" and "a great deal"), just for items 1 and 6:  

```
plot(poly6gb,1,items=c(1,6),levels=3:4)
```
- Plotting cumulative ICCs for the 3<sup>rd</sup> response or higher (i.e. "quite a lot" or "a great deal"), just for items 1 and 6:  

```
plot(poly6gb,1,items=c(1,6),levels=3,cumprob="high")
```
- Plotting cumulative ICCs for the second item response or lower (i.e. "none at all" or "not very much"), just for items 1 and 6:  

```
plot(poly6gb,1,items=c(1,6),levels=2,cumprob="low")
```

### 3. 1 latent trait; 1 group; 6 polytomous ordinal items

- Mplus input file: **1trait\_ordinal\_gb.inp**
- Model: 1 trait, 6 4-category items (police4 partl4 justice4 eu4 nato4 un4) treated as ordinal, 1 group = British respondents ('gb')
- R commands to read in the data and apply the LCAT function; view the results in two different formats, and reverse the direction of the trait if you wish, checking the result:

```
poly6gb<-lcat("1trait_ordinal_gb.out",sessionpath,addto=poly6gb)
print(poly6gb,2)
print(poly6gb,2,alt=T)
reorder(poly6gb,elements=2,traits=-1)
print(poly6gb,2)
```
- Some plots of ICCs:

```
plot(poly6gb,2,items=6,levels=1:4)
plot(poly6gb,2,items=1,levels=1:4)
plot(poly6gb,2,items=c(1,6),levels=1)
plot(poly6gb,2,items=1:6,levels=4)
plot(poly6gb,2,items=1:6,levels=2)
plot(poly6gb,2,items=1:6,levels=2,cumprob="high")
```

### 4. 2 correlated latent traits; 1 group; 6 binary items

- Mplus input file: **2trait\_corr\_binary\_gb.inp**
- Model: 2 traits with their covariance, 6 binary items (police2 partl2 justice2 load onto first trait and eu2 nato2 un2 onto second trait), 1 group = British respondents ('gb')
- R commands to read in the data (going back to the original object binary6gb) and apply the LCAT function; view the results in two different formats:

```
bin6gb<-lcat("2trait_corr_binary_gb.out",sessionpath,addto=bin6gb)
print(bin6gb,2)
print(bin6gb,2,alt=T)
```
- Keep the direction of the first trait the same (1) and reverse the direction of the second trait (-2) and check the results:

```
reorder(bin6gb,elements=2,traits=c(1,-2))
print(bin6gb,2)
```
- Some plots of ICCs – with new element required to specify which trait: trait=1 or trait=2:

```
plot(bin6gb,2,trait=1,items=1:3,levels=2)
plot(bin6gb,2,trait=2,items=4:6,levels=2)
```

## 5. 2 correlated latent traits; 1 group; 6 binary items with a cross-loading for one item

- Mplus input file: **2trait\_corr\_cl\_binary\_gb.inp**
- Model: 2 traits with their covariance, 6 binary items (police2 parl2 justice2 eu2 load onto first trait and eu2 nato2 un2 onto second trait, i.e. eu2 loads onto both traits), 1 group = British respondents ('gb')
- R commands to read in the data and apply the LCAT function; view the results in two different formats:  

```
bin6gb<-lcat("2trait_corr_cl_binary_gb.out",sessionpath,addto=bin6gb)
print(bin6gb,3)
print(bin6gb,3,alt=T)
```
- Reverse the direction of the (original) second trait (-2) and present it first in the results (list -2 first); keep the direction of the (original) first trait the same (1) and present it as the second trait (list 1 second), and check the results:  

```
reorder(bin6gb,elements=3,traits=c(-2,1))
print(bin6gb,3)
```
- Some plots of ICCs:  

```
plot(bin6gb,3,trait=1,items=4:6,levels=2)
plot(bin6gb,3,trait=2,items=1:4,levels=2)
```
- Print out the list of models in the object `binary6gb` to remind yourself which is which:  

```
bin6gb
```
- Likelihood ratio comparison test of the current model (with the cross-loading) with the previous nested model (without the cross-loading):  

```
lcat.lrtest(bin6gb,2,3)
```

## 6. 2 latent traits linked by a regression relationship; 1 group; 6 binary items

- Mplus input file: **2trait\_reg\_binary\_gb.inp**
- Model: 2 traits with trait 2 (trust in eu, nato and un) regressed onto trait 1 (trust in police, parliament and justice system), 6 binary items (police2 parl2 justice2 load onto first trait and eu2 nato2 un2 onto second trait), 1 group = British respondents ('gb')
- R commands to read in the data and apply the LCAT function; view the results in two different formats:  

```
bin6gb<-lcat("2trait_reg_binary_gb.out",sessionpath,addto=bin6gb)
print(bin6gb,4)
print(bin6gb,4,alt=T)
```
- Some plots of ICCs:  

```
plot(bin6gb,4,trait=1,items=1:3,levels=2)
plot(bin6gb,4,trait=2,items=4:6,levels=2)
```

## 7. 2 latent traits uncorrelated; 1 group; 6 binary items

- Mplus input file: **2trait\_uncorr\_binary\_gb.inp**
- Model: 2 traits with 6 binary items (police2 parl2 justice2 load onto first trait and eu2 nato2 un2 onto second trait), with covariance between traits constrained to be zero, 1 group = British respondents ('gb')
- R commands to read in the data and apply the LCAT function; view the results in two different formats:  

```
bin6gb<-lcat("2trait_uncorr_binary_gb.out",sessionpath,addto=bin6gb)
print(bin6gb,5)
print(bin6gb,5,alt=T)
```
- Some plots of ICCs:  

```
plot(bin6gb,5,trait=1,items=1:3,levels=2)
plot(bin6gb,5,trait=2,items=4:6,levels=2)
```
- Likelihood ratio comparison test of this model (with no covariance between traits) which is nested with the previous model (with the trait covariance):  

```
lcat.lrtest(bin6gb,4,5)
```

### Quitting the programme:

When you have finished working and go to shut down R, a dialogue box will appear asking whether you wish to 'save the workspace image'. Answer 'YES'. This will save the workspace so that when you return to the computer in the second class, you will be able to start from where you left off, and for example look at fit statistics for the model without having to reload the results from Mplus into R.