

Supplementary Material to “Measurement Invariance Via Equivalence Testing”

Ge Jiang, Yujiao Mai and Ke-Hai Yuan

Introduction

The supplementary material illustrates the use of the accompanying R package `equaltestMI`. The sample statistics from Table 1 of Lee and Al Otaiba (2015) are used as an example. The description of the data can be found in the original article and the results obtained from `equaltestMI` are discussed at length in the submitted article “Measurement Invariance Via Equivalence Testing”.

The R package `equaltestMI` is available on CRAN and can be downloaded for use on any R platform with version higher than 3.1.0. Users can pass different arguments to the main function `eqMI.main()` to examine measurement invariance using the conventional multiple-group approach or equivalence testing approach. Under the framework of equivalence testing, users obtain the minimum tolerable size (T-size) and adjusted cutoff values to evaluate the goodness-of-fit of each invariance test. The projection method is also available for testing the equality of latent means.

Part 1: R Script for Obtaining Results from Equivalence Testing and Projection Method

```
## load package
library(equaltestMI)

## sample statistics where M1 and M2 are sample means, and Cov1 and Cov2 are
## sample covariance matrices;
## group 1 = boys ineligible for free-reduced lunches
## group 2 = boys eligible for free-reduced lunches

setwd("C:/research/equaltestMI")
Group1 <- read.table('Group1.txt', header = TRUE)
Group2 <- read.table('Group2.txt', header = TRUE)
Group1 <- as.matrix(Group1)
Group2 <- as.matrix(Group2)
M1 <- Group1[1,]
M2 <- Group2[1,]
Cov1 <- Group1[2:7,]
Cov2 <- Group2[2:7,]
```

```
## lavaan model syntax
model <- '
AlphabetKnowledge =~ Letter_Name+ Letter_Sound
PhonologicalAwareness =~ Blending + Elision
Spelling =~ Real_Words + Pseudo_Words
'
```

```
## the results using equivalence testing and projection method
## full R output will be presented in Part 3
```

```
test <- eqMI.main(model = model,
  sample.nobs = c(78, 174),
  sample.mean = list(M1, M2),
  sample.cov = list(Cov1, Cov2),
  meanstructure = TRUE,
  output = 'both',
  quiet = FALSE,
  equivalence.test = TRUE, adjRMSEA = TRUE,
  projection = TRUE, bootstrap = FALSE)
```

Part 2: Sample Means and Covariance Matrices of the Example Data

Sample statistics for boys ineligible for free-reduced lunches (group 1):

Sample means:

```
## Letter_Name Letter_Sound Blending Elision Real_Words
## 45.26 40.45 10.91 6.51 23.88
## Pseudo_Words
## 14.12
```

Sample Covariance Matrix:

```
## Letter_Name Letter_Sound Blending Elision Real_Words
## Letter_Name 207.360 159.097 32.589 25.805 61.776
## Letter_Sound 159.097 280.228 42.888 36.748 76.123
## Blending 32.589 42.888 18.233 10.713 19.051
## Elision 25.805 36.748 10.713 20.070 20.372
## Real_Words 61.776 76.123 19.051 20.372 73.616
## Pseudo_Words 45.075 60.204 14.219 16.709 47.429
## Pseudo_Words
## Letter_Name 45.075
## Letter_Sound 60.204
## Blending 14.219
## Elision 16.709
## Real_Words 47.429
## Pseudo_Words 44.356
```

Sample statistics for boys eligible for free-reduced lunches (group 2):

Sample means:

```
## Letter_Name Letter_Sound Blending Elision Real_Words
##      41.32      34.88      9.08      4.45      19.24
## Pseudo_Words
##      11.07
```

Sample Covariance Matrix:

```
##          Letter_Name Letter_Sound Blending Elision Real_Words
## Letter_Name      295.840      232.200   38.996  20.174   67.593
## Letter_Sound      232.200      324.000   43.164  22.824   77.954
## Blending           38.996       43.164   19.010   9.260   23.428
## Elision            20.174       22.824    9.260  10.049   15.254
## Real_Words         67.593       77.954   23.428  15.254   64.320
## Pseudo_Words       57.771       60.458   16.272  11.042   38.411
##          Pseudo_Words
## Letter_Name        57.771
## Letter_Sound       60.458
## Blending           16.272
## Elision            11.042
## Real_Words         38.411
## Pseudo_Words       38.688
```

Part 3: Full R Output of the “test” object in Part 1

```
##
## ----- Equality of Population Covariance Matrices under NHT -----
##
##          Chisq Df      pvalue
## fit.pop.cov 48.85006 21 0.0005261173
##
## ----- Chi-Square and Chi-Square-Difference Test under NHT -----
##
##          Chisq Df      pvalue Chisq.diff Df.diff      pvalue
## fit.pop.cov      48.850 21      0.001
## fit.configural.g1  4.408  6      0.622
## fit.configural.g2 10.641  6      0.100
## fit.combine.groups 15.049 12
## fit.metric        20.033 15      0.171      4.984      3      0.173
## fit.residuals     42.512 21      0.004     22.479      6      0.001
## fit.varfactor     54.175 27      0.001     11.663      6      0.070
## fit.scalar        23.732 18      0.164      3.699      3      0.296
## fit.strong.means  41.066 21      0.006     17.334      3      0.001
## fit.strict.residuals 45.968 24      0.004     22.237      6      0.001
```

```

## fit.strict.means      63.630 27    0.000    17.662      3    0.001
##
## ----- T-size epsilon, RMSEA, and Adjusted Cutoff Values under ET -----
##
##              epsilon_t  RMESA_t  cut.01  cut.05  cut.08
## fit.pop.cov          0.209    0.141    0.076    0.097    0.121
## fit.configural.g1    0.028    0.097    0.116    0.133    0.157
## fit.configural.g2    0.071    0.154    0.116    0.133    0.157
## fit.metric           0.049    0.181    0.151    0.164    0.187
## fit.residuals        0.140    0.216    0.116    0.133    0.157
## fit.varfactor        0.078    0.161    0.116    0.133    0.157
## fit.scalar           0.040    0.163    0.151    0.164    0.187
## fit.strong.means     0.125    0.289    0.151    0.164    0.187
## fit.strict.residuals 0.138    0.215    0.116    0.133    0.157
## fit.strict.means     0.127    0.291    0.151    0.164    0.187
##
##              cut.10 goodness-of-fit
## fit.pop.cov          0.139                poor
## fit.configural.g1    0.175                excellent
## fit.configural.g2    0.175                fair
## fit.metric           0.205                fair
## fit.residuals        0.175                poor
## fit.varfactor        0.175                mediocre
## fit.scalar           0.205                close
## fit.strong.means     0.205                poor
## fit.strict.residuals 0.175                poor
## fit.strict.means     0.205                poor
##
##
## ----- Means of Latent and Specific Factors by the Projection Method
and under NHT -----
##
##              Chisq Df      pvalue
## fit.mvmean    22.388937  6 0.0010292258
## fit.common    19.433784  3 0.0002223613
## fit.specific  4.015386   3 0.2598074616
## Validity Index is 0.9885648
##
## ----- Means of Latent and Specific Factors by the Projection Method
and under ET -----
##
##              epsilon_t  RMESA_t  cut.01  cut.05  cut.08  cut.10
## fit.mvmean    0.139    0.215    0.116    0.133    0.157    0.175
## fit.common    0.137    0.302    0.151    0.164    0.187    0.205
## fit.specific  0.042    0.168    0.151    0.164    0.187    0.205
##
##              goodness-of-fit
## fit.mvmean                poor
## fit.common                poor
## fit.specific              fair

```

Part 4: Some Commonly Performed Analysis

1. results using conventional multiple-group SEM approach:

```
test1 <- eqMI.main(model = model,  
  sample.nobs = c(78, 174), sample.cov = list(Cov1, Cov2),  
  sample.mean = list(M1, M2), meanstructure = TRUE,  
  equivalence.test = FALSE, adjRMSEA = FALSE)
```

2. results using conventional multiple-group SEM approach with mean structure tested by projection method:

```
test2 <- eqMI.main(model = model,  
  sample.nobs = c(78, 174), sample.cov = list(Cov1, Cov2),  
  sample.mean = list(M1, M2), meanstructure = TRUE,  
  equivalence.test = FALSE, adjRMSEA = FALSE,  
  projection = TRUE)
```

3. results using equivalence testing:

```
test3 <- eqMI.main(model = model,  
  sample.nobs = c(78, 174), sample.cov = list(Cov1, Cov2),  
  sample.mean = list(M1, M2), meanstructure = TRUE,  
  equivalence.test = TRUE, adjRMSEA = FALSE)
```

4. results using equivalence testing and adjusted cutoff values:

```
test4 <- eqMI.main(model = model,  
  sample.nobs = c(78, 174), sample.cov = list(Cov1, Cov2),  
  sample.mean = list(M1, M2), meanstructure = TRUE,  
  equivalence.test = TRUE, adjRMSEA = TRUE)
```

5. analysis of 4 with mean structure tested by projection method:

```
test5 <- eqMI.main(model = model,  
  sample.nobs = c(78, 174), sample.cov = list(Cov1, Cov2),  
  sample.mean = list(M1, M2), meanstructure = TRUE,  
  equivalence.test = TRUE, adjRMSEA = TRUE,  
  projection = TRUE)
```

6. if any of the tests above evaluate only mean structure or only covariance structure, add the argument "structure = 'mean'" or "structure = 'covariance'", say test5 with only mean structure:

```
test6 <- eqMI.main(model = model, structure = 'mean',  
  sample.nobs = c(78, 174), sample.cov = list(Cov1, Cov2),  
  sample.mean = list(M1, M2), meanstructure = TRUE,  
  equivalence.test = TRUE, adjRMSEA = TRUE,  
  projection = TRUE)
```

7. if raw data are available, say the name of the raw data is 'literacy.dat' and the variable of group membership is 'FRL', then test5 is conducted as:

```
test7 <- eqMI.main(model = model, data = literacy.dat,  
  group = "FRL", meanstructure = TRUE,  
  equivalence.test = TRUE, adjRMSEA = TRUE,  
  projection = TRUE)
```

8. when raw data are available and project method is used, bootstrap resampling can be used to obtain empirical p-values of the tests conducted by project method:

```
test8 <- eqMI.main(model = model, data = literacy.dat,  
  group = "FRL", meanstructure = TRUE,  
  equivalence.test = TRUE, adjRMSEA = TRUE,  
  projection = TRUE, bootstrap = TRUE)
```

9. in any of the tests above, the users can turn out the printing of results (not recommended) though the results are still contained in test9\$eqMI.stat:

```
test9 <- eqMI.main(model = model, data = literacy.dat,  
  group = "FRL", meanstructure = TRUE,  
  equivalence.test = TRUE, adjRMSEA = TRUE,  
  projection = TRUE, bootstrap = TRUE,  
  quiet = TRUE)
```

Part 5: Arguments of the eqMI.main() Function

```
## The main function to test measurement invariance  
##  
## Description:  
##  
##     Test measurement invariance with equivalence testing, projection  
##     methods, and adjusted RMSEA cutoffs for two groups.  
##  
## Usage:  
##  
##     eqMI.main(..., output = "both", equivalence.test = TRUE, adjRMSEA = T  
RUE,  
##     projection = FALSE, bootstrap = FALSE, quiet = FALSE, B = 100,  
##     seed = 111)  
##  
## Arguments:  
##  
##     ...: The same arguments as for any lavaan model. See 'lavaan::sem'  
##     for more information.  
##  
##     Users must explicitly specify the name of the input elements  
##     for this function to catch. For example, specify 'data =  
##     HolzingerSwineford' instead just 'HolzingerSwineford'.  
##  
##     output: If the function prints out results of covariance structure,  
##     mean structure, or both. The value of 'output' must be  
##     'mean', 'covariance', or 'both'. When the tests involve mean  
##     structure ('output = 'mean' or 'both'), both the strong and  
##     the strict tests of measurement invariance will be conducted.  
##
```

```
## equivalence.test: If 'equivalence.test=TRUE', equivalence testing is
##      used for examining all statistics. RMSEA together with
##      conventional or adjusted cutoff values will be used to gauge
##      the goodness of fit.
##
## adjRMSEA: If 'adjRMSEA=TRUE', adjusted RMSEA cutoff values are used for
##      equivalence testing. See details in Yuan & Chan (2016).
##
## projection: If 'projection=TRUE', projection method is used to test the
##      equality of latent factor means. The advantage of the
##      projection method over conventional multiple-group SEM
##      approach is that the test of latent factor means can be
##      conducted even when the equality of intercepts do not hold.
##
## bootstrap: If 'bootstrap=TRUE', bootstrap is used to obtain empirical
##      p-values for testing the equality of cross-group latent
##      factor means.
##
##      quiet: If 'quiet=FALSE' (default), a summary is printed out
##      containing an overview of the different models that are
##      fitted, together with some model comparison tests and fit
##      measures. The results of equivalence testing will also be
##      printed if equivalence testing is used. If 'quiet=TRUE', no
##      summary is printed but results will be stored in the object.
##
##      B: The number of bootstrap samples used in bootstrap approach.
##
##      seed: The initial seed to generate bootstrap samples. Default at
##      111.
##
## Details:
##
##      An all-in-one function with several added options to conduct a
##      sequence of tests needed to evaluate MI. The chi-square
##      statistics, except the one for testing the equality of covariance
##      structure, are obtained based on 'lavaan::sem' function. The test
##      statistic of the covariance structure equality is obtained via the
##      method of Lagrangian multiplier. Equivalence testing is enabled by
##      setting 'equivalence.test=TRUE' and this function will calculate
##      T-size, RMSEA, and adjusted RMSEA cutoff values, and provide the
##      goodness-of-fit.
##
## Value:
##
##      A list is returned with:
##
##      'convention.sem' Result of conventional multiple-group SEM using
##      Lavaan. Returned object of 'eqMI.semtest'.
##
##      'projection.res' Results of projection methods on tests of latent
```

```

##          means. Returned object of 'eqMI.projection' and
##          'eqMI.bootstrap'.
##
##          'eqMI.stat' Test statistics, degrees of freedom, p-values, ncp,
##          T-sizes, RMSEAs, their cutoff values, and the goodness-of-fit
##          under equivalence testing. A formatted version of 'eqMI.stat'
##          is printed if 'quiet=FALSE'.
##
## References:
##
##          Deng, L., & Yuan, K. H. (2016). Comparing Latent Means Without
##          Mean Structure Models: A Projection-Based Approach. Psychometrika,
##          81(3), 802-829.
##
##          Yuan, K. H., & Chan, W. (2016). Measurement invariance via
##          multigroup SEM: Issues and solutions with chi-square-difference
##          tests. Psychological methods, 21(3), 405-426.
##
## Examples:
##
##          data(HolzingerSwineford)
##          semmodel<- '
##          L1 =~ V1 + V2 + V3
##          L2 =~ V4 + V5 + V6
##          L3 =~ V7 + V8
##          L4 =~ V9 + V10 + V11
##          '
##          # If raw data are available;
##
##          test <- eqMI.main(model = semmodel, data = HolzingerSwineford,
##          group = "school", meanstructure = TRUE,
##          output = 'both', quiet = FALSE,
##          equivalence.test = TRUE, adjRMSEA = TRUE,
##          projection = TRUE, bootstrap = FALSE)
##
##          # when only sample statistics are available;
##          # sample.cov need to be provided for tests of covariance structure;
##          # sample.mean need to be provided for tests of mean structure;
##
##          school1 <- subset(HolzingerSwineford, school==1)[-12]
##          school2 <- subset(HolzingerSwineford, school==2)[-12]
##          test <- eqMI.main(model = semmodel,
##          sample.nobs = c(nrow(school1), nrow(school2)),
##          sample.cov = list(cov(school1), cov(school2)),
##          sample.mean = list(colMeans(school1), colMeans(school2)),
##          meanstructure = TRUE, output = 'both', quiet = FALSE,
##          equivalence.test = TRUE, adjRMSEA = TRUE,
##          projection = TRUE, bootstrap = FALSE)
##
##

```