Measurement Invariance via Equivalence Testing and Projection Method

Ge Jiang, Yujiao Mai, and Ke-Hai Yuan

Introduction

This supplementary document 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 published article “Advances in Measurement Invariance and Mean Comparison of Latent Variables: Equivalence Testing and A Projection-Based Approach” <doi: 10.3389/fpsyg.2017.01823>.

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 (NHT) or equivalence testing (ET) 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.

Important Notes:

This package is developed for complete dataset with two groups/time points. Use of saturated models might lead to problems in calculation of adjusted RMSEA thresholds. Please consider alternative methods if you have datasets that do not satisfy the requirements.

Part 0: Installation

Users can install the package from CRAN:

```r
## load package
# install.packages("equaltestMI")
library(equaltestMI)
```

or install the most recent version from the maintainer’s GitHub repository:

```r
# install.packages("devtools")
# library(devtools)
# devtools::install_github("gabriellajg/equaltestMI", force=TRUE)
library(equaltestMI)
```

Part 1: Sample Means and Covariance Matrices of the Example Data

Load data first:
data(LeeAlOtaiba)
# contains sample covariance matrices and sample means of four groups

We will use two of the groups as illustration:

## group 1 = boys ineligible for free-reduced lunches
Group1 <- LeeAlOtaiba$BoysIneligible
Group1 <- as.matrix(Group1)

## group 2 = boys eligible for free-reduced lunches
Group2 <- LeeAlOtaiba$BoysEligible
Group2 <- as.matrix(Group2)

# sample means:
M1 <- Group1[,1]
M2 <- Group2[,1]

# sample covariance matrices:
Cov1 <- Group1[2:7,]
Cov2 <- Group2[2:7,]

Sample statistics for boys ineligible for free-reduced lunches (Group 1):
Sample means:
 |> Letter_Name  Letter_Sound  Blending  Elision  Real_Words  Pseudo_Words
#>  45.26  40.45  10.91  6.51  23.88  14.12
Sample Covariance Matrix:
 |> Letter_Name  Letter_Sound  Blending  Elision  Real_Words  Pseudo_Words
#> Letter_Name  207.360  159.097  32.589  25.805  61.776  45.075
#> Letter_Sound  159.097  280.228  42.888  36.748  76.123  60.204
#> Blending  32.589  42.888  18.233  10.713  19.051  14.219
#> Real_Words  61.776  76.123  19.051  20.372  73.616  47.429
#> Pseudo_Words  45.075  60.204  14.219  16.709  47.429  44.356

Sample statistics for boys eligible for free-reduced lunches (Group 2):
Sample means:
 |> Letter_Name  Letter_Sound  Blending  Elision  Real_Words  Pseudo_Words
#>  41.32  34.88  9.08  4.45  19.24  11.07
Sample Covariance Matrix:
 |> Letter_Name  Letter_Sound  Blending  Elision  Real_Words  Pseudo_Words
#> Letter_Name  295.840  232.200  38.996  20.174  67.593  57.771
#> Letter_Sound  232.200  324.000  43.164  22.824  77.954  60.458
#> Blending  38.996  43.164  19.010  9.260  23.428  16.272
#> Real_Words  67.593  77.954  23.428  15.254  64.320  38.411
#> Pseudo_Words  57.771  60.458  16.272  11.042  38.411  38.688
Part 2: R Script for Obtaining Results from Equivalence Testing and Projection Method

```r
## 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 = TRUE,
  equivalence.test = TRUE, adjRMSEA = TRUE,
  projection = TRUE, bootstrap = FALSE)
```

Part 3: Full R Output of the “test” object in Part 2

```r
#> #> ---------- 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  cut.10
#> fit.pop.cov 0.209 0.141 0.076  0.097  0.121  0.139
#> fit.configural.g1 0.028 0.097 0.116  0.133  0.157  0.175
#> fit.configural.g2 0.071 0.154 0.116  0.133  0.157  0.175
#> fit.metric 0.049 0.181 0.151  0.164  0.187  0.205
#> fit.residuals 0.140 0.216 0.116  0.133  0.157  0.175
#> fit.varfactor 0.078 0.161 0.116  0.133  0.157  0.175
#> fit.scalar 0.040 0.163 0.151  0.164  0.187  0.205
#> fit.strong.means 0.125 0.289 0.151  0.164  0.187  0.205
```
Part 4: Some Commonly Performed Analysis

1. results using conventional multiple-group SEM approach:

```r
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:

```r
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:

```r
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:

```r
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:

```r
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:

```r
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:

```r
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 by enabling bootstrap = TRUE.

```r
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 suppress the printing of results (not recommended) though the results are still contained in test9$eqMI.stat:

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

10. in any of the tests above, the users can allow partial invariance by adding ‘group.partial’:

```r
test10 <- eqMI.main(model = model, data = literacy.dat,
  group = "FRL", meanstructure = TRUE,
  group.partial = c("Spelling=Real_Words", "Blending-1"),
  equivalence.test = TRUE, adjRMSEA = TRUE,
  projection = TRUE, bootstrap = FALSE,
  quite = TRUE)
```
so that the loadings of ‘Spelling’ on ‘Real_Words’ and the intercept of ‘Blending’ are allowed to vary across groups.

Part 5: Help page of the eqMI.main() function

For a complete view of the help page of function eqMI.main(), please install R package printr and type ?eqMI.main in R console:

```r
#> Registered S3 method overwritten by 'printr':
#>   method          from
#>   knit_print.data.frame rmarkdown
#> Rendering development documentation for 'eqMI.main'
```