

# Appendix 2

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2023-11-03

## Overview

This is an overview of model selection, for the study entitled “The Pest Management Attitude scale: a tool for measuring consensus between experts and practitioners in invasion biology”. Let’s have a look at the dataset.

```
## 'data.frame': 322 obs. of 9 variables:
## $ ias.natconserv : num 2 3 2 3 3 3 3 3 2 ...
## $ ias.costbenefit : num 1 2 1 1 2 2 1 3 3 1 ...
## $ ias.nextgen : num 2 2 3 2 3 2 3 3 2 ...
## $ ias.nopriority : num -1 -2 1 -2 -1 0 -2 -1 -3 -1 ...
## $ ias.collateral : num 0 2 -1 1 2 1 3 3 -2 0 ...
## $ ias.interfere : num -2 2 -2 -2 -1 1 -3 -3 -2 0 ...
## $ ias.notenough : num 2 3 1 2 0 2 2 3 3 3 ...
## $ practitioner.dummy: Factor w/ 2 levels "Researcher","Practitioner": NA NA NA NA NA NA 1 1 1 1 ...
## $ taxa.type : chr "single" "single" "multiple" "multiple" ...
```

The dataset contains the variables called “ias.natconserv” (item NC in Fig. 1), “ias.costbenefit” (CB), “ias.nextgen” (NG), “ias.nopriority” (NP), “ias.collateral” (CD), “ias.interfere” (IN), “ias.notenough” (EC). Moreover, it contains a dummy variable that compares researchers versus practitioners (“practitioner.dummy”) and another variable called “taxa.type” comparing respondents that worked on a single taxonomic groups versus respondents that had worked with multiple taxa.

## A basic model

To begin, let’s fit a basic confirmatory factor analysis (CFA) and use with a robust estimator:

```
mod.a <- 'attitudes =~ NA*ias.natconserv + ias.costbenefit + ias.nextgen + ias.nopriority +
ias.collateral + ias.interfere + ias.notenough'
fit.a <- cfa(mod.a, data=d, std.ov= TRUE, std.lv=TRUE, estimator="MLM")
```

```
summary(fit.a, fit.measures=TRUE)
```

```
## lavaan 0.6-11 ended normally after 12 iterations
##
## Estimator ML
## Optimization method NLMINB
## Number of model parameters 14
##
## Number of observations 322
##
## Model Test User Model:
## Standard Robust
## Test Statistic 100.090 83.684
## Degrees of freedom 14 14
## P-value (Chi-square) 0.000 0.000
```

```

##      Scaling correction factor                      1.196
##      Satorra-Bentler correction
##
## Model Test Baseline Model:
##
##      Test statistic                      494.421      368.177
##      Degrees of freedom                      21          21
##      P-value                      0.000      0.000
##      Scaling correction factor                      1.343
##
## User Model versus Baseline Model:
##
##      Comparative Fit Index (CFI)                      0.818      0.799
##      Tucker-Lewis Index (TLI)                      0.727      0.699
##
##      Robust Comparative Fit Index (CFI)                      0.821
##      Robust Tucker-Lewis Index (TLI)                      0.732
##
## Loglikelihood and Information Criteria:
##
##      Loglikelihood user model (H0)                      -2997.617      -2997.617
##      Loglikelihood unrestricted model (H1)                  -2947.572      -2947.572
##
##      Akaike (AIC)                      6023.234      6023.234
##      Bayesian (BIC)                      6076.078      6076.078
##      Sample-size adjusted Bayesian (BIC)                  6031.671      6031.671
##
## Root Mean Square Error of Approximation:
##
##      RMSEA                      0.138      0.124
##      90 Percent confidence interval - lower                  0.113      0.101
##      90 Percent confidence interval - upper                  0.164      0.148
##      P-value RMSEA <= 0.05                      0.000      0.000
##
##      Robust RMSEA                      0.136
##      90 Percent confidence interval - lower                  0.109
##      90 Percent confidence interval - upper                  0.165
##
## Standardized Root Mean Square Residual:
##
##      SRMR                      0.079      0.079
##
## Parameter Estimates:
##
##      Standard errors                      Robust.sem
##      Information                      Expected
##      Information saturated (h1) model          Structured
##
## Latent Variables:
##
##      Estimate Std.Err z-value P(>|z|)
##      attitudes =~
##      ias.natconserv      0.701      0.082      8.519      0.000
##      ias.costbenefit      0.456      0.052      8.747      0.000
##      ias.nextgen      0.784      0.076     10.382      0.000

```

```
##      ias.nopriority    -0.550    0.056   -9.834    0.000
##      ias.collateral    -0.348    0.061   -5.741    0.000
##      ias.interfere     -0.479    0.054   -8.904    0.000
##      ias.notenough      0.422    0.071    5.911    0.000
##
## Variances:
##              Estimate Std.Err  z-value  P(>|z|)
##      .ias.natconserv    0.506    0.080    6.294    0.000
##      .ias.costbenefit    0.789    0.096    8.220    0.000
##      .ias.nextgen       0.382    0.090    4.250    0.000
##      .ias.nopriority    0.695    0.061   11.346    0.000
##      .ias.collateral    0.876    0.055   15.890    0.000
##      .ias.interfere     0.767    0.056   13.703    0.000
##      .ias.notenough     0.819    0.106    7.721    0.000
##      attitudes          1.000
```

Let's have a look at model fitness:

```
fitmeasures(fit.a, fit.measures = c("fmin", "chisq", "df", "pvalue", "cfi", "tli", "srmr", "rmsea"))
```

```
##      fmin  chisq      df  pvalue      cfi      tli      srmr  rmsea
##      0.155 100.090 14.000   0.000   0.818   0.727   0.079   0.138
```

Model fitness does not look bad. Let's look at the presence of potential correlations between observed variables in our model:

```
residuals(fit.a, type = "cor") #ias.interfere and ias.collateral covary
```

```
## $type
## [1] "cor.bollen"
##
## $cov
##              is.ntc is.cst is.nxt is.npr is.cll is.ntr is.ntn
## ias.natconserv    0.000
## ias.costbenefit -0.036  0.000
## ias.nextgen       0.021  0.039  0.000
## ias.nopriority   -0.018  0.060 -0.011  0.000
## ias.collateral    0.058 -0.037  0.086  0.019  0.000
## ias.interfere    -0.001  0.005  0.070 -0.008  0.381  0.000
## ias.notenough    -0.029  0.013  0.034  0.029  0.035 -0.001  0.000
```

Let's fit a second model, which allows "ias.collateral" and "ias.interfere" to covary:

```
mod.b <- 'attitudes =~ NA*ias.natconserv + ias.costbenefit + ias.nextgen + ias.nopriority +
          ias.collateral + ias.interfere + ias.notenough
          #####
          ias.collateral ~~ ias.interfere'
fit.b <- cfa(mod.b, data=d, std.ov= TRUE, std.lv=TRUE, estimator="MLM") #Satorra/Bentler correction
fitmeasures(fit.b, fit.measures = c("fmin", "chisq", "df", "pvalue", "cfi", "tli", "srmr", "rmsea"))
```

```
##      fmin  chisq      df  pvalue      cfi      tli      srmr  rmsea
##      0.023 14.884 13.000   0.315   0.996   0.994   0.029   0.021
```

Fitness indexes do not look bad. What about residual correlations between observed variables?

```
residuals(fit.b, type="cor") #ias.interfere and ias.collateral covary
```

```
## $type
## [1] "cor.bollen"
```

```
##
## $cov
##          is.ntc is.cst is.nxt is.npr is.cll is.ntr is.ntn
## ias.natconserv  0.000
## ias.costbenefit -0.033  0.000
## ias.nextgen     -0.001  0.027  0.000
## ias.nopriority  -0.024  0.055  0.002  0.000
## ias.collateral   0.003 -0.074  0.034  0.063  0.000
## ias.interfere    -0.040 -0.022  0.040  0.026  0.000  0.000
## iasnotenough    -0.030  0.013  0.018  0.027  0.003 -0.023  0.000
```

Correlations seem to be addressed. Now let's run a likelihood ratio test to compare the two models. We can compare the difference in the T statistics' values from the two models, which follows a chi-squared distribution:

```
lavTestLRT(fit.a, fit.b) #Significant differences

## Scaled Chi-Squared Difference Test (method = "satorra.bentler.2001")
##
## lavaan NOTE:
##   The "Chisq" column contains standard test statistics, not the
##   robust test that should be reported per model. A robust difference
##   test is a function of two standard (not robust) statistics.
##
##      Df      AIC      BIC    Chisq Chisq diff Df diff Pr(>Chisq)
## fit.b 13 5940.0 5996.6   14.884
## fit.a 14 6023.2 6076.1  100.090    47.755      1 4.829e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This second model looks better.

## Comparing respondents working on one, or more, taxa

It is time to test for invariance, between researchers working on a single taxonomic group of IAS and researchers working on multiple groups of IAS. To start with, let's test for some configural invariance. Under this invariance latent variable (LV) models have have the same structure in the group: same LVs, same indicator variables, same pattern of constrained and estimated parameters. Estimated coefficients might differ between groups, and thus LVs might not measure the same construct in each group. It is just a starting point towards more constrained invariances

```
mod <- 'attitudes =~ NA*ias.natconserv + ias.costbenefit + ias.nextgen + ias.nopriority +
        ias.collateral + ias.interfere + ias.notenough
        #-----
        ias.collateral ~~ ias.interfere'

fit.conf.inv <- cfa(mod, data = d, std.ov = TRUE, std.lv=TRUE, estimator="MLM",
                    group = "taxa.type")
```

Configural invariance seems to be respected. Now let's test for weak invariance, where factor loadings are the same across groups. Latent variances are allowed to vary among groups. Weak invariance provides moderate evidence that LVs are equivalent between groups, but only latent variances and covariances could be compared.

```
fit.weak.inv <- cfa(mod, data = d, std.ov = TRUE, std.lv=TRUE, estimator="MLM",
                    group = "taxa.type", group.equal = "loadings")
```

Weak invariance also seems to be respected. Now, let's test for strong invariance. For a given indicator variable, intercepts and LV means are the same among groups. Individuals at the same LV score have the same expected values of indicator variables. LV means, variances, and covariances can be compared. Group differences on strongly-invariant LVs, reflect real differences in LVs, as opposed to the difference caused by different measures.

```
fit.strong.inv <- cfa(mod, data = d, std.ov = TRUE, std.lv=TRUE, estimator="MLM",
  group = "taxa.type", group.equal = c("loadings", "intercepts"))
```

When comparing an unconstrained model with a model with configural, weak and strong invariance there seems to be no difference. Invariance seems to be respected.

```
lavTestLRT(fit.conf.inv, fit.weak.inv, fit.strong.inv)
```

```
## Scaled Chi-Squared Difference Test (method = "satorra.bentler.2001")
##
## lavaan NOTE:
##   The "Chisq" column contains standard test statistics, not the
##   robust test that should be reported per model. A robust difference
##   test is a function of two standard (not robust) statistics.
##
```

|                | Df | AIC    | BIC    | Chisq  | Chisq diff | Df diff | Pr(>Chisq) |
|----------------|----|--------|--------|--------|------------|---------|------------|
| fit.conf.inv   | 26 | 5978.1 | 6144.2 | 45.509 |            |         |            |
| fit.weak.inv   | 32 | 5970.9 | 6114.4 | 50.329 | 3.6785     | 6       | 0.7201     |
| fit.strong.inv | 38 | 5958.9 | 6079.7 | 50.329 | 0.0000     | 6       | 1.0000     |

```
fitmeasures(fit.conf.inv, c("cfi", "mfi", "rmsea", "srmr"))
```

```
##   cfi   mfi rmsea srmr
## 0.961 0.970 0.068 0.050
```

```
fitmeasures(fit.weak.inv, c("cfi", "mfi", "rmsea", "srmr"))
```

```
##   cfi   mfi rmsea srmr
## 0.963 0.972 0.060 0.055
```

```
fitmeasures(fit.strong.inv, c("cfi", "mfi", "rmsea", "srmr"))
```

```
##   cfi   mfi rmsea srmr
## 0.975 0.981 0.045 0.055
```

As invariance is respected, we can compare scores of the PMA scale, and loadings, between respondents with a different background. Namely, between respondents working on one taxa or on multiple taxa of IAS. Please, see Fig. 2 and Fig. 3 in the manuscript.

## Comparing researchers versus practitioners

Fitting a model with configural invariance:

```
dat <- d[which(!is.na(d$practitioner.dummy)),]
mod <- 'attitudes =~ NA*ias.natconserv + ias.costbenefit + ias.nextgen + ias.nopriority +
  ias.collateral + ias.interfere + ias.notenough
  #-----
  ias.collateral ~~ ias.interfere'

fit.conf.inv <- cfa(mod, data = dat, std.ov = TRUE, std.lv=TRUE, estimator="MLM",
  group = "practitioner.dummy")
```

Fitting a model with weak invariance:

```
fit.weak.inv <- cfa(mod, data = dat, std.ov = TRUE, std.lv=TRUE, estimator="MLM",
  group = "practitioner.dummy", group.equal = "loadings")
```

Fitting a model with strong invariance:

```
fit.strong.inv <- cfa(mod, data = dat, std.ov = TRUE, std.lv=TRUE, estimator="MLM",
  group = "practitioner.dummy", group.equal = c("loadings", "intercepts"))
```

Minor differences between unconstrained and constrained models, invariance seems to be respected:

```
lavTestLRT(fit.conf.inv, fit.weak.inv, fit.strong.inv)
```

```
## Warning in lavTestLRT(fit.conf.inv, fit.weak.inv, fit.strong.inv): lavaan WARNING: some restricted models; either these models are not nested, or
## the less restricted model failed to reach a global optimum.
```

```
## Scaled Chi-Squared Difference Test (method = "satorra.bentler.2001")
```

```
##
```

```
## lavaan NOTE:
```

```
## The "Chisq" column contains standard test statistics, not the
## robust test that should be reported per model. A robust difference
## test is a function of two standard (not robust) statistics.
```

```
##
```

```
##           Df      AIC      BIC  Chisq Chisq diff Df diff Pr(>Chisq)
## fit.conf.inv  26 5864.9 6030.2 43.024
## fit.weak.inv  32 5857.2 5999.9 47.299      3.4956      6      0.7446
## fit.strong.inv 38 5845.2 5965.4 47.299      0.0000      6      1.0000
```

```
fitmeasures(fit.conf.inv, c("cfi", "mfi", "rmsea", "srmr"))
```

```
##   cfi   mfi rmsea srmr
## 0.965 0.973 0.064 0.041
```

```
fitmeasures(fit.weak.inv, c("cfi", "mfi", "rmsea", "srmr"))
```

```
##   cfi   mfi rmsea srmr
## 0.969 0.976 0.055 0.046
```

```
fitmeasures(fit.strong.inv, c("cfi", "mfi", "rmsea", "srmr"))
```

```
##   cfi   mfi rmsea srmr
## 0.981 0.985 0.039 0.046
```

Invariance seems to be respected. To compare PMA scores and factor loadings see Fig. 2 and Fig. 3.

## Comparing models

We can compare our basic models, assuming no group difference, with a model accounting for respondent's experience with one or more taxa, and with another model accounting for practitioners/researchers:

```
mod <- 'attitudes =~ NA*ias.natconserv + ias.costbenefit + ias.nextgen + ias.nopriority +
  ias.collateral + ias.interfere + ias.notenough
#####
ias.collateral ~~ ias.interfere'
```

```
fit.a <- cfa(mod, data = dat, std.ov= TRUE, std.lv=TRUE, estimator="MLM")
```

```
fit.b <- cfa(mod, data = dat, std.ov= TRUE, std.lv=TRUE, estimator="MLM", group = "taxa.type")
```

```
fit.c <- cfa(mod, data = dat, std.ov= TRUE, std.lv=TRUE, estimator="MLM", group = "practitioner.dummy")
```

```

fitmeasures(fit.a, "tli") #Should be higher than 0.95

##    tli
## 0.987

fitmeasures(fit.b, "tli") #Should be higher than 0.95

##    tli
## 0.933

fitmeasures(fit.c, "tli") #Should be higher than 0.95

##    tli
## 0.944

fitmeasures(fit.a, "srmr") #Should be smaller than 0.08

##    srmr
## 0.031

fitmeasures(fit.b, "srmr") #Should be smaller than 0.08

##    srmr
## 0.05

fitmeasures(fit.c, "srmr") #Should be smaller than 0.08

##    srmr
## 0.041

fitmeasures(fit.a, "rmsea") #Its CI should be within 0.6-0.8

##    rmsea
##    0.03

fitmeasures(fit.b, "rmsea") #Its CI should be within 0.6-0.8

##    rmsea
##    0.071

fitmeasures(fit.c, "rmsea") #Its CI should be within 0.6-0.8

##    rmsea
##    0.064

```

Overall, it seems that there is no big difference between this model. And no strong effect of the group over PMA scores. We can just keep the simplest model.

## SEM and the effect of age

```

mod.sem <- 'attitudes =~ NA*ias.natconserv + ias.costbenefit + ias.nextgen + ias.nopriority +
           ias.collateral + ias.interfere + ias.notenough
           attitudes ~ age
           #####
           ias.collateral ~~ ias.interfere'

fit.sem <- cfa(mod.sem, data=d, std.ov= TRUE, std.lv=TRUE, estimator="MLM") #Satorra/Bentler correction
fitmeasures(fit.sem, fit.measures = c("fmin", "chisq", "df", "pvalue"))

##    fmin  chisq    df pvalue
## 0.052 25.855 19.000 0.134

```

```

bestfit <- fit.a

fitmeasures(bestfit, "cfi") #Should be higher than 0.95

##   cfi
## 0.992

fitmeasures(fit.sem, "cfi") #Should be higher than 0.95

##   cfi
## 0.981

fitmeasures(bestfit, "tli") #Should be higher than 0.95

##   tli
## 0.987

fitmeasures(fit.sem, "tli") #Should be higher than 0.95

##   tli
## 0.972

fitmeasures(bestfit, "srmr") #Should be smaller than 0.08

##   srmr
## 0.031

fitmeasures(fit.sem, "srmr") #Should be smaller than 0.08

##   srmr
## 0.042

fitmeasures(bestfit, "rmsea") #Its CI should be within 0.6-0.8

##   rmsea
##   0.03

fitmeasures(fit.sem, "rmsea") #Its CI should be within 0.6-0.8

##   rmsea
## 0.038

```

The age also seems not to have any strong effect on PMA scores.