Answers to exercises multigroup LVMs

```
library("lavaan")
```

Additional exercise: HADS

In the HADS anxiety subscale exercise in week 3 (IRT), we used a unidimensional model. That model did not fit very well. Therefore, we are going to use a two-dimensional model, suggested by Barth and Martin (2005). It consists of a Psychomotor Agitation (PAG) and a Psychic Anxiety (ANX) factor.

These are the items of the HADS: 1. I feel tense or wound up 2. I get a sort of frightened feeling as if something bad is about to happen 3. Worrying thoughts go through my mind 4. I can sit at ease and feel relaxed 5. I get a sort of frightened feeling like butterflies in the stomach 6. I feel restless and have to be on the move 7. I get sudden feelings of panic

a) Assess measurement invariance of the HADS Anxiety items with respect to gender ('geslacht'). Describe and interpret any differences you found.

```
library("foreign")
hads <- read.spss("HADS.sav", use.value.labels = TRUE, to.data.frame = TRUE)
summary(hads)
```

```
##  Respondentnummer    leeftijd           geslacht            HADS1
##  Min.   :500002   Min.   :18.00   een man   :217   bijna nooit : 43
##  1st Qu.:500162   1st Qu.:35.00   een vrouw :285   soms        :160
##  Median :500333   Median :43.00                    vaak        :202
##  Mean   :500335   Mean   :42.84                    bijna altijd: 97
##  3rd Qu.:500512   3rd Qu.:51.00
##  Max.   :500689   Max.   :80.00
##           HADS2              HADS3              HADS4              HADS5
##  bijna nooit :214   bijna nooit : 75   bijna altijd: 31   bijna nooit :179
##  soms        :151   soms        :175   vaak        : 81   soms        :170
##  vaak        :103   vaak        :180   soms        :219   vaak        :116
##  bijna altijd: 34   bijna altijd: 72   bijna nooit :171   bijna altijd: 37
##
##
##           HADS6              HADS7
##  bijna nooit : 67   bijna nooit :199
##  soms        :204   soms        :187
##  vaak        :167   vaak        :101
##  bijna altijd: 64   bijna altijd: 15
##
##
```

```
HADS.mod <- '
  PAG =~ HADS1 + HADS4 + HADS6
  ANX =~ HADS2 + HADS3 + HADS5 + HADS7
'
HADS.fit.conf <- cfa(HADS.mod, data = hads, group="geslacht",
                     ordered = paste0("HADS", 1:7))
```

```r
pars <- parameterestimates(HADS.fit.conf, standardized = TRUE)
pars[pars$se > 0, c(1:3, 5:7, 9, 13)]
```

```
##       lhs op   rhs group    est    se pvalue std.all
## 2     PAG =~ HADS4     1  0.777 0.049  0.000   0.695
## 3     PAG =~ HADS6     1  0.901 0.043  0.000   0.805
## 5     ANX =~ HADS3     1  0.989 0.048  0.000   0.826
## 6     ANX =~ HADS5     1  0.781 0.057  0.000   0.653
## 7     ANX =~ HADS7     1  0.944 0.051  0.000   0.789
## 8   HADS1  |    t1     1 -1.355 0.105  0.000  -1.355
## 9   HADS1  |    t2     1 -0.317 0.076  0.000  -0.317
## 10  HADS1  |    t3     1  0.893 0.086  0.000   0.893
## 11  HADS4  |    t1     1 -1.501 0.114  0.000  -1.501
## 12  HADS4  |    t2     1 -0.734 0.082  0.000  -0.734
## 13  HADS4  |    t3     1  0.392 0.077  0.000   0.392
## 14  HADS6  |    t1     1 -1.063 0.092  0.000  -1.063
## 15  HADS6  |    t2     1  0.119 0.075  0.111   0.119
## 16  HADS6  |    t3     1  1.048 0.091  0.000   1.048
## 17  HADS2  |    t1     1 -0.226 0.075  0.003  -0.226
## 18  HADS2  |    t2     1  0.550 0.079  0.000   0.550
## 19  HADS2  |    t3     1  1.529 0.116  0.000   1.529
## 20  HADS3  |    t1     1 -1.095 0.093  0.000  -1.095
## 21  HADS3  |    t2     1 -0.084 0.074  0.261  -0.084
## 22  HADS3  |    t3     1  1.048 0.091  0.000   1.048
## 23  HADS5  |    t1     1 -0.440 0.077  0.000  -0.440
## 24  HADS5  |    t2     1  0.560 0.079  0.000   0.560
## 25  HADS5  |    t3     1  1.529 0.116  0.000   1.529
## 26  HADS7  |    t1     1 -0.199 0.075  0.008  -0.199
## 27  HADS7  |    t2     1  0.769 0.083  0.000   0.769
## 28  HADS7  |    t3     1  1.910 0.152  0.000   1.910
## 36    PAG ~~   PAG     1  0.798 0.044  0.000   1.000
## 37    ANX ~~   ANX     1  0.698 0.045  0.000   1.000
## 38    PAG ~~   ANX     1  0.592 0.039  0.000   0.792
## 56    PAG =~ HADS4     2  0.703 0.069  0.000   0.624
## 57    PAG =~ HADS6     2  0.814 0.053  0.000   0.722
## 59    ANX =~ HADS3     2  1.052 0.062  0.000   0.848
## 60    ANX =~ HADS5     2  0.760 0.073  0.000   0.612
## 61    ANX =~ HADS7     2  0.980 0.052  0.000   0.789
## 62  HADS1  |    t1     2 -1.386 0.123  0.000  -1.386
## 63  HADS1  |    t2     2 -0.145 0.086  0.090  -0.145
## 64  HADS1  |    t3     2  0.832 0.097  0.000   0.832
## 65  HADS4  |    t1     2 -1.596 0.139  0.000  -1.596
## 66  HADS4  |    t2     2 -0.800 0.096  0.000  -0.800
## 67  HADS4  |    t3     2  0.435 0.088  0.000   0.435
## 68  HADS6  |    t1     2 -1.176 0.111  0.000  -1.176
## 69  HADS6  |    t2     2  0.075 0.085  0.379   0.075
## 70  HADS6  |    t3     2  1.274 0.116  0.000   1.274
## 71  HADS2  |    t1     2 -0.133 0.086  0.119  -0.133
## 72  HADS2  |    t2     2  0.678 0.093  0.000   0.678
## 73  HADS2  |    t3     2  1.449 0.127  0.000   1.449
## 74  HADS3  |    t1     2 -0.971 0.102  0.000  -0.971
## 75  HADS3  |    t2     2  0.098 0.085  0.249   0.098
## 76  HADS3  |    t3     2  1.088 0.106  0.000   1.088
## 77  HADS5  |    t1     2 -0.275 0.086  0.001  -0.275
```

```
## 78 HADS5  |    t2     2  0.448 0.088  0.000   0.448
## 79 HADS5  |    t3     2  1.356 0.121  0.000   1.356
## 80 HADS7  |    t1     2 -0.348 0.087  0.000  -0.348
## 81 HADS7  |    t2     2  0.693 0.093  0.000   0.693
## 82 HADS7  |    t3     2  1.849 0.166  0.000   1.849
## 90   PAG ~~   PAG     2  0.788 0.060  0.000   1.000
## 91   ANX ~~   ANX     2  0.649 0.055  0.000   1.000
## 92   PAG ~~   ANX     2  0.613 0.044  0.000   0.858
```

In both the female and male groups, we see substantial and significant loadings for all items. Also, the correlations between the PAG and ANX factors are significant and substantial, and latent variances are significant.

```
indices <- c("chisq.scaled", "df", "pvalue.scaled", "cfi.scaled", "srmr",
             "rmsea.scaled", "rmsea.ci.lower.scaled", "rmsea.ci.upper.scaled")
fitMeasures(HADS.fit.conf, indices)
```

```
##          chisq.scaled                df         pvalue.scaled
##                91.152            26.000                 0.000
##            cfi.scaled              srmr          rmsea.scaled
##                 0.982             0.047                 0.100
## rmsea.ci.lower.scaled rmsea.ci.upper.scaled
##                 0.078             0.123
```

CFI and SRMR indicate a well-fitting model, RMSEA does not. Graded Response Models are not very parsimonious by definition: a loading and multiple thresholds are estimated for every item. This often yields a relatively high RMSEA in these models.

```
residuals(HADS.fit.conf, type = "cor")
```

```
## $`een vrouw `
## $`een vrouw `$type
## [1] "cor.bollen"
##
## $`een vrouw `$cov
##       HADS1  HADS4  HADS6  HADS2  HADS3  HADS5  HADS7
## HADS1  0.000
## HADS4 -0.018  0.000
## HADS6 -0.030  0.077  0.000
## HADS2 -0.037 -0.089 -0.052  0.000
## HADS3  0.078 -0.029 -0.008  0.029  0.000
## HADS5  0.085  0.033  0.049 -0.101 -0.101  0.000
## HADS7 -0.037 -0.077 -0.001  0.055 -0.067  0.045  0.000
##
## $`een vrouw `$mean
## HADS1 HADS4 HADS6 HADS2 HADS3 HADS5 HADS7
##     0     0     0     0     0     0     0
##
## $`een vrouw `$th
## HADS1|t1 HADS1|t2 HADS1|t3 HADS4|t1 HADS4|t2 HADS4|t3 HADS6|t1 HADS6|t2
##        0        0        0        0        0        0        0        0
## HADS6|t3 HADS2|t1 HADS2|t2 HADS2|t3 HADS3|t1 HADS3|t2 HADS3|t3 HADS5|t1
##        0        0        0        0        0        0        0        0
## HADS5|t2 HADS5|t3 HADS7|t1 HADS7|t2 HADS7|t3
##        0        0        0        0        0
##
```

```
##
## $`een man`
## $`een man`$type
## [1] "cor.bollen"
##
## $`een man`$cov
##       HADS1  HADS4  HADS6  HADS2  HADS3  HADS5  HADS7
## HADS1  0.000
## HADS4 -0.033  0.000
## HADS6 -0.007  0.065  0.000
## HADS2 -0.014 -0.038 -0.032  0.000
## HADS3  0.023  0.043  0.045  0.007  0.000
## HADS5  0.031  0.004 -0.020 -0.098 -0.056  0.000
## HADS7 -0.001 -0.055 -0.073  0.056 -0.064  0.085  0.000
##
## $`een man`$mean
## HADS1 HADS4 HADS6 HADS2 HADS3 HADS5 HADS7
##     0     0     0     0     0     0     0
##
## $`een man`$th
## HADS1|t1 HADS1|t2 HADS1|t3 HADS4|t1 HADS4|t2 HADS4|t3 HADS6|t1 HADS6|t2
##        0        0        0        0        0        0        0        0
## HADS6|t3 HADS2|t1 HADS2|t2 HADS2|t3 HADS3|t1 HADS3|t2 HADS3|t3 HADS5|t1
##        0        0        0        0        0        0        0        0
## HADS5|t2 HADS5|t3 HADS7|t1 HADS7|t2 HADS7|t3
##        0        0        0        0        0
```

For women, there are two residual correlation < -0.1 between HADS5 and HADS2, and between HADS5 and HADS3.

For men, there are no residual correlations < -0.1 or $> .01$. The highest residual is between HADS5 and HADS2.

HADS2 and HADS5 have similar wordings, so adding a residual correlation between these two items makes sense from a substantive perspective.

```
modificationindices(HADS.fit.conf, sort = TRUE)[1:10,]
```

```
##       lhs op   rhs block group level    mi    epc sepc.lv sepc.all sepc.nox
## 113   ANX =~ HADS1     1     1     1 7.602  0.634   0.530    0.530    0.530
## 122 HADS4 ~~ HADS6     1     1     1 7.601  0.156   0.156    0.366    0.366
## 119 HADS1 ~~ HADS3     1     1     1 7.294  0.145   0.145    0.575    0.575
## 109   PAG =~ HADS2     1     1     1 7.009 -0.477  -0.426   -0.426   -0.426
## 111   PAG =~ HADS5     1     1     1 6.904  0.430   0.384    0.384    0.384
## 133 HADS2 ~~ HADS7     1     1     1 6.242  0.139   0.139    0.411    0.411
## 138   PAG =~ HADS3     2     2     1 5.467  0.660   0.586    0.586    0.586
## 164 HADS5 ~~ HADS7     2     2     1 5.148  0.141   0.141    0.291    0.291
## 134 HADS3 ~~ HADS5     1     1     1 4.768 -0.145  -0.145   -0.341   -0.341
## 132 HADS2 ~~ HADS5     1     1     1 4.519 -0.144  -0.144   -0.346   -0.346
```

Modification indices do not indicate the same parameters should be added for males and females.

I am actually quite satisfied with the model fit and will not make any post-hoc model adjustments. I proceed with assessing the equality of loadings:

```
HADS.fit.metr <- cfa(HADS.mod, data = hads, group = "geslacht",
                     ordered = paste0("HADS", 1:7),
```

```
                    group.equal = "loadings")
fitMeasures(HADS.fit.metr, indices)
```

```
##          chisq.scaled                    df         pvalue.scaled
##                78.449                31.000                 0.000
##            cfi.scaled                  srmr          rmsea.scaled
##                 0.987                 0.049                 0.078
## rmsea.ci.lower.scaled rmsea.ci.upper.scaled
##                 0.057                 0.100
```

```
lavTestLRT(HADS.fit.metr, HADS.fit.conf)
```

```
## Scaled Chi-Squared Difference Test (method = "satorra.2000")
##
## 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)
## HADS.fit.conf 26         48.206
## HADS.fit.metr 31         51.437     2.7994       5     0.7309
```

Model fit according to RMSEA has improved quite a bit, model fit has also improved according to CFI. The difference in χ^2 values is also not significant. Thus, equality of loadings between males and females appears tenable.

```
HADS.fit.scal <- cfa(HADS.mod, data = hads, group = "geslacht",
                    ordered = paste0("HADS", 1:7),
                    group.equal = c("loadings", "thresholds"))
fitMeasures(HADS.fit.scal, indices)
```

```
##          chisq.scaled                    df         pvalue.scaled
##               105.304                43.000                 0.000
##            cfi.scaled                  srmr          rmsea.scaled
##                 0.982                 0.048                 0.076
## rmsea.ci.lower.scaled rmsea.ci.upper.scaled
##                 0.058                 0.095
```

```
lavTestLRT(HADS.fit.metr, HADS.fit.scal)
```

```
## Scaled Chi-Squared Difference Test (method = "satorra.2000")
##
## 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)
## HADS.fit.metr 31         51.437
## HADS.fit.scal 43         61.991     16.765      12     0.1587
```

The difference in model fit is not significant according to the $\Delta\chi^2$ test. Also, CFI and SRMR indicate a well-fitting model, RMSEA value approaches an acceptable level.

I conclude that factor loadings and item thresholds, and thus also discrimination and difficulty parameters, are equal across gender.

b) I continue to assess structural invariance. I first test the equality of latent variances:

```
HADS.fit.var <- cfa(HADS.mod, data = hads, group = "geslacht",
                    ordered = paste0("HADS", 1:7),
                    group.equal = c("loadings", "thresholds", "lv.variances"))
fitMeasures(HADS.fit.var, indices)
```

```
##          chisq.scaled                    df         pvalue.scaled
##                98.009                45.000                 0.000
##            cfi.scaled                  srmr          rmsea.scaled
##                 0.985                 0.049                 0.069
## rmsea.ci.lower.scaled rmsea.ci.upper.scaled
##                 0.050                 0.087
```

```
lavTestLRT(HADS.fit.var, HADS.fit.scal)
```

```
## Scaled Chi-Squared Difference Test (method = "satorra.2000")
##
## 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)
## HADS.fit.scal 43         61.991
## HADS.fit.var  45         67.979     2.4066       2     0.3002
```

Equal latent variances seems tenable. I continue to test equality of latent covariances:

```
HADS.fit.covar <- cfa(HADS.mod, data = hads, group = "geslacht",
                    ordered = paste0("HADS", 1:7),
                    group.equal = c("loadings", "thresholds", "lv.variances",
                                    "lv.covariances"))
fitMeasures(HADS.fit.covar, indices)
```

```
##          chisq.scaled                    df         pvalue.scaled
##                95.409                46.000                 0.000
##            cfi.scaled                  srmr          rmsea.scaled
##                 0.986                 0.049                 0.066
## rmsea.ci.lower.scaled rmsea.ci.upper.scaled
##                 0.047                 0.084
```

```
lavTestLRT(HADS.fit.var, HADS.fit.covar)
```

```
## Scaled Chi-Squared Difference Test (method = "satorra.2000")
##
## 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)
## HADS.fit.var   45         67.979
## HADS.fit.covar 46         69.570    0.95187       1     0.3292
```

Equal latent covariances seems tenable also. I continue to test equality of latent means:

```
HADS.fit.means <- cfa(HADS.mod, data = hads, group = "geslacht",
                      ordered = paste0("HADS", 1:7),
                      group.equal = c("loadings", "thresholds", "lv.variances",
                                      "lv.covariances", "means"))
fitMeasures(HADS.fit.means, indices)
```

```
##          chisq.scaled                    df         pvalue.scaled
##                79.670                48.000                 0.003
##            cfi.scaled                   srmr          rmsea.scaled
##                 0.991                 0.049                 0.051
## rmsea.ci.lower.scaled rmsea.ci.upper.scaled
##                 0.030                 0.071
```

```
lavTestLRT(HADS.fit.means, HADS.fit.covar)
```

```
## Scaled Chi-Squared Difference Test (method = "satorra.2000")
##
## 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)
## HADS.fit.covar 46         69.57
## HADS.fit.means 48         70.60    0.59397       2     0.7431
```

Equal latent means seems tenable also. Note that our final model has good fit, according to robust CFI and RMSEA, as well as RMSEA.

c) We now fit one single model to the HADS data, and estimate the effect of age and gender on Physical Agitation and Anxiety:

```
head(hads$geslacht) # men will be the reference category
```

```
## [1] een vrouw  een man    een man    een man    een man    een man
## Levels: een man een vrouw
```

```
head(hads$leeftijd)
```

```
## [1] 30 55 37 43 55 66
```

```
hads$geslacht <- as.numeric(hads$geslacht) - 1
hads$interact <- hads$geslacht * hads$leeftijd
HADS.mod.int <- '
  PAG =~ HADS1 + HADS4 + HADS6
  ANX =~ HADS2 + HADS3 + HADS5 + HADS7
  PAG ~ interact + geslacht + leeftijd
  ANX ~ interact + geslacht + leeftijd
'
HADS.fit.int <- cfa(HADS.mod.int, data = hads, ordered = paste0("HADS", 1:7))
pars <- parameterestimates(HADS.fit.int, standardized = TRUE)
pars[pars$op == "~", c(1:7, 11)]
```

```
##    lhs op      rhs    est    se      z pvalue std.all
## 8  PAG  ~ interact  0.015 0.007  2.079  0.038   0.367
## 9  PAG  ~ geslacht -0.623 0.317 -1.969  0.049  -0.344
## 10 PAG  ~ leeftijd -0.012 0.005 -2.170  0.030  -0.163
## 11 ANX  ~ interact  0.014 0.006  2.153  0.031   0.379
```

```
## 12 ANX  ~ geslacht -0.591 0.294 -2.009  0.045  -0.355
## 13 ANX  ~ leeftijd -0.015 0.005 -3.122  0.002  -0.236
```

```
fitMeasures(HADS.fit.int, indices)
```

```
##          chisq.scaled                    df         pvalue.scaled
##                88.563                28.000                 0.000
##            cfi.scaled                  srmr          rmsea.scaled
##                 0.982                 0.045                 0.066
## rmsea.ci.lower.scaled rmsea.ci.upper.scaled
##                 0.051                 0.081
```

The model fits well according to all indices (RMSEA indicates adequate fit, though).

All effects have p-values $< .05$ (but note that it might be appropriate to apply a correction for multiple testing.

Women appear to have lower PAG and ANX than women. With increasing age, PAG and ANX becomes lower. The positive value for the interaction indicates that this effect does not exist for women, but only for men.