Part4_Analyses_on_Harmonized_Data

2024-09-18

Contents

This file assumes that the code in `Part1_Harmonization_continuous.Rmd`, `Part2_Harmonization_ordinal.Rmd`, and `Part3_Results.Rmd` have been run. These files result in the `df.rds` file that will be read in within the current file. If those files have not been run yet, please run the files before executing the code below.

Install and load packages, prepare data.

```
library(dplyr)
library(lavaan)
library(sirt)
library(mirt)
library(kableExtra)
library(here)
library(ggplot2)
library(umx)
# also install packages: haven, numDeriv
```

```
score_df_cont <- readRDS("rds/score_df_continuous.rds")
score_df_ord <- readRDS("rds/score_df_ord.rds")
df <- cbind(score_df_cont, score_df_ord[,c("approx_ord", "approx_ord_SE", "approx_ord_rel", "approx_ord
head(df, 2)
```

```
##      stu_id sample sex dropout i1 i2 i3 i4 i5 mean_score partial_cont
## ELS1 101101    ELS   0       0  2  1  2  2  1        1.6    -1.114292
## ELS2 101102    ELS   0       0  4  3  4  4  4        3.8     1.658808
##      partial_SE approx_cont approx_SE partial_rel approx_rel partial_ev
## ELS1   0.278666   -1.131463 0.2781254    0.927941  0.9282002 0.07765475
```

```
## ELS2   0.278666    1.661305 0.2781254    0.927941  0.9282002 0.07765475
##       approx_ev approx_ord approx_ord_SE approx_ord_rel approx_ord_ev
## ELS1 0.07735375  -1.018915     0.2476258      0.9386815    0.05755857
## ELS2 0.07735375   1.312507     0.2987173      0.9107680    0.08126969
```

```
dim(df)
```

```
## [1] 39700    22
```

```
# outcome variable: dropout
table(df$dropout)
```

```
##
##     0     1
## 36536  3164
```

```
round(table(df[df$sample == "ELS", ]$dropout) /
        sum(table(df[df$sample == "ELS", ]$dropout)), 3)
```

```
##
##     0     1
## 0.927 0.073
```

```
round(table(df[df$sample == "HSLS", ]$dropout) /
        sum(table(df[df$sample == "HSLS", ]$dropout)), 3)
```

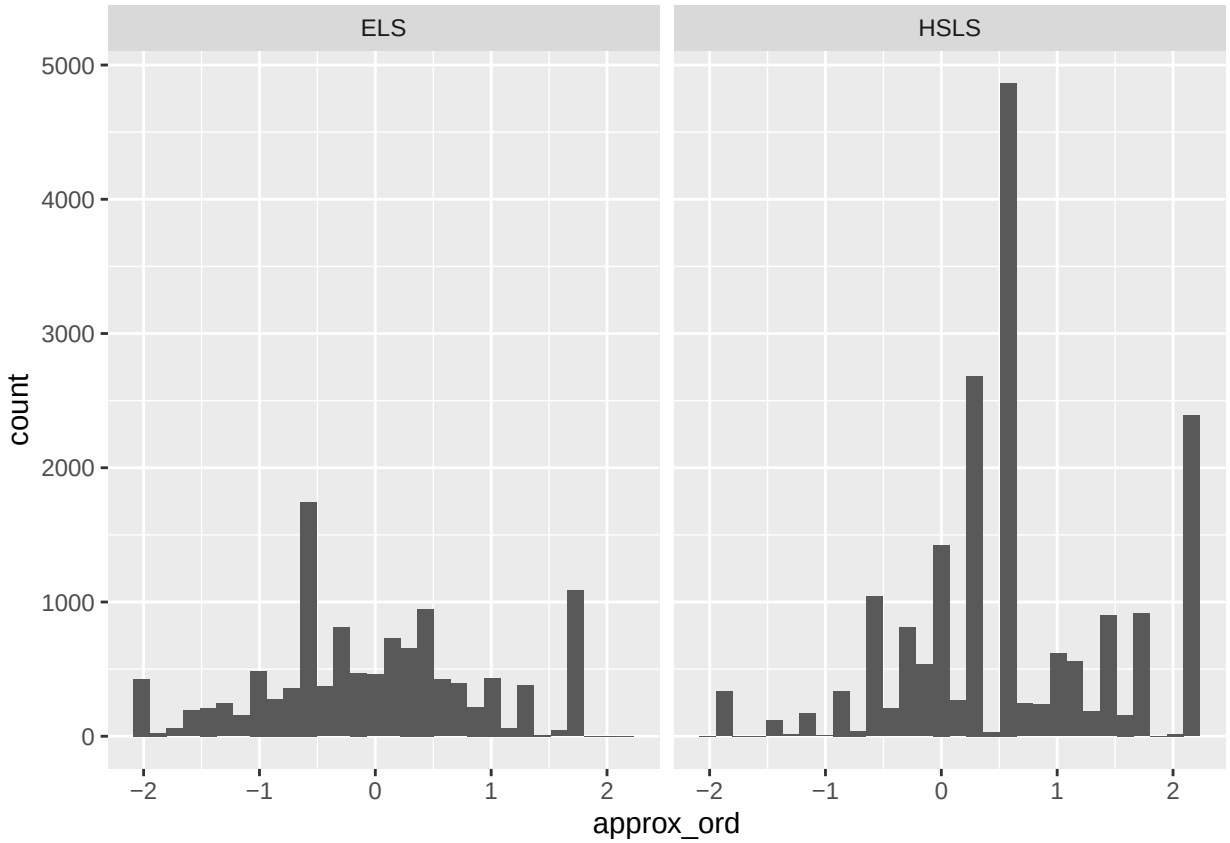
```
##
##     0     1
## 0.916 0.084
```

Descriptive Statistics

```
ggplot(df, aes(x = approx_ord)) +
  geom_histogram() +
  facet_wrap(~ sample)
```

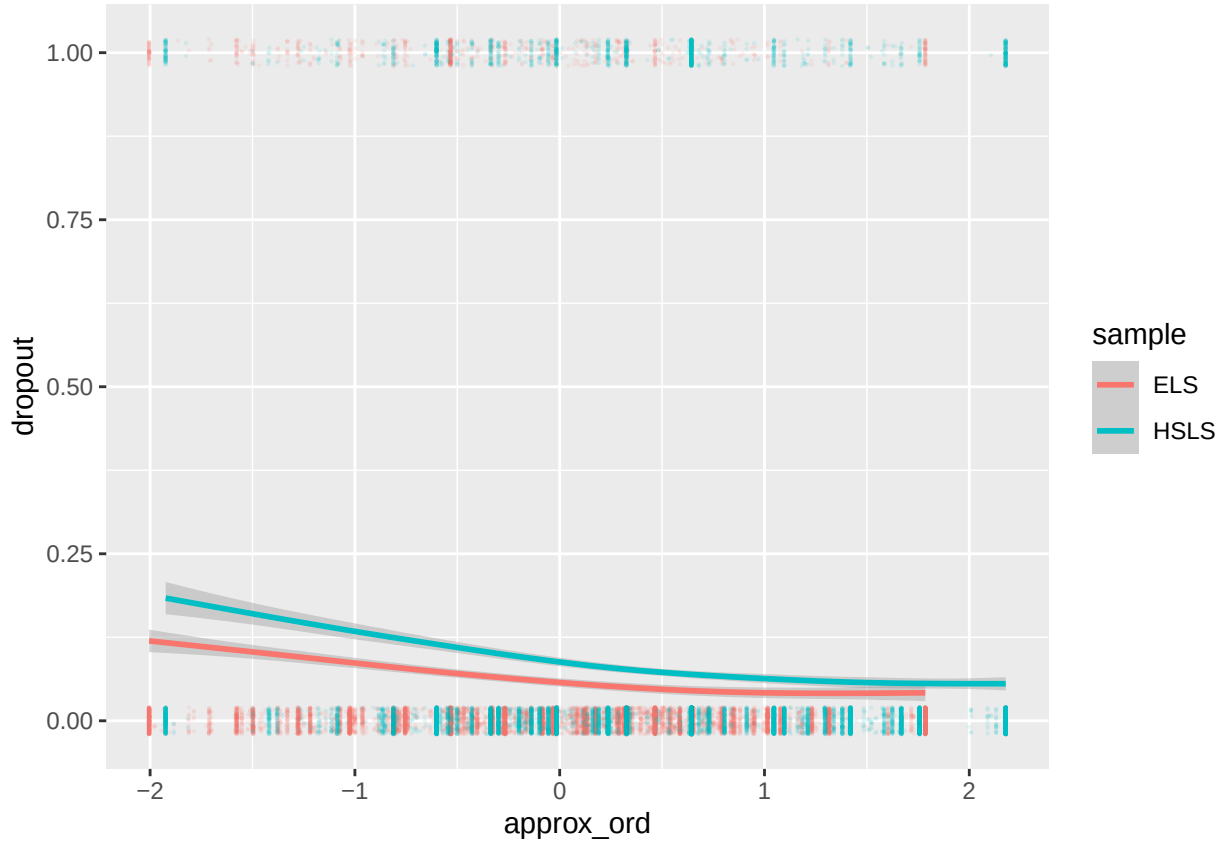
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 8951 rows containing non-finite values (`stat_bin()`).
```




```
ggplot(df, aes(x = approx_ord, y = dropout, col = sample)) +
  geom_jitter(width = 0, height = 0.02, alpha = 0.1,
              size = 0.1) +
  geom_smooth()
```

```
## `geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 8951 rows containing non-finite values (`stat_smooth()`).
## Warning: Removed 8951 rows containing missing values (`geom_point()`).
```



EAP Factor score regression (no reliability adjustment)

Using EAP scores to predict dropout with probit regression

```
# Warning: the code requires data to be sorted by `sample` before analyses
glm_approx_ord_int <- glm("dropout ~ approx_ord * sample", data = df,
                      family = "binomial")
summary(glm_approx_ord_int)
```

```
##
## Call:
## glm(formula = "dropout ~ approx_ord * sample", family = "binomial",
##     data = df)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -2.74290    0.03975 -69.007   <2e-16 ***
## approx_ord            -0.34968    0.04119  -8.489   <2e-16 ***
## sampleHSLS             0.43888    0.04949   8.869   <2e-16 ***
## approx_ord:sampleHSLS  0.01285    0.05086   0.253    0.801
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
```

```
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15731  on 30745  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15739
##
## Number of Fisher Scoring iterations: 5
```

```
# interaction not significant
glm_approx_ord_main <- glm("dropout ~ approx_ord + sample", data = df,
                     family = "binomial")
summary(glm_approx_ord_main)
```

```
##
## Call:
## glm(formula = "dropout ~ approx_ord + sample", family = "binomial",
##     data = df)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.74065    0.03868  -70.85   <2e-16 ***
## approx_ord  -0.34125    0.02416  -14.13   <2e-16 ***
## sampleHSLS   0.43833    0.04936    8.88   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15731  on 30746  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15737
##
## Number of Fisher Scoring iterations: 5
```

Using umx with EAP scores (pooled analysis without unreliability adjustment)

```
# create a dummy variable for the HSLS sample (n_group - 1 dummy variables needed)
df$HSLS <- 0
df$HSLS <- as.integer(df$sample == "HSLS")
```

```
# Recode discrete variable to be used with OpenMx
df$dropout_f <- mxFactor(df$dropout, levels = c(0, 1))
```

```
probitreg_umx_approx_ord <- umxRAM("
    dropout_f ~ approx_ord + HSLS
    dropout_f ~ 0 * 1
    dropout_f ~~ 1 * dropout_f
  ",
  data = df,
  tryHard = "ordinal")
```

[1] "Warning calling mxRefModels: mxRefModels can't handle all designs, including twin, and WLS https://github.com/OpenMx/OpenMx/issues/184"

Table 1: Parameter loadings for model 'm1'

	name	Estimate	SE	type
4	approx_ord_with_HSLS	0.150	0.003	Manifest Cov
1	approx_ord_to_dropout_f	-0.166	0.012	Manifest path
2	HSLS_to_dropout_f	0.176	0.02	Manifest path
7	one_to_approx_ord	0.364	0.006	Mean
8	one_to_HSLS	0.592	0.002	Mean
3	approx_ord_with_approx_ord	0.949	0.008	Residual
5	HSLS_with_HSLS	0.242	0.002	Residual
6	dropout_f_with_dropout_f	1.000	0	Residual

Algebra'threshMat' = 1.468CI95[1.439, 1.497]. p-value < 0.001

```
# plot(probitreg_umx_approx_ord)
```

Two-Stage Path Analysis with EAP scores

Adjusting for measurement error

```
# drop rows with missing reliability
df2 <- df[!is.na(df$approx_ord_rel), ]

# Reliability `approx_ord_rel` defined as 1 - approx_ord_SE^2 / psi_align_ord
# (computed for each observation using the psi value for the correct group, see
# `Part2_Harmonization_ordinal.Rmd` for details)

# Error variance `approx_ord_ev` defined as approx_ord_SE^2 * approx_ord_rel

probitreg_2spa_approx_ord <- umxRAM(
    "2spa",
    # Main effects of EAP scores and study indicators
    umxPath(c("eta", "ELS"), to = "dropout_f"),
    # Loading = reliability (as definition variable)
    umxPath("eta", to = "approx_ord", labels = "data.approx_ord_rel", free = FALSE),
    # Error variance (as definition variable)
    umxPath(var = "approx_ord", labels = "data.approx_ord_ev", free = FALSE),
    # Covariances of predictors
    umxPath(unique.pairs = c("eta", "ELS")),
    # Means of predictors
    umxPath(means = c("eta", "ELS")),
    # For model identification: Fix latent variate to be standard normal
    umxPath(v1m0 = "dropout_f"),
    data = df2,
    tryHard = "ordinal"
)
```

[1] "Warning calling mxRefModels: mxRefModels can't handle all designs, including twin, and WLS https://github.com/OpenMx/OpenMx/issues/184"

Table 2: Parameter loadings for model '2spa'

	name	Estimate	SE	type
7	ELS_with_eta	-0.583		Factor Cov
1	data.approx_ord_rel	0.939	0	Factor loading
2	eta_to_dropout_f	-0.259		Factor loading
3	ELS_to_dropout_f	4.785	67.334	Factor loading
6	eta_with_eta	1.104	0.01	Factor Variance
8	ELS_with_ELS	21.426		Factor Variance
9	one_to_eta	0.433	0.006	Mean
10	one_to_ELS	-5.308		Mean
4	data.approx_ord_ev	0.058	0	Residual
5	dropout_f_with_dropout_f	1.000	0	Residual

Algebra'threshMat' = 6.892CI95[-1152.99, 1166.775]. p-value = 0.991

Bartlett Factor score regression (no reliability adjustment)

Using Bartlett scores to predict dropout with probit regression

Bartlett scores computed using the approximate invariance model assuming continuous data.

```
glm_approx_cont_int <- glm("dropout ~ approx_cont * sample", data = df,
                      family = "binomial")
summary(glm_approx_cont_int)
```

```
##
## Call:
## glm(formula = "dropout ~ approx_cont * sample", family = "binomial",
##     data = df)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)            -2.74658    0.03990 -68.832   <2e-16 ***
## approx_cont            -0.32709    0.03787  -8.637   <2e-16 ***
## sampleHSLS              0.41022    0.04893   8.384   <2e-16 ***
## approx_cont:sampleHSLS -0.02738    0.04828  -0.567    0.571
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15718  on 30745  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15726
##
## Number of Fisher Scoring iterations: 5
```

```
# interaction not significant
glm_approx_cont_main <- glm("dropout ~ approx_cont + sample", data = df,
                      family = "binomial")
summary(glm_approx_cont_main)
```

```
##
## Call:
## glm(formula = "dropout ~ approx_cont + sample", family = "binomial",
##     data = df)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.75191    0.03892 -70.702   <2e-16 ***
## approx_cont -0.34396    0.02354 -14.614   <2e-16 ***
## sampleHSLS   0.41266    0.04891   8.436   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15718  on 30746  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15724
##
## Number of Fisher Scoring iterations: 5
```

Bartlett scores computed using the partial invariance model assuming continuous data.

```
glm_partial_cont_int <- glm("dropout ~ partial_cont * sample", data = df,
                      family = "binomial")
summary(glm_partial_cont_int)
```

```
##
## Call:
## glm(formula = "dropout ~ partial_cont * sample", family = "binomial",
##     data = df)
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -2.74672    0.03991 -68.826   <2e-16 ***
## partial_cont             -0.32764    0.03789  -8.648   <2e-16 ***
## sampleHSLS                0.42204    0.04911   8.594   <2e-16 ***
## partial_cont:sampleHSLS -0.07610    0.05099  -1.492    0.136
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15718  on 30745  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15726
##
## Number of Fisher Scoring iterations: 5
```

```
# interaction not significant
glm_partial_cont_main <- glm("dropout ~ partial_cont + sample", data = df,
                      family = "binomial")
summary(glm_partial_cont_main)
```

```
##
## Call:
## glm(formula = "dropout ~ partial_cont + sample", family = "binomial",
##     data = df)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.76050    0.03920 -70.430   <2e-16 ***
## partial_cont -0.36979    0.02549 -14.508   <2e-16 ***
## sampleHSLS    0.42649    0.04951   8.615   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15720  on 30746  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15726
##
## Number of Fisher Scoring iterations: 5
```

Using umx with Bartlett scores (pooled analysis without unreliability adjustment)

Bartlett scores computed using the approximate invariance model assuming continuous data.

```
probitreg_umx_approx_cont <- umxRAM("
    dropout_f ~ approx_cont + ELS
    dropout_f ~ 0 * 1
    dropout_f ~~ 1 * dropout_f
  ",
  data = df,
  tryHard = "yes")
```

[1] "Warning calling mxRefModels: mxRefModels can't handle all designs, including twin, and WLS https://github.com/OpenMx/OpenMx/issues/184"

Table 3: Parameter loadings for model 'm1'

	name	Estimate	SE	type
2	ELS_to_dropout_f	1.752	15.8	Factor loading
6	ELS_with_ELS	1.247	11.448	Factor Variance
4	approx_cont_with_ELS	0.221	6.862	Latent-Manifest Cov
1	approx_cont_to_dropout_f	-0.718	10.236	Manifest path
7	one_to_approx_cont	0.308	0.006	Mean
8	one_to_ELS	-0.155	9.329	Mean
3	approx_cont_with_approx_cont	0.948	0.008	Residual
5	dropout_f_with_dropout_f	1.000	0	Residual

Algebra'threshMat' = 2.577CI95[-64.146, 69.3]. p-value = 0.940

```
# plot(probitreg_umx_approx_cont)
```

Bartlett scores computed using the partial invariance model assuming continuous data.

```
probitreg_umx_partial_cont <- umxRAM("
    dropout_f ~ partial_cont + ELS
    dropout_f ~ 0 * 1
    dropout_f ~~ 1 * dropout_f
  ",
  data = df,
  tryHard = "yes")
```

[1] "Warning calling mxRefModels: mxRefModels can't handle all designs, including twin, and WLS https://github.com/OpenMx/OpenMx/issues/184"

Table 4: Parameter loadings for model 'm1'

	name	Estimate	SE	type
2	ELS_to_dropout_f	0.438	10.524	Factor loading
6	ELS_with_ELS	11.337	110.737	Factor Variance
4	ELS_with_partial_cont	1.123	20.825	Latent-Manifest Cov
1	partial_cont_to_dropout_f	-0.846	9.25	Manifest path
7	one_to_partial_cont	0.288	0.005	Mean
8	one_to_ELS	-5.168	99.356	Mean
3	partial_cont_with_partial_cont	0.833	0.007	Residual
5	dropout_f_with_dropout_f	1.000	0	Residual

Algebra'threshMat' = -0.094CI95[-109.409, 109.221]. p-value = 0.999

```
# plot(probitreg_umx_partial_cont)
```

Two-Stage Path Analysis with Bartlett scores

Adjusting for measurement error

```
# drop rows with missing reliability
df3 <- df[!is.na(df$approx_rel), ]

# Reliability set to 1 for Bartlett scores ("values = 1" below)
# Error variance `approx_ev` defined as approx_SE^2

probitreg_2spa_approx_cont <- umxRAM(
    "2spa",
    # Main effects of Bartlett scores and study indicators
    umxPath(c("eta", "ELS"), to = "dropout_f"),
    # Loading = reliability (as definition variable)
    umxPath("eta", to = "approx_cont", values = 1, free = FALSE),
    # Error variance (as definition variable)
    umxPath(var = "approx_cont", labels = "data.approx_ev", free = FALSE),
    # Covariances of predictors
    umxPath(unique.pairs = c("eta", "ELS")),
    # Means of predictors
    umxPath(means = c("eta", "ELS")),
    # For model identification: Fix latent variate to be standard normal
    umxPath(v1m0 = "dropout_f"),
    data = df3,
```

```
    tryHard = "yes"
)
```

[1] "Warning calling mxRefModels: mxRefModels can't handle all designs, including twin, and WLS https://github.com/OpenMx/OpenMx/issues/184"

Table 5: Parameter loadings for model '2spa'

	name	Estimate	SE	type
7	ELS_with_eta	-0.835	145.485	Factor Cov
1	eta_to_approx_cont	1.000	0	Factor loading
2	eta_to_dropout_f	0.011	34.041	Factor loading
3	ELS_to_dropout_f	0.181	4.966	Factor loading
6	eta_with_eta	0.862	0.008	Factor Variance
8	ELS_with_ELS	4.675	925.673	Factor Variance
9	one_to_eta	0.315	0.006	Mean
10	one_to_ELS	-2.601	272.966	Mean
4	data.approx_ev	0.077	0	Residual
5	dropout_f_with_dropout_f	1.000	0	Residual

Algebra'threshMat' = 1.097CI95[-113.001, 115.195]. p-value = 0.985

```
# drop rows with missing reliability
df4 <- df[!is.na(df$partial_rel), ]

# Reliability set to 1 for Bartlett scores ("values = 1" below)
# Error variance `partial_ev` defined as partial_SE^2

probitreg_2spa_partial_cont <- umxRAM(
    "2spa",
    # Main effects of Bartlett scores and study indicators
    umxPath(c("eta", "ELS"), to = "dropout_f"),
    # Loading = reliability (as definition variable)
    umxPath("eta", to = "partial_cont", values = 1, free = FALSE),
    # Error variance (as definition variable)
    umxPath(var = "partial_cont", labels = "data.partial_ev", free = FALSE),
    # Covariances of predictors
    umxPath(unique.pairs = c("eta", "ELS")),
    # Means of predictors
    umxPath(means = c("eta", "ELS")),
    # For model identification: Fix latent variate to be standard normal
    umxPath(v1m0 = "dropout_f"),
    data = df4,
    tryHard = "yes"
)
```

[1] "Warning calling mxRefModels: mxRefModels can't handle all designs, including twin, and WLS https://github.com/OpenMx/OpenMx/issues/184"

Table 6: Parameter loadings for model '2spa'

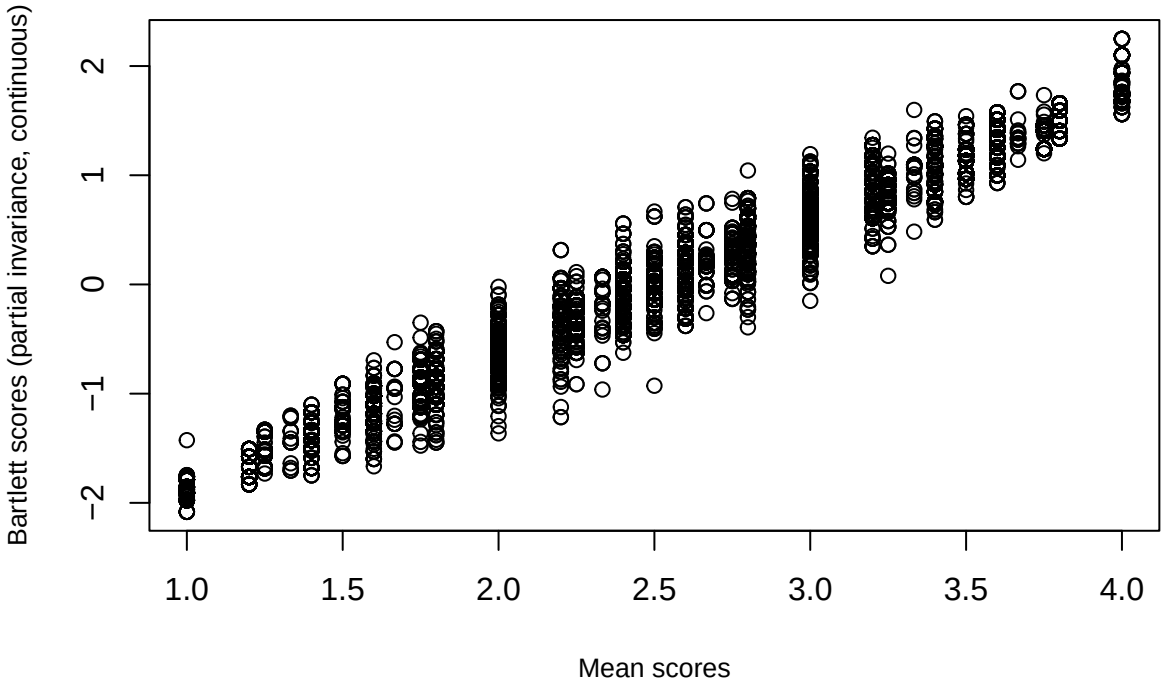
	name	Estimate	SE	type
7	ELS_with_eta	-1.310		Factor Cov
1	eta_to_partial_cont	1.000	0	Factor loading
2	eta_to_dropout_f	2.567		Factor loading
3	ELS_to_dropout_f	1.734		Factor loading
6	eta_with_eta	0.748	0.007	Factor Variance
8	ELS_with_ELS	4.664		Factor Variance
9	one_to_eta	0.298	0.005	Mean
10	one_to_ELS	-0.558		Mean
4	data.partial_ev	0.078	0	Residual
5	dropout_f_with_dropout_f	1.000	0	Residual

Algebra'threshMat' = 3.997CI95[-701.66, 709.654]. p-value = 0.991

Sensitivity Analysis

Using sum/mean scores

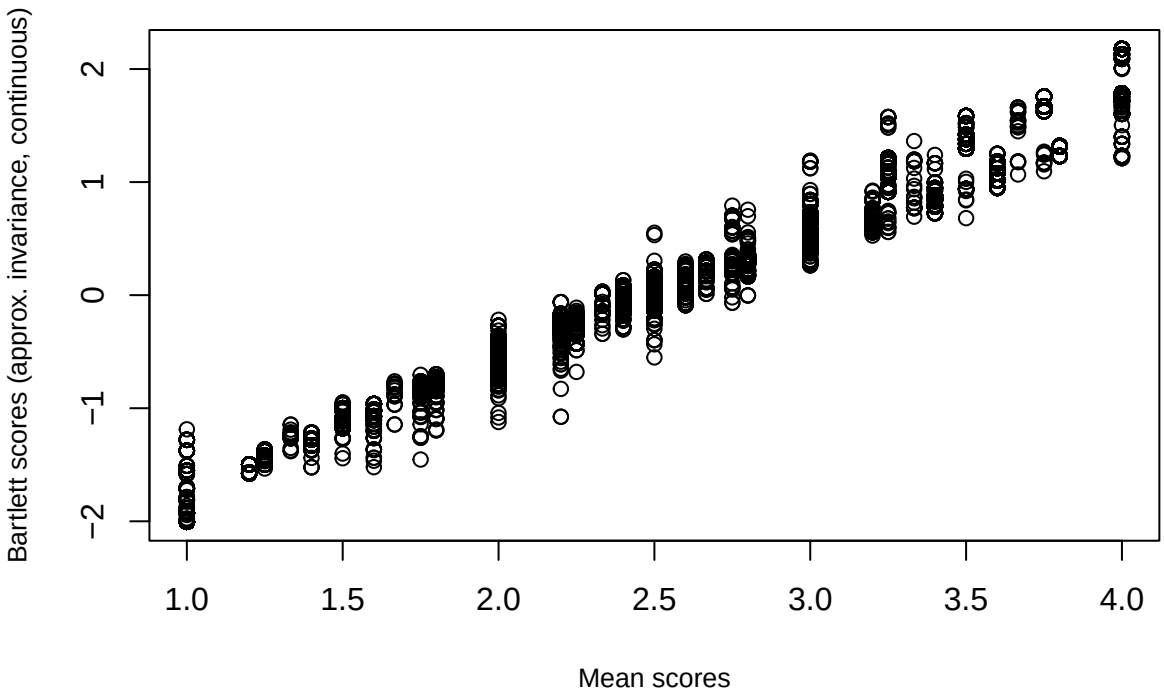
```
# Scatterplot
plot(x = df$mean_score, y = df$partial_cont, xlab = "Mean scores",
     ylab = "Bartlett scores (partial invariance, continuous)", cex.lab = 0.8)
```



```
cor(df$mean_score, df$partial_cont, use = "complete")
```

```
## [1] 0.9921757
```

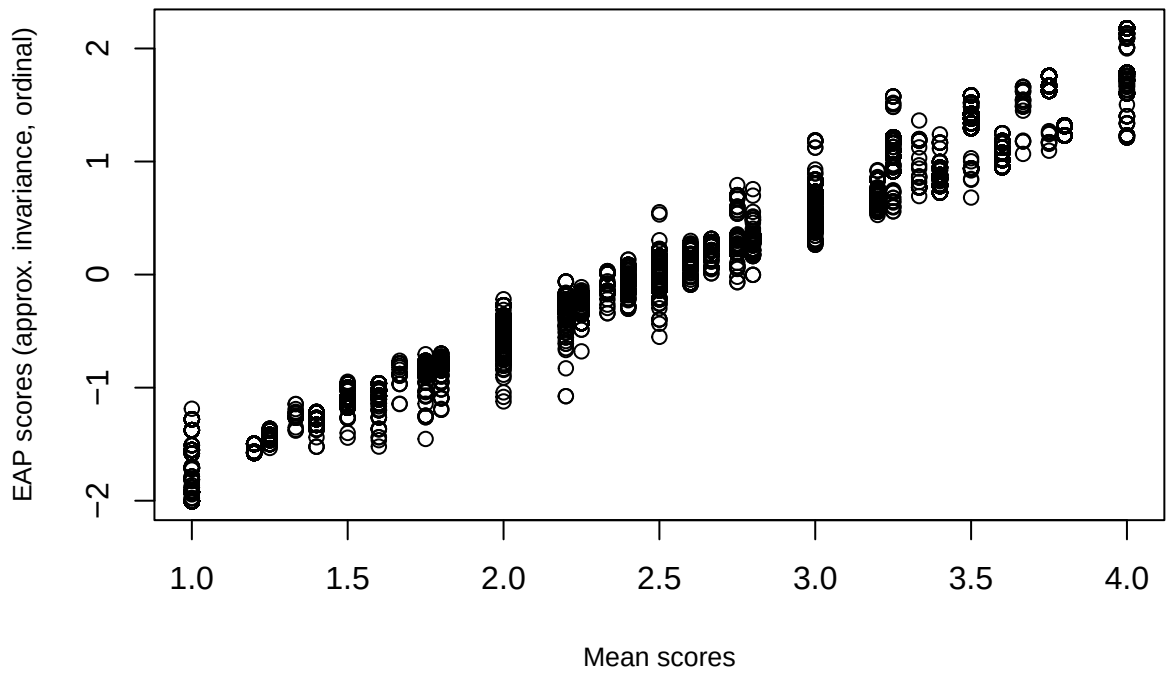
```
plot(x = df$mean_score, y = df$approx_ord, xlab = "Mean scores",
     ylab = "Bartlett scores (approx. invariance, continuous)", cex.lab = 0.8)
```




```
cor(df$mean_score, df$approx_cont, use = "complete")
```

```
## [1] 0.9925704
```

```
plot(x = df$mean_score, y = df$approx_ord, xlab = "Mean scores",
     ylab = "EAP scores (approx. invariance, ordinal)", cex.lab = 0.8)
```




```
cor(df$mean_score, df$approx_ord, use = "complete")
```

```
## [1] 0.9887612
```

Probit regression with mean scores

Note that the scale of the predictors are different, so the coefficients are not comparable.

```
# GLM (probit regression); interaction not significant
glm_meanscore <- glm("dropout ~ mean_score * sample", data = df,
                     family = "binomial")
summary(glm_meanscore)
```

```
##
## Call:
## glm(formula = "dropout ~ mean_score * sample", family = "binomial",
##     data = df)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)            -1.71965    0.11465 -14.998  < 2e-16 ***
## mean_score             -0.40697    0.04749  -8.570  < 2e-16 ***
## sampleHSLS              0.55232    0.16070   3.437 0.000589 ***
## mean_score:sampleHSLS -0.05095    0.06178  -0.825 0.409506
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15724  on 30745  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15732
##
## Number of Fisher Scoring iterations: 5
```

```r
# interaction not significant
glm_meanscore_main <- glm("dropout ~ mean_score + sample", data = df,
                      family = "binomial")
summary(glm_meanscore_main)
```

```
##
## Call:
## glm(formula = "dropout ~ mean_score + sample", family = "binomial",
##     data = df)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.65123    0.07873 -20.974   <2e-16 ***
## mean_score  -0.43713    0.03046 -14.349   <2e-16 ***
## sampleHSLS   0.42632    0.04937   8.635   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 15956  on 30748  degrees of freedom
## Residual deviance: 15725  on 30746  degrees of freedom
##   (8951 observations deleted due to missingness)
## AIC: 15731
##
## Number of Fisher Scoring iterations: 5
```