**Supplementary Materials for “Examining the impact of the Good ehaviour Game on health- and education-related outcomes for children: a cluster RCT and cost-consequence analysis”**

**Syntax for models not specified in the SAP by hypothesis**

In all exemplars below, the following variable names are used:

**TABLE 43. Variable coding**

|  |  |
| --- | --- |
| **Name** | **Description** |
| **Trial** | Allocation. Trial=1=GBG; Trial=0=control |
| **Gender** | Pupil’s gender. Gender=1=male; gender=0=female |
| **Fsm** | Eligibility for free school meals. Fsm=1=eligible; fsm=0=non-eligible |
| **Sen** | Special Education Needs. sen=1=special needs; sen=0=no special needs |
| **ks1** | Reading scores at KS1 |
| **condpr3b** | Conduct problems at follow-up. condpr3b=1=at risk; condpr3b=0=not at risk |
| **Risk** | Conduct problems at baseline. risk=1=at risk; risk=0=not at risk |
| **wb3** | Psychological wellbeing score at time 3 |
| **Schfsm** | Percentage of FSM pupils in school |
| **Schsize** | School size |
| **Scheal** | Percentage of pupils in school for whom English is an Additional Language |
| **schks1** | Percentage of pupils in school who reached level 4 at KS2 English and Maths |
| **Schcond** | School average for conduct problems at baseline |
| **school\_id** | School identifier |
| **Absence** | Number of sessions absent at a particular year |
| **Sessions** | Number of possible sessions at a particular year |
| **Baseline** | Rate of possible sessions attended at baseline (absence/sessions) |
| **Boyrisk** | Interaction between gender and risk |
| **Boytrial** | Interaction between gender and trial |
| **r\_trial** | Interaction between risk and trial |
| **boy\_r\_trial** | Interaction between gender, risk and trial |
| **c50** | Compliance. c50=1=complier; c50=0=non-complier |
| **condpr1** | Conduct problems score at baseline |
| **conc1** | Concentration problems score at baseline |
| **prosoc1** | Prosocial behaviour score at baseline |
| **sdqX\_Y** | Strengths and Difficulties Questionnaire Item “X” at time “Y” |

**Power analysis for binary outcome SDQ conduct problems**

title: Monte Carlo simulation for a multilevel logistic regression with conduct outcome

montecarlo:

names = y trial; ! y = conduct

patmiss = y (.15); !missingness set to 15% for the outcome

patprob = 1;

generate = y(1);

categorical = y;

nobservations = 3080;

ncsizes = 1;

csizes = 77 (40);

seed = 4533;

nreps = 10000;

between = trial;

cutpoints = trial (0); !50% allocation in each group

save = GBGMonteLogit;

analysis:

type= twolevel;

estimator = mlr;

algorithm = integration;

model population:

%within%

%between%

trial\*1;

[trial\*0];

y on trial\*-.38;

y\*.019;

[y$1\*2.25];

model:

%within%

%between%

y on trial\*-.38;

[y$1\*2.25];

y\*.019;

output: tech8 tech9;

**H1:** **2-level models for binary and continuous outcomes estimated via FIML**

This code presupposes the installation of R, R Studio and R package “MplusAutomation”. Indentation is not required. As this is Mplus syntax, variable names and commands are not case sensitive, but R objects and functions follow R conventions. Code chunks are separated by “#----“

#--------------------------------------------------

# ITT model for binary outcome (FIML)

#--------------------------------------------------

cond3\_itt <- mplusObject(

TITLE = "H1A. Conduct problems time 3 ITT FIML;",

VARIABLE = "between = trial schsize SchFSM;

within = FSM gender condpr1;

cluster = school\_id;

categorical = condpr3b;

usevariables = FSM gender

condpr1 trial schsize schfsm

condpr3b;",

ANALYSIS = "type = twolevel;

estimator = ML;

integration = montecarlo;",

MODEL = "%within%

condpr3b on FSM gender condpr1

condpr1;

FSM;

gender;

%between%

condpr3b on schsize SchFSM trial;

condpr3b;",

OUTPUT = "sampstat stand res cinterval;",

rdata = data)

cond3\_itt\_fit <- mplusModeler(cond3\_itt,

modelout = "cond3\_itt.inp",

run = 1L)

#-------------------------------------------------------

# ITT model for continuous outcomes (FIML)

#-------------------------------------------------------

wb3\_itt <- mplusObject(

TITLE = "H2B. Wellbeing time 3 subgroup FIML;",

VARIABLE = "between = trial schsize SchFSM;

within = FSM gender condpr1;

cluster = school\_id;

usevariables = FSM gender

condpr1 trial schsize schfsm

wb3;",

ANALYSIS = "type = twolevel;

estimator = ML;",

MODEL = "%within%

wb3 on FSM gender condpr1;

wb3;

condpr1;

FSM;

gender;

%between%

wb3 on schsize SchFSM trial;

wb3;",

OUTPUT = "sampstat stand res cinterval;",

rdata = data)

wb3\_itt\_fit <- mplusModeler(wb3\_itt,

modelout = "wb3\_itt.inp",

run = 1L)

**H1: 2-level negative binomial model for count data (Absences and exclusions)**

This code presupposes the installation of Stata 13 or above. “///” indicates that the code continues on the next line. Comments are preceded by “/\*”. Indentation is not required. “menbreg” is the Stata command for mixed-effects (multilevel) negative binomial regression.

menbreg absence /// /\* outcome

baseline gender fsm /// /\* pupil-level variables

trial schsize schfsm, /// /\* school-level variables

exposure(sessions) ///

|| school\_id:

**H2: 2-level models for binary and continuous outcomes estimated via FIML**

This code presupposes the installation of R, R Studio and R package “MplusAutomation”. Indentation is not required. As in Mplus[see above], variable names and commands are not case sensitive, but R objects and functions follow R conventions. Code chunks are separated by “#----“

#--------------------------------------------------

# Subgroup analysis model for binary outcome (FIML)

#--------------------------------------------------

cond3\_subgroup <- mplusObject(

TITLE = "H2A. Conduct problems time 3 subgroup FIML;",

VARIABLE = "between = trial schsize SchFSM;

within = FSM gender risk

boyrisk boytrial

boy\_r\_tr r\_trial;

cluster = school\_id;

categorical = condpr3b;

usevariables = FSM gender

risk trial schsize schfsm

condpr3b boyrisk boytrial

boy\_r\_tr r\_trial;",

DEFINE = "boyrisk = gender\*risk;

boytrial = gender\*trial;

boy\_r\_tr = gender\*risk\*trial;

r\_trial = risk\*trial;",

ANALYSIS = "type = twolevel;

estimator = ML;

integration = montecarlo;",

MODEL = "%within%

condpr3b on FSM gender risk

boyrisk boytrial boy\_r\_tr

r\_trial;

risk;

FSM;

gender;

boyrisk;

boytrial;

boy\_r\_tr;

r\_trial;

%between%

condpr3b on schsize SchFSM trial;

condpr3b;",

OUTPUT = "sampstat stand res cinterval;",

rdata = data)

cond3\_subgroup\_fit <- mplusModeler(cond3\_subgroup,

modelout = "cond3\_subgroup.inp",

run = 1L)

#-------------------------------------------------------

# Subgroup analysis model for continuous outcomes (FIML)

#-------------------------------------------------------

wb3\_subgroup <- mplusObject(

TITLE = "H2B. Wellbeing time 3 subgroup FIML;",

VARIABLE = "between = trial schsize SchFSM;

within = FSM gender risk

boyrisk boytrial

boy\_r\_tr r\_trial;

cluster = school\_id;

usevariables = FSM gender

risk trial schsize schfsm

wb3 boyrisk boytrial

boy\_r\_tr r\_trial;",

DEFINE = "boyrisk = gender\*risk;

boytrial = gender\*trial;

boy\_r\_tr = gender\*risk\*trial;

r\_trial = risk\*trial;",

ANALYSIS = "type = twolevel;

estimator = ML;",

MODEL = "%within%

wb3 on FSM gender risk

boyrisk boytrial boy\_r\_tr

r\_trial;

wb3;

risk;

FSM;

gender;

boyrisk;

boytrial;

boy\_r\_tr;

r\_trial;

%between%

wb3 on schsize SchFSM trial;

wb3;",

OUTPUT = "sampstat stand res cinterval;",

rdata = data)

wb3\_subgroup\_fit <- mplusModeler(wb3\_subgroup,

modelout = "wb3\_subgroup.inp",

run = 1L)

**H2: 2-level negative binomial model for count data (Absences and exclusions)**

This code presupposes the installation of Stata 13 or above. “///” indicates that the code continues on the next line. Comments are preceded by “/\*”. Indentation is not required. “menbreg” is the Stata command for mixed-effects (multilevel) negative binomial regression.

menbreg absence /// /\* outcome

baseline gender fsm risk /// /\* pupil-level variables

boyrisk /// /\* pupil-level interaction

boy\_r\_trial r\_trial boytrial /// /\* cross-level interactions

trial schsize schfsm, /// /\* school-level variables

exposure(sessions) ///

|| school\_id:

**H3: 2-level CACE model for binary and continuous outcomes**

This code presupposes the installation of R, R Studio and R package “MplusAutomation”. Indentation is not required. As in Mplus[see above], variable names and commands are not case sensitive, but R objects and functions follow R conventions. Code chunks are separated by “#----“

#-----------------------------------------------------

# Set up the model for binary outcome

#-----------------------------------------------------

cace\_model\_bin <- mplusObject(

TITLE = "CACE model for binary outcome.

Compliance = c50

Outcome = condpr3b (conduct problems);",

VARIABLE = "between = trial SchKS1 schsize schfsm SchCond scheal;

within = FSM SEN KS1 gender Conc1 condpr1 prosoc1;

cluster = school\_id;

categorical = c50 condpr3b;

classes = c(2);",

ANALYSIS = "type = twolevel mixture;

estimator = MLR;

starts = 2000 500;

processors = 10;

integration = montecarlo (500);",

DEFINE = "SchSize=SchSize/100;

SchFSM=SchFSM/10;

scheal=scheal/10;

SCHKS1=SCHKS1/10;

KS1=KS1/10;",

MODEL = "%WITHIN%

%overall%

c#1 on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

condpr3b on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

%c#1%

condpr3b on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

%c#2%

condpr3b on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

%BETWEEN%

%overall%

c#1 on SchSize SchFSM SchCond scheal SchKS1;

c#1\*1;

condpr3b on trial schsize schfsm SchCond scheal SchKS1;

condpr3b;

[condpr3b$1];

%c#1%

[c50$1@15];

condpr3b on schsize schfsm SchCond scheal SchKS1;

condpr3b on trial@0;

condpr3b;

[condpr3b$1];

%c#2%

[c50$1@-15];

condpr3b on schsize schfsm SchCond scheal SchKS1;

condpr3b on trial;

condpr3b;

[condpr3b$1];",

OUTPUT = "sampstat stand res tech8 tech7 tech1 tech3 cinterval;",

rdata = data)

#-----------------------------------------------------

# Fit the model (binary outcome)

#-----------------------------------------------------

cace\_model\_bin\_fit <- mplusModeler(cace\_model\_bin,

modelout = "cace\_model\_bin.inp",

run = 1L)

#-----------------------------------------------------

# Set up the model for continuous outcome

#-----------------------------------------------------

cace\_model\_cont <- mplusObject(

TITLE = "CACE model for continuous outcome.

Compliance = c50

Outcome = wb3 (wellbeing);",

VARIABLE = "between = trial SchKS1 schsize schfsm SchCond scheal;

within = FSM SEN KS1 gender Conc1 condpr1 prosoc1;

cluster = school\_id;

categorical = c50;

classes = c(2);",

ANALYSIS = "type = twolevel mixture;

estimator = MLR;

starts = 2000 500;

processors = 10;

integration = montecarlo (500);",

DEFINE = "SchSize=SchSize/100;

SchFSM=SchFSM/10;

scheal=scheal/10;

SCHKS1=SCHKS1/10;

KS1=KS1/10;",

MODEL = "%WITHIN%

%overall%

c#1 on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

wb3 on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

wb3;

%c#1%

wb3 on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

wb3;

%c#2%

wb3 on FSM SEN KS1 gender Conc1 condpr1 prosoc1;

wb3;

%BETWEEN%

%overall%

c#1 on SchSize SchFSM SchCond scheal SchKS1;

c#1\*1;

wb3 on trial schsize schfsm SchCond scheal SchKS1;

[wb3];

%c#1%

[c50$1@15];

wb3 on schsize schfsm SchCond scheal SchKS1;

wb3 on trial@0;

[wb3];

%c#2%

[c50$1@-15];

wb3 on schsize schfsm SchCond scheal SchKS1;

wb3 on trial;

[wb3];",

OUTPUT = "sampstat stand res tech8 tech7 tech1 tech3 cinterval;",

rdata = data)

#-----------------------------------------------------

# Fit the model (continuous outcome)

#-----------------------------------------------------

cace\_model\_cont\_fit <- mplusModeler(cace\_model\_cont,

modelout = "cace\_model\_cont.inp",

run = 1L)

**H3: Single-level CACE model for count outcomes**

This code presupposes the installation of Stata 15 or above. “///” indicates that the code continues on the next line. Indentation is not required. “baseline” is the prior measure of absence divided by prior measure of possible sessions. Standard errors are clustered by school (“school\_id”).

gsem (1.C: absence <- baseline gender fsm ///

sen ks1 trial@0 condpr1 conc1 prosoc1 ///

schsize schfsm schks1 schcond scheal, ///

exposure(sessions) poisson) ///

(2.C: absence <- baseline gender fsm ///

sen ks1 trial condpr1 conc1 prosoc1 ///

schsize schfsm schks1 schcond scheal, ///

exposure(sessions) poisson) ///

(1.C: c50 <- \_cons@-15, logit) ///

(2.C: c50 <- \_cons@15, logit) ///

(C <- baseline gender fsm ///

sen ks1 condpr1 ///

conc1 prosoc1 ///

schsize schfsm ///

schks1 schcond ///

scheal), ///

nocapslatent nolog ///

vce(cluster school\_id) lclass(C 2) ///

latent(C) startvalues(randomid, draws(20) seed(15))

**H4: 2-level model for KS2 reading scores**

This code presupposes the installation of Stata 13 or above. “///” indicates that the code continues on the next line. Comments are preceded by “/\*”. Indentation is not required. “mixed” is the Stata command for mixed-effects (multilevel) regression.

mixed reading /// /\* outcome

ks1 gender fsm /// /\* pupil-level variables

trial schsize schfsm, /// /\* school-level variables

|| school\_id:

Note: The other H4 models for continuous, binary and count variables are implemented in the exact same way as in H1, but changing the outcome variables. Instead of outcomes at time 3 (follow-up), the models are fitted on the outcomes at time 4 (12-month follow-up) or 5 (24-month follow-up).

**H5: Developmental cascades model using the RI-CLPM approach**

This exemplar code presupposes the installation of R, RStudio and the package “lavaan”. Indentation is not required. Comments are marked with “#” and code chunks are divided with “#-----”.

#-----------------------------------------------------

# 1. Model H0: Covariates fixed at 0

#------------------------------------------------------

m0 <- ‘

#######################

# MEASUREMENT MODEL #

#######################

# Constraints are needed for longitudinal measurement invariance

# Factor models for conduct at 3 waves (constrained).

FX3 =~ a\*sdq5\_3 + b\*sdq7\_3 + c\*sdq12\_3 + d\*sdq18\_3 + e\*sdq22\_3

FX4 =~ a\*sdq5\_4 + b\*sdq7\_4 + c\*sdq12\_4 + d\*sdq18\_4 + e\*sdq22\_4

FX5 =~ a\*sdq5\_5 + b\*sdq7\_5 + c\*sdq12\_5 + d\*sdq18\_5 + e\*sdq22\_5

# Factor models for emotional at 3 waves (constrained).

FY3 =~ f\*sdq3\_3 + g\*sdq8\_3 + h\*sdq13\_3 + i\*sdq16\_3 + j\*sdq24\_3

FY4 =~ f\*sdq3\_4 + g\*sdq8\_4 + h\*sdq13\_4 + i\*sdq16\_4 + j\*sdq24\_4

FY5 =~ f\*sdq3\_5 + g\*sdq8\_5 + h\*sdq13\_5 + i\*sdq16\_5 + j\*sdq24\_5

# threshold constraints conduct

sdq5\_3 | a1\*t1 + a2\*t2

sdq5\_4 | a1\*t1 + a2\*t2

sdq5\_5 | a1\*t1 + a2\*t2

sdq7\_3 | b1\*t1 + b2\*t2

sdq7\_4 | b1\*t1 + b2\*t2

sdq7\_5 | b1\*t1 + b2\*t2

sdq12\_3 | c1\*t1 + c2\*t2

sdq12\_4 | c1\*t1 + c2\*t2

sdq12\_5 | c1\*t1 + c2\*t2

sdq18\_3 | d1\*t1 + d2\*t2

sdq18\_4 | d1\*t1 + d2\*t2

sdq18\_5 | d1\*t1 + d2\*t2

sdq22\_3 | e1\*t1 + e2\*t2

sdq22\_4 | e1\*t1 + e2\*t2

sdq22\_5 | e1\*t1 + e2\*t2

# threshold constraints emotional

sdq3\_3 | f1\*t1 + f2\*t2

sdq3\_4 | f1\*t1 + f2\*t2

sdq3\_5 | f1\*t1 + f2\*t2

sdq8\_3 | g1\*t1 + g2\*t2

sdq8\_4 | g1\*t1 + g2\*t2

sdq8\_5 | g1\*t1 + g2\*t2

sdq13\_3 | h1\*t1 + h2\*t2

sdq13\_4 | h1\*t1 + h2\*t2

sdq13\_5 | h1\*t1 + h2\*t2

sdq16\_3 | i1\*t1 + i2\*t2

sdq16\_4 | i1\*t1 + i2\*t2

sdq16\_5 | i1\*t1 + i2\*t2

sdq24\_3 | j1\*t1 + j2\*t2

sdq24\_4 | j1\*t1 + j2\*t2

sdq24\_5 | j1\*t1 + j2\*t2

# Free latent means from t = 4 onwards

FX4 + FX5 + FY4 + FY5 ~ 1

################

# BETWEEN PART #

################

# Random intercepts as latent factors

RIX =~ 1\*FX3 + 1\*FX4 + 1\*FX5

RIY =~ 1\*FY3 + 1\*FY4 + 1\*FY5

RIZ =~ 1\*zread3 + 1\*zread4 + 1\*zread5

# Residual variances of all factor variables fixed at 0.

FX3 ~~ 0\*FX3

FX4 ~~ 0\*FX4

FX5 ~~ 0\*FX5

FY3 ~~ 0\*FY3

FY4 ~~ 0\*FY4

FY5 ~~ 0\*FY5

zread3 ~~ 0\*zread3

zread4 ~~ 0\*zread4

zread5 ~~ 0\*zread5

###############

# WITHIN PART #

###############

WFX3 =~ 1\*FX3

WFX4 =~ 1\*FX4

WFX5 =~ 1\*FX5

WFY3 =~ 1\*FY3

WFY4 =~ 1\*FY4

WFY5 =~ 1\*FY5

WZ3 =~ 1\*zread3

WZ4 =~ 1\*zread4

WZ5 =~ 1\*zread5

# Lagged effects between the within-person centred latent variables.

WFX4 + WFY4 + WZ4 ~ WFX3 + WFY3 + WZ3

WFX5 + WFY5 + WZ5 ~ WFX4 + WFY4 + WZ4

# Correlations within the same wave.

WFX3 ~~ WFY3

WFX3 ~~ WZ3

WFY3 ~~ WZ3

WFX4 ~~ WFY4

WFX4 ~~ WZ4

WFY4 ~~ WZ4

WFX5 ~~ WFY5

WFX5 ~~ WZ5

WFY5 ~~ WZ5

##########################

# ADDITIONAL CONSTRAINTS #

##########################

# Correlations between-factors and within-factors set to 0 at all waves

RIX + RIY + RIZ ~~ 0\*WFX3 + 0\*WFY3 + 0\*WZ3 + 0\*WFX4 + 0\*WFY4 + 0\*WZ4 + 0\*WFX5 + 0\*WFY5 + 0\*WZ5

# Covariances (observed conduct)

# item 5 all time points

sdq5\_3 ~~ sdq5\_4

sdq5\_3 ~~ sdq5\_5

sdq5\_4 ~~ sdq5\_5

# item 7 all time points

sdq7\_3 ~~ sdq7\_4

sdq7\_3 ~~ sdq7\_5

sdq7\_4 ~~ sdq7\_5

# item 12 all time points

sdq12\_3 ~~ sdq12\_4

sdq12\_3 ~~ sdq12\_5

sdq12\_4 ~~ sdq12\_5

# item 18 all time points

sdq18\_3 ~~ sdq18\_4

sdq18\_3 ~~ sdq18\_5

sdq18\_4 ~~ sdq18\_5

# item 22 all time points

sdq22\_3 ~~ sdq22\_4

sdq22\_3 ~~ sdq22\_5

sdq22\_4 ~~ sdq22\_5

# Covariances (observed emotional)

# item 3 all time points

sdq3\_3 ~~ sdq3\_4

sdq3\_3 ~~ sdq3\_5

sdq3\_4 ~~ sdq3\_5

# item 8 all time points

sdq8\_3 ~~ sdq8\_4

sdq8\_3 ~~ sdq8\_5

sdq8\_4 ~~ sdq8\_5

# item 13 all time points

sdq13\_3 ~~ sdq13\_4

sdq13\_3 ~~ sdq13\_5

sdq13\_4 ~~ sdq13\_5

# item 16 all time points

sdq16\_3 ~~ sdq16\_4

sdq16\_3 ~~ sdq16\_5

sdq16\_4 ~~ sdq16\_5

# item 24 all time points

sdq24\_3 ~~ sdq24\_4

sdq24\_3 ~~ sdq24\_5

sdq24\_4 ~~ sdq24\_5

#################################################

##### time-invariant covariates fixed at 0 ######

#################################################

# “shrisk” is derived as such: shrisk=FSM+SEN

# trial=0=control; trial=1=intervention

# gender=0=female; gender=1=male

FX3 + FX4 + FX5 ~ 0\*trial + 0\*gender + 0\*shrisk

FY3 + FY4 + FY5 ~ 0\*trial + 0\*gender + 0\*shrisk

zread3 + zread4 + zread5 ~ 0\*trial + 0\*gender + 0\*shrisk

'

#------------------------------------------------------------

# 2. Fit model H0

#------------------------------------------------------------

m0\_fit <- cfa(m0, cluster= "school\_id", data = data,

estimator = "WLSMV", mimic = "mplus",

parameterization = "theta", zero.keep.margins=TRUE,

missing = "pairwise", std.lv=T,

ordered = c("sdq5\_3", "sdq7\_3", "sdq12\_3", "sdq18\_3",

"sdq22\_3", "sdq5\_4", "sdq7\_4", "sdq12\_4", "sdq18\_4", "sdq22\_4", "sdq5\_5", "sdq7\_5", "sdq12\_5", "sdq18\_5", "sdq22\_5", "sdq3\_3", "sdq8\_3", "sdq13\_3", "sdq16\_3", "sdq24\_3", "sdq3\_4", "sdq8\_4", "sdq13\_4", "sdq16\_4", "sdq24\_4", "sdq3\_5", "sdq8\_5", "sdq13\_5", "sdq16\_5", "sdq24\_5"))

#-----------------------------------------------------

# 3. Model H1: Trial, gender and shared risk freely estimated.

#------------------------------------------------------

# Copy previous model and name it “m1”.

# Replace the last chunk “time-invariant covariates fixed at 0” with:

# (Remove “” as necessary)

“#################################################

## time-invariant covariates constrained to ######

## equality across time (“cn” constraints) ######

#################################################

FX3 + FX4 + FX5 ~ cn13\*trial + cn23\*gender + cn33\*shrisk

FY3 + FY4 + FY5 ~ cn14\*trial + cn24\*gender + cn34\*shrisk

zread3 + zread4 + zread5 ~ cn15\*trial + cn25\*gender + cn35\*shrisk”

#------------------------------------------------------------

# 4. Fit model H1

#------------------------------------------------------------

m1\_fit <- cfa(m1, cluster= "school\_id", data = data,

estimator = "WLSMV", mimic = "mplus",

parameterization = "theta", zero.keep.margins=TRUE,

missing = "pairwise", std.lv=T,

ordered = c("sdq5\_3", "sdq7\_3", "sdq12\_3", "sdq18\_3",

"sdq22\_3", "sdq5\_4", "sdq7\_4", "sdq12\_4", "sdq18\_4", "sdq22\_4", "sdq5\_5", "sdq7\_5", "sdq12\_5", "sdq18\_5", "sdq22\_5", "sdq3\_3", "sdq8\_3", "sdq13\_3", "sdq16\_3", "sdq24\_3", "sdq3\_4", "sdq8\_4", "sdq13\_4", "sdq16\_4", "sdq24\_4", "sdq3\_5", "sdq8\_5", "sdq13\_5", "sdq16\_5", "sdq24\_5"))

#------------------------------------------------------------

# 5. Compare nested model H0 and H1

#------------------------------------------------------------

lavTestLRT(m0\_fit, m1\_fit)