Random Intercept Latent Transition Analysis (RI-LTA) with {MplusAutomation}

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A tutorial replicating the analyses presented in Muthén & Asparouhov (2020)

• Hidden Markov Models • Simulation • 2 Applied Examples • Invariance •

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Contents

Source citation: Muthén, B. & Asparouhov, T. (2020). Latent Transition Analysis with Random Intercepts (RI-LTA). Under review. Version 3.

- This tutorial was made with the intention of having readers following along in the original article. Many of the important concepts relevant to RI-LTA, discussed extensively in Muthén & Asparouhov (2020), are not included here.
- All content & concepts closely follow Muthén & Asparouhov (2020).
- All models are estimated with Mplus version 8.4 (Muthén & Muthén, 1998 - 2017) via the interface R (R Core Team, 2017) package {`MplusAutomation`} (Hallquist & Wiley, 2018).

- The article, data, and all corresponding `Mplus` scripts can be found here: https://www.statmodel.com/RI-LTA.shtml

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Sections of Muthén & Asparouhov (2020) paper:

1. Introduction
2. Regular LTA
3. Random Intercept RI-LTA
4. Relations to other multi-level models
5. Monte Carlo simulation study
6. Applications of RI-LTA using two data examples (Mood data & Dating data)

Introducing the LTA & RI-LTA models

Parameters of regular LTA model

- T: number of time points (t a discrete timepoint)
- C_t: categrorical latent variable at time t
- U_{rit}: latent class indicator for indicator r, subject i, and time t
- M: number of categories for observed indicators
- K: number of classes for latent variable C_t (k a discrete class)
- τ: transition probability, $P(C_t = k|C_{t-1} = m)$
- ω_{rk}: item and class specific threshold on the inverse logit scale
- π_k: class size for each of C_t latent variables

Interpreting LTA paramaters: Classification error & transition probabilities (τ)

Table 1: LTA estimates for the Life satisfaction example

Measurement probabilities

Observed response	Latent class: Unsatisfied	Latent class: Satisfied
Unsatisfied	0.855	0.163 (Classification error)
Satisfied	0.145 (Classification error)	0.837

Time 1 latent class probabilities

Unsatisfied: 0.395 Satisfied: 0.605

Transition probabilities for Time 1 (rows) to Time 2 (columns)

	Unsatisfied	Satisfied
Unsatisfied	T1 UNS / T2 UNS 1.000	T1 UNS / T2 SAT 0.000
Satisfied	0.126 T1 SAT / T2 UNS	0.874 T1 SAT / T2 SAT

STABILITY

Figure 1: Picture adapted from Muthén & Asparouhov (2020).

Common LTA assumptions

- Conditional independence: Indicators are assumed to be independent after conditioning upon class (k)
- Markov property: C_t is only influenced by C_{t-1}. Also commonly called "lag-1 effects"
- Measurement invariance: of latent class indicators across Time points
- Stationary invariance: transition probabilities are fixed (invariant) across time points

Note: All model assumptions listed above may be relaxed to better fit a particular data context.

Related longitudinal models

Each of these models separates out `stable between-subject` differences from `within-subject` variance:

Latent trait-state model

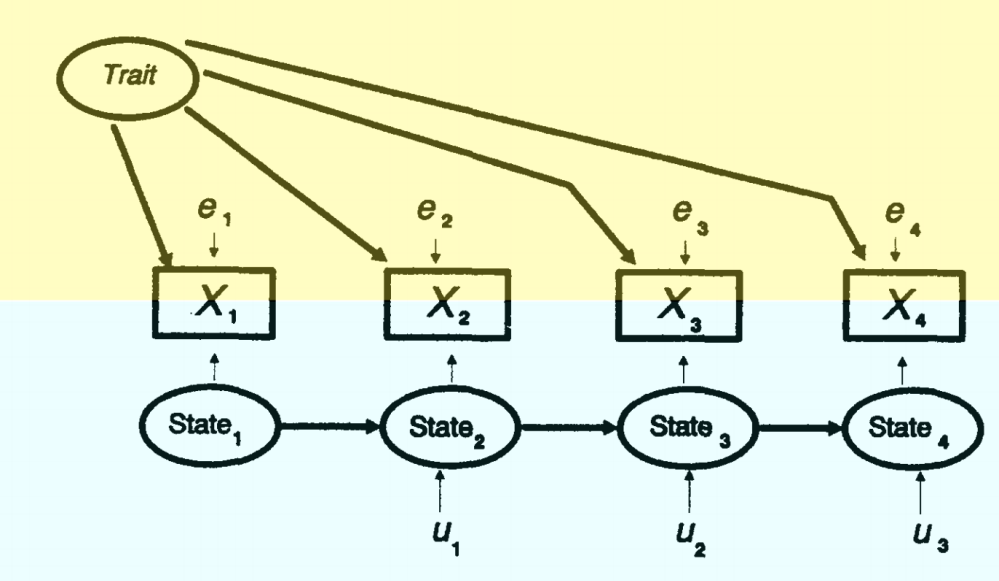


Figure 2: Latent trait-state model. Picture adapted from Kenny & Zustra (1995).

Random intercept cross-lagged panel model (RI-CLPM)

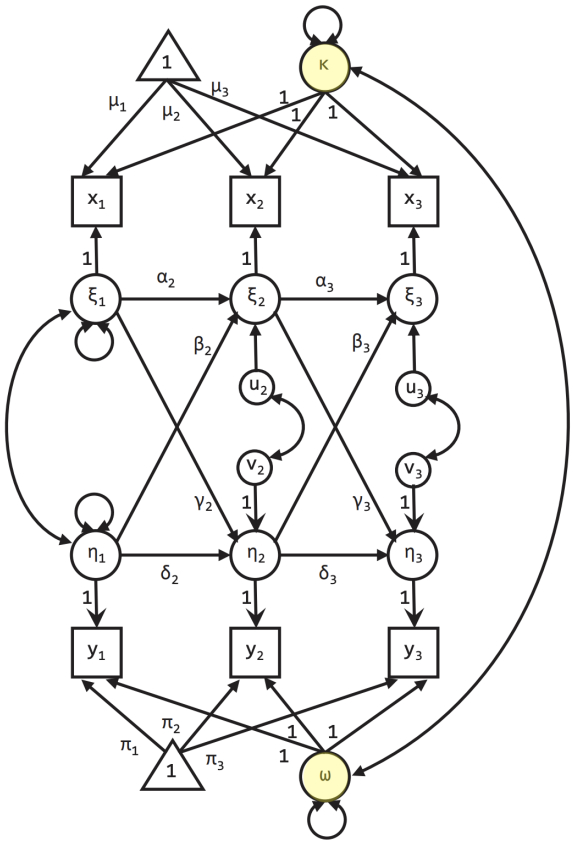


Figure 3: Random intercept cross-lagged panel model. Picture is adapted from Hamaker et al., (2015).

Random intercept LTA model specification details

Continuous random intercept LTA model, unique parameters (p.11-15):

- f_i: The continuous random intercept latent factor. Distributed $N = (0, 1)$
- λ_r: The factor loadings for each latent class indicator U_{rit} which are held equal across time points (time-invariant).

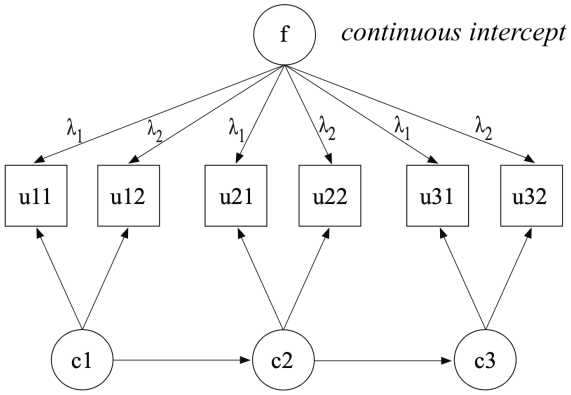


Figure 4a: Picture adapted from Muthén & Asparouhov (2020).

Binary random intercept LTA model, unique parameters (p.15-17):

- I_k: The binary random intercept latent class variable with $k = 2$.

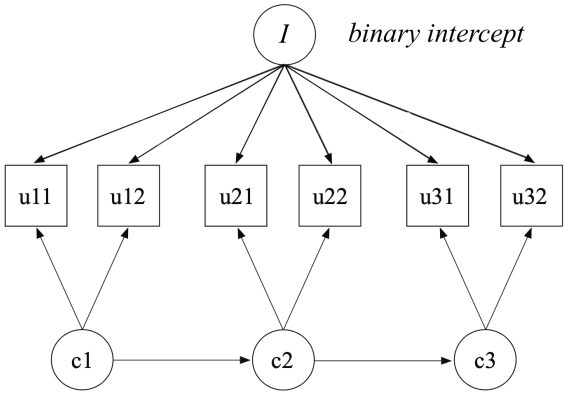


Figure 4b: Picture adapted from Muthén & Asparouhov (2020).

Critique of traditional LTA model:

a. Generally, the central interest in LTA is *state* changes across time points.
b. Given **a** is true, stable individual differences (between-subject variation) or *trait* variance should be separated to isolate changes in states (within-subject variation) across time.
c. If between-subject variation is not accounted for using the random-intercept approach, transition probability estimates may be significantly biased.

d. Intuitively, removing between-subject variation is a logical step in the same manner that repeated measure designs parse out this random effect.

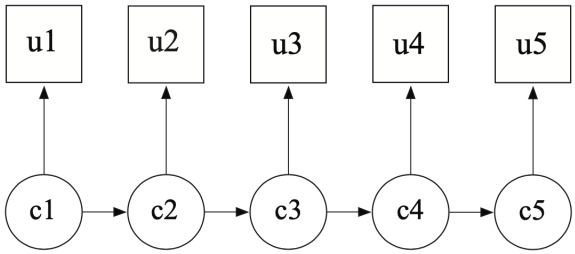


Figure 5: LTA with 1 binary indicator (u) at 5 time points. Picture from Muthén & Asparouhov (2020).

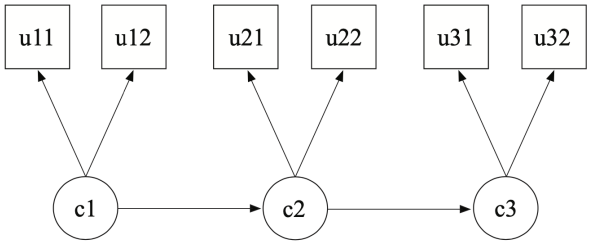


Figure 6: LTA with 2 binary indicator at 3 time points. Picture from Muthén & Asparouhov (2020).

Monte Carlo simulation study

Population & model characteristics:

a. 5 binary indicators (U_{rit})
b. categorical latent variables C_t: Latent variables are generated to have 2 latent classes ($K = 2$)

- class 1: logit values set to 1 (probability = 0.731) across all indicators
- class 2: logit values set to -1 (probability = 0.269) across all indicators
- Probability of class membership at time 1: .5 ($C_{k=1}$) and .5 ($C_{k=2}$)

c. random intercept continuous latent factor (f)

- loadings (λ_i): set to 2
- mean is fixed to 0, variance is fixed to 1

d. transition probabilities

- TRANS11 = .622
- TRANS21 = .500

e. sample size conditions (N): 500, 1000, 2000, 4000

Simulation (1): Regular LTA model matching data generation (Time points = 2)

- data generated = regular LTA
- model = regular LTA

Note: sample size not varied due to high performance and parameter coverage for the N=500 condition

```
lta_01  <- mplusObject(

  TITLE = "model01_regular_lta",

  MONTECARLO =
     "NAMES = u11-u15 u21-u25;
        GENERATE = u11-u15 u21-u25(1);
        CATEGORICAL = u11-u15 u21-u25;
        GENCLASSES = c1(2) c2(2);
        CLASSES = c1(2) c2(2);
        NOBSERVATIONS = 500;
        NREPS = 500;",

  ANALYSIS =
      "TYPE = MIXTURE;
       ESTIMATOR = ML;
         processors = 8;",

  MODELPOPULATION =
      "%OVERALL%
      [c1#1-c2#1*0];      ! latent intercepts at 0?
      c2#1 on c1#1*0.5;   ! transition probability at .5


  MODEL POPULATION-c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL POPULATION-c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
```

```
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521); ",

  MODEL =
    "%OVERALL%
     [c1#1-c2#1*0] (par1-par2);
     c2#1 on c1#1*0.5 (par11);

  MODEL c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521);",

  MODELCONSTRAINT =
       "! Compute joint and marginal probabilities:
        New(
        trans11*.622 trans12*.378 trans21*.5 trans22*.5
        prob11*.5 prob12*.5 prob21*.561 prob22*.439);

        trans11 = 1/(1+exp(-(par2+par11)));
        trans12 = 1-trans11;
        trans21 = 1/(1+exp(-par2));
        trans22 = 1- trans21;
        ! marginal probabilities at T1 and T2:
        prob11 = 1/(1+exp(-par1));
        prob12 = 1 - prob11;
        prob21 = prob11*trans11+prob12*trans21;
        prob22 = 1- prob21;",

  OUTPUT = "")

lta_01_fit <- mplusModeler(lta_01,
                           dataout=here("sim1_LTA", "sim1_lta01.dat"),
                           modelout=here("sim1_LTA", "sim1_lta01.inp"),
                           check=TRUE, run = TRUE, hashfilename = FALSE)
```

Simulation (2): Regular LTA model matching data generation (Time points = 3)

- data generated = regular LTA

- model = regular LTA

Note: sample size not varied

```
lta_02  <- mplusObject(

  TITLE = "model02_regular_lta",

  MONTECARLO =
     "NAMES = u11-u15 u21-u25 u31-u35;
        GENERATE = u11-u15 u21-u25 u31-u35(1);
        CATEGORICAL = u11-u15 u21-u25 u31-u35;
        GENCLASSES = c1(2) c2(2) c3(2);
        CLASSES = c1(2) c2(2) c3(2);
        NOBSERVATIONS = 500;
        NREPS = 500;",

  ANALYSIS =
      "TYPE = MIXTURE;
       ESTIMATOR = ML;
         processors = 8;",

  MODELPOPULATION =
      "%OVERALL%
      [c1#1-c3#1*0];      !
      c2#1 on c1#1*0.5;   ! transition probability at .5
      c3#1 on c2#1*0.5;   !

  MODEL POPULATION-c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL POPULATION-c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521);

  MODEL POPULATION-c3:
        %c3#1%
        [u31$1*1] (p111); [u32$1*1] (p211); [u33$1*1] (p311);
        [u34$1*1] (p411); [u35$1*1] (p511);
        %c3#2%
      [u31$1*-1] (p121); [u32$1*-1] (p221); [u33$1*-1] (p321);
      [u34$1*-1] (p421); [u35$1*-1] (p521); ",

  MODEL =
    "%OVERALL%
```

```
    [c1#1-c3#1*0] (par1-par3);
    c2#1 on c1#1*0.5 (par11);
    c3#1 on c2#1*0.5;

  MODEL c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521);

  MODEL c3:
        %c3#1%
        [u31$1*1] (p111); [u32$1*1] (p211); [u33$1*1] (p311);
        [u34$1*1] (p411); [u35$1*1] (p511);
        %c3#2%
      [u31$1*-1] (p121); [u32$1*-1] (p221); [u33$1*-1] (p321);
      [u34$1*-1] (p421); [u35$1*-1] (p521); ",

  MODELCONSTRAINT =
       "! Compute joint and marginal probabilities:
        New(
        trans11*.622 trans12*.378 trans21*.5 trans22*.5
        prob11*.5 prob12*.5 prob21*.561 prob22*.439);

        trans11 = 1/(1+exp(-(par2+par11)));
        trans12 = 1-trans11;
        trans21 = 1/(1+exp(-par2));
        trans22 = 1- trans21;
        !marginal probabilities at T1 and T2:
        prob11 = 1/(1+exp(-par1));
        prob12 = 1 - prob11;
        prob21 = prob11*trans11+prob12*trans21;
        prob22 = 1- prob21;",

  OUTPUT = "")

lta_02_fit <- mplusModeler(lta_02,
                           dataout=here("sim1_LTA", "sim1_lta02.dat"),
                           modelout=here("sim1_LTA", "sim1_lta02.inp"),
                           check=TRUE, run = TRUE, hashfilename = FALSE)
```

Simulation (3): Regular LTA model misspecified relative to data generation (Time points = 3)

- data generated = RI-LTA
- model = regular LTA

```
lta_03  <- mplusObject(

TITLE = "model02_regular_lta",

MONTECARLO =
   "NAMES = u11-u15 u21-u25 u31-u35;
      GENERATE = u11-u15 u21-u25 u31-u35(1);
      CATEGORICAL = u11-u15 u21-u25 u31-u35;
      GENCLASSES = c1(2) c2(2) c3(2);
      CLASSES = c1(2) c2(2) c3(2);
      NOBSERVATIONS = 500;
      NREPS = 500;",

ANALYSIS =
    "TYPE = MIXTURE;
     ESTIMATOR = ML;
       processors = 8;",

MODELPOPULATION =
    "%OVERALL%
    [c1#1-c3#1*0];      !
    c2#1 on c1#1*0.5;   ! transition probability at .5
    c3#1 on c2#1*0.5;   !

MODEL POPULATION-c1:
    %c1#1%
    [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
    [u14$1*1] (p411); [u15$1*1] (p511);
      %c1#2%
      [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
      [u14$1*-1] (p421); [u15$1*-1] (p521);

MODEL POPULATION-c2:
    %c2#1%
    [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
    [u24$1*1] (p411); [u25$1*1] (p511);
      %c2#2%
    [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
    [u24$1*-1] (p421); [u25$1*-1] (p521);

MODEL POPULATION-c3:
      %c3#1%
      [u31$1*1] (p111); [u32$1*1] (p211); [u33$1*1] (p311);
      [u34$1*1] (p411); [u35$1*1] (p511);
      %c3#2%
    [u31$1*-1] (p121); [u32$1*-1] (p221); [u33$1*-1] (p321);
    [u34$1*-1] (p421); [u35$1*-1] (p521); ",
```

```
  MODEL =
    "%OVERALL%
     [c1#1-c3#1*0] (par1-par3);
     c2#1 on c1#1*0.5 (par11);
     c3#1 on c2#1*0.5;

  MODEL c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521);

  MODEL c3:
        %c3#1%
        [u31$1*1] (p111); [u32$1*1] (p211); [u33$1*1] (p311);
        [u34$1*1] (p411); [u35$1*1] (p511);
        %c3#2%
      [u31$1*-1] (p121); [u32$1*-1] (p221); [u33$1*-1] (p321);
      [u34$1*-1] (p421); [u35$1*-1] (p521); ",

  MODELCONSTRAINT =
       "! Compute joint and marginal probabilities:
        New(trans11*.622 trans12*.378 trans21*.5 trans22*.5
        prob11*.5 prob12*.5 prob21*.561 prob22*.439);

        trans11 = 1/(1+exp(-(par2+par11)));
        trans12 = 1-trans11;
        trans21 = 1/(1+exp(-par2));
        trans22 = 1- trans21;
        !marginal probabilities at T1 and T2:
        prob11 = 1/(1+exp(-par1));
        prob12 = 1 - prob11;
        prob21 = prob11*trans11+prob12*trans21;
        prob22 = 1- prob21;",

  OUTPUT = "")

lta_03_fit <- mplusModeler(lta_03,
                           dataout=here("sim1k_LTA", "sim03_lta.dat"),
                           modelout=here("sim1k_LTA", "sim03_lta.inp"),
                           check=TRUE, run = TRUE, hashfilename = FALSE)
```

Simulation (4) step 1: RI-LTA model matching data generation (sample size varied)

Data generated by RI-LTA model (Time points = 2)

Vary sample size: Estimate RI-LTA models with T = 2 for sample sizes 500, 1000, 1500, 2000, 2500

```
# looping over N-sizes conditions

t2_rilta  <- lapply(1:5, function(k) {
  t2_nsize  <- mplusObject(

  TITLE = "T2RILTA - vary n-size",

    MONTECARLO =
glue("NAMES = u11-u15 u21-u25;
        GENERATE = u11-u15 u21-u25(1);
        CATEGORICAL = u11-u15 u21-u25;
        GENCLASSES = c1(2) c2(2);
        CLASSES = c1(2) c2(2);
        NOBSERVATIONS = {k*500};
        SEED = 3252020;
        NREPS = 5; !rep number reduced for demo (real sim use 500,1000)
      repsave = all;
      save = {k}_t2n500rep*.dat;
      RESULTS = t2results{k}.csv;"),

  ANALYSIS =
      "TYPE = MIXTURE;
       algorithm = integration;
         processors = 8;",

  MODELPOPULATION =
      "%OVERALL%

      [c1#1-c2#1*0];
      c2#1 on c1#1*0.5;

      f by u11-u15*2 (p1-p5)
           u21-u25*2 (p1-p5);

        f@1; [f@0]; ! set factor variance to 1 and mean to 0

  MODEL POPULATION-c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL POPULATION-c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
```

```
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521); ",

  MODEL =
    "%OVERALL%

    [c1#1-c2#1*0] (par1-par2);
    c2#1 on c1#1*0.5 (par11);

    f by u11-u15*2 (p1-p5)
         u21-u25*2 (p1-p5);

    f@1; [f@0];

  MODEL c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521);",

  MODELCONSTRAINT =
       "! Compute joint and marginal probabilities:
        New(
        trans11*.622 trans12*.378 trans21*.5 trans22*.5
        prob11*.5 prob12*.5 prob21*.561 prob22*.439);
        trans11 = 1/(1+exp(-(par2+par11)));
        trans12 = 1-trans11;
        trans21 = 1/(1+exp(-par2));
        trans22 = 1- trans21;
        !marginal probabilities at T1 and T2:
        prob11 = 1/(1+exp(-par1));
        prob12 = 1 - prob11;
        prob21 = prob11*trans11+prob12*trans21;
        prob22 = 1- prob21;"
)

t2_nsize.fit <- mplusModeler(t2_nsize,
                dataout=here("sim2_RI1", "t2_nsize_sim.dat"),
                modelout=sprintf(here("sim2_RI1", "%d_t2_nsize_sim.inp"), k),
                check=TRUE, run = TRUE, hashfilename = FALSE)
})
```

Coerce the simulation `results` output files to format for readable tables

```
sim2 <- here("sim2_RI1")

fs::dir_ls(sim2)

all_csv <- fs::dir_ls(sim2, regexp = "\\.csv$")

all_results <- fs::dir_ls(sim2, regexp = "\\.csv$") %>%
  map_dfr(read.csv, sep = " ", header = F)

all_results2 <- as.data.frame(format(all_results,scientific=F))

fit_results <- all_results2 %>% slice(8:nrow(all_results2)) %>%
 slice(which(row_number() %% 9 == 1)) %>%
 select(V1:V8)

fit_results2 <- fit_results %>%
 mutate(Condition = as.array(rep(1:5, each = 5))) %>%
 mutate(Rep_Num = as.array(rep(1:5, 5))) %>%
 purrr::modify_if(is.character, as.numeric) %>%
 select(9:10,1:8) %>%
 rename(
      H0_LL = V1,
   Free_Par = V2,
        AIC = V3,
        BIC = V4,
       aBIC = V5,
    Chi_Val = V6,
    Chi_DF  = V7,
      Chi_P = V8) %>%
  mutate(Condition = factor(Condition,
          labels = c(`1` = "N=500", `2` = "N=1000", `3`= "N=1500",
                     `4` = "N=2000",`5` = "N=2500")))
```

Make table with each replication by condition as separate row

```
fit_results2 %>%
  kable(booktabs = T) %>%
  kable_styling(latex_options = c("scale_down", linesep = ""),
                full_width = F,
                position = "left")
```

Condition	Rep_Num	H0_LL	Free_Par	AIC	BIC	aBIC	Chi_Val	Chi_DF	Chi_P
N=500	1	-2749.594	18	5535.188	5611.051	5553.918	1009.2829	1005	0.4561013
N=500	2	-2837.305	18	5710.609	5786.472	5729.339	915.8423	1005	0.9791113
N=500	3	-2696.120	18	5428.241	5504.104	5446.971	929.1771	1005	0.9573538
N=500	4	-2797.659	18	5631.318	5707.181	5650.048	1004.4552	1005	0.4989226
N=500	5	-2705.927	18	5447.854	5523.717	5466.584	926.4994	1005	0.9627697
N=1000	1	-5603.975	18	11243.950	11332.289	11275.120	1024.1379	1005	0.3303167
N=1000	2	-5505.977	18	11047.955	11136.294	11079.125	1001.1806	1005	0.5280763
N=1000	3	-5481.085	18	10998.169	11086.509	11029.340	1021.8583	1005	0.3487154
N=1000	4	-5460.839	18	10957.677	11046.017	10988.848	1061.5608	1005	0.1050173
N=1000	5	-5504.614	18	11045.228	11133.567	11076.398	1001.5850	1005	0.5244777
N=1500	1	-8314.668	18	16665.337	16760.975	16703.794	1044.2702	1005	0.1895410
N=1500	2	-8288.039	18	16612.078	16707.716	16650.535	997.3942	1005	0.5616700
N=1500	3	-8176.377	18	16388.755	16484.393	16427.212	1044.0734	1005	0.1907027
N=1500	4	-8232.702	18	16501.404	16597.042	16539.861	932.0613	1005	0.9508393
N=1500	5	-8229.723	18	16495.447	16591.085	16533.904	1003.7668	1005	0.5050511
N=2000	1	-11120.646	18	22277.292	22378.108	22320.921	1079.7151	1005	0.0503255
N=2000	2	-10956.236	18	21948.473	22049.289	21992.102	1071.1954	1005	0.0721377
N=2000	3	-10944.488	18	21924.975	22025.792	21968.605	956.0701	1005	0.8631720
N=2000	4	-11069.375	18	22174.750	22275.566	22218.379	1016.2641	1005	0.3954395
N=2000	5	-11081.107	18	22198.213	22299.030	22241.843	1098.7629	1005	0.0204558
N=2500	1	-13841.245	18	27718.490	27823.323	27766.132	1044.0597	1005	0.1907837
N=2500	2	-13750.826	18	27537.653	27642.486	27585.295	1081.9365	1005	0.0456181
N=2500	3	-13674.066	18	27384.133	27488.966	27431.775	1015.0062	1005	0.4062080
N=2500	4	-13918.484	18	27872.968	27977.801	27920.610	1057.3389	1005	0.1225054
N=2500	5	-13851.295	18	27738.590	27843.423	27786.232	1010.9299	1005	0.4416170

Make table with each condition as separate row (averaged across replications)

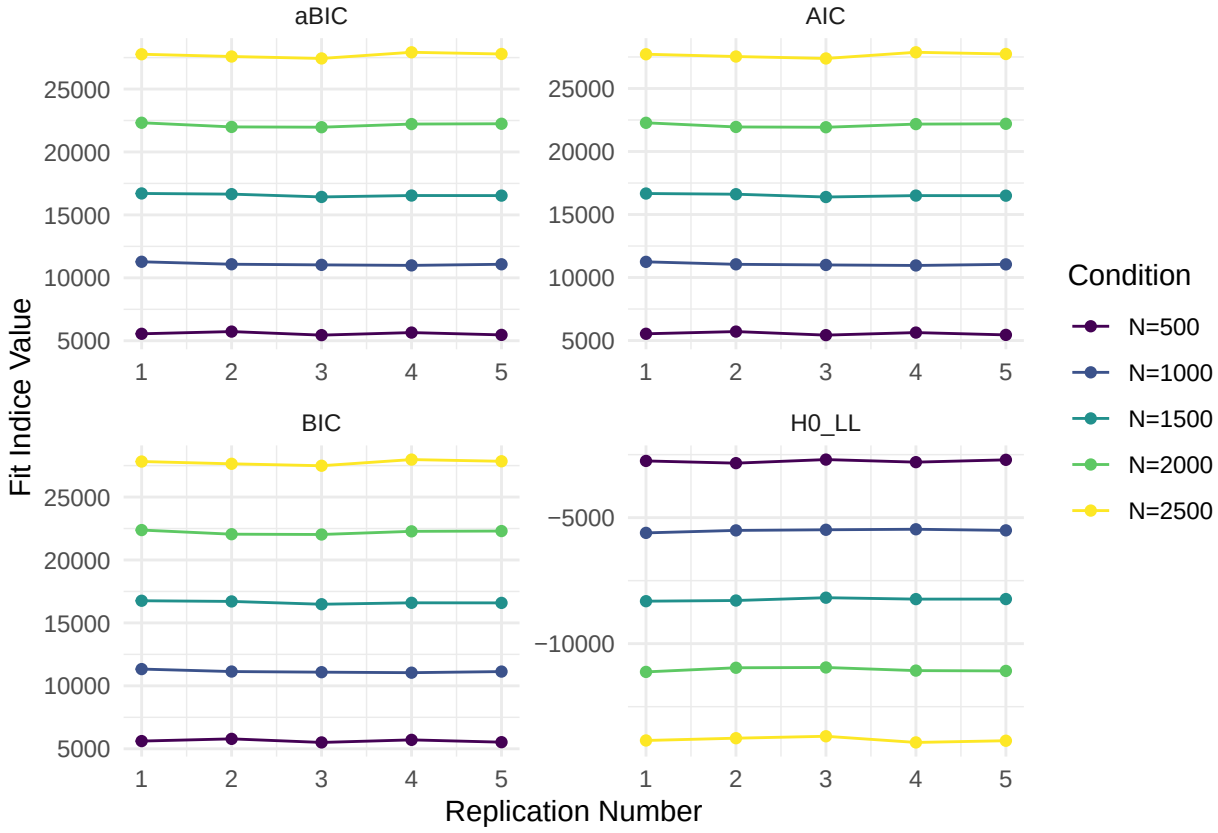
```
fit_by_cond <- fit_results2 %>%
  group_by(Condition) %>%
  summarize(
    avg_H0_LL = mean(H0_LL),
    avg_Par   = mean(Free_Par),
    avg_AIC   = mean(AIC),
    avg_BIC   = mean(BIC),
    avg_aBIC  = mean(aBIC),
    avg_Chi_Val = mean(Chi_Val),
    avg_Chi_DF  = mean(Chi_DF),
    avg_Chi_P   = mean(Chi_P),
  ) %>%
  bind_rows(summarise_all(., funs(if(is.numeric(.)) mean(.) else "Total"))) %>%
  adorn_rounding(digits = 2)


fit_by_cond %>%
  kable(booktabs = T) %>%
  kable_styling(latex_options = c("scale_down", linesep = ""),
                full_width = F,
                position = "left")
```

Condition	avg_H0_LL	avg_Par	avg_AIC	avg_BIC	avg_aBIC	avg_Chi_Val	avg_Chi_DF	avg_Chi_P
N=500	-2757.32	18	5550.64	5626.50	5569.37	957.05	1005	0.77
N=1000	-5511.30	18	11058.60	11146.94	11089.77	1022.06	1005	0.37
N=1500	-8248.30	18	16532.60	16628.24	16571.06	1004.31	1005	0.48
N=2000	-11034.37	18	22104.74	22205.56	22148.37	1044.40	1005	0.28
N=2500	-13807.18	18	27650.37	27755.20	27698.01	1041.85	1005	0.24
Total	-8271.69	18	16579.39	16672.49	16615.32	1013.94	1005	0.43

```r
fit_long <- fit_results2 %>%
  select(1:3,5:8) %>%
  pivot_longer(H0_LL:aBIC,              # gathering columns
               names_to = "variable", # new column >> names
               values_to = "value")   # new column >> values

fit_long %>%
  ggplot(., aes(x=Rep_Num,
                y=value,
                group=Condition,
                color=Condition)) +
  geom_point() +
  geom_line() +
  scale_color_viridis_d() +
  facet_wrap(~variable, scales = "free") +
  theme_minimal() +
  labs(x= "Replication Number",
       y= "Fit Indice Value")
```



```
ggsave(here("figures", "fit_results.png"), height = 6, width = 8)
```

Simulation (4) step 2: RI-LTA model matching data generation (Time points = 2)

```
replist_m1 <- read.csv(here("sim2_RI1", "1_t2n500replist.dat"),
                       header = F)


s2_rilta_1  <- mplusObject(

  TITLE = "m01_step2_ri_lta_t2",

  DATA =
  glue("{as.list.data.frame(here('sim2_RI1', '1_t2n500replist.dat;'))}
  type = montecarlo;"),

  VARIABLE =
     "NAMES = u11-u15 u21-u25 class1 class2;
        usev = u11-u25;
        CATEGORICAL = u11-u15 u21-u25;

        CLASSES = c1(2) c2(2);",

  ANALYSIS =
      "TYPE = MIXTURE;
       algorithm = integration;
         processors = 8;",

  MODEL =
    "%OVERALL%

    [c1#1-c2#1*0] (par1-par2);
    c2#1 on c1#1*0.5 (par11);

  MODEL c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
```

```
      [u24$1*-1] (p421); [u25$1*-1] (p521);",

  MODELCONSTRAINT =
       "! Compute joint and marginal probabilities:
        New(
        trans11*.622 trans12*.378 trans21*.5 trans22*.5
        prob11*.5 prob12*.5 prob21*.561 prob22*.439);

        trans11 = 1/(1+exp(-(par2+par11)));
        trans12 = 1-trans11;
        trans21 = 1/(1+exp(-par2));
        trans22 = 1- trans21;
        !marginal probabilities at T1 and T2:
        prob11 = 1/(1+exp(-par1));
        prob12 = 1 - prob11;
        prob21 = prob11*trans11+prob12*trans21;
        prob22 = 1- prob21;")



# does not work (unable to save as dataframe without rownames)
s2_rilta_1_fit <- mplusModeler(s2_rilta_1,
                               modelout=here("sim2_RI1", "step2_rilta_1.inp"),
                               check=TRUE, run = FALSE, hashfilename = FALSE)

#SOLUTION: must edit input file, copy and paste following filepath (overwrite previous): "/Users/agarbe

runModels(here("sim2_RI1", "step2_rilta_1.inp"))
```

Simulation (5) step 1: RI-LTA model matching data generation (Time points = 3)

```
# looping over sample sizes

t3_rilta  <- lapply(1:5, function(k) {
  t3_nsize  <- mplusObject(

  TITLE = "T3RILTA - vary n-size",

    MONTECARLO =
glue("NAMES = u11-u15 u21-u25 u31-u35;
        GENERATE = u11-u15 u21-u25 u31-u35(1);
        CATEGORICAL = u11-u15 u21-u25 u31-u35;
        GENCLASSES = c1(2) c2(2) c3(2);
        CLASSES = c1(2) c2(2) c3(2);
        NOBSERVATIONS = {k*500};
      SEED = 3252020;
        NREPS = 5; !rep number reduced for demo (real sim use 500,1000)
      repsave = all;
```

```
    save = {k}_t3n500rep*.dat;
    RESULTS = t3results{k}.csv;"),

ANALYSIS =
    "TYPE = MIXTURE;
     algorithm = integration;
       processors = 8;",

MODELPOPULATION =
    "%OVERALL%

    [c1#1-c3#1*0];
    c2#1 on c1#1*0.5;
    c3#1 on c2#1*0.5;

    f by u11-u15*2 (p1-p5)
         u21-u25*2 (p1-p5)
         u31-u35*2 (p1-p5);

      f@1; [f@0];

MODEL POPULATION-c1:
    %c1#1%
    [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
    [u14$1*1] (p411); [u15$1*1] (p511);
      %c1#2%
      [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
      [u14$1*-1] (p421); [u15$1*-1] (p521);

MODEL POPULATION-c2:
    %c2#1%
    [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
    [u24$1*1] (p411); [u25$1*1] (p511);
      %c2#2%
    [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
    [u24$1*-1] (p421); [u25$1*-1] (p521);

MODEL POPULATION-c3:
      %c3#1%
      [u31$1*1] (p111); [u32$1*1] (p211); [u33$1*1] (p311);
      [u34$1*1] (p411); [u35$1*1] (p511);
      %c3#2%
    [u31$1*-1] (p121); [u32$1*-1] (p221); [u33$1*-1] (p321);
    [u34$1*-1] (p421); [u35$1*-1] (p521); ",


MODEL =
  "%OVERALL%

   [c1#1-c3#1*0] (par1-par3);

  c2#1 on c1#1*0.5 (par11);
  c3#1 on c2#1*0.5;
```

```
    f by u11-u15*2 (p1-p5)
         u21-u25*2 (p1-p5)
         u31-u35*2 (p1-p5);

      f@1; [f@0];

  MODEL c1:
    %c1#1%
    [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
    [u14$1*1] (p411); [u15$1*1] (p511);
      %c1#2%
      [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
      [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL c2:
    %c2#1%
    [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
    [u24$1*1] (p411); [u25$1*1] (p511);
      %c2#2%
    [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
    [u24$1*-1] (p421); [u25$1*-1] (p521);

  MODEL c3:
      %c3#1%
      [u31$1*1] (p111); [u32$1*1] (p211); [u33$1*1] (p311);
      [u34$1*1] (p411); [u35$1*1] (p511);
      %c3#2%
    [u31$1*-1] (p121); [u32$1*-1] (p221); [u33$1*-1] (p321);
    [u34$1*-1] (p421); [u35$1*-1] (p521); ",

  MODELCONSTRAINT =
     "! Compute joint and marginal probabilities:
      New(
      trans11*.622 trans12*.378 trans21*.5 trans22*.5
      prob11*.5 prob12*.5 prob21*.561 prob22*.439);

      trans11 = 1/(1+exp(-(par2+par11)));
      trans12 = 1-trans11;
      trans21 = 1/(1+exp(-par2));
      trans22 = 1- trans21;
      !marginal probabilities at T1 and T2:
      prob11 = 1/(1+exp(-par1));
      prob12 = 1 - prob11;
      prob21 = prob11*trans11+prob12*trans21;
      prob22 = 1- prob21;"
)

t3_nsize.fit <- mplusModeler(t3_nsize,
                             modelout= sprintf(here("sim3_RI2", "%d_t3_nsize_sim.inp"), k),
                             check=TRUE, run = TRUE, hashfilename = FALSE)
})
```

Simulation (5) step 2: RI-LTA model matching data generation (Time points = 3)

for condition: N = 500

```
replist_m2 <- read.csv(here("sim3_RI2", "1_t3n500replist.dat"),
                       header = F) %>% remove_rownames()



s2_rilta_2  <- mplusObject(

  TITLE = "m01_step2_ri_lta_t2",

  DATA =
  glue("{here('sim2_RI1', '1_t3n500replist.dat;')}
      type = montecarlo;"),

  VARIABLE =
     "NAMES = u11-u15 u21-u25 u31-u35
      class1 class2 class3;
      usev = u11-u35;
        CATEGORICAL = u11-u15 u21-u25 u31-u35;
        CLASSES = c1(2) c2(2) c3(2); ",

  ANALYSIS =
      "TYPE = MIXTURE;
       algorithm = integration;
         processors = 8;",

  MODEL =
    "%OVERALL%
      [c1#1-c3#1*0] (par1-par3);
      c2#1 on c1#1*0.5 (par11);
      c3#1 on c2#1*0.5;

  MODEL c1:
      %c1#1%
      [u11$1*1] (p111); [u12$1*1] (p211); [u13$1*1] (p311);
      [u14$1*1] (p411); [u15$1*1] (p511);
        %c1#2%
        [u11$1*-1] (p121); [u12$1*-1] (p221); [u13$1*-1] (p321);
        [u14$1*-1] (p421); [u15$1*-1] (p521);

  MODEL c2:
      %c2#1%
      [u21$1*1] (p111); [u22$1*1] (p211); [u23$1*1] (p311);
      [u24$1*1] (p411); [u25$1*1] (p511);
        %c2#2%
      [u21$1*-1] (p121); [u22$1*-1] (p221); [u23$1*-1] (p321);
      [u24$1*-1] (p421); [u25$1*-1] (p521);

  MODEL c3:
        %c3#1%
```

```
        [u31$1*1] (p111); [u32$1*1] (p211); [u33$1*1] (p311);
        [u34$1*1] (p411); [u35$1*1] (p511);
        %c3#2%
       [u31$1*-1] (p121); [u32$1*-1] (p221); [u33$1*-1] (p321);
       [u34$1*-1] (p421); [u35$1*-1] (p521); ",

  MODELCONSTRAINT =
       "! Compute joint and marginal probabilities:
        New(
        trans11*.622 trans12*.378 trans21*.5 trans22*.5
        prob11*.5 prob12*.5 prob21*.561 prob22*.439);

        trans11 = 1/(1+exp(-(par2+par11)));
        trans12 = 1-trans11;
        trans21 = 1/(1+exp(-par2));
        trans22 = 1- trans21;
        !marginal probabilities at T1 and T2:
        prob11 = 1/(1+exp(-par1));
        prob12 = 1 - prob11;
        prob21 = prob11*trans11+prob12*trans21;
        prob22 = 1- prob21;")

# does not work (unable to save as dataframe without rownames)

s2_rilta_2_fit <- mplusModeler(s2_rilta_2,
                               modelout=here("sim3_RI2", "step2_rilta_t3.inp"),
                               check=TRUE, run = FALSE, hashfilename = FALSE, writeData = 'never')

#SOLUTION: must edit input file, copy and paste following filepath (overwrite previous): "/Users/agarbe

runModels(here("sim3_RI2", "step2_rilta_t3.inp"))
```

Analysis of 2 applied data examples

LTA model varients:

a. regular LTA
b. continuous random intercept
c. binary random intercept

Additionally, the LTA variants above are incorporated with the following modeling extensions:

- mover-stayer model component (i.e., a higher-order latent class variable)
- cross-group invariance (i.e., analogous to a MIMIC model or a grouping covariate)
- additional covariates and/or outcomes

Choice of model is based on the `BIC`:

$$BIC = -2 * LogLikelihood + p * ln(N)$$

- P = number of parameters
- N = Sample size

Mood data example (Eid & Langeheine, 2003)

- Sample size (N) = 494
- Time points = 4 (3-weeks apart)
- Mixture model (LCA)
  - 2 binary indicators (Ui)
  - 2 latent classes ($C_{k=2}$)
- Indicators - participants rated momentary sadness and unhappiness
  - Likert ranging from 1 (not at all) to 5 (very much) recoded to binary:
    - Category 1 = "not at all"
    - Category 2 = all other categories
- Assumptions:
  1. Stationarity invariance (across 3 transition matrices; following models in Eid & Langeheine, 2003)
  2. Longitudinal invariance (across the 4 time point latent variables)

Models considered for the mood example:

- Models 1-3 standard analyses
- Models 4-6 Mover-Stayer analysis (mover-stayer factor has $k = 2$)

Table 5: Model fitting results for the Mood data

Model	# parameters	loglikelihood	BIC
Standard			
1 Regular LTA	7	-2053	4150
2 RI-LTA, binary RI[1]	10	-2028	4118
3 RI-LTA, continuous RI	9	-2019	4093
Mover-Stayer			
4 Regular LTA	8	-2037	4123
5 RI-LTA, binary RI[2]	11	-2017	4101
6 RI-LTA, continuous RI	10	-2017	4096

[1] Model 2 is model 2 in Table 1 of Eid and Langeheine (2003).
[2] Model 5 is model 5 in Table 1 of Eid and Langeheine (2003).

Figure 7: Picture adapted from Muthén & Asparouhov (2020).

Comparison of LTA modeling approaches to mood data

Mood Model 1 - Regular LTA

Read in the `Mood` data file

```
mood_data <-  read_csv(here("data", "eid-langeheine-mood.csv"), col_names = FALSE)

colnames(mood_data) <-  c("u11", "u12", "u21", "u22", "u31", "u32", "u41", "u42", "freq", "est", "sd")
```

```
m1_mood  <- mplusObject(

  TITLE =
     "Eid 2003 data: T=4, N=494, P=2, C=2
      Regular LTA, stationary",

  VARIABLE =
     "usev = u11-u42;
      freqweight = freq;
      categorical = u11-u42;
      classes = c1(2) c2(2) c3(2) c4(2);",

  ANALYSIS =
     "type = mixture;
      proc = 8;
      starts = 400 100;",

  MODEL =
     "%OVERALL%
      [c2#1 - c4#1] (p0);

        c4#1 on c3#1 (pt);
      c3#1 on c2#1 (pt);
        c2#1 on c1#1 (pt);

    ! csharp by;
    ! csharp by c1#1@1 c2#1@1 c3#1@1;
    ! csharp*0.5; [csharp@0]; csharp with f@0;
    ! csharp on w*1;

    MODEL c1:
        %c1#1%
        [u11$1] (1);   [u12$1] (2);
        %c1#2%
        [u11$1] (11);  [u12$1] (12);

    MODEL c2:
        %c2#1%
        [u21$1] (1);  [u22$1] (2);
        %c2#2%
```

```
        [u21$1] (11); [u22$1] (12);

    MODEL c3:
        %c3#1%
        [u31$1] (1);  [u32$1] (2);
        %c3#2%
        [u31$1] (11); [u32$1] (12);

    MODEL c4:
        %c4#1%
        [u41$1] (1);  [u42$1] (2);
        %c4#2%
        [u41$1] (11); [u42$1] (12); ",

  OUTPUT = "tech1 tech15;",

  usevariables = colnames(mood_data),
  rdata = mood_data)

m1_mood.fit <- mplusModeler(m1_mood,
                            modelout=here("mood_mplus", "m1_mood.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Mood Model 2 - RI-LTA, binary RI

NOTE: use of `update()`, selected syntax is used from base model `m1_mood`

```
m2_mood  <- update(m1_mood,

  TITLE = ~
     "Eid 2003 data: T=4, N=494, P=2, C=2
      Model 2",

  VARIABLE = ~
     "usev = u11-u42;
      categorical = u11-u42;
      classes = t(2) c1(2) c2(2) c3(2) c4(2);
      freqweight = freq;",

  MODEL = ~
 "%OVERALL%
      ! stationary markov

      [c2#1-c4#1] (p0);

      c4 on c3 (pt);
      c3 on c2 (pt);
      c2 on c1 (pt);
```

```
MODEL t.c1:
! (item,t class, c class): 8 tau's total
    %t#1.c1#1%
    [u11$1] (p111); [u12$1] (p211);
    %t#1.c1#2%
    [u11$1] (p112); [u12$1] (p212);
    %t#2.c1#1%
    [u11$1] (p121); [u12$1] (p221);
    %t#2.c1#2%
    [u11$1] (p122); [u12$1] (p222);

MODEL t.c2:
    %t#1.c2#1%
    [u21$1] (p111); [u22$1] (p211);
    %t#1.c2#2%
    [u21$1] (p112); [u22$1] (p212);
    %t#2.c2#1%
    [u21$1] (p121); [u22$1] (p221);
    %t#2.c2#2%
    [u21$1] (p122); [u22$1] (p222);

 MODEL t.c3:
    %t#1.c3#1%
    [u31$1] (p111); [u32$1] (p211);
    %t#1.c3#2%
    [u31$1] (p112); [u32$1] (p212);
    %t#2.c3#1%
    [u31$1] (p121); [u32$1] (p221);
    %t#2.c3#2%
    [u31$1] (p122); [u32$1] (p222);

MODEL t.c4:
    %t#1.c4#1%
    [u41$1] (p111); [u42$1] (p211);
    %t#1.c4#2%
    [u41$1] (p112); [u42$1] (p212);
    %t#2.c4#1%
    [u41$1] (p121); [u42$1] (p221);
    %t#2.c4#2%
    [u41$1] (p122); [u42$1] (p222); ",

MODELCONSTRAINT = ~
   "! each item has intercept, loading on trait, loading on occasion
    ! so no trait-occasion interaction
        New(i1 i2 lt1 lt2 lo1 lo2);
        p111 = i1;
        p112 = i1 + lo1;
        p121 = i1 + lt1;
        p122 = i1 + lo1 + lt1;
        p211 = i2;
        p212 = i2 + lo2;
        p221 = i2 + lt2;
        p222 = i2 + lo2 + lt2;")
```

```
m2_mood.fit <- mplusModeler(m2_mood,
                            dataout =here("mood_mplus", "m1_mood.dat"),
                            modelout=here("mood_mplus", "m2_mood.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Mood Model 3 - RI-LTA, Continuous RI

NOTE: use of `update()`, selected syntax is used from base model `m1_mood`

```
m3_mood  <- update(m1_mood,

  TITLE = ~
     "Eid 2003 data: T=4, N=494, P=2, C=2
      Model 3 - RI Continuous",

  ANALYSIS = ~ .+
     "algorithm = integration;
      integration = 30;",

  MODEL = ~
     "%OVERALL%

    ! Stationarity imposed:
     [c2#1 - c4#1] (p0);

     c4#1 on c3#1 (pt);
     c3#1 on c2#1 (pt);
     c2#1 on c1#1 (pt);

     f by u11-u12* (p1-p2)
          u21-u22* (p1-p2)
          u31-u32* (p1-p2)
          u41-u42* (p1-p2);
     f@1; [f@0];

     MODEL c1:
         %c1#1%
         [u11$1] (1);   [u12$1] (2);
         %c1#2%
         [u11$1] (11);  [u12$1] (12);

     MODEL c2:
         %c2#1%
         [u21$1] (1);  [u22$1] (2);
         %c2#2%
         [u21$1] (11); [u22$1] (12);
```

```
    MODEL c3:
        %c3#1%
        [u31$1] (1);  [u32$1] (2);
        %c3#2%
        [u31$1] (11); [u32$1] (12);

    MODEL c4:
        %c4#1%
        [u41$1] (1);  [u42$1] (2);
        %c4#2%
        [u41$1] (11); [u42$1] (12); ",

   OUTPUT = ~.+ "tech8;",

  usevariables = colnames(mood_data),
  rdata = mood_data)

m3_mood.fit <- mplusModeler(m3_mood,
                            dataout =here("mood_mplus", "m1_mood.dat"),
                            modelout=here("mood_mplus", "m3_mood.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Mood Model 4 - Regular LTA - Mover-Stayer

```
m4_mood  <- mplusObject(

  TITLE =
     "Eid 2003 data: T=4, N=494, P=2, C=2
      Model 4 - Regular LTA, Mover-Stayer",

  VARIABLE =
     "usev = u11-u42;
      categorical = u11-u42;
      classes = cb(2) c1(2) c2(2) c3(2) c4(2);
      freqweight = freq;",

  ANALYSIS =
     "type = mixture;
      proc = 8;
      starts = 80 16;
      parameterization = probability;",

  MODEL =
     "%OVERALL%

    MODEL cb:
      %cb#1% ! Stationary movers
      c4 on c3 (pt1-pt2);
```

```
      c3 on c2 (pt1-pt2);
      c2 on c1 (pt1-pt2);

      %cb#2% ! Stayers
      c2#1 on c1#1@1; c2#1 on c1#2@0;
      c3#1 on c2#1@1; c3#1 on c2#2@0;
      c4#1 on c3#1@1; c4#1 on c3#2@0;

    MODEL c1:
        %c1#1%
        [u11$1] (1);   [u12$1] (2);
        %c1#2%
        [u11$1] (11);  [u12$1] (12);

    MODEL c2:
        %c2#1%
        [u21$1] (1);  [u22$1] (2);
        %c2#2%
        [u21$1] (11); [u22$1] (12);

    MODEL c3:
        %c3#1%
        [u31$1] (1);  [u32$1] (2);
        %c3#2%
        [u31$1] (11); [u32$1] (12);

    MODEL c4:
        %c4#1%
        [u41$1] (1);  [u42$1] (2);
        %c4#2%
        [u41$1] (11); [u42$1] (12); ",

  OUTPUT = "tech1 tech10 tech15;",

  usevariables = colnames(mood_data),
  rdata = mood_data)

m4_mood.fit <- mplusModeler(m4_mood,
                            dataout =here("mood_mplus", "m1_mood.dat"),
                            modelout=here("mood_mplus", "m4_mood.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Mood Model 5 - RI-LTA, binary RI, Mover-Stayer

```
m5_mood  <- mplusObject(

  TITLE =
     "Eid 2003 data: T=4, N=494, P=2, C=2
```

```
    Model 5 - RI-LTA, binary RI, Mover-Stayer",

VARIABLE =
   "usev = u11-u42;
    categorical = u11-u42;
    classes = t(2) cb(2) c1(2) c2(2) c3(2) c4(2);
    freqweight = freq;",

ANALYSIS =
   "type = mixture;
    proc = 8;
    starts = 320 80;
    parameterization = probability;",

MODEL =
   "%OVERALL%

  MODEL cb:
      %cb#1% ! Stationary movers
      c4 on c3 (pt1-pt2);
      c3 on c2 (pt1-pt2);
      c2 on c1 (pt1-pt2);

      %cb#2% ! Stayers
      c2#1 on c1#1@1; c2#1 on c1#2@0;
      c3#1 on c2#1@1; c3#1 on c2#2@0;
      c4#1 on c3#1@1; c4#1 on c3#2@0;

MODEL t.c1:
    %t#1.c1#1%
    [u11$1] (p111); [u12$1] (p211);
    %t#1.c1#2%
    [u11$1] (p112); [u12$1] (p212);
    %t#2.c1#1%
    [u11$1] (p121); [u12$1] (p221);
    %t#2.c1#2%
    [u11$1] (p122); [u12$1] (p222);

MODEL t.c2:
    %t#1.c2#1%
    [u21$1] (p111); [u22$1] (p211);
    %t#1.c2#2%
    [u21$1] (p112); [u22$1] (p212);
    %t#2.c2#1%
    [u21$1] (p121); [u22$1] (p221);
    %t#2.c2#2%
    [u21$1] (p122); [u22$1] (p222);

 MODEL t.c3:
    %t#1.c3#1%
    [u31$1] (p111); [u32$1] (p211);
    %t#1.c3#2%
    [u31$1] (p112); [u32$1] (p212);
```

```
      %t#2.c3#1%
      [u31$1] (p121); [u32$1] (p221);
      %t#2.c3#2%
      [u31$1] (p122); [u32$1] (p222);

  MODEL t.c4:
      %t#1.c4#1%
      [u41$1] (p111); [u42$1] (p211);
      %t#1.c4#2%
      [u41$1] (p112); [u42$1] (p212);
      %t#2.c4#1%
      [u41$1] (p121); [u42$1] (p221);
      %t#2.c4#2%
      [u41$1] (p122); [u42$1] (p222); ",

  MODELCONSTRAINT =
     "! each item has intercept, loading on trait, loading on occasion
      ! so no trait-occasion interaction
          New(i1 i2 lt1 lt2 lo1 lo2);
          p111 = i1;
          p112 = i1 + lo1;
          p121 = i1 + lt1;
          p122 = i1 + lo1 + lt1;
          p211 = i2;
          p212 = i2 + lo2;
          p221 = i2 + lt2;
          p222 = i2 + lo2 + lt2;",

  OUTPUT = "tech1 tech10 tech15;",

  usevariables = colnames(mood_data),
  rdata = mood_data)

m5_mood.fit <- mplusModeler(m5_mood,
                            dataout =here("mood_mplus", "m1_mood.dat"),
                            modelout=here("mood_mplus", "m5_mood.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Mood Model 6 - RI-LTA - Continuous RI, Mover-Stayer

```
m6_mood  <- mplusObject(

  TITLE =
     "Eid 2003 data: T=4, N=494, P=2, C=2
      Model 6 - RI-LTA, Continuous RI, Mover-Stayer",

  VARIABLE =
     "usev = u11-u42;
```

```
    categorical = u11-u42;
    classes = cb(2) c1(2) c2(2) c3(2) c4(2);
    freqweight = freq;",

ANALYSIS =
   "type = mixture;
    algorithm = integration;
    integration = 30;
    proc = 8;
    starts = 320 80;
    parameterization = probability;",

MODEL =
   "%OVERALL%

    f by u11-u12* (p1-p2)
         u21-u22* (p1-p2)
         u31-u32* (p1-p2)
         u41-u42* (p1-p2);
      f@1; [f@0];

  MODEL cb:
      %cb#1% ! Stationary movers
      c4 on c3 (pt1-pt2);
      c3 on c2 (pt1-pt2);
      c2 on c1 (pt1-pt2);

      %cb#2% ! Stayers
      c2#1 on c1#1@1; c2#1 on c1#2@0;
      c3#1 on c2#1@1; c3#1 on c2#2@0;
      c4#1 on c3#1@1; c4#1 on c3#2@0;

  MODEL c1:
      %c1#1%
      [u11$1] (1);   [u12$1] (2);
      %c1#2%
      [u11$1] (11);  [u12$1] (12);

  MODEL c2:
      %c2#1%
      [u21$1] (1);  [u22$1] (2);
      %c2#2%
      [u21$1] (11); [u22$1] (12);

  MODEL c3:
      %c3#1%
      [u31$1] (1);  [u32$1] (2);
      %c3#2%
      [u31$1] (11); [u32$1] (12);

  MODEL c4:
      %c4#1%
      [u41$1] (1);  [u42$1] (2);
```

```
        %c4#2%
        [u41$1] (11); [u42$1] (12); ",


  OUTPUT = "tech1;",

  usevariables = colnames(mood_data),
  rdata = mood_data)

m6_mood.fit <- mplusModeler(m6_mood,
                            dataout =here("mood_mplus", "m1_mood.dat"),
                            modelout=here("mood_mplus", "m6_mood.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating data example (section 6.2; Lanza & Collins, 2008)

- National Longitudinal Survey of Youth (NLSY97)
- Sample size (N) = 2,937
- Time points = 3 (1 year apart)

Mixture model (LCA) - 4 ordinal and binary indicators (Ui) - 5 latent classes ($C_{k=5}$)

Indicators: - Past-year number of dating partners (0,1,2,more) - year 98 = u11, year 99 = u21, year 00 = u31 - Past-year sex (no, yes) - year 98 = u12, year 99 = u22, year 00 = u32 - Past-year number of sexual partners (0,1,2,more) - year 98 = u13, year 99 = u23, year 00 = u33 - Past-year STD (no, yes) - year 98 = u14, year 99 = u24, year 00 = u34

Latent class labels (Lanza & Collins model):

1. Nondaters
2. Daters
3. Monogomous
4. Multipartner safe
5. Multipartner exposed

Assumptions: (following models in Eid & Langeheine, 2003)

Applied to dating models 1 - 15

1. Longitudinal invariance (across the 3 time point latent variables)
2. Stationarity invariance (across the 2 transition matrices)

Models considered for the dating example:

- Models 1-3: Standard analyses (Regular, Binary RI, Continuous RI)

- Models 4-6: Mover-Stayer analysis (Regular, Binary RI, Continuous RI)
- Models 7-10: Group-invariance MIMIC (grouping variable is male-female)
- Models 11-15: Adding 4 covariates and their interactions ***

Table 7: Model fitting results for the Dating data

Model	# parameters	loglikelihood	BIC
Standard			
1 Regular LTA	49	-16202	32796
2 RI-LTA, binary RI	53	-16056	32535
3 RI-LTA, continuous RI	52	-16043	32502
Mover-Stayer			
4 Regular LTA	50	-16194	32787
5 RI-LTA, binary RI	54	-16053	32536
6 RI-LTA, continuous RI	53	-16041	32506

Figure 8: Picture adapted from Muthén & Asparouhov (2020).

Read in the `Dating` datafile

```
date_data <-  read_csv(here("data", "LanzaCollinsLTA.csv"), col_names = FALSE) %>%
  select(1:25) # select variables used in analysis

colnames(date_data) <-  c(
    "id", "gender", "male", "dates_98","dates_99","dates_00","par_98",
    "par_99","par_00","u11", "u21", "u31", "age_fd", "u12", "u22", "u32",
    "u13", "u23","u33","u14","u24","u34","safe_98","safe_99","safe_00")
```

Comparison of LTA modeling approaches to the dating data example

Dating Model 1 - Regular LTA

```
m1_date <- mplusObject(

  TITLE =
    "Dating Model 1 - Regular LTA - Invariance
     Lanza-Collins 2008 Developmental Psychology",

  VARIABLE =
     "usev = u11 u13 u14
                 u21 u23 u24
```

```
                u31 u33 u34;

    categorical = u11-u34;
    missing = all(999);
    classes = c1(5) c2(5) c3(5);",

ANALYSIS =
   "type = mixture;
    processors = 8;
    starts = 160 40;",

MODEL =
"%Overall%

    [c2#1 c3#1] (int1);
    [c2#2 c3#2] (int2);
    [c2#3 c3#3] (int3);
    [c2#4 c3#4] (int4);

    c2 on c1 (trans1-trans16); !!! Stationary transition assumption !!!
    c3 on c2 (trans1-trans16);

Model c1:
  %c1#1%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
  %c1#2%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
  %c1#3%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
  %c1#4%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
  %c1#5%
  [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

Model c2:
  %c2#1%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
  %c2#2%
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
  %c2#3%
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
  %c2#4%
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
  %c2#5%
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

Model c3:
  %c3#1%
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
  %c3#2%
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
  %c3#3%
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
```

```
    %c3#4%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);",

  OUTPUT = "tech1 tech15 svalues;",

  usevariables = colnames(date_data),
  rdata = date_data)

m1_date.fit <- mplusModeler(m1_date,
                            modelout=here("date_mplus", "m1_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 2 - RI-LTA, binary RI

```
m2_date <- mplusObject(

  TITLE =
    "Lanza-Collins 2008 Developmental Psychology
     Dating Model 2 - N=2937, T=3, P=4, C=5",

  VARIABLE =
     "usev = u11 u13 u14
                 u21 u23 u24
                 u31 u33 u34;

      categorical = u11-u34;
      missing = all(999);
      classes = t(2) c1(5) c2(5) c3(5);",

  ANALYSIS =
     "type = mixture;
      processors = 8;
      starts = 320 80;",

  MODEL =
 "%Overall%

      [c2#1 c3#1] (int1);
      [c2#2 c3#2] (int2);
      [c2#3 c3#3] (int3);
      [c2#4 c3#4] (int4);

      c2 on c1 (trans1-trans16); !!! Stationary transition assumption !!!
      c3 on c2 (trans1-trans16);

  Model t.c1:
    %t#1.c1#1%
```

```
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p111-p115);
    %t#1.c1#2%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p121-p125);
    %t#1.c1#3%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p131-p135);
    %t#1.c1#4%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p141-p145);
    %t#1.c1#5%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p151-p155);

    %t#2.c1#1%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p211-p215);
    %t#2.c1#2%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p221-p225);
    %t#2.c1#3%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p231-p235);
    %t#2.c1#4%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p241-p245);
    %t#2.c1#5%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p251-p255);

  Model t.c2:
    %t#1.c2#1%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p111-p115);
    %t#1.c2#2%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p121-p125);
    %t#1.c2#3%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p131-p135);
    %t#1.c2#4%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p141-p145);
    %t#1.c2#5%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p151-p155);

    %t#2.c2#1%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p211-p215);
    %t#2.c2#2%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p221-p225);
    %t#2.c2#3%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p231-p235);
    %t#2.c2#4%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p241-p245);
    %t#2.c2#5%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p251-p255);

  Model t.c3:
    %t#1.c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p111-p115);
    %t#1.c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p121-p125);
    %t#1.c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p131-p135);
    %t#1.c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p141-p145);
```

```
    %t#1.c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p151-p155);

    %t#2.c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p211-p215);
    %t#2.c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p221-p225);
    %t#2.c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p231-p235);
    %t#2.c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p241-p245);
    %t#2.c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p251-p255);",

   MODELCONSTRAINT =
     "new(a1-a3 b12-b15 b22-b25 b32-b35
      t1-t3 tau11 tau21 tau12 tau22 tau13
      tau23 tau14 tau24 tau15 tau25);
! t class 1:
      p111 = a1;                      ! c-class 1:
      p112 = a1+exp(tau11);           ! 2nd tau for 3-cat item
      p113 = a2;
      p114 = a2+exp(tau21);           ! 2nd tau for 3-cat item
      p115 = a3;
      p121 = a1+b12;                  ! c-class 2:
      p122 = a1+exp(tau12)+b12;
      p123 = a2+b22;
      p124 = a2+exp(tau22)+b22;
      p125 = a3+b32;
      p131 = a1+b13;                  ! c-class 3:
      p132 = a1+exp(tau13)+b13;
      p133 = a2+b23;
      p134 = a2+exp(tau23)+b23;
      p135 = a3+b33;
      p141 = a1+b14;                  ! c-class 4:
      p142 = a1+exp(tau14)+b14;
      p143 = a2+b24;
      p144 = a2+exp(tau24)+b24;
      p145 = a3+b34;
      p151 = a1+b15;                  ! c-class 5:
      p152 = a1+exp(tau15)+b15;
      p153 = a2+b25;
      p154 = a2+exp(tau25)+b25;
      p155 = a3+b35;
! t class 2:
      p211 = a1+t1;                   ! c-class 1:
      p212 = a1+exp(tau11)+t1;        ! 2nd tau for 3-cat item
      p213 = a2+t2;
      p214 = a2+exp(tau21)+t2;        ! 2nd tau for 3-cat item
      p215 = a3+t3;
      p221 = a1+b12+t1;               ! c-class 2:
      p222 = a1+exp(tau12)+b12+t1;
      p223 = a2+b22+t2;
```

```
      p224 = a2+exp(tau22)+b22+t2;
      p225 = a3+b32+t3;
      p231 = a1+b13+t1;               ! c-class 3:
      p232 = a1+exp(tau13)+b13+t1;
      p233 = a2+b23+t2;
      p234 = a2+exp(tau23)+b23+t2;
      p235 = a3+b33+t3;
      p241 = a1+b14+t1;               ! c-class 4:
      p242 = a1+exp(tau14)+b14+t1;
      p243 = a2+b24+t2;
      p244 = a2+exp(tau24)+b24+t2;
      p245 = a3+b34+t3;
      p251 = a1+b15+t1;               ! c-class 5:
      p252 = a1+exp(tau15)+b15+t1;
      p253 = a2+b25+t2;
      p254 = a2+exp(tau25)+b25+t2;
      p255 = a3+b35+t3;",

  OUTPUT = "tech1;",

  usevariables = colnames(date_data),
  rdata = date_data)

m2_date.fit <- mplusModeler(m2_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m2_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 3 - RI-LTA, continuous RI

NOTE: use of `update()`, selected syntax is used from base model `m1_date`

```
m3_date <- update(m1_date,

    TITLE = ~
    "Dating Model 3 - Continuous RI-LTA - invariance
     Lanza-Collins 2008 Developmental Psychology",

    ANALYSIS = ~.+
      "algorithm = integration;",

    MODEL = ~
      "%Overall%
      [c2#1 c3#1] (int1);
      [c2#2 c3#2] (int2);
      [c2#3 c3#3] (int3);
      [c2#4 c3#4] (int4);

      c2 on c1 (trans1-trans16);  !!! Stationary transition assumption !!!
      c3 on c2 (trans1-trans16);

      f by u11-u14* (lam1-lam3)
```

```
      u21-u24* (lam1-lam3)
      u31-u34* (lam1-lam3);
      f@1; [f@0];

  Model c1:
    %c1#1%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

  Model c2:
    %c2#1%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
    %c2#2%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);",

    MODELCONSTRAINT = ~ "",

    OUTPUT = ~
      "tech1 tech15 svalues;")

m3_date.fit <- mplusModeler(m3_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m3_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 4 - Regular LTA, Mover-Stayer

```
m4_date <- mplusObject(

    TITLE =
    " Dating Model 4 - Lanza-Collins 2008 Developmental Psychology
     Continuous RI-LTA",

    VARIABLE =
      "usev = u11 u13 u14
              u21 u23 u24
              u31 u33 u34;

       categorical = u11-u34;
       missing = all(999);
       classes = cb(2) c1(5) c2(5) c3(5);",

    ANALYSIS =
      "type = mixture;
       starts =  100 20;
       processors = 8;
       parameterization = probability;",

    MODEL =
  "%Overall%

  Model cb:

  %cb#1%
      c2 on c1 (pt1-pt20);  !!! Stationary transition assumption !!!
      c3 on c2 (pt1-pt20);

  %cb#2% !!! Stayer class.  Going row by row: !!!
      c2#1 on c1#1@1; c2#2 on c1#1@0; c2#3 on c1#1@0; c2#4 on c1#1@0;
      c2#1 on c1#2@0; c2#2 on c1#2@1; c2#3 on c1#2@0; c2#4 on c1#2@0;
      c2#1 on c1#3@0; c2#2 on c1#3@0; c2#3 on c1#3@1; c2#4 on c1#3@0;
      c2#1 on c1#4@0; c2#2 on c1#4@0; c2#3 on c1#4@0; c2#4 on c1#4@1;
      c2#1 on c1#5@0; c2#2 on c1#5@0; c2#3 on c1#5@0; c2#4 on c1#5@0;

      c3#1 on c2#1@1; c3#2 on c2#1@0; c3#3 on c2#1@0; c3#4 on c2#1@0;
      c3#1 on c2#2@0; c3#2 on c2#2@1; c3#3 on c2#2@0; c3#4 on c2#2@0;
      c3#1 on c2#3@0; c3#2 on c2#3@0; c3#3 on c2#3@1; c3#4 on c2#3@0;
      c3#1 on c2#4@0; c3#2 on c2#4@0; c3#3 on c2#4@0; c3#4 on c2#4@1;
      c3#1 on c2#5@0; c3#2 on c2#5@0; c3#3 on c2#5@0; c3#4 on c2#5@0;

  Model c1:
    %c1#1%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
```

```
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

  Model c2:
    %c2#1%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
    %c2#2%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);",

    OUTPUT = "tech1;",

    usevariables = colnames(date_data),
    rdata = date_data)

m4_date.fit <- mplusModeler(m4_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m4_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 5 - RI-LTA, binary RI, Mover-Stayer

NOTE: use of `update()`, selected syntax is used from base model `m2_date`

```
m5_date <- update(m2_date,

  TITLE = ~
    "Lanza-Collins 2008 Developmental Psychology
     Dating Model 5a - RI-LTA, binary RI, Mover-Stayer",

  VARIABLE = ~
     "usev = u11 u13 u14
                 u21 u23 u24
                 u31 u33 u34;
```

```
    categorical = u11-u34;
    missing = all(999);
    classes = t(2) cb(2) c1(5) c2(5) c3(5);",

ANALYSIS = ~.+
   "parameterization = probability;",

MODEL = ~
"%Overall%

Model cb:

%cb#1%
    c2 on c1 (pt1-pt20);  !!! Stationary transition assumption !!!
    c3 on c2 (pt1-pt20);

%cb#2% !!! Stayer class !!!
    c2#1 on c1#1@1; c2#2 on c1#1@0; c2#3 on c1#1@0; c2#4 on c1#1@0;
    c2#1 on c1#2@0; c2#2 on c1#2@1; c2#3 on c1#2@0; c2#4 on c1#2@0;
    c2#1 on c1#3@0; c2#2 on c1#3@0; c2#3 on c1#3@1; c2#4 on c1#3@0;
    c2#1 on c1#4@0; c2#2 on c1#4@0; c2#3 on c1#4@0; c2#4 on c1#4@1;
    c2#1 on c1#5@0; c2#2 on c1#5@0; c2#3 on c1#5@0; c2#4 on c1#5@0;

    c3#1 on c2#1@1; c3#2 on c2#1@0; c3#3 on c2#1@0; c3#4 on c2#1@0;
    c3#1 on c2#2@0; c3#2 on c2#2@1; c3#3 on c2#2@0; c3#4 on c2#2@0;
    c3#1 on c2#3@0; c3#2 on c2#3@0; c3#3 on c2#3@1; c3#4 on c2#3@0;
    c3#1 on c2#4@0; c3#2 on c2#4@0; c3#3 on c2#4@0; c3#4 on c2#4@1;
    c3#1 on c2#5@0; c3#2 on c2#5@0; c3#3 on c2#5@0; c3#4 on c2#5@0;

Model t.c1:
  %t#1.c1#1%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p111-p115);
  %t#1.c1#2%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p121-p125);
  %t#1.c1#3%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p131-p135);
  %t#1.c1#4%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p141-p145);
  %t#1.c1#5%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p151-p155);

  %t#2.c1#1%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p211-p215);
  %t#2.c1#2%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p221-p225);
  %t#2.c1#3%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p231-p235);
  %t#2.c1#4%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p241-p245);
  %t#2.c1#5%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p251-p255);

Model t.c2:
```

```
    %t#1.c2#1%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p111-p115);
    %t#1.c2#2%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p121-p125);
    %t#1.c2#3%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p131-p135);
    %t#1.c2#4%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p141-p145);
    %t#1.c2#5%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p151-p155);

    %t#2.c2#1%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p211-p215);
    %t#2.c2#2%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p221-p225);
    %t#2.c2#3%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p231-p235);
    %t#2.c2#4%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p241-p245);
    %t#2.c2#5%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p251-p255);

  Model t.c3:
    %t#1.c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p111-p115);
    %t#1.c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p121-p125);
    %t#1.c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p131-p135);
    %t#1.c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p141-p145);
    %t#1.c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p151-p155);

    %t#2.c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p211-p215);
    %t#2.c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p221-p225);
    %t#2.c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p231-p235);
    %t#2.c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p241-p245);
    %t#2.c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p251-p255);" )

m5_date.fit <- mplusModeler(m5_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m5_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 6 - RI-LTA, continuous RI, Mover-Stayer

```
m6_date <-  mplusObject(

  TITLE =
    "Dating Model 6a - RI-LTA, continuous RI, Mover-Stayer
     Lanza-Collins 2008 Developmental Psychology",

  VARIABLE =
     "usev = u11 u13 u14
                 u21 u23 u24
                 u31 u33 u34;

      categorical = u11-u34;
      missing = all(999);
      classes = cb(2) c1(5) c2(5) c3(5);",

  ANALYSIS =
    "type = mixture;
     starts =  100 20;
     processors = 8;
     parameterization = probability;
     algorithm = integration;",

  MODEL =
   "%Overall%

    f by u11-u14* (lam1-lam3)
    u21-u24* (lam1-lam3)
    u31-u34* (lam1-lam3);
    f@1; [f@0];

  Model cb:

  %cb#1% !!! Stationary transition assumption !!!
      c2 on c1 (pt1-pt20);
      c3 on c2 (pt1-pt20);

  %cb#2% !!! Stayer class.  Going row by row: !!!
      c2#1 on c1#1@1; c2#2 on c1#1@0; c2#3 on c1#1@0; c2#4 on c1#1@0;
      c2#1 on c1#2@0; c2#2 on c1#2@1; c2#3 on c1#2@0; c2#4 on c1#2@0;
      c2#1 on c1#3@0; c2#2 on c1#3@0; c2#3 on c1#3@1; c2#4 on c1#3@0;
      c2#1 on c1#4@0; c2#2 on c1#4@0; c2#3 on c1#4@0; c2#4 on c1#4@1;
      c2#1 on c1#5@0; c2#2 on c1#5@0; c2#3 on c1#5@0; c2#4 on c1#5@0;

      c3#1 on c2#1@1; c3#2 on c2#1@0; c3#3 on c2#1@0; c3#4 on c2#1@0;
      c3#1 on c2#2@0; c3#2 on c2#2@1; c3#3 on c2#2@0; c3#4 on c2#2@0;
      c3#1 on c2#3@0; c3#2 on c2#3@0; c3#3 on c2#3@1; c3#4 on c2#3@0;
      c3#1 on c2#4@0; c3#2 on c2#4@0; c3#3 on c2#4@0; c3#4 on c2#4@1;
      c3#1 on c2#5@0; c3#2 on c2#5@0; c3#3 on c2#5@0; c3#4 on c2#5@0;

  Model c1:
    %c1#1%
```

```
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

  Model c2:
    %c2#1%
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
    %c2#2%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);",

    usevariables = colnames(date_data),
    rdata = date_data)

m6_date.fit <- mplusModeler(m6_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m6_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Example - Cross-group Invariance (MIMIC)

Comparing **Regular LTA** to **RI-LTA**

Dating Model 7, Regular LTA, non-invariance

```
m7_date <- mplusObject(

    TITLE =
    "Dating Model 7, Regular LTA,  non-invariance
     Lanza-Collins 2008 Developmental Psychology",

    VARIABLE =
      "usev = u11 u13 u14
                u21 u23 u24
                u31 u33 u34
                male;        !!! grouping covariate !!!

    categorical = u11-u34;
    missing = all(999);

    classes = c1(5) c2(5) c3(5);",

    ANALYSIS =
    "type = mixture;
     starts =  320 80;
     processors = 8;",

    MODEL =
      "%Overall%
       c1 on male;

      c2#1 on male (int1); c3#1 on male (int1);
      c2#2 on male (int2); c3#2 on male (int2);
      c2#3 on male (int3); c3#3 on male (int3);
      c2#4 on male (int4); c3#4 on male (int4);

        c2 on c1 (trans1-trans16);
        c3 on c2 (trans1-trans16);

      u11-u34 on male@0;

  Model c1:
    %c1#1%!
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

  Model c2:
    %c2#1%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p11-p15);
```

```
    %c2#2%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p51-p55);",

    OUTPUT =  "",

    usevariables = colnames(date_data),
    rdata = date_data)


m7_date.fit <- mplusModeler(m7_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m7_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 8, Regular LTA, invariance

NOTE: use of `update()`, selected syntax is used from base model `m7_date`

```
m8_date <- update(m7_date,

    TITLE = ~
    "Dating Model 8, Regular LTA, invariance
     Lanza-Collins 2008 Developmental Psychology",

    ANALYSIS = ~
    "type = mixture;
     starts =  160 40;
     processors = 8;",

    MODEL = ~
      "%Overall%
       c1 on male;
```

```
    c2#1 on male (int1); c3#1 on male (int1);
    c2#2 on male (int2); c3#2 on male (int2);
    c2#3 on male (int3); c3#3 on male (int3);
    c2#4 on male (int4); c3#4 on male (int4);

      c2 on c1 (trans1-trans16);
      c3 on c2 (trans1-trans16);

    u11-u34 on male@0;

Model c1:
  %c1#1%!
    u11-u14 on male (d11-d13);   !!! cross-group invariance equality constraints !!!
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
  %c1#2%
    u11-u14 on male (d21-d23);
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
  %c1#3%
    u11-u14 on male (d31-d33);
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
  %c1#4%
    u11-u14 on male (d41-d43);
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
  %c1#5%
    u11-u14 on male (d51-d53);
  [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

Model c2:
  %c2#1%
    u21-u24 on male (d11-d13);   !!! cross-group invariance equality constraints !!!
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
  %c2#2%
    u21-u24 on male (d21-d23);
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
  %c2#3%
    u21-u24 on male (d31-d33);
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
  %c2#4%
    u21-u24 on male (d41-d43);
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
  %c2#5%
    u21-u24 on male (d51-d53);
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

Model c3:
  %c3#1%
    u31-u34 on male (d11-d13);   !!! cross-group invariance equality constraints !!!
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
  %c3#2%
    u31-u34 on male (d21-d23);
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
  %c3#3%
    u31-u34 on male (d31-d33);
```

```
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
      u31-u34 on male (d41-d43);
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
      u31-u34 on male (d51-d53);
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);")

m8_date.fit <- mplusModeler(m8_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m8_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 9, RI-LTA, non-invariance

NOTE: use of `update()`, selected syntax is used from base model `m7_date`

```
m9_date <- update(m7_date,

    TITLE = ~
    "Dating Model 9, Regular LTA, non-invariance
     Lanza-Collins 2008 Developmental Psychology",

        ANALYSIS = ~
       "algorithm = integration;
        stscale = 1;",

    MODEL = ~
      "%Overall%
       c1 on male;

      c2#1 on male (int1); c3#1 on male (int1);
      c2#2 on male (int2); c3#2 on male (int2);
      c2#3 on male (int3); c3#3 on male (int3);
      c2#4 on male (int4); c3#4 on male (int4);

      c2 on c1 (trans1-trans16);
      c3 on c2 (trans1-trans16);

      f by u11-u14* (lam1-lam3)  !!! continuous random intercept !!!
      u21-u24* (lam1-lam3)
      u31-u34* (lam1-lam3);
      f@1; [f@0];

      u11-u34 on male@0;

  Model c1:
    %c1#1%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
```

```
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
    [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

  Model c2:
    %c2#1%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p11-p15);
    %c2#2%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p51-p55);",

    OUTPUT = ~ "tech15;")

m9_date.fit <- mplusModeler(m9_date,
                            dataout=here("date_mplus", "date.dat"),
                            modelout=here("date_mplus", "m9_date.inp"),
                            check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 10, RI-LTA, invariance

NOTE: use of `update()`, selected syntax is used from base model `m9_date`

```
m10_date <- update(m9_date,

    TITLE = ~
    "Dating Model 10, Regular LTA, invariance
     Lanza-Collins 2008 Developmental Psychology",

    ANALYSIS = ~
```

```
  "type = mixture;
   starts =  400 100; !!! estimation time ~ > 30 minutes !!!
   proc = 8;
   algorithm = integration;
   integration = 30;",

  MODEL = ~
    "%Overall%
     c1 on male;

    c2#1 on male (int1); c3#1 on male (int1);
    c2#2 on male (int2); c3#2 on male (int2);
    c2#3 on male (int3); c3#3 on male (int3);
    c2#4 on male (int4); c3#4 on male (int4);

    c2 on c1 (trans1-trans16);
    c3 on c2 (trans1-trans16);

    f by u11-u14* (lam1-lam3)  !!! continuous random intercept !!!
    u21-u24* (lam1-lam3)
    u31-u34* (lam1-lam3);
    f@1; [f@0];

    u11-u34 on male@0;

Model c1:
  %c1#1%!
    u11-u14 on male (d11-d13);   !!! cross-group invariance equality constraints !!!
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
  %c1#2%
    u11-u14 on male (d21-d23);
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
  %c1#3%
    u11-u14 on male (d31-d33);
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
  %c1#4%
    u11-u14 on male (d41-d43);
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
  %c1#5%
    u11-u14 on male (d51-d53);
  [u11$1 u11$2 u13$1 u13$2 u14$1] (p51-p55);

Model c2:
  %c2#1%
    u21-u24 on male (d11-d13);   !!! cross-group invariance equality constraints !!!
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
  %c2#2%
    u21-u24 on male (d21-d23);
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p21-p25);
  %c2#3%
    u21-u24 on male (d31-d33);
  [u21$1 u21$2 u23$1 u23$2 u24$1] (p31-p35);
  %c2#4%
```

```
      u21-u24 on male (d41-d43);
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
      u21-u24 on male (d51-d53);
    [u21$1 u21$2 u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
      u31-u34 on male (d11-d13);   !!! cross-group invariance equality constraints !!!
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
      u31-u34 on male (d21-d23);
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
      u31-u34 on male (d31-d33);
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
      u31-u34 on male (d41-d43);
    [u31$1 u31$2 u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
      u31-u34 on male (d51-d53);
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);")

m10_date.fit <- mplusModeler(m10_date,
                             dataout=here("date_mplus", "date.dat"),
                             modelout=here("date_mplus", "m10_date.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)
```

Adding covariates and interactions to the dating example

Four binary covariates:

- gender: 0 = Female, 1 = Male
- cigarettes: 0 = Did not use, 1 = Used in past year
- drunk: 0 = Did not use, 1 = Used in past year
- marijuana: 0 = Did not use, 1 = Used in past year

Dating Model 11 - regular LTA - main effects

```
m11_date <- mplusObject(

    TITLE =
    "Dating Model 11, regular LTA, main effects
     Lanza-Collins 2008 Developmental Psychology",
```

```
  VARIABLE =
    "usev = u11 u13 u14
              u21 u23 u24
              u31 u33 u34
              male x11 x12 x13;   !!! grouping covariate !!!

  categorical = u11-u34;
  missing = all(999);

  classes = c1(5) c2(5) c3(5);",

  ANALYSIS =
  "type = mixture;
   starts =  320 80;
   processors = 8;",

  MODEL =
    "%Overall%
     [c2#1 c3#1] (int1);
     [c2#2 c3#2] (int2);
     [c2#3 c3#3] (int3);
     [c2#4 c3#4] (int4);

     c2 on c1 (trans1-trans16);
     c3 on c2 (trans1-trans16);

     c1 on male x11 x12 x13;

     c2 on male x11 x12 x13 (slp1-slp16);
     c3 on male x11 x12 x13 (slp1-slp16);

Model c1:
  %c1#1%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
  %c1#2%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
  %c1#3%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
  %c1#4%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
  %c1#5%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p51-p55);

Model c2:
  %c2#1%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
  %c2#2%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p21-p25);
  %c2#3%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p31-p35);
  %c2#4%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p41-p45);
  %c2#5%
```

```
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);",

    OUTPUT = "tech15;",

    usevariables = colnames(date_data),
    rdata = date_data)

m11_date.fit <- mplusModeler(m11_date,
                             dataout=here("date_mplus", "date.dat"),
                             modelout=here("date_mplus", "m11_date.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 12 - regular LTA - main effects & gender interaction effects

NOTE: use of `update()`, selected syntax is used from base model `m11_date`

```
m12_date <- update(m11_date,

    TITLE = ~
    "Dating Model 12, regular LTA - main effects and gender interaction effects
     Lanza-Collins 2008 Developmental Psychology",

    ANALYSIS = ~.+
    "stscale = 1;",

    MODEL = ~
      "%Overall%
       [c2#1 c3#1] (int1);
       [c2#2 c3#2] (int2);
       [c2#3 c3#3] (int3);
       [c2#4 c3#4] (int4);

       c2 on c1 (trans1-trans16);
       c3 on c2 (trans1-trans16);

       c1 on male x11 x12 x13;

       c2 on male x11 x12 x13 (slp1-slp16);
```

```
      c3 on male x11 x12 x13 (slp1-slp16);

  Model c1:
    %c1#1%
      c2 on male (tr1-tr4);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
      c2 on male (tr21-tr24);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
      c2 on male (tr31-tr34);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
      c2 on male (tr41-tr44);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
      c2 on male (tr51-tr54);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p51-p55);

  Model c2:
    %c2#1%
      c3 on male (tr1-tr4);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
    %c2#2%
      c3 on male (tr21-tr24);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
      c3 on male (tr31-tr34);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
      c3 on male (tr41-tr44);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
      c3 on male (tr51-tr54);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);")

m12_date.fit <- mplusModeler(m12_date,
                  dataout=here("date_mplus", "date.dat"),
                  modelout=here("date_mplus", "m12_date.inp"),
                  check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 13 - RI-LTA - continuous RI

NOTE: use of `update()`, selected syntax is used from base model `m11_date`

```
m13_date <- update(m11_date,

    TITLE = ~
    "Dating Model 13 - RI-LTA - continuous RI
     Lanza-Collins 2008 Developmental Psychology",

    ANALYSIS = ~
     "type=mixture;
      starts = 480 160;
      processors = 8;
      algorithm=integration;
      integration = 30;
      stscale = 1;",

    MODEL = ~
      "%Overall%
       [c2#1 c3#1] (int1);
       [c2#2 c3#2] (int2);
       [c2#3 c3#3] (int3);
       [c2#4 c3#4] (int4);

       c2 on c1 (trans1-trans16);
       c3 on c2 (trans1-trans16);

       f by u11-u14* (lam1-lam3)
       u21-u24* (lam1-lam3)
       u31-u34* (lam1-lam3);
       f@1; [f@0];

       f on male x11 x12 x13;

  Model c1:
    %c1#1%
      c2 on male (tr1-tr4);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
      c2 on male (tr21-tr24);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
      c2 on male (tr31-tr34);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
      c2 on male (tr41-tr44);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
      c2 on male (tr51-tr54);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p51-p55);
```

```
  Model c2:
    %c2#1%
      c3 on male (tr1-tr4);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
    %c2#2%
      c3 on male (tr21-tr24);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
      c3 on male (tr31-tr34);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
      c3 on male (tr41-tr44);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
      c3 on male (tr51-tr54);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);")

m13_date.fit <- mplusModeler(m13_date,
                   dataout=here("date_mplus", "date.dat"),
                   modelout=here("date_mplus", "m13_date.inp"),
                   check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 14 - RI-LTA - continuous RI - main effects

NOTE: use of `update()`, selected syntax is used from base model `m11_date`

```
m14_date <- update(m11_date,

    TITLE = ~
    "Dating Model 14 - continuous RI - main effects
     Lanza-Collins 2008 Developmental Psychology",

    ANALYSIS = ~
     "type=mixture;
      starts = 320 80;
      processors = 8;
      algorithm=integration;",
```

```
  MODEL = ~
    "%Overall%
     [c2#1 c3#1] (int1);
     [c2#2 c3#2] (int2);
     [c2#3 c3#3] (int3);
     [c2#4 c3#4] (int4);

     c2 on c1 (trans1-trans16);
     c3 on c2 (trans1-trans16);

     f by u11-u14* (lam1-lam3)
     u21-u24* (lam1-lam3)
     u31-u34* (lam1-lam3);
     f@1; [f@0];

     f on male x11 x12 x13;

     c1 on male x11 x12 x13;
     c2 on male x11 x12 x13 (slp1-slp16);
     c3 on male x11 x12 x13 (slp1-slp16);

Model c1:
  %c1#1%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
  %c1#2%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
  %c1#3%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
  %c1#4%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
  %c1#5%
  [u11$1 u11$2  u13$1 u13$2 u14$1] (p51-p55);

Model c2:
  %c2#1%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
  %c2#2%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p21-p25);
  %c2#3%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p31-p35);
  %c2#4%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p41-p45);
  %c2#5%
  [u21$1 u21$2  u23$1 u23$2 u24$1] (p51-p55);

Model c3:
  %c3#1%
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
  %c3#2%
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
  %c3#3%
  [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
  %c3#4%
```

```
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);")

m14_date.fit <- mplusModeler(m14_date,
                  dataout=here("date_mplus", "date.dat"),
                  modelout=here("date_mplus", "m14_date.inp"),
                  check=TRUE, run = TRUE, hashfilename = FALSE)
```

Dating Model 15 - RI-LTA - continuous RI - main effects & gender interaction effects

NOTE: use of `update()`, selected syntax is used from base model `m11_date`

```
m15_date <- update(m11_date,

    TITLE = ~
    "Dating Model 15 - RI-LTA - continuous RI - main effects and gender interaction effects
     Lanza-Collins 2008 Developmental Psychology",

    ANALYSIS = ~
     "type=mixture;
      starts = 320 80;
      processors = 8;
      integration = 20;
      algorithm=integration;",

    MODEL = ~
      "%Overall%
       [c2#1 c3#1] (int1);
       [c2#2 c3#2] (int2);
       [c2#3 c3#3] (int3);
       [c2#4 c3#4] (int4);

       c2 on c1 (trans1-trans16);
       c3 on c2 (trans1-trans16);

       f by u11-u14* (lam1-lam3)
       u21-u24* (lam1-lam3)
       u31-u34* (lam1-lam3);
       f@1; [f@0];

       f on male x11 x12 x13;

       c1 on male x11 x12 x13;
       c2 on male x11 x12 x13 (slp1-slp16);
       c3 on male x11 x12 x13 (slp1-slp16);

  Model c1:
    %c1#1%
```

```
      c2 on male (tr1-tr4);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p11-p15);
    %c1#2%
      c2 on male (tr21-tr24);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p21-p25);
    %c1#3%
      c2 on male (tr31-tr34);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p31-p35);
    %c1#4%
      c2 on male (tr41-tr44);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p41-p45);
    %c1#5%
      c2 on male (tr51-tr54);
    [u11$1 u11$2  u13$1 u13$2 u14$1] (p51-p55);

  Model c2:
    %c2#1%
      c3 on male (tr1-tr4);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p11-p15);
    %c2#2%
      c3 on male (tr21-tr24);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p21-p25);
    %c2#3%
      c3 on male (tr31-tr34);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p31-p35);
    %c2#4%
      c3 on male (tr41-tr44);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p41-p45);
    %c2#5%
      c3 on male (tr51-tr54);
    [u21$1 u21$2  u23$1 u23$2 u24$1] (p51-p55);

  Model c3:
    %c3#1%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p11-p15);
    %c3#2%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p21-p25);
    %c3#3%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p31-p35);
    %c3#4%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p41-p45);
    %c3#5%
    [u31$1 u31$2  u33$1 u33$2 u34$1] (p51-p55);")

m15_date.fit <- mplusModeler(m15_date,
                  dataout=here("date_mplus", "date.dat"),
                  modelout=here("date_mplus", "m15_date.inp"),
                  check=TRUE, run = TRUE, hashfilename = FALSE)
```

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UC SANTA BARBARA