

Mixture Modeling for Lifespan Developmental Research

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Acknowledgements

Both authors were supported by a grant from the Social Science and Humanity Research Council of Canada (435-2018-0368).

This is the prepublication version of the following manuscript:

Morin, A., & Litalien, D. (2019). [Mixture modeling for lifespan developmental research](#). In *Oxford Research Encyclopedia of Psychology*. Oxford University Press. doi: <http://dx.doi.org/10.1093/acrefore/9780190236557.013.364>

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Summary

As part of the Generalized Structural Equation Modeling framework, mixture models are person-centered analyses seeking to identify distinct subpopulations, or profiles, of participants differing quantitatively and qualitatively from one another on a configuration of indicators and/or relations among these indicators. Mixture models are typological (resulting in a classification system), probabilistic (each participant having a probability of membership into all profiles based on prototypical similarity), and exploratory (the optimal model is typically selected based on a comparison of alternative specifications) in nature, and can take different forms. Latent profile analyses seek to identify subpopulations of participants' differing from one another on a configuration of indicators and can be extended to factor mixture analyses allowing for the incorporation of latent factors to the model. In contrast, mixture regression analyses seek to identify subpopulations of participants' differing from one another in terms of relations among profile indicators. These analyses can be extended to the multiple-group and/or longitudinal analyses, allowing researchers to conduct tests of profile similarity across different samples of participants or time points, and latent transition analyses can be used to assess probabilities of profiles transition over time among a sample of participants (i.e., within person stability and change in profile membership). Finally, growth mixture analyses are built from latent curve models and seek to identify subpopulations of participants following quantitatively and qualitatively distinct trajectories over time. All of these models can accommodate covariates, used either as predictors, correlates or outcomes, and can even be extended to tests of mediation and moderation.

Keywords: Person-Centered Analyses, Mixture Modeling, Latent Profile Analyses, Multigroup Latent Profile Analyses, Mixture Regression, Latent Transition, Longitudinal Profile Similarity, Growth Mixture.

Introduction

Describing, explaining, and predicting psychological characteristics and behaviors among developing individuals, and understanding how and why they fluctuate and evolve over time are central questions for researchers interested in lifespan development. The sheer complexity of our object of research – humans – is drastically increased when considered within a time perspective and calls for equally complex analytical procedures. Fortunately, as developmental researchers, we live in very exciting times of fast-paced methodological developments coupled with exponentially increasing levels of computing power and user-friendly statistical packages. This fast-paced evolution is not, however, without a cost for applied researchers: That of having to keep up with these developments despite often lacking the formal technical training required to do so in an efficient manner. Marsh and Hau (2007) introduced the term “substantive-methodological synergies” to describe collaborative efforts of knowledge translation through which statistical advanced are used to address applied research questions as a favored way of reinstating communications between applied researchers and statistical experts. Core to this process is the availability of user-friendly non-technical introductions to these advanced methodologies. With this in mind, the present chapter was written in order to provide a broad introduction to the application of person-centered mixture modeling methods most useful to lifespan developmental researchers. A special attention will be given to longitudinal mixture models allowing to capture interindividual differences in intraindividual developmental processes (Ram & Grimm, 2007).

Various analytic methods are available to help researchers better understand developmental changes or trends among individuals. Five decades ago, Cohen (1968) proposed multiple regression as a generic framework able to capture linear or polynomial relations between continuous or categorical predictors, their interactions, and a continuous outcome variable. Ten years later, Knapp (1978) established multiple regression as a special case of canonical correlation analysis, allowing for the simultaneous consideration of multiple outcomes. Canonical correlation was itself rapidly superseded by latent variable models (e.g., confirmatory factor analyses – CFA: Jöreskog, 1969; structural equation models – SEM; Jöreskog, 1970), an even broader analytical framework through which chains of relations could be estimated between continuous latent variables (i.e., factors) corrected for measurement error (Bagozzi, Fornell, & Larcker, 1981). A subsequent development came from the incorporation of mixture modeling methods into a Generalized SEM (GSEM) framework (Muthén, 2002; Skrondal & Rabe-Hesketh, 2004). In and of themselves, mixture models have been around for decades (Gibson, 1959; Lazarsfeld & Henry, 1968; McLachlan & Peel, 2000). However, it is their integration within GSEM and the creation of user-friendly statistical packages (e.g., Latent GOLD: Vermunt & Magidson, 2005; Mplus: Muthén & Muthén, 2018) that have contributed to the increasing popularity of these models. Mixture modeling is a model-based approach to classification, based on the assumption that a sample includes a mixture of subpopulations. Through it, GSEM makes it possible to estimate of relations between any type of continuous and categorical observed and latent variables.

Variable-Centered versus Person-Centered Analyses

To better understand GSEM, let us first consider one key defining characteristic of CFA and SEM models. These models are *variable-centered*: They assume that all individuals are drawn from a single population, and yield results that reflect a synthesis, or average, of the relations observed among all members of the sample. In contrast, mixture modeling and GSEM are *person-centered*: They relax this assumption of population homogeneity, allowing all or part of any CFA/SEM model to differ across unobserved subpopulations of participants referred to as *latent profiles* (when defined from continuous indicators) or *latent classes* (when defined from categorical indicators). The person-centered approach thus adopts a more holistic view of individuals than the variable-centered approach, and affords the opportunity to consider the

combined effects of any number of variables in a way that would be hard to address using traditional variable-centered analyses of interactions (e.g., Morin, Morizot, Boudrias, & Madore, 2011). However, the person-centered approach requires a paradigmatic shift in the way research questions are framed, moving away from a correlational view focusing on relations among variables to a configurational approach centered on persons (Delbridge & Fiss, 2013), and has long been considered as a method of choice in developmental research (Bergman & Magnusson, 1997).

In GSEM, the latent profiles reflect relatively homogenous subpopulations of participants differing qualitatively and quantitatively from one another (Morin & Marsh, 2015) in relation to: (a) their configuration of a set of observed and/or latent variable(s), and/or (b) relations among observed and/or latent variables (Borsboom, Mellenbergh, & Van Heerden, 2003). Mathematically, these subpopulations, or profiles, are reflected via the estimation of a latent categorical variable. Despite our focus on these approaches, it is important to acknowledge that mixture modeling and GSEM are not the only way to apply person-centered analyses. In particular, evolving clustering procedures deserve a specific mention (for a review, see Brusco, Steinley, Cradit, & Singh, 2011). Still, being model-based and anchored into the SEM framework, GSEM affords an arguably more flexible way to incorporate predictors and outcomes of profiles directly into the model (Petras & Masyn, 2010), to account for longitudinal dependencies inherent in longitudinal data (but see Hofmans, Vantilborgh, & Solinger, 2018), and to assess chains of relations among a variety of continuous and categorical latent variables (McLarnon and O'Neill, 2018).

Person-Centered Analyses: Three Defining Characteristics

Within GSEM, person-centered analyses present three key defining characteristics (Morin, Bujacz, & Gagné, 2018). First, they are *typological* in nature, resulting in a classification system designed to categorize individuals more accurately into qualitatively and quantitatively distinct subpopulations or profiles.

Second, the identified latent profiles are *prototypical* in nature, with each participant having a probability of membership in every profile based on their degree of similarity with the profile's specific configuration. In GSEM, each profile thus reflects a latent (i.e., inferred, unobserved) prototypical subpopulation to which each participant has a probability of corresponding based on their degree of prototypical similarity with the profile's specific configuration. More precisely, whereas classical cluster analytic methods result in a "physical" (i.e., deterministic) classification of participants into profiles (but see Gabriel et al., 2018), GSEM rather results in a probabilistic classification system. Taking these probabilities into account as part of the model thus provides a way to control for the measurement errors inherent in this classification process. Thus, just like latent CFA/SEM factors incorporated a correction for the measurement errors present at the item level, latent profiles are similarly controlled for classification errors.

Finally, person-centered analyses are *exploratory* from a methodological perspective, as solutions including different numbers of profiles are typically contrasted in order to select the optimal solution in a mainly exploratory manner. This does not mean that they cannot be used for confirmatory purposes (for a more extensive discussion, see Morin et al., 2018). Moreover, a more methodologically confirmatory approach to the estimation of mixture models has been proposed for fields of research advanced enough to support the generation of a priori hypotheses regarding the nature of profiles (Schmiege, Masyn, & Bryan, 2018). However, even in these contexts, the a priori model would still need to be contrasted with unconstrained exploratory models to show that their fit to the data remains comparatively acceptable. In practice, the optimal number of profiles is most commonly determined based on inspection of: (a) the substantive meaning and theoretical conformity of the solution; (b) the statistical adequacy of the solution; (c) statistical indicators (additional details on the technicalities of model estimation

and use of statistical indicators to select the optimal solution are provided in Appendix A of the online supplements). Because of this exploratory nature, a key consideration is the empirical demonstration of the meaningfulness of the profiles. To support a substantive interpretation, analysts need to embark on a construct validation process aiming to demonstrate that the profiles: (a) are theoretically meaningful, either by supporting a priori hypotheses or by being able to generate new perspectives; (b) have heuristic value, by being able to provide a practically useful representation, (c) are meaningfully related to key predictors, outcomes, or correlates, and (d) generalize to new samples (Marsh, Lüdtke, Trautwein, & Morin, 2009; Morin, Morizot, et al., 2011).

In the following chapter, we propose a user-friendly description of various types of mixture models available to lifespan development researchers, with a specific focus on longitudinal models. However, before moving on to longitudinal models, we first provide a basic introduction to the estimation of mixture models, with a focus on Latent profile analyses (LPA), Factor Mixture Analyses (FMA), mixture regression analyses (MRA), and tests of profile similarity. We then address models with more direct relevance to longitudinal analyses, including longitudinal tests of profile similarity, latent transition analyses (LTA), and growth mixture analyses (GMA). We finish by a consideration of mixture models including covariates, either through direct inclusion or auxiliary approaches. We also provide additional information and comprehensive syntaxes in appendices to guide the reader in conducting these analyses using the Mplus package. More specifically, these appendices include technical considerations in the estimation of mixture models (Appendix A), Mplus input code for the estimation of the various mixture models presented (Appendix B).

Typical Mixture Models

Latent Profile Analyses

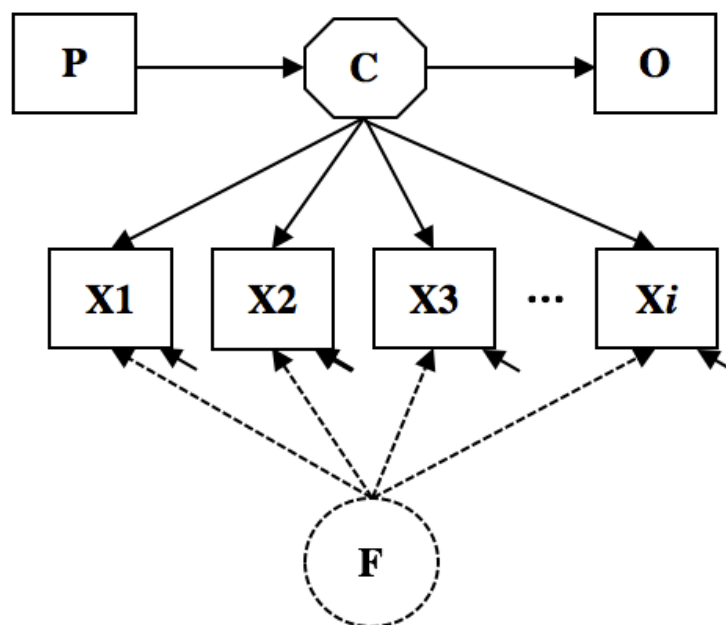


Figure 1. Latent Profile and Factor Mixture Analyses

This model estimates k latent profiles (C_1 to C_k) differing from one another based on their configuration on i indicators (X_1 to X_i). Predictors (P) and outcomes (O) can be integrated to the model, where P influences the likelihood of membership into the latent profiles, and the likelihood of membership into the latent profiles influences O . In factor mixture analyses, k latent profiles and j common factors (F_1 to F_j ; illustrated by the dotted ellipse and factor loadings) are simultaneously estimated from the same i indicators (X_1 to X_i).

Arguably, the most basic type of mixture models are latent profile analyses (LPA) or latent class analyses (LCA). LPA simply seek to identify subpopulations of participants differing from one another on their configuration on a series of continuous variables (e.g., Lubke & Muthén, 2005), whereas LCA does so based on a series of categorical indicators. Although the present chapter focuses on continuous indicators, which are most commonly used in developmental research, all of the models presented in this chapter can easily be extended to categorical or count variables, in which case “profiles” should be referred to as “classes”. LPA are illustrated in Figure 1, where the octagon represents the latent categorical variable C reflecting k distinct latent profiles (C1 to C k) defined as a function of a configuration of scores obtained on a series of i manifest indicators (squares X1 to Xi). In this figure, the additional squares represent manifest predictors (P) and outcome (O) variables, while the circle represent a continuous latent factor, three components discussed later. At its most basic level, a typical LPA solution estimates k latent profiles from a series of i indicators, and would be expressed as (e.g., Peugh & Fan, 2013):

$$\sigma_i^2 = \sum_{k=1}^K \pi_k (\mu_{ik} - \mu_i)^2 + \sum_{k=1}^K \pi_k \sigma_{ik}^2 \quad (1)$$

This model decomposes the variance into between-profile (the first term) and within-profile (the second term) components, where the profile-specific means (μ_{ik}) and variances (σ_{ik}^2) are expressed as a function of a density parameter π_k reflecting the proportion of participants corresponding to each profile. However, more constrained types of LPA models can be estimated while allowing profiles to be defined only on the basis of the indicators means ($\sigma_{ik}^2 = \sigma_i^2$; Peugh & Fan, 2013) and remain the default parameterization of LPA in some statistical packages, such as Mplus (Muthén, & Muthén, 2018). Relaxing this default helps to obtain less biased parameter estimates (Peugh & Fan, 2013), and provides an arguably more realistic representation of the data than relying on artificial constraints through which the level of inter-individual variability is forced to be equivalent across profiles (Morin, Maïano, et al., 2011). It should be noted that mixture models remain complex and computer-intensive, and have a tendency to converge on improper solutions, or to fail to converge. When this occurs, the model might have been overparameterized (e.g., too many profiles, too many parameters freely estimated) and more parsimonious models involving class-invariant variances ($\sigma_{ik}^2 = \sigma_i^2$) should be pursued. Our recommendation is to always start with theoretically “optimal” models, and then reduce model complexity when necessary.

LPA can easily accommodate a variety of continuous, ordinal and categorical measurement scales (McLachlan & Peel, 2000), take into account a multilevel structure (Mäkikangas et al., 2018), and make it possible to assess the added value of alternative specifications (free estimation of indicators variance, inclusion of correlated uniquenesses or method factors, etc.) in terms of improvements in the relative fit of the model.

Although they are typically estimated based on cross-sectional data, LPA can still be used to address various developmental research questions. For instance, this approach is particularly helpful to investigate how various dimensions of multidimensional measures combine, to identify the optimal number of patterns (profiles) that are need to summarize the various scores combinations observed within a specific population, and can even be used to contrast the profiles obtained among distinct samples of participants. For instance, Chen, Morin, Parker, and Marsh (2015) used LPA to better capture life satisfaction across the post-school transition. Based on three domains of life satisfaction (achievement, family, and leisure), they identified seven distinct profiles that proved to be highly similar across multiple measurement occasions. Profiles indicators do not need to tap into a single overarching conceptual field in order to be informative. For example, Orpinas, Raczynski, Peters, Colman, and Bandalos (2015) conducted

LPA to predict high-school dropout from the assets and maladaptive behaviors of sixth graders rated by their teachers. They identified seven students' profiles that they placed on a continuum in accordance to their probabilities of dropping out of high school. Investigating children that has been exposed to violence, McDonald, Graham-Bermann, Maternick, Ascione, and Williams (2016) identified three socioemotional functioning profiles based on six indicators of adjustment, and went on the identify a variety of risk and protective factors of membership into these profiles.

Factor Mixture Analyses

The GSEM framework is not limited to the sole consideration of latent categorical variables, but allows for the simultaneous inclusion of latent continuous (factors) variables within the same model and even from the same set of indicators (as illustrated in the dotted part of Figure 1). Factor Mixture Analyses (FMA) can be used to investigate the underlying continuous or categorical nature of psychological constructs (Clark et al., 2013; Masyn, Henderson, & Greenbaum, 2010), to test the measurement invariance of psychometric measures across unobserved subpopulations (Tay, Newman, & Vermunt, 2011), or simply to control for a general tendency shared among indicators in order to estimate latent profiles controlled for this shared tendency (Morin & Marsh, 2015). Interestingly, in a study mentioned in the previous section, Chen et al. (2015) relied on FMA, rather than LPA, in order to be able to identify profiles based the three life satisfaction domains properly disaggregated from participants' global levels of life satisfaction across domains.

Mixture Regression Analyses

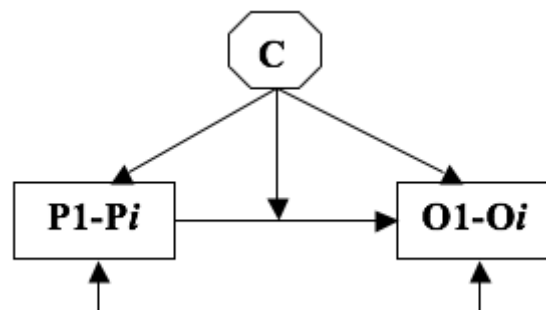


Figure 2. Mixture Regression Analyses

This model estimates k latent profiles ($C1$ to Ck) differing at the level of relations (regressions) among a set of predictors ($P1$ to Pi) and outcomes ($O1$ to Oi). Mixture regression analyses identify subpopulations among which these relations differ. It can also be combined with latent profile analyses to identify profiles differing on the basis of both these relations, but also the configuration of indicators.

Mixture regression analyses (MRA) are illustrated in Figure 2 and seek to identify latent profiles differing from one another at the level of estimated relations (regressions) between constructs (Van Horn et al., 2009). Thus, whereas LPAs regroup participants based on their configuration on a set of indicators (e.g., personality dimensions), MRA identify subpopulations in which the relations among constructs (e.g., relations between personality dimensions and psychopathology) differ. In MRA, outcome's means and variances (representing the intercepts and residuals of the regression equation) need to be freely estimated across profiles, in addition to the regression slope itself, in order to obtain profile-specific regression equations. More complex applications are also possible, such as combining LPA and MRA to identify subpopulations differing based on both a configuration of indicators, and relations between these indicators (Chénard-Poirier, Morin, & Boudrias, 2017) or mixture SEM models in order to identify profiles defined based on relations estimated between latent

constructs corrected for measurement errors (Henson, Reise, & Kim, 2007).

Despite its flexibility, and relevance to both cross-sectional and longitudinal analyses, MRA has been rarely used in research so far. As an example, Lanza, Cooper, and Bray (2014) relied on MRA to study relations between adolescent delinquency and a series of eight well-established risk factors. Their results revealed five latent profiles of adolescents presenting different levels of delinquency and differentiated patterns of associations with the various risk factors leading them to propose intervention strategies tailored to profile membership. MRA have also been used to identify profiles characterized by distinct patterns of associations between family, school, and peer relationships and suicide attempts among Asian American adolescents (Wong & Maffini, 2011) or between family resources and academic achievement (Van Horn et al., 2009). Likewise, Morin, Scalas, and Marsh (2015) conducted hybrid mixture SEM analyses to test whether a theoretical model of self-concept formation applied differentially to certain subpopulations. Their results suggested that the effects of actual appearance self-perceptions on the self-esteem of adolescents and young adults increased as their ideal appearance standards increased.

Multiple Group Tests of Profile Similarity

As noted at the end of the Introduction, a key component of the construct validation process required to assess the meaningfulness of the person-centered solution involves the demonstration that this solution generalizes to new samples. Arguably, evidence of generalizability in the context of person-centered research is typically built on an accumulation of studies (e.g., Kabins, Xu, Bergman, Berry, & Wilson, 2016; Meyer & Morin, 2016). This accumulation of results is required to differentiate the core set of profiles that emerge with regularity across studies, from the more peripheral set of profiles that emerge irregularly under specific conditions (Solinger, Van Olffen, Roe & Hofmans, 2013). However, an additional key feature of GSEM is the ability to systematically assess the extent to which a specific person-centered solution (e.g., LPA, MRA) would be replicated across distinct samples of participants. A comprehensive methodological framework designed to guide the realization of such tests of profile similarity in the LPA context was proposed by Morin, Meyer, Creusier, and Biétry (2016), and extended to MRA analyses by Morin and Wang (2016). The sequence of similarity tests involved in this approach are summarized in Table 1, and the implementation of this framework is covered in the online supplements.

This framework represents another key advantage of GSEM relative to the cluster analytic approach, and makes it possible to assess the extent to which a specific solution can be assumed to generalize across subpopulations defined based gender, cultures, educational levels, or age groups. Guided by this framework, Litalien, Morin, and McInerney investigated the extent to which adolescents' achievement goal profiles, and the predictors and outcomes of these profiles, were similar across gender (2017a) and cultures (2017b). Although results from these two studies suggest more similarities than differences across subgroups, they also revealed valuable distinctions (e.g., cultural differences in the structure of a specific profile, group-based differences in the prevalence of specific profiles, and distinct patterns of predictive associations).

Table 1
Tests of Profile Similarity

Test	Description
A – Configural Similarity	<ul style="list-style-type: none"> ✓ Configural similarity assesses whether same number of latent profiles are identified in all groups. ✓ Configural similarity is a prerequisite to all further tests. ✓ Lack of configural similarity: The latent profiles differ across groups and require a qualitative comparison process.
B – Structural Similarity	<ul style="list-style-type: none"> ✓ Structural similarity assesses whether within-profile levels on the indicators are the same in all groups (i.e., whether profile structure remains unchanged). ✓ Configural and structural similarity are prerequisite to all further tests, but partial structural similarity is possible. ✓ Lack of partial structural similarity: The latent profiles differ across groups and require a qualitative comparison process. ✓ Prerequisite: Configural similarity.
C – Dispersion Similarity	<ul style="list-style-type: none"> ✓ Dispersion similarity assesses whether levels of within-profile variability are the same in all groups. ✓ Partial dispersion similarity is possible. ✓ Lack of dispersion similarity: The level of inter-individual differences among profile members changes across groups. ✓ Not applicable when profile indicators are categorical. ✓ Prerequisite: Configural and structural similarity.
D – Distributional Similarity	<ul style="list-style-type: none"> ✓ Distributional similarity assesses whether the relative size of the profiles are the same in all groups. ✓ The size of all profiles needs to be either similar or not across pairs of groups, but partial distributional similarity is possible across different pairs of groups (e.g., Group 1 and be similar to Group 2, but different than Group 3). ✓ Lack of distributional similarity: The size of the profiles differs across groups. ✓ Prerequisite: Configural and structural similarity.
E – Predictive Similarity	<ul style="list-style-type: none"> ✓ Predictive similarity assesses if the effects of predictors on profile membership are the same in all groups. ✓ Predictors of profile membership are directly included to the most similar (A-D) model. This step is only appropriate when predictors are included in the study. ✓ The effects of any single predictor need to be either similar or not across pairs of groups, but partial predictive similarity is possible across different pairs of groups, or across different predictors. ✓ Lack of predictive similarity: The effects of predictors on profile membership differ across groups. ✓ Prerequisite: Configural and structural similarity.
F – Explanatory Similarity	<ul style="list-style-type: none"> ✓ Explanatory similarity assesses if the effects of profile membership on outcome levels are the same in all groups. ✓ Outcomes of profile membership are directly included to the most similar (A-D) model. This step is only appropriate when outcomes are included in the study. ✓ Partial explanatory similarity is possible. ✓ Lack of explanatory similarity: The effects of profile membership on the outcomes differ across groups. ✓ Prerequisite: Configural and structural similarity.
G – Regression Similarity	<ul style="list-style-type: none"> ✓ Regression similarity assesses if the regressions that define the mixture regression profiles are the same in all groups. ✓ This step is only relevant in mixture regression analyses, and forms the second step of the sequence for these analyses. ✓ Partial similarity is possible. ✓ Lack of partial regression similarity: The latent profiles differ across groups and require a qualitative comparison process. ✓ Prerequisite: Configural similarity.
Recommended order	<p>Steps that are a prerequisite to subsequent steps are bolded. Latent Profile Analyses: A-B-C-D-E-F Mixture Regression Analyses: A-G-B-C-D-E-F</p>

Longitudinal Mixture Models

Longitudinal Tests of Profile Similarity and Latent Transition Analyses

Of particular interest to developmental researchers is the analysis of longitudinal data. In this context, a key strength of the GSEM framework is the ability to incorporate more than one latent categorical variable (reflecting the profiles) in the same model. At the most basic level, this feature can be used to incorporate, into a single model, a series of time-specific LPA solutions (e.g., one LPA solution describing the Time 1 profiles and a second LPA solution describing the Time 2 profiles) based on the same set of indicators. Importantly, such model can be used to test for the similarity of latent profile solutions across time points using an approach similar to that described in the present section for the multi-group context. Longitudinal tests of profile similarity are particularly useful for the assessment of stability and change over time, or developmental period, in the number, structure, inter-individual variability or frequency of the identified latent profiles, and can be extended to tests of predictive and explanatory similarity in terms of associations between the profiles, their predictors, and their outcomes over time. Kam, Morin, Meyer, and Topolnytsky (2016) refer to such longitudinal tests of profile similarity as tests of *within-sample stability*.

Kam et al. (2016) also mention that longitudinal data also makes it possible to assess a second form of profile stability related to the assessment of whether individual membership in specific profiles remains stable over time. They refer to this second form as *within-person stability*. However, this second type of test requires the conversion of the longitudinal LPA model into a Latent Transition Analysis (LTA) model, illustrated in Figure 3. In addition to the estimation of LPA solutions at multiple time points, LTA also take into account the connections (i.e., individual transitions in profile membership) between the time specific LPA solutions (Collins & Lanza, 2009). It is important to keep in mind that LTAs can theoretically be used to model the connections between any type of mixture models (Nylund-Gibson, Grimm, Quirk, & Furlong, 2014).

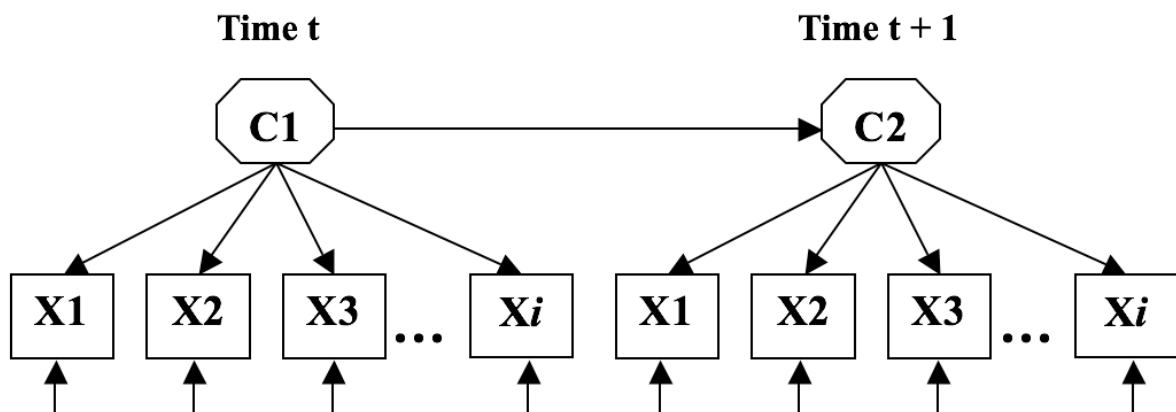


Figure 3. Latent Transition Analyses

This model estimates C latent profiles at two separate time points (C1 and C2), and the probabilities for individuals to transition from C1 to C2 over time. Latent transition analyses can be used to assess the invariance of a latent profile solution over time. However, latent transition analyses do not require the mixture model estimated at C1 to be equivalent to the mixture model estimated at C2.

In its simplest expression, LTA estimates LPA solutions based on the same set of indicators and including the same number of profiles at both time points. In this specific context, LTA should be built from the most *similar* longitudinal LPA model (i.e., after the longitudinal tests of configural, structural, dispersion, and distributional similarity, or tests of *within-sample*

similarity, have been conducted), but before the incorporation of predictors and outcomes to the model (i.e., before conducting tests of predictive and explanatory similarity) (e.g., Gillet, Morin, & Reeve, 2017). Including predictors and outcomes to the LTA, rather than to the simple longitudinal LPA, presents two key advantages. First, it provides a way to assess associations that take into account the within-person stability of profile membership, which is akin to controlling for the stability of profile membership (e.g., Gillet et al., 2017). Second, this conversion also makes it possible to add an additional step in the tests of predictive similarity to assess whether the predictors can influence specific profile transitions (e.g., Ciarrochi, Morin, Sahdra, Litalien, & Parker, 2017).

Although the tests of profile similarity proposed by Morin, Meyer, et al. (2016) for the multiple group context can easily be applied to the longitudinal context via the estimation of a longitudinal LPA model (see the online supplements for an illustration), the conversion of the most similar longitudinal LPA to a LTA is not as straightforward in the presence of distributional similarity (i.e., when the size of the profiles are equal across time). In this context, typical equality constraints cannot be directly imposed on the relative size of the profiles given that the parameter reflecting the class probability at each subsequent time point reflect in fact the “intercepts” of the regression of the time-specific profiles on the profiles estimated at the previous time points. In this context, a more extended approach, which is fully exposed and illustrated in a webnote (Morin & Litalien, 2017), is required. We reinforce that this more complex approach is only required in the presence of distributional similarity, whereas any other longitudinal LPA solution can be converted to a LTA model using the online supplements accompanying this chapter.

Interestingly, studies in developmental psychology have relied on LTA to better capture changes among various developmental indicators. For instance, Ciarrochi et al. (2017) investigated the stability of combinations of social support from various sources (parents, teachers, and peers) and their associations with well-being among adolescents. They identified six profiles that were similar in Grade 8th and 11th (configural, structural, and dispersion), but that differed in size (distributional). In addition, adolescents in either low or high support profiles tended to remain in similar profiles over this 3-year period, whereas moderate profiles showed greater instability. LTA has also been applied to study the development of cognitive abilities among elementary school pupils (Rinne, Ye, & Jordan, 2017) and the stability of University students' motivation profiles (Gillet et al., 2017).

Growth Mixture Analyses

Growth mixture analyses (GMA), illustrated in Figure 4, seek to identify latent subpopulations of participants following distinct longitudinal trajectories on one – or many – indicator(s) over time. GMA are built from latent curve models (LCM, for a comprehensive introduction to LCM, see Bollen and Curran, 2006). In LCM, indicators are assessed over multiple time points and trajectories at the sample level are estimated through a random intercept factor (representing the level on the repeated measure at the first time point) and random slope(s) factor(s; reflecting through different functions the change occurring over time in the repeated measures) that are allowed to differ across individuals. In its simplest expression, GMA extract latent profiles differing on the average of these growth factors (i.e., presenting a different average intercept and slope factors). GMA thus identify subgroups (i.e., profiles) that follow distinct longitudinal trajectories (e.g., Morin, Maïano et al. 2011). More complex GMA may extract subgroups differing on all LCM parameters, and may even allow for the extraction of subgroups with trajectories following distinct functional forms (linear, quadratic, etc.). GMA are particularly well-suited to investigations of the effects of longitudinal development, interventions, or life transitions.

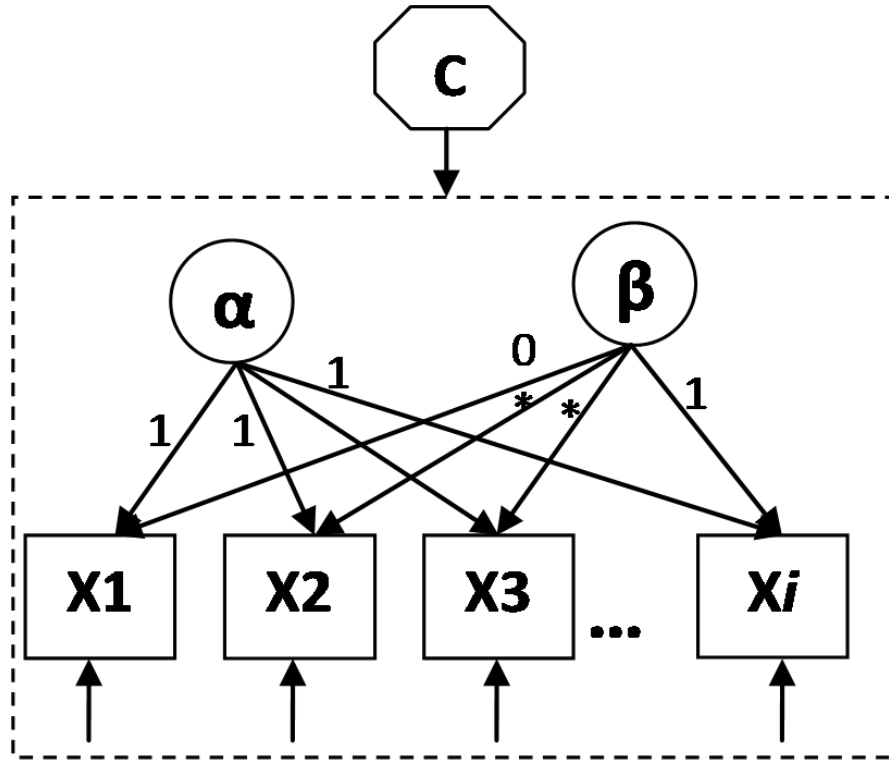


Figure 4. Growth Mixture Analyses

This model estimates C latent profiles presenting different longitudinal trajectories on one or more variables over i time points. Individual trajectories are estimated through a latent growth model, any part of which is allowed to differ across profiles.

A linear GMA for the repeated measure y_{it} for individual i at time t is estimated within k distinct levels ($k = 1, 2, \dots, K$) of the unobserved latent categorical variable c representing the profiles, with each individual having a probability of membership in the k levels.

$$y_{it} = \sum_{k=1}^K p_k [\alpha_{iyk} + \beta_{iyk} \lambda_t + \varepsilon_{yitk}] \quad (2)$$

$$\alpha_{iyk} = \mu_{\alpha yk} + \zeta_{\alpha yik} \quad (3)$$

$$\beta_{iyk} = \mu_{\beta yk} + \zeta_{\beta yik} \quad (4)$$

The k subscript indicates that most parameters are allowed to differ across profiles. This means that each profile can be defined by its own LCM. In these equations, α_{iyk} and β_{iyk} represent the random intercept and random linear slope of the trajectory for individual i in profile k ; $\mu_{\alpha yk}$ and $\mu_{\beta yk}$ represent the average intercept and linear slope in profile k and $\zeta_{\alpha yik}$ and $\zeta_{\beta yik}$ represent the variability of the intercepts and slopes across cases within profiles. ε_{yitk} represents the time- individual- and class- specific residuals. These residuals are generally allowed to vary across time. p_k defines the probability that an individual i belongs to a specific class (k) with all $p_k \geq 0$ and $\sum_{k=1}^K p_k = 1$. The variance parameters ($\zeta_{\alpha yik}, \zeta_{\beta yik}$) have a mean of zero and a Φ_{yk} variance-covariance matrix:

$$\Phi_{yk} = \begin{bmatrix} \psi_{\alpha\alpha yk} & \\ \psi_{\alpha\beta yk} & \psi_{\beta\beta yk} \end{bmatrix} \quad (5)$$

In these models, time is represented by λ_t , the factor loading matrix relating the time-specific indicators to the linear slope factor. Time is coded to reflect the passage of time and thus needs to reflect the interval between measurement points. Assuming a study including four equally spaced monthly measurement points of anxiety taken among students entering high school, it is reasonable to set the intercept at Time 1 [$E(\alpha_{iyk}) = \mu_{y1k}$]. Thus, for a linear GMA, time would be coded $\lambda_1 = 0$, $\lambda_2 = 1$, $\lambda_3 = 2$, $\lambda_4 = 3$, leading to the estimation of profiles in which the intercept factors would reflect the average level of anxiety exhibited by the member of the profile when entering high school (Time 1) and the slope factor would reflect the average rate of monthly change in anxiety levels characterizing profile members. For additional discussion of time codes, the readers should consult Biesanz, Deeb-Sossa, Papadakis, Bollen, and Curran (2004) and Metha and West (2000).

Functional Forms (Shape) for the Trajectories

Linear

When working with GMA, a first important consideration involves the expected shape, or functional form, of the trajectories. The most common functional forms are polynomial, in which the two most frequently used operationalizations are linear and quadratic trajectories. Equations 2 to 5 described the linear GMA model. This model assumes that all longitudinal trajectories will be linear, characterized either by a steady increase over time, a steady decrease over time, or longitudinal stability. Because the intercepts and slopes factors of estimated as part of these models are random parameter, a specific intercept and slope value will be ascribed to each individuals, and time-specific individual deviations from this straight line will be absorbed as part of the time-specific residuals. This is the most common form of GMA, and its estimation requires a minimum of three measurement points. Still, in the absence of change over time (when the linear slope mean and variance are 0), an intercept-only model could be sufficient. Likewise, when participants all share a common starting point, a model including only a random slope (and no random intercept) could be sufficient.

Quadratic

A quadratic GMA involves adds one additional slope factor to the model (e.g., Diallo, Morin, & Parker, 2014) in order to represent curvilinear trajectories (U-shape, or inverted U-shape). In this model, α_{iyk} remains defined as in Equation 2, λ_t remains coded as in the linear model, and β_{1iyk} and β_{2iyk} respectively represent the random linear and quadratic slopes for individual i in profile k .

$$y_{it} = \sum_{k=1}^K p_k [\alpha_{iyk} + \beta_{1iyk} \lambda_t + \beta_{2iyk} \lambda_t^2 + \varepsilon_{yitk}] \quad (6)$$

$$\beta_{1iyk} = \mu_{\beta 1yk} + \zeta_{\beta 1yik} \quad (7)$$

$$\beta_{2iyk} = \mu_{\beta 2yk} + \zeta_{\beta 2yik} \quad (8)$$

$$\Phi_{yk} = \begin{bmatrix} \Psi_{\alpha\alpha yk} & & \\ \Psi_{\alpha\beta 1yk} & \Psi_{\beta 1\beta 1yk} & \\ \Psi_{\alpha\beta 2yk} & \Psi_{\beta 1\beta 2yk} & \Psi_{\beta 2\beta 2yk} \end{bmatrix} \quad (9)$$

The estimation of a quadratic GMA requires four time points. In a quadratic model, the second slope factor, used to represent the curvature of the trajectories, is defined using the square of the time codes used in the linear model. Whereas a linear model can easily be interpreted without a graphical display by considering the initial level (the intercept factor) and rate of change over time (the slope factor) corresponding to each profile, a quadratic model is best interpreted by using a graphical representation of the trajectories. However, it is interesting

to note that the average inflexion point of the trajectories (the bottom of the U-shape curve, or the top of the inverted U-shape curve) can be calculated $\mu_{\beta_{1,yk}}$ as $-\mu_{\beta_{1,yk}} / 2\mu_{\beta_{2,yk}}$. Because the intercept, linear slope, and quadratic slope factor are all random effects, the quadratic model provides a high level of flexibility in allowing for the representation of different functional forms across profiles in the same model. For instance, a profile associated with a quadratic slope factor of 0 would follow a mainly linear trajectory, and a profile associated with a linear and quadratic slope factors of 0 would follow a stable (flat) trajectory (for an example, see Morin, Maïano et al., 2011).

Piecewise

Piecewise GMA are particularly useful when there is an expected transition point over the course of the study (transition, intervention, etc.). Piecewise models allow for the estimation of a change in the direction of longitudinal trajectories before and after a transition point. Typically, this is reflected by the integration of two linear slopes to the model, the first representing the pre-transition slope, and the second representing the post-transition slope (e.g., Diallo & Morin, 2015):

$$y_{it} = \sum_{k=1}^K p_k [\alpha_{iyk} + \beta_{1iyk} \lambda_{1t} + \beta_{2iyk} \lambda_{2t} + \varepsilon_{yitk}] \quad (10)$$

In this model, α_{iyk} is defined as in Equation 3, Φ_{yk} is defined as in Equation 9, β_{1iyk} and β_{2iyk} are linear slopes reflecting the growth occurring before and after the transition point. In this model, two distinct sets of time scores λ_{1t} and λ_{2t} are used to reflect the passage of time before, and after the transition. Assuming a study including six equally spaced measurements points with an intercept located at Time 1 [$E(\alpha_{iyk}) = \mu_{y1k}$], and a transition point located after the third time point, λ_{1t} would be coded $\{0, 1, 2, 2, 2, 2\}$ for time $\lambda_{1t=1}$ to $\lambda_{1t=6}$ (reflecting linear growth for the first three time points after which the equal loadings allow the remaining growth information to be absorbed by the second linear slope factor) and λ_{2t} would be $\{0, 0, 0, 1, 2, 3\}$ for time $\lambda_{2t=1}$ to $\lambda_{2t=6}$ (reflecting linear growth between the last three time points).

Piecewise GMA require at least two measurement points before and after the transition point, with five measurement points in total (e.g., Diallo & Morin, 2015). Diallo and Morin (2015) note, however, that convergence problems are frequent when estimating a piecewise model using only two measurement point before (but not after), the transition point. With additional time points, the piecewise model may be extended to model curvilinear trends. Despite their flexibility, piecewise models require an a priori knowledge of the exact location of the transition point, which is also assumed to be the same for all members of a specific profile, but could be allowed to differ across profiles. When the turning point is not known a priori but suspected to exist (e.g., to identify how long after entry into high school students typically take to change their life rhythm), then it is possible to estimate a linear LCM as part of preliminary analyses, and to examine the modification indices associated with the loadings on the slope factor to locate the turning point (see Kwok, Luo, & West, 2010).

Latent Basis

A limitation of typical implementations of GMA is that the same functional form needs to be estimated in all profiles. This requirement is not, however, as restrictive as it seems given that it is easy to constrain one or many of the slope factors to be zero in specific profiles. For instance, by constraining the quadratic slope to be zero in one profile within a quadratic GMA, one constrains this profile to follow a linear trajectory. Similarly, by constraining the second slope to be equal to the first one in a piecewise model, one constrains the trajectories to follow the same course before and after the transition point. Similarly, the piecewise model could be modified to incorporate a distinct transition in each profile. More restrictive is the fact that all

of these models involve estimating profiles that remain within the same family of polynomial trajectories (i.e., it is not possible to estimate exponential, logistic, and quadratic trajectories within the same model).

The latent basis model provides an interesting workaround this limitation. In LCM/GMA, only two time codes λ_t need to be fixed to 0 and 1 for identification purposes, while the remaining codes can be freely estimated (Bollen & Curran, 2006; Grimm, Ram, & Estabrook, 2016; Ram & Grim, 2009). The slope factor thus represents the total change occurring between these two time points, and the loadings reflect the proportion of that total change occurring at specific time points. When these loadings are freely estimated across profiles, the latent basis model thus provides a way to estimate completely distinct trajectories across profiles (for an example, see Morin, Mañano, Marsh, Nagengast, & Janosz, 2013), without imposing any functional shape.

The latent basis model is expressed as in Equations 2 to 5, but $t-2$ time codes are freely estimated in λ_t . This model further provides the possibility to freely estimate these $t-2$ time codes in all profiles so that λ_t becomes λ_{tk} , allowing for the extraction of trajectories differing completely in shape across profiles. In this model, $\mu_{\beta_{yk}}$ then reflects the total change occurring between the two time points codes 0 and 1, and the freely estimated loadings represent the proportion of change ($\mu_{\beta_{yk}}$) occurring at each specific time point (and are associated with profile-specific statistical significance tests).

Additional Non-linear Specifications

For a description of additional functional forms (exponential, logistic, gompertz, etc.), interested readers should consult Blozis (2007), Browne and Du Toit (1991), and Grimm et al. (2016). However, it is important to note that in these more complex operationalizations, the non-linear parameter describing the functional form would always be non-random. In more practical terms, if we take the example of an exponential trajectories, this means that despite the fact that the total amount of change occurring over time would be allowed to differ across individuals and profiles, the exponential shape itself would be assumed to be the same across all individuals and profiles.

Alternative Parameterizations

As noted above in the Latent Profile Analysis section, LPA can be estimated using more or less restricted parameterizations depending on whether the variances of the profile indicators are constrained to be equal across profiles or not. GMA are even more complex given that the profiles can be defined allowing any or all parameters from a LCM (the mean of the growth factors, the variances-covariances of the growth factors, the time-specific residuals) to be freely estimated in all profiles or not. However, fully-variant GMA are seldom estimated, potentially because these more complex models tend to more frequently run into estimation and convergence problems.

Among the simpler parameterizations, Nagin's (1999) group-based latent class growth analysis (LCGA) constrains the variances of the growth factors (e.g., α_{iyk} , β_{1iyk} , β_{2iyk}) to be exactly zero (i.e., a fixed effects model), thus taking out the latent variance-covariance matrix from the model ($\Phi_{yk} = 0$). LCGA thus force all members of the profile to follow the exact same trajectory, absorbing any deviation from this trajectory into the time-specific residuals. LCGA also typically assumes these time-specific residuals to be equal across profiles ($\varepsilon_{yitk} = \varepsilon_{yit}$). Another common restricted GMA is linked to the defaults of the Mplus package (Muthén & Muthén, 2018), which freely estimate $\mu_{\alpha_{yk}}$, $\mu_{\beta_{1yk}}$ and $\mu_{\beta_{2yk}}$ in all profiles but constrain the latent variance-covariance parameters and the time-specific residuals to be equal

across the profiles ($\Phi_{yk} = \Phi_y$ and $\varepsilon_{yitk} = \varepsilon_{yit}$). A final type of restriction, stemming from the multilevel growth modeling tradition (Li & Hser, 2011; Tofighi & Enders, 2007), would be to set the time-specific residuals to equality across time points (homoscedastic), while allowing them to differ ($\varepsilon_{yitk} = \varepsilon_{yik}$) or not ($\varepsilon_{yitk} = \varepsilon_{yi}$) across profiles. This restriction relies on the assumption that the model explains individuals' responses equally well across time points.

In discussing these restrictions, Morin, Maïano et al. (2011) presented them as untested invariance assumptions that are unlikely to hold in real life and generally fails to be supported when empirically tested. Using a real data set, they further showed that these restricted parameterizations could result in drastically different conclusions. Unfortunately, arguments supporting the adequacy of these restricted parameterizations are seldom provided in applied research, and tests of these assumptions (which are easy to conduct using the information criteria and LRTs) are almost never implemented (but see Muthén, 2004; Reinecke & Seddig, 2011). An extensive simulation study conducted by Diallo, Morin, and Lu (2016) supported Morin, Maïano et al. (2011) conclusions, leading them to recommend that the LCGA parameterization should be avoided and that, whenever possible, GMA should be estimated while allowing all model parameters to be freely estimated in all profiles. However, this recommendation comes with the recognition that this free estimation of all model parameters is not always possible due to the tendency of these more complex models to converge on improper solutions, or not to converge at all (Diallo et al., 2016), which is typically taken to reflect overparameterization and the need to rely on simpler models (e.g., Bauer & Curran, 2003; Chen, Bollen, Paxton, Curran, & Kirby, 2001).

As for LPA, more flexible models are thus likely to provide a much richer perspective, although the ability to estimate more flexible models is likely to be limited with smaller samples, or fewer time points. For this reason, we recommend to always start with the estimation of more complex models allowing the profiles to be defined based on the complete LCM, and then to slowly impose constraints when less restricted models fail to converge on proper solutions. It should be noted that, as for LCM, sample size issues for GMA are not limited to the number of participants, but it is also necessary to take into account the number of measurement points so that more measurement occasions can offset sample size limitations (Diallo & Morin, 2015; Diallo, Morin, & Parker, 2014).

In sum, whenever possible, we suggest that GMA be estimated with a fully independent within-profile LCM: $\mu_{\alpha yk}$, $\mu_{\beta 1 yk}$, $\mu_{\beta 2 yk}$, $\zeta_{\alpha yik}$, $\zeta_{\beta 1 yik}$, $\zeta_{\beta 2 yik}$, Φ_{yk} , ε_{yitk} , and even λ_{tk} in latent basis models. Should GMM users face convergence problems, we suggest that the following sequence of constraints should be implemented: (1) $\varepsilon_{yitk} = \varepsilon_{yik}$; (2) $\varepsilon_{yitk} = \varepsilon_{yit}$; (3) $\Phi_{yk} = \Phi_y$; (4) $\varepsilon_{yitk} = \varepsilon_{yi}$; (5) $\Phi_{yk} = \Phi_y$ and $\varepsilon_{yitk} = \varepsilon_{yik}$; (6) $\Phi_{yk} = \Phi_y$ and $\varepsilon_{yitk} = \varepsilon_{yit}$; (7) $\Phi_{yk} = \Phi_y$ and $\varepsilon_{yitk} = \varepsilon_{yi}$. However, this sequence should not be followed blindly and should be adapted to the specific research question and context.

The Role of Time

One critical issue that often tends to be misunderstood or ignored in applied research is that LCM/GMA estimate longitudinal trajectories defined as a function of time. Thus, a strong assumption of these models is that the trajectories can be assessed as a function of a meaningful time referent (Metha & West, 2000). For instance, although modeling longitudinal trajectories as a function of the time of measurement might make sense for a cohort of children all recruited at the same age or developmental period, it might not make sense in a study of high schoolers recruited across all grade levels. In this second context, a more meaningful metric of time might be required. For studies relying on participants differing from one another in terms of age (or grade level in educational studies, or even tenure level in organizational studies), Metha and West (2000) proposed an easy-to-implement test to assess whether it would be proper to rely

on uniform time codes based on the time of measurement despite this variation. More precisely, they noted that age (or grade level, or tenure) could be considered to be negligible when: (1) the regression of the intercept of a LCM on age is equal to the slope factor, and (2) the regression of the slope factor on age of this LCM is equal to zero. In the online supplements, we show how to conduct this verification.

Still, there will be situations in which age (or grade level, or tenure) ends up having a non-negligible impact on individual trajectories, or when one would specifically want to model growth trajectories as a function of individually-varying time codes. For this specific context, Grimm et al. (2016) proposed a simple approach, which we illustrate at the end of the online supplements, allowing researchers to estimate trajectories based on individually-varying time codes reflecting participants' age, grade-level, or tenure. This approach can easily be extended for studies in which participants are simply not measured at the same moment.

Mixture Modeling with Covariates

A major advantage of GSEM over other types of person-centered analyses comes from the possibility to directly include covariates (predictors, correlates or outcomes; see Model 1 in Figure 1) to the model. By combining analyses, this direct inclusion of covariates helps to limit Type 1 errors and can reduce biases in the estimation of the relationships between covariates and the profiles (Bolck, Croon, & Hagenars, 2004). Covariates can be conceptualized as having an impact on profile membership (predictors), as being impacted by profile membership (outcomes), or as being related to profile membership with no assumption of directionality of the associations (correlates). Because these three types of covariates are included using different approaches, this distinction needs to be made a priori, on the basis of theoretical expectations and research background. After years of oscillating between alternative recommendations, a series of statistical simulation studies have established that covariates should be included to the model once the optimal unconditional solution has been selected (Diallo, Morin, & Lu, 2017a; Hu, Leite, & Gao, 2017; Nylund-Gibson, & Masyn, 2016), rather than included from the start before having selected the model including the most optimal number of profiles. Likewise, including covariates to the final unconditional model should not modify the nature of the profiles, given that such a change would indicate a violation of the assumption that the direction of the relation goes from the predictors to the profiles, or from the profiles to the outcomes (Marsh et al., 2009; Morin, Morizot et al., 2011).

Direct Inclusion

With these caveats in mind, there is a general recognition of the advantage of the direct inclusion approach of predictors and outcomes directly into the final retained solution (e.g., Diallo & Lu, 2017). To ensure that such inclusion does not result in a switch in profile definition, it is often useful to estimate the conditional model (the model with covariates) using starts values taken from the final unconditional model (the model without covariates) while turning off the random start function (that is no longer useful). With the outcomes, this direct inclusion approach involves their specification as additional profile indicators, and provide a way to conduct specific tests of mean differences in outcomes levels across profiles (see the online supplements for examples of this approach). Using this direct inclusion approach for the predictors results in the estimation of a multinomial logistic regression representing the relations between the predictor and the likelihood of membership into the various profiles. In multinomial logistic regressions, each predictor has $k-1$ (with k being the number of profiles) effects for each possible pairwise comparison of profiles. The regression coefficients reflect the expected increase, for each unit of increase in the predictor, in the log-odds of the outcome (the probability of membership in one profile versus another). Odds ratios (OR) are also typically reported, and reflect the change in the likelihood of membership in a target profile versus a comparison profile for each unit of increase in the predictor (e.g., OR = 2 means that each unit of increase in the predictor is associated with participants being twice more likely to be member

of the target, versus comparison, profile).

Automated Auxiliary Approaches

However, in many situations, covariate inclusions will result in a change in profile definition. Fortunately, a variety of “auxiliary”, or inactive, approaches have been proposed to allow for the estimation of associations between profiles and covariates without allowing these covariates to change the nature of the profiles (Asparouhov & Muthén, 2014; Lanza, Tan & Bray, 2013; Vermunt, 2010; for an illustration see Wickrama et al., 2016). So far, three main approaches exist, and have been automated in the Mplus statistical package. The first of these approaches, is usually referred to as the BCH approach (and is implemented in Mplus using the BCH function) in reference to its development by Bolck et al. (2004), despite the fact that this approach was improved by Vermunt (2010; also see Bakk, Tekle, & Vermunt, 2013). Essentially, the BCH approach conducts a weighted multiple group comparison in which the weights are a function of the classification probabilities. This approach is limited to the consideration of continuous outcomes. The second auxiliary approach is model based and was proposed by Lanza et al. (2013) to contrast profiles on the basis of continuous (using the DCON function in Mplus) or categorical outcome variables (using the DCAT function in Mplus). This approach regresses the profiles on the outcomes, before reversing this link function using Bayes’ theorem. The third auxiliary approach, the so-called “three-step” approach (Asparouhov & Muthén, 2014; Vermunt, 2010), relies on the modal profile membership obtained from the final unconditional model (step 1), which is then used as a nominal profile indicator in the estimation of a new latent profile solution in which classification logits are used to retain a probability-based classification (step 2). This new solution is then used in further analyses (step 3). This three step approach can be used both for predictors (using the R3STEP function in Mplus) or outcomes (using the DU3STEP function in Mplus, or the DE3STEP function should one want the outcome variances to be set to equality across profiles).

So far, statistical research on the relative efficacy of these approaches shows that they all tend to perform well, although they all present limitations in specific conditions (Asparouhov & Muthén, 2014; Bakk, Oberski, & Vermunt, 2016; Bakk & Vermunt, 2016; Bakk et al., 2013; Collier & Leite, 2017; Lanza et al., 2013; McLarnon & O’Neill, 2018; Vermunt, 2010). For example: (a) the Lanza et al. (2013) approach tends to underperform when outcomes’ variances are unequal across class and entropy is low; (b) the BCH approach may sometimes fail, resulting in extreme or impossible parameter estimates, and does not perform as well when the entropy or sample sizes are low; (c) the three-step approach sometimes still results in a shift in profile definition. Our own experiences with these approaches suggests that, when they perform correctly, they all tend to produce similar estimates, although the standard errors of these estimates are sometimes lower (showing greater precision) with the Lanza et al. (2013) approach, which also tends to present lower type 1 error rates (Collier & Leite, 2017).

Correlates

We have so far discussed the inclusion of predictors and outcomes to the model. When considering correlates, Meyer and Morin (2016) have previously recommended yet another, older, auxiliary approach (implemented via the E function in Mplus) relying on a Wald chi-square test of statistical significance based on pseudo-class draws (Asparouhov & Muthén, 2007; Wang, Brown, & Bandeen-Roche, 2005), as this approach does not assume directionality in the associations between profiles and correlates. Still, the weaker performance of this approach in the aforementioned simulation studies suggests that it could possibly be replaced by any of the other auxiliary approaches designed for outcome variables.

Manual Auxiliary Approaches

A key limitation of all of the automated auxiliary approaches comes from the fact that they are unable to simultaneously consider predictors and outcomes variables, chains of relations (i.e., mediation, moderation), or outcome levels corrected for some controlled variables.

Likewise, these approaches cannot be used in models involving more than one latent categorical variables, such as in multiple group tests of profile similarity, or LTA. For most of contexts involving a single latent categorical variable, it is however possible to manually implement both the BCH and the three-step approaches, although the manual BCH approach has limitations related to missing data. However, only the three-step approach can be implemented in models involving more than one latent categorical variable. Interested readers can consult McLarnon and O'Neill (2018) in which the manual implementation of both the BCH and three-step approaches is illustrated for tests of mediation, moderations, and controlled-based mean comparisons involving LPA. Likewise, Morin and Litalien (2017) discuss the manual implementation of the three-step approach in models including more than one latent categorical variable.

Growth Mixture Analyses with Covariates

Covariate questions are slightly more complex in the context of GMA, given that predictions can involve the intercept and slope factors, in addition to profile membership in a way that could easily become mind-boggling. To simplify prediction issues in the context of GMA, Morin et al. (2012, 2013) suggest that it might be preferable to rely on a stepwise approach to the incorporation of predictors, in which a null effects model (i.e., predictors effects are constrained to be zero) is compared to a series of alternative models in which the predictors are allowed to sequentially predict: a) profile membership; b) profile membership and the growth factors; c) profile membership and the growth factors in a way that differs across profiles. Selection of the optimal model can then be helped by a consideration of model fit information. A similar procedure could be implemented with outcomes, as well as with time-varying covariates (Diallo, Morin, & Lu, 2017b) which could be allowed to predict the repeated measure in a way that is identical across profiles and time points and then allowed to differ across profiles and/or time points. For situations in which covariates result in change in profile membership, the aforementioned BCH and three-step procedures could easily be implemented manually in combination with the extraction of factor scores representing the intercept and slope factors to allow for the estimation of the same sequence of predictive tests.

Conclusion

In this chapter, we presented a broad introduction to person-centered mixture modeling, with a more specific focus on longitudinal applications, and tried to illustrate the heuristic potential of this methodological framework for lifespan developmental research. As noted in this chapter, mixture modeling is an exploratory person-centered method that is typological and prototypical in nature, through which individuals are classified in subgroups (or class) based on their characteristics. We would like to remind the reader that person- and variable-centered approaches should be viewed as complementary, rather than as opposite, and can be combined to provide a more complete view of the same reality. Following Marsh and Hau (2007) call for substantive-methodological synergy, we sought to provide a user-friendly introduction to these complex models, aiming to help developmental researchers to better understand and apply these advanced methodologies. We hope that we achieved this objective, and that reading this chapter will motivate readers to pursue their exploration in a more autonomous manner, and help them to generate and test creative research ideas. Still, it is important to keep in mind that, irrespective of our ability to achieve this objective, mixture models remain complex, and quite challenging for inexperienced researchers. We thus recommend to start with simpler models (LPAs, LPAs with covariates, FMAs), before moving on to more complex models (multiple-group LPAs, or LTAs), and to even more complex models (MRAs and GMAs). We hope that the various possibilities offered by these models will motivate lifespan developmental researchers to overcome this complexity.

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**Supplements for:
Mixture Modeling for Lifespan Developmental Research**

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Acknowledgements. The authors want to thank Matthew J.W. McLarnon for picking up a few mistakes in an earlier version of this document.

Appendix A

Technical Considerations in the Estimation of Mixture Models

Mixture Indicators

Mixture models are most often estimated using scale scores on the various indicators of interest (i.e., taking the sum or average on the items used to assess a component and using this aggregated score as the indicator). The limitation of this approach is that scale scores are known to be tainted by (or uncorrected for) measurement error. In contrast, latent variable (i.e., models where the items are used to estimate latent factors, which are then used as mixture indicators) are naturally controlled for measurement error (e.g., Bollen, 1989). Unfortunately, applications of fully latent mixture models are still few (e.g., Morin, Scalas, & Marsh, 2015), which can be explained by computational complexity of mixture models which makes it often impossible to implement a fully latent approach due to nonconvergence or convergence on improper solutions. An alternative is to rely on factor scores taken from preliminary measurement models (e.g., Kam, Morin, Meyer, & Topolnytsky, 2015; Morin & Marsh, 2015). Although factors scores do not explicitly control for measurement errors as well as latent variables, they do provide a partial implicit control for measurement errors (by giving more weight to more reliable item). As such, they tend to provide researchers with a stronger alternative than scale scores. In addition, factors scores tend to preserve the nature of the underlying measurement structure (e.g., methodological controls, bifactor models, cross-loadings) far better than scale scores (Morin, Boudrias et al., 2016, 2017). A third advantage of factor scores, which appears to be critically important in the context of cross cultural and/or longitudinal research is that preliminary measurement models can be used to systematically assess the measurement invariance of the measures across groups and/or time points (Millsap, 2011). Factor scores can then be saved from the most invariant measurement model, thus ensuring the comparability of the results across groups or time points. A final advantage of factors scores comes from their natural standardization, making them directly and easily interpretable with a mean of zero and a variance of one.

Random Starts

Technically, mixture models are estimated through an iterative process that risks converging on a local solution rather than on a true maximum likelihood when starts values are not adequate (Hipp & Bauer, 2006). For this reason, best practice is to estimate mixture models using multiple set of random start values, and allowing these starts values to iterate sufficiently (Hipp & Bauer, 2006; McLachlan & Peel, 2000). Despite a general recognition that “the more, the better” applies to random starts, increasing the number of random starts also requires substantially more computational time. In practice, our recommendation is to use at least 3000 sets of random starts, 100 iterations for each of these sets of starts values, and to retain at least the 100 best sets of starts values for final stage optimization. These values can be increased to 5000, 200, and 200 when the final solution is not sufficiently replicated. We see these values as a minimum that can be increased as needed, and often use even larger values in our own research (e.g., 10000, 1000, 500).

Class Enumeration

Alternative solutions including different number of latent profiles (from one to a number typically above theoretical expectations but generally lower than 10) are typically contrasted in order to select the final solution. Selection of the optimal number of profiles is determined based on inspection of: (a) the substantive meaning and theoretical conformity of the solution; (b) the statistical adequacy of the solution and (c) statistical indicators. We focus here on these statistical indicators: The Akaike Information Criterion (AIC), the Consistent AIC (CAIC), the Bayesian information criterion (BIC), and the sample-adjusted BIC (SABIC). Although the CAIC is not routinely provided in the Mplus statistical package, it can be easily calculated as BIC + the number of free parameters. A lower value on these indicators suggests a better-fitting

model. Classical likelihood ratio tests (LRT) are appropriate for the comparisons of nested models based on the same variables and number of profiles, but inappropriate for class enumeration purposes. For this purpose, two LRT approximations are available: The Lo, Mendel and Rubin's (2001) LRT (the standard and adjusted version of this test typically yield the same conclusions), and the Bootstrap LRT (BLRT; McLachlan & Peel, 2000). These tests compare a k -profile model with a $k-1$ -profile model. Non-significant p values indicate that the $k-1$ profile model should be retained. Finally, although it should not be used for class enumeration purposes the entropy provides a summary indicator of classification accuracy, with larger values (closer to 1) indicating fewer classification errors.

Multiple simulation studies (for a recent review, see Diallo, Morin, & Lu, 2016) indicate that four of these indicators (CAIC, BIC, ABIC, and BLRT) are particularly effective, while the AIC and LMR/ALMR should not be used (Diallo, Morin, & Lu, 2016, 2017; Henson et al., 2007; McLachlan & Peel, 2000; Nylund, Asparouhov, & Muthén, 2007; Peugh & Fan, 2013; Tein, Coxe, & Cham, 2013; Tofighi & Enders, 2008; Tolvanen, 2007; Yang, 2006). When these indicators fail to retain the optimal model, the BIC and CAIC tend to underestimate the true number of profiles, while the AIC, ABIC, and BLRT tend to overestimate it. A recent simulation study (Diallo, Morin, & Lu, 2017) further suggests that the BIC and CAIC should be privileged under conditions of high entropy ($\geq .800$), whereas the ABIC and BLRT perform better in conditions of low entropy ($\leq .600$). However, these indicators are heavily influenced by sample size (Marsh et al., 2009), which means that with a sufficiently large sample, they may keep on suggesting the addition of profiles without ever converging on a preferable solution. When this happens, it is recommended to present these indicators in the format of "elbow plots" (Morin, Maïano, et al., 2011; Petras & Masyn, 2010). These plots illustrate the gains in fit associated with the addition of profiles, and the point after which the slope flattens is typically indicates the optimal number of profiles.

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Appendix B

Mplus Input Code for the Estimation of Mixture Models

In Mplus syntax, text sections preceded by an exclamation mark (!) are annotations.

DATA

The first part of the Mplus syntax identify the data set to be used in the analysis. If the data set is in the same folder as the input file (which we recommend), only the name of the data set needs to be indicated. If the data set is in another folder, then the full path needs to be specified. Here, the data set is labeled “filename.dat” and is located in the same folder.

```
DATA:
FILE IS filename.dat;
```

VARIABLE

In the VARIABLE section, the NAMES function identifies all variables included in the data set, in order of appearance. The USEVARIABLES function defines the variables to be used in the analysis. The MISSING function defines the missing data code (we typically use the same code for all variables). The IDVARIABLE function defines the unique identifier for participants. The CLASSES function defines the number of latent profiles to be estimated (here 3). The USEOBS function can be used to limit the estimation to a subset of participants. In this example, the function would limit the estimation to females (identified in the variable Gender, coded 1: males; 2: females). The CLUSTER function can be used to define the unique identifier for a clustering (level 2) variable to be controlled in the analysis (e.g., classrooms).

```
VARIABLE:
NAMES = ID Gender Classroom Pred1 Pred2 Cor1 Cor2 Out1 Out2 IND1_T1 IND2_T1
IND3_T1 IND1_T2 IND2_T2 IND3_T2;
USEVARIABLES = IND1_T1 IND2_T1 IND3_T1;
MISSING = all (999);
IDVARIABLE = ID;
CLASSES = c (3);
! CLUSTER = Classroom;
! USEOBS Gender EQ 2;
```

ANALYSIS:

The ANALYSIS section describes the analysis itself. Here, we request the estimation of a mixture model (TYPE = MIXTURE) including a correction for the nesting of participants within a higher level unit (i.e., classrooms) (TYPE = COMPLEX) and using the robust maximum likelihood estimator (ESTIMATOR = MLR). STARTS = 3000 100 requests 3000 sets of random start values, with the best 100 of these starts retained for final stage optimization. STITERATIONS = 100 requests that all random starts be allowed 100 iterations. PROCESS = 3 uses 3 of the available processors to speed up the estimation.

```
Analysis:
TYPE = MIXTURE COMPLEX;
ESTIMATOR = MLR; PROCESS = 3;
STARTS = 3000 100; STITERATIONS = 100;
```

The best way to ensure that the final solution represents a true maximum likelihood rather than a local solution is to increase the number of starts values. As part of the output, Mplus provides the loglikelihood values associated with all of the random starts retained for the final stage optimization. It will also indicate how many of the start value runs did not converge.

RANDOM STARTS RESULTS RANKED FROM THE BEST TO THE WORST
LOGLIKELIHOOD VALUES

15 perturbed starting value run(s) did not converge.

Final stage loglikelihood values at local maxima, seeds, and initial stage start numbers:

-6095.887	991399	1433
-6095.887	165268	2436
-6095.887	551639	55
-6095.887	58353	1723
-6095.887	168648	1788
-6095.887	445692	2796
-6095.887	973369	202
-6095.887	623887	2611
-6096.828	163110	584
-6096.828	762461	425
-6096.828	62715	2599
-6104.647	264951	1130
-6104.647	930872	277
-6104.647	670998	1876
-6104.698	98068	998
-6105.491	361131	2563

...

In this example, the best loglikelihood value was replicated 8 times (in bold, the number of times the value of -6095.887 appears in the first column), which is satisfactory. Although no clear-cut rule exists, we suggest that solutions should be replicated at least 3 times. Failing to do so, additional tests should be conducted while increasing the number of start values and/or iterations or using user-defined starts values. For instance, the starts values from the best fitting non-replicated solution are provided when requesting SVALUES in the output section of the syntax. These starts values can be used in the model section while keeping the random starts function active (we provide an example below). The second column provides the model seed associated with each random start. Using the seed provides an easy way to replicate the final solution (or any other solution) while decreasing computational time. To do so, the following ANALYSIS section can be used to replicate the above solution. This seed however will not ensure that the solution is replicated if additional covariates are added to the model (SVALUES then need to be used).

```
Analysis:
TYPE = MIXTURE COMPLEX;
ESTIMATOR = MLR;
PROCESS = 3;
STARTS = 0;
OPTSEED = 991399;
STITERATIONS = 100;
```


MODEL

In between the ANALYSIS and OUTPUT section, the MODEL section describes the specific analysis to be conducted. We provide code, in sequence, for each of the models described in the manuscript.

OUTPUT

The last section of the syntax covers specific sections of the output that are requested. Here we request standardized model parameters (STDYX), sample statistics (SAMPSTAT), confidence intervals (CINTERVAL), the starts values corresponding to the solution (SVALUES), the residuals (RESIDUAL), the arrays of parameter specifications and starting values (TECH1), the profile-specific sample characteristics (TECH7), the LMR and aLMR (TECH11), and the BLRT (TECH14).

OUTPUT:

```
STDYX SAMPSTAT CINTERVAL SVALUES RESIDUAL TECH1 TECH7 TECH11  
TECH14;
```

Latent Profile Analysis

The MODEL section includes an %OVERALL% section describing the global relations estimated among the constructs, and profile specific statements (here %c#1% to %c#3%, where c corresponds to the label used to define the categorical latent variable in the CLASSES command of the VARIABLE: section, and the number 1 to k refers to the specific value of this variable (the specific profile). Here, no relations are estimated between the variables so nothing appears in the %OVERALL% section. In this example, three profiles are estimated from three indicators taken at the first time point (IND1_T1, IND2_T1, and IND3_T1). The profile specific sections request that the means (indicated by the name of the variable between brackets []) and variances (the names only) of the indicators be freely estimated in all profiles.

```
MODEL:
%OVERALL%
%c#1%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
%c#2%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
%c#3%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
```

Profiles can also be estimated with equal variances across profiles:

```
MODEL:
%OVERALL%
%c#1%
[IND1_T1 IND2_T1 IND3_T1];
%c#2%
[IND1_T1 IND2_T1 IND3_T1];
%c#3%
[IND1_T1 IND2_T1 IND3_T1];
```

And with correlated uniquenesses (correlations are identified by WITH) among all profile indicators (not recommended), where the correlations are invariant across profiles:

```
MODEL:
%OVERALL%
IND1_T1 WITH IND2_T1 IND3_T1; IND2_T1 WITH IND3_T1;
%c#1%
[IND1_T1 IND2_T1 IND3_T1]; IND1_T1 IND2_T1 IND3_T1;
%c#2%
[IND1_T1 IND2_T1 IND3_T1]; IND1_T1 IND2_T1 IND3_T1;
%c#3%
[IND1_T1 IND2_T1 IND3_T1]; IND1_T1 IND2_T1 IND3_T1;
```

With correlated uniquenesses among all profile indicators (not recommended) where the correlations are freely estimated in all profiles:

```
MODEL:
%OVERALL%
IND1_T1 WITH IND2_T1 IND3_T1; IND2_T1 WITH IND3_T1;
%c#1%
[IND1_T1 IND2_T1 IND3_T1]; IND1_T1 IND2_T1 IND3_T1;
IND1_T1 WITH IND2_T1 IND3_T1; IND2_T1 WITH IND3_T1;
%c#2%
[IND1_T1 IND2_T1 IND3_T1]; IND1_T1 IND2_T1 IND3_T1;
IND1_T1 WITH IND2_T1 IND3_T1; IND2_T1 WITH IND3_T1;
%c#3%
[IND1_T1 IND2_T1 IND3_T1]; IND1_T1 IND2_T1 IND3_T1;
IND1_T1 WITH IND2_T1 IND3_T1; IND2_T1 WITH IND3_T1;
```

When SVALUES are requested, the output will include a section similar to the following. This section can be cut-and-pasted and used as a replacement of the MODEL section in conjunction with the STARTS function set to 0 (STARTS = 0) to replicate the final solution. This function is particularly useful when one wants to include covariates in a model while making sure that the final unconditional LPA solution remains unchanged.

```
MODEL COMMAND WITH FINAL ESTIMATES USED AS STARTING VALUES
%OVERALL%
[ c#1*-0.93515 ];
[ c#2*0.49113 ];
%C#1%
[ IND3_T1*0.39664 ];
[ IND2_T1*-0.93155 ];
[ IND1_T1*-1.59367 ];
IND3_T1*1.59137;
IND2_T1*2.12542;
IND1_T1*0.53789;
%C#2%
[IND3_T1*-0.15201 ];
[IND2_T1*-0.29812 ];
[IND1_T1*-0.18248 ];
IND3_T1*0.72513;
IND2_T1*0.43116;
IND1_T1*0.42376;
%C#3%
[IND3_T1*0.08333 ];
[IND2_T1*0.86526 ];
[IND1_T1*0.94111 ];
IND3_T1*1.13489;
IND2_T1*0.48030;
IND1_T1*0.44053;
```

Latent Profile Analysis with Covariates

Predictors

Direct inclusion of predictors to the model is done by way of a multinomial logistic regression where the predictors are specified as having an impact on profile membership (c#1-c#2 ON Pred1 Pred2; one less statement than the total number of profiles is necessary) in the %OVERALL% section.

```
MODEL:
%OVERALL%
c#1-c#2 ON Pred1 Pred2;
%c#1%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
%c#2%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
%c#3%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
```

To ensure that the nature of the profiles remains unchanged by the inclusion of predictors, the SVALUES from the final solution can be used, and the random starts function turned off (STARTS = 0;). If this is not sufficient, the class specific (%C#1% to %C#3%) starts values can be fixed (using @ rather than *). The starts values used in the %OVERALL% section to describe the class probabilities should not be fixed ([c#1*-0.93515];

```
%OVERALL%
[ c#1*-0.93515 ]; [ c#2*0.49113 ];
c#1-c#2 ON Pred1 Pred2;
%C#1%
[ IND3_T1*0.39664 ]; [ IND2_T1*-0.93155 ]; [ IND1_T1*-1.59367 ];
IND3_T1*1.59137; IND2_T1*2.12542; IND1_T1*0.53789;
%C#2%
[IND3_T1*-0.15201 ]; [IND2_T1*-0.29812 ]; [IND1_T1*-0.18248 ];
IND3_T1*0.72513; IND2_T1*0.43116; IND1_T1*0.42376;
%C#3%
[IND3_T1*0.08333 ]; [IND2_T1*0.86526 ]; [IND1_T1*0.94111 ];
IND3_T1*1.13489; IND2_T1*0.48030; IND1_T1*0.44053;
```

Among all available AUXILIARY approaches, the R3STEP (see Asparouhov & Muthén, 2014) is the most naturally suited to predictors. This approach is similar to the multinomial logistic regression described above, but explicitly tests whether including the predictors resulted in a change in the nature of the profile. When this occurs (and the previous direct approaches do not work), then predictors need to be treated as correlates. To use this approach, the following line of code needs to be included to the VARIABLE section (in bold). The Model section remains unchanged (the use of start values may help).

```
VARIABLE:
NAMES = ID Gender unit Pred1 Pred2 Cor1 Cor2 Out1 Out2 IND1_T1 IND2_T1 IND3_T1
IND1_T2 IND2_T2 IND3_T2;
USEVARIABLES = IND1_T1 IND2_T1 IND3_T1;
MISSING = all (999);
IDVARIABLE = ID;
CLASSES = c (3);
AUXILIARY = Pred1 (R3STEP) Pred2 (R3STEP);
```

Outcomes

The direct inclusion of outcomes involves adding them as additional mixture indicators, preferably while using the SVALUES from the final solution to ensure stability in the nature of the profiles. Parameter labels are given to the means of the outcome variables in each profile (in parentheses), and these labels can be used with the MODEL CONSTRAINT command to provide tests of significance of differences between profiles on the various outcomes.

```
%OVERALL%
[ c#1*-0.93515 ]; [ c#2*0.49113 ];
%C#1%
[ IND3_T1*0.39664 ]; [ IND2_T1*-0.93155 ]; [ IND1_T1*-1.59367 ];
IND3_T1*1.59137; IND2_T1*2.12542; IND1_T1*0.53789;
[Out1] (oa1); [Out2] (ob1);
%C#2%
[IND3_T1*-0.15201 ]; IND2_T1*-0.29812 ]; [IND1_T1*-0.18248 ];
IND3_T1*0.72513; IND2_T1*0.43116; IND1_T1*0.42376;
[Out1] (oa2); [Out2] (ob2);
%C#3%
[IND3_T1*0.08333 ]; [IND2_T1*0.86526 ]; [IND1_T1*0.94111 ];
IND3_T1*1.13489; IND2_T1*0.48030; IND1_T1*0.44053;
[Out1] (oa3); [Out2] (ob3);
MODEL CONSTRAINT:
! New parameters are created using this function and reflect pairwise mean differences between
! profiles. (e.g., y12 reflect the differences between the means of profiles 1 and 2 on Out1)
NEW (y12);
y12 = oa1-oa2;
NEW (y13);
y13 = oa1-oa3;
NEW (y23);
y23 = oa2-oa3;
NEW (z12);
z12 = ob1-ob2;
NEW (z13);
z13 = ob1-ob3;
NEW (z23);
z23 = ob2-ob3;
```

Three AUXILIARY approaches (see Asparouhov & Muthén, 2014) are available. The first one is similar to the R3STEP approach and tests the degree to which continuous outcomes change the nature of the profiles. This approach can either allow for the variances of the outcomes to be freely estimated in all profiles (DU3STEP) or invariant across profiles (DE3STEP). A more recent alternative (BCH) has been shown to outperform these approaches, while ensuring the stability of the profile solutions. Finally, a last approach also ensures the stability of the profile solution, while accommodating continuous (DCON) and categorical (DCAT) outcomes.

```
! Pick between these alternatives:
AUXILIARY = Out1 (DU3STEP) Out2 (DU3STEP);
AUXILIARY = Out1 (DE3STEP) Out2 (DE3STEP);
AUXILIARY = Out1 (BCH) Out2 (BCH);
AUXILIARY = Out1 (DCON) Out2 (DCON);
AUXILIARY = Out1 (DCAT) Out2 (DCAT);
```

Correlates

Correlates can be incorporated to the model via the Auxiliary (e) approach.

```
AUXILIARY = Cor1 (e) Cor2 (e);
```

Factor Mixture Analysis

Presented next is the input for the factor mixture analyses that can be used as a way to control for global levels shared among the indicators (e.g., global levels of life satisfaction) in order to estimate clearer latent profiles. The only difference with the previous LPA models is the introduction of a common factor model in the %OVERALL% section. This factor model is specified as invariant across profiles. This common factor is labeled G, and defined by the same indicators that are used to estimate the latent profiles (BY defines factor loadings). All loadings on this factor are freely estimated (the * associated with the first indicators overrides the default of constraining the loading of the first factor to be 1). The factor variance thus needs to be fixed to 1 for identification purposes (the @ is used to fix a parameter to a specific value). Because the intercepts of the indicators of this factor will be freely estimated across profiles, the factor means needs to be fixed to 0 for identification purposes.

```
MODEL:
%OVERALL%
G BY IND1_T1* IND2_T1 IND3_T1;
G@1;
[G@0];
%c#1%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
%c#2%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
%c#3%
[IND1_T1 IND2_T1 IND3_T1];
IND1_T1 IND2_T1 IND3_T1;
```

Multiple-Group Latent Profile Analyses: Configural Similarity

In the VARIABLE section, the multiple groups need to be defined using the KNOWCLASS function, which uses a label (here we use cg) to define this new grouping variable. In our example, we use two subgroups referring to males and females. However, more than two groups can be used for any relevant subpopulation or subgroups (e.g., cultural groups). Here, the levels of this grouping variable are defined as: (a) including participants with a value of 1 (males) on the variable Gender, and (b) including participants with a value of 2 (females) on the variable Gender. There are now two “latent” grouping variables, C estimated as part of the model estimation (the profiles) and having k levels (here we are still working with a 3-profile solution) and CG reflecting the observed subgroups (Gender) with 2 levels. Participants are allowed to be cross classified.

```
KNOWCLASS = cg (Gender = 1 Gender = 2);
CLASSES = cg (2) c (3);
```

The %OVERALL% section is used to indicate that the class sizes are freely estimated in all observed samples (males and females) using the ON function (reflecting regressions) indicating that profile membership is conditional on gender. Once again, $k-1$ statements are required (i.e., 2 for a 3-profile model). Profile-specific statements are then defined using a combination of the known classes CG and the estimated classes C. Similar labels in parentheses identify parameters that are estimated to be equal across groups. Here, none of the labels are shared between groups, so that the means and variances are freely estimated in all combinations of profiles across gender. Lists of constraints (m1-m3) apply to the parameters in order of appearance (m1 applies to IND1_T1, m2 to IND2_T1, m3 to IND3_T1).

```
%OVERALL%
c#1 on cg#1; c#2 on cg#1;

%cg#1.c#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3);
IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%cg#1.c#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6);
IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%cg#1.c#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9);
IND1_T1 IND2_T1 IND3_T1 (v7-v9);

%cg#2.c#1%
[IND1_T1 IND2_T1 IND3_T1] (mm1-mm3);
IND1_T1 IND2_T1 IND3_T1 (vv1-vv3);
%cg#2.c#2%
[IND1_T1 IND2_T1 IND3_T1] (mm4-mm6);
IND1_T1 IND2_T1 IND3_T1 (vv4-vv6);
%cg#2.c#3%
[IND1_T1 IND2_T1 IND3_T1] (mm7-mm9);
IND1_T1 IND2_T1 IND3_T1 (vv7-vv9);
```

Multiple-Group Latent Profile Analyses: Structural Similarity

The only difference between this model and the previous one is that the means are constrained to be equal across gender within each profile using identical labels in parentheses. Labels in bold were modified from the previous model.

```
%OVERALL%
c#1 on cg#1; c#2 on cg#1;

%cg#1.c#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3);
IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%cg#1.c#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6);
IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%cg#1.c#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9);
IND1_T1 IND2_T1 IND3_T1 (v7-v9);

%cg#2.c#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3);
IND1_T1 IND2_T1 IND3_T1 (vv1-vv3);
%cg#2.c#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6);
IND1_T1 IND2_T1 IND3_T1 (vv4-vv6);
%cg#2.c#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9);
IND1_T1 IND2_T1 IND3_T1 (vv7-vv9);
```

Multiple-Group Latent Profile Analyses: Dispersion Similarity

The only difference between this model and the previous one is that the variances are constrained to be equal across gender within each profile using identical labels in parentheses. Labels in bold were modified from the previous model.

```
%OVERALL%
c#1 on cg#1; c#2 on cg#1;

%cg#1.c#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3);
IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%cg#1.c#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6);
IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%cg#1.c#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9);
IND1_T1 IND2_T1 IND3_T1 (v7-v9);

%cg#2.c#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3);
IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%cg#2.c#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6);
IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%cg#2.c#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9);
IND1_T1 IND2_T1 IND3_T1 (v7-v9);
```


Multiple-Group Latent Profile Analyses: Distributional Similarity

The only difference between this model and the previous one is that nothing appears in the %OVERALL% section of the input to reflect the fact that the sizes of the profiles are no longer conditional on gender (or group membership).

```
%OVERALL%
```

```
%cg#1.c#1%
```

```
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
```

```
%cg#1.c#2%
```

```
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
```

```
%cg#1.c#3%
```

```
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
```

```
%cg#2.c#1%
```

```
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
```

```
%cg#2.c#2%
```

```
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
```

```
%cg#2.c#3%
```

```
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
```

Multiple-Group Latent Profile Analyses with Predictors: Relations Freely Estimated Across Subgroups

This model uses the SVALUES associated with the previous model of distributional similarity (specified as * followed by the value of the estimated parameters), and simply include predictor effects on profile membership (c#1-c#2 ON Pred1 Pred2;). To allow these effects to be freely estimated across gender, they need to be constrained to 0 in the %OVERALL% section, and freely estimated in both gender groups in a new section of the input specifically referring to CG. See all sections in bold.

```

%OVERALL%
[ cg#1*-0.00217 ]; [ c#1*-0.93515 ]; [ c#2*0.49113 ];
c#1-c#2 ON Pred1@0 Pred2@0;
%CG#1.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
%CG#1.C#2%
[IND3_T1*-0.15201 ] (m4); IND2_T1*-0.29812 ] (m5); [IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
%CG#1.C#3%
[IND3_T1*0.08333 ] (m7); [IND2_T1*0.86526 ] (m8); [IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
%CG#2.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
%CG#2.C#2%
[IND3_T1*-0.15201 ] (m4); IND2_T1*-0.29812 ] (m5); [IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
%CG#2.C#3%
[IND3_T1*0.08333 ] (m7); [IND2_T1*0.86526 ] (m8); [IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
MODEL cg:
%cg#1%
c#1-c#2 ON Pred1 Pred2;
%cg#2%
c#1-c#2 ON Pred1 Pred2;

```

Multiple-Group Latent Profile Analyses with Predictors: Predictive Similarity

This model is almost identical to the previous one. In order for the effects of the predictors to be constrained to similarity across gender, they simply need to be specified as freely estimated in the %OVERALL% section (c#1-c#2 ON Pred1 Pred2;), while taking out the gender specific sections. See the code line in bold.

```
%OVERALL%
[ cg#1*-0.00217 ]; [ c#1*-0.93515 ]; [ c#2*0.49113 ];
c#1-c#2 ON Pred1 Pred2;
%CG#1.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
%CG#1.C#2%
[IND3_T1*-0.15201 ] (m4); IND2_T1*-0.29812 ] (m5); [IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
%CG#1.C#3%
[IND3_T1*0.08333 ] (m7); [IND2_T1*0.86526 ] (m8); [IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
%CG#2.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
%CG#2.C#2%
[IND3_T1*-0.15201 ] (m4); IND2_T1*-0.29812 ] (m5); [IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
%CG#2.C#3%
[IND3_T1*0.08333 ] (m7); [IND2_T1*0.86526 ] (m8); [IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
```

Multiple-Group Latent Profile Analyses with Outcomes: Relations Freely Estimated Across Subgroups

This model also uses the SVALUES associated with the model of distributional similarity. Here, we simply request the free estimation of the distal outcome means in all profiles across gender ([Out1 Out2]). We also use labels in parentheses to identify these new parameters, which will then be used in a new MODEL CONSTRAINT section to request tests of the significance of mean differences between profiles within genders.

```
%OVERALL%
[ cg#1*-0.00217 ]; [ c#1*-0.93515 ]; [ c#2*0.49113 ];
%CG#1.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
[Out1] (oa1);
[Out2] (ob1);
%CG#1.C#2%
[ IND3_T1*-0.15201 ] (m4); [ IND2_T1*-0.29812 ] (m5); [ IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
[Out1] (oa2);
[Out2] (ob2);
%CG#1.C#3%
[ IND3_T1*0.08333 ] (m7); [ IND2_T1*0.86526 ] (m8); [ IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
[Out1] (oa3);
[Out2] (ob3);
%CG#2.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
[Out1] (oaa1);
[Out2] (obb1);
%CG#2.C#2%
[ IND3_T1*-0.15201 ] (m4); [ IND2_T1*-0.29812 ] (m5); [ IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
[Out1] (oaa2);
[Out2] (obb2);
%CG#2.C#3%
[ IND3_T1*0.08333 ] (m7); [ IND2_T1*0.86526 ] (m8); [ IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
[Out1] (oaa3);
[Out2] (obb3);

MODEL CONSTRAINT:
NEW (y12); y12 = oa1-oa2;
NEW (y13); y13 = oa1-oa3;
NEW (y23); y23 = oa2-oa3;
NEW (z12); z12 = ob1-ob2;
NEW (z13); z13 = ob1-ob3;
NEW (z23); z23 = ob2-ob3;
NEW (yy12); yy12 = oaa1-oaa2;
NEW (yy13); yy13 = oaa1-oaa3;
NEW (yy23); yy23 = oaa2-oaa3;
NEW (zz12); zz12 = obb1-obb2;
NEW (zz13); zz13 = obb1-obb3;
NEW (zz23); zz23 = obb2-obb3;
```

Multiple-Group Latent Profile Analyses with Outcomes: Explanatory Similarity

This model is almost identical to the previous one except that the parameter labels are used to constrain the outcome means to be invariant across gender. As a result, less lines of code are required in the MODEL CONSTRAINT section.

```

%OVERALL%
[ cg#1*-0.00217 ]; [ c#1*-0.93515 ]; [ c#2*0.49113 ];
%CG#1.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
[Out1] (oa1);
[Out2] (ob1);
%CG#1.C#2%
[IND3_T1*-0.15201 ] (m4); [IND2_T1*-0.29812 ] (m5); [IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
[Out1] (oa2);
[Out2] (ob2);
%CG#1.C#3%
[IND3_T1*0.08333 ] (m7); [IND2_T1*0.86526 ] (m8); [IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
[Out1] (oa3);
[Out2] (ob3);
%CG#2.C#1%
[ IND3_T1*0.39664 ] (m1); [ IND2_T1*-0.93155 ] (m2); [ IND1_T1*-1.59367 ] (m3);
IND3_T1*1.59137 (v1); IND2_T1*2.12542 (v2); IND1_T1*0.53789 (v3);
[Out1] (oa1);
[Out2] (ob1);
%CG#2.C#2%
[IND3_T1*-0.15201 ] (m4); [IND2_T1*-0.29812 ] (m5); [IND1_T1*-0.18248 ] (m6);
IND3_T1*0.72513 (v4); IND2_T1*0.43116 (v5); IND1_T1*0.42376 (v6);
[Out1] (oa2);
[Out2] (ob2);
%CG#2.C#3%
[IND3_T1*0.08333 ] (m7); [IND2_T1*0.86526 ] (m8); [IND1_T1*0.94111 ] (m9);
IND3_T1*1.13489 (v7); IND2_T1*0.48030 (v8); IND1_T1*0.44053 (v9);
[Out1] (oa3);
[Out2] (ob3);

MODEL CONSTRAINT:
NEW (y12); y12 = oa1-oa2;
NEW (y13); y13 = oa1-oa3;
NEW (y23); y23 = oa2-oa3;
NEW (z12); z12 = ob1-ob2;
NEW (z13); z13 = ob1-ob3;
NEW (z23); z23 = ob2-ob3;

```

Mixture Regression Analysis

Mixture regression analyses specify a regression model in the %OVERALL% section of the input indicating here that Out1 (an outcome of interest) is regressed (ON) a series of predictors from (IND1_T1 IND2_T1 IND3_T1). Then, the profile-specific sections of the input request that these regression coefficients be freely estimated in all profiles. In the basic mixture regression model, the mean and variance of the outcome(s) also need to be freely estimated in each profile as they respectively reflect the intercepts and residuals of the regressions.

```
%OVERALL%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
Out1; [Out1];
%c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
Out1; [Out1];
%c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
Out1; [Out1];
```

A more flexible (and realistic) representation also freely estimates the means (and variances) of the predictors in each profile, resulting in a hybrid model that combines LPA (for predictors) and mixture regressions and provides results indicating how the regression differs as a function of latent profiles of employees defined based on their configuration on the predictors.

```
%OVERALL%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
Out1 IND1_T1 IND2_T1 IND3_T1; [Out1 IND1_T1 IND2_T1 IND3_T1];
%c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
Out1 IND1_T1 IND2_T1 IND3_T1; [Out1 IND1_T1 IND2_T1 IND3_T1];
%c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
Out1 IND1_T1 IND2_T1 IND3_T1; [Out1 IND1_T1 IND2_T1 IND3_T1];
```

Multiple Group Mixture Regression Analysis: Configural Similarity

This set-up is highly similar to the one used for the multiple groups LPA models. Here again, the KNOWCLASS option is used to define the gender groups in the VARIABLE section:

```
KNOWCLASS = cg (gender = 1 gender = 2);
CLASSES = cg (2) c (3);
```

Then the Model section describes the model of configural similarity.

```
%OVERALL%
c#1 on cg#1;
c#2 on cg#1;
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (rr1-rr3);
Out1 IND1_T1 IND2_T1 IND3_T1 (mm1-mm4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv1-vv4);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (rr11-rr13);
Out1 IND1_T1 IND2_T1 IND3_T1 (mm11-mm14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv11-vv14);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (rr21-rr23);
Out1 IND1_T1 IND2_T1 IND3_T1 (mm21-mm24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv21-vv24);
```

Multiple Group Mixture Regression Analysis: Regression Similarity

The only difference between this model and the previous one is that the regression coefficients are constrained to be equal across gender within each profile using identical labels in parentheses. Labels in bold were modified from the previous model.

```
%OVERALL%
c#1 on cg#1; c#2 on cg#1;
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (mm1-mm4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv1-vv4);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (mm11-mm14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv11-vv14);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (mm21-mm24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv21-vv24);
```


Multiple Group Mixture Regression Analysis: Structural Similarity

Means of both predictors and outcome are constrained to be equal across gender within each profile using identical labels in parentheses.

```

%OVERALL%
c#1 on cg#1; c#2 on cg#1;
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv1-vv4);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv11-vv14);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (vv21-vv24);

```

Multiple Group Mixture Regression Analysis: Dispersion Similarity

Variances are constrained to be equal across gender within each profile using identical labels in parentheses.

```
%OVERALL%
c#1 on cg#1; c#2 on cg#1;
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
```

Multiple Group Mixture Regression Analysis: Distributional Similarity

The statements making profile membership conditional on gender are simply taken out.

```

%OVERALL%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);

```

Multiple Group Mixture Regression Analysis with Predictors: Relations Freely Estimated Across Subgroups

To ensure stability, starts values from the previously most invariant solution should be used (not illustrated here). To allow these effects to be freely estimated across gender, they need to be constrained to 0 in the %OVERALL% section, and freely estimated in both gender groups in a new section of the input specifically referring to CG.

```

%OVERALL%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
c#1-c#2 ON Pred1@0 Pred2@0;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
MODEL cg:
%cg#1%
c#1-c#2 ON Pred1 Pred2;
%cg#2%
c#1-c#2 ON Pred1 Pred2;

```

Multiple Group Mixture Regression Analysis with Predictors: Predictive Similarity

To ensure stability, starts values from the previously most invariant solution should be used.

```

%OVERALL%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
c#1-c#2 ON Pred1 Pred2;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);

```

**Multiple Group Mixture Regression Analysis with Outcomes: Relations Freely
Estimated Across Subgroups**

To ensure stability, starts values from the previously most invariant solution should be used.

```
%OVERALL%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
[Out2] (oa1);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
[Out2] (oa2);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
[Out2] (oa2);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
[Out2] (oaa1);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
[Out2] (oaa2);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
[Out2] (oaa3);
```

MODEL CONSTRAINT:

```
NEW (y12); y12 = oa1-oa2;
NEW (y13); y13 = oa1-oa3;
NEW (y23); y23 = oa2-oa3;
NEW (yy12); yy12 = oaa1-oaa2;
NEW (yy13); yy13 = oaa1-oaa3;
NEW (yy23); yy23 = oaa2-oaa3;
```

Multiple Group Mixture Regression Analysis with Outcomes: Explanatory Similarity

To ensure stability, starts values from the previously most invariant solution should be used.

```

%OVERALL%
Out1 ON IND1_T1 IND2_T1 IND3_T1;
%cg#1.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
[Out2] (oa1);
%cg#1.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
[Out2] (oa2);
%cg#1.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
[Out2] (oa2);
%cg#2.c#1%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r1-r3);
Out1 IND1_T1 IND2_T1 IND3_T1 (m1-m4);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v1-v4);
[Out2] (oa1);
%cg#2.c#2%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r11-r13);
Out1 IND1_T1 IND2_T1 IND3_T1 (m11-m14);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v11-v14);
[Out2] (oa2);
%cg#2.c#3%
Out1 ON IND1_T1 IND2_T1 IND3_T1 (r21-r23);
Out1 IND1_T1 IND2_T1 IND3_T1 (m21-m24);
[Out1 IND1_T1 IND2_T1 IND3_T1] (v21-v24);
[Out2] (oa3);

```

MODEL CONSTRAINT:

NEW (y12); y12 = oa1-oa2;

NEW (y13); y13 = oa1-oa3;

NEW (y23); y23 = oa2-oa3;

Longitudinal Latent Profile Analysis: Configural Similarity

The estimation of a longitudinal latent profile analysis is highly similar to the estimation of a multiple-group LPA with the exception that the latent categorical variable representing the observed group that was defined using the KNOWCLASS function (CG in the previous examples) is now replaced by another unknown latent categorical variable representing profiles groups estimated at another time point.

```
CLASSES = c1 (3) c2 (3);
```

Because of the similarity of the inputs, we do not comment the sequence of similarity tests in the next sections. In this model, two sections of the input are used to define the profiles estimated at the first (MODEL C1:) and second (MODEL C2:) time points, where the profiles are defined by distinct variables reflecting the mixture indicators measured at either the first (e.g., IND1_T1) or second (e.g., IND1_T2) time point.

```
%OVERALL%
MODEL C1:
%c1#1%
 [IND1_T1 IND2_T1 IND3_T1] (m1-m3);
IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%c1#2%
 [IND1_T1 IND2_T1 IND3_T1] (m4-m6);
IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%c1#3%
 [IND1_T1 IND2_T1 IND3_T1] (m7-m9);
IND1_T1 IND2_T1 IND3_T1 (v7-v9);
MODEL C2:
%c2#1%
 [IND1_T2 IND2_T2 IND3_T2] (mm1-mm3);
IND1_T2 IND2_T2 IND3_T2 (vv1-vv3);
%c2#2%
 [IND1_T2 IND2_T2 IND3_T2] (mm4-mm6);
IND1_T2 IND2_T2 IND3_T2 (vv4-vv6);
%c2#3%
 [IND1_T2 IND2_T2 IND3_T2] (mm7-mm9);
IND1_T2 IND2_T2 IND3_T2 (vv7-vv9);
```


Longitudinal Latent Profile Analysis: Structural Similarity

```

%OVERALL%
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (vv1-vv3);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (vv4-vv6);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (vv7-vv9);

```

Longitudinal Latent Profile Analysis: Dispersion Similarity

```

%OVERALL%
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);

```

Longitudinal Latent Profile Analysis: Distributional Similarity

Labels are used to request that the sizes of the profiles be invariant over time.

```
%OVERALL%
[ c1#1] (p1);
[ c1#2] (p2);
[ c2#1] (p1);
[ c2#2] (p2);
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);
```

Latent Transition Analysis (From a LPA Model of Dispersion Similarity)

In the basic LTA model, the %OVERALL% section states that membership into the profiles at the second time point (C2) are conditional on membership in the profiles estimated at the first time points (C1). This is necessary to estimate the individual transition probabilities over time. This is the only change (see in bold) that is required to convert a longitudinal LPA model to a LTA model. However, keep in mind that the procedure required to convert a LPA model of distributional similarity) to a LTA is more complex (for details, see Morin & Litalien, 2017: <https://smslabstats.weebly.com/webnotes.html>)

```
%OVERALL%
c2 on c1;
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);
```

Latent Transition Analysis with Predictors: Relations freely estimated across profiles and time points

To ensure stability, starts values from the previously most invariant solution should be used. In this model, the effects of the predictors are allowed to differ across time points. In addition, the effects of the predictors of Time 2 profiles are also allowed to differ across Time 1 profiles in order to assess their specific role in the prediction of specific profile-to-profile transitions.

```
%OVERALL%
c2 on c1;
[ c1#1] (p1); [ c1#2] (p2);
[ c2#1] (p1); [ c2#2] (p2);
c1 ON Pred1;
c2 ON Pred2;
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
c2 ON Pred2;
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
c2 ON Pred2;
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
c2 ON Pred2;
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);
```

Latent Transition Analysis with Predictors: Relations freely estimated across time points

To ensure stability, starts values from the previously most invariant solution should be used.

```
%OVERALL%
c2 on c1;
[ c1#1] (p1); [ c1#2] (p2);
[ c2#1] (p1); [ c2#2] (p2);
c1 ON Pred1;
c2 ON Pred2;
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);
```

Latent Transition Analysis with Predictors: Predictive Similarity

To ensure stability, starts values from the previously most invariant solution should be used.

```
%OVERALL%
c2 on c1;
[ c1#1] (p1); [ c1#2] (p2);
[ c2#1] (p1); [ c2#2] (p2);
c1 ON Pred1 (pr1-pr2); ! one less label than the number of latent profiles
c2 ON Pred2 (pr1-pr2);
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);
```

Latent Transition Analysis with Outcomes: Relations freely estimated across time points

To ensure stability, starts values from the previously most invariant solution should be used.

```

%OVERALL%
c2 on c1;
[ c1#1] (p1); [ c1#2] (p2);
[ c2#1] (p1); [ c2#2] (p2);
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
[Out1] (oa1);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
[Out1] (oa2);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
[Out1] (oa3);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
[Out2] (ob1);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
[Out2] (ob2);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);
[Out2] (ob2);
MODEL CONSTRAINT:
NEW (y12); y12 = oa1-oa2;
NEW (y13); y13 = oa1-oa3;
NEW (y23); y23 = oa2-oa3;
NEW (z12); z12 = ob1-ob2;
NEW (z13); z13 = ob1-ob3;
NEW (z23); z23 = ob2-ob3;

```

Latent Transition Analysis with Outcomes: Explanatory Similarity

To ensure stability, starts values from the previously most invariant solution should be used.

```

%OVERALL%
c2 on c1;
[ c1#1] (p1); [ c1#2] (p2);
[ c2#1] (p1); [ c2#2] (p2);
MODEL C1:
%c1#1%
[IND1_T1 IND2_T1 IND3_T1] (m1-m3); IND1_T1 IND2_T1 IND3_T1 (v1-v3);
[Out1] (oa1);
%c1#2%
[IND1_T1 IND2_T1 IND3_T1] (m4-m6); IND1_T1 IND2_T1 IND3_T1 (v4-v6);
[Out1] (oa2);
%c1#3%
[IND1_T1 IND2_T1 IND3_T1] (m7-m9); IND1_T1 IND2_T1 IND3_T1 (v7-v9);
[Out1] (oa3);
MODEL C2:
%c2#1%
[IND1_T2 IND2_T2 IND3_T2] (m1-m3); IND1_T2 IND2_T2 IND3_T2 (v1-v3);
[Out2] (oa1);
%c2#2%
[IND1_T2 IND2_T2 IND3_T2] (m4-m6); IND1_T2 IND2_T2 IND3_T2 (v4-v6);
[Out2] (oa2);
%c2#3%
[IND1_T2 IND2_T2 IND3_T2] (m7-m9); IND1_T2 IND2_T2 IND3_T2 (v7-v9);
[Out2] (oa3);
MODEL CONSTRAINT:
NEW (y12); y12 = oa1-oa2;
NEW (y13); y13 = oa1-oa3;
NEW (y23); y23 = oa2-oa3;

```

Linear Growth Mixture Analysis

In LCM, the “I S |” function serves as a shortcut to define longitudinal intercepts and slope parameters and are generally followed by a specification of the time-varying indicators and their time codes (loadings on the slope factor). In this input, we request the means of the intercepts and slope factors ([I S];), their variances (I S;), their covariances (I WITH S;), and all time specific residuals (IND1_T1, IND1_T2, IND1_T3, IND1_T4, IND1_T5, IND1_T6;) be freely estimated in all profiles. We assume here six repeated measures of a specific indicator (IND1_T1), equally spaced, with an intercept located at Time 1.

```
%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
```

The following function provides plots of the trajectories.

```
PLOT:
TYPE IS PLOT3;
SERIES = IND1_T1- IND1_T6 (*);
```

As noted in the main manuscript, simpler parameterizations are possible should this fully variant model fail to converge on proper solutions. Our preference is to test these alternatives in the following order: C-B-A-D-F-E-G.

Alternative A – Class-Invariant Latent Variance-Covariance Matrix

```
%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
```

Alternative B – Class-Invariant Residuals

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
I S; I WITH S;
%c#2%
[I S];
I S; I WITH S;
%c#3%
[I S];
I S; I WITH S;

```

Alternative C – Homoscedastic Residuals (equal across time points)

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R2);
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R3);

```

Alternative D – Class-Invariant Homoscedastic Residuals (equal across time points)

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);

```


Alternative E – Class-Invariant Latent Variance-Covariance Matrix and Class-Invariant Residuals

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
%c#2%
[I S];
%c#3%
[I S];

```

Alternative F – Class-Invariant Latent Variance-Covariance Matrix and Homoscedastic Residuals

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);
%c#2%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R2);
%c#3%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R3);

```

Alternative G – Class-Invariant Latent Variance-Covariance Matrix and Class-Invariant Homoscedastic Residuals

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);
%c#2%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);
%c#3%
[I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (R1);

```

Quadratic Growth Mixture Analysis

A quadratic slope factor (Q) is simply added to the previous model.

```
%OVERALL%
I S Q | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
I S Q;
[I S Q];
I WITH S Q;
S WITH Q;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
I S Q;
[I S Q];
I WITH S Q;
S WITH Q;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
I S Q;
[I S Q];
I WITH S Q;
S WITH Q;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
```

Piecewise Growth Mixture Analysis

Two linear slope factors (S1 and S2) can be defined to represent change before and after the transition point.

```
%OVERALL%
I S1 | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@2 IND1_T5@2 IND1_T6@2;
I S2 | IND1_T1@0 IND1_T2@0 IND1_T3@0 IND1_T4@1 IND1_T5@2 IND1_T6@3;
%c#1%
I S1 S2;
[I S1 2];
I WITH S1 S2;
S1 WITH S2;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
I S1 S2;
[I S1 2];
I WITH S1 S2;
S1 WITH S2;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
I S1 S2;
[I S1 2];
I WITH S1 S2;
S1 WITH S2;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
```

Latent Basis Growth Mixture Analysis

In a latent basis model, two loadings (typically the first and last) need to be respectively fixed to 0 and 1 (@0 and @1) while the others are freely estimated. Here, we also request that these be freely estimated in all profiles by repeating this function in the profile-specific sections.

```
%OVERALL%
I S | IND1_T1@0 IND1_T2* IND1_T3* IND1_T4* IND1_T5* IND1_T6@1;
%c#1%
I S | IND1_T1@0 IND1_T2* IND1_T3* IND1_T4* IND1_T5* IND1_T6@1;
I S;
[I S];
I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
I S | IND1_T1@0 IND1_T2* IND1_T3* IND1_T4* IND1_T5* IND1_T6@1;
I S;
[I S];
I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
I S | IND1_T1@0 IND1_T2* IND1_T3* IND1_T4* IND1_T5* IND1_T6@1;
I S;
[I S];
I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
```

Metha and West (2000) Test

When participants' differ from one another on age (or any other meaningful time-related variable) Metha and West (2000) note that these individual variations can be considered to be negligible when the following two conditions are met: (1) the regression of the intercept of a LCM on age is equal to the slope factor, and (2) the regression of the slope factor on age of this LCM is equal to zero. Testing these conditions simply involve contrasting a typical LCM model incorporating age as a predictor of the intercept and slope factors to one in which these two conditions are imposed on the model. If the second, and more constrained model, fit as well as the first one, then the impact of age can be considered to be negligible.

Initial Model:

```
VARIABLE:
NAMES = ID age IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
USEVARIABLES = age IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
MISSING = all (999);
IDVARIABLE = ID;
ANALYSIS:
ESTIMATOR = MLR;
MODEL:
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
I ON Age;
S ON Age;
```

Constrained Model:

```
MODEL:
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
I ON Age (c1);
[S] (c1);
S ON Age@0;
```

Age-Defined Linear Growth Mixture Analysis

To estimate growth mixture analysis where age (or any other individually varying variable) is used to defined the Time codes, this specific variable needs to be identified using the CONSTRAINT command of the variable section (this command identified variables used only in the MODEL CONSTRAINT SECTION). The loadings on the slope factor (representing the time code), rather than being fixed to specific values, are assigned a label (here L1 to L6). Using this approach involves that one has to rely on the complete specification of the LCM model (without being able to use the short cut function linked to the | function). To apply this complete specification, one also has to constraint the time specific intercepts to the 0, and to request the free estimation of the intercept and slope factor means in the %OVERALL% section. In the present example, we define trajectories defined on the basis of age (coded in years), and want to set the intercept of the trajectories to 10 years old (corresponding to the age of the youngest participant at Time 1). Measurement point are taken at annual intervals equal for all participants. If measurement intervals also differ across participants, then one AGE variable would be required for each time of measurement. With this approach, time-specific residuals should be specified as homoscedastic (equal across time points) as the alternative approach of allowing them to differ across time of measurement would be inconsistent with the definition of time codes that ignore the time of measurement. The PLOT function does not work in this context, so that the trajectories would need to be graphed manually. This model is illustrated on the following page:

```

VARIABLE:
NAMES = ID age IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
USEVARIABLES = IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
MISSING = all (999);
IDVARIABLE = ID;
Constraint = age;
ANALYSIS:
TYPE = MIXTURE COMPLEX;
ESTIMATOR = MLR; PROCESS = 3;
STARTS = 3000 100; STITERATIONS = 100;
MODEL:
%OVERALL%
I BY IND1_T1@1 IND1_T2@1 IND1_T3@1 IND1_T4@1 IND1_T5@1 IND1_T6@1;
S BY IND1_T1* (L1)
      IND1_T2 (L2)
      IND1_T3 (L3)
      IND1_T4 (L4)
      IND1_T5 (L5)
      IND1_T6 (L6);
I S; I WITH S; [I S];
[IND1_T1@0 IND1_T2@0 IND1_T3@0 IND1_T4@0 IND1_T5@0 IND1_T6@0];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#1%
I S; I WITH S; [I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (r1);
%c#2%
I S; I WITH S; [I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (r2);
%c#3%
I S; I WITH S; [I S];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (r3);
MODEL CONSTRAINT:
L1 = AGE - 10;
L2 = AGE - 10 + 1;
L3 = AGE - 10 + 2;
L4 = AGE - 10 + 3;
L5 = AGE - 10 + 4;
L6 = AGE - 10 + 5;

```

Age-Defined Quadratic Growth Mixture Analysis

A similar approach can be used for a quadratic model (or any other polynomial models).

```

MODEL:
%OVERALL%
I BY IND1_T1@1 IND1_T2@1 IND1_T3@1 IND1_T4@1 IND1_T5@1 IND1_T6@1;
S BY IND1_T1* (L1)
      IND1_T2 (L2)
      IND1_T3 (L3)
      IND1_T4 (L4)
      IND1_T5 (L5)
      IND1_T6 (L6);
Q BY IND1_T1* (Q1)
      IND1_T2 (Q2)
      IND1_T3 (Q3)
      IND1_T4 (Q4)
      IND1_T5 (Q5)
      IND1_T6 (Q6);
I S Q; I WITH S Q; S WITH Q; [I S Q];
[IND1_T1@0 IND1_T2@0 IND1_T3@0 IND1_T4@0 IND1_T5@0 IND1_T6@0];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#1%
I S Q; I WITH S Q; S WITH Q; [I S Q];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (r1);
%c#2%
I S Q; I WITH S Q; S WITH Q; [I S Q];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (r2);
%c#3%
I S Q; I WITH S Q; S WITH Q; [I S Q];
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6 (r3);
MODEL CONSTRAINT:
L1 = AGE - 10;
L2 = AGE - 10 + 1;
L3 = AGE - 10 + 2;
L4 = AGE - 10 + 3;
L5 = AGE - 10 + 4;
L6 = AGE - 10 + 5;
Q1 = (AGE - 10)**2;
Q2 = (AGE - 10+1)**2;
Q3 = (AGE - 10+2)**2;
Q4 = (AGE - 10+3)**2;
Q5 = (AGE - 10+4)**2;
Q6 = (AGE - 10+5)**2;

```

Growth Mixture Analysis: Time-Invariant Predictors***Null-Effects Model***

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
C ON Pred1@0 Pred2@0;
I ON Pred1@0 Pred2@0;
S ON Pred1@0 Pred2@0;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;

```

Effects on Class Membership

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
C ON Pred1 Pred2;
I ON Pred1 @0 Pred2@0;
S ON Pred1 @0 Pred2@0;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;

```


Effects on Class Membership and Class-Invariant Effects on the Growth Factors

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
C ON Pred1 Pred2;
I ON Pred1 Pred2;
S ON Pred1 Pred2;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;

```

Effects on Class Membership and Class-Varying Effects on the Growth Factors

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
C ON Pred1 Pred2;
I ON Pred1 Pred2;
S ON Pred1 Pred2;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
I ON Pred1 Pred2;
S ON Pred1 Pred2;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
I ON Pred1 Pred2;
S ON Pred1 Pred2;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
I ON Pred1 Pred2;
S ON Pred1 Pred2;

```

Growth Mixture Analysis: Time-Invariant Outcomes

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
[Out1] (oa1); [Out2] (ob1);
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
[Out1] (oa2); [Out2] (ob2);
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
[Out1] (oa3); [Out2] (ob3);
MODEL CONSTRAINT:
NEW (y12);
y12 = oa1-oa2;
NEW (y13);
y13 = oa1-oa3;
NEW (y23);
y23 = oa2-oa3;
NEW (z12);
z12 = ob1-ob2
NEW (z13);
z13 = ob1-ob3;
NEW (z23);
z23 = ob2-ob3;

```

Growth Mixture Analysis: Time-Varying Predictors***Null-Effects Model***

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
IND1_T1 ON PredT1@0;
IND1_T2 ON PredT2@0;
IND1_T3 ON PredT3@0;
IND1_T4 ON PredT4@0;
IND1_T5 ON PredT5@0;
IND1_T6 ON PredT6@0;
[PredT1] (m1); [PredT2] (m2); [PredT3] (m3); [PredT4] (m4); [PredT5] (m5); [PredT6] (m6);
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;

```

Effects Free to Vary Across Time Points

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
IND1_T1 ON PredT1;
IND1_T2 ON PredT2;
IND1_T3 ON PredT3;
IND1_T4 ON PredT4;
IND1_T5 ON PredT5;
IND1_T6 ON PredT6;
[PredT1] (m1); [PredT2] (m2); [PredT3] (m3); [PredT4] (m4); [PredT5] (m5); [PredT6] (m6);
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;

```

Effects Free to Vary Across Time Points and Profiles

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
IND1_T1 ON PredT1;
IND1_T2 ON PredT2;
IND1_T3 ON PredT3;
IND1_T4 ON PredT4;
IND1_T5 ON PredT5;
IND1_T6 ON PredT6;
[PredT1] (m1); [PredT2] (m2); [PredT3] (m3); [PredT4] (m4); [PredT5] (m5); [PredT6] (m6);
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
IND1_T1 ON PredT1;
IND1_T2 ON PredT2;
IND1_T3 ON PredT3;
IND1_T4 ON PredT4;
IND1_T5 ON PredT5;
IND1_T6 ON PredT6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
IND1_T1 ON PredT1;
IND1_T2 ON PredT2;
IND1_T3 ON PredT3;
IND1_T4 ON PredT4;
IND1_T5 ON PredT5;
IND1_T6 ON PredT6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
IND1_T1 ON PredT1;
IND1_T2 ON PredT2;
IND1_T3 ON PredT3;
IND1_T4 ON PredT4;
IND1_T5 ON PredT5;
IND1_T6 ON PredT6;

```

Effects Free to Vary Across Profiles but Not Time Points

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
IND1_T1 ON PredT1;
IND1_T2 ON PredT2;
IND1_T3 ON PredT3;
IND1_T4 ON PredT4;
IND1_T5 ON PredT5;
IND1_T6 ON PredT6;
[PredT1] (m1); [PredT2] (m2); [PredT3] (m3); [PredT4] (m4); [PredT5] (m5); [PredT6] (m6);
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
IND1_T1 ON PredT1 (r1);
IND1_T2 ON PredT2 (r1);
IND1_T3 ON PredT3 (r1);
IND1_T4 ON PredT4 (r1);
IND1_T5 ON PredT5 (r1);
IND1_T6 ON PredT6 (r1);
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
IND1_T1 ON PredT1 (r2);
IND1_T2 ON PredT2 (r2);
IND1_T3 ON PredT3 (r2);
IND1_T4 ON PredT4 (r2);
IND1_T5 ON PredT5 (r2);
IND1_T6 ON PredT6 (r2);
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
IND1_T1 ON PredT1 (r3);
IND1_T2 ON PredT2 (r3);
IND1_T3 ON PredT3 (r3);
IND1_T4 ON PredT4 (r3);
IND1_T5 ON PredT5 (r3);
IND1_T6 ON PredT6 (r3);

```

Effects Constrained to Equality Across Time Points and Profiles

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
IND1_T1 ON PredT1 (r1);
IND1_T2 ON PredT2 (r1);
IND1_T3 ON PredT3 (r1);
IND1_T4 ON PredT4 (r1);
IND1_T5 ON PredT5 (r1);
IND1_T6 ON PredT6 (r1);
[PredT1] (m1); [PredT2] (m2); [PredT3] (m3); [PredT4] (m4); [PredT5] (m5); [PredT6] (m6);
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;

```

Growth Mixture Analysis: Time-Varying Outcomes

In the following inputs, we allow the full regression equation (slope, intercepts, residuals) associated with the time-varying-outcomes to differ or not across profiles and time points. Simpler models relying on the slopes only can be estimated (without the greyscale part). Alternatively, equality constraints can be imposed (and tested) in sequence, starting with the slopes, then the intercepts, and then the residuals.

Null-Effects Model

```
%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
OutT1 ON IND1_T1@0;
OutT2 ON IND1_T2@0;
OutT3 ON IND1_T3@0;
OutT4 ON IND1_T4@0;
OutT5 ON IND1_T5@0;
OutT6 ON IND1_T6@0;
[OutT1] (m1); [OutT2] (m2); [OutT3] (m3); [OutT4] (m4); [OutT5] (m5); [OutT6] (m6);
%c#1%
[I S]; I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S]; I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S]; I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
```

Effects Free to Vary Across Time Points

```
%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
OutT1 ON IND1_T1;
OutT2 ON IND1_T2;
OutT3 ON IND1_T3;
OutT4 ON IND1_T4;
OutT5 ON IND1_T5;
OutT6 ON IND1_T6;
[OutT1] (m1); [OutT2] (m2); [OutT3] (m3); [OutT4] (m4); [OutT5] (m5); [OutT6] (m6);
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
```

Effects Free to Vary Across Time Points and Profiles

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
OutT1 ON IND1_T1;
OutT2 ON IND1_T2;
OutT3 ON IND1_T3;
OutT4 ON IND1_T4;
OutT5 ON IND1_T5;
OutT6 ON IND1_T6;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
OutT1 ON IND1_T1;
OutT2 ON IND1_T2;
OutT3 ON IND1_T3;
OutT4 ON IND1_T4;
OutT5 ON IND1_T5;
OutT6 ON IND1_T6;
[OutT1] (m1); [OutT2] (m2); [OutT3] (m3); [OutT4] (m4); [OutT5] (m5); [OutT6] (m6);
OutT1 (v1); OutT2 (v2); OutT3 (v3); OutT4 (v4); OutT5 (v5); OutT6 (v6);
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
OutT1 ON IND1_T1;
OutT2 ON IND1_T2;
OutT3 ON IND1_T3;
OutT4 ON IND1_T4;
OutT5 ON IND1_T5;
OutT6 ON IND1_T6;
[OutT1] (n1); [OutT2] (n2); [OutT3] (n3); [OutT4] (n4); [OutT5] (n5); [OutT6] (n6);
OutT1 (vv1); OutT2 (vv2); OutT3 (vv3); OutT4 (vv4); OutT5 (vv5); OutT6 (vv6);
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
OutT1 ON IND1_T1;
OutT2 ON IND1_T2;
OutT3 ON IND1_T3;
OutT4 ON IND1_T4;
OutT5 ON IND1_T5;
OutT6 ON IND1_T6;
[OutT1] (p1); [OutT2] (p2); [OutT3] (p3); [OutT4] (p4); [OutT5] (p5); [OutT6] (p6);
OutT1 (vvv1); OutT2 (vvv2); OutT3 (vvv3); OutT4 (vvv4); OutT5 (vvv5); OutT6 (vvv6);

```


Effects Free to Vary Across Profiles but Not Time Points

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
OutT1 ON IND1_T1;
OutT2 ON IND1_T2;
OutT3 ON IND1_T3;
OutT4 ON IND1_T4;
OutT5 ON IND1_T5;
OutT6 ON IND1_T6;
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
OutT1 ON IND1_T1 (o1);
OutT2 ON IND1_T2 (o1);
OutT3 ON IND1_T3 (o1);
OutT4 ON IND1_T4 (o1);
OutT5 ON IND1_T5 (o1);
OutT6 ON IND1_T6 (o1);
[OutT1] (m1); [OutT2] (m1); [OutT3] (m1); [OutT4] (m1); [OutT5] (m1); [OutT6] (m1);
OutT1 (v1); OutT2 (v1); OutT3 (v1); OutT4 (v1); OutT5 (v1); OutT6 (v1);
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
OutT1 ON IND1_T1 (o2);
OutT2 ON IND1_T2 (o2);
OutT3 ON IND1_T3 (o2);
OutT4 ON IND1_T4 (o2);
OutT5 ON IND1_T5 (o2);
OutT6 ON IND1_T6 (o2);
[OutT1] (m2); [OutT2] (m2); [OutT3] (m2); [OutT4] (m2); [OutT5] (m2); [OutT6] (m2);
OutT1 (v2); OutT2 (v2); OutT3 (v2); OutT4 (v2); OutT5 (v2); OutT6 (v2);
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
OutT1 ON IND1_T1 (o3);
OutT2 ON IND1_T2 (o3);
OutT3 ON IND1_T3 (o3);
OutT4 ON IND1_T4 (o3);
OutT5 ON IND1_T5 (o3);
OutT6 ON IND1_T6 (o3);
[OutT1] (m3); [OutT2] (m3); [OutT3] (m3); [OutT4] (m3); [OutT5] (m3); [OutT6] (m3);
OutT1 (v3); OutT2 (v3); OutT3 (v3); OutT4 (v3); OutT5 (v3); OutT6 (v3);

```

Effects Constrained to Equality Across Time Points and Profiles

```

%OVERALL%
I S | IND1_T1@0 IND1_T2@1 IND1_T3@2 IND1_T4@3 IND1_T5@4 IND1_T6@5;
OutT1 ON IND1_T1 (o1);
OutT2 ON IND1_T2 (o1);
OutT3 ON IND1_T3 (o1);
OutT4 ON IND1_T4 (o1);
OutT5 ON IND1_T5 (o1);
OutT6 ON IND1_T6 (o1);
[OutT1] (m1); [OutT2] (m1); [OutT3] (m1); [OutT4] (m1); [OutT5] (m1); [OutT6] (m1);
OutT1 (v1); OutT2 (v1); OutT3 (v1); OutT4 (v1); OutT5 (v1); OutT6 (v1);
%c#1%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#2%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;
%c#3%
[I S];
I S; I WITH S;
IND1_T1 IND1_T2 IND1_T3 IND1_T4 IND1_T5 IND1_T6;

```