2022

**Mis-Specification of Functional Forms in Growth Mixture Modeling: A Monte Carlo Simulation**

Richa Ghevarghese  
*University of Denver*

---

Follow this and additional works at: [https://digitalcommons.du.edu/etd](https://digitalcommons.du.edu/etd)

Part of the Developmental Psychology Commons, Educational Assessment, Evaluation, and Research Commons, Higher Education Commons, and the Statistical Methodology Commons

---

**Recommended Citation**

[https://digitalcommons.du.edu/etd/2048](https://digitalcommons.du.edu/etd/2048)

---

This Dissertation is brought to you for free and open access by the Graduate Studies at Digital Commons @ DU. It has been accepted for inclusion in Electronic Theses and Dissertations by an authorized administrator of Digital Commons @ DU. For more information, please contact jennifer.cox@du.edu,dig-commons@du.edu.
Mis-Specification of Functional Forms in Growth Mixture Modeling: A Monte Carlo Simulation

Abstract
Growth mixture modeling (GMM) is a methodological tool used to represent heterogeneity in longitudinal datasets through the identification of unobserved subgroups following qualitatively and quantitatively distinct trajectories in a population. These growth trajectories or functional forms are informed by the underlying developmental theory, are distinct to each subgroup, and form the core assumptions of the model. Therefore, the accuracy of the assumed functional forms of growth strongly influences substantive research and theories of growth. While there is evidence of mis-specified functional forms of growth in GMM literature, the weight of this violation has been largely overlooked. Current solutions to circumvent assumption violations to functional forms of growth are reliant on theory and inferences yielded from previous research. However, the low frequency of systematic replications of study assumptions implies that developmental theories may not always suggest the correct functional form for a given growth phenomenon. The current dissertation is an examination of GMM assumption violation to the functional form of growth. The simulation study quantitatively contrasted the measured differences between the true population model to a series of mis-specified models where the outcome appropriateness was measured using latent classes and model fit indices. Results of the simulation study revealed two key takeaways. Firstly, that the fit indices of the mis-specified models consistently selected the correct number of classes present in the sample. However, closer examination of the mixing proportion of these latent classes revealed that individual's probability of membership to the latent classes was compromised for the mis-specified models. Secondly, the type of functional form mis-specified (i.e., a simple linear or quadratic or complex Gompertz) determined how visible the effects of the mis-specification would be to the researcher. The implications of these findings are further discussed in this paper along with directions for future research.

Document Type
Dissertation

Degree Name
Ph.D.

Department
Quantitative Research Methods

First Advisor
Denis Dumas

Keywords
Developmental studies, Functional form analysis, Growth mixture modeling, Growth trajectories, Latent growth curve modeling, Trend analysis

Subject Categories
Developmental Psychology | Education | Educational Assessment, Evaluation, and Research | Higher Education | Statistical Methodology | Statistics and Probability

Publication Statement
Copyright is held by the author. User is responsible for all copyright compliance.

This dissertation is available at Digital Commons @ DU: https://digitalcommons.du.edu/etd/2048
Mis-specification of Functional Forms in
Growth Mixture Modeling: A Monte Carlo Simulation

A Dissertation
Presented to
the Faculty of the Morgridge College of Education
University of Denver

In Partial Fulfillment
of the Requirements for the Degree
Doctor of Philosophy

by
Richa Ghevarghese
June 2022
Advisor: Dr. Denis Dumas
Abstract

Growth mixture modeling (GMM) is a methodological tool used to represent heterogeneity in longitudinal datasets through the identification of unobserved subgroups following qualitatively and quantitatively distinct trajectories in a population. These growth trajectories or functional forms are informed by the underlying developmental theory, are distinct to each subgroup, and form the core assumptions of the model. Therefore, the accuracy of the assumed functional forms of growth strongly influences substantive research and theories of growth. While there is evidence of mis-specified functional forms of growth in GMM literature, the weight of this violation has been largely overlooked. Current solutions to circumvent assumption violations to functional forms of growth are reliant on theory and inferences yielded from previous research. However, the low frequency of systematic replications of study assumptions implies that developmental theories may not always suggest the correct functional form for a given growth phenomenon. The current dissertation is an examination of GMM assumption violation to the functional form of growth. The simulation study quantitatively contrasted the measured differences between the true population model to a series of mis-specified models where the outcome appropriateness was measured using latent classes and model
fit indices. Results of the simulation study revealed two key takeaways. Firstly, that the fit indices of the mis-specified models consistently selected the correct number of classes present in the sample. However, closer examination of the mixing proportion of these latent classes revealed that individual’s probability of membership to the latent classes was compromised for the mis-specified models. Secondly, the type of functional form mis-specified (i.e., a simple linear or quadratic or complex Gompertz) determined how visible the effects of the mis-specification would be to the researcher. The implications of these findings are further discussed in this paper along with directions for future research.
# Table of Contents

Abstract ii

Table of Contents iv

List of Figures viii

List of Tables ix

**Chapter One: Fundamentals of Growth Mixture Modeling** 1

Longitudinal Data: An Overview of Methodological Advances 6
Why Growth Mixture Modeling? 8
The Role of Growth Curves in Growth Modeling 10

**Chapter Two: Literature Review** 15

Traditional Growth Models 16
Contemporary Growth Model 17
Multilevel Modeling 18
Structural Equation Modeling 19

The Fundamentals of Growth Curve Modeling 21
Latent Growth Curve Models (LGCM) 22
Fixed Effects and Random Effects 23
The Unconditional Linear LGCM 24
Change Hypotheses and the Role of Functional Forms 27
Individual Level Analysis 28
Group Level Analysis 29

Mixture Modeling 30
Growth Mixture Modeling 31
Model Specification 34
Number of Latent Classes 35
Latent Class Membership 36
Model Selection and Interpretation 38

Mathematical Representation of a 2-Class Means GMM 39
The Pitfalls in GMM Applications 40
The Issue of Optimal Solutions in GMM 41
Criteria for Model Fit 42
Limited Generalizability of GMM Solutions 43
Effect of Violations to Assumptions 43
Insufficient Critical Replications 44
Chapter Three : Methodology  
- The Gompertz GMM  
- Simulation Design  
- Manipulated Design Conditions  
  - Mixing Proportions of the Latent Classes  
  - Degree of Class Separation  
- Comparison of True Model versus Mis-specified Models  
  - Model Evaluation Criteria  
- Diagnostic Tests  

Chapter Four : Results  
- Convergence Rate  
- Preliminary Dataset Check for Trend Using a One-way ANOVA  
- Performance of Fit Indices and Class Enumeration  
- Results of Linear Mis-specification at 4 Timepoints  
  - Four Timepoints, Low-class Separation, Equal and Unequal Mixing Proportions  
  - Four Timepoints, Medium-class Separation, Equal and Unequal Mixing Proportions  
- Results of Linear Mis-specification at 8 Timepoints  
  - Eight Timepoints, Low-class Separation, Equal and Unequal Mixing Proportions  
  - Eight Timepoints, Medium-class Separation, Equal and Unequal Mixing Proportions  
- Results of Latent Basis Models at 8 Timepoints  
  - Eight Timepoints, Low-class Separation, Equal and Equal Mixing Proportions  
  - Eight Timepoints, Medium-class Separation, Equal and Equal Mixing Proportions  
- Results Of Gompertz Mis-specified Models at 4 Timepoints  
  - Four Timepoints, Low-class Separation, Equal and Unequal Mixing Class Proportion  
  - Four Timepoints, Medium-class Separation, and Equal and Unequal Mixing Proportions  
- Results of Gompertz Mis-specified Models at 8 Timepoints  
  - Eight Timepoints and Equal Mixing Proportions at Low-class Separation  
  - Eight Timepoints, Medium-class Separation, and Equal and Unequal Mixing Proportions  
- Latent Class Assignment  

v
List of Figures

Chapter Three: Methodology

Figure 1  Data Generating Model for the 2-Class GMM at Four Repeated Measures  67
Figure 2  Process of Analyses of Alternative Functional Forms Fit to the Data.  74

Chapter Four: Results

Figure 3  Eight Timepoints and Unequal Mixing Proportions at The Three Levels of Latent Class Separation of The Mis-specified Linear Growth Trajectory  111
Figure 4  Behavior of the Standardized Residuals in a PP Plot  112
Figure 5  Graph of the Standardized Residual Values by Outcome and Predicted for Unequal Mixing Proportion  114
Figure 6  Standardized Residual Values of the Linear Mis-specified Model at Equal Mixing Proportions  118
Figure 7  Behavior of the Standardized Residual at Equal Mixing Proportions  119
Figure 8  Graph of the Standardized Residual Values by Outcome and Predicted for Equal Mixing Proportion  120
List of Tables

Chapter Three: Methodology

Table 1 Fixed Design Condition 65
Table 2 Manipulated Design Conditions 66
Table 3 Estimates for the Population Model: 2-Class GMM means+pattern 68
Table 4 Sample Table of Fit Statistics for the Linear-GMM (will be created for each functional form) 75

Chapter Four: Results

Table 5 Convergence Rate of Original Simulated Models and Mis-specified Models 79
Table 6 Results of One-Way ANOVA at 4 timepoints 81
Table 7 Results of One-Way ANOVA at 8 timepoints 81
Table 8 Results of Multiple Comparisons Tukey HSD Test for all groups at 4 timepoints 82
Table 9 Results of Multiple Comparisons Tukey HSD Test for the statistically significant groups at 8 timepoints 83
Table 10 Results of the 12 Original Simulated Data Generated Models 85
Table 11 Differences from the Original Model Fit Indices of The Three Growth Trajectories at The Various Manipulated Design Conditions 86
Table 12 Fit Indices for the 2-Class Original Versus Linear Mis-specified Growth Trajectory at Low-class Separation 94
Table 13 Fit Indices for the 2-Class Original Versus Linear Mis-specified Growth Trajectory at Medium-class Separation 94
Table 14 Fit Indices for the 2-Class Original Versus Linear Mis-specified Growth Trajectory at High-class Separation 98
Table 15 Changes to Individuals’ Assignment to Latent Classes 108
Chapter One: Fundamentals of Growth Mixture Modeling

In any scientific study using quantitative methods, fitting of a hypothesized model to the data relies on core assumptions which inform choice of the methodology, thereby critically informing substantive findings (Fan et al., 2016). This implies that incorrect assumptions, consequently, can yield misleading substantive findings. In the area of Growth Mixture Modeling, this unfortunate scenario may be more common than previously thought, especially in cases where the functional form of growth is mis-specified (Infurna & Luthar, 2017). This dissertation stems from ontological discussions regarding the validity of assumptions that drive a researcher’s selection of a growth trajectory when modeling the attribute being measured in a population. Given that individuals learn in varying ways (Shah et al., 2013) and that there exists a plethora of functional forms from which to choose (Adolph et al., 2008), it is surprising that the literature on developmental studies is saturated with the use of linear, quadratic, and occasionally exponential growth curves (i.e., limited progress has been made toward understanding the process of developmental change). Furthermore, discussions relating to functional forms in the literature deal primarily with explorations in modeling the linearity and nonlinearity of growth trajectories, not necessarily entertaining the possibility of other potentially less popular patterns of growth.
Hence, the first harbinger of an underlying issue is that there isn't a thorough and rigorous investigation into discovering the possible fit of other functional forms. Second, the checks in place to guide researchers in ensuring selection of the correct functional form are rendered incomplete by what is currently possible through advances in statistical software, and through the proliferation of longitudinal data pertaining to the educational achievement of students in the US (Dumas & McNeish, 2017). This dissertation focuses on identifying the correctness (i.e., true alignment) of a functional form with the underlying developmental theory of a researcher's assertion regarding the shape of growth. It is carried out by testing the fit of typical as well as atypical growth trajectories defining the shape of learning behaviors in an individual.

The two common checks for correctness of functional form are reliance on theory and previously published research. In this specific context of capturing and modeling growth, the interconnectedness of theory and referencing published research forms a symbiotic relationship. The inferences obtained from this combination reinforce the assumptions regarding the choice of trajectory corresponding to the development of an attribute in an individual. The challenge that emerges from solely relying on theory and published research is the repeated modeling of biases which stem from the belief that a certain growth assumption is theoretically sound. Typically, this belief is corroborated when multiple papers showcase the same results; however, as exemplified by Infurna and Luthar (2017), similarity of results across studies is meaningless when these similarities are the result of retaining the same \textit{a priori} assumptions regarding growth instead of
testing different assumptions. The former is dangerous to scientific discipline because it negatively influences comprehension of the underlying theory.

Therefore, a logical first step towards this issue is to draw attention to the dearth of evidence in published literature challenging contemporary assumptions of growth trajectories in learning and the implications these hold in the field of psychological studies.

When considering this issue within the context of growth mixture modeling (GMM), the tension is further intensified due to added complexities contributed by the methodology itself. GMM is a methodological tool used to represent heterogeneity in longitudinal datasets through the identification of unobserved subgroups that follow qualitatively and quantitatively distinct trajectories (Diallo et al., 2016; Morin et al., 2011). However, when applying GMM, the extracted unobserved subgroups can be vulnerable to non-normality in the dataset among other issues. Specifically, there exists a high probability for the overextraction of subgroups (i.e., the extraction of more than the true number of latent classes in the dataset) and issues with convergence and non-normality of the data (Bauer & Curran, 2003). In GMM, drawing from the underlying development theory, the analyst asserts a growth trajectory for each perceived subgroup in the population (i.e., each subgroup is typically defined by its own growth trajectory), and the final number of subgroups decided upon are the result of convergence and good model fit. Good model fit is determined by examination of fit indices. The functional form of growth is not known \textit{a priori}, rather it is hypothesized and consequently
confirmed via the extraction of latent classes. It is possible for an overextraction of latent classes to falsely indicate good model fit, for which reason GMM is considered an exploratory methodology, to be used cautiously with guidance from appropriate theory (Ram & Grimm, 2009). Therefore, the soundness of theory is crucial in order for a practitioner of this methodology to be confident in the \textit{a priori} assumptions and \textit{post hoc} inferences from using a GMM.

There are three important irreconcilable issues that stem from the present solutions available in the selection of functional forms that map onto the underlying developmental theory, namely that 1) mis-specified functional forms are commonplace in the literature (Infurna & Luthar, 2016); 2) GMM practitioners aware of the fragility of the methodology typically stay within the bounds of what is safe (i.e., using parameters that ensure model convergence; Ram & Grimm, 2009); and 3) given that individuals learn in varying ways, the lack of a disruption in the manner in which functional forms are perceived for the last several decades in educational psychology holds negative implications for whether all possibilities of learning trajectories are truly being captured. The use of established development theory and published research have their place in equipping analysts in coming as close as possible to choosing the correct functional form to represent the diverse ways in which individuals learn and to represent the subgroups that capture the differences between functional forms present in a given population.
However, as previously stated, advances in longitudinal research, types of growth modeling possibilities, and software packages currently available present opportunities to rethink what is currently accepted as the standard for the correct specification of functional forms.

Given that unintentional mis-specification of functional forms is likely common, the objective of this dissertation is to add another check in place that analysts can use to know whether the assumptions of growth imposed on a model accurately represent the underlying theory. Additionally, it will highlight other functional forms that could describe growth albeit forms that are less commonly observed. When it comes to modeling attempts to capture growth in an individual (and in a population), the typical practice in GMM has been to use fit indices to retain the models with good fit, and disregard those with poor fit (Hu & Bentler, 1998; Ram & Grimm, 2009). The model with good fit confirms the accuracy of functional forms and the number of unobservable subgroups present in that population. The few studies in GMM that have explored the intentional mis-specification of GMM assumptions concentrate on the role of fit indices in class extraction (e.g., Nylund et al., 2007; Diallo et al., 2016; McNeish & Harring, 2017). However, there are no simulation studies intentionally violating the assumption of growth for the purpose of measurably quantifying the similarities and dissimilarities between the functional forms within latent classes of the true population model and the functional forms within latent classes of the mis-specified models. The purpose of looking at the issue from this perspective is to observe the behavior of fit indices in the
context of mis-specified functional forms to identify spurious classes and trajectories more easily when they do occur under the most seemingly seamless GMM applications. As mentioned already, the timing of such an endeavor that offers researchers an opportunity to reliably revive the conversation regarding functional forms stems from the combination of advances in longitudinal research and statistical methodologies handling growth analysis. Each of these will be explored in further detail in the rest of this chapter.

**Longitudinal Data: An Overview of Methodological Advances**

The use of longitudinal datasets expands the frontier of research possibilities because it allows for the utilization of all of the data collected relative to the limiting practice of selecting data to intentionally fit a specific analytical technique (Grimm et al., 2017). The exploration of research possibilities and opportunities using longitudinal datasets has revolutionized the types of research questions that could be asked regarding changes undergone by the attribute being measured. Several advantages are associated with engaging in longitudinal research. Of specific note is its ability to model and capture complex representations of growth yielded from the density of repeated measures. Longitudinal research offers the ability to ask more nuanced research questions which has led to the development of statistical frameworks, (i.e., the structural equation modeling (SEM) and multilevel modeling (MLM) frameworks). Each framework was developed to answer similar research questions with a different emphasis on the evaluation of model fit. Tucker and Rao (1958) presented the idea of generalized learning curves within the structural equation modeling (SEM) context, representing the fundamental aspects of
change that all individuals shared. For several decades, individual growth modeling (Wishart, 1958) and generalized learning curves (Tucker & Rao, 1958) were the primary techniques used to examine growth in individuals over time.

As the literature and general comprehension of growth processes increased, Laird and Ware (1982) introduced the idea of multilevel modeling (MLM), suggesting that growth could be measured at level-1 (within-individuals) and level-2 (between-individuals) simultaneously, implying the ability to study between-person differences in within-person change. MLM techniques conceptualized from the development of linear mixed-effects models further enhanced growth modeling by highlighting common misconceptions addressing theories articulated by growth models regarding an individual's initial status and rates of change and the types of growth trajectories that are possible to model.

In tandem, Meredith and Tisak (1990) showcased use of the SEM framework to fit latent curve models, illustrating how linear growth models can be specified as a restricted confirmatory factor analysis with a means and a covariance structure. McArdle (1988) extended the use of growth models into the multivariate space, proposing that growth models could study the development of two or more processes as well as changes in latent variables. At the turn of the century, advances in computational technology increased the possibility of examining nonlinear mixed-effect models, which allowed for the examination of between-person differences in a wider set of within-person change models in the MLM framework; in the SEM framework, parameters from nonlinear
mixed-effects models were seen to be obtainable through Taylor series expansions (Grimm et al., 2016). Consequently, analysts discovered that using the MLM or SEM frameworks to fit the same model yielded identical results.

While the choice of framework is a matter of preference and could depend on the software being utilized, some models are more easily illustrated in one over the other framework. Specifically relevant to this study, the choice to represent growth mixture modeling (GMM) using an SEM framework stems from the software challenges associated with presenting GMM as an MLM. However, both frameworks are used illustratively in this study to increase clarity of the topic being researched.

**Why Growth Mixture Modeling?**

The methodological choice of GMM is ideal to focus initial efforts in uncovering whether educational researchers have truly understood and capitalized on the diversity present in learning trajectories among individuals. GMM is a powerful and versatile statistical technique that has gained popularity across the social science, educational, and health disciplines. Morin et al. (2011) have ascribed GMM's popularity to its ability to overcome the primary challenge associated with conventional (as well as contemporary) growth models (i.e., the assumption that all individuals are drawn from a single population) by representing longitudinal heterogeneity by identifying subgroups (latent classes) following qualitatively and quantitatively distinct trajectories. Simply stated, GMM is used to identify the optimal number of latent subgroups showing distinct patterns of longitudinal change in an outcome variable. This benefit of GMM makes it a
viable and increasingly popular statistical tool across scientific disciplines. For example, in a study by Orylska et al. (2019), the authors explored the possible presence of different trajectories of learning efficiency during a working memory (WM) training program for young children diagnosed with Attention Deficit Hyperactivity Disorder (ADHD), compared with a typically developing (TD) control group. Using GMM, they attempted to infer whether learning trajectories and outcomes differed between simple and complex training tasks. Their use of GMM stemmed from the lack of scientific rigor present in existing WM studies, thus calling into question the use of goodness of fit indices and whether it accurately reflected the heterogeneous symptom profile in ADHD. While there is substantive credence to their findings, of immediate relevance to this dissertation are two key takeaways: (1) the advantage GMM provides in investigating individual differences in a given attribute through analyzing trajectories of learning performance across individuals and (2) the implications of the inferences from the study in adding to and corroborating the literature on the development of key cognitive skills known to impact learning (the results of their study held policy implications relating to changes that could be made in an educational context for the benefit of children and young people).

In the context of education, it is unrealistic to believe that a full and complete understanding of learning trajectories can truly be achieved in any single investigation, by the very nature of learning trajectories being dynamically and intricately woven together with the unique qualities that make up an individual. However, it is possible to make great strides in advancing the discipline of educational psychology by allowing the
perspective that individuals possess qualitatively distinct developmental trajectories that change through the course of an individual's life to inform scientific thought processes in educational psychology. While GMM can be used to identify whether subgroups exist within the population that follow qualitatively distinct developmental trajectories, of greater relevance to this dissertation is that GMM can be wielded as a powerful tool in uncovering whether the resultant trajectory defined by the subgroups represents an accurate taxonomy of learning and to test the potential of other trajectories of learning.

The Role of Growth Curves in Growth Modeling

Given that one cannot truly know the distribution of a population from which observations are drawn or know *a priori* the shape of growth for any individual in a population, analysts rely on theory to guide model assumptions incorporated in the building of growth models. Mathematically, as represented by a growth curve, the process by which a learning trajectory develops is measured by the functional form of growth which specifies that the amount of change the measured attribute exhibits across the individuals of interest must be functionally related to time (i.e., time-related change must be occurring). For example, if a developmental process displays linear change, then a straight line, (i.e., \( Y = a + bX \)), describes growth of an attribute (Burchinal & Appelbaum, 1991). Growth curves are one of the more valuable estimable pieces of information provided from repeated measures data and require three vital conditions to be met in order to be estimated from repeated measure observations:
1. the attribute must be defined by the same latent construct across measurement occasions
2. the attribute is being measured the same way, or by the same instrument across measurement occasions (i.e., vertically scaled scores are being modeled)
3. the attribute is measured in a manner that reflects the true developmental functions estimated from the data (i.e., the estimated growth curves are describing the underlying developmental process with scores that reflect the actual amount of the attribute possessed by a given individual at a given time)

Growth models are effective in presenting a narrative of what the analyst believes the data are measuring, making the use of inferences to inform model assumptions a critical aspect of growth modeling. Present day growth models are centric to the concept of intraindividual changes and interindividual differences in intraindividual change (Grimm et al., 2016). Simply put, the building of growth models is founded on the ability to examine within-person change and between-person differences in within-person change. The anatomy of growth models can be summed up as follows: (1) an individual's observed trajectory can be described by a mathematical function of time and noise (error); (2) the parameters of the function represent specific meaningful aspects of the intraindividual change process; and (3) variations in those parameters constitute information about interindividual differences in the change process. The implications hold that in a given population, the functional form within one latent class can dramatically differ from another latent class in the same population.
GMM is being widely used to detect the presence of latent classes, or unobserved subgroups in a population of interest, and, consequently, its ability to address nuanced research questions regarding the within-person change function has made it an appealing statistical tool for measuring growth. However, despite its statistical appeal, GMM is fraught with methodological concerns in its application. Specifically, a major area largely unexplored in the GMM literature is whether the functional form that is fit to the data truly reflects the underlying individual growth trajectory. Evident in the literature are studies of model-based functional forms of growth that incorrectly represent the longitudinal profiles of population growth trajectories. The implications for the mis-specification of functional forms are critical for several reasons, one of them being the intensive investment of time, resources, and monetary resources that goes into collecting longitudinal data. The other reason has to do with inference. Formally, the purpose of this dissertation is to test GMM's ability to extract the correct number of latent classes when the assumption of the functional form of growth for the true model has been violated. From prior research it can be inferred that given GMM's fragility to assumption violations, complex manipulation of functional forms is typically avoided. In fact, as a methodology, there are obvious areas that have been extensively researched (e.g., the role of fit indices) and other areas of substantive importance that have been overlooked (e.g., violation of assumptions of the functional forms of growth).

To reiterate, the correct functional form to fit to the data can be extremely challenging to know a priori, therefore, analysts use theoretical underpinnings to guide
the methodological decision making. However, an interesting phenomenon observed among practitioners of GMM has been the replication of studies, carrying forward the same set of theoretical assumptions that guided the very first exploration of the attribute being studied. Systematic methodological biases in scientific research such as this compromise both theory (inference informs theory), and subsequent applications of GMM modeled after the theorized functional form of growth. The perpetuation of potentially problematic methodological choices in GMM stems from it being a challenging methodology to implement with issues ranging from improper solutions, overextraction of classes (a routine feature), and sensitivity of parameter estimates to starting values. Therefore, methodologists have preferred to apply GMM within the bounds of what has been observed to cause model convergence; decisions are made in applications of GMM to avoid model specifications that lead to incomplete solutions. An indirect consequence has been an avoidance by analysts to apply complex functional forms in GMM studies. When it comes to modeling complex functional forms in GMM, there is one study by Grimm, Ram, and Estabrook (2010) where they use a Gompertz GMM to examine nonlinear change patterns in a population being measured on the development of reading skills during childhood.

**Objective of the Study**

The dearth of complexly modeled functional forms in GMM, and the danger of limited critical replications, (i.e., replication of GMM studies with modifications to the guiding assumptions of growth), highlight a gap this dissertation aims at addressing.
Popular in GMM literature has been the focused effort to check assumptions under the modeling of the null hypothesis, (i.e., when the model is correct). Further, the risk of model nonconvergence has resulted in methodologists ignoring important elements of the GMM methodology that could truly set it apart when it comes to the examination of between-person differences in within-person change. Contrary to the conventional process of testing the correctness of model-fit, this dissertation will examine the effects of intentionally mis-specifying the functional form of growth in a Monte Carlo simulation study. The goal is to study the performance of fit indices in extracting the correct number of latent classes under a series of modeling conditions. Finally, these results will be compared with the findings of the true model, to shed light on GMM's ability to discriminate an incorrectly fitting model from the true model. The overarching objective is to showcase the ease with which a mis-specified functional form can incorrectly inform substantive inferences and the high likelihood that mis-specified functional forms are the norm, not the exception due to the oftentimes undetectable nature of mis-specified growth function.
Chapter Two: Literature Review

This dissertation is a study of GMM and the effects of assumption violations in its application. A thorough understanding of the characteristic features of GMM and its correct application relies on a host of components related to the ways in which growth proceeds in a population. The goal of this literature review is to provide a detailed argument for the need of methodological explorations in GMM especially as continual advances in the software used to assess complex change trajectories are being refined, thereby presenting the opportunity for gaps in the methodology of GMM to be addressed.

Growth: An Introduction to Longitudinal Research

A central concern of longitudinal research among educational researchers is the description of patterns of growth (i.e., stability and change). Growth in the context of this study can be understood as the process of change occurring in an entity over a finite set of time points (for example, vocabulary development in children). Growth and change as such are normal features of biological, psychological, and sociological phenomena. Contained in the measurement of growth is the ability to examine (and describe) the process of change, thus making measurement of change a fundamental concern to almost all scientific disciplines. Researchers use a longitudinal research design to achieve this because longitudinal research is the measurement of the same individuals repeatedly assessed over a certain number of time points (Stull, 2008; Duncan & Duncan, 2009).
A variety of techniques aimed at examining change exist, driven by different research questions, data structures, and statistical models, therefore, there is not one statistical procedure that acts as a panacea for the analysis of longitudinal data. In fact, the uses of longitudinal research are as wide as they are varied, and techniques of modeling growth can be categorized as traditional growth models and contemporary growth models. The following section delves further into the groundwork laid by traditional growth modeling techniques, and the impetus for their advancement.

Growth Models: Traditional to Contemporary Analyses of Change

**Traditional Growth Models**

Traditionally, approaches in modeling growth focused on homogeneous populations and the assessment of change based on group means. Specifically, computed scores are group means (not individual scores), and the variance obtained around the group mean indicates the degree to which individual change scores differ from the group mean. In experimental research designs (example, pre-test versus post-test), analyses assessing whether two groups exhibited different amounts of change in their mean score involved differences of mean tests such as t-tests, repeated measures analysis of variance (ANOVA), analysis of covariance (ANCOVA), or multivariate analysis of variance (MANOVA) (Stull, 2008); nonexperimental research designs involved multiple regression as well as various methods for analyzing raw change scores (difference scores) and residualized change scores (Stull, 2008; Curran et al., 2010). The challenge with these approaches, however, is that group means can mask the individual change scores at each measurement occasion because differences among individual subjects are treated as
error variance, effectively disguising valuable information regarding the individual change function. Therefore, in spite of the improvements to traditional growth modeling approaches, the models fail in accommodating increasingly complex developmental theories (Muthén & Curran, 1997).

An increase in the complexity of theoretical models that attempt to explain behavior from a developmental perspective warrants the ability to perform a nuanced examination of the individual change function. The gap in traditional growth functions has been addressed by development of methodologies identifying larger frameworks in which to capture a more complete picture of the analysis of change. One such framework in the analysis of repeated measures data is latent growth modeling, described by Duncan and Duncan (2009) as an “influential statistical revolution.” It is a useful tool in analyzing longitudinal data because it can track trajectories and changes of a phenomena by comparing lines of change across a set of individuals in order to determine the overall model’s line of change (Burant, 2016). This framework of growth and change analysis sets the stage for GMM and will be explored in detail in sections to follow.

**Contemporary Growth Model**

Contemporary growth modeling techniques focus on the variability around the group mean. This variability is the result of individuals possessing slopes ranging from flat lines, to lines that change dramatically between repeated measures. Simply stated, the graduation from traditional growth modeling techniques to contemporary growth techniques stemmed from the research interest in analyzing change
explicitly at an individual level (i.e., modeling the change that was previously hidden in the error term). The two components of individual change are initial status, and the functional form of growth (i.e., the growth curve or growth trajectory). The two main frameworks developed to handle the inclusion of an individual change function (i.e., intraindividual change) are multilevel modeling (MLM) and structural equation modeling (SEM).

**Multilevel Modeling**

MLM is a technique for analyzing growth with two or more levels of examination. For example, MLM is typically used when individuals are nested within groups or observations are nested within individuals. At the first level each individual has an intercept, and a slope of change calculated for their growth curve. At the second level, the slope for each individual is assessed as the dependent variable of analysis. MLM takes into account dependency between observations (an improvement from conventional growth techniques) and provides a method of estimating growth curve models (GCM) to yield correct standard error for parameter estimates, correct significance tests, and confidence intervals (Wu et al., 2009; Curran et al. 2010; Wickrama et al., 2016). MLM is also known as hierarchical linear modeling (HLM), random effects models, or random coefficients model.
**Structural Equation Modeling**

SEM is another technique of growth analysis. In contrast to MLM, SEM can model measurement error in key constructs thereby obtaining more precise estimates of the relationships among latent constructs (Stull, 2008). Additionally, it allows for the simultaneous examination of relationships among multiple dependent variables and allows for multiple intercepts and slopes to covary. This feature yields information on how one variable changes in relation to other variables and also provides overall fit of the model to the data.

The central advantage of advances from traditional to contemporary growth modeling approaches is the ability to answer research questions that deal with how change proceeds within an individual (i.e., intraindividual change), while simultaneously answering questions about how change proceeds between individuals (i.e., interindividual changes). For example, Burant (2008) used the SEM framework to apply LGCM to study individual differences in depressive symptoms over a year for older patients discharged from hospitalization, effectively handling measurement error, and gathering additional information to inform the construct under study while determining similarities and differences among individuals’ manifestation of depressive symptoms. Unlike traditional growth modeling techniques, LGCM is able to handle interindividual differences in intraindividual change, thus providing increased substantial evidence to the construct being studied and information on formulating a sound hypothesis in relation to growth and change studies.
When it comes to analyzing the data from longitudinal datasets, there are several statistical techniques from which to choose (Hox & Stoel, 2005; Curran et al., 2010). In recent years (with advances in software packages), the statistical technique of growth curve modeling (GCM) has gained prominence because it is able to estimate the parameters in a population where all the individuals are assumed to have growth curves of the same functional form (e.g., linear), but with parameters that differ in describing their curves. GCM analysis can be used to obtain a description of the mean growth in a population, while providing some explanation for the variability between subjects in the parameters that describe their growth curves (i.e., interindividual differences in intraindividual change; Hox & Stoel, 2005). GCM can be approached from the MLM or the SEM framework. As described above, each statistical framework offers its own unique advantage to the analysis of growth models, and both can be used to formulate equivalent models that provide identical estimates. For the purpose of this study, the primary difference between MLM and SEM (also the reason for selecting the SEM framework in this study) is that the latter framework of analysis uses latent variables to account for the relationship between the observed variables, thus the title “latent growth curve modeling.” Furthermore, GMM is a subgroup analysis based on latent relationships between the observed and latent variables.
The Fundamentals of Growth Curve Modeling

A fundamental assumption of the growth curve methodology is that change is systematically related to the passage of time. Briefly, contemporary growth modeling techniques introduce the ability to describe intraindividual variability in intraindividual patterns of change over time. These techniques are collectively referred to as “growth curve modeling,” a broad term describing an array of statistical models for repeated measures data (Bollen & Curran, 2006; Stull, 2008). GCM stems from three different disciplines: in psychology, the study of development is carried out within the SEM framework and referred to as “latent curve analysis” (Meredith & Tisak, 1990); in statistics and biostatistics, it is emphasized as random coefficient regression models for longitudinal data (Rao, 1965); and in the field of education, hierarchical linear modeling (HLM) developed within the MLM framework.

GCM defines a discrete set of analytical approaches estimating between-person differences in within-person change, and these within-person patterns of change are often referred to as growth curves. Furthermore, these growth curves vary from person to person, depending on the characteristics of an individual's longitudinal profile (e.g., within-person trajectories can show no-change over time [flat], or systematically increase or decrease, or be linear or curvilinear in form). Its widespread utility stems from the flexibility it offers in addressing different types of research questions in longitudinal analysis, while simultaneously providing a nuanced focus on the continuous process of individual development. Some examples of growth curve modeling techniques include
multilevel models of change, latent trajectory analysis, latent curve modeling, and mixed-effects models of change (Karney & Bradbury, 1995; Curran et al., 2010).

As mentioned already, GCM can be addressed within a SEM or MLM framework. Conceptually, GCM is a two-stage process, where in the first stage, the repeated measures data are used to estimate the individual’s trajectory by fitting a regression line that plots the variables being measured for each individual over time. In the first stage, the estimated parameters are of interest as opposed to the observed variables. In the second stage, the parameters of the individual growth curves are treated as new outcome variables to be explained by other contextual variables in a between-persons analysis (Duncan et al., 2011). Specifically, the individual regression equations for all of the individuals are summarized to obtain an average intercept (i.e., the mean of the variable at the first time point) and an average slope for all individuals, each with its own variance (Karney & Bradbury, 1995; Wickrama et al., 2016).

**Latent Growth Curve Models (LGCM)**

The term *latent* growth curve is rooted in the exploratory factor analysis (EFA) and principal components analysis (PCA) literature. Similar to a CFA, covariances among repeated measures can be modeled and the factors are then conceptualized as aspects of change, and loadings are interpreted as the parameters representing the dependence of the repeated measures on the latent aspects of change.

LGCM is a special case of SEM, sharing many of its strengths and weaknesses. To reiterate, SEM is a modeling framework for testing the hypothesized patterns of
relationships among sets of variables, of which some are observed, and others are latent or unobserved (Preacher et al., 2008). In this regard, the latent variables serve as a proxy for the construct under study that cannot be directly observed. The latent variables are represented by measured indicator variables, and factor loadings capture the effect of latent variables on their indicators.

### Fixed Effects and Random Effects

GCM, at its very basic level, is composed of fixed and random effects that capture the collection of individual trajectories over time (Curran et al., 2010; Wickrama et al., 2016). In a GCM, the fixed and random effects are responsible for capturing the growth characteristics for the group and for the individuals within the group. The average slope is obtained after all the individual regression equations are estimated, and that estimate comprises the fixed effect of the model. Together with the average slope (i.e., rate of change), the fixed effect defines the underlying growth trajectory in the model.

The random effect is the variance around the group mean which can be interpreted as estimates of the between-person variability in the individual intercepts and slopes. It is useful in explaining the behavior of growth parameters. A small random effect measured by a smaller variance of the intercept and slope indicates that the parameters defining the growth trajectory are more similar across the sample of individuals; conversely, a large random effect measured by a large variance of intercepts and slopes indicates greater individual differences in the magnitude of the trajectory parameters around the mean values. A situation of the random effect equaling zero is
possible, where all the individuals share a single trajectory of growth or share the same trajectory parameters (Curran et al., 2010). The goal of GCM is to then incorporate theoretically driven covariates that could explain this variation (e.g., why is the initial level higher for some individuals than for others?).

Drawing from the published works of Curran, Obeidat and Losardo (2010), and Wickrama, Lee, O’Neal, and Lorenz (2016), the basic linear growth curve model is specified; the no-growth or intercept only model and the linear growth model. The purpose of mathematically and figuratively beginning with the linear model is because it is straightforward and easily extends into the multiple-group growth curve perspective and then into the GMM framework.

The Unconditional Linear LGCM

In this section, the mathematical formulation of a LGCM is explained to further the understanding of components related to GMM. In discussing growth models, linear models are often the starting point because of their simplicity in explaining within-person change. A LGCM can be represented in terms of a data model which depicts the relationship between the factors and the repeated measures of y.

\[ y = \tau_y + A_y \eta + \epsilon \] (1)

The LGCM in matrix notation represents,

1. \( p \times 1 \) vector of observations \((y)\), as a linear function of intercepts \((\tau_y, p \times 1)\)
2. \( m \) latent variables representing aspects of change \((\eta, m \times 1)\)
3. disturbance terms \((\epsilon, p \times 1)\)
4. factor loadings as regression coefficients ($\Lambda_y, p \times m$).

In its expanded form, i.e., $m = 2$ ($m = 1$ for no-growth or intercept only, $m = 2$ for linear model),

$$y_{ti} = \lambda_{1t} \eta_{1i} + \lambda_{2t} \eta_{2i} + \epsilon_{ti}$$

(2)

here, the score at occasion $t$ for individual $i$, as a function of the two latent variables $\eta_{1i}$ and $\eta_{2i}$. The latent variables may be expressed as functions of the latent means $\alpha_1$ and $\alpha_2$, and $\epsilon_{ti}$ are individual deviations from the means.

$$\eta_{1i} = \alpha_1 + \zeta_{1i}$$

(2.1)

$$\eta_{2i} = \alpha_2 + \zeta_{2i}$$

(2.2)

The latent variables make up the random coefficients, the means make up the fixed effects, and the residuals make up the random effects in the model.

From the data model, a covariance and a mean structure can be derived as the repeated measures of $y$ as functions of model parameters. They differ from the data model in that they do not contain scores for individuals on the factors (e.g., intercept and slope factors). The mean structure represents the population means of those repeated measures of $y$ as functions of model parameters, (i.e., it represents the population means of observed variables) ($\mu_y, p \times 1$) as functions of intercepts ($\tau_y, p \times 1$) and latent variable means ($\alpha, m \times 1$). In the covariance structure, the variances and covariances of observed variables ($\Sigma, p \times p$) are represented as functions of factor loadings ($\Lambda_y$), factor variances
and covariances ($\Psi$, $m \times m$), and disturbance variances and covariances ($\Theta_\varepsilon$, $p \times p$), as written respectively (Preacher et al., 2008):

$$\Sigma = \Lambda_y \Psi \Lambda_y' + \Theta_\varepsilon$$  \hspace{1cm} (3) \\
$$\mu_y = \tau_y + \Lambda_y \alpha$$  \hspace{1cm} (4)

Therefore, in the SEM framework, the parameters of interest for a LGCM are contained in the matrices $\Lambda_y$, $\Psi$, and $\Theta_\varepsilon$ and the vector $\alpha$, collectively known as the latent growth vectors.

For example, in a given sample with $Y_1$ through $Y_5$ repeated measures, equally spaced, the change in $Y$ being modeled as a function of two latent growth vectors will have two columns in the loading matrix $\Lambda_y$. The intercept loading values will be fixed at 1, to indicate the influence of a constant on the repeated measures, and the slope loadings fixed to a linear progression to represent linearly increasing growth over time. This is also a representation of the hypothesized trajectories or functional form of growth. Furthermore, by specifying the covariance paths among factors, the ability to ask specific questions about the rate of growth is made possible (for example: is the rate of growth in some variable related to initial status?).

$$\Lambda_y = \begin{bmatrix} 1 & 0 & 1 & 1 & 1 & 2 & 1 & 3 & 1 & 4 \end{bmatrix}$$  \hspace{1cm} (5)

In $\Lambda_y$, the elements in the first column constrained to 1 reflect each individual’s intercept remaining constant over the repeated measures. And the linear progression in the second columns reflects the hypothesized functional form of growth with equally spaced time intervals.
In the $\Psi$ variance-covariance matrix, the elements include the intercept variance $\Psi_{11}$, the slope variance $\Psi_{22}$, and the covariance of the intercept and the slope $\Psi_{21}$. The $\alpha$ matrix represents regression coefficients, and specifically, $\alpha_2$ represents the expected change in the outcome variable associated with a change of one unit in the time metric.

$$\theta_\varepsilon = [\theta_\varepsilon \ 0 \ \theta_\varepsilon \ 0 \ 0 \ \theta_\varepsilon \ 0 \ 0 \ 0 \ \theta_\varepsilon \ 0 \ 0 \ 0 \ 0 \ \theta_\varepsilon]$$  \hspace{1cm} (7)

Lastly, the elements of the $\Theta_\varepsilon$ matrix are variances and covariances of disturbance terms, representing the portion of the variance in the data not associated with the hypothesized latent curves. The off-diagonal terms in $\Theta_\varepsilon$ are fixed to zero to represent the hypothesis that disturbances are uncorrelated over time. This completes a no-growth and a linear LGCM which may be extended to incorporate predictors of intercept and/or slope, parallel growth curves for multiple outcomes, and parameter constraints (e.g., the covariance of the intercept and slope may be constrained to zero; Preacher et al., 2008).

**Change Hypotheses and the Role of Functional Forms**

The formulation of a change hypothesis is a critical first step in the study of change. Conceptually, a change hypothesis provides insight to how observed scores relate to the time metric at the individual change function, and where in this change function the interindividual differences manifest (Grimm et al., 2017). The change hypothesis provides overall direction for what the analyst believes about the behavior of the growth parameters (intercepts and slopes) in the model, and how to build the model to fit the data.
The change hypothesis is captured by an empirical representation of the change. Specifically, a mathematical process of representation describes the relationship between the time metric and the observed scores. The components of change include: (1) mean change (means); (2) extent of interindividual differences in change (covariances); and (3) pattern or functional form of change. At the individual-level, the goal is to describe how the process of growth and change unfolds within an individual (i.e., how development is proceeding within an individual). Additionally, given that there are several individual trajectories, each following a distinct functional form, the goal at the individual change level is to find an accurate mathematical representation of an individual’s growth process.

At the group-level, the goal is to capture differences in the observed trajectories.

**Individual Level Analysis**

The manner in which the functional form is summarized is a challenging process as it must be a balance of (1) uncomplicated, (2) correct identification of the individual change patterns, and (3) provide meaningful information about the individual. Grimm, Ram and Estabrook (2017) have posited that researchers inevitably prioritize one of the above three checks for an appropriate functional form, exampling the common use (or overuse) of the linear growth model to describe each individual’s functional form by two parameters: the intercept and the slope (which would be linear). The use of two parameters to describe within-person change is a suitable starting point but simultaneously poses the threat of oversimplification of a more complex change process, and loss of individual nuances of change if it remains the only functional form examined.
for the representation of the change process. The consideration of theory and use of time-varying covariates also affect the individual change theory.

Ram and Grimm (2009) used the latent basis model to example how the functional form of the individual change trajectory is understood. Using SEM specifications, $A_0$, a fixed vector of 1, at four occasions of measurement $t = 0$ to 4 ($A_0 = 1, 1, 1, 1$) captures stability, and $A_1$ captures the occasion-to-occasion changes or pattern of change as dictated by the data. For a linear growth model, $A_1 = [0, .125, .250, 1]$ or for a quadratic growth model, $A_1 = [0, .015, .062, 1]$.

**Group Level Analysis**

The group level analysis examines the changes that occur between individuals (individuals who share homogeneity in the changes they experience are typically grouped together). At this level, the goal is to determine which parameters (means, covariances, and functional form) of the individual change model are allowed to vary over persons. Following with the example of a linear growth model, change is captured in varying the only two growth parameters across persons. This implies that the between-person differences are captured in these two particular aspects of change (intercept and the slope). Determining which parameters to vary across individuals is driven by theory, therefore in more complex models, not all the parameters are selected to be varied across individuals. Simply put, theoretical notions are necessary to drive the location of between-person differences in change (Grimm et al., 2017). Marceau et al. (2011) exampled this in their use of logistic models to describe individual changes in the
development of puberty. Specifically, the differences in changes that occur between individuals were captured using two parameters (inflection point and rate of change to the upper asymptote), even though in a logistic model four parameters of change describe the process of development (the lower and upper asymptote describing the pre-existing level of an attribute and potential level of an attribute, respectively, inflection point and rate of change to the upper asymptote). The researchers decided on these two parameters as per the specification of their study and what made sense from an interpretation standpoint to understand developmental differences between individuals on their observed trajectories.

**Mixture Modeling**

Mixture modeling is a statistical technique utilized in situations with a mixture of observed and unobserved variables, which can be a combination of continuous or discrete variables. Mixture modeling techniques are identified by other names depending on the cross section of continuous or discrete observed variables with latent variables. For example, extensions of mixture models include item response theory (IRT) and factor analysis where the observed variables are discrete and the latent variables are continuous. Other examples are latent class analysis (LCA) and GMM, where conversely, the observed variables are continuous, and the latent variables are discrete. These arrays of models are collectively referred to as latent variable models.

Mixture modeling primarily deals with the recovery of hidden groups from observed data, specifically concerning itself with discrete latent variables. These discrete latent variables form hidden groups where within each group individuals share
characteristics (e.g., have similar responses according to some variables or have similar change patterns) that are possibly different from other groups in the observed data. These groups can be thought about as "classes" or "mixture components," or as categories of unobserved nominal or ordinal variables which cannot be observed through the data itself but through statistical analysis (Muthen, 2004). Mixture modeling techniques afford researchers the ability to uncover unobserved heterogeneity in a population, find substantively meaningful groups of people, and obtain the distributions within such groups and the probability of an individual's membership to the different groups.

**Growth Mixture Modeling**

GMM has increased in frequency of use across the social and behavioral sciences in recent years. It is a close relative to latent class growth analysis (LCGA) and stands at the intersection of LGCM, and finite mixture modeling, where its core assumption is that the data are drawn from a finite number of heterogeneous subpopulations. For example, as an advanced growth modeling technique, the research objective in GMM is to study individual changes on a construct, and interindividual differences in those changes based on the construct. In an examination of reading skills in children’s kindergarten to second grade years, a researcher might be interested in evidence that interindividual differences in improved reading skills are better represented by considering more than one typology, (i.e., a potential group of individuals who have a typical slope of readings skills and a group of individuals who have a less typical slope of reading skills). The pattern of change is of interest here to identify individuals who are likely to be in one group versus
the other and develop mechanisms to address growth or gaps in readings skills among children. The finite mixture component of GMM divides the population into an unknown number of exhaustive and mutually exclusive subpopulations. Ram and Grimm (2008) formally described GMM as the process of identifying multiple unobserved subpopulations in order to describe how longitudinal change proceeds within each unobserved subpopulation and examine differences in change among the unobserved subpopulations. Simply put, the primary goal of GMM is to identify the underlying subgroups or latent classes in a population exhibiting qualitatively distinct patterns of change. This can be written as the distribution of an observed outcome $Y_i$ in,

$$
\int (Y_i) = \sum_{k=1}^{K} [Pr(C_i = k) \int (Y_i | C_i = k)]
$$

(8)

where, $C_i$ represents the latent class membership for individual $i$, $K$ is the total number of latent classes, $Pr(C_i = k)$ is the mixing proportion for Class $k$, and $\int (Y_i | C_i = k)$ is the class specific response distribution of $Y_i$.

GMM, an extension of the multiple-group modeling technique, shares similarities and differences. While both techniques are similar in the assumption of multivariate normality in the distribution of intercepts and slopes within latent classes and nonnormality across latent classes, they differ in how they handle the identification of classes. Unlike the multiple-group technique, GMM handles the identification of classes in a post-hoc manner, classifying individuals thought to share homogeneity in growth characteristics into groups where each group underlying the data is different from the
others (i.e., individuals within a group share the same growth trajectories while differing from individuals in other groups). Unlike multiple-group modeling, GMM is an exploratory analysis, used when the researcher must discover how to split the data. This particular feature of GMM is met with caution when it comes to the interpretation of its results, as sole reliance on model parameters to describe underlying subgroups is circumstantial evidence and can be misleading regarding the true number of latent classes in the population.

**Building a GMM**

Given the fragile nature of class determination in a GMM, it is vital to its application that there exists a strong link between theory to inform the GMM hypothesis and method for the purpose of a sound analytical strategy. The use of theory in tandem with previous empirical findings and initial examination of the data helps direct the researcher in correctly inferring 1) the number of unobserved subgroups expected in the analysis; 2) expected subgroup differences in terms of mean change; 3) extent of interindividual differences in change; and 4) the pattern of change.

**Baseline or Invariance Model**

A GMM begins with a *single-group* representation of change which is searched for following usual growth curve modeling procedures where a series of models (e.g., no growth, linear, quadratic, latent basis, etc.) are fit to the full data. This baseline single-group growth curve model serves as a starting point from which the exploration for unobserved groups proceeds. The baseline model or the invariance model treats all
potential groups underlying the data as having identical growth patterns, means, variances, and covariances (i.e., all parameters are constrained to be equivalent across groups). The assumption driving this step is that the group underlying the data is homogeneous, and thus, the goal is to determine the most appropriate mathematical, and empirical representation of change in the homogeneous group (Ram & Grimm, 2009; Grimm et al., 2016). Proceeding from the single-group baseline model, the intent of the GMM analysis is to obtain a better and more complete representation of the data by allowing for the possibility of multiple unobserved groups. This step is intended to corroborate with the hypothesis formulated and provide a purposeful direction in which to approach the data.

Model Specification

The best fitting model is searched for through the specification and estimation of a series of models. As previously mentioned, the successful application of a GMM hinges on formulating an expectation of the number of subgroups underlying the data and being informed on how these subgroups are expected to differ in terms of mean change, extent of interindividual differences in change, and the pattern of intraindividual change. Simply put, the researcher believes there to be latent subgroups in the population, and the process of searching them out implies specifying how the groups differ on means, extent of changes observed between groups, and pattern of change (i.e., trajectory of growth) within individuals. Therefore, following a well-specified research question, a total of four
models are fit: the baseline model (as described already) and three group difference models.

1. Means model: The first group difference model allows the assumed number of latent groups in the dataset to differ among groups with respect to the mean change function of the growth factors (i.e., the intercept and slope).

2. Covariance model: The second group difference model, measuring the extent of interindividual differences between groups, allows the means and variances (and covariances) of the growth factors to differ among groups.

3. Pattern of intraindividual change: The last group difference model, in addition to the means and covariances, allows for the pattern or shape (i.e., the functional form of growth within groups) of change to differ among groups. This is the defining feature of a GMM analysis, invoking the belief that individuals in a given population measured longitudinally will showcase a trajectory of individual growth different from another individual in the population. Individuals homogeneous in their growth trajectories are categorized into groups and each group varies on one or all of the three group differences (mean, covariances, and pattern of change).

**Number of Latent Classes**

To reiterate, these latent subgroups are identified *post hoc*; therefore, it is critically important to formulate theoretically sound expectations of the number of groups present in the population of interest. When using GMM to unearth latent classes in a population, a latent grouping variable $c$ is used to indicate the number of classes.
theorized and thus expected to exist. Model parameters are estimated for each latent class and the probability that each individual is a member of each group. For example, if the population of interest is hypothesized as having two subgroups (e.g., "high risk for opioid addiction" and "low risk for opioid addiction"), to quantify whether a) two subgroups truly exist and b) assess how these groups differ from each other, the researcher specifies a 2-Class (means) model, a 2-Class (means + covariance) model, and a 2-Class (means + covariance + pattern) model followed by a set of 3-class group difference models because the process of confirming an accurate number of classes requires the iterative examination of one more than the expected number of latent subgroups. This process of iterative examination allows the possibility to reject models that have weak statistical evidence for the number of latent classes present in the dataset.

**Latent Class Membership**

The membership of individuals in latent classes relies on which variables and random effects are included as latent class indicators and the specifications of the within-class joint distribution of those latent class indicators. Simply stated, latent class membership is determined by the class-specific model parameters. As such, latent class membership is unobserved, and indicators for the latent class variable include observed, or latent, variables that differ in values between individuals in the population due to latent class membership as well as model parameters that are permitted to be class-specific, making them the random effects or individually varying parameters in the model. The class-specific joint distribution of the observed and latent variables as well as random
effects characterize these latent classes. Therefore, the estimation of the optimal number, size or proportion of classes, and corresponding model parameter estimates depends on how latent classes are characterized.

**Model Fit to the Data**

In order to determine whether a model is a good representation of the data, comparisons are made among all the models, using fit indices generated. Fit indices help in assessing model fit to the data which also implies a simultaneous confirmation of the most likely number of subgroups underlying the population. It is important to bear in mind that good model fit simultaneously confirms the extracted number of latent classes. Simply put, the finality of the decision to keep a model reinforces the theory driving the number of classes extracted (i.e., the number of subgroups that make up the population of interest), thus making model selection a critical last step.

**Model Estimation**

The GMM is estimated using maximum likelihood (ML) or Bayesian methods. Depending on the statistical program being used, the estimation process follows either an expectation-maximization (EM) procedure (e.g., Mplus) or Markov Chain Monte Carlo procedures (e.g., AMOS). The latent group classification variable is specified (e.g., c = 2, 3, 4, so on), and through iterative procedures, parameter estimates and posterior estimates are obtained indicating the probability of individuals’ membership in each of the possible groups to maximize the likelihood of the data given the model parameters.
(for ML) or to estimate the posterior mean for the parameters given the data (for the Bayesian approach) (Ram & Grimm, 2009).

**Model Selection and Interpretation**

As mentioned above, model selection is a critical last step. Published literature emphasizes building a defensible judgment about the optimal model using a combination of model results, theory, and fit statistics. Given that an array of models are typically fit to the data before the best-fitting one is selected, a systematic approach to sifting through comparable models is necessary. Researchers are encouraged to pay specific attention to parameter estimates that are out of bounds (e.g., negative variances) among other problems in estimation, knowing that not all solutions obtained during model estimation will be useful. As previously mentioned, model selection is made using fit indices, where lower values indicate better-fitting models (Muthén, 2003; Nylund et al., 2007). Popular fit indices used in a GMM are the Bayesian Information Criterion (BIC), Akaike Information Criterion (AIC), and Adjusted BIC. In addition, the Vuong–Lo–Mendell–Rubin likelihood ratio test (VLMRLRT) and Adjusted Lo–Mendell–Rubin likelihood ratio test (Adjusted LRT) are used to quantify specific comparisons between the model of interest and a model with one fewer class, where a significance test (p < .05) of the VLMR-LRT or Adjusted LRT indicates that the model with C – 1 classes should be rejected in favor of the model with C classes. Other thresholds that help in model selection include comparison to the baseline model, and confidence with which individuals have been classified as belonging to the latent classes. The use of an entropy
statistic value, which ranges from 0.00 to 1.00, indicates the conditional probabilities of individuals’ group membership, where high values of entropy (> .80) indicate that individuals are classified with confidence. It also holds implications for good separation between latent classes implying that there is no overlap between the latent classes.

**Mathematical Representation of a 2-Class Means GMM**

GMMs are commonly fit in the SEM framework. This is in part due to the limited MLM software capabilities available in handling this type of analysis. The linear GMM is written as follows in a SEM framework, where $y_i^k$ is a T x 1 vector of the repeatedly measured observed scores for individual i in class k. T represents the number of repeated measures based on the stipulated time metric. $\Lambda$ is a T x 2 matrix of factor loadings defining the latent variable intercept and slope, $\eta_i^k$ is the 2 x 1 vector of latent factor (intercept and slope) scores for individual i in class k, and $u_i^k$ is a T x 1 vector of unique scores for individual i in class k.

$$y_i^k = \Lambda \eta_i^k + u_i^k$$  \hspace{1cm} (9)

The latent factor scores are written such that $\alpha^k$ is a 2 x 1 vector of latent factor means for class k and $\xi_i^k$ is a 2 x 1 vector of residual deviations for individual i in class k.

$$\eta_i^k = \alpha^k + \xi_i^k$$  \hspace{1cm} (10)

The within-class model implied mean and covariance structure is as follows:

$$\mu_i^k = \Lambda \alpha^k$$

(11) The elements of the covariance structure $\Sigma^k$, is $\psi^k$ a 2 x 2 latent covariance matrix.
for class $k$ and $\Theta^k$ is a $T \times T$ diagonal residual covariance matrix for class $k$.

$$\Sigma^k = \Lambda \psi^k \Lambda' + \Theta^k$$

(12)

A valuable highlight is to note the pervasiveness of $k$ in the models. In the first model, the invariance model, the data are modeled as though they are sampled from a single nonmixture population (i.e., there are no class specific differences). In the second model, the means model, the latent variable means are allowed to be class specific (i.e., $\alpha^k$). In the third model, the means and covariance model, the latent variable means, variances, and covariances are class specific (i.e., $\alpha^k$ and $\psi^k$). In the last model, the pattern models the means, covariances, and residual variances, and all estimated parameters of the model are class specific (i.e., $\alpha^k$, $\psi^k$ and $\Theta^k$).

The Pitfalls in GMM Applications

GMM is a powerful tool in understanding and describing interindividual differences in intraindividual change. Its ability in addressing nuanced research questions regarding the within-person change function has made it an appealing statistical tool for measuring growth and increased its utility across the sciences. However, GMM continues to be a methodology that is challenging to implement with issues ranging from improper solutions, overextraction of classes (a routine feature), and sensitivity of parameter estimates to starting values. As a result, a common caution to those interested in conducting GMMs is to avoid its application to overly complex developmental theories (Ram & Grimm, 2009; Preacher et al., 2010; Grimm et al., 2016).
There is merit to treading with caution; however, an unintended consequence has been few cutting-edge developments in testing the bounds of GMM as a methodology. As such, while complex developmental theories are the norm when assessing human behavior and learning, the combination of modeling simple (e.g., linear and quadratic models) developmental theories with low-risk applications of GMM begs the question of whether GMM is being utilized to its full ability and whether typical growth trajectories truly measure the underlying developmental hypothesis or mask complexities in developmental theories. These create the need for expanding the manner in which GMM can be used. As a step in that direction, the following section will explore major areas that remain unclear in the application of GMM. They are related to latent class extraction (or enumeration), effects of violations of GMM assumptions in arriving at an optimal GMM solution, and the dearth of sufficient critical replications in GMM studies. Consequently, these issues directly impact understanding and interpretation of the functional form of growth between latent classes.

**The Issue of Optimal Solutions in GMM**

An optimal solution in GMM is a concert of good model fit and correct enumeration of latent classes (i.e., determining the number of classes). Additionally, the strategy that guides accurate extraction of latent classes relies on development hypotheses set *a priori* which inform the expectation of the number of classes to be extracted. However, obtaining a trustworthy solution in a GMM analysis is a time-consuming
process of varying the sets of starting values used. The combination of uncertainty embedded in the mixture component, along with the unpredictability associated with possible class assignments (Grimm et al., 2017), pose a continual challenge to reaching an optimal solution in a GMM analysis.

**Criteria for Model Fit**

Given the critical role of latent classes in interpreting results and making inferences, GMM is challenging to apply because researchers lack a single commonly accepted set of best model fit criteria to agree upon the correct number of classes. Tofighi and Enders (2008) have classified these fit indices into three major categories: information-based criteria, nested model likelihood ratio tests, and goodness-of-fit measures. The current practice of extracting classes in a GMM involves the combination of a variety of fit indices, theory, and published research. Conversely, when it comes to the utility of fit indices in class determination, Bauer and Curran (2003) have held a different opinion relative to other experts in the field. They presented the case that using fit indices to identify the presence of latent classes is not evidence of heterogeneity in a population, as fit indices can also be used to approximate homogeneous but undefined distributions. Given that the fit indices cannot be used to distinguish between the two functions of the model, there is a need for alternative benchmarks of correct latent class identification.
Limited Generalizability of GMM Solutions

Once an optimal solution has been achieved in GMM, the generalizability of that solution for further analyses must be a constrained effort (i.e., generalizability of GMM solutions is atypical compared to generalizability of the results from other statistical tests). While the successful fit of an optimal model to the data holds meaning within the immediate context of the study, it is possible for these solutions to mean little outside of it due to the varying constraints and assumptions often applied to secure an optimal solution in GMM. Specifically, consider that a GMM solution provides information on an individual's membership into latent classes based on an approximation of their predicted probability of class membership. However, using the established groups (confirmed by GMM) in subsequent analyses (e.g., regression of subgroup membership on explanatory variables) trades an approximation of an individual’s membership for exact membership (i.e., 85% certainty in class membership to 100%). The implications for artificially removing the original uncertainty associated with an individual's membership to a group is to substantiate literature with potentially compromising inferences (McIntosh, 2012).

Effect of Violations to Assumptions

Following the thread of latent classes, and their extraction and inference, Curran and Bauer (2003) highlighted that critical to the extraction of latent classes is the operating assumption regarding normality of the data. They showed that in a GMM
application, a multiple-class model could easily be estimated from a single-group population distribution when the assumption of normality is violated. More plainly, within-class nonnormality leads to the spurious extraction of too many latent classes. Furthermore, they criticized the practice of relying on strong substantive theory indicating population heterogeneity to guide the interpretation of the model. Specifically, their concern was that using a GMM to test the hypothesis that the population is heterogeneous, and subsequently determining that multiple latent classes are optimal for the data, does not confirm heterogeneity of the population. Instead, with the intent to raise an awareness of alternative interpretations of GMM solutions, they reasoned that additional classes improving model fit could very well be the result of other factors (e.g., an irregular but homogeneous distribution of repeated measures). In the vein of within-class assumptions, Bauer and Curran (2003) also showed that model mis-specification, for example, mis-specifying the within-class covariance structure, leads to the extraction of an incorrect number of classes.

**Insufficient Critical Replications**

The linear change model is the most common of functional forms modeled in a GMM. To this effect, a majority of GMM literature has consisted of a high frequency of linear and polynomial models (e.g., quadratic, cubic). In fact, there is a surprising lack of complex functional forms modeled via GMM. Grimm, Ram, and Estabrook (2017) have encouraged considering multiple types of change models, given that individuals follow
linear as well as nonlinear trajectories of growth. However, methodological decisions in conducting a GMM are weighed against the dilemma of whether model convergence will be achieved. In applications regarding GMM analysis, it is well known that increasing model complexity simultaneously increases the chances of model nonconvergence. As a result, usual (typical) applications of GMM proceed in an analytic approach consistent with theories emphasizing population heterogeneity in patterns of change over time (Bauer & Curran, 2003). Put differently, the combination of time constraints, computational burdens, and relative simplicity with which GMM can be suited to a researcher’s purposes has resulted in little attention being given to testing the statistical boundaries of a GMM’s capabilities.

Conversely, in an interesting experiment, Infurna and Luthar (2017) have cautioned against blind reliance on inferences from GMM solutions to inform subsequent analyses (i.e., using the results of a GMM as the truth about a population). In their paper on spousal loss, the authors highlighted an important methodological consideration regarding the replication of biases across studies. They discovered that findings from GMM were highly influenced by the a priori assumptions applied before running the models and that the study of resilience was saturated with similar findings across several different GMM applications. They pointed out that the empirical accumulation of evidence stemming from the same a priori assumptions applied across studies contributed compromising inferences to the literature on resilience. Highlighting the Larzelere et al. (2015) argument for “critical replications” of studies (as opposed to
“exact replications”), the authors changed two *a priori* assumptions to the same dataset, getting different results in return.

Aside from the obvious implication stemming from their study that violations of GMM assumptions directly impact the type of functional forms and number of latent class trajectories extracted, they also highlighted the dangerous practice of taking the results from one GMM analysis as strong evidence for the underlying developmental theory without some attempt at replicating the results. Infurna and Luthar’s (2017) study examining the methodological pitfalls of a GMM application is one among a handful of its kind. Another study testing the characteristic features of GMM as a methodology is Bauer and Curran’s (2003) research presenting alternative arguments to conventional ideas of the role of strong theoretical background and fit indices in latent class identification.

**Objective of the Present Study**

The purpose of this study is to determine the effect of violating the assumption of functional forms of growth on class extraction and the optimal GMM solution. Taken together, the pitfalls of GMM directly threaten the credibility of the hypothesized feature of intraindividual growth trajectories and the modeling of functional forms. For reasons already covered (systematic versus critical replications), there is little in the literature specific to GMM in terms of incorrectly applied functional forms. Furthermore, while there are ample studies documenting the performance accuracy of fit indices extracting
latent classes, there is little available regarding the misidentification of intraindividual growth trajectories (i.e., the violation of the assumption of change developing in an individual). That said, in the broader context of longitudinal studies and growth modeling, the idea of modeling the incorrect functional form has received some attention.

Whittaker and Khojastesh (2017), in a study of fit indices in the LGM context, recognized that the frequency of using linear functional forms to model growth stems in small part from theoretical underpinnings, but mostly because linear trajectories are the simplest to model with respect to interpretation. They point out that not all functional forms are linear and incorrect modeling can lead to biased estimates of interest in a growth curve model. Therefore, in an attempt to alert the analyst to whether the correct functional form has been identified, Whittaker and Khojastesh’s (2017) study determined that when using the information-based criteria CAIC, the BIC, the nBIC, and the HQIC they can confidently select the linear model among a set of competing models, regardless of the number of measurement occasions or sample sizes (directly relating to their study). Furthermore, they determined that the information-based criteria that selected the quadratic growth model or the cubic growth model with six measurement occasions is most likely credible, as the information-based criteria performs with better accuracy with more measurement occasions in tandem with a large sample size.

In a simulation study examining the functional form of growth, Diallo, Morin, and Parker (2014) attempted to detect nonlinear trends when present in the data. In the context of latent curve models (LCM), the authors utilized simulated data to investigate
the power of LCMs in detecting the mean of the quadratic slope, Type I error rates, and rates of nonconvergence during the estimation of quadratic LCMs. Their study was aimed at addressing the gap in the literature indicating extensive use of LCMs for the analysis of longitudinal data, yet very few studies were available in which systematic estimates of the statistical power of the LCM to detect specific types of development (linear, quadratic, exponential, etc.) were examined. Instead, they found that most statistical studies of the power of LCMs were concerned with the capacity of these models to detect between-group differences rather than with the ability of these models to correctly detect one or more parameters used to characterize the shape of the estimated trajectories.

In a substantive application, Infurna and Luthar (2017) addressed the controversy that resilience to major life stressors is not as common as had been empirically shown in GMM analysis. Directly citing GMM as the basis for the incorrect inference of resilience being the typical pattern of response among adults exposed to traumatic life events, the authors modified GMM assumptions by allowing for differences in within-group variability across the different trajectories and greater within-group variability was allowed for among individuals in the trajectory marked by substantial initial declines following the stressor, and then subsequent recovery. Compared to previous results from the same data, by reassessing the assumptions underlying the functional form of growth, the authors found that their results varied dramatically indicating those who were seen to be previously resilient were in fact not, and the model suggested a single group solution characteristic of recovery.
Broadly speaking, the issues that stem from violations of functional forms in growth modeling have received a cursory glance in longitudinal data analysis; however, when it comes to GMM, a methodology easily susceptible to challenges with convergence, the effects of direct mis-specification of functional forms is largely unexplored. Given GMMs’ inability to provide an optimal solution in the face of assumption violations, their performance is not expected to be different when it comes to functional forms. However, the objective of this study is not to prove the sensitivity of fit indices to mis-specified GMMs, rather it is to provide a concentrated look at the performances of fit indices, and number of classes extracted in a badly mis-specified GMM, relative to the correct GMM model. It is important to note that, in any substantive application of GMM, the functional form can be extremely difficult to know \textit{a priori}, and therefore the fitting of incorrect functional forms is likely a common occurrence in the literature. The goal of this dissertation is to be able to craft a new look into the capacity and functioning of a GMM in this real-world situation in which the functional form is mis-specified.
Chapter Three : Methodology

The following growth mixture modeling (GMM) simulation study aims at examining how violations of the assumptions of latent class growth trajectories impact model fit. Framed in the context of an empirical comparison between a true model and a series of mis-specified models, the extent and implications of the effects of these violations will be measured through sensitivity of model fit indices and enumeration of latent classes.

The study’s aim is directly supported by utilizing the Monte Carlo simulation technique of data generation. Specifically, its ability to generate sample data with known population parameters and fit indices for assessing model fit to the data (Nylund et al., 2007) makes it an ideal choice to conduct a comparative exploration of parameter estimates and model fit indices yielded from mis-specified models against the same for the true model. The simulation will be a combination of fixed and manipulated design conditions to investigate the environments in which the mis-specified models yield the correct and incorrect number of latent classes with good or poor model fit. While sufficient literature provides evidence that assumption violations in GMM yield an untrustworthy extraction of latent classes (Bauer & Curran, 2003; Enders & Tofighi, 2008), this has been a concentrated effort under the modeling of the correct growth function. In tandem with knowing the behavior of model fit indices under correct model
specification, Maiti and Mukherjee (1991) highlighted the need for studies that examine how model fit indices degrade under model mis-specification. Given the relative newness of the GMM methodology and the challenges associated with class extraction, extensive research on how it performs under model mis-specification will contribute to an increased awareness of its application in substantive research. The hypothesis undergirding this study is that GMM will exhibit meaningful variability in its performance at recovering the population parameters in all the mis-specified models (Nylund et al., 2007).

Population Model

The dataset for the simulation study will be generated according to the following conditions. A systematic review of substantive applications of GMM evidence between two and three subgroups in a given population with functional forms similar to the ones specified in this study (see e.g., Ram & Grimm, 2007; Tofiqhi & Enders, 2007). Therefore, drawing from common data structures found in psychology and the behavioral sciences (Tofiqhi & Enders, 2007), the population model consists of two subgroups defined by their growth trajectories across timepoints. One group will exhibit an initial elevated growth trajectory level that over time moves toward a lower asymptote at a relatively stable pace and the second group will consist of growth trajectories that grow in a less steep but stable manner over time, (i.e., a quadratic growth trajectory and a linear growth trajectory, respectively). Conceptually, these two groups can be thought of as a "problem class" and a "zero class" (Tofiqhi & Enders, 2007), or "high stress group" and "typical group" (Ram & Grimm, 2007). Other assumptions include a normal distribution
of the indicator variables and the residual variances being homoscedastic, uncorrelated (i.e. \( \theta = \theta^2 I_n \)), and invariant across classes (\( \theta^k = \theta \) for all \( k \)).

Two design decisions that will be made to improve convergence and ensure existence of a global solution are the exclusion of covariates and fixing the residual variables to be equal. A useful advantage of the GMM approach is the ability to include multiple covariates (i.e., predictors or distal outcomes) in order to explain both within- and between-class variability simultaneously (Wickrama et al., 2016). However, to manage the scope of the study, negotiating tradeoffs between the advantages and disadvantages of various simulation designs was made in relation to the study's intended aim (Skrondal, 2000). Jung and Wickrama (2007) have also highlighted the need for careful consideration of research goals in tandem with model complexity in order to avoid convergence problems, improper solutions, and overall model instability.

In this vein, the second decision deals with setting residual variances and growth factor variances and covariances to be invariant across classes. Constraining the model reduces the number of free parameters that have to be estimated which in turn increases the chance of the existence of a global solution. Setting up these assumptions is reasonable given that Bauer and Curran (2003) showed in a simulation study minimal difference in the prediction of class membership when factor variances were allowed to vary relative to when they were constrained (Li, 2013). Lastly, external validity of the study is enhanced by using parameter estimates used in similar simulation studies.
The population GMM formula expressed as follows:

\[ Y[t]_n = \sum_{c=1}^{C} \pi_{nc}(g_{0nc}A[t]_0 + g_{1nc}A[t]_1 + g_{2nc}A[t]_2 + \epsilon[t]_{nc}) \]  

(13)

given,

\[ 0 \leq \pi_{nc} \leq 1 \text{ and } \sum_{c=1}^{C} \pi_{nc} = 1 \]  

(13.1)

where, the \( \pi_{nc} \) represents the probability of an individual's membership to a class, c. The grouping variable c is unobserved. \( Y[t]_n \) is the observed longitudinal data or individuals’ scores on variable Y repeatedly measured at times \( t = 1 \) to 4. It is described by three latent variables \( g_{0nc}, g_{1nc}, g_{2nc} \) and three basis vectors \( A[t]_0, A[t]_1, A[t]_2 \).

\( A[t]_0 \) represents the intercept and is a fixed vector of 1. \( A[t]_1 \) and \( A[t]_2 \) represent a linear and a quadratic slope, respectively. GMM allows researchers the ability to examine within-person change and between-person differences in within-person change (Ram & Grimm, 2007); however, in this study the extent of group differences examined will be restricted to mean change and patterns of change between groups. Specifically, the mean intercept and slopes will not be allowed to covary, thus eliminating the estimation of a covariance matrix. As mentioned above, this decision stems from the need to maintain an uncomplicated simulation environment to successfully isolate the true effects of mis-specified functional forms within latent classes. The application of a GMM begins with specifying a baseline single-group model \( 1 - Class_{baseline} \), to serve as the starting point from which the exploration for unobserved groups will proceed (Ram & Grimm, 2009).
The baseline model precedes the specification and estimation of the true model (i.e., the 2-Class GMM). A series of models will be specified to examine how the two unobserved groups might differ (Ram & Grimm, 2009). The first group difference model will be a $2 - \text{Class}_{\text{means}}$ model, where the two groups are allowed to differ with respect to the mean change function. The next model will be a $2 - \text{Class}_{\text{means} + \text{pattern}}$, where the two groups are allowed to differ with respect to the pattern of growth (Ram & Grimm, 2009). Following the 2-Class GMM, a 3-Class GMM will be fit to the data to accommodate the possibility of one more latent class, following GMM best practices (Ram & Grimm, 2009). Although it is known a priori that only two latent classes are present in the data, a $3 - \text{Class}_{\text{means}}$ and $3 - \text{Class}_{\text{means} + \text{patterns}}$ will be estimated and model fit monitored using fit indices (Ram & Grimm, 2009). The expectation is that the 2-Class GMM will be the best fitting model. In Mplus, the exact number of categories/groups in the latent c variable and which parameters may differ among groups will be specified for each model thereby invoking the assumptions laid out in the description of the population model (Ram & Grimm, 2009).

Once the baseline model and the true model have been established, the latent basis model will be fit to the data, followed by the linear model, the Gompertz model, and the Michaelis Menten. The latent basis GMM is expected to validate the true model by confirming the presence of two latent classes. From there, the linear GMM, the Gompertz, and the Michaelis Menten are expected to yield poor model fit to the data by over- or underextracting latent classes. To reiterate, the true model is correctly identified.
by the correct extraction of two latent classes and good model fit. The mis-specified models in the study will be examined for how close, exact, or far they are from correct class extraction and performance of fit indices to the true model.

**The Baseline Model**

The preliminary step in specifying the GMM is to establish a baseline or invariance model (Ram & Grimm, 2007). In the baseline model, the two subgroups underlying the data will be set to have identical growth patterns, means, variances, and covariances (Ram & Grimm, 2007). Specifically, all the parameters will be constrained to be equivalent across groups and a single-group assumption will be imposed on the dataset (Ram & Grimm, 2007; Soloski & Durtschi, 2019). The purpose of the baseline model is to provide information about overall fit of the data to a trajectory with a single shape or form before accounting for heterogeneity in the trajectories (Wickrama et al., 2016). The benefit of this approach is the identification of distinct classes prior to conducting GMM (Jung & Wickrama, 2007; Ram & Grimm, 2009).

In this study, the baseline model will be established using a special type of GMM: a latent class growth analysis (LCGA), also referred to as a semiparametric group-based modeling (Nagin, 1999; Wickrama et al., 2016). Using LCGA, the number of distinct trajectories to be extracted from the data will be specified and the model with trajectories that best fit the data will be selected (Andruff et al., 2009). This type of GMM only estimates means and fixes within-class variances and covariances to zero (Wickrama et al., 2016), invoking the belief that individuals within classes are homogeneous.
Researchers evaluate which model provides the best fit to the data by interpreting and comparing both the fit statistics and the posterior probabilities for each model tested (Andruft et al., 2009).

The Latent Basis

The latent basis growth model or the unstructured model is an exploratory model in which the shape or functional form of change is not specified \textit{a priori} (Ram & Grimm, 2009); instead the model is used to derive the optimal shape of change from the data (Cameron et al., 2013). This feature of the latent basis model makes it a choice selection in this study as it provides a mis-specified representation of the nonlinear change trajectories modeled by the true population model (Ram & Grimm, 2007). Since the LB-GMM derives the optimal shape of the underlying growth trajectories without \textit{a priori} specification, it will be used to validate the 2-class GMM (i.e., the true population model underlying the simulated dataset).

The population model postulated by the LB-GMM is as follows:

$$Y[t]_n = \sum_{c=1}^{C} \pi_{nc} (g_{0nc}A[t]_0 + g_{1nc}A[t]_1 + \epsilon[t]_{nc})$$

(14)

where intraindividual change is invoked via the vectors $A[t]_0$ and $A[t]_1$, respectively. $A[t]_0$ represents the initial measurement and thus will be fixed at 1. The elements of $A[t]_1$ will be fixed at 0 for the first basis coefficient and 1 for the last basis coefficient. This specification will enable interpretation of the intercept and scaling of the latent
slope. Using the identification of $\alpha_t$ can be interpreted as the proportion of the total amount of change between the first and the last occasion that occurred up to a given time $t$ (Ram & Grimm, 2007). The two random variables representing interindividual differences in intraindividual change are invoked via $g_{one}$ and $g_{inc}$ which capture interindividual differences at the initial level of measurement and interindividual differences in the total amount of change, respectively.

Leaning on SEM notation for further clarification, the $\Lambda$ matrix for the latent basis growth model with four occasions of measurement can be specified as:

$$\Lambda = \begin{bmatrix} 1 & 0 & 1 & \lambda_{22} & 1 & \lambda_{23} & 1 & 1 \end{bmatrix} \quad (15)$$

The second column which defines the shape factor has three unknown loadings to be estimated from the data (Grimm et al., 2017). The hypothesis here is that when the latent basis population model is fit to the data, it will extract two underlying subgroups with the correct growth trajectory specification.

The level-2 equation for the latent basis growth model is:

$$g_{0i} = \beta_{0i} + d_{0i} \quad (16.1)$$

$$g_{1i} = \beta_{1i} + d_{1i} \quad (16.2)$$

where, the fixed effect parameters for the intercept and shape factor are represented by $\beta_{0i}$ and $\beta_{1i}$, respectively, and the random effect parameters, (i.e., the individual deviations
from the growth factors) $d_{0i}$ and $d_{1i}$, are assumed to follow a multivariate normal distribution with zero means, estimated variances, and covariances (Grimm et al., 2016).

$$d_{0i}, d_{1i} \sim \text{MVN } ([0 
0 ] [\sigma_1^2 \sigma_{21} \sigma_2^2 ] )$$  \hspace{1cm} (16.3)

**The Linear GMM**

The expectation for incorrectly fitting the Linear GMM to the true population model data is as follows:

$H_0$: Mis-specifying the functional form in the true model with a linear trajectory has no effect on correct class extraction.

$H_1$: Mis-specifying the functional form in the true model with a linear trajectory has an effect on correct class extraction.

Although the population model for the linear GMM appears similar to the latent basis growth model, it differs in how intraindividual change and interindividual differences in change are understood and specified by the model.

The population model postulated by the Linear GMM is as follows:

$$\gamma[t]_n = \sum_{c=1}^{C} \pi_{nc} (g_{0nc}A[t]_0 + g_{1nc}A[t]_1 + \epsilon[t]_{nc})$$  \hspace{1cm} (17)

where intraindividual change is invoked via the vectors $A[t]_0$ and $A[t]_1$, respectively, implying individuals differ from one another in their latent intercept, $g_0$, and their latent
slopes, $g_1$. The vector $A[t]_0$ represents the initial measurement and captures flat aspects of intraindividual change. Its basis coefficients will be fixed at 1. $A[t]_1$ is another vector of intraindividual change to the model describing aspects of straight-line growth and decline in the measured construct. The basis coefficients for the latent slope are defined as,

$$(t - c_0)c_1$$

where $t$ is measurement occasion, $c_0$ and $c_1$ are constants. In the current study, with four equally spaced time points and a linear growth model, the $A$ matrix is specified as:

$$A = \begin{bmatrix} 1 & 0 & -V_{@1} & V_{@1} \\ 1 & 1 & -V_{@2} & V_{@2} \\ 1 & 2 & -V_{@3} & V_{@3} \\ 1 & 3 & -V_{@4} & V_{@4} \end{bmatrix}$$

(17.2)

The level-2 equation for the latent basis growth model is,

$$g_{0i} = \beta_{0i} + d_{0i}$$

(17.3)

$$g_{1i} = \beta_{1i} + d_{1i}$$

(17.4)

where the fixed effect parameters for the intercept and shape factor are represented by $\beta_{0i}$ and $\beta_{1i}$, respectively, and the random effect parameters, (i.e., the individual deviations from the growth factors) $d_{0i}$ and $d_{1i}$, are assumed to follow a multivariate normal distribution with zero means, estimated variances, and covariances.

$$d_{0i}, d_{1i} \sim \text{MVN}([0 \ 0 \ | \sigma_1^2 \ \sigma_{21} \ \sigma_2^2])$$

(17.5)
The hypothesis here is that when the linear population model is fit to the data, it will extract the incorrect number of latent classes, although the precise manner of its incorrect class extraction is not known.

**The Gompertz GMM**

The Gompertz curve is very relevant in the context of learning and development. The literature review on longitudinal reading data evidence the Gompertz curve to be the most appropriate model in handling variation in the rate of approach to the asymptote, timing of accelerated changes, and total amount of change to the upper asymptote (Grimm et al., 2010). In the following simulation study, the data will be fit to the mis-specified Gompertz model and the estimated parameters will be compared to the parameters of the true model.

\[ H_0: \text{Mis-specifying the functional form in the true model with a Michaelis Menten curve has no effect on correct class extraction.} \]

\[ H_1: \text{Mis-specifying the functional form in the true model with a Michaelis Menten curve has an effect on correct class extraction. The Gompertz curve can be written as:} \]

\[
Y[t]_n = \sum_{c=1}^{C} \pi_{nc} (b_{0nc} + b_{1nc}[\exp(-\exp(-b_{2nc}(t - b_{3nc})))] + e_{nct}) \tag{18}
\]

where the instantaneous rate of change

\[
t = b_{3n} \text{ equals } (b_{1n}b_{2n}/e) \tag{18.1}
\]
$b_0$ is the individual total amount of change from the lower to the upper asymptotes. It will be set at -4 following specifications from Ram and Grimm's (2009) Gompertz GMM. It represents the total amount of expected change in the measured variable and because the lower asymptote is invariant over individuals, the upper potential of the measured variable for each individual is controlled by $b_{2n}$, the individual rate of approach to the asymptote. It controls how quickly change occurs for each individual from the point of inception of change. $b_{3n}$ is the timing of accelerated changes for individual n and is referred to as the timing parameter. It represents the time when each individual's learning rate reaches its maximum. The latent random coefficients which enter the model nonlinearly will be fixed at 0 but the latent variable means will be estimated parameters in the equations for the partial derivatives in $\Lambda$ and therefore will be estimated in the model.

Simulation Design

This simulation design comprises the fixed and manipulated design conditions that will be applied to the true model and each of the mis-specified models. The sample size is the only fixed factor design that will be included in the study. The manipulated design conditions are:

- mixing proportion of latent classes
- latent class separation
- number of repeated measures
Fixed Design Conditions

Sample Size

GMM is a large sample size statistical technique (Ram & Grimm, 2007); however, how large a sample is necessary for GMM analysis depends on the factors that play a role in the identification and description of unobserved subgroups. Ram and Grimm (2007) have advised that each substantive GMM application be evaluated in relation to the particulars of the data, model, and theoretical underpinnings of the study. After review of several published simulations on GMM applications, the sample size in this study is fixed at 1000 (see, e.g., Nylund et al., 2007; Tofghi & Enders, 2007). This is a typical sample size given the varied range of 500 to 5000 observed in published literature (Tofghi & Enders, 2007; Li, 2016). Varying the levels of sample size is a commonly observed manipulated design condition in simulated applications of GMM and much information has been generated over the years regarding its impact on class identification. Therefore, in order to manage scope of the study and explore less common and perhaps more interesting, manipulated design conditions, sample size is a fixed design condition in this study.

Table 1 Fixed Design Condition

<table>
<thead>
<tr>
<th>Factor</th>
<th>Fixed value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample size</td>
<td>1000</td>
</tr>
</tbody>
</table>
Manipulated Design Conditions

Mixing Proportions of the Latent Classes

Tofighi and Enders (2007) evidenced that mixing proportions affects class enumeration. The mixing proportion parameter $p_k$, which describes the probability of an individual’s membership to class $k$ with all $P_k > 0$ and $\sum_{k=1}^{K} P_k = 1$, will be modeled as a balanced design (50:50) and as an unbalanced design (30:70). The reason for selecting these two specific levels of mixing proportions stems from what is commonly observed in similar simulated GMM studies. The mixing proportion condition directly influences the number of latent classes recovered during the estimation process. Typically observed is that a balanced design performs better in recovering the expected number of classes, while an unbalanced design has a more variable performance. However, the mixing proportion of 30:70 was selected out of other more extreme conditions such as 20:80 (known to have been simulated in a few GMM studies), because it is expected to have a better rate of convergence of the models as seen in Tofighi and Enders (2007) simulated study of class recovery under various fit indices.

Degree of Class Separation

Mixture class separation refers to the amount of overlap between growth trajectories for the latent classes. The purpose of including it as a manipulated design condition is because accuracy of estimation is impacted by quality of class separation (Depaoli, 2013). Specifically, poor separation between growth trajectories, (i.e., isomorphic growth trajectories), impact the accuracy with which individuals are assigned
into latent classes (Depaoli, 2013). It is commonly used as a simulation condition in analysis of latent classes for the purpose of determining the impact of class separation on entropy values. Since individuals’ assignment to the correct latent classes underscores the true underlying growth trajectory, quality of separation (i.e., high, medium or low) between the growth trajectories speaks to the models’ confidence in assigning individuals to their respective classes. Mixture class separation is manipulated by varying the growth factors, the intercept, and the slope defined through a multivariate Mahalanobis calculation (MD; Mahalanobis, 1936). Following notations specified by McLachlan and Peel (2000), the MD between two latent classes is written as follows:

$$\text{MD} = \Delta = [(\mu_1 - \mu_2)'\Sigma^{-1}(\mu_1 - \mu_2)]$$

(20)

where $\Sigma^{-1}$ represents the inverse of the covariance matrix of individual’s growth parameters, and $\mu_1$ and $\mu_2$ terms represent the mean intercept and mean slope for each trajectory in the first and second latent classes.

As previously iterated, one trajectory is the “problem class” or “high stress” class. Using this trajectory, class separation between subsequent classes will be determined in relation to the trajectory set for the first latent class (Depaoli, 2013). The second latent class presents a “zero class” or “normal” latent growth trajectory and following guidelines stipulated by Lubke and Muthén (2005), the second latent class will be fixed as having a high latent class separation from the first class by setting the MD at 2.0 (see e.g., Depaoli, 2013).
From there, class separation will be modeled according to the benchmarks of the MD representing high, medium, and poor class separation (Lubke & Muthén, 2005).

**Number of Measurement Occasions**

Parameter estimates increase in precision relative to the number of data points collected per individual in the sample (Duncan et al., 2006). It is typically the case in substantive (as well as simulated) GMM applications that the number of measurement occasions are between three and four measures (Masyn & Brown, 2001; Jung & Wickrama, 2007). However, correct class enumeration (and composition) is improved with greater time points to measure curvature of growth. Therefore, in this dissertation, each model will be examined at four and eight repeated measures. According to Vickers (2003), fixing the repeated measures at four yields reasonable power to detect change and approximate potential nonlinear growth trajectories. The choice of eight time points stems from Muthén and Curran’s (1997) recommendation of at least five or greater repeated measure indicators given the potential issues of convergence that could arise with a small number of indicators.
Table 2

Manipulated Design Conditions

<table>
<thead>
<tr>
<th>Factor</th>
<th>Levels</th>
</tr>
</thead>
<tbody>
<tr>
<td>Degree of class separation</td>
<td>High</td>
</tr>
<tr>
<td></td>
<td>Medium</td>
</tr>
<tr>
<td></td>
<td>Low</td>
</tr>
<tr>
<td>Mixing proportion</td>
<td>Level 1: Balanced (50:50)</td>
</tr>
<tr>
<td></td>
<td>Level 2: Unbalanced (30:70)</td>
</tr>
<tr>
<td>Repeated measures</td>
<td>Level 1: 4 timepoints</td>
</tr>
<tr>
<td></td>
<td>Level 2: 8 timepoints</td>
</tr>
</tbody>
</table>

In summary, three levels of class separation, two levels of mixing proportion, and two levels of repeated measures are used in the experimental design, which results in $3 \times 2 \times 2 = 12$ cells. Since three functional form models (quadratic, linear, Gompertz, latent Basis) are examined under each of these cells, the total number of conditions is $12 \times 4 = 48$. Altogether, 100 replications will be used to achieve convergence to the global solution across all functional forms in each cell of the design. In methodological studies focused on GMM, the minimum number of replications has been found to be 100 to achieve stable distributional properties and empirical critical values (e.g., Asparouhov & Muthén, 2013).
Table 3 represents the information that will be included for the true model as well as the fitted models (the models with the mis-specification to the functional forms). Data will be generated and analyzed using Mplus Version 7.11 (Muthén & Muthén, 1998–2020).

Figure 1
Data Generating Model for the 2-Class GMM at Four Repeated Measures
Table 3

Estimates for the Population Model: 2-Class GMM means+pattern

<table>
<thead>
<tr>
<th></th>
<th>Class 1</th>
<th>Class 2</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sample size</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Average probability of class membership</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Latent variable means</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Intercept mean, g0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Slope mean, g1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Slope loadings, A1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Time 1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Time 2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Time 3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Time 4</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Comparison of True Model versus Mis-specified Models**

The process of model selection in GMM, described as an “art,” does not hinge on a single statistic, or rely on a deterministic set of rules highlighting the best model (Ram & Grimm, 2009). Rather, using a combination of model results, theory, and fit statistics, a defensible judgement about the optimal model is made. It is the subjective nature in which model selection proceeds in GMM that requires studies be critically replicated for accurate outcomes. Generally, the objective of model selection is to determine the most reasonable representation of the data; therefore, two aspects of the models are considered:

- Optimal number of unobserved groups
- The type and extent of differences between and within those groups
In Mplus, an EM procedure will be used to obtain maximum likelihood estimates of all model parameters and individual posterior probabilities will be derived from those estimates. Since this dissertation is centered on the mis-specification of the growth function between latent classes, and mis-specification is known to directly impact class enumeration, the typical GMM model selection process is not appropriate to understand or draw conclusions from the output. The objective for this study is to make specific conclusions about the undetected use of incorrect functional forms in substantive literature; therefore, determining the effect and severity of functional form mis-specification on class enumeration requires comparative analysis between the series of GMMs per functional form.

*Model Evaluation Criteria*

As part of the preliminary analysis of the dataset a one-way ANOVA will be conducted to determine the possible presence of trends. In this study, the time variable will serve as the categorical independent variable and the outcome variable will serve as the continuous dependent variable. Although the one-way ANOVA can’t confirm the type of trend (i.e., linear or quadratic) present in the dataset, it is useful in allowing the researcher to determine if proceeding with a computationally intensive GMM is feasible as it provides information on whether the outcome is significantly different for at least one time point. Furthermore, the one-way ANOVA will be applied to two of the twelve simulated datasets (i.e., the dataset that doesn’t have the functional form mis-specification). The reason that the one-way ANOVA is conducted for only two of the
twelve datasets is because the same results can be expected to be yielded from each of the simulated datasets. Additionally, the preliminary ANOVA test is included to illustrate as an example the merit to corroborating GMM with other statistical techniques.

The models will be evaluated on the following criteria:

*Entropy.* Individual’s group membership is expected to fluctuate in the series of mis-specified GMMs, therefore entropy will provide a summary indicator of how conditional probabilities of individuals’ group membership fluctuate between the mis-specified models to the true population model. It is a standardized index ranging from 0 to 1 of model-based classification accuracy where higher values indicate improved enumeration accuracy thereby signaling distinct class separation (Wickrama et al., 2016).

*Fit indices.* The information criteria-AIC and BIC across several simulation studies, are shown to be more resilient to mis-specification. These indices will be monitored according to the typical benchmark of lowest value indicating the better fitting model. However, the models with the lowest information criteria will be used to rank the other mis-specified models in order of mis-specification severity as a function of the group trajectories. The information criteria (IC) are computed using the deviance statistics (-2 log-likelihood values), number of model parameters (p), and sample size (n) (Wickrama et al., 2016; Tofigli & Enders, 2007). These fit indices impose a parameterization penalty for the number of parameters and small sample size (Wickrama et al., 2016). Therefore, they are scaled such that a lower value represents better fit among several plausible models (Nylund et al., 2007; Tofigli & Enders, 2007; Wickrama et al., 2016). The
following study will utilize the Bayesian information criterion (BIC; Sclove, 1987) which is known for its consistency (i.e., it is known to select the correct model more frequently as the sample size increases and also in cases of model mis-specification). Although the IC applies a different penalty for the number of model parameters, sample size, or both, leading to the possibility of each pointing to a different class solution as the best model (Nylund et al., 2007), drawing from published applications of GMM, it is possible to hypothesize the behavior of the IC in relation to the true model and the mis-specified models.

\[
BIC = -2 \log L + p(\log(n)) \tag{21}
\]

Although the sample size is fixed in this study, following the mathematical underpinning of the BIC, it will favor the latent basis model and the linear model while rejecting the more complex models.

**Number of latent classes.** The number of latent classes yielded from the mis-specified models will be compared to the true number of classes present in the sample (i.e., the number of latent classes simulated from the data-generating model).

**Diagnostic Tests**

Two diagnostic tests will be included in the study. The first test will be an *a priori* test using a one-way ANOVA and a Tukey HSD group difference test in order to form a general visual hypothesis of the pattern of growth trends present in the dataset. The second will be a post-hoc test of the residuals of the fitted models that shares the closest resemblance to the original mode.
The a priori test of a one-way ANOVA, followed by a Tukey HSD test will be useful in indicating the types of growth patterns present in the dataset. The one-way ANOVA will be conducted on two of the simulated datasets. The expectation is that the one-way ANOVA would indicate significance for mean differences across the timepoints in the dataset since it is being run on the simulated datasets. Therefore, results of the one-way ANOVA will be included for only two of the datasets which are:

- 4 timepoints, high-class separation and an unequal mixing proportion
- 8 timepoints had an equal mixing class proportion at low-class separation

Including the one-way ANOVA serves to test the merit of incorporating a corroborating statistical technique to assist the researcher applying a GMM methodology in forming appropriate hypothesis regarding functional forms present in the dataset. In this dataset, the dependent variable is the continuous outcome variable and independent variable is the categorical time variable measured at 4 and 8 timepoints.

A post-hoc test, a mixed-effects model analysis will be conducted on the fitted model(s) whose mis-specified fit indices and entropy values closely resemble the original model. The purpose of incorporating a mixed model will be to investigate the behavior of the residuals of the mis-specified models in order to show case a closer look at the regression lines per latent class in the fitted model. It can be the case that one (or more) of the fitted models appear to be the true model. Therefore, the mixed effects model would serve the purpose of diagnosing in which latent class do the residuals show errant behavior along the regression line. Additionally, a follow-up mixed-effects model would
highlight the insufficiency of the GMM selection criteria in identifying the correct model.

Ultimately, the one of the goals of this simulation study is to draw conclusions about the impact of mis-specifications to functional forms and necessity of developing either *a priori* or post-hoc tests (or both) to serve as an empirical check in detecting an incorrect functional form prior to generalizing results to substantive literature.

Following is a figure to represent the process of applying each of the four alternative functional forms to the true population dataset. It is followed by a sample table of fit statistics for the Linear-GMM. The sample table will be created for each of the models with an alternative functional form and compared to the results of the baseline model and the true population model.
Figure 2

Process of Analyses of Alternative Functional Forms Fit to the Data

FDC and MDC represent fixed design conditions and manipulated design conditions respectively; “A” is the true population dataset generating model; “B” is the first alternative model fit to A where the dashed lines represent the first simple manipulated functional form of a latent basis growth model; “C” is the second alternative model fit to A where the dashed lines represent the second simple manipulated functional form of a
linear growth curve; “D” is the third alternative model fit to A where the dashed lines represent the first complex manipulated functional form of a Gompertz growth model.

Table 4
Sample Table of Fit Statistics for the Linear-GMM (will be created for each functional form)

<table>
<thead>
<tr>
<th></th>
<th>1-Class Baseline</th>
<th>Linear-GMM</th>
<th>Linear-GMM</th>
<th>Linear-GMM</th>
<th>Linear-GMM</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2-Class Means</td>
<td>2-Class Means</td>
<td>3-Class Means</td>
<td>3-Class Means + Patterns</td>
<td></td>
</tr>
<tr>
<td>Repeated</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Measures</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sample size</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nc = 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nc = 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fit Statistics</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AIC</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BIC</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Chapter Four: Results

The following dissertation is a comparative analysis of the impact of growth trajectory mis-specifications (ranging from a simple linear, latent basis to the complex Gompertz curve) on analysis and interpretation of GMM results.

The research question was addressed through a Monte Carlo simulation conducted in Mplus version 8.8 where 12 simulated datasets were generated and then analyzed using GMM in a series of simulated models under the manipulated design conditions of timepoints, mixing proportions, and separation of latent classes. Each model per manipulated design condition was analyzed for fit ranging from 1-class to 3-classes, thereby resulting in the analysis of 36 GMM models in totality. The models were then assessed to make conclusions regarding convergence rates among mis-specified models, behavior of the fit indices, and performance of class enumeration. Additionally, a one-way ANOVA was conducted on the original models to serve as a precursory look at the dataset to determine the appropriateness of applying a GMM. And as a post-hoc measure, a mixed model was conducted to the mis-specified model with the closest resemblance to the original model. The dual purpose of the mixed model was to provide a visual representation of the performance of the standardized residual values of the selected mis-specified model and to determine the efficacy of corroborating a GMM analysis with a follow-up statistical technique.
In this vein, the chapter is methodically laid out in three sections that contrast the mis-specified models to the original models to address the research question. Beginning with the first section, the convergence rate per mis-specified growth trajectory is presented in comparison to that of the original simulated models to observe challenges (if any) to model convergence. Following is the assessment of model fit typical to GMM where the mis-specified models are compared to their original model counterparts in order to determine quality of mis-specified model fit to the data. Lastly, a one-way ANOVA was conducted to graphically determine the behavior of the residuals between the original simulated model and the mis-specified models.

**Convergence Rate**

A prominent challenge in GMM analysis, especially when using EM algorithm for fitting finite mixture models, relates to convergence issues, (i.e., nonconvergence of models or multiple local maxima). Given this context, it seems useful to include how well the models converged across the mis-specified growth trajectories and manipulated design conditions. Before proceeding, it is important to stipulate the inclusion criteria considered in relation to the convergence of the models for the purposes of this dissertation. Given the complexity of estimation with GMMs, researchers define and interpret “nonconvergence” according to the research question being addressed. In this case, drawing from McNeish and Harring’s (2021) most recent work on convergence solutions in GMM, if likelihood optimization could not be completed using Mplus’s default criteria (500 EM algorithm iterations, convergence criteria of 1E-5) or
if a replication produced a solution with admissible solutions with one set of starting values but the same likelihood could not be reproduced for a different set of starting values, the replication was convergent for the purposes of this dissertation (in spite of the implication of local maxima). The purpose of employing a less restrictive convergence rule was to accommodate for the complexity posed by modeling a Gompertz curve as a mis-specified growth curve. Therefore, the replications are counted as converged any time optimization was completed with admissible parameter estimates.

Each cell of the design was replicated 500 times. From Table 5, the 12 original simulated models achieved convergence rates of 97% (and greater). Similarly, the models with the linear mis-specification and the latent basis models converged equally as well with convergence rates between 90–100%. The models that saw more frequent issues associated with convergence rates were the Gompertz models. Although all the Gompertz models converged, for the model at four timepoints, equal mixing proportion and medium separation, the convergence rate was at 62.2%, implying that the results derived from this model were based on roughly 300 (and fewer) replications. This model had the lowest rate of convergence. The Gompertz model at 4 time points, medium-class separation and equal mixing proportions converged without replicating the best log likelihood information for the model fit. The recommended program solution was to increase the number of random starts. The same warning message was generated when the Gompertz model was modeled at 8 time points and unequal mixing proportions.
Lastly, when observed at high-class separation, the Gompertz model at all levels of the manipulated design conditions converged without being able to replicate the best log likelihood criteria.

Table 5

Convergence Rate of Original Simulated Models and Mis-specified Models

<table>
<thead>
<tr>
<th>Sample size</th>
<th>Class separation</th>
<th>Timepoints</th>
<th>Mixing proportions</th>
<th>Original model</th>
<th>Linear</th>
<th>Latent basis</th>
<th>Gompertz</th>
</tr>
</thead>
<tbody>
<tr>
<td>1000</td>
<td>LCS 4 30</td>
<td>96.8</td>
<td>100</td>
<td>97.8</td>
<td>96.8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LCS 4 50</td>
<td>96.4</td>
<td>93.4</td>
<td>96.4</td>
<td>94.4</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LCS 8 30</td>
<td>100</td>
<td>99.8</td>
<td>92</td>
<td>99.4</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LCS 8 50</td>
<td>100</td>
<td>99.8</td>
<td>91.6</td>
<td>95.8</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MCS 4 30</td>
<td>97.8</td>
<td>100</td>
<td>98</td>
<td>76.2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MCS 4 50</td>
<td>97.8</td>
<td>100</td>
<td>99.6</td>
<td>62.2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MCS 8 30</td>
<td>100</td>
<td>99.8</td>
<td>92</td>
<td>94.4a</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MCS 8 50</td>
<td>100</td>
<td>99.4</td>
<td>93</td>
<td>96.2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HCS 4 30</td>
<td>97</td>
<td>100</td>
<td>94.4</td>
<td>93.8a</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HCS 4 50</td>
<td>97.4</td>
<td>100</td>
<td>99.6</td>
<td>65.6a</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HCS 8 30</td>
<td>100</td>
<td>100</td>
<td>92</td>
<td>90.6a</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HCS 8 50</td>
<td>100</td>
<td>99.8</td>
<td>90.6</td>
<td>97.6</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Note. Values are reported as percentages. LCS = low-class separation; MCS = medium-class separation; HCS = high-class separation.

a the best log-likelihood value for these models couldn’t be replicated

Preliminary Dataset Check for Trend Using a One-way ANOVA

Inclusion of the one-way ANOVA in this specific study comes with some caveats to be discussed further. However, its inclusion is reasonable since a priori knowledge of whether a longitudinal-type analysis (for example, GLMM or GMM) is at all opportune serves as a practical first step in justifying a time-intensive GMM application. The one-way ANOVA conducted in this study was run in the open-source statistical software program R version 3.1.
To conceive a preliminary exploration into the presence of a trend in the dataset as the first step to GMM, the decision was made to treat time as the categorical independent variable. Time is the number of equidistant points along which scores for individuals in a sample was measured. The dependent variable is the outcome across the timepoints. The independent variable was “time” which had either 4 levels or 8 levels depending on the dataset.

Since the one of the goals of incorporating the one-way ANOVA was to illustrate the merit of incorporating a preliminary analysis prior to a GMM application, this point was exampled with two out of the original twelve simulated datasets. The datasets used were the models at 4 and 8 timepoints. The model at 4 timepoints had high-class separation and an unequal mixing proportion. And the model measured at 8 timepoints had an equal mixing class proportion at low-class separation. These datasets were arbitrarily picked. The one-way ANOVA was conducted to compare the effect of the time variable on the outcome variable. Results from the one-way ANOVA revealed that there was a statistically significant difference in the outcome between at least two of the timepoints. Upon further inspection Tukey’s HSD Test for multiple comparisons found that the mean of the outcome was positive and increasing with a statistically significant mean difference in both the 4 timepoints and the 8 timepoints. Table 8 and Table 9 includes the results from the Tukey test for the time periods that were statistically significant. The Tukey test revealed that the outcome increased with time and suggested a trend. It is worthwhile to note here that ANOVA is applicable for a continuous dependent
variable, and a categorical independent variable, hence time was treated as a categorical variable. The use of a one-way ANOVA in this study serves more as a directionally relevant perspective for corroborating statistical techniques possible with GMM.

Table 6
Results of One-Way ANOVA at 4 timepoints

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Time</strong></td>
<td>3</td>
<td>208</td>
<td>69.29</td>
<td>16.6</td>
<td>1.02e-10 ***</td>
</tr>
<tr>
<td><strong>Residual</strong></td>
<td>3996</td>
<td>16680</td>
<td>4.17</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>3999</td>
<td>16888</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 7
Results of One-Way ANOVA at 8 timepoints

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Time</strong></td>
<td>7</td>
<td>5702</td>
<td>814.5</td>
<td>23.53</td>
<td>&lt;2e-16 ***</td>
</tr>
<tr>
<td><strong>Residual</strong></td>
<td>7992</td>
<td>276652</td>
<td>34.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>7999</td>
<td>282354</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Table 8

Results of Multiple Comparisons Tukey HSD Test for all groups at 4 timepoints

<table>
<thead>
<tr>
<th>Time</th>
<th>Time</th>
<th>Diff</th>
<th>lower limit</th>
<th>Upper limit</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>1</td>
<td>0.1445185</td>
<td>-0.0903141</td>
<td>0.3793511</td>
<td>0.3892074</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>0.3421997</td>
<td>0.10736708</td>
<td>0.5770322</td>
<td>0.0010488</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>0.6077255</td>
<td>0.37289287</td>
<td>0.842558</td>
<td>0.0000000</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>0.1976811</td>
<td>-0.0371515</td>
<td>0.4325137</td>
<td>0.1337016</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>0.4632069</td>
<td>0.22837434</td>
<td>0.6980395</td>
<td>0.0000025</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>0.2655258</td>
<td>0.03069321</td>
<td>0.5003584</td>
<td>0.0192719</td>
</tr>
</tbody>
</table>

*Note.* These are results for the original model at 4 timepoints, unequal class proportion and high-class separation
Table 9

Results of Multiple Comparisons Tukey HSD Test for the statistically significant groups at 8 timepoints

<table>
<thead>
<tr>
<th>Time</th>
<th>Time</th>
<th>Diff</th>
<th>Lower limit</th>
<th>Upper limit</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5</td>
<td>1.050188</td>
<td>0.2524896</td>
<td>1.8478864</td>
<td>0.0017033</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>1.4923637</td>
<td>0.69466528</td>
<td>2.2900621</td>
<td>0.0000004</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>1.9400974</td>
<td>1.14239903</td>
<td>2.7377958</td>
<td>0.0000000</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>2.5409463</td>
<td>1.74324795</td>
<td>3.3386447</td>
<td>0.0000000</td>
</tr>
<tr>
<td>2</td>
<td>5</td>
<td>0.8994166</td>
<td>0.10171824</td>
<td>1.697115</td>
<td>0.0146477</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>1.3415923</td>
<td>0.54389392</td>
<td>2.1392907</td>
<td>0.0000097</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>1.7893261</td>
<td>0.99162768</td>
<td>2.5870245</td>
<td>0.0000000</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>2.390175</td>
<td>1.59247659</td>
<td>3.1878734</td>
<td>0.0000000</td>
</tr>
<tr>
<td>3</td>
<td>6</td>
<td>1.1113879</td>
<td>0.31368948</td>
<td>1.9090863</td>
<td>0.0006398</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>1.5591216</td>
<td>0.76142323</td>
<td>2.35682</td>
<td>0.0000001</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>2.1599705</td>
<td>1.36227215</td>
<td>2.9576689</td>
<td>0.0000000</td>
</tr>
<tr>
<td>4</td>
<td>6</td>
<td>0.8105043</td>
<td>0.0128059</td>
<td>1.6082027</td>
<td>0.0432922</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>1.2582381</td>
<td>0.46053966</td>
<td>2.0559364</td>
<td>0.0000483</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>1.859087</td>
<td>1.06138857</td>
<td>2.6567854</td>
<td>0.0000000</td>
</tr>
<tr>
<td>5</td>
<td>7</td>
<td>0.8899094</td>
<td>0.09221104</td>
<td>1.6876078</td>
<td>0.0165596</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>1.4907584</td>
<td>0.69305995</td>
<td>2.2884567</td>
<td>0.0000000</td>
</tr>
<tr>
<td>6</td>
<td>8</td>
<td>1.0485827</td>
<td>0.25088427</td>
<td>1.8462811</td>
<td>0.0017462</td>
</tr>
</tbody>
</table>

Note. These are results for the original model at 8 timepoints, equal class proportion and low-class separation

Performance of Fit Indices and Class Enumeration

The class enumeration and fit indices for the original 12 simulated models are listed in Table 10. These models were simulated to replicate a typical 2-class model where one class follows a linear trajectory, and the other class a quadratic growth trajectory. All the models successfully converged, and the best log likelihood was
replicated for each model. Differences were observed between the results from the manipulated factors. Models with an equal mixing proportion showed an entropy of > 0.8 compared to the models with unequal mixing proportions. The combination of low-class separation, fewer time points of measurement, and unequal class proportions yielded the lowest entropy value of 0.37.
Table 10
Results of the 12 Original Simulated Data Generated Models

<table>
<thead>
<tr>
<th></th>
<th>High Class Separation</th>
<th>Medium Class Separation</th>
<th>Low Class Separation</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>4.50  4.30  8.50  8.30</td>
<td>4.50  4.30  8.50  8.30</td>
<td>4.50  4.30  8.50  8.30</td>
</tr>
<tr>
<td>Sample size</td>
<td>1000  1000  1000  1000</td>
<td>1000  1000  1000  1000</td>
<td>1000  1000  1000  1000</td>
</tr>
<tr>
<td>Free parameters</td>
<td>14    14    18    18</td>
<td>14    14    18    18</td>
<td>14    14    18    18</td>
</tr>
<tr>
<td>AIC</td>
<td>11709.8  12645.5  26418.4  11685.7</td>
<td>12492.9  24207.2  24941.7</td>
<td>11487.0  12266.9  24286.7  24862.8</td>
</tr>
<tr>
<td>BIC</td>
<td>11778.5  12714.2  24193.6  26506.7</td>
<td>11754.4  12561.7  24295.5  25030.1</td>
<td>11555.7  12335.6  24375.0  24951.2</td>
</tr>
<tr>
<td>SABIC</td>
<td>11734.1  12669.7  24136.4  26449.6</td>
<td>11710.0  12517.2  24238.4  24972.9</td>
<td>11511.3  12291.1  24317.8  24894.0</td>
</tr>
<tr>
<td>Entropy</td>
<td>0.83  0.53  0.72  0.65</td>
<td>0.81  0.45  0.83  0.79</td>
<td>0.8  0.37  0.89  0.71</td>
</tr>
</tbody>
</table>
Table 11

Differences from the Original Model Fit Indices of The Three Growth Trajectories at The Various Manipulated Design Conditions

<table>
<thead>
<tr>
<th>4 Timepoints</th>
<th>MD</th>
<th>Model</th>
<th>Mixing proportion</th>
<th>AIC</th>
<th>BIC</th>
<th>Entropy</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCS</td>
<td>Linear</td>
<td>50-50</td>
<td>631.3</td>
<td>611.6</td>
<td>9%</td>
<td></td>
</tr>
<tr>
<td>MCS</td>
<td>Linear</td>
<td>50-50</td>
<td>622.6</td>
<td>603.0</td>
<td>10%</td>
<td></td>
</tr>
<tr>
<td>LCS</td>
<td>Linear</td>
<td>50-50</td>
<td>11.5</td>
<td>8.1</td>
<td>58%</td>
<td></td>
</tr>
<tr>
<td>HCS</td>
<td>Linear</td>
<td>30-70</td>
<td>240.4</td>
<td>220.8</td>
<td>7%</td>
<td></td>
</tr>
<tr>
<td>MCS</td>
<td>Linear</td>
<td>30-70</td>
<td>226.5</td>
<td>206.8</td>
<td>0%</td>
<td></td>
</tr>
<tr>
<td>LCS</td>
<td>Linear</td>
<td>30-70</td>
<td>229.0</td>
<td>209.4</td>
<td>6%</td>
<td></td>
</tr>
<tr>
<td>Timepoints</td>
<td>MD</td>
<td>Model</td>
<td>Mixing proportion</td>
<td>AIC</td>
<td>BIC</td>
<td>Entropy</td>
</tr>
<tr>
<td>------------</td>
<td>----</td>
<td>---------</td>
<td>-------------------</td>
<td>-----</td>
<td>-----</td>
<td>---------</td>
</tr>
<tr>
<td>HCS</td>
<td>Latent Basis</td>
<td>50-50</td>
<td>18.5</td>
<td>28.3</td>
<td>0%</td>
<td></td>
</tr>
<tr>
<td>MCS</td>
<td>Latent Basis</td>
<td>50-50</td>
<td>19.2</td>
<td>29.1</td>
<td>0%</td>
<td></td>
</tr>
<tr>
<td>LCS</td>
<td>Latent Basis</td>
<td>50-50</td>
<td>-404.9</td>
<td>-395.1</td>
<td>30%</td>
<td></td>
</tr>
<tr>
<td>HCS</td>
<td>Latent Basis</td>
<td>30-70</td>
<td>24.6</td>
<td>34.5</td>
<td>3%</td>
<td></td>
</tr>
<tr>
<td>MCS</td>
<td>Latent Basis</td>
<td>30-70</td>
<td>105.2</td>
<td>115.0</td>
<td>1%</td>
<td></td>
</tr>
<tr>
<td>LCS</td>
<td>Latent Basis</td>
<td>30-70</td>
<td>103.7</td>
<td>113.6</td>
<td>-4%</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Timepoints</th>
<th>MD</th>
<th>Model</th>
<th>Mixing proportion</th>
<th>AIC</th>
<th>BIC</th>
<th>Entropy</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCS</td>
<td>Gompertz</td>
<td>50-50</td>
<td>29.4</td>
<td>63.8</td>
<td>0%</td>
<td></td>
</tr>
<tr>
<td>MCS</td>
<td>Gompertz</td>
<td>50-50</td>
<td>28.5</td>
<td>62.9</td>
<td>-1%</td>
<td></td>
</tr>
<tr>
<td>LCS</td>
<td>Gompertz</td>
<td>50-50</td>
<td>327.6</td>
<td>361.9</td>
<td>1%</td>
<td></td>
</tr>
<tr>
<td>HCS</td>
<td>Gompertz</td>
<td>30-70</td>
<td>33.3</td>
<td>67.7</td>
<td>-19%</td>
<td></td>
</tr>
<tr>
<td>MCS</td>
<td>Gompertz</td>
<td>30-70</td>
<td>19.4</td>
<td>53.7</td>
<td>-18%</td>
<td></td>
</tr>
<tr>
<td>LCS</td>
<td>Gompertz</td>
<td>30-70</td>
<td>17.2</td>
<td>51.4</td>
<td>-24%</td>
<td></td>
</tr>
<tr>
<td>Timepoints</td>
<td>MD</td>
<td>Model</td>
<td>Mixing proportion</td>
<td>AIC</td>
<td>BIC</td>
<td>Entropy</td>
</tr>
<tr>
<td>------------</td>
<td>-----</td>
<td>------------------------</td>
<td>-------------------</td>
<td>------</td>
<td>------</td>
<td>---------</td>
</tr>
<tr>
<td></td>
<td>HCS</td>
<td>Linear</td>
<td>50-50</td>
<td>0.4</td>
<td>5.3</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>MCS</td>
<td>Linear</td>
<td>50-50</td>
<td>1.3</td>
<td>6.2</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>LOW</td>
<td>Linear</td>
<td>50-50</td>
<td>0.5</td>
<td>5.4</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>HCS</td>
<td>Linear</td>
<td>30-70</td>
<td>2.0</td>
<td>6.9</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>MCS</td>
<td>Linear</td>
<td>30-70</td>
<td>1.8</td>
<td>6.7</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>LCS</td>
<td>Linear</td>
<td>30-70</td>
<td>1.3</td>
<td>6.2</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>HCS</td>
<td>Latent Basis</td>
<td>50-50</td>
<td>298.8</td>
<td>328.2</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>MCS</td>
<td>Latent Basis</td>
<td>50-50</td>
<td>538.3</td>
<td>567.8</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>LCS</td>
<td>Latent Basis</td>
<td>50-50</td>
<td>312.4</td>
<td>341.8</td>
<td>1%</td>
</tr>
<tr>
<td></td>
<td>HCS</td>
<td>Latent Basis</td>
<td>30-70</td>
<td>930.8</td>
<td>960.3</td>
<td>1%</td>
</tr>
<tr>
<td></td>
<td>MCS</td>
<td>Latent Basis</td>
<td>30-70</td>
<td>315.8</td>
<td>345.3</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>LCS</td>
<td>Latent Basis</td>
<td>30-70</td>
<td>314.4</td>
<td>343.9</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>HCS</td>
<td>Gompertz</td>
<td>50-50</td>
<td>816.5</td>
<td>791.9</td>
<td>9%</td>
</tr>
<tr>
<td></td>
<td>MCS</td>
<td>Gompertz</td>
<td>50-50</td>
<td>112.1</td>
<td>166.2</td>
<td>13%</td>
</tr>
<tr>
<td></td>
<td>LCS</td>
<td>Gompertz</td>
<td>50-50</td>
<td>272.2</td>
<td>326.2</td>
<td>0%</td>
</tr>
<tr>
<td></td>
<td>HCS</td>
<td>Gompertz</td>
<td>30-70</td>
<td>133.0</td>
<td>187.1</td>
<td>0%</td>
</tr>
</tbody>
</table>
Note. HCS = high-class separation, MCS = medium-class separation, LCS = low-class separation. The (-) in the entropy value differences implies an improvement of the entropy to the mis-specified model (from the original).

The percentage of correctly identified groups by the AIC and BIC favoring the 2-class models over the 1-class and 3-class models per manipulated condition was 100%, (i.e., the fit indices in tandem with the entropy values identified in spite of the mis-specification the presence of two latent classes per model). Furthermore, there was consistent agreement between the AIC and the BIC in relation to fit of the mis-specified model to the data. The differences in the fit indices (AIC and BIC values) for each mis-specified model compared to the original models ranged from 0–960 points. For example, it can be observed from Table 11 that the AIC and BIC values of the latent basis model at eight timepoints, low-class separation (MD = 1.1), and unequal mixing class proportions had a large deviation (AIC = 930 points and BIC = 960 points) from the fit indices of the original model. Directing focusing on the performance of the AIC given the model mis-specification conditions showed some models with minimal differences in fit (compared to the original AIC indices). For example, some of the mis-specified models (16%) had less than 2-point difference in the AIC between the mis-specified model and the original i.e., the difference ranged between 0.4 - 1.3 points, interestingly with no changes to the entropy values.
In tandem, the BIC of these same models showed less than 7-point difference in the BIC between the mis-specified model and the original i.e., the difference ranged between 5.3 – 6.2 points (with no changes to the entropy values).

Of all the models, the linear mis-specified model at eight timepoints came the closest to resembling the original model across the manipulated factors of timepoints, mixing proportions, and latent class separation. The fit indices considered to inform fit of the mis-specified model to the original data were the AIC, the BIC, and the entropy value. From Table 9, it can be observed that compared to the other models, the fit indices of the linear mis-specification at eight timepoints had minimal to no differences compared to the original model, implying that the mis-specified model had a relatively similar fit to the data as the original model. In tandem, there were no changes to the entropy values for the linear mis-specified model at eight timepoints compared to the models per manipulated design condition.

In contrast, the latent basis models and the Gompertz growth curve mis-specification at eight timepoints showed the largest deviation, (i.e., the worst fit) compared to the original models (and their counterpart models at four timepoints) across the fit indices and entropy values. In the case of the Gompertz mis-specified model the respective entropy values and the large deviation in the fit indices of the AIC and BIC values were in tandem with entropy values that showed improvement, decline, and in some cases no change compared to the original models. The Gompertz models were the
only ones fraught with model termination issues and lack of replication of the best log
likelihood values thereby rendering the entropy values as untrustworthy.

**Results of Linear Mis-specification at 4 Timepoints**

For each model with a mis-specified growth trajectory and the latent basis model,
one through three classes were fit to the original simulated dataset to generate model
parameters in order to make a comparative analysis on fit of the mis-specified models to
the data. Included in this section are the fit indices and parameter information only for the
mis-specified model that shared the closest resemblance to the original model.

**Four Timepoints, Low-class Separation, Equal and Unequal Mixing Proportions**

The linear mis-specification at four timepoints, low-class separation condition,
and equal mixing proportions had a much smaller difference in fit compared to the same
model when the mixing proportion was modified to be unequal. Observed when there
was an equal mixing proportion, the better fitting model was the 2-class linear mis-
specified model compared to the 1-class and 3-class model. While there was only a small
difference in fit indices between the mis-specified linear model and the original (AIC =
11.5, BIC = 8.1), the mis-specified model’s ability to discriminate between the number
of classes present in the dataset steeply deteriorated (58%) as observed by the entropy of
0.22. The same model with an unequal mixing class proportion favored the 2-class linear
mis-specified model relative to the 1-class and 3-class model. However, the fit indices of
the mis-specified linear model had a large deviation (AIC = 229, BIC = 209.4) from the
fit indices of the original, interestingly with an entropy of 1 suggesting an excellent
assignment of individual’s class membership.

Four Timepoints, Medium-class Separation, Equal and Unequal Mixing Proportions

At a medium (MD = 2.3) separation between latent classes for both conditions of
equal and unequal mixing class proportion, the correct number of groups or the 2-class
linear mis-specified model was selected (relative to the 1-class and 3-class model). The
fit indices of the mis-specified model experienced a large deviation (AIC = 622.6, BIC
= 603) from that of the original. Interestingly, relative to the fit indices, the mis-specified
model’s ability to discriminate the number of classes present in the model showed a less
steep (10%) decline (compared to the same model at low-class separation).

When an unequal mixing class proportion was modeled, the deviation of the fit indices of
the mis-specified model from the original was comparatively smaller (AIC = 226.5, BIC
= 206.8) compared to the mis-specified model with equal class proportion. Of note is
that there was no change to the model’s ability to assign individual’s class membership.

Four Timepoints, High-class Separation, Equal and Unequal Mixing Proportions

At high-class separation (MD = 3.1) observed at both conditions of equal and
unequal mixing class proportion, the correct number of groups or the 2-class linear mis-
specified model was selected (relative to the 1-class and 3-class model). A large deviation
(AIC = 631.3, BIC = 611.6) of the fit indices of the mis-specified model was observed
and, similar to the same model at medium-class separation, the mis-specified model’s
ability to discriminate the number of classes present in the model had a less steep (9%) decline.

When modeled to have an unequal mixing class proportion, there was still a large deviation \((AIC = 240, BIC = 220.8)\) of the fit indices of the mis-specified model from the original and the model’s ability to discriminate the number of classes present in the model had a less steep decline (7%) compared to the linear mis-specification model at four timepoints, and low-class separation. As far as entropy, the low-class separation condition showed the poorest evaluation of individual’s class assignment which remains true to the literature.
Results of Linear Mis-specification at 8 Timepoints

Table 12

Fit Indices for the 2-Class Original Versus Linear Mis-specified Growth Trajectory at Low-class Separation

<table>
<thead>
<tr>
<th>Linear mis-specification</th>
<th>Number of classes</th>
<th>Clas size</th>
<th>Timepoints</th>
<th>Low</th>
<th>Free parameters</th>
<th>Log likelihood</th>
<th>AIC</th>
<th>BIC</th>
<th>Entropy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Original</td>
<td>2-Class</td>
<td>50-50</td>
<td>8</td>
<td>1.1</td>
<td>18</td>
<td>-12125.3</td>
<td>24286.7</td>
<td>24375.0</td>
<td>0.89</td>
</tr>
<tr>
<td></td>
<td>1-Class</td>
<td>50-50</td>
<td>8</td>
<td>1.1</td>
<td>13</td>
<td>-15771.2</td>
<td>31568.5</td>
<td>31632.3</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>2-Class</td>
<td>50-50</td>
<td>8</td>
<td>1.1</td>
<td>19</td>
<td>-12124.6</td>
<td>24287.1</td>
<td>24380.4</td>
<td>0.89</td>
</tr>
<tr>
<td></td>
<td>3-Class</td>
<td>50-50</td>
<td>8</td>
<td>1.1</td>
<td>17</td>
<td>-15585.3</td>
<td>31204.5</td>
<td>31288.0</td>
<td>0.8</td>
</tr>
<tr>
<td>Original</td>
<td>2-Class</td>
<td>30-70</td>
<td>8</td>
<td>1.1</td>
<td>18</td>
<td>-12413.4</td>
<td>24862.8</td>
<td>24951.2</td>
<td>0.71</td>
</tr>
<tr>
<td></td>
<td>1-Class</td>
<td>30-70</td>
<td>8</td>
<td>1.1</td>
<td>13</td>
<td>-16181.7</td>
<td>32389.3</td>
<td>32453.1</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>2-Class</td>
<td>30-70</td>
<td>8</td>
<td>1.1</td>
<td>19</td>
<td>-12413.1</td>
<td>24864.1</td>
<td>24957.4</td>
<td>0.71</td>
</tr>
<tr>
<td></td>
<td>3-Class</td>
<td>30-70</td>
<td>8</td>
<td>1.1</td>
<td>17</td>
<td>-16162.1</td>
<td>32358.3</td>
<td>32441.7</td>
<td>0.42</td>
</tr>
</tbody>
</table>

Note. Entropy based measures are undefined for models with 1-class. Low represents low-class separation.

Eight Timepoints, Low-class Separation, Equal and Unequal Mixing Proportions

When the number of timepoints was increased at low-class separation, the linear mis-specified model at both an equal mixing proportion and unequal mixing proportion favored the correct number of groups or the 2-class linear mis-specified model as the better fitting model (relative to the 1-class and 3-class models).
The fit indices at equal class proportions barely deviated (AIC = 0.5 BIC = 5.4) from the fit indices of the original model. The same was true for the model when assumed to have an unequal mixing class proportion (AIC = 1.3 BIC = 6.2). Furthermore, there was no change in the entropy between the mis-specified model and the original model to suggest the mis-specified model’s inability to classifying individuals according to their respective class probabilities.
Table 13

Fit Indices for the 2-Class Original Versus Linear Mis-specified Growth Trajectory at Medium-class Separation

<table>
<thead>
<tr>
<th>Linear mis-specification</th>
<th>Number of classes</th>
<th>Class size</th>
<th>Medium</th>
<th>Free parameters</th>
<th>Log likelihood</th>
<th>AIC</th>
<th>BIC</th>
<th>Entropy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Original</td>
<td>2-Class</td>
<td>50-50</td>
<td>2.3</td>
<td>18</td>
<td>-12085.6</td>
<td>24207.2</td>
<td>24295.5</td>
<td>0.83</td>
</tr>
<tr>
<td></td>
<td>1-Class</td>
<td>50-50</td>
<td>2.3</td>
<td>17</td>
<td>-12732.9</td>
<td>25499.8</td>
<td>25583.2</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>2-Class</td>
<td>50-50</td>
<td>2.3</td>
<td>19</td>
<td>-12085.2</td>
<td>24208.5</td>
<td>24301.7</td>
<td>0.83</td>
</tr>
<tr>
<td></td>
<td>3-Class</td>
<td>50-50</td>
<td>2.3</td>
<td>17</td>
<td>-15492.6</td>
<td>31019.2</td>
<td>31102.7</td>
<td>0.91</td>
</tr>
<tr>
<td>Original</td>
<td>2-Class</td>
<td>30-70</td>
<td>2.3</td>
<td>18</td>
<td>-12452.9</td>
<td>24941.7</td>
<td>25030.1</td>
<td>0.79</td>
</tr>
<tr>
<td></td>
<td>1-Class</td>
<td>30-70</td>
<td>2.3</td>
<td>17</td>
<td>-12746.3</td>
<td>25526.5</td>
<td>25610.0</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>2-Class</td>
<td>30-70</td>
<td>2.3</td>
<td>19</td>
<td>-12452.8</td>
<td>24943.5</td>
<td>25036.8</td>
<td>0.79</td>
</tr>
<tr>
<td></td>
<td>3-Class</td>
<td>30-70</td>
<td>2.3</td>
<td>17</td>
<td>-16250.4</td>
<td>32534.9</td>
<td>32618.3</td>
<td>0.55</td>
</tr>
</tbody>
</table>

Note. Entropy based measures are undefined for models with 1-class. Medium represents medium-class separation. These are the fit indices for the 2-Class model at 8 timepoints.
Eight Timepoints, Medium-class Separation, Equal and Unequal Mixing Proportions

At medium-class separation, the 2-class linear mis-specified model continued to be favored as the better fitting model (relative to the 1-class and 3-class models) at both equal and unequal class proportions. The fit indices at equal class proportions barely deviated (AIC = 1.3, BIC = 6.2) from the fit indices of the original model. The same was true for the model when assumed to have an unequal mixing class proportion (AIC = 1.8, BIC = 6.7). Furthermore, there was no change in the entropy between the mis-specified model and the original model to suggest the mis-specified model’s inability to classify individuals according to their respective class probabilities.
Table 14

Fit Indices for the 2-Class Original Versus Linear Mis-specified Growth Trajectory at High-class Separation

<table>
<thead>
<tr>
<th>Linear mis-specification</th>
<th>Number of classes</th>
<th>Class size</th>
<th>Time points</th>
<th>High</th>
<th>Free parameters</th>
<th>Log likelihood</th>
<th>AIC</th>
<th>BIC</th>
<th>Entropy</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Original</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2-Class</td>
<td>50-50</td>
<td>8</td>
<td>3.1</td>
<td>18</td>
<td>-12034.6</td>
<td>24105.2</td>
<td>24193.6</td>
<td>0.72</td>
<td></td>
</tr>
<tr>
<td>1-Class</td>
<td>50-50</td>
<td>8</td>
<td>3.1</td>
<td>16</td>
<td>-15313.6</td>
<td>30659.3</td>
<td>30737.8</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>2-Class</td>
<td>50-50</td>
<td>8</td>
<td>3.1</td>
<td>19</td>
<td>-12033.8</td>
<td>24105.6</td>
<td>24198.9</td>
<td>0.72</td>
<td></td>
</tr>
<tr>
<td>3-Class</td>
<td>50-50</td>
<td>8</td>
<td>3.1</td>
<td>17</td>
<td>-15223.9</td>
<td>30481.8</td>
<td>30565.2</td>
<td>0.9</td>
<td></td>
</tr>
<tr>
<td><strong>Original</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2-Class</td>
<td>30-70</td>
<td>8</td>
<td>3.3</td>
<td>18</td>
<td>-13191.2</td>
<td>26418.4</td>
<td>26506.7</td>
<td>0.64</td>
<td></td>
</tr>
<tr>
<td>1-Class</td>
<td>30-70</td>
<td>8</td>
<td>3.3</td>
<td>14</td>
<td>-16795.0</td>
<td>33618.0</td>
<td>33686.7</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>2-Class</td>
<td>30-70</td>
<td>8</td>
<td>3.3</td>
<td>19</td>
<td>-13191.2</td>
<td>26420.4</td>
<td>26513.6</td>
<td>0.64</td>
<td></td>
</tr>
<tr>
<td>3-Class</td>
<td>30-70</td>
<td>8</td>
<td>3.3</td>
<td>17</td>
<td>-16780.5</td>
<td>33594.9</td>
<td>33678.4</td>
<td>0.35a</td>
<td></td>
</tr>
</tbody>
</table>

*Note.* The original implies the original data generating model and its parameters. No entropy values for 1-class models.

a Residual covariance matrix is not positive definite.

High refers to high class separation.
Eight Timepoints, High-class Separation, Equal and Unequal Mixing Proportions

Similar to the results at low and medium-class separation, at high-class separation, the 2-class linear mis-specified model continued to be favored as the better fitting model (relative to the 1-class and 3-class models) at both equal and unequal class proportions. The fit indices at equal class proportions had a small deviation (AIC = 0.4, BIC = 5.3) from the fit indices of the original model. The same was true for the model when assumed to have an unequal mixing class proportion (AIC = 2, BIC = 6.9). Furthermore, there was no change in the entropy between the mis-specified model and the original model to suggest the mis-specified model’s inability to classifying individuals according to their respective class probabilities.

Results of Latent Basis Models at 4 Timepoints

Four Timepoints, Low-class Separation, Equal and Unequal Mixing Proportions

Observed at the low-class separation (MD = 1.1) condition the latent basis growth trajectory was utilized favoring the 2-class latent basis model as the better fitting model (compared to the 1-class and 3-class model) in under both conditions of equal and unequal mixing class proportion. Compared to the medium and high-class separation conditions, the fit indices had a large positive deviation (AIC = -404.9, BIC = -395.1) from the fit indices of the original model implying the better fitting model to be the latent basis model; however, the model’s ability to discriminate between the number of classes present in the dataset steeply deteriorated (30%) from the original. When modeled with an unequal mixing class proportion, the fit indices of the latent basis model had a large
deviation (AIC = 103.7, BIC = 113.6) from the original; however, the latent basis’s ability to assign individual’s class membership improved (4%).

*Four Timepoints, Medium-class Separation, Equal and Unequal Mixing Proportions*

Observed at the medium-class separation (MD = 2.3) and equal mixing proportions, the better fitting model was the 2-class latent basis model compared to the 1-class and 3-class model (where the 3-class model encountered issues in replicating the best log likelihood value). This held true across conditions of equal and unequal mixing proportions. The fit indices of the latent basis model at medium-class separation showed a small difference (AIC = 19.2, BIC = 29.1) from the fit indices of the original model with no changes to the latent basis’s ability in confidently assigning individual’s class membership. At unequal mixing proportions, the fit indices of the latent basis model at medium-class separation showed a large difference (AIC = 105.2, BIC = 115) from the fit indices of the original model. However, given the large difference in the fit indices between the original model and the latent basis model, there was only a slight deterioration (~1%) to the latent basis’s ability in confidently assigning individual’s class membership.

*Four Timepoints, High-class Separation, Equal and Unequal Mixing Proportions*

Observed at the high-class separation (MD = 3.1) and equal mixing proportions, the better fitting model was the 2-class latent basis model compared to the 1-class and 3-class model (where the 3-class model encountered issues in replicating the best log likelihood value). This held true across conditions of equal and unequal mixing
proportions. The fit indices of the latent basis model at high-class separation and equal mixing class proportion showed a medium sized deviation ($AIC = 19.2$, $BIC = 28.3$) from the fit indices of the original, and there were once again no changes to the latent basis’s ability in confidently assigning individual’s class membership. At the unequal mixing class proportion, the model encountered issues in replicating with the best log likelihood value for the 1-class and the 3-class model. The fit indices of the latent basis model at high-class separation showed a medium sized difference ($AIC = 105.2$, $BIC = 115$) from the fit indices of the original model. Furthermore, the latent basis models’ ability to confidently assign individual’s class membership to the latent classes deteriorated (1%) from the original model.

**Results of Latent Basis Models at 8 Timepoints**

*Eight Timepoints, Low-class Separation, Equal and Equal Mixing Proportions*

When the number of measurement points are increased, at low-class separation ($MD = 1.1$) and equal mixing proportions, the better fitting model was the 2-class latent basis model compared to the 1-class and 3-class model. This held true for the unequal mixing class condition as well. At the low-class separation condition, the fit indices of the latent basis model showed a large difference ($AIC = 312$, $BIC = 341.8$) from the fit indices of the original model with minimal deterioration (~1%) to the latent basis’s ability in confidently assigning individual’s class membership to latent classes.

Similarly, when modeled assuming an unequal mixing class proportion, a large difference ($AIC = 314$, $BIC = 343.9$) was also observed, however, there were no changes to the
latent basis’s ability in confidently assigning individual’s class membership to latent classes.

**Eight Timepoints, Medium-class Separation, Equal and Equal Mixing Proportions**

When the number of measurement points are increased, at medium-class separation (MD = 2.3), for both equal and unequal mixing proportions, the better fitting model was the 2-class latent basis model compared to the 1-class and 3-class model. At the medium-class separation condition, the fit indices of the latent basis model showed a large difference (AIC = 538.3, BIC = 341.8) from the fit indices of the original model. The same held true for the model with an unequal mixing class proportion (AIC = 315, BIC = 345.3) with no changes to the latent basis’s ability in confidently assign individual’s class membership to latent classes.

**Eight Timepoints, High-class Separation, Equal and Unequal Mixing Class Proportion**

When the number of measurement points are increased, at high-class separation (MD = 3.1), for both equal and unequal mixing proportions, the better fitting model was the 2-class latent basis model compared to the 1-class and 3-class model. At the high-class separation condition, the fit indices of the latent basis model showed large difference (AIC = 298.8, BIC = 328.8) from the fit indices of the original model. The same model when assumed to have an unequal mixing class proportion, showed the largest difference (AIC = 930.8, BIC = 960.3) of any of the previous models.
The same held true for the model with an unequal mixing class proportion (AIC = 315, BIC = 345.3) with no changes to the latent basis’s ability in confidently assigning individual’s class membership to latent classes.

**Results Of Gompertz Mis-specified Models at 4 Timepoints**

*Four Timepoints, Low-class Separation, Equal and Unequal Mixing Class Proportion*

Observed at the low-class separation (MD = 1.2) for both equal and unequal mixing proportions, the better fitting model was the 2-class Gompertz compared to the 1-class and 3-class model. Additionally, the 2-class and the 3-class encountered issues in replicating the best log likelihood value. The fit indices of the Gompertz mis-specified model at low-class separation showed a large difference (AIC = 327.6, BIC = 361.9) from the fit indices of the original model implying a far worse fit of the mis-specified model to the data. Interestingly, the entropy of the mis-specified model showed hardly any deterioration (~1%) to confidently assigning individual’s class membership. The same model (MD = 1) when there was an unequal mixing class proportion, did not encounter issues in replicating with the best log likelihood value. The fit indices of the Gompertz mis-specified model at low-class separation (AIC = 17.2, BIC = 51.4) showed a small difference from the fit indices of the original model and the entropy vastly improved (24%) with the Gompertz mis-specification implying the model’s ability to confidently assign individual’s class membership.
Four Timepoints, Medium-class Separation, and Equal and Unequal Mixing Proportions

Observed at the medium-class separation (MD = 2.3) for both equal and unequal mixing proportions, the better fitting model was the 2-class Gompertz (where the 3-class model encountered issues in replicating the best log likelihood value). The fit indices of the Gompertz mis-specified model at medium-class separation (AIC = 28.5, BIC = 62.9) showed a medium sized difference from the fit indices of the original model, though the entropy of the mis-specified model showed slight improvement (~1%) to confidently assigning individual’s class membership. The same model when there was an unequal mixing class proportion (MD = 2.4) did not encounter issues in replicating with the best log likelihood value. The fit indices of the Gompertz mis-specified model at medium-class separation showed a medium difference (AIC = 19.4, BIC = 53.7) from the fit indices of the original model and the entropy vastly improved (24%) with the Gompertz mis-specification, implying the model’s ability to confidently assign individual’s class membership.

Four Timepoints, High-class Separation, Equal and Unequal Mixing Proportions

Observed at the high-class separation (MD = 3.1) for both equal and unequal mixing proportions, the better fitting model was the 2-class Gompertz compared to the 1-class and 3-class model (where the 2-class model encountered issues in replicating the best log likelihood value). The fit indices of the Gompertz mis-specified model at high-class separation showed a medium-sized difference (AIC = 29.4, BIC = 63.8) from the
fit indices of the original model and there was no noticeable change to the entropy of the mis-specified model. The same model when there was an unequal mixing class proportion (MD = 3.4) did not encounter issues in replicating with the best log likelihood value. The fit indices of the Gompertz mis-specified model at high-class separation showed a medium difference (AIC = 33.3, BIC = 67.7) from the fit indices of the original model and the entropy improved (19%) with the Gompertz mis-specification, implying the model’s ability to confidently assign individual’s class membership.

Results of Gompertz Mis-specified Models at 8 Timepoints

Eight Timepoints and Equal Mixing Proportions at Low-class Separation

Observed at the low-class separation (MD = 1.1) for both equal and unequal mixing proportions, the Gompertz mis-specified model encountered found the better fitting model was the 2-class Gompertz model compared to the 1-class and 3-class model. The fit indices of the Gompertz mis-specified model at low-class separation showed a large sized difference from the fit indices of the original model (AIC = 272.2, BIC = 326.2). In tandem, the entropy of the mis-specified model remained the same showing no change in the model’s confidence in assigning individual’s class membership. The same model when there was an unequal mixing class proportion (MD = 1.1) also encountered numerous issues with the model not terminating normally, and issues of model nonidentification. The fit indices of the Gompertz mis-specified model at low-class separation showed a large difference (AIC = 678.9, BIC = 654.3) from the fit indices
of the original model and the entropy saw a small decline (3%) with the Gompertz mis-
specification

_Eight Timepoints, Medium-class Separation, and Equal and Unequal Mixing Proportions_

Observed at the medium-class separation (MD = 2.3) for both equal and unequal mixing proportions, the better fitting model was the 2-class Gompertz model compared to the 1-class and 3-class model. The fit indices of the Gompertz mis-specified model at medium-class separation showed a large sized difference from the fit indices of the original model. In tandem, the entropy of the mis-specified model showed decline (13%) from the original. The same model when there was an unequal mixing class proportion (MD = 2.3) found the better fitting model to be the 2-class model compared to the 1-class and 3-class model. Similarly, to the previous model, the fit indices of the Gompertz mis-specified model at medium-class separation showed a large difference from the fit indices of the original model and the entropy saw a small decline (3%) with the Gompertz mis-specification.

_Eight Timepoints, High-class Separation, and Equal and Unequal Mixing Proportions_

Observed at the high-class separation (MD = 3.14) and equal mixing proportions, the better fitting model was the 2-class Gompertz model compared to 3-class model (where the 1-class and 2-class model encountered issues in termination and replicating the best log likelihood value, respectively). The fit indices of the Gompertz mis-specified model at high-class separation showed a large sized difference from the fit
indices of the original model. In tandem, the entropy of the mis-specified value declined (9%) from the original confirming poor fit of the model to the data.

The same model when there was an unequal mixing class proportion (MD = 3.4) found the better fitting model to be the 2-class model compared to the 1-class and 3-class model. In this case, both the 2-class and the 3-class model were challenged in model termination and replicating the best log likelihood value. The fit indices of the Gompertz mis-specified model at high-class separation showed a large difference from the fit indices of the original model and the lack of change in the entropy remained suggested clearly an extremely poor fit of the model to the data.

**Latent Class Assignment**

The latent class assignment of individual’s membership is presented in Table 15. The table includes the original model and the models with the mis-specified functional forms. For each of the four functional forms presented, the probability of individuals’ latent class assignment is included for each of the manipulated design conditions that were included in the study. The change columns are the proportions of change the mis-specified models experienced relative to the original model.

It can be observed that at 4 timepoints, unequal mixing proportion and low-class separation, the model was unable to correctly assign individuals to the latent classes. The worst performing model was the linear mis-specification which assigned all the individuals to the second latent class leaving the first latent class at zero. Similarly, the latent basis and the model including a Gompertz curve mis-specification also had
incorrectly proportioned class membership. For example, the original dataset used in the mis-specification of the Gompertz curve was generated with a 30:70 mixing class proportion. However, when fit with a Gompertz curve, the model yielded a latent class assignment that disproportionately assigned 51 individuals to the first latent class (compared to 170), and 949 individuals to the second latent class (compared to 830). Although, the most extreme impact to latent class assignment was observed at the low-class separation condition, all the fitted models experienced a certain amount of inaccuracy to individual’s class membership to the latent classes.
Table 15
Changes to Individuals’ Assignment to Latent Classes

<table>
<thead>
<tr>
<th>Timepoints</th>
<th>Mixing Class Proportion</th>
<th>Class Separation</th>
<th>Original</th>
<th>Change</th>
<th>Linear</th>
<th>Latent Basis</th>
<th>Gompertz</th>
<th>Change</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Unequal</td>
<td>Low</td>
<td>170</td>
<td>830</td>
<td>17:83</td>
<td>0</td>
<td>1000</td>
<td>0:1</td>
</tr>
<tr>
<td></td>
<td>Medium</td>
<td>182</td>
<td>818</td>
<td>91:409</td>
<td>33</td>
<td>967</td>
<td>33:967</td>
<td>825</td>
</tr>
<tr>
<td></td>
<td>Medium</td>
<td>509</td>
<td>491</td>
<td>509:491</td>
<td>509</td>
<td>491</td>
<td>509:491</td>
<td>482</td>
</tr>
<tr>
<td></td>
<td>Medium</td>
<td>293</td>
<td>707</td>
<td>293:707</td>
<td>293</td>
<td>707</td>
<td>293:707</td>
<td>704</td>
</tr>
<tr>
<td></td>
<td>High</td>
<td>298</td>
<td>702</td>
<td>149:351</td>
<td>298</td>
<td>702</td>
<td>149:351</td>
<td>354</td>
</tr>
</tbody>
</table>

Note. The change columns represent the changes to the probability of individuals’ class assignment between the original model and each of the models with the altered functional form.
Graphical Representation of the Standardized Residual Values of the Linear Mis-specified Model at 8 Timepoints

A mixed-effects model was conducted in STATA using the data generated from Mplus version 8.8. This methodology was employed to further examine the mis-specified model whose fit indices and entropy values closely resembled those of the original model. From Table 11, it can be observed that there were no changes to the entropy of the 2-class linear model compared to the original model implying that the model correctly detected the presence of two classes in the dataset. In spite of a mis-specification to the functional form, the model was confident regarding its assignment of individuals to the latent classes. Additionally, from Table 15 it can be observed that the class proportions did not change when there was an unequal mixing proportion condition at medium and high-class separation.

Given that the 2-class linear model was a mis-specification that still yielded the correct number of classes and class assignment, the purpose of the mixed-effects model was to further inspect the behavior of the residuals per latent class of the model. Since there is a priori knowledge that the model is incorrect, but the GMM selection criteria vetted the model as correct. Therefore, plotting and examining the residuals would reveal whether there was a trustworthy pattern of the spread of the residual values along the regression line. This analysis was run in STATA and conducted for each of the manipulated design conditions.
In STATA, the predicted values of the outcome were generated, and the residuals for each latent class were obtained and saved from the outcome and the predicted values. These residuals were then standardized in order to better interpret the results. Three types of graphs were plotted using the generated residuals – the PP plot, the QQ plot and the line plot.

From Figure 3 and Figure 6, the QQ plot, examining the behavior of the residuals in the linear mis-specified model at unequal and equal class proportions, and at all three levels of class separation, class 1 showed a relatively normal spread of the residual values along the regression line. In class 2 however, it can be observed that at the tail ends of the regression line the residual values deviated away from the regression line. Though not entirely suspicious, further examination of the PP plots (Figure 4), which looks at the behavior of the residuals around the center of the line, showed a normal class 1; however, class 2 yielded problematic behavior of the residuals. This makes sense given that the growth trajectory of the second latent class was modified. From Figure 6, the same implication holds for equal mixing proportions. The QQ plot reveals that class 1 has a fairly normal spread of residual values around the regression line including the tail ends; however, class 2 shows errant behavior of the residuals. Interestingly, closer examination of the PP plot, which holds the same implication for low and medium-class separation (as the results from the PP plot of the unequal class separation), shows at high-class separation an abnormal spread of the residuals around the center of the regression line for both classes. While the results from the GMM analysis revealed that the mis-specified
linear model at eight timepoints could be assumed to be a good fit of the model to the data, not delving further into the behavior of the residuals would lead to an erroneous inference of the GMM results. However, an examination of the residuals showcased the drawbacks of relying solely on GMM results to make substantive inferences.

**Plots of the Standardized Residual Values of The Linear Mis-specified Model at Eight Timepoint for Each Manipulated Condition**

Figure 3

Eight Timepoints and Unequal Mixing Proportions at The Three Levels of Latent Class Separation of The Mis-specified Linear Growth Trajectory
Note. QQPlot of the standardized residual values of the linear mis-specified model at (A) low-class separation; (B) medium-class separation; (C) high-class separation at Eight timepoints at unequal mixing proportions

Figure 4

Behavior of the Standardized Residuals in a PP Plot
Note. PP Plot of the standardized residual values of the linear mis-specified model at (A) low-class separation; (B) medium-class separation; (C) high-class separation at Eight timepoints at unequal mixing proportions.
Figure 5

Graph of the Standardized Residual Values by Outcome and Predicted for Unequal Mixing Proportion

(A)
Figure 6

Standardized Residual Values of the Linear Mis-specified Model at Equal Mixing Proportions

(A)

(B)

(C)

Note. QQPlot of the standardized residual values of the linear mis-specified model at (A) low-class separation; (B) medium-class separation; (C) high-class separation at eight timepoints at equal mixing proportions
Figure 7

Behavior of the Standardized Residual at Equal Mixing Proportions

(A)

(B)

(C)

Note. PP Plot of the standardized residual values of the linear mis-specified model at (A) low-class separation; (B) medium-class separation; (C) high-class separation at eight timepoints at equal mixing proportions.
Figure 8

Graph of the Standardized Residual Values by Outcome and Predicted for Equal Mixing Proportion

(A)
Chapter Five : Discussion

The research question that sparked this dissertation endeavor was “what is the impact of a mis-specified growth curve in GMM as it relates to substantive inference?”

Two compelling reasons that justified asking this question were:

- overlooked mis-specified growth curves in GMM
- the standard that correct class extraction implies successful GMM application

Presence of Mis-specified Growth Curves in GMM

Earlier in this study the argument was presented for the prevalence and potential frequency of mis-specified functional forms in GMM. It was theorized as a gap due to the undetectable consequence of functional form mis-specification to substantive inference and the dearth of studies exploring the issue. A feature inherent to the methodology that lends itself to functional form mis-specification is the role and influence of a priori assumptions in GMM. In GMM literature there is that a researcher’s underlying assumptions about how individuals develop on a construct, if not reappraised by another when looking to replicate findings, prompt the proliferation of methodological biases that consequently influence substantive inferences.
For example, in the field of resilience, Infurna and Luthar (2016) contended against claims by Bonanno et al. (2011) who used GMM to surmise that 60% of their sample fell in the latent class of resilient individuals. Modifying the a priori assumption allowing for within-class variability, Infurna and Luthar (2016) replicated the study using the same data and concluded instead that approximately 40% of the sample followed the functional form defining the resilient trajectory. Therefore, for almost a decade, 20% of the sample was described with an incorrect functional form and erroneously specified as falling in the class of individuals exhibiting resilience to major life stressors. Their intended focus in using GMM was to reassess the number of latent classes correctly extracted in resilience studies to ultimately challenge the norm that resilience is a unidimensional construct. However, their study inadvertently highlighted that incorrect functional form assumptions in GMM have both methodological and substantive implications.

While the specific exploration of mis-specified functional form in GMM has not received the kind of attention it deserves, this is not to say that functional form mis-specification has not been previously studied in cluster analysis or latent class type analysis. A study by Usami, Jacobucci, and Hayes (2019) looked at the effect of functional form mis-specification to assess the robustness of a latent growth curve model (LGCM) based-SEM Trees for detecting population heterogeneity. It appears that the interest is present in the overarching field of latent class and latent growth curve analysis and attention to the role of mis-specification of functional forms to inference.
The Standard of Correct Class Extraction

Over the last decade, the focus in refining the GMM methodology has largely been concerned with another characteristic feature of the methodology, namely the enumeration of latent classes. GMM is a contemporary statistical methodology designed to identify latent trajectory classes based on longitudinal growth data. It is a combination of latent growth curve and mixture models, and therefore can simultaneously estimate trajectories of change and infer subgroups of individuals with distinct multivariate normal distributions (Infurna & Luthar, 2016). Capitalizing on its ability to uncover latent subgroups, GMM has been widely applied to a diverse number of fields; however, the prevalent issues of overextraction of latent classes present with GMM has focused researchers’ efforts toward resolving this methodological challenge. Consequently, addressing the challenge of overextraction of latent classes led to a decade long study of appropriate accompanying fit indices to be used when applying GMM analysis to determine the number of subgroups in a sample. This is mentioned to underscore the two primary focus areas to which extensive attention has been directed in attempts to refine the methodology. Eventually, in a study by Ram and Grimm (2009), GMM was appropriately described as an exploratory methodology and recommendations were made that it be used for exploratory purposes within the context of longitudinal data.
Conceptualizing the Research Question

As mentioned earlier, the research question aimed at unearthing the ways in which mis-specified functional forms influenced substantive inference within the GMM context. In order to answer this question, a 2-class population model with one linear class, and one quadratic class, was hypothesized as is typical in a GMM study. The population model was then simulated in a Monte Carlo simulation under the manipulated conditions of varying timepoints (4 timepoints and 8 timepoints), mixing class proportion (50:50 and 30:70), and latent class separation (low, medium, and high). The fixed design factor was the sample size of n = 1000. In total 12 models representing the original models were simulated and each model was then evaluated with a linear, latent basis, and Gompertz growth curve resulting in the comparative analysis of 36 models. Under these conditions, the effect of functional form mis-specification was assessed on class assignment and class extraction, where class assignment is a look at the proportion of individuals in a given latent class and class extraction is a look at the number of latent classes extracted. The comparisons between the mis-specified models and the original simulated models were gauged on rate of convergence, fit indices, and entropy.

The Need for Studying Functional Form Mis-specification

Given that the past several years has seen extensive research in refining the GMM methodology with popular focus on the performance of fit indices in correct class extraction, this study aimed at a comparative assessment across the 36 models to draw
conclusions using the previously specified measures (fit indices and entropy) on the effect of mis-specification of functional forms to GMM results. GMM being an exploratory technique affords researchers the opportunity to continue to iron out methodological challenges, one such being GMM’s inability to identify scenarios when an incorrect latent class growth trajectory is being modeled. The purpose of this simulation study was to address the need researchers and practitioners have in apprehending mis-specified functional forms when using GMM. The consequence of not confronting the issue of pervasive methodological biases is that a group of individuals following a different growth curve than what is assumed can be entirely missed.

Discussion of Simulation Results

The two major takeaways in exploring the research question regarding the effects of functional form mis-specification in GMM were:

- Expected class enumeration does not imply accurate capture of functional forms in a sample
- Type of curve modeled (simple or complex) holds implications for visibility of the mis-specification

Expected Class Enumeration Doesn’t Imply All Possible Functional Forms Identified

In GMM, the researcher’s expectation of the number of latent classes that GMM should extract isn’t the same as the correct number of underlying latent classes present in a sample. Fastidious care to ensure that a GMM application yields the expected number
of latent classes is important. However, treating this as the standard implies an inaccurate representation of the underlying growth trajectories defining a sample which in turn compromise theories of development. The practical implications are that erroneous inferences undermine effectiveness of learning interventions and overlooks groups of individuals whose functional forms of learning trajectories perhaps differ from the researcher’s a priori assumptions. Shader (2021) similarly suggests caution when interpreting GMM results as often incorrect inferences tend to be reified in the literature.

The purpose of conducting a simulation was to look at an array of models that are challenging to observe in real-world applications. It can be assumed using the examples of the mis-specified models in this study that in a real-world context, the performance of the fit indices, in tandem with the convergence rates and extraction of the expected classes would lead a researcher to select a mis-specified model as the true model. For example, in this study there was a 100% agreement of the AIC and the BIC fit indices across the latent classes per mis-specified model. More precisely, each model with a mis-specified growth curve was modeled as a 1-class, 2-class and 3-class GMM. The 2-class GMM model was favored by both the AIC and BIC in all 36-models. For two out of the three functional forms modeled, the convergence rates were good and for the third functional form the convergence rates were predictably acceptable given the complexity of modeling the Gompertz.
This is mentioned to underscore that using the current selection process of the hypothesized GMM would support the selection of a mis-specified model. The example of the mis-specified model at 4 and 8 timepoints serves as a particularly interesting example to challenge this argument.

**Mixing Proportion**

In practical application the mixing proportion of latent classes can be balanced (equal) or unbalanced (unequal) and there can be varying degrees of unbalanced class proportions that can be modeled though sometimes at the cost of convergence issues and model non-identification. Table 11 represents the assignment of individuals’ membership to the latent classes. The 2-class models were favored by the fit indices for each of the functional forms modeled. However, even though the models with mis-specified functional forms correctly identified the datasets as having two classes, the mixing proportion of classes changed across most of the models compared to the original.

A look at the model with 4 timepoints, equal mixing proportions and low-class separation shows that somewhere between the original model and the model with the linear mis-specification, the latent class assignment changed from an equal mixing proportion to an unequal mixing proportion (36:64). More clearly stated, when the incorrect functional form was modeled, individuals who identified with either a linear or quadratic functional form originally were conformed to a trajectory of development that inaccurately represented the true trajectory of their growth. Similarly, when the mis-specification was more complex such as the Gompertz curve, though the fit indices
selected two classes as the number present in the data, the mixing proportion changed
from equal to represent an unequal mixing proportion (69:31).

**Latent Class Separation**

Another clear observation was that the severity of the issue of mis-assignment of
individuals’ membership to the latent classes increased when there was little delineation
between the separation of the latent classes. Further examination of the latent class
separation showed a typical trend common to GMMs where models at high-class
separation and equal mixing proportions yielded little to no change in the entropy values.
Recall that the entropy value signals the model’s confidence in the accuracy of
assignment of individuals’ membership to latent classes. Predictably as the separation
between classes diminished so did the accuracy of the entropy values. A general trend
observed was that at medium-class separation and equal class proportions, the entropy
declined from the original simulated model’s entropy on average by 10%, however, the
same model at low-class separation saw the entropy value decline by greater than 50%
(see low-class separation at four time points from Table 8). Given that mixture class
separation between latent classes in GMMS is often characterized by how
similar/different the growth trajectories are between the latent classes (Depaoli, 2013),
this pattern of diminishing entropy values from the high to low latent class separation is
typical. It is expected at low-class separation between the growth trajectories that greater
would be the model’s challenge in accurately assigning individuals into latent classes.
This argument explains why the linear mis-specified model at 4 timepoints, low-class
separation, and equal mixing proportions would have the greatest decline in entropy value of all the mis-specified models.

**Mis-specification in GMMs Obscured by Type of Functional Form**

The second key takeaway from this simulation experiment was that models with a simple mis-specification to the functional form (i.e., a linear or a quadratic curve) are better able to mask the incorrectness of the functional form, elevating the risks of accepting this type of mis-specified model as the true model. The reason being that when it comes to a simple functional form mis-specification both linear and quadratic latent growth curves can express monotone increasing trajectories that the simulated longitudinal dataset indicate (Usami et al., 2018). The issue is further complicated when fit indices agree, good entropy values are yielded, and there are no issues with convergence. Convergence rate from the thirty-six simulated models and the corresponding growth trajectory mis-specification suggested that the models with the linear mis-specification had between a 97-100% convergence rate at each simulated condition. The convergence rates for the latent basis models landed in a similar range. Since non-convergence or multiple local maxima are common problems in using EM algorithm for fitting finite mixture models, it is especially critical in GMMS to know the complexity of the growth trajectory before beginning the modeling process. As such, the more complex the functional form, greater is the visibility into the model indicating inappropriate fit the data. For example, modeling the mis-specification of a Gompertz...
curve revealed the most difficulty (of all the models) in converging to a proper solution. Additionally, the Gompertz models that did eventually converge saw issues with non-replication of the best log likelihood value which rendered the results somewhat suspect. Though these results from the Gompertz model are not unexpected given that modeling a Gompertz curve in a GMM under typical modeling scenarios is a complex task, the emphasis here is that the effect of mis-specifying a complex functional form could be easier to not overlook compared to modeling a simple functional form.

Timepoints

It is theorized that when the number of timepoints are increased (in this case from 4 to 8 time points), the model is better able to capture the growth curve (Ram & Grimm, 2007). All the models except for the linear model at 8 time points yielded results that were to be expected based on this theory. It is of particular interest to note that when the conditions of balanced/unbalanced mixing class proportions and three levels of class separation with the mis-specified linear growth trajectory were extended from 4 to 8 time points, the model yielded results closely resembling the original simulated model. The linear mis-specified model at 8 timepoints showed minimal differences from the original and would look like the model of choice were there no original model to which to compare the functional form mis-specification. Observed from Table 7, the fit indices for the linear mis-specified model were in some cases less than half of a point different from the fit indices of the original model. However, although the model looked very
similar to the original, a mixed model analysis revealed an erratic behavior of the residuals around the regression line for the class with the mis-specification.

**Implications**

GMM is better suited to use as a constrained exploratory technique whose results are corroborated by other statistical methodologies such as a mixed-effects model to confirm results especially in situations when fitting simpler polynomial functional forms to the model as functional form mis-specification is the most hidden with simpler functional forms. As an a priori analysis of the dataset, conducting a trend analysis implemented as an ANOVA would benefit the researcher in visualizing the dataset before choosing to apply a GMM. Given that GMM can be both time and computationally intensive, visualizing the dataset would provide the researcher with an idea of the feasibility of applying a GMM. A trend analysis conducted in ANOVA would especially suit a repeated measures dataset since it is commonly applied to data that has been collected over time or when a single independent variable has been manipulated to observe its effects on a response variable. Specifically, since the a priori goal isn’t to determine the number of classes present or the functional form of each latent class, visualizing the dataset prior to application of a GMM would assist the researcher in forming appropriate methodological ideas of the types of functional forms to specify.

A trend analysis tests the hypothesis that the means of the ordered groups change in a linear or higher order (polynomial) fashion. It would yield according to the grouping
variable created, the pattern or shape of the relationship between the independent variable and the dependent variable. Using this simulation, a trend analysis would be set up to analyze time as the independent grouping variable, and the outcome per time point would be the continuous dependent variable. A trend analysis is different from a one-way ANOVA in that the groups have an order. Therefore, in this study, the results would not have differed from a one-way ANOVA versus a trend analysis conducted in ANOVA. However, if the complexity of the simulation model were increased with inclusion of covariates, a trend analysis would better accommodate the a priori step of confirming the types of functional forms to specify to the model. And would also assist in discovering functional forms that are not as commonly used by researchers in the field.

The findings from this study showcase that while it is possible to model an incorrect functional form that yields the correct (expected) number of latent classes, the results are an erroneous mixing proportion in the latent classes in the model. The changed latent class membership when the functional form is mis-specified highlights the possibility of certain individuals’ developmental curves underlying a sample being overlooked or incorrectly classified. This suggest that researchers must exercise caution when using GMM to confirm a priori assumptions given the dangers of relying solely on the standard of correct class extraction in GMM. In this vein, for a practitioner extending GMM to newer fields of research, success of a GMM application could be conceptualized as not only correct class extraction or behavior of fit indices but as testing the efficacy of different functional forms to the dataset and examining the behavior of the residuals of
the selected model. There are many strengths to GMM and one of the more understood ones is its conceptualization as a methodology to uncover growth trajectories inherent to a sample but not as familiar to the researcher.

Limitations

The study has several limitations. Firstly, the mis-specified functional form was applied to only one of the two latent classes in the model. In order to construct a complete understanding of the effects of functional forms mis-specification to the model, and substantive inferences, the study could have benefitted from functional form mis-specifications in both the latent classes. Secondly, the change in mixing proportion to latent classes under a mis-specified functional form was only briefly covered in this study. However, extensive research into why the mixing proportion changes and the effects of imposing model constraints and its resulting effects on the conditions of model mis-specification would add further clarity to the findings from this study. Lastly, the modeling of the Gompertz curve is a complex task and there is evidence of only one study having used this type of curve. Therefore, including another type of sigmoid curve that is more complex than the typical polynomial curve would contribute to better understanding the effects of functional form mis-specification in the case of complex curves, and also improve generalizability of the results.
Conclusions and Future Directions

It was interesting to note that contrary to the common narrative is that traditional GMM often overextracts latent classes (Shader, 2021), in the modeling scenarios of mis-specified growth trajectories, out of the 1-class and 3-class models, most of the times the 2-class models were favored in the mis-specified models. However, these results were yielded from a simulated study where the mis-specification was restricted to only one latent class. It would be interesting to observe resultant differences in parameters, fit indices, class enumeration, and class assignment when the first latent class and then, both latent classes, were to have a mis-specified functional form. The Mahalanobis distance was used to measure the distance between the latent classes when modeling the three levels of class separation. The process of using the Mahalanobis distance to manipulate latent class separation was tedious and complex. Given that the entropy also reveals how confident the model is in delineating the classes present in the model, there is a viable opportunity for uncovering the specific empirical connection between the Mahalanobis distance and the entropy values to improve the process of manipulation of latent class separation in a simulation study.

GMM’s ability to identify multiple unobserved subpopulations, each with a unique growth trajectory and simultaneously describe longitudinal change within each unobserved subpopulation has caused its wide-spread adoption in the research sciences.
While extensive attention over the years has been devoted to the correct determination of the number of latent classes present in a sample, this study highlights the inadequacy of relying on that standard alone. The findings from this dissertation reveal that mis-specification of functional forms result in an inaccurate mixing proportion of latent classes. This implies that individuals whose functional forms don’t match the assumptions of the developmental process being studied could be overlooked when using GMM which holds negative implications for informing and developing of theories of growth. Furthermore, the effects of mis-specified functional forms that are polynomial in nature are more challenging to recognize than for example, a sigmoid (i.e., Gompertz curve) functional forms. Unfortunately, since polynomial functional forms are frequently observed in GMM applications, the possibility of erroneous inferences being a likelihood rather than a chance occurrence are more than likely.

The study and exploration of mis-specification relating to functional forms are common research goals in other fields that use predictive modeling (such as econometrics) where the refining of substantive inferences inform key policy making decisions. Similarly, in the field of education, where the refining and development of growth theories critically inform learning interventions and programs in the classroom, it is imperative that all possible functional forms underlying a sample are identified. Although having a priori assumptions of the expected number of latent classes present in a population provide a directional starting point, it is valuable in tandem to model theoretically relevant, even if not as familiar functional forms to discover more (or less)
latent classes present in a population. Given that individuals are unique and follow distinctly different growth trajectories, GMM serves as a useful methodology in broadening the horizon of what is known and possible as it relates to growth and developmental theories in the social sciences.
References


https://doi.org/10.1007/s00180-018-0815-x

