A LONGITUDINAL BEHAVIOR GENETIC MODEL FOR ORDERED CATEGORICAL VARIABLES

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by

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A LONGITUDINAL BEHAVIOR GENETIC MODEL

FOR OREDERED CATETORICAL VARIABLES

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Abstract

A developmental behavior genetic model is proposed for the analysis of longitudinal twin data consisting of ordered categorical variables. In this model, the genetic growth curve model (McArdle, 1986; McArdle et al., 1998) was combined with a latent response variable model for ordered categorical variables. In the growth part of the proposed model, proportional changes in response categories across time were modeled as a growth curve in which mean and variance changes in underlying continuous variables are modeled. In the biometric part of the model, these growth factors were decomposed into genetic and environmental components. The model was applied to simulated data sets generated under varying conditions of model complexity. Parameters were successfully estimated in all conditions although estimates of standard errors were biased and statistical powers to detect non-zero parameters were weak for some parameters. Possible solutions for these irregularities were discussed. Despite these limitations, the relative contributions of genetic and environmental components on growth factors were well estimated. Possible refinement of simulation analysis and expansion of the proposed model for multiple indicators at each measurement occasion were discussed.

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Chapter 1: BACKGROUND

Quantitative behavior genetic models have been used to quantify the heritability of phenotypic behaviors (Martin & Eaves, 1977; Neale & Cardon, 1992). In their basic form, quantitative behavior genetics models, also known as ACE models (Loehlin, 1998) or Genetic Factor Models (Neale & Cardon, 1992), are factor analytic approaches that decompose the variability of a phenotypic variable across individuals into latent factors which represent biometric components: An additive genetic factor (*A* factor), a common environmental factor (*C* factor), and a unique environmental factor (*E* factor). Quantitative behavior genetics models have been expanded to incorporate more complicated data structures such as multiple indicators for a phenotype (Neale & Cardon, 1992), group comparisons of biometric components (Dolan, Molenaar & Boomsma 1991), and gene-environment interactions as well as non-additive genetic factors (Dick, Rose, Viken, Kaprio, & Koskenvuo, 2001; Dolan, Molenaar, & Boomsma, 1991; Neale & Cardon, 1992; Purcell, 2002).

As genetically informative longitudinal data from twins have become available, behavior genetics models have been expanded to identify genetic and environmental effects on developmental changes of phenotype behaviors. In early studies of longitudinal twin data, it was found that genetic components are important to determine both physical growth (Vandenberg & Falkner, 1965) and cognitive abilities (Matheny, 1983; 1990; Wilson, 1983). Vandenberg and Falkner (1965) compared regression coefficients of heights on a time variable (days) between twins and found that regression coefficients were significantly different between dizygotic (DZ, fraternal) twin pairs, but were not

significantly different between monozygotic (MZ, identical) twin pairs. In later analyses of cognitive abilities (Matheny, 1983; 1990; Wilson, 1983), correlations of MZ twin pairs showed more congruence on the test scores of cognitive abilities than of DZ twin pairs.

Recent studies of longitudinal twin data have employed factor analysis and structural equation models in order to estimate genetic and environmental contributions as latent variables. Two primary types of models have been developed for the analysis of longitudinal twin data: the Genetic Simplex Model (Dolan, Molenaar and Boomsma, 1991; Eaves, Long, and Heath, 1986; Neale and Cardon, 1992) and the growth curve model with biometric factor structures (McArdle 1986; McArdle, Prescott, Hamagami, & Horn, 1998; McArdle & Hamagami 2003; Neale & McArdle 2003). In the genetic simplex model, the score at each measurement consists of a true score and a corresponding error term. The true score at each measurement has genetic and environmental sources affected by the genetic and environmental sources at previous measurement occasions. The genetic simplex model does not assume specific shapes of growth curves, and can capture any shape of growth trajectories.

McArdle (1986), also McArdle et al. (1998), applied a biometric factor structure to the growth curve model in order to estimate genetic and environmental influences on developmental changes of phenotype variables. This model will be referred to as the genetic growth curve model in the following. The genetic growth curve model can be divided into two parts: a growth part and a biometric part. In the growth part, changes of repeatedly measured variables are represented as a function of time through growth parameters which are an intercept and rates of change. Growth parameters vary across

individual, and, in the biometric part, variability growth parameters across individuals are decomposed into contributions from genetic and environmental factors.

The genetic growth curve model has been employed in many subsequent studies in order to determine the genetic and environmental contributions to mean and variance changes of phenotype variables across time (McArdle, 1986; McArdle et al., 1998; McGue & Christensen, 2001; McGue & Christensen, 2002; Reynolds et al., 2002; Finkel et al., 2003; McArdle & Hamagami, 2003; Reynolds et al., 2005). Research employing the genetic growth curve model has focused on cognitive ability and the variables used in these studies were test scores from well-developed measures, measured as continuous variables which meet the assumptions of factor analytic models. For example, McArdle et al. used processing speed; McGue and Christensen used composite scores; and Reynolds et al. used percentage and principal component scores. However, psychological measurements often take the form of ordered categorical variables with a few response categories. Such variables cannot be directly used within the genetic growth curve model due to the violations of assumptions required for factor analytic models (Bollen, 1989; Bollen & Curran, 2006). Given that ordered categorical variables are prevalent forms of psychological measurements, enabling the use of ordered categorical variables within genetic growth curve model is a substantial expansion of developmental behavior genetics studies.

Ordered categorical variables can be incorporated within the biometric growth model by employing latent response variable methods. Directly applying factor analytic models to ordered categorical variables, by treating them as continuous variables, violates the assumptions required for factor analytic models and leads to the incorrect chi-square

tests and biased standard errors (Bollen 1989; Bollen and Curran 2006). However, methods of modeling ordered categorical variables within factor analytic models have been developed from different disciplines such as factor analytic models (Muthén, 1984; Muthén & Muthén, 2002; Takane & de Leeuw, 1987) and the Item Response Theory (Embretson & Reise, 2000; Samejima, 1996). Common for these approaches, observed categorical variables are assumed to be categorizations of underlying continuous variables and the information on the underlying continuous variables are derived from proportions of response categories of observed categorical variables. The method of modeling underlying continuous variables have been employed in behavior genetics studies to incorporate ordered categorical variables (Prescott, 2004; Cho, Wood, & Heath, 2009). In a previous study (Cho, Wood, & Heath, 2009), group differences of response proportions of ordered categorical variables were decomposed into biometric factors by mapping the differences of proportions of response categories between groups onto mean and variance differences of the underlying continuous variables.

In this study, this logic is expanded to longitudinal contexts for behavior genetic analysis of phenotypes measured by ordered categorical variables. In order to model repeatedly measured ordered categorical variables, the genetic growth curve model is applied to continuous variables that are assumed to underlie observed categorical variables. In case of repeatedly measured ordered categorical variables, proportions of response categories vary across time. Thus, modeling the underlying continuous variables is possible by mapping proportional changes of response categories across times onto the mean and variance changes of the underlying continuous variables. This requires further

consideration of model specification and identifications which are more complicated than in cases of analyzing continuous variables.

In the following chapters, descriptions of the proposed model and the results from simulation analyses are provided. Chapter 2 provides theoretical basis of proposed model. The proposed model is described in Chapter 3 which includes the reviews of genetic factor model (Martin & Eaves, 1977; Neale and Cardon 1992), growth curve model and genetic growth curve model. Chapter 3 provides theoretical and conceptual explanations of the mapping longitudinal changes of response proportions onto the mean and variance changes of underlying continuous variables and how the genetic and environmental components are decomposed from these changes. The genetic growth curve model employed in this study is largely based on the model proposed by McArdle (1986) and McArdle et al. (1998). Model specification is detailed in Chapter 3 especially focusing on parameter constraints and identifications. In Chapter 4, the proposed model is applied to generated data sets in order to check its performance in various conditions. Finally, Chapter 5 summarizes the results of simulation and discusses the limitations and further elaborations of the new model.

Chapter 2: THE GENETIC FACTOR AND THE GENETIC GROWTH CURVE MODEL

Overview of the Genetic Factor Model

The genetic factor model is an application of factor analytic models that decomposes genetic and environmental components from the variances of phenotype variables collected from twins. Data from twins are important in behavior genetic studies because twins have naturally controlled genotypes: identical twins (monozygotic, MZ twins) share identical genes and fraternal twins (dizygotic, DZ twins) share half of their genes. In the univariate genetic factor model, variance of a phenotype variable from twins is decomposed into three biometric factors: additive genetic (A), common environmental (C), and unique environmental (E) factors. Let phenotype variables from twins in a pair as Y_1 and Y_2, genetic factor model can be expressed in a matrix form as:

$$\begin{pmatrix} Y_1 \\ Y_2 \end{pmatrix} = \begin{pmatrix} \lambda_A & \lambda_C & \lambda_E & 0 & 0 & 0 \\ 0 & 0 & 0 & \lambda_A & \lambda_C & \lambda_E \end{pmatrix} \begin{pmatrix} A_1 \\ C_1 \\ E_1 \\ A_2 \\ C_2 \\ E_2 \end{pmatrix}. \quad (1)$$

For j-th twin ($j = \{1, 2\}$), factor A_j, C_j, and E_j represent the additive genetic factor, environmental component common to both twins, and environmental component unique to each of twins, respectively. In univariate genetic factor models, phenotype variables do not have residual terms because the E factor cannot be distinguished from residual terms. λ_A, λ_C, and λ_E are the factor loadings from factor A_j, C_j, and E_j, respectively, to phenotype variable Y_j. λ_A, λ_C, and λ_E do not have subscript j because factor loadings are symmetrical

between twins. Factor loadings represent the relative contributions of genetic and environmental factors on phenotype variables.

Genetic and environmental factors are defined by the correlations of these factors between twins. Correlation between additive genetic factors is set to unity for MZ twins and 0.5 for DZ twins because monozygotic twin pairs shares same genotype and dizygotic twin pairs shares half of their genes (Neale & Cardon, 1992, p. 60-68 for the derivation of these correlations). The correlation of common environmental (*C*) factors between twins is set to unity because *C* factor represents the environment common to both twins. Finally, correlation of unique environmental (*E*) factors between twins is set to zero because the *E* factor represent environment that is not shared by twins. Thus the correlation matrix of $(A_1\ C_1\ E_1\ A_2\ C_2\ E_2)^T$ is

$$\text{corr}(A_1\ \ C_1\ \ E_1\ A_2\ \ C_2\ \ E_2)^T = \begin{pmatrix} 1 & & & & & \\ 0 & 1 & & \text{symmetric} & & \\ 0 & 0 & 1 & & & \\ r & 0 & 0 & 1 & & \\ 0 & 1 & 0 & 0 & 1 & \\ 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}, \tag{2}$$

where $r = 1$ for MZ twin pairs and $r = 0.5$ for DZ twin pairs.

Not all parameters can be identified from this model unless constraints on some parameters are applied. In the model in Equation (1), λ's represent relative contributions of genetic and environmental factors to the variance of the phenotype variable. To secure identification of the λ's, means and variances of biometric factors are set to zero and one so that λ's can be estimated without further constraints. Thus the modeled covariance matrix between Y_1 and Y_2 from the model in Equation (1) and (2) is

$$\text{cov}(Y_1, Y_2) = \begin{pmatrix} \lambda_A^2 + \lambda_C^2 + \lambda_E^2 & \lambda_A^2 + \lambda_C^2 \\ \lambda_A^2 + \lambda_C^2 & \lambda_A^2 + \lambda_C^2 + \lambda_E^2 \end{pmatrix} \text{ for MZ twin pairs and}$$

$$\text{cov}(Y_1, Y_2) = \begin{pmatrix} \lambda_A^2 + \lambda_C^2 + \lambda_E^2 & 0.5\lambda_A^2 + \lambda_C^2 \\ 0.5\lambda_A^2 + \lambda_C^2 & \lambda_A^2 + \lambda_C^2 + \lambda_E^2 \end{pmatrix} \text{ for DZ twin pairs.} \quad (3)$$

In Equations (3), the squares of factor loadings represent the relative contributions of genetic and environmental factors to the variance of a phenotype variable. The genetic factor model described above is based on several assumptions. First, no correlations are assumed among additive genetic, common environmental, and unique environmental factors within a twin. Second there is no gene × environment interaction. Third, only an additive genetic factor is considered and any non-additive gene effects, such as dominant gene effects, are not considered. Finally, random mating of parents is assumed. These assumptions are common for multivariate genetic factor models explained below.

More often, psychological constructs are measured by multiple indicator variables rather than by a single variable. Two types of genetic factor models have been developed for phenotypes measured by multiple indicators (Neale & Cardon, 1991). In the independent pathway model (also known as the biometric model), each of multiple indicators are decomposed by genetic and environmental components common to all indicator variables. In the common pathway model (also known as the psychometric model), genetic and environmental components are decomposed from a common latent factor extracted from multiple indicators. For example, with four indicators for a phenotype, Y_{1j} through Y_{4j} for twin j, where $j = \{1, 2\}$, the independent pathway model is represented in a matrix form as below.

$$\begin{pmatrix} Y_{11} \\ Y_{21} \\ Y_{31} \\ Y_{41} \\ Y_{12} \\ Y_{22} \\ Y_{32} \\ Y_{42} \end{pmatrix} = \begin{pmatrix} \lambda_{A1} & \lambda_{C1} & \lambda_{E1} & 0 & 0 & 0 \\ \lambda_{A2} & \lambda_{C2} & \lambda_{E2} & 0 & 0 & 0 \\ \lambda_{A3} & \lambda_{C3} & \lambda_{E3} & 0 & 0 & 0 \\ \lambda_{A4} & \lambda_{C4} & \lambda_{E4} & 0 & 0 & 0 \\ 0 & 0 & 0 & \lambda_{A1} & \lambda_{C1} & \lambda_{E1} \\ 0 & 0 & 0 & \lambda_{A2} & \lambda_{C2} & \lambda_{E2} \\ 0 & 0 & 0 & \lambda_{A3} & \lambda_{C3} & \lambda_{E3} \\ 0 & 0 & 0 & \lambda_{A4} & \lambda_{C4} & \lambda_{E4} \end{pmatrix} \begin{pmatrix} A_1 \\ C_1 \\ E_1 \\ A_2 \\ C_2 \\ E_2 \end{pmatrix} + \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \varepsilon_4 \\ \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \varepsilon_4 \end{pmatrix} \quad (4)$$

Unlike the univariate model, a multivariate genetic factor model can isolate the residual term (ε_p) specific to each variable and the *E* factor common to all phenotype indicators. As in the univariate genetic factor model, biometric factors are scaled to have means of zero and variances of one and factor loadings from biometric factors to indicator variables are estimated without further constraints being applied to factor loadings. Factor loadings represent the relative contributions of *A*, *C*, and *E* factors to the variance of each indicator variable. Since variances of biometric factors are set to one, the covariance structure of biometric factors are defined as correlation matrix as in Equation (2). Thus, from Equations (2) and (4), modeled covariance matrices of Y_{i1} and Y_{i2} ($i = \{1, 2, 3, 4\}$) for MZ and DZ twins are

$$\begin{pmatrix} \lambda_{Ai}^2 + \lambda_{Ci}^2 + \lambda_{Ei}^2 + \theta_i & \lambda_{Ai}^2 + \lambda_{Ci}^2 \\ \lambda_{Ai}^2 + \lambda_{Ci}^2 & \lambda_{Ai}^2 + \lambda_{Ci}^2 + \lambda_{Ei}^2 + \theta_i \end{pmatrix} \text{ for MZ twin pairs and}$$

$$\begin{pmatrix} \lambda_{Ai}^2 + \lambda_{Ci}^2 + \lambda_{Ei}^2 + \theta_i & 0.5\lambda_{Ai}^2 + \lambda_{Ci}^2 \\ 0.5\lambda_{Ai}^2 + \lambda_{Ci}^2 & \lambda_{Ai}^2 + \lambda_{Ci}^2 + \lambda_{Ei}^2 + \theta_i \end{pmatrix} \text{ for DZ twin pairs.}$$

In the common pathway or psychometric model, instead of having independent paths from biometric factors to each variable, a single latent factor extracted from multiple indicators is decomposed into genetic and environmental factors. This type of

model can incorporate psychometric factor structure into the genetic factor model. For example, for a phenotype construct measured by four indicators, Y_{1j} through Y_{4j}, the common pathway model can be represented in a matrix form as:

$$\begin{pmatrix} Y_{11} \\ Y_{21} \\ Y_{31} \\ Y_{41} \\ Y_{12} \\ Y_{22} \\ Y_{32} \\ Y_{42} \end{pmatrix} = \begin{pmatrix} \lambda_1 & 0 \\ \lambda_2 & 0 \\ \lambda_3 & 0 \\ \lambda_4 & 0 \\ 0 & \lambda_1 \\ 0 & \lambda_2 \\ 0 & \lambda_3 \\ 0 & \lambda_4 \end{pmatrix} \begin{pmatrix} L_1 \\ L_2 \end{pmatrix} + \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \varepsilon_4 \\ \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \varepsilon_4 \end{pmatrix}, \text{ where } \begin{pmatrix} L_1 \\ L_2 \end{pmatrix} = \begin{pmatrix} \gamma_A & \gamma_C & \gamma_E & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_A & \gamma_C & \gamma_E \end{pmatrix} \begin{pmatrix} A_1 \\ C_1 \\ E_1 \\ A_2 \\ C_2 \\ E_2 \end{pmatrix}. \quad (5)$$

L_j are, for twin j the latent factors which are measured by the four indicator variables. L_j are decomposed into biometric factors A_j, C_j, and E_j. γ_A, γ_C, and γ_E are the factor loadings from A_j, C_j, and E_j factors, respectively, to factor L_j. With unit variances of biometric factors the modeled covariance matrix between Y_{i1} and Y_{i2} is

$$\begin{pmatrix} \lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 + \lambda_i^2\gamma_E^2 + \theta_i & \lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 \\ \lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 & \lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 + \lambda_i^2\gamma_E^2 + \theta_i \end{pmatrix} \text{ for MZ twin pairs and}$$

$$\begin{pmatrix} \lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 + \lambda_i^2\gamma_E^2 + \theta_i & 0.5\lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 \\ 0.5\lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 & \lambda_i^2\gamma_A^2 + \lambda_i^2\gamma_C^2 + \lambda_i^2\gamma_E^2 + \theta_i \end{pmatrix} \text{ for DZ twin pairs.}$$

Latent factors, L_j, need to be scaled to identify the factor loadings in Equation (5). In factor analysis models, scales of the latent variables are usually reference to one of their indicators of which factor loading is set to one. Alternatively one can set the variances of latent factors to unity and estimate the factor loadings without constraints. Different identification constraints lead to the changes in scales of latent factors and different solutions of parameter estimates, but relative contributions of biometric factors

to the variance of the *L* factors do not change. In both models, the residual of each variable can have an item-specific biometric factor structure. Alternatively, especially when the item specific biometric factor structure is not of interest, allowing covariance of each item between twins, which vary across different types of twins, is sufficient to incorporate item specific covariance structure (Prescott 2004; Cho, Wood, & Heath, 2009).

Overview of the Genetic Growth Curve Model

The growth curve and genetic factor models are integrated in the genetic growth curve model. The genetic growth curve model was proposed by McArdle (1986) (see also McArdle, et al., 1998) and employed in subsequent studies in order to determine the heredity of developmental changes in cognitive abilities (McGue & Christensen, 2001; McGue & Christensen, 2002; Reynolds, Finkel, Gatz, & Pedersen 2002; Finkel, Reynolds, McArdle, Gatz, & Pedersen, 2003; McArdle & Hamagami, 2003; Reynolds, Finkel, McArdle, Gatz, Berg, & Pedersen, 2005).

Data for the genetic growth curve model are multivariate data repeatedly measured from twins. Twins in a pair have parallel repeated measurements. The genetic growth curve model can be considered as a longitudinal extension of the multivariate genetic factor model. Specifically, the genetic growth curve model is in the form of the common pathway model, because common growth factors from repeatedly measured indicator variables are decomposed into biometric factors. To illustrate the genetic growth curve model, let Y_{tj} as a repeatedly measured phenotype variable measured from *j*-th twin (j=$\{1, 2\}$) at time *t*, where $t = \{1, 2, \cdots, T\}$. Genetic growth curve model can be divided into two parts: growth part and biometric part. In the growth part, the change of

repeatedly measured phenotype is captured by growth factors. For example, with $T = 4$, the matrix form of the growth part is

$$\begin{pmatrix} Y_{11} \\ Y_{21} \\ Y_{31} \\ Y_{41} \\ Y_{12} \\ Y_{22} \\ Y_{32} \\ Y_{42} \end{pmatrix} = \begin{pmatrix} 1 & \lambda_1 & 0 & 0 \\ 1 & \lambda_2 & 0 & 0 \\ 1 & \lambda_3 & 0 & 0 \\ 1 & \lambda_4 & 0 & 0 \\ 0 & 0 & 1 & \lambda_1 \\ 0 & 0 & 1 & \lambda_2 \\ 0 & 0 & 1 & \lambda_3 \\ 0 & 0 & 1 & \lambda_4 \end{pmatrix} \begin{pmatrix} I_1 \\ S_1 \\ I_2 \\ S_2 \end{pmatrix} + \begin{pmatrix} \varepsilon_{11} \\ \varepsilon_{21} \\ \varepsilon_{31} \\ \varepsilon_{41} \\ \varepsilon_{12} \\ \varepsilon_{22} \\ \varepsilon_{32} \\ \varepsilon_{42} \end{pmatrix}. \quad (6)$$

In Equation (6), Y_{tj} at each measurement occasion is explained by growth factors I_j and S_j. I_j is the intercept factor common to all occasions of measurements, which is defined by setting all factor loadings for Y_{tj} to one. S_j is a slope factor, which is a rate of change. Factor loading from S_j to Y_{tj}, λ_t, can be set to values representing certain forms of growth trajectories or freed to be estimated with minimal identification constraints. Constraints on λ_t required to identify the growth part of the model is discussed in the following sections. λ_t are constrained equal across twins.

In the biometric part, intercepts and slope factors are decomposed into genetic and environmental factors in the biometric part as expressed in the following equation.

$$\begin{pmatrix} I_1 \\ S_1 \\ I_2 \\ S_2 \end{pmatrix} = \begin{pmatrix} \gamma_{AI} & \gamma_{CI} & \gamma_{EI} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_{AS} & \gamma_{CS} & \gamma_{ES} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \gamma_{AI} & \gamma_{CI} & \gamma_{EI} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_{AS} & \gamma_{CS} & \gamma_{ES} \end{pmatrix} \begin{pmatrix} A_{I1} \\ C_{I1} \\ E_{I1} \\ A_{S1} \\ C_{S1} \\ E_{S1} \\ A_{I2} \\ C_{I2} \\ E_{I2} \\ A_{S2} \\ C_{S2} \\ E_{S2} \end{pmatrix} \quad (7)$$

In Equation (7), A_{Ij}, C_{Ij}, and E_{Ij} are, for the j-th twin, biometric factors, which are additive genetic, common environmental, and unique environmental factors, respectively, of intercept factor I_j. A_{Ij}, C_{Ij}, and E_{Ij} will be referred to as I-biometric factors. A_{Sj}, C_{Sj}, and E_{Sj} are biometric factors for slope factor S_j and will be referred to as S-biometric factors. γ_{AI}, γ_{CI}, and γ_{EI} are factor loadings from I-biometric factors to I_j. γ_{AS}, γ_{CS}, and γ_{ES} are factor loadings from S-biometric factors to S_j. Estimates of factor loadings from biometric factors to growth factors represent the relative contributions of biometric factors to growth factors. Subscript j is omitted from the factor loadings because the factor loadings for both twins in the same pair are set to be equal. In Equation (7) growth factors do not have disturbance terms because unique environmental factor E_j cannot be distinguished from the disturbance term of the growth factors.

As was the case with the models presented earlier, not all parameters in the model in Equations (6) and (7) can be identified without applying further constraints. Parameter constraints required for the identification of the growth curve model also apply for the growth part of the genetic growth curve model in Equation (6). In Equation (6), not all λ_t

and means and elements of variance/covariance matrix of growth factors can be identified simultaneously. Fixing one of the λ_t to zero and another factor loading to any non-zero constant (usually to one) can identify the remaining factor loadings, which are not fixed to constants, as well as the mean vector and elements of variance/covariance matrix of *I* and *S* factors (McArdle, 1986; McArdle & Epstein, 1987). Two fixed factor loadings provide the scales of *I* and *S* factors from which the mean vector and variance/covariance matrix of growth factors and remaining factor loadings are identified.

Although two factor loadings are fixed to constants, any shape of growth trajectory can still be captured with this setting. This is done by estimating the rest of factor loadings which are not fixed to constants. Factor loadings not fixed to constants are estimated proportional to the mean difference between the points at which factor loadings are set to zero and one. The minimal requirement for the number of measurement occasions in this setting is three repeated measurements (Bollen & Curran, 2006). As mentioned earlier, any shape of growth trajectory can be captured, but, for more meaningful interpretation of the *S* factors, certain forms of growth trajectories are often assumed. The most common form of growth trajectory is linear trajectories in which λ_t are set to chronological time corresponding to each measurement occasion. In cases of linear growth, the *S* factor is interpreted as a slope of linear function of repeated measurements, regressed on chronological time. It is also possible to add more growth factors, such as quadratic or cubic slopes, or to specify the slope factor as a parameter for other structured pattern of growth trajectories (McArdle et al., 1998; Neale & McArdle, 2003; Finkel et al., 2005; Reynolds et al., 2005) to accommodate more complicated forms of growth trajectories.

In the biometric part of the genetic growth factor model, even after growth factors are scaled as described above, biometric factors are latent and must be scaled to identify their mean vector and a variance/covariance matrix as well as factor loadings from biometric factors to growth factors, γ's. As in the univariate and multivariate genetic factor models, with means and variances of biometric factors set to zero and one, respectively, a variance/covariance matrix of biometric factors are estimated as a correlation matrix and γcan be estimated without further constraints. The model above implies that the mean changes of Y_{tj} are determined by growth factors, and the individual variabilities of growth factors around their means are decomposed into genetic and environmental components (McArdle, 1986; McArdle et al., 1998). Since means of biometric factors are set to zero, the mean of Y_{tj}, μ_t, is determined by the intercepts of I and S factors, α_I and α_S, respectively, and factor loadings from S factor, λ_t.

$$\mu_{tj} = \alpha_I + \lambda_t \alpha_S \tag{8}$$

The covariance structure among biometric factors is

$$\mathrm{Cov}\begin{pmatrix} A_{I1} \\ C_{I1} \\ E_{I1} \\ A_{S1} \\ C_{S1} \\ E_{S1} \\ A_{I2} \\ C_{I2} \\ E_{I2} \\ A_{S2} \\ C_{S2} \\ E_{S2} \end{pmatrix} = \begin{pmatrix} 1 & & & & & & & & & & & \\ 0 & 1 & & & & & & & & & & \\ 0 & 0 & 1 & & & & & & & & & \\ 0 & 0 & 0 & 1 & & & & & & & & \\ 0 & 0 & 0 & 0 & 1 & & & & & & & \\ 0 & 0 & 0 & 0 & 0 & 1 & & & & & & \\ r & 0 & 0 & 0 & 0 & 0 & 1 & & & & & \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & & & & \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & & & \\ 0 & 0 & 0 & r & 0 & 0 & 0 & 0 & 0 & 1 & & \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix} \text{ symmetric} . \tag{9}$$

In Equation (9), r is the correlation between additive genetic factors between twins. $r = 1$ for MZ twin pairs and $r = 0.5$ for DZ twin pairs. Factor loadings from biometric factors to growth factors, γ's, represent the relative contributions of growth factors to the variances of growth factors and the model-implied variances of Y_{tj} are

$$\text{var}(Y_{tj}) = \gamma_{AI}^2 + \gamma_{CI}^2 + \gamma_{EI}^2 + (\gamma_{AS}\lambda_t)^2 + (\gamma_{CS}\lambda_t)^2 + (\gamma_{ES}\lambda_t)^2 + \theta_{tj} \quad (10)$$

$$\text{cov}(Y_{t1}, Y_{t2}) = \gamma_{AI}^2 r + \gamma_{CI}^2 + \gamma_{AS}^2 r + \gamma_{CS}^2 . \quad (11)$$

Covariances between any two measurement occasions are

$$\text{cov}(Y_{tj}, Y_{uj}) = \gamma_{AI}^2 + \gamma_{CI}^2 + \gamma_{EI}^2 + \gamma_{AS}^2\lambda_t\lambda_u + \gamma_{CS}^2\lambda_t\lambda_u + \gamma_{ES}^2\lambda_t\lambda_u . \quad (12)$$

θ_{tj} is the residual variance of Y_{tj}.

More parameters can be added to the model in Equation (6) through (12). First, the model in Equation (6) through (12) does not include the covariance between I and S factors. Covariance between intercept and slope factors varies depending on the shape of growth trajectories and the centering of time variable (Hancock & Choi, 2006; Rovine & Molenaar, 1998; Wood & Jackson, under review). The covariance between I and S factors can be incorporated into the model by allowing covariances of biometric factors for the I and S factors within twins. Alternatively, McArdle et al. (1998) allowed factor loadings from S-biometric factors to I factor. With this setting, covariances between the I and S factors are captured by the factor loadings from the S-biometric factors to the I and S factors. The factor loadings from the S-biometric factor to the I factor can also be used to test if the same biometric factors operate on both I and S factors. In this study, this alternative setting was used to capture the covariance between the I and S factors, instead of allowing covariances between biometric factors for I and S factors. Second, as in a multivariate genetic factor model, the residuals of Y_{tj} may have item-specific biometric

factor structures. The biometric factor structure of residuals can be included by allowing biometric factors specific to each measurement occasion. Usually, however, those specific biometric components are not of interest and, in those cases, allowing covariances between Y_{t1} and Y_{t1}, which vary between MZ and DZ twin groups, is sufficient to incorporate residual biometric factor structure.

Chapter 3: THE GENETIC GROWTH CURVE MODEL FOR ORDERED CATEGORICAL VARIABLES

Factor Analytic Models with Ordered Categorical Variables

The genetic growth curve model is an application of factor analytic models which requires normally distributed continuous variables. However, measurements in psychology are often in the form of categorical variables with only a few response categories. In the case that response categories are ordered, such as Likert or attitude scales, these categorical variables are assumed to be categorizations of an unobserved continuum. Binary variables can also be regarded as a special case of ordered categorical variables with only two response categories. Even if an underlying continuum is assumed, treating ordered categorical variables as continuous variables, and using them in factor analytic models as such, violates assumptions required for structural equation models (Babakus, Ferguson, & Joreskog, 1987; Bollen, 1989; Johnson & Creech, 1983; Lubke & Muthén, 2004; Olsson, 1979). First, even if the measurement model holds for underlying continuous variables, it does not necessarily holds for the observed continuous variable. Second, the distributions of ordered categorical variables cannot be equal to the distributions of underlying continuous variables, because observed categorical variables are sparse categorization of the underlying continuous variables. Finally, these violations of assumptions lead to the violation of the covariance structure hypothesis. Even though the modeled covariance structure may hold for the covariance matrix of underlying continuous variables, it does not necessarily extend to the covariance matrix of observed categorical variables.

To circumvent these problems, corrective methods of analyzing ordered categorical variables within factor analytic and structural equation models have been developed from different perspectives, including Item Response Theory (Embretson & Reise, 2000; Samejima, 1996) and factor analysis of ordered categorical variables (Muthén, 1984; Muthén & Muthén, 2002; Takane & de Leeuw, 1987). Common to these procedures is providing methods of modeling underlying continuous variables, instead of observed categorical variables, through the proportions of response categories. In order to describe this method, suppose Y^* is a latent continuous variable that underlies corresponding observed ordered categorical indicator variable *Y*. Let *Y* has *C* response categories and assume Y^* measures a single latent factor η, for simplicity of illustration. The measurement model of Y^* is

$$Y^* = \nu + \lambda \eta + \varepsilon \ . \tag{13}$$

ν is the intercept, ε is residual of Y^*, and λ is the factor loading from η to Y^*. From Equation (13), the mean and variance of Y^*, μ^* and σ^{*2}, respectively, are given as:

$$\mu^* = \nu + \lambda \alpha \text{ and } \sigma^{*2} = \lambda^2 \varphi + \theta \ . \tag{14}$$

α and φ are the mean and variance of latent variable η, respectively, and θ is the variance of residual ε. Since the measurement model in Equation (13) holds for Y^*, and not for *Y*, Y^* needs to be linked with *Y*. Since *Y* is assumed to be a categorization of Y^*, the proportions of response categories of *Y* are linked with Y^*, through *C* - 1 thresholds. Thresholds are cut-off scores that categorize Y^* into *Y*.

$$Y = \begin{cases} 1, & \text{if } Y^* \le \tau_1 \\ 2, & \text{if } \tau_1 < Y^* \le \tau_2 \\ \vdots & \\ C-1, & \text{if } \tau_{C-2} < Y^* \le \tau_{C-1} \\ C, & \text{if } \tau_{C-1} < Y^* \end{cases} \tag{15}$$

τ_c is c-th threshold. Figure 1 conceptualizes mapping of Y onto Y^* with four ordered response categories.

This formulation requires assumptions on the distribution function of underlying continuous variable Y^* in order to estimate thresholds and means and variances of underlying continuous variables. Usually, underlying continuous variables are assumed to be distributed as multivariate normal, and thus the marginal distribution of an underlying continuous variable is normal. With the normality assumption on the distribution of Y^*, from Equations (13) through (15), the modeled marginal probability that the response of Y is less than c-th category, given η, is determined as

$$P(Y \le c \mid \eta) = \Phi\left[\frac{\tau_c - (\nu + \lambda\,\eta)}{\sqrt{\theta}}\right], \tag{16}$$

and thus the probability that the response of Y_i is in the c-th category is

$$P(Y = c \mid \eta) = \Phi\left[\frac{\tau_c - (\nu + \lambda\,\eta)}{\sqrt{\theta}}\right] - \Phi\left[\frac{\tau_{c-1} - (\nu + \lambda\,\eta)}{\sqrt{\theta}}\right],$$

where Φ is the probability density function of the standard normal distribution. Sample estimate of $P(Y_i \le c)$ is sample response proportion that Y_i is less or equal to response category c. Bivariate marginal probability of two ordered categorical variables Y_i and Y_k is determined as

$$P(Y_i \leq c\ , Y_k \leq d\ ) = \int_{-\infty}^{(\sigma_i^*)^{-1}(\tau_c - \mu_i^*)} \int_{-\infty}^{(\sigma_k^*)^{-1}(\tau_d - \mu_k^*)} \phi_2(Y_i^*, Y_k^*) dY_i^* dY_k^*,$$

wehre $\phi_2(Y_i^*, Y_k^*)$ is a bivariate standard normal probability density function with correlation parameter between Y_i and Y_k, ρ_{ik}. ρ_{ik} is estimated as a polychoric correlation (or a tetrachoric correlation in the case of dichotomous variables) between a pair of ordered categorical variables.

Even with a normality assumption on the distribution of underlying continuous variables, thresholds, mean, and variance of an underlying continuous variable cannot be simultaneously estimated. The distributions of underlying continuous variables is usually set to standard normal and, from Equation (16), thresholds are estimated as *z*-scores corresponding to the cumulative proportions of response categories. With the assumption of standard normality of Y^*, the residual variance of Y^*, θ, is determined as a residual from σ^{*2} which is set to one.

$$\theta = 1 - \lambda^2 \varphi$$

However, it is not necessary to set the distributions of underlying continuous variables to standard normal with the mean of zero and unit variance. With a normality assumption of underlying continuous variables, their means and variances can be set to any values while thresholds are estimated accordingly. Allowing for the possibility of having the distributions of underlying continuous variables other than standard normal is especially important when analyzing data from multiple groups or repeated measurements. This is because the differences of means and variances of underlying continuous variables between groups or repeated measurements can be estimated, instead of being set to constants, by applying appropriate constraints on thresholds (Bollen & Curran, 2006; Cho,

et al., 2009; Mehta, Neale, & Flay, 2004; Muthén & Asparouhov, 2002). For more detail, an explanation of estimating mean and variance changes across time is included in the following section.

The Genetic Growth Curve Model of Ordered Categorical Variables

The genetic growth curve model and a method of factor analysis of ordered categorical variables are combined to enable the genetic growth curve model to incorporate ordered categorical variables. In order to incorporate ordered categorical variables, the genetic growth curve model is applied to underlying continuous variables. However, as discussed in the previous chapter, the assumption of standard normality on the distributions of underlying continuous variables is not appropriate for modeling repeatedly measured ordered categorical variables. In order to model the change of repeatedly measured ordered categorical variables within the growth curve model, information on the mean changes, as well as covariance structure among underlying continuous variables across time, is required. By assuming the distributions of the underlying continuous variables as standard normal, however, means and variances of underlying continuous variables are set to zero and one, respectively, so that no information exists on mean and variance changes in the underlying continuous variables over time.

When modeling repeatedly measured ordered categorical variables, mean vector and covariance matrix of underlying continuous variables can be estimated based on proportional changes of response categories of observed categorical variables (Bollen & Curran, 2006; Cho, et al., 2009; Mehta, et al., 2004; Muthén & Asparouhov, 2002). In case of repeatedly measured continuous variables, means and variances vary across time.

However, in the case of repeatedly measured ordered categorical variables, the proportions of response categories vary over time. To model the changes of repeatedly measured ordered categorical variables in the growth part of the genetic growth curve model, proportional differences over time should be mapped onto mean and variance differences of underlying continuous variables. However, with a standard normality assumption on the distributions of underlying continuous variables, proportional differences of response categories are captured by threshold differences across time because the distributions of underlying continuous variables are fixed to standard normal, and thresholds are estimated as *z*-scores corresponding to the cumulative proportions of response categories at each time point.

For illustration, let Y_t as a repeatedly measured ordered categorical variable at time t with three response categories. With three waves, let observed response proportions of first, second, and third response categories be 75%, 20%, and 5% for Y_1; 40%, 30%, and 30% for Y_2; and 10% and 20% and 70% for Y_3. With the distributions of Y_t are fixed to standard normal at all waves, thresholds vary as response proportions change over time (Figure 2). There are two thresholds for each variable, because Y_t have three response categories, and thresholds (solid vertical lines in Figure 2) are estimated as *z*-scores corresponding to cumulative proportions of response categories. Thus, for three waves, first and second thresholds $\{\tau_1, \tau_2\}$ are: {0.6744, 1.6449} for Y_1; {-0.2533, 0.6744} for Y_2; and {-1.2816, -0.5244} for Y_3. Even though thresholds change as proportions of response categories change over time, there is no information to be modeled within the growth curve because means and variances of underlying continuous variables are fixed to zero and one, respectively, at all waves.

The information on mean and variance changes of underlying continuous variables can be derived from proportional changes of the response categories such that the growth curve model can be applied (Muthén & Asparouhov, 2002; Mehta et al., 2004; Bollen & Curran, 2006). Unlike in the previous example, in which distributions were fixed and thresholds change as response proportions change, here the differences in means and variances over time can be estimated while the thresholds are fixed to constants. Given that each Y_t has three or more response categories, fixing two thresholds of Y_t provides reference points by which the mean and variance of Y_t^* are estimated. Letting z_{t1} and z_{t2} be two z-scores corresponding to cumulative response proportions of first and second response categories, respectively, of Y_t, mean and standard deviation, μ^*_t and σ^*_t, respectively, of Y_t^* are estimated from following equations.

$$\frac{\tau_1 - \mu_t^*}{\sigma_t^*} = z_{t1} \ , \ \frac{\tau_2 - \mu_t^*}{\sigma_t^*} = z_{t2}$$

τ_1 and τ_2 are two fixed thresholds ($\tau_1 < \tau_2$). Subscript t, which represents t-th measurement occasion, is omitted from τ's because same values of fixed thresholds are used across all waves. Thus, μ_t^* and σ_t^* can be expressed as

$$\mu_t^* = \frac{\tau_1 z_{t2} - \tau_2 z_{t1}}{z_{t2} - z_{t1}} \ , \tag{17}$$

$$\sigma_t^* = \frac{\tau_2 - \tau_1}{z_{t2} - z_{t1}} \text{, and} \tag{18}$$

the covariance between time t and u is

$$\sigma_{tu}^* = \sigma_t^* \rho_{tu} \sigma_u^* . \tag{19}$$

When τ_1 and τ_2 are fixed to constants, the mean vector and covariance matrix can be estimated from Equation (17) through (19) because the cumulative proportions and *z*-scores are given from data. Any two thresholds can be set to any values as long as $\tau_1 < \tau_2$. Commonly, first two thresholds are set to zero and one (Bollen & Curran, 2006; Mehta, et al., 2004).

Figure 3 shows the changes of distributions of underlying continuous variables for the same proportional changes as in Figure 2. Fixing two thresholds, τ_{t1} and τ_{t2} to zero and one, respectively, means (dashed vertical lines) and standard deviations change as: (μ_1^* = -0.6951, σ_1^* = 1.0305) for Y_1^*; (μ_2^* = 0.2731, σ_2^* = 1.0778) for Y_2^*; and (μ_2 = 1.6926, σ_3^* = 1.3207) for Y_3^*. Thus, covariance matrix and mean vector of underlying continuous variables of repeatedly measured ordered categorical variables can be derived from changes of response proportions using the Equations (17) through (19).

In case of binary variables, there is only one threshold for a binary variable, because the number of thresholds is the number of response categories minus one. As seen in Equations (17) and (18), at least two thresholds are needed to estimate the mean and variance of an underlying continuous variable. Thus, in case of binary variables, not both mean and variance of an underlying continuous variable can be estimated in the way explained above. Mean vector of repeatedly measured binary variables can be estimated by setting variances and thresholds of underlying continuous variables to a constant. However, conceptually, assuming constant variances of underlying continuous variables over time are may not be viable since it is not likely that the variances of repeatedly measured variables remain constant over time. Thus, unless further assumption on variances of underlying continuous variables is available, the variances of underlying

continuous variables should not be set to a constant and the method explained in this study is not applicable to binary variables.

Mean and variance changes in underlying continuous variables derived from proportional changes of response categories are modeled within the growth part of the genetic growth curve model in Equation (6) and (7). With four measurement occasions, Y_{1j} through Y_{4j}, of repeated ordered categorical variables, the model is expressed as

$$\begin{pmatrix} Y_{11}^* \\ Y_{21}^* \\ Y_{31}^* \\ Y_{41}^* \\ Y_{12}^* \\ Y_{22}^* \\ Y_{32}^* \\ Y_{42}^* \end{pmatrix} = \begin{pmatrix} 1 & \lambda_1 & 0 & 0 \\ 1 & \lambda_2 & 0 & 0 \\ 1 & \lambda_3 & 0 & 0 \\ 1 & \lambda_4 & 0 & 0 \\ 0 & 0 & 1 & \lambda_1 \\ 0 & 0 & 1 & \lambda_2 \\ 0 & 0 & 1 & \lambda_3 \\ 0 & 0 & 1 & \lambda_4 \end{pmatrix} \begin{pmatrix} I_1 \\ S_1 \\ I_2 \\ S_2 \end{pmatrix} + \begin{pmatrix} \varepsilon_{11}^* \\ \varepsilon_{21}^* \\ \varepsilon_{31}^* \\ \varepsilon_{41}^* \\ \varepsilon_{12}^* \\ \varepsilon_{22}^* \\ \varepsilon_{32}^* \\ \varepsilon_{42}^* \end{pmatrix}. \quad (20)$$

In Equation (20), Y_{tj}^* are the underlying continuous variable of Y_{tj} and ε_{ti}^* are their residuals. I_j and S_j are the intercept and slope factors, respectively, for j-th twin. As explained in Equations (17) and (18), given there are three or more response categories, two fixed thresholds are required to estimate mean and variance changes in the underlying continuous variables. Any pair of thresholds can be chosen to be fixed, but, usually, first two thresholds are set to zero and one at all measurement occasions ($\tau_{11} = \tau_{21} = \tau_{31} = \tau_{41} = 0$ and $\tau_{12} = \tau_{22} = \tau_{32} = \tau_{42} = 1$). τ_{tk} is k-th threshold of Y_{tj}. Twins in the same pair has symmetric parameters, so, selected thresholds are fixed to the same values across twins and across measurement occasions. Parameters in the growth part can be identified with conventional identification constraints on the factor loadings, in which one of λ_t is fixed to zero and another factor loading fixed to any non-zero value

(commonly one) so that remaining factor loadings and the mean vector and covariance matrix of growth factors are identified (McArdle & Epstein, 1987). As in growth curve models, the growth part requires three or more repeated measurements for each twin to identify the model (Bollen & Curran, 2006).

In the biometric part, relative contributions of genetic and environmental factors on growth factors I_j and S_j are estimated as latent variables.

$$\begin{pmatrix} I_1 \\ S_1 \\ I_2 \\ S_2 \end{pmatrix} = \begin{pmatrix} \gamma_{AI} & \gamma_{CI} & \gamma_{EI} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_{AS} & \gamma_{CS} & \gamma_{ES} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \gamma_{AI} & \gamma_{CI} & \gamma_{EI} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_{AS} & \gamma_{CS} & \gamma_{ES} \end{pmatrix} \begin{pmatrix} A_{I1} \\ C_{I1} \\ E_{I1} \\ A_{S1} \\ C_{S1} \\ E_{S1} \\ A_{I2} \\ C_{I2} \\ E_{I2} \\ A_{S2} \\ C_{S2} \\ E_{S2} \end{pmatrix} \quad (21)$$

Biometric factors are set to have means of zero and standard deviations of one so that factor loadings from biometric factors to growth factors are estimated without further constraints. With this setting, mean changes of underlying continuous variables are determined by growth factors and individual variances of growth factors are decomposed into the contributions of biometric factors (McArdle, 1986; McArdle & Hamagami, 2003; McArdle et al., 1998). The mean of y_t^* is determined as,

$$\mu_t^* = \alpha_I + \lambda_t \alpha_S . \quad (22)$$

With the same covariance structure of biometric factors as in Equation (9), model implied variances and covariances between underlying continuous variables are

$$\text{var}(Y_{tj}^*) = \gamma_{AI}^2 + \gamma_{CI}^2 + \gamma_{EI}^2 + \gamma_{AS}^2\lambda_t^2 + \gamma_{CS}^2\lambda_t^2 + \gamma_{ES}^2\lambda_t^2 + \theta_{tj}\,, \tag{23}$$

$$\text{cov}(Y_{tj}^*, Y_{uj}^*) = \gamma_{AI}^2 + \gamma_{CI}^2 + \gamma_{EI}^2 + \gamma_{AS}^2\lambda_t\,\lambda_u + \gamma_{CS}^2\lambda_t\,\lambda_u + \gamma_{ES}^2\lambda_t\,\lambda_u\,, \text{ and} \tag{24}$$

$$\text{cov}(Y_{t1}^*, Y_{t2}^*) = \gamma_{AI}^2 r + \gamma_{CI}^2 + \gamma_{AS}^2 r + \gamma_{CS}^2\,. \tag{25}$$

cov(Y_{tj}^*, Y_{uj}^*) is the covariance between time *t* and *u* and cov(Y_{t1}^*, Y_{t2}^*) is covariance between twins at the same time point. θ_{tj} is the variance of residual ε_{tj}^*. Factor loadings from biometric factors to growth factors represent relative contributions of biometric factors to growth factors, and, since the variances of biometric factors are set to one, the squares of factor loadings from biometric factors to growth factors are the variances of growth factors accounted for by biometric factors. With normality assumption on the distributions of underlying continuous variables, probability of Y_{tj} falls into category *c* given growth factors and biometric factors is

$$\begin{aligned}
&P(y_{tj} = c \mid I_j, S_j, A_{Ij}, C_{Ij}, E_{Ij}, A_{Sj}, C_{Sj}, E_{Sj}) \\
&\quad = P(y_{tj} \le c \mid I_j, S_j, A_{Ij}, C_{Ij}, E_{Ij}, A_{Sj}, C_{Sj}, E_{Sj}) \\
&\qquad - P(y_{tj} \le c-1 \mid I_j, S_j, A_{Ij}, C_{Ij}, E_{Ij}, A_{Sj}, C_{Sj}, E_{Sj}) \\
&= \Phi\left[\frac{\tau_c - \{\kappa_I + \gamma_{AI}A_{Ij} + \gamma_{CI}C_{Ij} + \gamma_{EI}E_{Ij} + \lambda_t\,(\kappa_S + \gamma_{AS}A_{Sj} + \gamma_{CS}C_{Sj} + \gamma_{ES}E_{Sj})\}}{\sqrt{\theta_t^*}}\right] \\
&\quad - \Phi\left[\frac{\tau_{c-1} - \{\kappa_I + \gamma_{AI}A_{Ij} + \gamma_{CI}C_{Ij} + \gamma_{EI}E_{Ij} + \lambda_t\,(\kappa_S + \gamma_{AS}A_{Sj} + \gamma_{CS}C_{Sj} + \gamma_{ES}E_{Sj})\}}{\sqrt{\theta_t^*}}\right].
\end{aligned}$$

Φ is cumulative probability density function of standard normal distribution.

Parameters representing covariance between *I* and *S* factors and residual biometric factor structures can be added. As pointed out in Chapter 2, the covariance between *I* and *S* factors can be incorporated by allowing factor loadings from *S*- biometric factors to I factor (McArdle et al., 1998). These factor loadings can also be used to test if there are common biometric factors that affect both *I* and *S* factors. Denoting the factor loadings

from A_S, C_S, and E_S factors to I factor as γ_{ASI}, γ_{CSI}, and γ_{ESI}, respectively, model implied variances and covariances in Equation (23) through (25) need to be adjusted as follows.

$$\begin{aligned}\text{var}(Y_{tj}^*) = {} & \gamma_{AI}^2 + \gamma_{CI}^2 + \gamma_{EI}^2 + \gamma_{AS}^2\lambda_t^2 + \gamma_{CS}^2\lambda_t^2 + \gamma_{ES}^2\lambda_t^2 \\ & + \gamma_{AIS}^2 + \gamma_{CIS}^2 + \gamma_{EIS}^2 + 2(\gamma_{AIS}\gamma_{AS} + \gamma_{CIS}\gamma_{CS} + \gamma_{EIS}\gamma_{ES}) + \theta_{tj}\end{aligned} \tag{26}$$

$$\begin{aligned}\text{cov}(Y_{tj}^*, Y_{uj}^*) = {} & \gamma_{AI}^2 + \gamma_{CI}^2 + \gamma_{EI}^2 + \gamma_{AS}^2\lambda_t\lambda_u + \gamma_{CS}^2\lambda_t\lambda_u + \gamma_{ES}^2\lambda_t\lambda_u \\ & + \gamma_{AIS}\gamma_{AS}(\lambda_t + \lambda_u) + \gamma_{CIS}\gamma_{CS}(\lambda_t + \lambda_u) + \gamma_{EIS}\gamma_{ES}(\lambda_t + \lambda_u)\end{aligned} \tag{27}$$

$$\text{cov}(Y_{t1}^*, Y_{t2}^*) = \gamma_{AI}^2 r + \gamma_{CI}^2 + \gamma_{AS}^2 r + \gamma_{CS}^2 + \gamma_{AIS}^2 r + \gamma_{AIS}^2 r \tag{28}$$

In addition to the biometric factor structure for the growth factors, residuals of each of the repeated measurements can have biometric factor structure. It is possible to add a biometric factor structure for each residual, which can also be captured by allowing covariances between θ_{t1} and θ_{t2}, which vary across MZ and DZ twins. These covariances can capture biometric factor structures of residuals with fewer parameters than having a biometric factor structure for residuals especially when it is not of interest.

The model proposed above is presented in Figure 4. A path diagram in Figure 4 follows the conventional notation for presenting factor analytic models. Rectangles are observed variables and circles are latent variables. Underlying continuous variables, Y_{tj}^* in circles, are linked with their observed categorical variables, Y_{tj} in rectangles. Single headed arrows represent the regressional relationships and double headed arrows represent correlational relationships. Arrows from each triangle represent the mean/intercept.

The weighted least square is a commonly used estimation method for derived mean vector and a covariance matrix of underlying continuous variables. Most of commonly used estimators, can yield consistent estimates of parameters from derived

polychoric covariance matrix, but it has been pointed out that resulting chi-square tests and standard errors are often inaccurate for some estimators, such as maximum likelihood, generalized least square, and unweighted least square (Bollen, 1989; Bollen & Curran, 2006; Muthén, 1984). A weighted least square with an optimal weight matrix, which is the covariance matrix of the elements of the derived covariance matrix, is a better estimator, but it requires large sample sizes and computational capacity. Alternatives to the optimal weight matrix have been suggested such as the weighted least square using diagonals of optimal weight matrix (Browne, 1984; Jöreskog & Sörbom, 1981; Muthén, du Toit, & Spisic, D. 1997) and the adjusted maximum likelihood method (Jöreskog, Sörbom, du Toit, & du Toit, 1999; Satora, 1992). This requires reasonably smaller sample sizes and less computational resources.

In order to implement this framework, structural equation software is needed that is capable of correctly estimating the parameters from the derived mean vectors and covariance matrix of underlying continuous variables. The software must also allow explicit constraints on thresholds so that appropriate sets of equality constraints can be applied across time and longitudinal changes of mean and variance can be estimated. In this study, Mplus (Muthén & Muthén, 2007) was used to generate and analyze the data sets. In Mplus, the default estimator for ordered categorical variables is weighted least square with a diagonal weight matrix, and standard errors and mean- and variance-adjusted chi-square test statistics that use a full weight matrix (WLSMV) (Muthén & Asparouhov, 2002; Muthén & Muthén, 2007). Mplus also allows explicit constraints on thresholds.

Analyzing ordered categorical variables, Mplus provides two alternative parameterizations of the variances of underlying continuous variables: the Delta and Theta parameterizations. Within the Delta parameterization, the variance of each underlying continuous variable is parameterized by means of scale factor, Δ, which is the inverse of standard deviation of the underlying continuous variable. Using the Delta parameterization, Δ are estimated, and residual variances, denoted as θ, are determined as residuals from the variance of the underlying continuous variable, which is Δ^{-2}.

$$\theta = \Delta^{-2} - \lambda^2 \varphi \tag{29}$$

The correlation ρ_{ik} between two underlying continuous variables, Y_i^* and Y_k^*, is

$$\rho_{ik} = \Delta_i \sigma_{ik} \Delta_k .$$

Scale factors are set to one by default, to identify the model used in single group and cross-sectional analyses. However, in multiple group analyses or longitudinal analyses, it is not necessary to fix scale factors of all variables to a constant, and differences between groups or measurement occasions can be estimated.

Theta parameterization is another parameterization method in Mplus for categorical data analysis. Theta parameterization estimates residual variances, θ, and variances of underlying continuous variables are not estimated and are computed as $\sigma^2 = \Delta^{-2} = \lambda^2 \varphi + \theta$. Delta parameterization is known to have computational advantages over theta parameterization in parameter estimation (Muthén & Asparouhov, 2002) and specifying variance differences of underlying continuous variables is easier in the delta parameterization.

Chapter 4: ANALYSIS OF GENERATED DATA SETS

In this chapter, the proposed model is applied to generated datasets in order to investigate the performance of the model in varying conditions. Simulations began with data sets generated from the base model. The base model is a relatively simple model with rather restrictive conditions that can rarely be satisfied in real data analysis. In later sections the models used to generate data sets were expanded to incorporate more complicated models with increased number of parameters to be estimated. A Monte-Carlo simulation module built in Mplus (version 5, Muthén & Muthén 2007) was used to generate the data sets. The data sets were generated with varying conditions. Some conditions were common to all models used for data generation. The conditions of data generations common to all simulated data sets are shown in Table 1. Table 2 lists the parameters that varied by different conditions of data generations. To generate ordered categorical variables, continuous data were generated from specified conditions, and were categorized using thresholds of $\tau_1 = 0$ and $\tau_2 = 1$, which is in accordance with the assumption of underlying continuous variables.

Simulation 1: The Base Model

In the first set of simulations, data sets were generated from the base model which has the minimum number of parameters to be estimated. Values of the parameter used in base model to generate the data sets follow. 1) The proportions of the variance of *I* factor accounted for by *A*, *C*, and *E* factors were $p_{IA} = 0.5$, $p_{IC} = 0.3$, and $p_{IE} = 0.2$, respectively. 2) The proportions of the variance of *S* factor accounted for by *A*, *C*, and *E* factors were $p_{SA} = 0.5$, $p_{SC} = 0.3$, and $p_{SE} = 0.2$. 3) Correlation between *I* and *S* factors was $\rho_{IS} = 0$. 4) Residual covariances between twins were set to zero. Data sets were generated with four

different sample sizes of 1000, 2000, 3000 and 4000 twin pairs. The same numbers of pairs were assigned to both MZ and DZ twin groups. Continuous datasets were generated first and they were then converted into categorical data using the thresholds $\tau_1 = 0$ and $\tau_2 = 1$.

The base model used to generate the data sets is the simplest model that captures linear growth trajectory, as well as contributions of genetic and environmental factors on growth factors. The analytic model was identical to the model used to generate the data sets. This is a favorable condition of data analysis to yield stable estimations of parameters and their standard errors with minimum sample sizes. The sample sizes were varied as 1000, 2000, 3000, and 4000 twin pairs in order to check the required sample size. Also, changes in the parameter estimates were checked for different values of fixed thresholds. In the real data analyses, the population values of thresholds, that categorize the underlying continuum, cannot be known and arbitrary values of fixed thresholds are used. Since different values of fixed thresholds change the values of parameter estimates, it was important to investigate its effect on heritability estimates.

Before the continuous variables generated from the model were converted into ordered categorical variables, generated data were analyzed in their original continuous forms. The following parameters were estimated in the analytic model: factor loadings from biometric factors to growth factors (γ_{AI}, γ_{CI}, γ_{EI}, γ_{AS}, γ_{CS}, and γ_{ES}), intercepts of growth factors (α_I and α_S), and residual variances (θ_1, θ_2, θ_3, and θ_4). The results from different sample sizes were summarized in Tables 3 through 6.

In Table 3 through 6, the chi-square rejection rate, RMSEA, CFI, and TLI are presented to show overall fit of the analytic model. The chi-square rejection rate is the

proportion of replications in which chi-square values were larger than the 95% quantile of chi-square distribution with the corresponding degree of freedom. If the chi-square distribution is well approximated, chi-square rejection rate should be close to 0.05. Chi-square rejection rates well above 0.05 indicates that the analytic model is rejected in too many replications and chi-square test failed to detect the correct model at $\alpha = 0.05$ level. Means and standard deviations of CFI and TLI across replications were presented. The column labeled as "*Pop. Values*" presents the population values of the parameters used to generate the datasets. The column labeled as "*Est. Avg.*" presents the averages of parameter estimates across replications. If the parameter is estimated without bias, values in "*Est. Avg.*" should be close to the values in the column of "*Pop. Values*". The column labeled as "*Est. SD*" presents the standard deviations of parameter estimates across replications. The standard deviations of parameter estimates are equivalent to standard errors of parameter estimates, given that the number of replications is sufficiently large. The column labeled as "*Average SE*" contains averages of standard errors of the parameter estimates across replications. If the standard errors of parameter estimates were unbiased, the values in the column "*Average SE*" should be close to "*Est. SD*". The column of "*95% Coverage*" presents the proportions of replications in which 95% confidence intervals contain population values. With $\alpha = 0.05$, "*95% coverage*" should be close to 0.95. The column labeled as "*Sig. Coeff.*" shows the proportions of replications in which the hypothesis test, of whether parameter is equal to zero, is rejected. When the population value of a parameter is not equal to zero, values in the column of "*Sig. Coeff.*" estimates the statistical power of detecting non-zero parameters. If the true population value of a parameter is equal to zero, percentage estimates type I error rate

(Muthén and Muthén 2002; Muthén & Muthén 2007). Residual variances, $\{\theta_1, \theta_2, \theta_3, \theta_4\}$, in Tables 3 through 6 were presented only for the first twins in the MZ group. Although the residual variances were not constrained to be equal across twins and across MZ and DZ twin groups, similar patterns were observed across twins and across MZ and DZ twin groups, as such presenting all the residuals in the tables would not be necessary.

In the analysis of the continuous data sets, fit indices indicated that overall fit is within acceptable level. All of the average estimates were very close to the population values used to generate the data sets regardless of sample sizes, which indicated that the parameters estimates were unbiased. The rest of the results indicated desirable properties of parameter estimation. The average standard errors of the parameter estimates were close to the standard deviations of the parameter estimates, except for γ_{CI}, where the average standard error was overestimated when sample size was the smallest (n = 1000; estimation SD was 0.108 and average SE was 0.622). However, given that the percentage of significant coefficients (column "*Sig. Coeff.*") of γ_{CI} is 0.942, which represents the statistical power to detect non-zero parameters, it is likely that overestimated standard error is due to few extreme values of estimated standard errors. This pattern of overestimated standard errors will be examined in the analyses of categorized data in later sections. 95% coverages of parameter estimates were close to 0.95 for all parameters. In the column of "Sig. Coeff.", it can be seen that all parameters were estimated with appropriate levels of power or type I error rates. The results were almost identical from the analysis of the data sets with n = 3000 and with n = 4000, in terms of fit indices and parameter estimations. Overall, the parameter estimates and their standard errors were well estimated using the original form of continuous variables.

Next, the data sets generated from the base model were categorized into ordered categorical variables with three response categories using thresholds $\tau_1 = 0$ and $\tau_2 = 1$. The proposed model was applied to estimate parameters from the categorized data. In the analytic model, the following parameters were estimated: factor loadings from biometric factors to growth factors (γ_{AI}, γ_{CI}, γ_{EI}, γ_{AS}, γ_{CS}, and γ_{ES}), intercepts of growth factors (α_I and α_S), and scale factors of Y_{tj} (Δ_1, Δ_2, Δ_3, and Δ_4). Instead of residual variances being estimated, scale factors, which are the inverses of standard deviation of each variable, were estimated because delta parameterization within Mplus was used, as in Equation (29). As explained in preceding sections, delta parameterization estimates the variances of Y_{jt}^* by means of scale factors, Δ_{tj}, and the residual variances, θ_{tj}, are determined as the residuals from the scale factors given the latent factors. Given the biometric factors and factor loadings from them, the residual variance of Y_{tj}^* is

$$\theta_{tj} = \Delta_{tj}^{-2} - \sqrt{\gamma_{AI}^2 + \gamma_{CI}^2 + \gamma_{EI}^2 + \gamma_{ASI}^2 + \gamma_{CSI}^2 + \gamma_{ESI}^2 + \gamma_{AS}^2\lambda_t^2 + \gamma_{CS}^2\lambda_t^2 + \gamma_{ES}^2\lambda_t^2} \quad . \qquad (30)$$

Computed residual variances were also presented in the tables of results labeled as θ_t, but they do not have standard errors and other properties because they were not estimated parameters.

In Tables 7 through 10, values of fixed thresholds used to analyze the categorized data were same as the values used to categorize continuous data, $\tau_1 = 0$ and $\tau_2 = 1$. Thus, it was expected that parameter estimates from the analysis of categorized variables should be close to their population values and parameter estimates from the analysis of continuous data. Fit indices indicated that the analytic model fits well to the data. In all sample sizes, chi-square rejection rates were lower than 0.05. RMSEAs were within 0.05, the common acceptance criteria. Averages of CFI and TLI were almost perfect with

values of one and nearly no variances. Average estimates were close to their population values indicating that the parameters were successfully estimated without biases. No parameter estimate significantly deviated from its population value. Standard errors of most parameters were well estimated, but standard errors of following parameter estimates deviated from their population values (standard deviations of estimates, column "*Est. SD*") by more than 10%: γ_{ASI}, γ_{CI}, γ_{CSI}, γ_{ESI}, and γ_{CS} when n = 1000; γ_{AI}, γ_{ASI}, γ_{CI}, γ_{CSI}, and γ_{EI} when n = 2000; and γ_{CI} when n = 3000 and n = 4000. Average standard values that deviated from their population values by more than 10% are boldfaced in the Tables 7 through 10.

Given that the proportions of significant coefficients (column "*Sig. Coeff.*"), which represent statistical powers, for the parameters whose average standard errors were overestimated were within acceptable level (larger than 0.8), it is likely that these overestimated averages of standard errors were due to few extreme values of the estimated standard errors. For example, estimates of standard errors of γ_{CI}, when n = 1000, over replications were plotted in Figures 5 and 6. In Figure 5, there were few estimated standard errors, of which values were extremely large. It is highly likely that these values inflated the average estimate of the standard error of γ_{CI} in Table 7.

Looking closer, in Figure 6, the Y axis was rescaled to have a range of 0 to 2. Most of the estimated standard errors were clustered around the horizontal line representing the population value of the standard error of γ_{CI} (the standard deviation of the parameter estimates). However, considerable numbers of standard errors were overestimated to some extent and the distribution of the standard errors of γ_{CI} is positively skewed with a few extreme outliers. Similar patterns were found for other parameters whose standard

errors were overestimated when n = 1000 (γ_{ASI}, γ_{CSI}, γ_{ESI}, and γ_{CS} in Figures 6 through 9, respectively) and when n = 2000 (γ_{AI}, γ_{ASI}, γ_{CI}, γ_{CSI}, and γ_{EI}, figures are not presented). In the analysis of the data sets with n = 3000, just the standard error of γ_{CI} was overestimated with only a few extreme values (Figure 11). The result from the analysis of data sets with n = 4000 yielded almost identical result as the result from the analysis of data sets with n = 3000.

From the result, it can be concluded that at least 3000 pairs of twins are required to obtain stable estimations of standard errors. It should also be noted that, however, even though there were some outliers that led to inflated averages of standard errors of some parameters, the level of statistical power to detect the significant parameters was well controlled within the desired level (> 0.8). Given this result, it would be informing to check the results from the modified analytic models in which unnecessary parameters, of which values were set to zero in the model used to generate the data sets, removed. The estimation of standard errors is usually more stable with the models with fewer parameters to be estimated. In the following analysis, the same data sets used in the Table 7 through 10 were analyzed using the modified analytic model. In the modified analytic model, γ_{ASI}, γ_{CSI}, and γ_{ESI}, whose population values were zero, were not estimated and constrained to zero.

Results of analyses of the data sets, generated from the base model, using the modified analytic model are in Table 11 through 14. Unlike the result in Table 7, only the standard error of γ_{CI} was overestimated even when the sample size was the smallest (n = 1000, Table 11). This was consistent with the results from the analysis of continuous variables. Few extreme values of estimated standard errors inflated the average standard

error (Figure 12). In the analyses of data sets with larger sample sizes (n = 2000, 3000, and 4000; in Table 12 – 14), no inflated averages of standard errors were observed and standard errors of all parameter estimates were very close to the standard deviations of parameter estimates.

These results indicate that the simpler model is more likely to yield stable estimations of standard errors and models with more parameters require larger sample sizes (larger than 3000 pairs of twins) to obtain unbiased estimations of standard errors. Although some anomalies exist on the estimations of standard errors, considering other properties of analysis, including overall fit indices, parameter estimations and their standard errors, statistical powers, and type I error rates, the proposed model performs reasonably well with the data sets generated from the base model. Also, it is important to note that the relative contributions of biometric factors to the variances of the growth factors, which are the squares of the factor loadings from biometric factors to the growth factors, were successfully estimated.

In the next set of simulation analyses, several different sets of fixed thresholds were used in the analytic models, of which values were different from the values used to categorize the continuous datasets. The underlying continuous variables are unobserved and population values of the thresholds cannot be known in real data analyses. In the analysis of ordered categorical variables, thresholds needs to be fixed to arbitrary constants in order to estimate mean and variance changes of underlying continuous variables over time. It is common to set the first and second thresholds to zero and one, respectively. In the previous analysis, because generated datasets used in the first simulation have been categorized using thresholds of zero and one, resulting parameter

estimates using the analytic models with fixed threshold values of zero and one (in Tables 7 through 14) were close to those from the analyses of continuous data sets (Tables 3 through 6). It should be again noted, however, that in real data analysis population values of thresholds cannot be known and that using different thresholds will results in different parameter estimates.

Specifically, changes of the values of fixed thresholds change the locations and scales of the underlying continuous variables and lead to the changes of Δ_{tj}, κ_I, κ_S, and all γ's. This section describes how the changes in thresholds affect these parameter estimates in cases of linear growth, but the results apply to other types of growth trajectories. In cases of linear growth, with minimal identification conditions (i.e. with three measurement occasions and λ_1, λ_2, and λ_3, set to 0, 1, and 2, respectively), means and standard deviations of growth factors are identified as follows (Bollen & Curran 2006).

$$\mu_I = \mu_1^* \tag{31}$$

$$\mu_S = \mu_2^* - \mu_1^* \tag{32}$$

$$\sigma_I^2 = 2\sigma_{12}^* - \sigma_{12}^* \tag{33}$$

$$\sigma_S^2 = \frac{\sigma_{23}^* - \sigma_{13}^*}{2} \tag{34}$$

where σ_{tu}^* is the covariance of the underlying continuous variables between time t and u. From Equations (17), (31) and (32), μ_I and μ_S are

$$\mu_I = \frac{\tau_1 z_{12} - \tau_2 z_{11}}{z_{12} - z_{11}} \text{ and} \tag{35}$$

$$\mu_S = \frac{(\tau_2 - \tau_1)(z_{21} z_{12} - z_{22} z_{11})}{(z_{22} - z_{21})(z_{12} - z_{11})}, \text{ respectively.} \tag{36}$$

The mean of *I* factor is the mean at the first wave, which is computed as in Equation (35), given the proportions of response categories and fixed thresholds. From Equation (35), the mean of *I* factor changes by τ_1 and τ_2, given z_1 and z_2 from data. It can be seen from Equation (36) that, using different thresholds, μ_S changes proportional to the difference between two new thresholds. To derive the variances of *I* and *S* factors, σ^2_I and σ^2_S, respectively, Equation (18) is revisited.

$$\sigma_t^* = \frac{\tau_2 - \tau_1}{z_{t2} - z_{t1}}$$

From Equations (18), (33), and (34), the variances of intercept and slope factors, σ^2_I and σ^2_S, respectively, are

$$\sigma_I^2 = (\tau_2 - \tau_1)^2 \left(\frac{2\rho_{12}}{(z_{11} - z_{12}) - (z_{21} - z_{22})} - \frac{\rho_{13}}{(z_{11} - z_{12}) - (z_{31} - z_{32})} \right) \text{and} \qquad (37)$$

$$\sigma_S^2 = \frac{(\tau_2 - \tau_1)^2}{2} \left(\frac{\rho_{23}}{(z_{21} - z_{22})(z_{31} - z_{32})} - \frac{\rho_{13}}{(z_{11} - z_{12})(z_{31} - z_{32})} \right). \qquad (38)$$

$\rho_{\underline{tu}}$ is the polychoric correlation between *t*-th and *u*-th measurements. From Equation (37) and (38), the standard deviations of *I* and *S* factors are proportional to difference between τ_1 and τ_2. When different sets of fixed thresholds are used, factor loadings from biometric factors to *I* and *S* factors vary proportional to the difference between two fixed thresholds because those factor loadings are proportional to the variances of *I* and *S* factors. In the simulation analysis described in the following sections, the estimates of the factor loadings are compared with the population values correctly adjusted by the changes of the fixed thresholds, as described above.

Two sets of thresholds different from the thresholds used to categorize continuous data were used for the analysis of the same categorized data sets used in Tables 7 through 14. The analytic models were the same as the model used to yield the results in Tables 11 through 14, yet different sets of fixed thresholds were used. Samples sizes were set to 3000 pairs (1500 pairs for each of MZ and DZ twin group), which yielded reliable estimates of the standard errors in previous analyses.

The first set of thresholds was $\tau_1 = 0$ and $\tau_2 = 0.5$ and the results are presented in Table 15. Population values of parameters were adjusted accordingly. In Table 15, as explained in Equations (37) and (38), the factor loadings from biometric factors to growth factors were half of the values of the factor loadings when $\tau_1 = 0$ and $\tau_2 = 1$ because the difference between the new set of thresholds were half of the original set of thresholds. The intercept of *I* factor, α_I, was not changed because the mean of Y_1 did not change with the new threshold values (Equation (31)and (35)). The intercept of *S* factor, α_S, was changed from 1 to 0.5 (Equation (36)). As expected, fit indices were identical to the result using fixed $\tau_1 = 0$ and $\tau_2 = 1$ (Table 13) because location and scale changes of the underlying continuous variables would not affect the overall fit of the model. Estimates of parameters and their standard errors were very close to their population values without noticeable bias. Statistical powers and type I error rates were well controlled within acceptable levels. Generating the data sets, relative contributions of additive genetic, common environmental, and unique environmental factors to the variances of biometric factors were set to 50%, 30%, and 20%, respectively, for both *I* and *S* factors. Although the factor loadings had been changed by changing the values of fixed thresholds, the

relative contributions of biometric factors estimated the same in the result using the fixed values of thresholds $\tau_1 = 0$ and $\tau_2 = 1$.

The result of an analysis using another set of threshold values, $\tau_1 = 1$ and $\tau_2 = 1.5$, yielded the same pattern (Table 16). With this set of threshold values, the intercept of the *I* factor changed to one from zero due to the location changes of underlying continuous variables. Other estimates and fit indices remained identical to the result in Table 15 because the difference between τ_1 and τ_2 did not change. The results in Tables 15 and 16 show that, although different values of fixed thresholds result in different estimates of parameters, the estimates of relative contributions of biometric factors to the variances of growth factors were maintained. This point is critical, because the relative contributions of biometric factors are the most important parameters of the proposed model and any sets of fixed thresholds can be used to correctly estimate relative contributions of biometric factors to growth factors.

Simulation 2: Models with non-zero I-S covariance and residual covariances

In this section, the data sets were generated from more complicated models which incorporate all of the parameters in the model in Figure 4. In addition to the parameters in the base model, the models used to generate datasets in this section contain following parameters: the covariance between *I* and *S* factors by means of factor loadings from *S*-biometric factors to *I* factors (γ_{ASI}, γ_{CSI}, and γ_{ESI}), the residual covariances between twins (θ_{12}), and the factor loadings from *S* factor (λ_3 and λ_4). Sample sizes were set to $n = 4000$ (2000 for each of the MZ and DZ groups) to secure stable estimates of standard errors and $\tau_1 = 0$ and $\tau_2 = 1$ were used to categorize continuous variables. Residual covariances between twins were set to the desired values by means of residual covariances between

twins that vary by zygosity. Generating data sets, biometric factor structure was assumed for residuals of repeated measurements and relative contributions from additive genetic, common environmental, and unique environmental factors were set to 30%, 30%, and 40%, respectively. This setting resulted in a covariance of residuals between twins 0.300 for MZ twin pairs and 0.225 for DZ twin pairs.

The correlation between *I* and *S* factors was set to low ($\rho_{IS} = 0.2$), moderate ($\rho_{IS} = 0.4$), and high ($\rho_{IS} = 0.7$). To set the covariance between *I* and *S* factors, instead of having the covariance between biometric factors for *I* and *S* factors, the model used in data generation and analysis followed McArdle et al.'s (1998) model, which allowed factor loadings from *S*-biometric factors, A_I, C_I, and E_I, to the *I* factor, γ_{ASI}, γ_{CSI}, and γ_{ESI}, respectively. These factor loadings are referred to as γ_{*SI} collectively, in the rest of the paper. γ_{*SI} factor loadings can also be used to test whether there are common biometric factors which affect both *I* and *S* factors, as suggested in McArdle et al (1998). However, specifying *I* and *S* covariance using γ_{*SI} factors is rather complicated in that $\{\gamma_{ASI}, \gamma_{CSI}, \gamma_{ESI}\}$ and $\{\gamma_{AI}, \gamma_{CI}, \gamma_{EI}\}$ change simultaneously depending on the covariance between *I* and *S* factors. In order to set the covariance between *I* and *S* factors at desired values, formulas in Equation (39) were used.

$$\gamma_{ASI} = \frac{\sigma_I \rho_{IS} p_{\rho A}}{\sqrt{p_{SA}}},\ \gamma_{ESI} = \frac{\sigma_I \rho_{IS} p_{\rho C}}{\sqrt{p_{SC}}},\ \text{and}\ \gamma_{ESI} = \frac{\sigma_I \rho_{IS} p_{\rho E}}{\sqrt{p_{SE}}} \tag{39}$$

Given γ_{ASI}, γ_{CSI}, and γ_{ESI}, factor loadings from A_{Ij}, S_{Ij}, and E_{Ij} to the *I* factor, γ_{AI}, γ_{CI}, and γ_{EI} are determined as

$$\gamma_{AI} = \sqrt{p_{IA}\sigma_I^2 - \gamma_{ASI}},\ \gamma_{CI} = \sqrt{p_{IC}\sigma_I^2 - \gamma_{CSI}},\ \text{and}\ \gamma_{EI} = \sqrt{p_{IE}\sigma_I^2 - \gamma_{ESI}}. \tag{40}$$

In Equations (39) and (40), $p_{\rho A}$, $p_{\rho C}$, and $p_{\rho E}$ are the proportions of correlation contributed by correlations between *A*, *C*, and *E* factors. Definitions of other parameters can be found in Table 2. Given the parameters in Table 2, γ_{ASI}, γ_{CSI}, γ_{ESI}, γ_{AI}, γ_{CI}, and γ_{EI} are determined as in Equations (39) and (40). Equations (39) and (40) were derived from following three equations.

$$\sigma_I^2 = \gamma_{AI}^2 + \gamma_{ASI}^2 + \gamma_{CI}^2 + \gamma_{CSI}^2 + \gamma_{EI}^2 + \gamma_{ESI}^2$$

$$\sigma_S^2 = \gamma_{AS}^2 + \gamma_{CS}^2 + \gamma_{ES}^2$$

$$\rho_{IS} = \gamma_{AI}\gamma_{ASI} + \gamma_{CI}\gamma_{CSI} + \gamma_{EI}\gamma_{ESI}$$

In the analytic models, instead of setting the factor loadings from *S* factors to Y_t, λ_t, to constants, the last two factor loadings, λ_3 and λ_4, were estimated while λ_1 and λ_2 were fixed to zero and one, respectively, which are the minimal identification constraints of λ_t (McArdle & Epstein, 1987). Although the λ_t were set to {0, 1, 2, 3} in the models used to generate the data sets, the analytic model can capture any shape of growth trajectories other than linear curve by estimating λ_3 and λ_4. Also, residual covariances between twin pairs were estimated in the analytic model. Residual covariances were constrained equal across repeated measurements and were freed to vary between MZ and DZ twin groups. Residuals of measurements were assumed to have the same biometric factor structures. In order to capture the biometric factor structure for residuals, covariances of residuals between twins were allowed which vary by zygosity.

The results of this analysis are in Tables 17 through 19. Fit indices suggest that the analytic model fits well to the generated data sets. Chi-square test rejection rates indicated that the analytic models were rejected in less than 5% of replications. Other fit

indices, such as CFI, TLI, and RMSEA, were within acceptable levels. Averages estimates of all parameters were close to their population values regardless of the levels of ρ_{IS}. Fewer standard errors of parameter estimates were biased when the correlation between *I* and *S* factors was low (ρ_{IS} = 0.2; Table 17) or moderate (ρ_{IS} = 0.4; Table 18) than when ρ_{IS} was high (ρ_{IS} = 0.7; Table 19). Averages of standard errors that exceeded their population values by more than 10% were presented in boldface in Tables 17 through 19. When ρ_{IS} was low (ρ_{IS} = 0.2; Table 17), average standard errors were overestimated for γ_{AI} (*average SE* = 0.107 and *Estimation SD* = 0.094) and γ_{CI} (*average SE* = 0.158 and *Estimation SD* = 0.158). When ρ_{IS} was moderate (ρ_{IS} = 0.4; Table 18), average standard errors were overestimated for γ_{AI} (*average SE* = 0.145 and *Estimation SD* = 0.126) and γ_{CI} (*average SE* = 0.441 and *Estimation SD* = 0.142). When ρ_{IS} was high (ρ_{IS} = 0.7; Table 19), average standard errors were overestimated for following parameters: γ_{AI} (*average SE* = 0.405 and *Estimation SD* = 0.144), γ_{ASI} (*average SE* = 0.111 and *Estimation SD* = 0.089), γ_{CI} (*average SE* = 0.475 and *Estimation SD* = 0.137), γ_{EI} (*average SE* = 0.324 and *Estimation SD* = 0.090), γ_{ESI} (*average SE* = 0.059 and *Estimation SD* = 0.050) and γ_{AS} (*average SE* = 0.057 and *Estimation SD* = 0.051).

Given the overall results, it is possible that sample size was too small to obtain unbiased estimates of the standard errors. In order to determine the sample size that is sufficient for an unbiased estimation of standard errors, data with different sample sizes were generated and analyzed using the same analytic models used in Tables 17-19. In Figures 12-14, the proportions of the bias of three chosen parameters, γ_{AI}, γ_{CI}, and γ_{EI} (of which estimates of standard errors were especially problematic in Tables 17-19) were plotted against varying sample size. Proportions of bias was computed as

$$\frac{\text{average of estimated } SE}{SD \text{ of parameter estimates}} \times SD \text{ of parameter estimates}.$$

Sample sizes varied by 1000 pairs. In Figures 12-14, it is shown that larger sample sizes were required to obtain unbiased estimates of standard errors as the *I*-*S* correlation increased. At a low *I*-*S* correlation (ρ_{IS} = 0.2; Figure 13), bias of the standard errors of γ_{AI} was maintained within 10% from n = 5000 and biases of γ_{CI} was maintained within 10% from n = 6000. When *I*-*S* correlation was moderate (ρ_{IS} = 0.4; Figure 14), bias of the standard errors of γ_{AI} and γ_{EI} were maintained within 10% from n = 5000, and the bias of γ_{CI} was lower than 10% from n = 11000. Much larger sample sizes were required when *I*-*S* correlation was high (ρ_{IS} = 0.7; Figure 15). Biases of the standard errors were maintained within 10% from n = 17000, and n = 19000 for γ_{EI} and γ_{AI}, respectively. However, for γ_{CI}, sample size of n = 22000 was still not sufficient to obtain the unbiased estimate of the standard error.

In the analysis of this set of generated data sets, statistical powers, shown in the column of "*Sig. Coeff.*", were not at acceptable levels for some non-zero parameters. When ρ_{IS} was low (ρ_{IS} = 0.2; Table 17), statistical powers were not sufficient for γ_{ASI} (% significant coefficients = 0.173), γ_{CSI} (% significant coefficients = 0.061) and γ_{ESI} (% significant coefficients = 0.214). With a moderate level of ρ_{IS} (ρ_{IS} = 0.4; Table 18), statistical powers were below acceptable levels for γ_{ASI} (% significant coefficients = 0.641), γ_{CSI} (% significant coefficients = 0.303) and γ_{ESI} (% significant coefficients = 0.780). When ρ_{IS} level was high (ρ_{IS} = 0.7; Table 19), statistical powers below acceptable levels were observed for γ_{AI} (% significant coefficients = 0.708), γ_{CI} (% significant coefficients = 0.678) and γ_{EI} (% significant coefficients = 0.785), but the statistical

powers of these parameters were close to the acceptable level, unlike the analyses of the data generated with low and moderate levels of ρ_{IS}. The lack of statistical powers of γ_{AI}, γ_{CI}, and γ_{EI}, when ρ_{IS} was high, were likely due to overestimated standard errors given that the estimates of γ_{AI}, γ_{CI}, and γ_{EI} were also accompanied by highly overestimated standard errors.

Factor loadings with insufficient statistical power were the factor loadings to *I* factor from biometric factors, which, as seen from Equations (39) and (40), vary simultaneously depending on *I*-*S* covariance. As *I*-*S* covariance increases $\{\gamma_{ASI}, \gamma_{CSI}, \gamma_{ESI}\}$ become larger relative to $\{\gamma_{AI}, \gamma_{CI}, \gamma_{EI}\}$. As seen from the results in Tables 17 through 19, among $\{\gamma_{ASI}, \gamma_{CSI}, \gamma_{ESI}\}$ and $\{\gamma_{AI}, \gamma_{CI}, \gamma_{EI}\}$, insufficient statistical power was observed for those values that were relatively smaller compared to their counterparts. When ρ_{IS} was low and moderate, the sizes of γ_{ASI}, γ_{CSI}, and γ_{ESI} (of which statistical powers were less than 0.8) were relatively smaller compared to γ_{AI}, γ_{CI}, and γ_{EI}. Similarly, when ρ_{IS} was high, the sizes of γ_{AI}, γ_{CI}, and γ_{EI} become smaller relative to γ_{ASI}, γ_{CSI}, and γ_{ESI}, and the statistical power of γ_{AI}, γ_{CI}, and γ_{EI} were not sufficient. Although the results are not presented, these patterns of insufficient statistical power were not observed in the analysis of the continuous data sets.

McArdle, et al. (1998) suggested that γ_{ASI}, γ_{CSI}, and γ_{ESI} can be used to test whether there are biometric factors that affect both *I* and *S* factors. However, given insufficient statistical powers of these factor loadings in simulation analyses, testing hypotheses regarding these factor loadings could lead to incorrect conclusions. Moreover, removing factor loadings that are tested not statistically different from zero can be detrimental to the parameter estimation and overall fit of the model. In Table 20, the

same data sets used in Table 18 were analyzed using the analytic model with γ_{ASI}, γ_{CSI}, and γ_{ESI}, of which statistical powers were below the acceptable level in Table 18, constrained to zero.

In Table 20, although estimations of standard errors were improved for the remaining parameters (only the standard error of γ_{CS} was biased), fit indices and parameter estimation were much worse than those of Table 18. Chi-square rejection rate was 1.000, which means the analytic model was rejected in all replications. Although no noticeable difference was observed for CFI and TLI (CFI = 0.999, TLI = 0.999), RMSEA was higher than in Table 18 (RMSEA = 0.034). Averages of CFI and TLI were slightly less than one (CFI = 0.999, TLI = 0.999). Also, considerably more parameter estimates (γ_{AI}, γ_{CI}, γ_{AS}, γ_{CS}, γ_{ES}, Δ_1, Δ_3, and Δ_4) were biased. Parameter estimates deviated from their population values more than 10% were presented in boldface in Table 20. Moreover, noticeable changes in the estimates of remaining parameters after removing insignificant parameters may indicate that those parameters should not removed from the model.

The most important objective of the proposed model is to determine the relative contributions of genetic and environmental components to developmental changes. The factor loadings from biometric factors to growth factors estimate these relative contributions. From this perspective, the proposed model was able to successfully recover the relative contributions of genetic and environmental components on growth factors, by yielding unbiased estimates the factor loadings from biometric factors to the growth factors. However, testing the common biometric factor for both *I* and *S* factors using the proposed model, as McArdle et al. (1998) suggested, may lead to incorrect conclusions, due to insufficient statistical power for some of the related parameters. In the next

simulation analysis, an alternative model specification that can improve the estimations of standard errors was investigated.

Simulation 3: Alternative model specification with zero I-S covariance

In this set of simulation analysis, the analytic model with an alternative specification, in which γ_{*SI} factor loadings were set to zero, was used to analyze the same data sets used in Table 19, as a solution for overestimated standard errors and insufficient statistical powers. In the analyses of data sets with non-zero *I-S* covariance (Tables 17-19), biased estimations of standard errors and insufficient statistical powers were found for the parameters that vary by level of *I-S* covariance (γ_{AI}, γ_{SI}, γ_{EI}, γ_{ASI}, γ_{CSI}, and γ_{ESI}). Such anomalies were found for more parameters as *I-S* correlation is high (Table 17-19, and were minimized when *I-S* covariance was zero (Tables 11-14). Given these observations, estimations of standard errors and statistical powers may be improved if the analytic model can be specified with zero covariance between *I* and *S* factors, thus no γ_{*SI} loadings.

Covariance between *I* and *S* factors changes by the location of the reference point for the *I* factor (Hancock & Choi, 2006; Rovine & Molenaar, 1998) and, in case of linear growth curves, the point at which σ_I^2 is minimized and σ_{IS} is zero can be found (Hancock & Choi, 2006). If the model is specified with a constraint of $\sigma_{IS} = 0$ (equivalent to setting γ_{*SI} to zero) while λ_t are freely estimated, λ_t are estimated with the reference point for the *I* factor at which σ_I is minimized and σ_{IS} is zero, even if such point is out of the bound of the time period of repeated measurements. Changes in the location and scale of time measures are reflected by the changes in λ_t. For the same data, different sets of λ_t yield the same estimated mean vector and variance/covariance matrix of repeated

measurements and identical model fits. Thus, the analytic model can be specified with zero *I*-*S* covariance by allowing λ_t is freely estimated. To see if this alternative model specification improves the estimation of standard errors and statistical powers, in this set of simulation analyses, analytic models with this alternative model specification was used to analyze the same data sets used in Table 19 (high *I*-*S* covariance condition, $\rho_{IS} = 0.7$). In Table 19, overestimated standard errors and insufficient statistical powers were more noticeable than in low or moderate *I*-*S* covariance conditions (Table 17-18).

In order to find the reference point for the *I* factor that minimizes σ_I^2 and removes *I*-*S* covariance, the derivation introduced by Hancock and Choi (2006) was used here. In this derivation, the measure of time, λ_t, is expressed as a linear combinations of a *baseline shift coefficient*, *a*, and a *scale coefficient*, *b*.

$$\lambda_t = a + tb,\ t = \{0, 1, 2, \cdots, T\} \tag{41}$$

In Equation (41), a baseline shift coefficient *a* represents the distance between the reference point for *I* factor, where λ_t is set to zero, and the first measurement occasion, in the unit of scale coefficient, *b*. For example, in the case where $\lambda_t = \{0, 1, 2, 3\}$, $a = 0$ and $b = 1$, meaning that the reference point for the *I* factor is the first measurement occasion and the time measure is in unit scale. In the case of $\lambda_t = \{1, 3, 5, 7\}$, $a = 1$ and $b = 2$, meaning that the reference point for *I* factor is at one unit below the first measurement occasion, and the unit of time measure is doubled. Therefore, the point at which σ_{IS} is minimized can be found by finding the corresponding value of *a*.

Intercepts and elements of the variance/covariance matrix of the *I* and *S* factors from linear growth curve models with different sets of λ_t can be converted into one another using corresponding *a* and *b* coefficients. Given a linear growth curve, intercepts

and elements of the variance/covariance matrices of the *I* and *S* factors from two different sets of λ_t with $\{a_1, b_1\}$ and $\{a_2, b_2\}$ have the following relationship (Hancock & Choi, 2006). Let μ_{I1}, μ_{S1}, σ_{I1}^2, σ_{S1}^2, and σ_{IS1} be intercepts and elements of variance/covariance matrix of *I* and *S* factors using $\{a_1, b_1\}$. μ_{I2}, μ_{S2}, σ_{I2}^2, σ_{S2}^2, and σ_{IS2}, corresponding parameters from the analytic model using $\{a_2, b_2\}$, can be computed as follows.

$$\mu_{I2} = \mu_{I1} + \left(a_1 - \frac{b_1}{b_2} a_2 \right) \mu_{S1} \tag{42}$$

$$\mu_{S2} = \frac{b_1}{b_2} \mu_{S1} \tag{43}$$

$$\sigma_{I2}^2 = \sigma_{I1}^2 + 2\left(a_1 - \frac{b_1}{b_2} a_2 \right) \sigma_{IS1} + \left(a_1 - \frac{b_1}{b_2} a_2 \right)^2 \sigma_{S1}^2 \tag{44}$$

$$\sigma_{IS2} = \frac{b_1}{b_2} \sigma_{IS1} + \frac{b_1}{b_2} \left(a_1 - \frac{b_1}{b_2} a_2 \right) \sigma_{S1}^2 \tag{45}$$

$$\sigma_{S2}^2 = \left(\frac{b_1}{b_2} \right)^2 \sigma_{S1}^2 \tag{46}$$

a coefficient that minimizes σ_{I2}^2 can be found by differentiating Equation (44) with respect to *a*. Let a_* as the coefficient *a* that minimizes σ_{I2}^2,

$$a_* = \frac{b_*}{b_1} \frac{\sigma_{IS1}}{\sigma_{S1}^2} + \frac{b_*}{b_1} a_1 \tag{47}$$

In Equation (47), b_* is *b* coefficient coupled with a_*, which needs to be fixed to an arbitrary value in order to obtain a_*.

Let the baseline shift coefficient and scale coefficient in the simulation model a_0 and b_0, respectively. Then, $a_0 = 0$ and $b_0 = 1$ and means and elements of variances/covariance matrix of *I* and *S* factors are designated to be $\mu_{I0} = 0$, $\mu_{S0} = 1$, σ_{I0}^2

= σ_{S0}^2 = 1, and σ_{IS0} = 0.7. Holding $b_* = b_0$ and substituting other parameters in Equation (47), a_* is computed as 0.7 yielding λ_t = {0.7, 1.7, 2.7, 3.7}. This means that the baseline reference point that minimizes σ_{IS} is at 0.7 units below the first measurement occasion. Under this model specification, from Equations (42) through (46), μ_{I*} = -0.7, μ_{S*} = 1, σ_{I*}^2 = 0.51, σ_{S*}^2 = 0.49, and σ_{IS*} = 0. It must be noted that, σ_{IS*} = 0, and thus γ_{*SI} can be set to zero.

Specifying the analytic model, one λ_t needs to be fixed to a constant to secure model identification. Fixing one λ_t to a constant and setting σ_{IS} to zero provides a reference point and a scale of time measure by which rest of λ_t, and intercepts and a variance/covariance matrix of *I* and *S* factors can be estimated. Two analytic models with λ_1 fixed to different values were used to analyze the data sets generated with high *I*-*S* correlation condition (ρ_{IS} = 0.7) used in Table 19. In the first analytic model, λ_1 was fixed at 0.7, which is the value of a_* derived above while *b* coefficient was held at one. Hence the baseline shift coefficient and scale coefficient for the first analytic model were a_1 = 0.7 and b_1 = 1, respectively. Derived values of intercepts and elements of variance/covariance matrix were computed above (μ_{I1} = -0.7, μ_{S1} = 1, σ_{I1}^2 = 0.51, σ_{S1}^2 = 0.49, and σ_{IS1} = 0) and factor loadings from biometric factors were adjusted accordingly.

In the real data analyses, however, it should be noted that the value of a_* cannot be known and the value of fixed λ_t is arbitrary. Changes in the fixed value of λ_t may result in the changes of scale coefficient *b*, which lead to corresponding changes of the values of intercept and elements of variance/covariance matrix of *I* and *S* factors. Despite these changes, the model fit and the reference point for *I* factor do not change, and thus the alternative model specification without γ_{*SI} loadings can still be applied with arbitrary

value of fixed λ_t. The model with an arbitrary value of fixed λ_t was tested in the analysis using the analytic model with λ_1 fixed to one. With this setting the distance between the reference point and the first measurement occasion stretches to one from 0.7, and the baseline shift and scale coefficients change as $a_2 = 1$ and $b_2 = 1/0.7 = 1.429$. With this setting, intercepts and elements of variance/covariance matrix of *I* and *S* factors are adjusted as: $\mu_{I2} = -0.7$, $\mu_{S2} = 0.7$, $\sigma_{I2}^2 = 0.51$, $\sigma_{S2}^2 = 0.49$, and $\sigma_{IS2} = 0$. It needs to be noted that the covariance between *I* and *S* factors is still kept at zero.

Table 21presents the summary of results from the analysis of continuous data, which was generated with high *I*-*S* covariance condition ($\sigma_{IS} = 0.7$), using analytic models with two different constraints on λ_t; $\lambda_1 = 0.7$ and $\lambda_1 = 1$. Population values were adjusted for the corresponding values of λ_1. Fit indices show that analytic models with these different constraints on λ_t fitted equally well to the data. Columns of average estimates and average standard errors show that, in both analytic models, parameter estimates and their standard errors were estimated close to their population values.

Table 22 and 23 are the summary of results from the analyses of categorized data sets using the analytic models with constraints of $\lambda_1 = 0.7$ and $\lambda_1 = 1$, respectively. The analytic models reflected in Tables 22 and 23 are the same as the analytic model used in Table 19, with the exception that γ_{*SI} were removed and λ_1 was fixed to a constant, while the rest of λ_t were freely estimated. Both analytic models, using different fixed values of λ_1, fitted well to the data and fit statistics from both models were identical. Parameters were estimated without noticeable biases from the adjusted population values. Although the reference point for *I* factor is outside the bounds of the measurement occasions, relative contributions of the biometric factors to the variance of the *I* factor were

maintained at the same levels as in the result from the analytic model with a reference point for *I* factor being the first measurement occasion (Table 19). Standard errors were still overestimated for some parameters as average standard errors γ_{AI} and γ_{CI} deviated from their population values by more than10%. However, standard errors of fewer parameters were overestimated compared to the result in Table 19, where standard errors of γ_{AI}, γ_{ASI}, γ_{CI}, γ_{CSI}, γ_{EI}, γ_{ESI}, and γ_{AS} deviated from their population values by more than 10%. Also, it is notable that insufficient statistical power was found only for γ_{CI} in Table 22 and no such lack of statistical power was found in Table 23. These results show that alternative model specification, which can remove σ_{IS}, can improve the estimation of standard errors and statistical powers.

Simulation 4: Data sets with varying levels of heritability

In this section data sets were generated with varying levels of the heritability of the growth factors. In the simulation studies of binary and ordinal data, statistical powers of detecting correct models differed across levels of heritability (Ramakrishnan, Meyer, Goldberg, & Henderson 1996); Kuhnert & Do 2003). In both studies, both the classical univariate behavior genetics model (i.e. the ACE model) and an alternative approach (the Bayesian hierarchical model) did not perform well with low (10-20%) or moderate (40-50%) levels of heritability in terms of detecting correct models. In this set of simulation analyses, heritability was varied as low (20%), moderate (50%), and high (70%) to examine if there are any differences in the statistical powers to detect the correct models and parameter estimations.

The following conditions are common to the models generate the data sets across different levels of heritability. 1) λ_t were set to the values that represent linear growth, {0,

1, 2, 3}, and, in the analytic models, λ_3 and λ_4 were estimated while λ_1 and λ_2 were set to zero and one, respectively. 2) The correlation between *I* and *S* factors were set to 0.4. 3) Sample sizes were $n = 4000$. 4) Residual covariances were set to 0.3 for MZ twin pairs and 0.225 for DZ twin pairs and are estimated in the analytic models. 5) Variances of both *I* and *S* factors were set to unity. What varied across data generations were the relative contributions of *A*, *C*, and *E* factors to the variances of *I* and *S* factors. Heritability was varied by manipulating the contribution of *A* factor. In the low heritability condition, relative proportions of *A*, *C*, and *E* factors for growth factors were set to 20%, 60%, and 20%, respectively. For moderate level of heritability, relative proportions were set to 50%, 30%, and 20%. In the high heritability condition, relative proportions were set to 70%, 20%, and 10%. The factor loadings from the biometric factors to growth factors were set to the values derived from the Equations (39) and (40), considering the *I*-*S* correlation and relative contributions of biometric factors to growth factors.

The results of analyses with varying levels of heritability are in Tables 24 through 26. The patterns of results were similar to those found in *Simulation 2*. Differences in the statistical powers to detect correct models were measured by chi-square rejection rates in this study. Across different heritability conditions, differences in statistical power was not as noticeable as found in Ramakrishnan et al. (1996) and Kuhnert and Do (2003), but there still were minor differences in the rejection rates of the analytic models. At $\alpha = 0.05$ level, the proportion of rejected analytic models was relatively low when heritability was low (20%, χ^2 rejection rate = 0.037; Table 24) compared to the moderate (50%; χ^2 rejection rate = 0.053, Table 25) and high (70%, χ^2 rejection rate = 0.058; Table 26)

heritability conditions. RMSEA, CFI, and TLI indicated a good fit of the analytic model to the generated data sets in all conditions. Estimation of standard errors and statistical powers showed same pattern as those in Simulation 2. Overestimated standard errors were found for the factor loadings to the *I* factor. Insufficient statistical powers were observed for the parameters with relatively smaller effect sizes. Specifically, when *I*-*S* correlation was small ($\rho_{IS} = 0.2$) or moderate ($\rho_{IS} = 0.4$), factor loadings γ_{ASI}, γ_{CSI}, and γ_{ESI}, with insufficient statistical powers, were relatively smaller than factor loadings γ_{AI}, γ_{CI}, and γ_{EI}. On the other hand, when *I*-*S* correlation was high ($\rho_{IS} = 0.7$), statistical powers of γ_{AI}, γ_{CI}, and γ_{EI}, relatively smaller than γ_{ASI}, γ_{CSI}, and γ_{ESI}, were not within acceptable level.

Chapter 5: DISCUSSION AND FUTURE AGENDA

Discussion

In this study, a genetic growth curve model for ordered categorical variables was proposed. This model can be used in determining genetic and environmental influences on developmental changes of phenotypes which are measured by ordered categorical variables. Given that ordered categorical variables are common in psychological measurements, the model proposed in this study is useful to developmental behavior genetics studies. To incorporate ordered categorical variables, proportional differences across repeatedly measured ordered categorical variables were mapped onto mean and variance differences of underlying continuous variables. Growth factors explain the mean and variance changes of underlying continuous variables, in the growth part of genetic growth curve model. In the biometric part, the variances of growth factors are decomposed into biometric factors. From the analyses of simulated data sets, parameter estimates were close to their population values, showing that heritability of growth factors were successfully estimated by the proposed model, even with relatively smaller sample sizes. However, there still remained undesirable properties observed in parameter estimations. Estimations of the standard errors of some parameters tend to be biased due to unstable estimates of standard errors, especially with smaller sample sizes and models with more parameters to be estimated. In addition, statistical powers of some non-zero factor loadings, especially with relatively smaller effect sizes, were not maintained within acceptable level. This may cause difficulty in model modifications.

Unstable estimations of standard errors were observed for the factor loadings from biometric factors to *I* factor. These factor loadings are related to *I*-*S* covariance,

because they vary by the level of *I*-*S* covariance (Equations (39) and (40)). Standard errors of such factor loadings were positively biased, especially when the *I*-*S* correlation was high. When the the *I*-*S* correlation was zero, standard errors were better estimated and only the standard error of γ_{CI} was overestimated, given the sample sizes were sufficiently large (more than $n = 3000$). With a correctly specified model, in which unnecessary factor loadings were constrained to zero, the standard error of only γ_{CI} was biased at the smallest sample size ($n = 1000$). Also, lack of statistical powers of detecting non-zero parameters was observed for the factor loadings from biometric factors to the *I* factor, especially when such factor loadings have relatively small effect sizes. McArdle et al. (1998) suggested the use of factor loadings from the *S*-biometric factors to the *I* factor to test the hypothesis of common biometric factors between the two. However, given that related factor loadings are especially problematic in terms of standard errors and statistical powers, such hypothesis testing may lead to an incorrect conclusion. As seen in Table 20, incorrect model specification led to a high rejection rate of the correct model, from the chi-square test, and biased estimates of parameters.

Given that the factor loadings that vary by the levels of *I*-*S* covariance were especially problematic, an alternative specification of the model, in which *I*-*S* covariance is set to zero, may yield better estimations of standard errors. As a solution for overestimated standard errors and insufficient statistical powers, an alternative model specification with zero covariance between *I* and *S* factors was tested. This alternative model specification can yield an equally well-fitting model while covariance between *I* and *S* factors are set to zero. From the result of the analyses using the analytic models with this alternative specification, fewer parameters had overestimated standard errors

and insufficient statistical powers, compared to the analysis of same data sets using the original analytic model.

Although this alternative model specification has an advantage of providing better estimates of standard errors and more statistical powers, its application can be limited for following reasons. First, the derivation of a_* and other parameters described in Simulation 3 only applies for linear growth curves. For other forms of growth curves, such as quadratic or cubic, a_* and other parameters would need to be derived accordingly and it may not be possible to derive a_* for the growth trajectories without structured forms. More importantly, the *I* factor and its variance decomposition may not have the same interpretation as in the analysis using the original analytic model. In the applications of the growth curve model, the *I* factor is interpreted as the status of a phenotype at the time of interest - often the initial status - at which λ_t is set to zero. With alternative model specification described in Simulation 3, the reference point is estimated and it may not be the point of interest and even out of the bound of measurement occasions. When the reference point for *I* factor is estimated outside the bound of measurement occasions, the *I* factor is the hypothetical status of a phenotype at the estimated reference point, at which the variance of a phenotype is minimized. In that case, although relative contributions of biometric factors were maintained at the estimated reference point (Table 21- 23), variance decomposition of the *I* factor may not be as meaningful as in the original analytic model. Using the analytic models with alternative model specification, the variance decomposition of the *I* factor is on the hypothetical variance of a phenotype at the estimated reference point. Meanwhile, the *S* factor and its

variance decomposition can still be interpreted in the same manner as in the original analytic model.

It must be noted that, analysis of categorized data require relatively large sample sizes. It has been observed that stable estimations of standard errors and the statistical powers to detect some non-zero parameters required relatively larger sample sizes than the sample sizes required in the analyses of continuous data sets. As shown in Tables 11 through 14, analyses of categorized data sets using modified analytic models, in which unnecessary parameters were constrained to zero, required relatively smaller sample sizes than those required in the analyses of the same data sets using the original analytic models. In the analyses of data generated from the models with all parameters (Table 18-20), biases of standard errors and insufficient statistical powers were observed even with relatively a large sample size (n = 4000). Also, required sample sizes are even larger as the *I-S* covariance increases (Figures 12 through 14). Therefore specifying the model without *I-S* covariance, as described in Simulation 3, may also help reducing required sample size.

In order to model the longitudinal changes in the response proportions, two thresholds are fixed, and the information on mean and variance changes of underlying continuous variables is derived from changes in proportions of response categories. This method is equivalent to assuming that the properties of measurements are invariant and the properties of subjects change over time. However, the threshold invariance does not necessarily hold in all cases. It is possible that thresholds changes while means and variances of underlying continuous variables are invariant, or thresholds, means, and

variances of underlying continuous variables change simultaneously. Unless further information is available, this is difficult determine.

There have not been many studies on this topic, but Mehta et al. (2004) have suggested a formula to test the threshold invariance between different measurement occasions. This formula was based on the fact that, when threshold invariance holds, the standard deviation of an underlying continuous variable based on any pair of thresholds should be the same. However, the use of this method to test the thresholds invariance is limited, in that it cannot detect the non-invariance of the thresholds if the thresholds vary additively or proportionally by the same amount for all thresholds at different time points. In such cases, the thresholds invariance cannot be distinguished from mean and variance changes of underlying continuous variables by the formula suggested by Mehta et al. (2004). Also this formula only applies where there are more than two thresholds because two thresholds are required to be constrained equal across time, to derive the mean and variance changes of underlying continuous variables. With more than three response categories, and thus with more than two thresholds, it is possible to estimate the rest of thresholds, and compare models with minimally constrained thresholds and with fully invariant thresholds in order to test partial invariance of thresholds. However, with three response categories, the means and variances of underlying continuous variables are just identified and there are no additional degrees of freedom left to test partial thresholds invariance. Threshold invariance of repeatedly measured ordered categorical variables is an important assumption, and this topic would benefit from further studies.

The described method of modeling repeatedly measured ordered categorical variables cannot be applied to binary variables unless further information is available. To

model proportional changes of response categories across repeated measurements, the mean and variance differences across underlying continuous variables are derived from proportional differences of response categories by fixing two thresholds to constants. For each ordered categorical variables, there are ($C - 1$) thresholds, where C is the number of response categories. Binary variables can be treated as special cases of ordered categorical variables with two response categories, and, since there are two response categories, each binary variable has only a single threshold. In the analysis of ordered categorical variables, two parameters among mean, variance and thresholds should be fixed to constants for each underlying continuous variable in order to estimate the rest of the parameters. Since there is only a single threshold in the case of binary variables, another parameter should also be fixed to a constant. It is possible to constrain the variances of underlying continuous variables to a constant and estimate mean change over time. However, fixing the variances of underlying continuous variables to a constant may not be appropriate for longitudinal data, in that it is not reasonable to assume constant variance over time. Thus, unless further information is available on the variances of underlying continuous variables over time, longitudinal binary variables cannot be modeled by fixing their variances to a constant.

In the genetic growth curve model, the interpretations of growth factors are more important than in other contexts, because individual variation of growth factors are decomposed into biometric factors. In case of linear growth curves, in which λ_t are fixed to the values representing chronological time, the interpretations of growth factors are straightforward. The I factor is the initial status of the measured phenotype and the S factor is the rate of the change. The entire growth trajectory can be captured by these two

growth factors, and biometric factor decompositions have meaningful interpretation. However, a very limited range of growth trajectories has linear form of growth.

With the minimal identification constraints on factor loadings, λ_t, fixing one of λ_t to zero and another to a non-zero constant, any shape of growth trajectory can be captured by estimating the λ_t that are not fixed to constants (McArdle, 1986; McArdle & Epstein, 1987; McArdle, et al., 1998). With this setting, the *I* factor is the status of the phenotype at the point where λ_t is set to zero and the *S* factor is the difference between the time points where λ_t is zero and λ_t is one. In order to describe the growth trajectory with this setting, not only growth factors but also estimated factor loadings should be considered. In the biometric part, however, individual variability of growth factors is decomposed into biometric factors, but the variabilities of λ_t are not considered.

More complicated growth trajectories than linear growth can be incorporated without estimating λ_t. Nonlinear patterns of growth trajectories can be incorporated by including factors for quadratic or cubic curves (Finkel et al., 2005; Reynolds et al., 2005). Growth factors for piecewise growth (Li, Duncan, Duncan, & Hops, 2001; Chou, Yang, Pentz, & Hser, 2004) or practice effect (McArdle et al., 1998) can also be included to incorporate different patterns of growth at different periods of time. Neale and McArdle (2000) proposed a method of modeling complicated growth patterns by utilizing structured factor loadings. They characterized typical patterns of human growth with three parameters: initial status, rate of change, and an asymptote. These parameters are estimated as latent factors, defined by factor loadings from them to Y_t fixed to the structured values that represent initial status, rate of change, and asymptote. This method is promising, because typical human growth patterns are described by few parameters,

and each growth factor has a straightforward interpretation that allows more meaningful biometric factor decomposition.

Future Agenda

The model proposed in this study has been focused on phenotype behaviors measured by a single indicator variable at each measurement occasion. However, it is common that psychological measurements consist of multiple indicators for a phenotype construct, and thus incorporating multiple indicators is important in studying psychological phenotypes. Hence one important expansion of the proposed model will be to incorporate multiple indicators for a phenotype behavior, at each measurement occasion.

Within behavior genetics studies, phenotypes measured by multiple indicators have frequently been analyzed with univariate model, by using summary scores such as sums or means. However, it has been pointed out that using summary scores can yield biased parameter estimates, especially when the factorial invariance between twins does not hold (Neale, Lubke, Aggen, & Dolan, 2005). With multiple indicators for a phenotype, the presence of factorial invariance between twins, as well as across measurement occasions, is a testable hypothesis. Moreover, it has also been pointed out that the growth model with multiple indicators has advantages, in that it allows the separation of measurement errors from time-dependent disturbance terms (Bollen & Curran, 2006; Duncan & Duncan, 1996; Ferrer, Balluerka, & Widaman, 2008; McAardle, 1988).

Incorporating multiple ordered categorical indicators within the proposed model involves modification of the growth part of the model. Several studies have discussed the use of multiple indicators in the growth curve model (Bollen & Curran, 2006; Duncan & Duncan, 1996; Ferrer, Balluerka, & Widaman, 2008; McAardle, 1988), but no research

has been focused on multiple ordered categorical indicators of a phenotype behavior. Thus, rather than describing general issues in the use of multiple indicators within the growth curve model, this section focuses on issues in incorporating multiple ordered categorical indicators.

As stated above, using multiple ordered categorical indicators in the proposed model involves modification of the growth part of the proposed model. There are mainly two types of growth curve models of multiple indicators: the curves-of-factors and the factors-of-curves (Duncan & Duncan, 1996; McAardle, 1988). In the curves-of-factors model, also known as second order growth model, the growth curve model is applied to the factors extracted from multiple indicators. The factors-of-curve model estimates common factors from the separate growth factors of each of the multiple indicators. The curve-of-factor model is more common form of multiple indicator growth curve model, because it conforms to psychometric factor structures. The next section focuses on this form of multiple indicator growth curve model.

Unlike the growth curve model with continuous indicators, modeling ordered categorical variables requires additional considerations regarding the model identification and factorial invariance in that underlying continuous variables are modeled through thresholds and response proportions. In the second order growth curve model, parallel factors are extracted across measurement occasions from repeatedly measured indicator variables. Identification constraints should allow estimations of the mean vector and variance/covariance matrix of parallel factors, and tests of factorial invariance across measurement occasions.

Relevant discussions can be found in Millsap & Yun-Tein (2004) and Cho, Wood & Heath (2009), in the context of multiple group factor analysis of ordered categorical variables. Millsap & Yun-Tein (2004) discussed factorial invariance across groups, in general multiple group factor analysis of ordered categorical variables. They also derived minimal identification constraints that enable estimations of differences of factor means and variances across groups. Cho, Wood & Heath (2009) extended Millsap & Yun-Tein's study to behavior genetics models and proposed a model that decomposes group differences of phenotypes measured by ordered categorical variables. They derived minimal identification conditions specific to multiple group genetic factor analysis of ordered categorical variables. The model specified with minimal identification constraints can be compared with more restricted models, in which more parameters are constrained across groups, to test factorial invariance across groups. Although those studies focused on multiple group analyses, the same logic is applicable across time in a longitudinal context, because, in the second order growth models, parallel factors are extracted from repeatedly measured multiple indicators. Even though Millsap and Yun-Tein (2004) and Cho, Wood and Heath (2009) provided useful discussions that can be applied to the second order growth curve models with multiple ordered categorical indicators, there have been no studies that specifically discussed second order growth curve models with ordinal indicators and this is an important topic that requires further studies.

The proposed model has yet to be tested using the data sets generated from more realistic conditions, especially with varying patterns of missing data and sparse cells. First of all, analyzing data generated with varying patterns of missing, including patterns of missing data that violates the assumption of missing at random, would be informative.

Generated data sets used in the simulation analysis comprised complete data with sufficient counts of response categories at all occasions. In longitudinal data analyses, however, attrition of participants is common. Also, patterns of missing data can be more complicated in the longitudinal data collected from twins. Twin pairs may not always have parallel measurements, due to the attrition and/or missing data of one of twins. In the analysis of ordered categorical variables, response categories with too few counts can also complicate the estimation of parameters in the model. The impact of sparse cells in the analysis of ordered categorical variables has not been of much interest, especially in the context of longitudinal data analysis. Sparse cells can be more problematic in longitudinal data analyses when there are radical changes over time in the distributions of underlying continuous variables. When the distribution of an underlying continuous variables representing one time point deviates from the distribution at another point of time, with fixed thresholds, it is possible that some response categories may not have sufficient counts which may prevent stable estimations of parameters.

Given that many psychological measurements collect ordered categorical variables, the ability to incorporate such variables reflects substantial expansion within developmental behavior genetics studies. Any phenotype behavior repeatedly measured from twins, by ordered categorical variables, can benefit from this study. The proposed model has yet to be elaborated to incorporate more complicated situations, the model and the results from the simulation analysis have provided the necessary basis for further elaboration. In future studies, the proposed model will be applied to newly available real data, since data with varying real conditions will help to check the performance of the model. Overall, necessary foundation has been established to test the proposed model

using real data and to elaborate the proposed model to incorporate real-life data complications into the analysis, making the model an effective tool for longitudinal behavior genetic studies.

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Figure 1. Mapping of response proportions of observed categorical variable *Y* onto underlying continuous variables Y^*

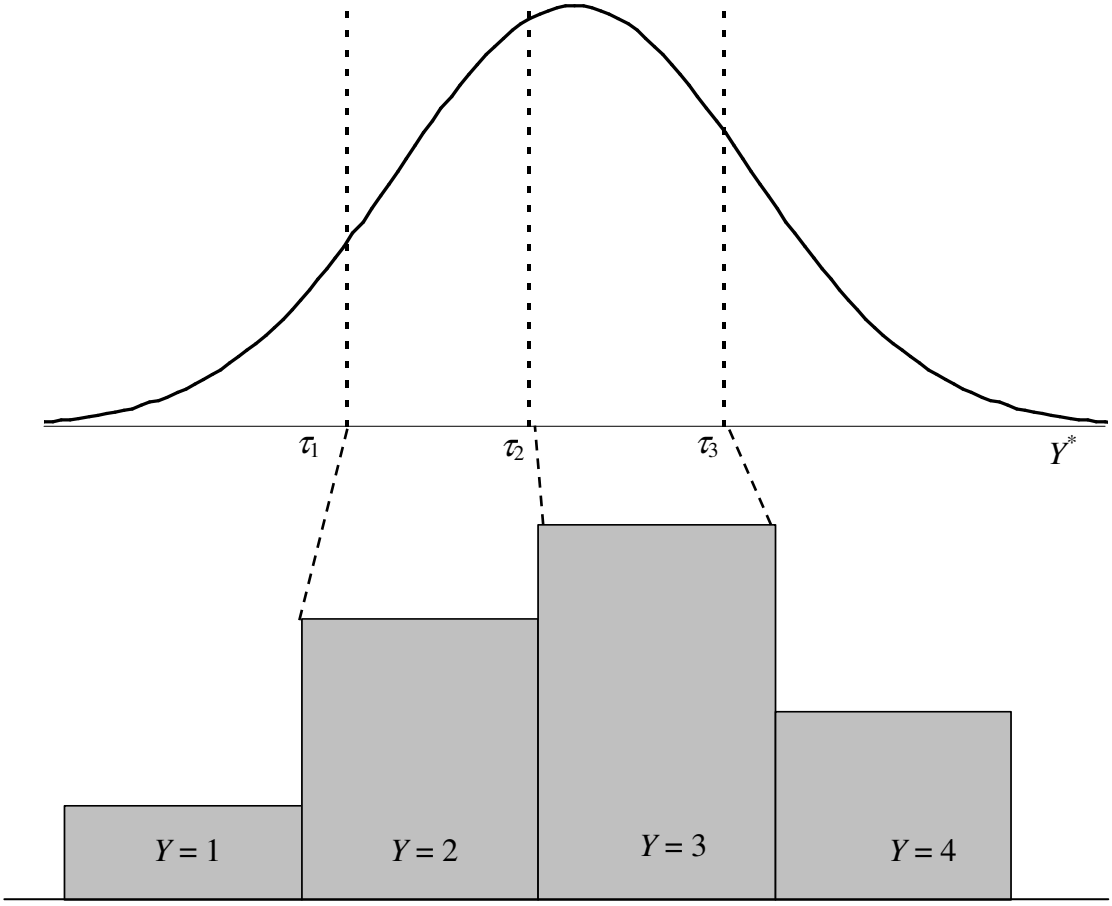

Figure 2. The change of thresholds by the changes of response proportions, while distributions of underlying continuous variables are fixed to standard normal.

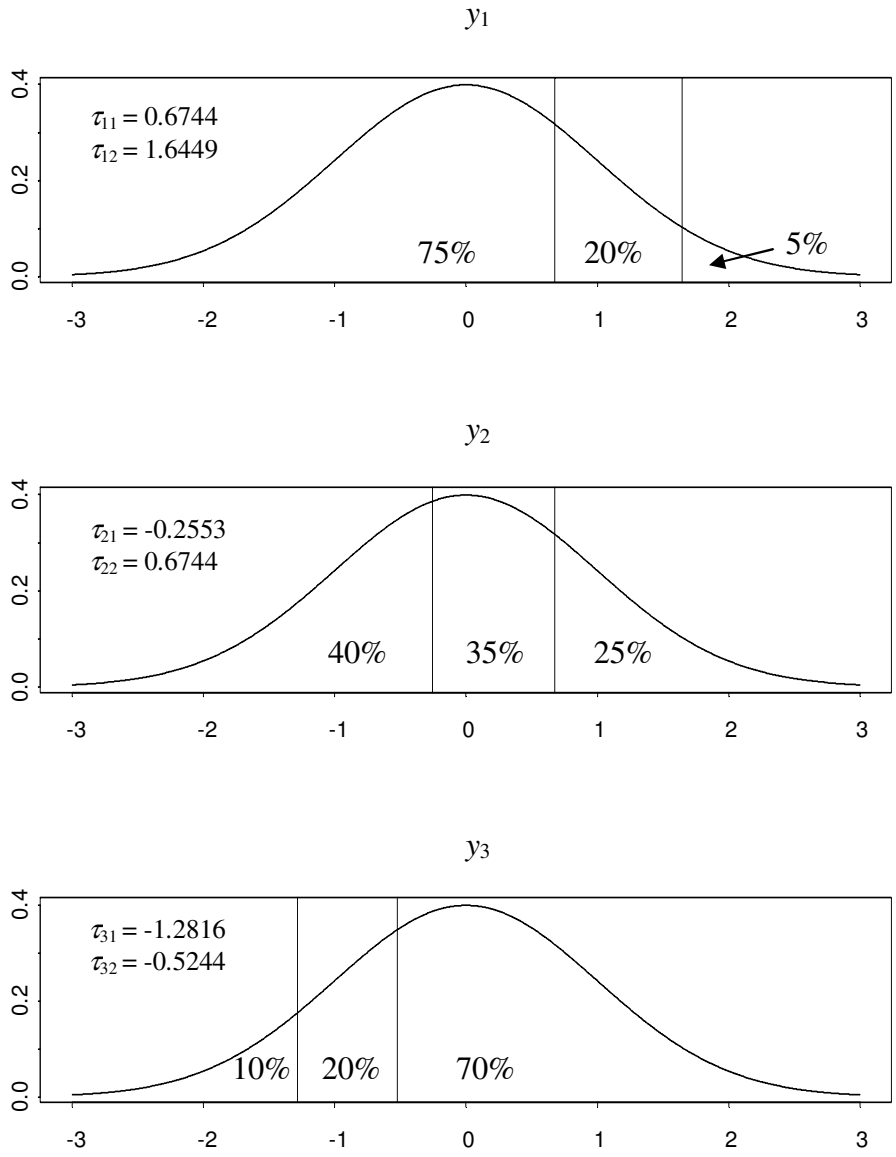

Figure 3. The change of means and variances of underlying continuous variables by the change of response proportions of observed categorical variables changes, while two thresholds are fixed to $\{\tau_1 = 0,\ \tau_2 = 1\}$.

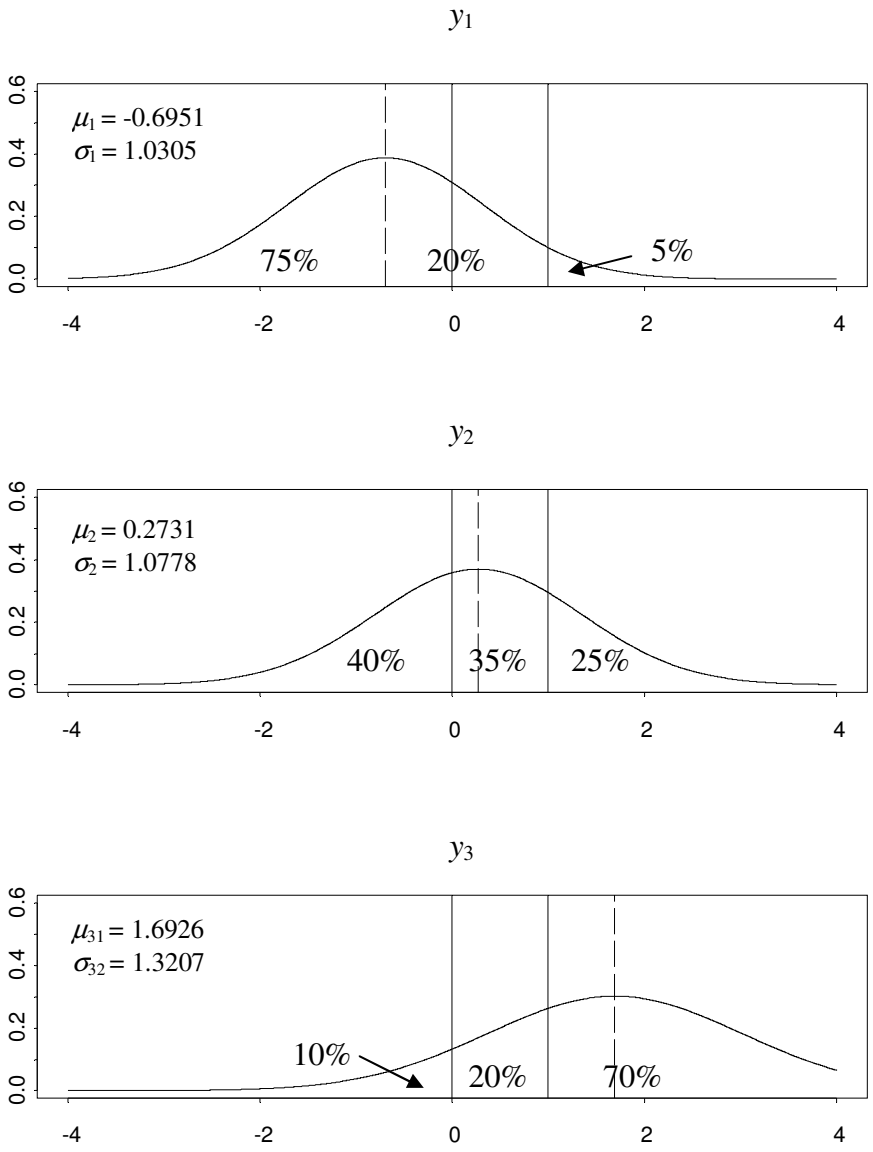

Figure 4. The Path diagram of genetic growth curve model of ordered categorical variables in Equations (23) and (24).

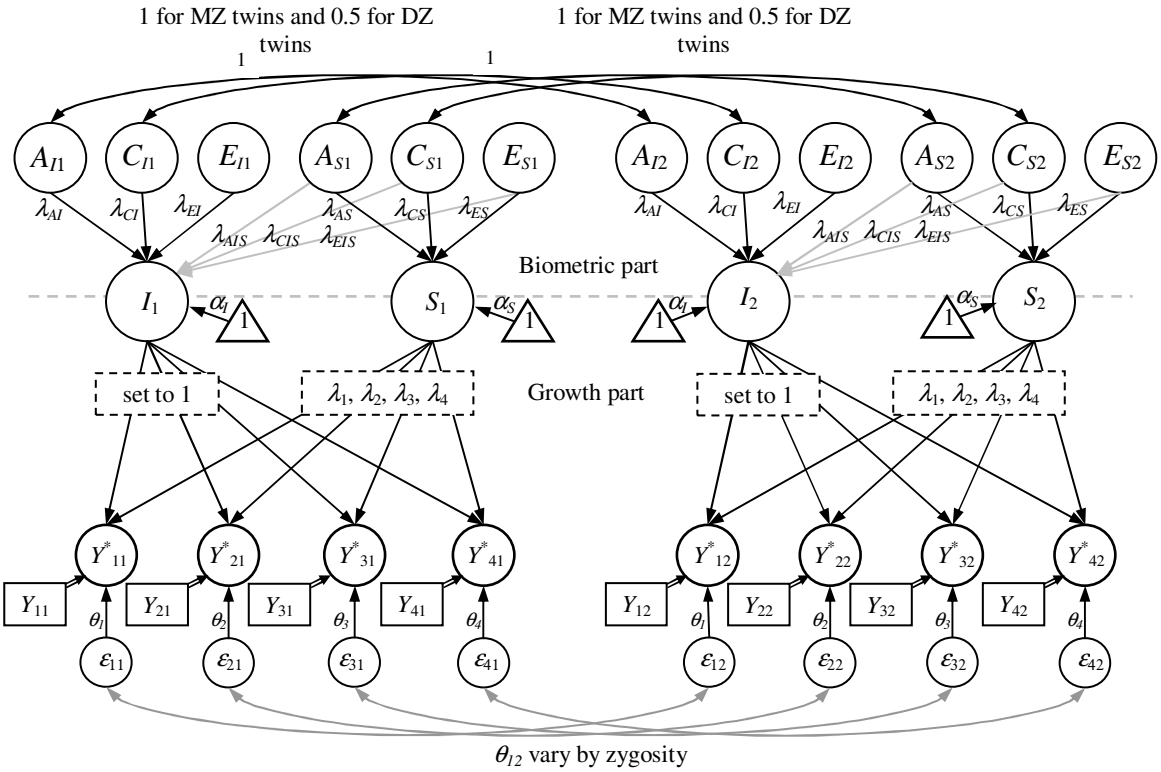

Figure 5. Estimated standard errors of γ_{CI} (n = 1000) by replications.

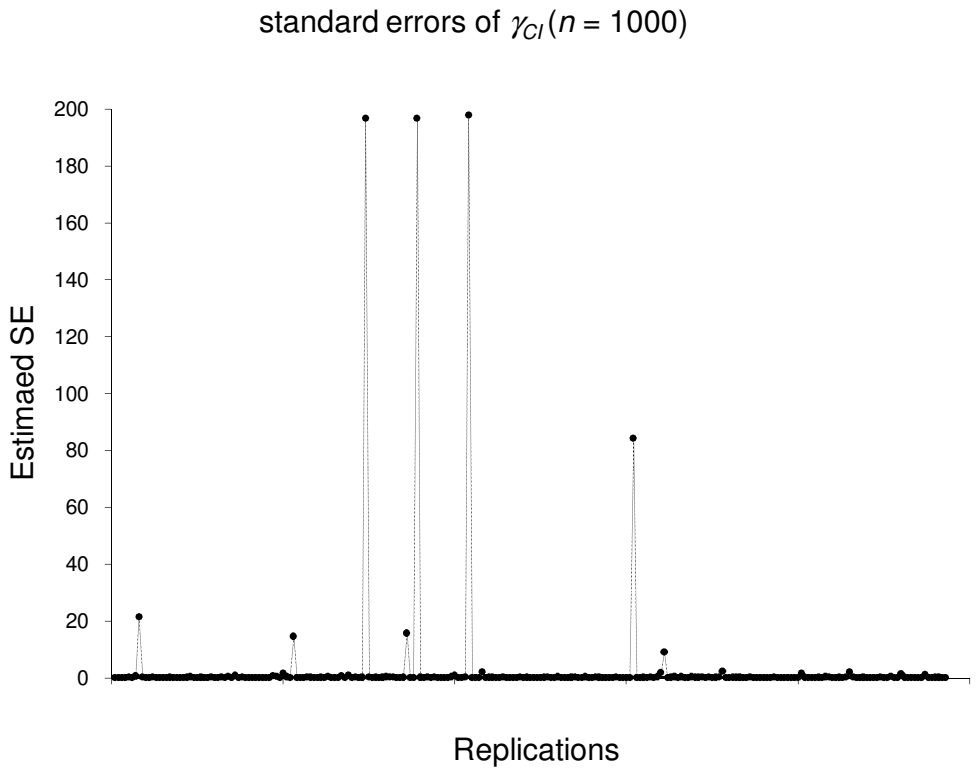

Figure 6. Estimated standard errors of γ_{CI} (n = 1000) by replications with differently scaled Y axis: ranges from 0 to 2.

Note: Horizontal line is the SD of the estimates of γ_{CI} over replications (0.149), which is the population value of standard errors.

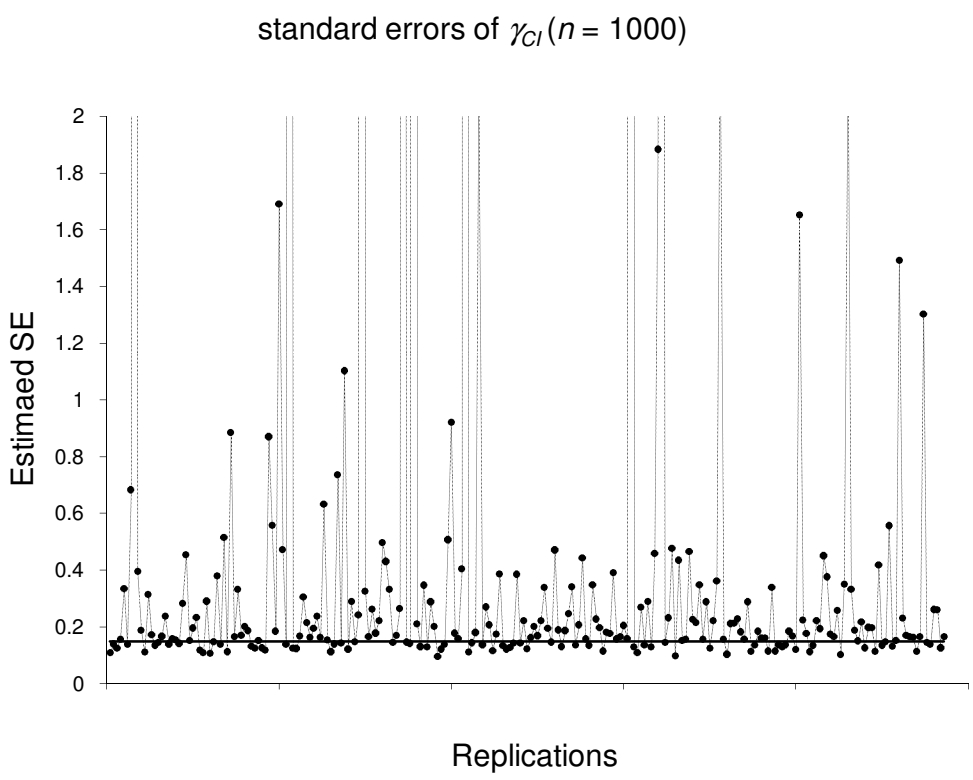

Figure 7. Estimated standard errors of γ_{ASI} (n = 1000) by replications.

Note: Horizontal line is the SD of the estimates of γ_{ASI} over replications (0.220), which is the population value of standard errors.

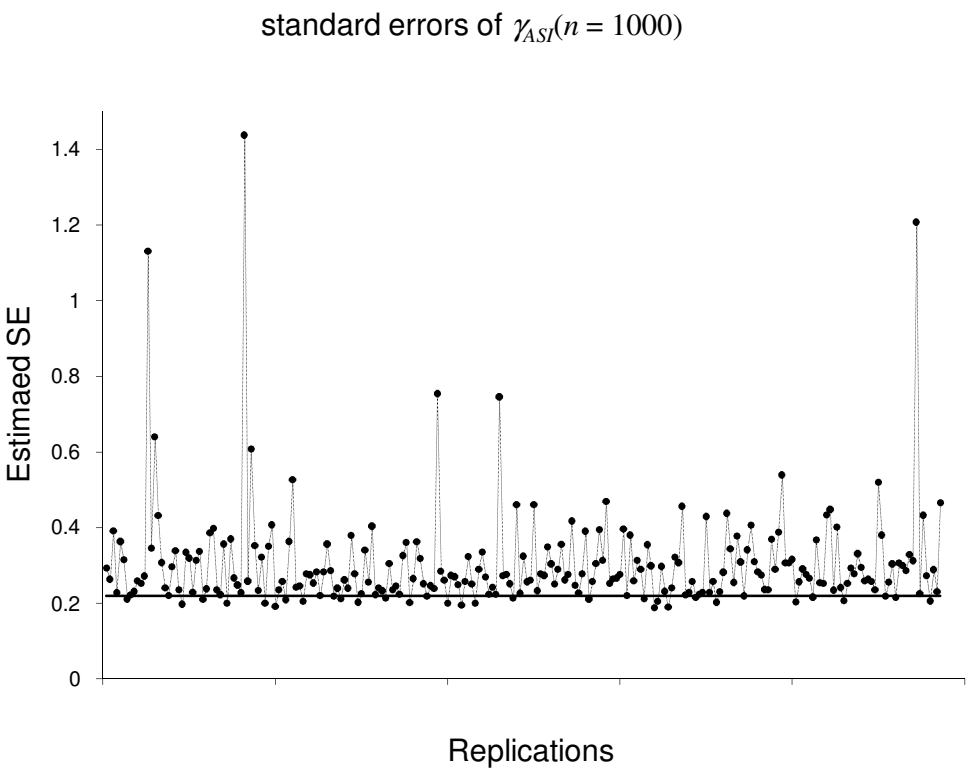

Figure 8. Estimated standard errors of γ_{CSI} (n = 1000) by replications.

Note: Horizontal line is the SD of the estimates of γ_{ASI} over replications (0.223), which is the population value of standard errors.

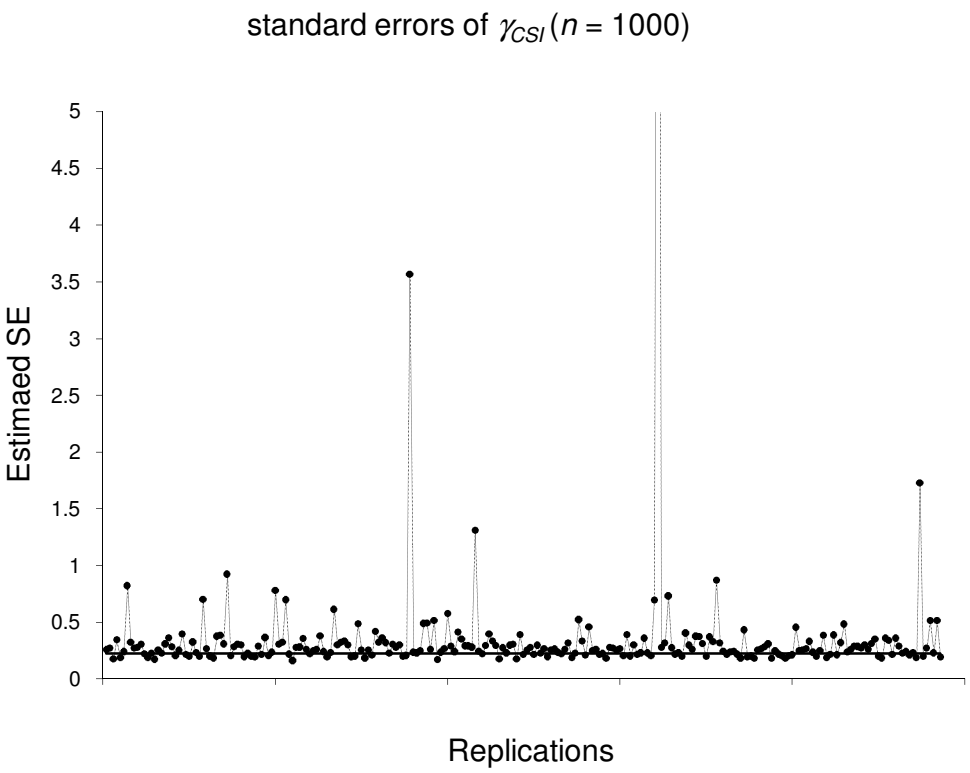

Figure 9. Estimated standard errors of γ_{ESI} (n = 1000) by replications.

Note: Horizontal line is the SD of the estimates of γ_{ASI} over replications (0.127), which is the population value of standard errors.

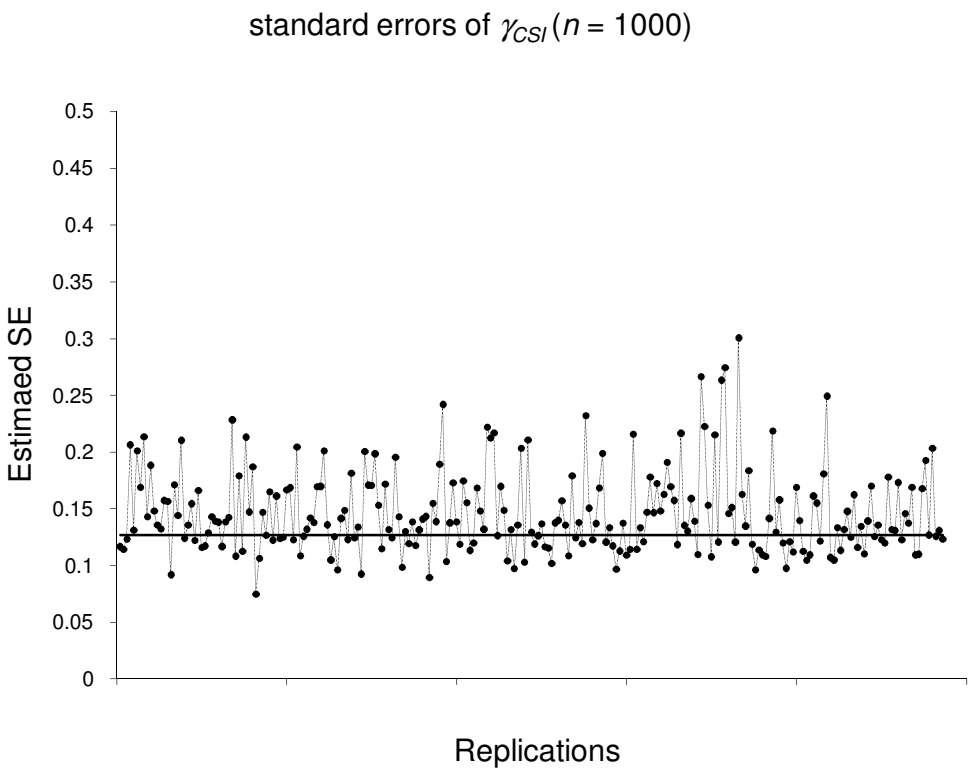

Figure 10. Estimated standard errors of γ_{CSI} (n = 1000) by replications.

Note: Horizontal line is the SD of the estimates of γ_{ASI} over replications (0.136), which is the population value of standard errors.

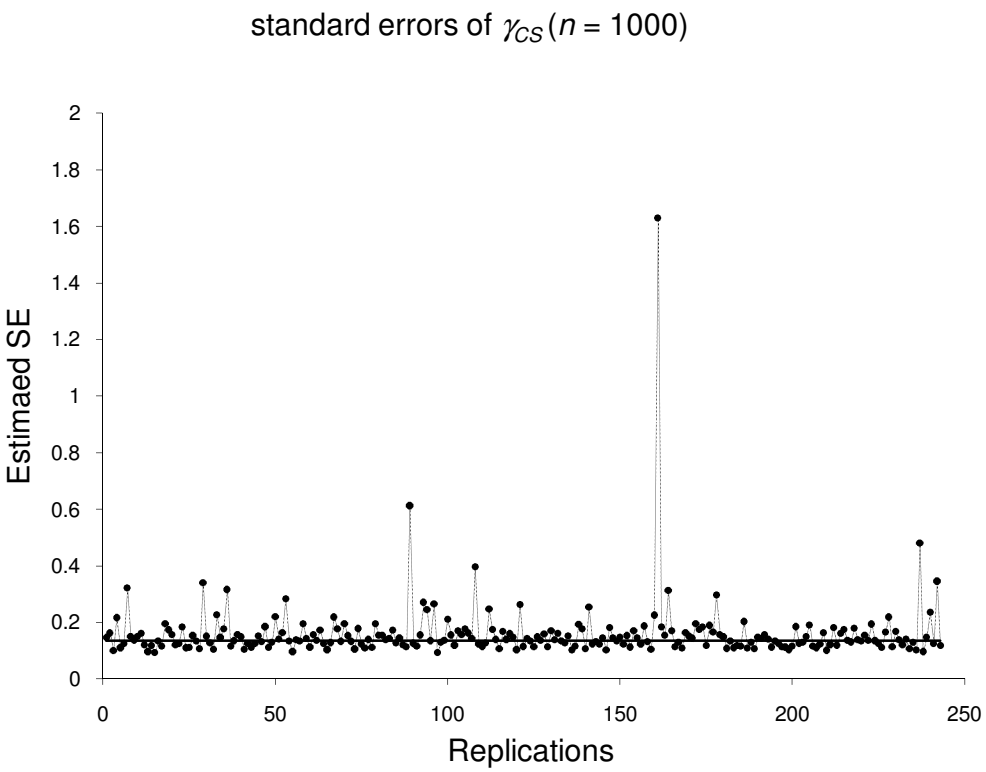

Figure 11. Estimated standard errors of γ_{CI} (n = 3000) by replications.

Note: Horizontal line is the SD of the estimates of γ_{ASI} over replications (0.112), which is the population value of standard errors.

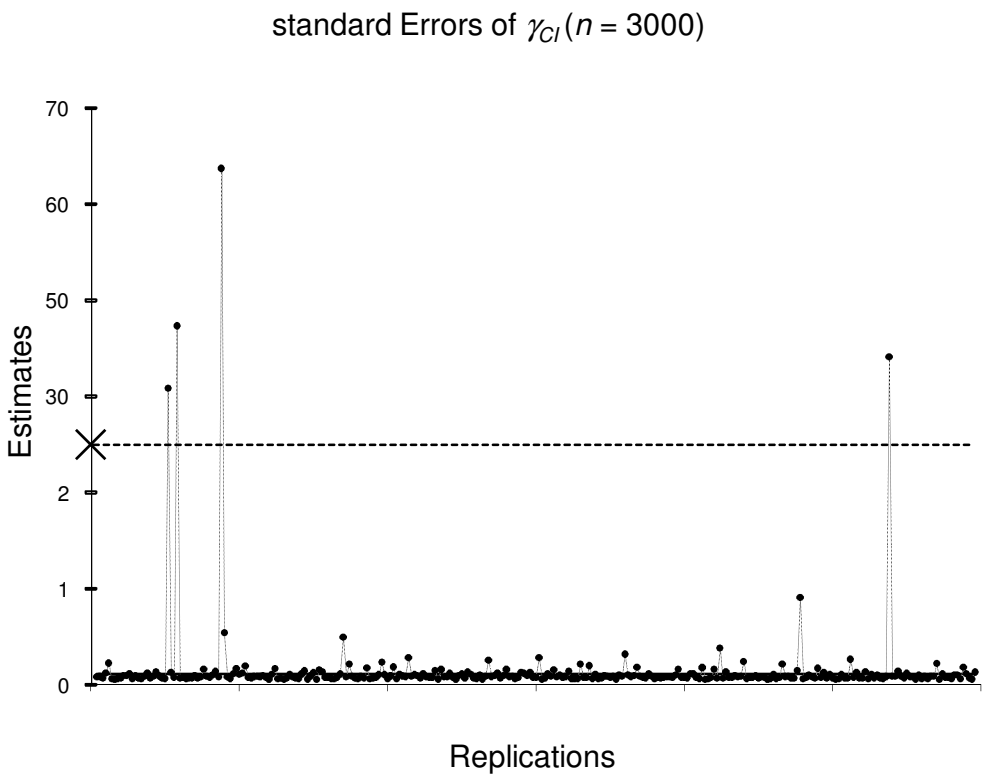

Figure 12. Estimated standard errors of γ_{CI} (n = 1000) by replications from the modified analytic model.

Note: Horizontal line is the SD of the estimates of γ_{ASI} over replications (0.149), which is the population value of standard errors.

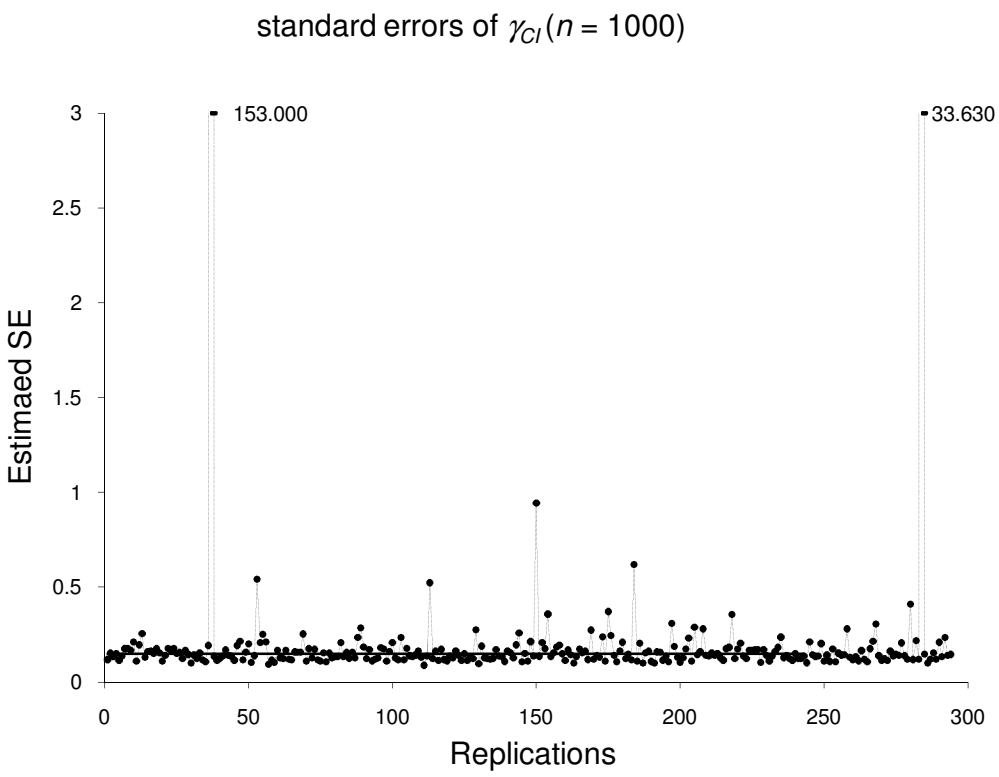

Figure 13. Biases of standard errors when *I-S* correlation was low (ρ_{IS} = 0.2).

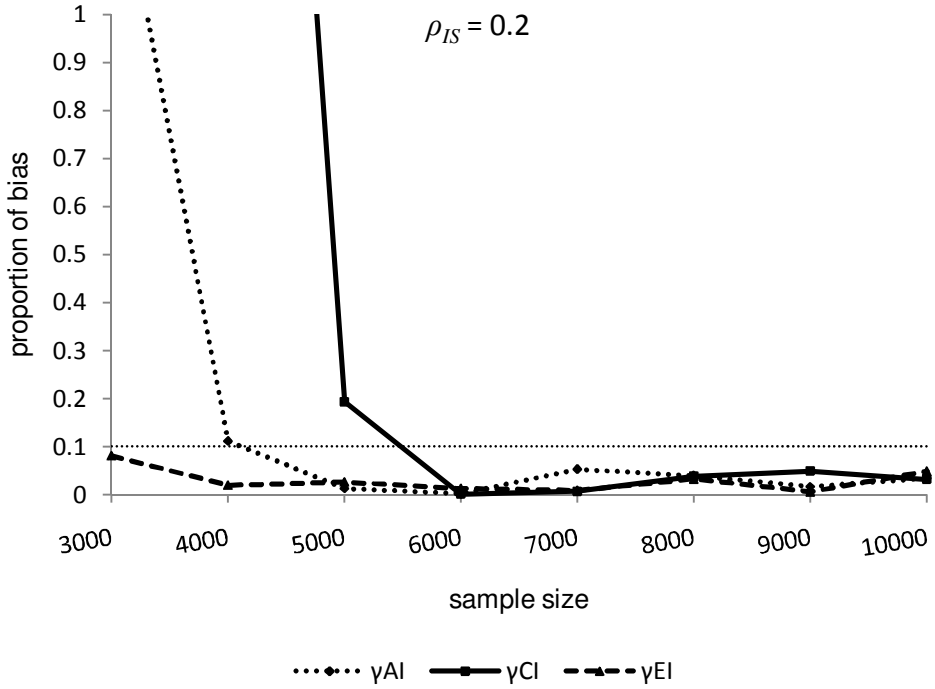

Figure 14. Biases of standard errors when *I*-*S* correlation was moderate (ρ_{IS} = 0.4).

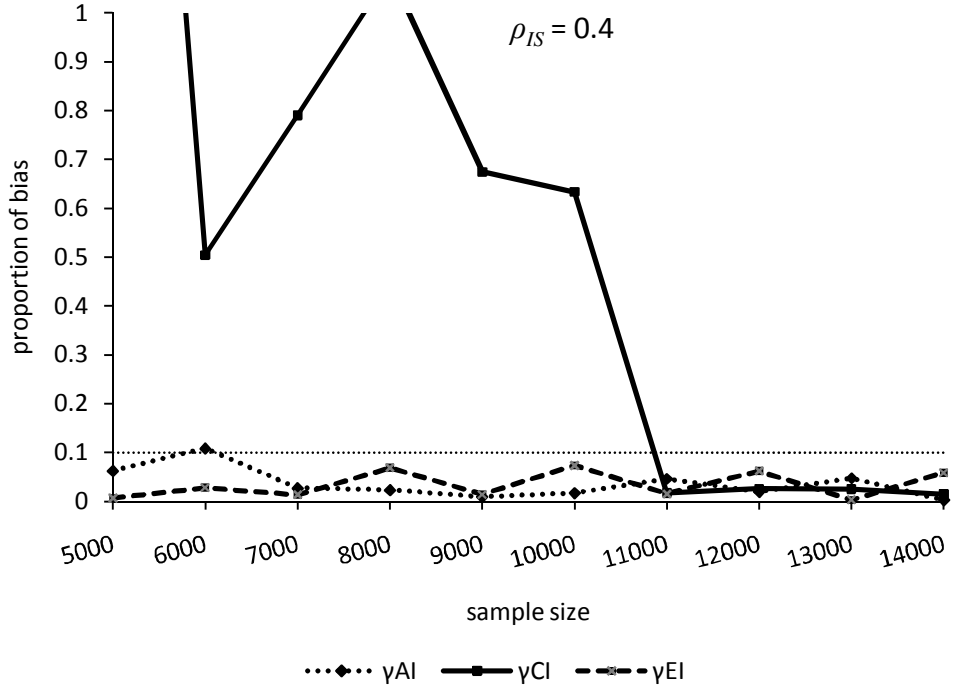

Figure 15. Biases of standard errors when *I*-*S* correlation was high (ρ_{IS} = 0.7).

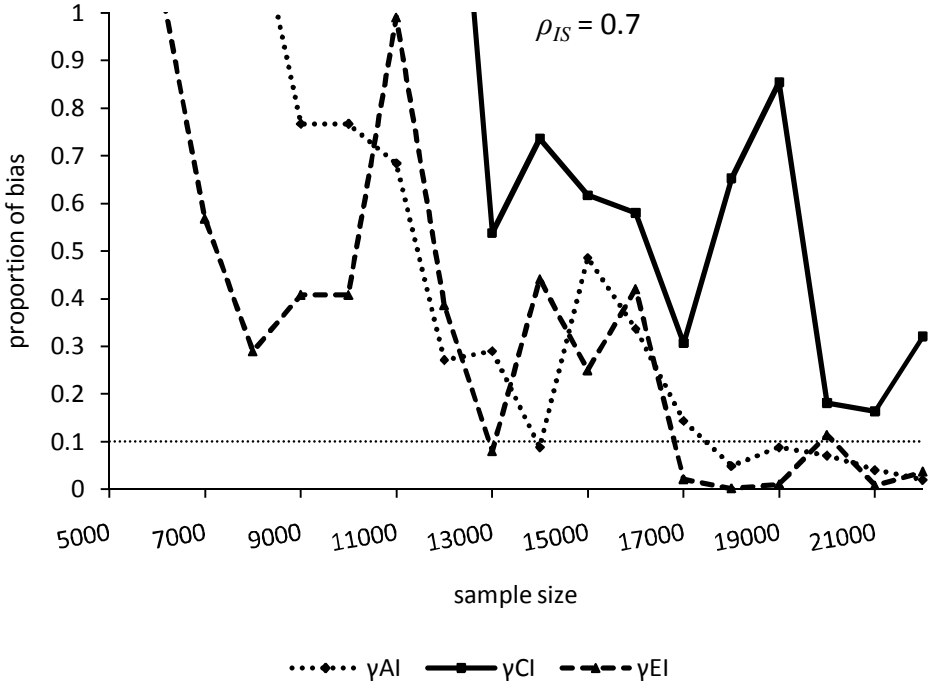

Table 1. Conditions of data generation common to all simulated data sets

c1) The datasets were generated with four waves: $T = 4$

c2) The number of replications was 300.

c3) Same numbers of twin pairs were assigned to MZ and DZ twin groups.

c4) No other growth factors were used than intercept (*I*) and slope (*S*) factors.

c5) Three biometric factors were used to decompose the variances of *I* and *S* factors, which were additive genetic factors (*A* factors); environmental factors common to both twins in a pair (*C* factors); and environmental factors unique to each twin (*E* factors).

c6) Intercepts of *I* and *S* factors were set to zero and one, respectively: $\alpha_I = 0$, $\alpha_S = 1$.

c7) Variances of *I* and *S* factors were set to one: $\sigma_I^2 = \sigma_S^2 = 1$.

c8) Factor loadings from S factor to Y_{tj} were set to the values represent linear growth: $\{\lambda_1, \lambda_2, \lambda_3, \lambda_4\} = \{0, 1, 2, 3\}$.

c9) Residual variances of Y_{1j} through Y_{2j} were set to 0.5: $\theta_1 = \theta_2 = \theta_3 = \theta_4 = 0.5$.

c10) To generate ordered categorical variables, continuous data were generated first and were categorized using thresholds of $\tau_1 = 0$ and $\tau_2 = 1$.

Table 2. Parameters varied by different data generations

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p1) The proportions of the variance of *I* factor accounted for by *A*, *C*, and *E* factors: p_{IA}, p_{IC}, and p_{IE}.

p2) The proportions of the variance of *S* factor accounted for by *A*, *C*, and *E* factors: p_{SA}, p_{SC}, and p_{SE}.

p3) Correlation between *I* and *S* factors: ρ_{IS}.

p4) The proportions of ρ_{IS} accounted for by correlations between *A*, *C*, and *E* factors: $p_{\rho A}$, $p_{\rho C}$, and $p_{\rho E}$.

p5) Sample size *n*.

p6) Residual covariances between twins: θ_{12}

Table 3. Analysis of continuous data generated from the base model (n = 1000)

Parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.692	0.094	0.093	0.966	0.994
γ_{CI}	0.548	0.525	0.108	**0.622**	0.976	0.942
γ_{EI}	0.447	0.442	0.043	0.045	0.972	1.000
γ_{AS}	0.707	0.703	0.058	0.056	0.952	1.000
γ_{ASI}	0.000	0.002	0.104	0.103	0.958	0.042
γ_{CS}	0.548	0.541	0.074	0.070	0.966	1.000
γ_{CSI}	0.000	0.004	0.121	0.123	0.950	0.050
γ_{ES}	0.447	0.446	0.023	0.022	0.954	1.000
γ_{ESI}	0.000	0.002	0.048	0.047	0.948	0.052
α_I	0.000	0.000	0.031	0.032	0.952	0.048
α_S	1.000	1.001	0.029	0.030	0.950	1.000
θ_1	0.500	0.497	0.056	0.057	0.948	1.000
θ_2	0.500	0.500	0.042	0.040	0.934	1.000
θ_3	0.500	0.496	0.052	0.051	0.942	1.000
θ_4	0.500	0.502	0.093	0.095	0.952	1.000
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.008	0.999	1.000	0.047		
SD	0.009	0.001	0.001			

Table 4. Analysis of continuous data generated from the base model (n = 2000)

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.702	0.065	0.064	0.956	1.000
γ_{CI}	0.548	0.537	0.072	0.074	0.956	0.994
γ_{EI}	0.447	0.444	0.030	0.032	0.966	1.000
γ_{AS}	0.707	0.705	0.041	0.039	0.954	1.000
γ_{ASI}	0.000	0.002	0.070	0.072	0.964	0.036
γ_{CS}	0.548	0.544	0.050	0.049	0.942	1.000
γ_{CSI}	0.000	0.002	0.082	0.085	0.970	0.030
γ_{ES}	0.447	0.447	0.017	0.016	0.940	1.000
γ_{ESI}	0.000	0.001	0.035	0.034	0.942	0.058
α_I	0.000	-0.001	0.022	0.022	0.954	0.046
α_S	1.000	1.001	0.021	0.021	0.948	1.000
θ_1	0.500	0.497	0.039	0.040	0.958	1.000
θ_2	0.500	0.499	0.028	0.029	0.954	1.000
θ_3	0.500	0.497	0.036	0.036	0.950	1.000
θ_4	0.500	0.506	0.067	0.068	0.952	1.000
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.005	1.000	1.000	0.063		
SD	0.007	< 0.001	< 0.001			

Table 5. Analysis of continuous data generated from the base model (n = 3000)

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.041	0.045	0.970	1.000
γ_{CI}	0.548	0.548	0.047	0.050	0.966	1.000
γ_{EI}	0.447	0.446	0.021	0.022	0.962	1.000
γ_{AS}	0.707	0.707	0.028	0.028	0.962	1.000
γ_{ASI}	0.000	0.003	0.052	0.051	0.942	0.058
γ_{CS}	0.548	0.546	0.035	0.034	0.948	1.000
γ_{CSI}	0.000	0.000	0.062	0.059	0.930	0.070
γ_{ES}	0.447	0.447	0.011	0.011	0.948	1.000
γ_{ESI}	0.000	-0.001	0.024	0.024	0.948	0.052
α_I	0.000	-0.001	0.016	0.016	0.974	0.026
α_S	1.000	1.001	0.015	0.015	0.954	1.000
θ_1	0.500	0.500	0.029	0.029	0.952	1.000
θ_2	0.500	0.499	0.020	0.020	0.954	1.000
θ_3	0.500	0.497	0.026	0.025	0.938	1.000
θ_4	0.500	0.503	0.048	0.048	0.946	1.000
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.004	1.000	1.000	0.050		
SD	0.005	< 0.001	< 0.001			

Table 6. Analysis of continuous data generated from the base model (n = 4000)

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.041	0.045	0.970	1.000
γ_{CI}	0.548	0.548	0.047	0.050	0.966	1.000
γ_{EI}	0.447	0.446	0.021	0.022	0.962	1.000
γ_{AS}	0.707	0.707	0.028	0.028	0.962	1.000
γ_{ASI}	0.000	0.003	0.052	0.051	0.942	0.058
γ_{CS}	0.548	0.546	0.035	0.034	0.948	1.000
γ_{CSI}	0.000	0.000	0.062	0.059	0.930	0.070
γ_{ES}	0.447	0.447	0.011	0.011	0.948	1.000
γ_{ESI}	0.000	-0.001	0.024	0.024	0.948	0.052
α_I	0.000	-0.001	0.016	0.016	0.974	0.026
α_S	1.000	1.001	0.015	0.015	0.954	1.000
θ_1	0.500	0.500	0.029	0.029	0.952	1.000
θ_2	0.500	0.499	0.020	0.020	0.954	1.000
θ_3	0.500	0.497	0.026	0.025	0.938	1.000
θ_4	0.500	0.503	0.048	0.048	0.946	1.000
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.004	1.000	1.000	0.047		
SD	0.005	< 0.001	< 0.001			

Table 7. Analysis of categorized data generated from the base model (n = 1000)

parameter	Pop. values	Est. cont.	Est. Avg	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.692	0.690	0.137	0.145	0.983	0.952
γ_{ASI}	0.000	0.002	0.050	0.220	**0.305**	0.996	0.004
γ_{CI}	0.548	0.525	0.546	0.149	**0.795**	0.952	0.844
γ_{CSI}	0.000	0.004	-0.005	0.223	**0.373**	0.992	0.008
γ_{EI}	0.447	0.442	0.450	0.070	0.067	0.963	0.990
γ_{ESI}	0.000	0.002	0.002	0.127	**0.146**	0.967	0.033
γ_{AS}	0.707	0.703	0.704	0.110	0.109	0.946	0.997
γ_{CS}	0.548	0.541	0.535	0.136	**0.524**	0.952	0.874
γ_{ES}	0.447	0.446	0.447	0.045	0.044	0.963	1.000
α_I	0.000	0.000	-0.004	0.034	0.037	0.959	0.041
α_S	1.000	1.001	1.008	0.042	0.043	0.973	1.000
Δ_1	0.817	0.832	0.818	0.047	0.048	0.949	1.000
Δ_2	0.632	0.641	0.629	0.023	0.023	0.014	1.000
Δ_3	0.426	0.431	0.425	0.017	0.016	0.031	1.000
Δ_4	0.309	0.311	0.307	0.014	0.013	0.207	1.000
θ_1	0.500	0.497	0.496				
θ_2	0.500	0.500	0.609				
θ_3	0.500	0.496	0.521				
θ_4	0.500	0.502	0.586				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.008	1.000	1.000	0.038			
SD	0.012	< 0.001	< 0.001				

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

Table 8. Analysis of categorized data generated from the base model (n = 2000)

parameter	Pop. values	Est. cont.	Est. Avg	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.702	0.666	0.153	**1.273**	0.986	0.888
γ_{ASI}	0.000	0.002	0.018	0.164	**0.199**	0.990	0.010
γ_{CI}	0.548	0.537	0.511	0.148	**2.540**	0.969	0.815
γ_{CSI}	0.000	0.002	0.012	0.163	**0.205**	0.983	0.017
γ_{EI}	0.447	0.444	0.428	0.096	**0.591**	0.955	0.913
γ_{ESI}	0.000	0.001	0.007	0.098	0.102	0.976	0.024
γ_{AS}	0.707	0.705	0.699	0.095	0.096	0.976	1.000
γ_{CS}	0.548	0.544	0.543	0.097	0.105	0.976	0.969
γ_{ES}	0.447	0.447	0.447	0.042	0.044	0.976	1.000
α_I	0.000	-0.001	-0.002	0.027	0.026	0.958	0.042
α_S	1.000	1.001	1.002	0.032	0.030	0.941	1.000
Δ_1	0.817	0.824	0.815	0.035	0.036	0.948	1.000
Δ_2	0.632	0.637	0.631	0.018	0.017	0.000	1.000
Δ_3	0.426	0.429	0.427	0.013	0.012	0.000	1.000
Δ_4	0.309	0.310	0.308	0.009	0.009	0.031	1.000
θ_1	0.500	0.497	0.496				
θ_2	0.500	0.499	0.609				
θ_3	0.500	0.497	0.521				
θ_4	0.500	0.506	0.586				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.006	1.000	1.000	0.038			
SD	0.008	< 0.001	< 0.001				

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

Table 9. Analysis of categorized data generated from the base model (n = 3000)

parameter	Pop. values	Est. Avg. cont.	Est. Avg	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.675	0.099	0.102	0.980	0.973
γ_{ASI}	0.000	0.003	0.018	0.139	0.137	0.960	0.040
γ_{CI}	0.548	0.548	0.527	0.112	**0.432**	0.953	0.933
γ_{CSI}	0.000	0.000	0.001	0.144	0.138	0.946	0.054
γ_{EI}	0.447	0.446	0.440	0.054	0.055	0.960	0.993
γ_{ESI}	0.000	-0.001	0.000	0.071	0.071	0.946	0.054
γ_{AS}	0.707	0.707	0.704	0.061	0.067	0.970	1.000
γ_{CS}	0.548	0.546	0.547	0.069	0.072	0.970	1.000
γ_{ES}	0.447	0.447	0.445	0.032	0.031	0.936	1.000
α_I	0.000	-0.001	-0.001	0.018	0.018	0.963	0.037
α_S	1.000	1.001	1.000	0.022	0.021	0.956	1.000
Δ_1	0.817	0.820	0.818	0.024	0.025	0.960	1.000
Δ_2	0.632	0.635	0.633	0.013	0.012	0.000	1.000
Δ_3	0.426	0.428	0.426	0.009	0.008	0.000	1.000
Δ_4	0.309	0.309	0.309	0.007	0.007	0.000	1.000
θ_1	0.500	0.500	0.459				
θ_2	0.500	0.499	0.539				
θ_3	0.500	0.497	0.508				
θ_4	0.500	0.503	0.538				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.005	1.000	1.000	0.047			
SD	0.006	< 0.001	< 0.001				

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

Table 10. Analysis of categorized data generated from the base model (n = 4000)

Parameter	Pop. values	Est. Avg. cont.	Est. Avg	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.675	0.099	0.102	0.980	0.973
γ_{ASI}	0.000	0.003	0.018	0.139	0.137	0.960	0.040
γ_{CI}	0.548	0.548	0.527	0.112	**0.432**	0.953	0.933
γ_{CSI}	0.000	0.000	0.001	0.144	0.138	0.946	0.054
γ_{EI}	0.447	0.446	0.440	0.054	0.055	0.960	0.993
γ_{ESI}	0.000	-0.001	0.000	0.071	0.071	0.946	0.054
γ_{AS}	0.707	0.707	0.704	0.061	0.067	0.970	1.000
γ_{CS}	0.548	0.546	0.547	0.069	0.072	0.970	1.000
γ_{ES}	0.447	0.447	0.445	0.032	0.031	0.936	1.000
α_I	0.000	-0.001	-0.001	0.018	0.018	0.963	0.037
α_S	1.000	1.001	1.000	0.022	0.021	0.956	1.000
Δ_1	0.817	0.820	0.818	0.024	0.025	0.960	1.000
Δ_2	0.632	0.635	0.633	0.013	0.012	0.000	1.000
Δ_3	0.426	0.428	0.426	0.009	0.008	0.000	1.000
Δ_4	0.309	0.309	0.309	0.007	0.007	0.000	1.000
θ_1	0.500	0.500	0.459				
θ_2	0.500	0.499	0.539				
θ_3	0.500	0.497	0.508				
θ_4	0.500	0.503	0.538				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.005	1.000	1.000	0.047			
SD	0.006	< 0.001	< 0.001				

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

Table 11. Analysis of categorized data generated from the base model using the modified analytic model (n = 1000)

parameter	Pop. values	Est. Avg. cont.	Est. Avg	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.690	0.138	0.145	0.980	0.949
γ_{CI}	0.548	0.548	0.546	0.149	**0.919**	0.952	0.843
γ_{EI}	0.447	0.446	0.434	0.096	0.093	0.956	0.928
γ_{AS}	0.707	0.707	0.704	0.110	0.109	0.945	0.997
γ_{CS}	0.548	0.546	0.534	0.135	0.139	0.956	0.874
γ_{ES}	0.447	0.447	0.446	0.052	0.050	0.939	1.000
α_I	0.000	-0.001	-0.004	0.034	0.037	0.962	0.038
α_S	1.000	1.001	1.008	0.042	0.043	0.973	1.000
Δ_1	0.817	0.820	0.815	0.045	0.048	0.956	1.000
Δ_2	0.632	0.635	0.628	0.025	0.025	0.031	1.000
Δ_3	0.426	0.428	0.425	0.018	0.017	0.058	1.000
Δ_4	0.309	0.309	0.307	0.014	0.013	0.222	1.000
θ_1	0.500	0.500	0.417				
θ_2	0.500	0.499	0.284				
θ_3	0.500	0.497	0.525				
θ_4	0.500	0.503	0.202				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.009	1.000	1.000	0.058			
SD	0.012	< 0.001	< 0.001				

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

Table 12. Analysis of categorized data generated from the base model using the modified analytic model (n = 2000)

Parameter	Pop. values	Est. Avg. cont.	Est. Avg	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.701	0.099	0.098	0.967	0.997
γ_{CI}	0.548	0.548	0.543	0.113	0.110	0.957	0.970
γ_{EI}	0.447	0.446	0.444	0.046	0.047	0.950	1.000
γ_{AS}	0.707	0.707	0.701	0.080	0.076	0.947	1.000
γ_{CS}	0.548	0.546	0.544	0.089	0.088	0.953	0.987
γ_{ES}	0.447	0.447	0.448	0.031	0.031	0.950	1.000
α_I	0.000	-0.001	-0.002	0.027	0.026	0.950	0.050
α_S	1.000	1.001	1.002	0.032	0.030	0.943	1.000
Δ_1	0.817	0.820	0.815	0.032	0.033	0.957	1.000
Δ_2	0.632	0.635	0.631	0.018	0.017	0.000	1.000
Δ_3	0.426	0.428	0.427	0.012	0.011	0.000	1.000
Δ_4	0.309	0.309	0.309	0.009	0.009	0.013	1.000
θ_1	0.500	0.500	0.515				
θ_2	0.500	0.499	0.614				
θ_3	0.500	0.497	0.518				
θ_4	0.500	0.503	0.600				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.006	1.000	1.000	0.047			
SD	0.008	< 0.001	< 0.001				

Table 13. Analysis of categorized data generated from the base model using the modified analytic model (n = 3000)

parameter	Pop. values	Est. Avg. cont.	Est. Avg	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.700	0.062	0.068	0.970	1.000
γ_{CI}	0.548	0.548	0.548	0.064	0.073	0.963	1.000
γ_{EI}	0.447	0.446	0.446	0.032	0.033	0.963	1.000
γ_{AS}	0.707	0.707	0.708	0.049	0.053	0.963	1.000
γ_{CS}	0.548	0.546	0.544	0.058	0.060	0.960	1.000
γ_{ES}	0.447	0.447	0.445	0.024	0.022	0.920	1.000
α_I	0.000	-0.001	-0.001	0.018	0.018	0.963	0.037
α_S	1.000	1.001	1.000	0.021	0.021	0.960	1.000
Δ_1	0.817	0.820	0.818	0.023	0.024	0.953	1.000
Δ_2	0.632	0.635	0.633	0.012	0.012	0.000	1.000
Δ_3	0.426	0.428	0.427	0.008	0.008	0.000	1.000
Δ_4	0.309	0.309	0.309	0.007	0.006	0.000	1.000
θ_1	0.500	0.500	0.478				
θ_2	0.500	0.499	0.522				
θ_3	0.500	0.497	0.496				
θ_4	0.500	0.503	0.532				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.005	1.000	1.000	0.060			
SD	0.006	< 0.001	< 0.001				

Table 14. Analysis of categorized data generated from the base model using the modified analytic model (n = 4000)

Parameter	Pop. values	Est. Avg. cont.	Est. Avg	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.707	0.698	0.700	0.062	0.068	0.970	1.000
γ_{CI}	0.548	0.548	0.548	0.064	0.073	0.963	1.000
γ_{EI}	0.447	0.446	0.446	0.032	0.033	0.963	1.000
γ_{AS}	0.707	0.707	0.708	0.049	0.053	0.963	1.000
γ_{CS}	0.548	0.546	0.544	0.058	0.060	0.960	1.000
γ_{ES}	0.447	0.447	0.445	0.024	0.022	0.920	1.000
α_I	0.000	-0.001	-0.001	0.018	0.018	0.963	0.037
α_S	1.000	1.001	1.000	0.021	0.021	0.960	1.000
Δ_1	0.817	0.820	0.818	0.023	0.024	0.953	1.000
Δ_2	0.632	0.635	0.633	0.012	0.012	0.000	1.000
Δ_3	0.426	0.428	0.427	0.008	0.008	0.000	1.000
Δ_4	0.309	0.309	0.309	0.007	0.006	0.000	1.000
θ_1	0.500	0.500	0.478				
θ_2	0.500	0.499	0.522				
θ_3	0.500	0.497	0.496				
θ_4	0.500	0.503	0.532				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate			
Average	0.005	1.000	1.000	0.060			
SD	0.006	< 0.001	< 0.001				

Table 15. Analysis of categorized data generated from the base model using the fixed thresholds $\tau_1 = 0$ and $\tau_2 = 0.5$ ($n = 3000$)

Parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.354	0.350	0.031	0.034	0.970	1.000
γ_{CI}	0.274	0.274	0.032	0.036	0.963	1.000
γ_{EI}	0.224	0.223	0.016	0.016	0.963	1.000
γ_{AS}	0.354	0.354	0.025	0.026	0.963	1.000
γ_{CS}	0.274	0.272	0.029	0.030	0.960	1.000
γ_{ES}	0.224	0.222	0.012	0.011	0.920	1.000
α_I	0.000	0.000	0.009	0.009	0.963	0.037
α_S	0.500	0.500	0.011	0.011	0.960	1.000
Δ_1	1.633	1.635	0.047	0.048	0.953	1.000
Δ_2	1.265	1.266	0.024	0.023	0.940	1.000
Δ_3	0.853	0.853	0.016	0.016	0.930	1.000
Δ_4	0.617	0.618	0.013	0.013	0.927	1.000
θ_1	0.125	0.120				
θ_2	0.125	0.131				
θ_3	0.125	0.124				
θ_4	0.125	0.133				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.005	1.000	1.000	0.060		
SD	0.006	0.000	0.000			

Table 16. Analysis of categorized data generated from the base model using the fixed thresholds $\tau_1 = 1$ and $\tau_2 = 1.5$ ($n = 3000$)

Parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE	95% coverage	Sig. Coeff.
γ_{AI}	0.354	0.350	0.031	0.034	0.970	1.000
γ_{CI}	0.274	0.274	0.032	0.036	0.963	1.000
γ_{EI}	0.224	0.223	0.016	0.016	0.963	1.000
γ_{AS}	0.354	0.354	0.025	0.026	0.963	1.000
γ_{CS}	0.274	0.272	0.029	0.030	0.960	1.000
γ_{ES}	0.224	0.222	0.012	0.011	0.920	1.000
α_I	1.000	1.000	0.009	0.009	0.963	1.000
α_S	0.500	0.500	0.011	0.011	0.960	1.000
Δ_1	1.633	1.635	0.047	0.048	0.953	1.000
Δ_2	1.265	1.266	0.024	0.023	0.940	1.000
Δ_3	0.853	0.853	0.016	0.016	0.930	1.000
Δ_4	0.617	0.618	0.013	0.013	0.927	1.000
θ_1	0.125	0.120				
θ_2	0. 125	0.131				
θ_3	0. 125	0.124				
θ_4	0. 125	0.133				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.005	1.000	1.000	0.060		
SD	0.006	0.000	0.000			

Table 17. Analysis of categorized data generated from more complicated model with low cov (I, S) (ρ_{IS} = 0.2, n = 4000)

Parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.**
λ_2	2.000	2.003	0.048	0.049	0.959	1.000
λ_3	3.000	3.005	0.102	0.100	0.966	1.000
γ_{AI}	0.693	0.670	0.094	**0.107**	0.973	0.990
γ_{ASI}	0.141	0.151	0.119	0.127	0.969	**0.173**
γ_{CI}	0.537	0.513	0.106	**0.158**	0.976	0.905
γ_{CSI}	0.109	0.115	0.127	0.134	0.973	**0.061**
γ_{EI}	0.438	0.429	0.064	0.063	0.959	0.983
γ_{ESI}	0.089	0.092	0.067	0.069	0.959	**0.214**
γ_{AS}	0.707	0.708	0.063	0.068	0.980	1.000
γ_{CS}	0.548	0.543	0.068	0.075	0.976	1.000
γ_{ES}	0.447	0.445	0.031	0.031	0.952	1.000
α_I	0.000	-0.001	0.019	0.020	0.963	0.037
α_S	1.000	1.001	0.026	0.027	0.966	1.000
Δ_1	0.816	0.818	0.014	0.014	0.949	1.000
Δ_2	0.587	0.587	0.010	0.010	0.952	1.000
Δ_3	0.398	0.398	0.008	0.009	0.963	1.000
Δ_4	0.292	0.292	0.009	0.010	0.963	1.000
θ_{12} MZ	0.300	0.299	0.030	0.028	0.932	1.000
θ_{12} DZ	0.225	0.225	0.030	0.030	0.949	1.000
θ_1	0.500	0.488				
θ_2	0.500	0.527				
θ_3	0.500	0.512				
θ_4	0.500	0.423				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.004	1.000	1.000	0.044		
SD	0.006	0.000	0.000			

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

** Proportions of significant coefficients less than 0.8 for non-zero parameters were bold faced.

Table 18. Analysis of categorized data generated from more complicated model with moderate cov (*I*, *S*) (ρ_{IS} = 0.4, n = 4000)

Parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.**
λ_2	2.000	2.002	0.052	0.051	0.941	1.000
λ_3	3.000	3.010	0.099	0.101	0.965	1.000
γ_{AI}	0.648	0.611	0.126	**0.145**	0.979	0.906
γ_{ASI}	0.283	0.295	0.121	0.133	0.979	**0.641**
γ_{CI}	0.502	0.471	0.142	**0.441**	0.955	0.805
γ_{CSI}	0.219	0.222	0.129	0.140	0.972	**0.303**
γ_{EI}	0.410	0.396	0.082	**0.115**	0.930	0.920
γ_{ESI}	0.179	0.183	0.070	0.071	0.962	**0.780**
γ_{AS}	0.707	0.707	0.064	0.069	0.969	1.000
γ_{CS}	0.548	0.544	0.068	0.076	0.976	1.000
γ_{ES}	0.447	0.444	0.031	0.031	0.951	1.000
α_I	0.000	0.000	0.019	0.020	0.965	0.035
α_S	1.000	1.000	0.026	0.027	0.965	1.000
Δ_1	0.816	0.818	0.014	0.015	0.943	1.000
Δ_2	0.550	0.551	0.010	0.010	0.933	1.000
Δ_3	0.375	0.375	0.009	0.009	0.951	1.000
Δ_4	0.278	0.278	0.009	0.009	0.951	1.000
θ_{12} MZ	0.300	0.298	0.031	0.028	0.916	1.000
θ_{12} DZ	0.225	0.224	0.031	0.030	0.930	1.000
θ_1	0.500	0.475				
θ_2	0.500	0.528				
θ_3	0.500	0.476				
θ_4	0.500	0.448				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.005	1.000	1.000	0.053		
SD	0.006	0.000	0.000			

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

** Proportions of significant coefficients less than 0.8 for non-zero parameters were bold faced.

Table 19. Analysis of categorized data generated from more complicated model with high cov (*I*, *S*) (ρ_{IS} = 0.7, n = 4000)

Parameter	Pop. Values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.**
λ_2	2.000	1.999	0.044	0.043	0.931	1.000
λ_3	3.000	2.999	0.086	0.083	0.948	1.000
γ_{AI}	0.505	0.444	0.144	**0.405**	1.000	**0.708**
γ_{ASI}	0.495	0.506	0.089	**0.111**	0.991	1.000
γ_{CI}	0.391	0.384	0.137	**0.475**	0.961	**0.678**
γ_{CSI}	0.383	0.377	0.091	**0.114**	0.987	0.970
γ_{EI}	0.319	0.304	0.090	**0.324**	0.961	**0.785**
γ_{ESI}	0.313	0.316	0.050	**0.059**	0.979	1.000
γ_{AS}	0.707	0.702	0.051	**0.057**	0.983	1.000
γ_{CS}	0.548	0.549	0.055	0.062	0.974	1.000
γ_{ES}	0.447	0.446	0.023	0.025	0.970	1.000
α_I	0.000	0.000	0.017	0.016	0.936	0.064
α_S	1.000	1.002	0.023	0.023	0.944	1.000
Δ_1	0.816	0.817	0.013	0.012	0.924	1.000
Δ_2	0.506	0.507	0.007	0.008	0.949	1.000
Δ_3	0.347	0.348	0.007	0.007	0.958	1.000
Δ_4	0.261	0.262	0.007	0.007	0.970	1.000
θ_{12} MZ	0.300	0.300	0.022	0.023	0.948	1.000
θ_{12} DZ	0.225	0.222	0.025	0.024	0.931	1.000
θ_1	0.500	0.486				
θ_2	0.500	0.485				
θ_3	0.500	0.460				
θ_4	0.500	0.535				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate*		
Average	0.004	1.000	1.000	0.034		
SD	0.006	0.000	0.000			

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

** Proportions of significant coefficients less than 0.8 for non-zero parameters were bold faced.

Table 20. Analysis of the same data used in Table 18 using modified analytic model

parameter	Pop. values	Est. Avg.*	Est. SD	Avg. SE**	95% coverage	Sig. Coeff.
λ_2	2.000	1.634	0.033	0.031	0.000	1.000
λ_3	3.000	2.110	0.050	0.050	0.000	1.000
γ_{AI}	0.648	**1.075**	0.071	0.072	0.003	1.000
γ_{CI}	0.502	**0.585**	0.101	0.109	0.809	0.987
γ_{EI}	0.410	0.411	0.040	0.041	0.960	1.000
γ_{AS}	0.707	**0.860**	0.050	0.053	0.181	1.000
γ_{CS}	0.548	**0.443**	0.079	**0.091**	0.987	0.963
γ_{ES}	0.447	**0.316**	0.025	0.025	0.000	1.000
α_I	0.000	-0.091	0.023	0.024	0.030	0.970
α_S	1.000	1.117	0.028	0.028	0.007	1.000
Δ_1	0.816	**0.695**	0.015	0.013	0.000	1.000
Δ_2	0.550	0.563	0.009	0.009	0.701	1.000
Δ_3	0.375	**0.455**	0.007	0.008	0.000	1.000
Δ_4	0.278	**0.393**	0.008	0.008	0.000	1.000
θ_{12} MZ	0.300	0.181	0.026	0.026	0.013	1.000
θ_{12} DZ	0.225	0.153	0.040	0.038	0.520	0.977
θ_1	0.500	0.416				
θ_2	0.500	0.445				
θ_3	0.500	0.319				
θ_4	0.500	0.194				
Fit indices	RMSEA	CFI	TLI	χ^2 rejection rate		
Average	0.034	0.999	0.999	1.000		
SD	0.003	0.000	0.000			

* Average parameter estimates deviated from their population values by more than 10% were bold faced.

** Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

Table 21. Analysis of continuous data sets using the alternative model specification with zero γ_{*SI}.

constraint	$\lambda_1 = 0.7$				$\lambda_1 = 1$			
parameter	Pop. Values	Est. Avg.	SD	SE Avg.	Pop. Values	Est. Avg.	SD	SE Avg.
λ_2	1.700	1.701	0.021	0.021	2.429	2.429	0.030	0.029
λ_3	2.700	2.701	0.037	0.036	3.858	3.858	0.053	0.052
λ_4	3.700	3.702	0.055	0.054	5.287	5.288	0.079	0.077
γ_{AI}	0.505	0.503	0.038	0.037	0.505	0.503	0.038	0.037
γ_{CI}	0.391	0.391	0.047	0.046	0.391	0.391	0.047	0.046
γ_{EI}	0.319	0.319	0.016	0.016	0.319	0.319	0.016	0.016
γ_{AS}	0.707	0.705	0.022	0.022	0.495	0.494	0.016	0.015
γ_{CS}	0.548	0.549	0.028	0.026	0.383	0.384	0.020	0.018
γ_{ES}	0.447	0.447	0.010	0.009	0.313	0.313	0.007	0.006
α_I	-0.700	-0.699	0.018	0.017	-0.700	-0.699	0.018	0.017
α_S	1.000	1.001	0.022	0.022	0.700	0.700	0.016	0.015
θ_1	0.500	0.502	0.021	0.021	0.500	0.502	0.021	0.021
θ_2	0.500	0.500	0.017	0.016	0.500	0.500	0.017	0.016
θ_3	0.500	0.500	0.022	0.022	0.500	0.500	0.022	0.022
θ_4	0.500	0.498	0.041	0.040	0.500	0.498	0.041	0.040
θ_{12} MZ	0.300	0.300	0.018	0.018	0.300	0.300	0.018	0.018
θ_{12} DZ	0.225	0.225	0.017	0.017	0.225	0.225	0.017	0.017
	Fit statistics							
	χ^2 rejection rate	CFI	TLI	RMSEA	χ^2 rejection rate	CFI	TLI	RMSEA
Mean	0.030	1	1	0.004	0.030	1	1	0.004
Std		0	0	0.005		0	0	0.005

Table 22. Analysis of categorized data sets using the alternative model specification with zero γ_{*SI} and $\lambda_1 = 0.7$.

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.**
λ_2	1.700	1.698	0.041	0.041	0.946	1.000
λ_3	2.700	2.694	0.084	0.084	0.950	1.000
λ_4	3.700	3.693	0.140	0.139	0.939	1.000
γ_{AI}	0.505	0.474	0.116	**0.142**	0.993	0.853
γ_{CI}	0.391	0.389	0.118	**0.363**	0.950	**0.748**
γ_{EI}	0.319	0.315	0.067	0.062	0.950	0.953
γ_{AS}	0.707	0.707	0.043	0.044	0.953	1.000
γ_{CS}	0.548	0.548	0.045	0.048	0.957	1.000
γ_{ES}	0.447	0.449	0.020	0.021	0.953	1.000
α_I	-0.700	-0.702	0.033	0.033	0.939	1.000
α_S	1.000	1.004	0.042	0.041	0.939	1.000
Δ_1	0.816	0.816	0.012	0.012	0.950	1.000
Δ_2	0.506	0.507	0.008	0.008	0.939	1.000
Δ_3	0.347	0.348	0.007	0.007	0.932	1.000
Δ_4	0.261	0.261	0.007	0.007	0.946	1.000
θ_{12} MZ	0.300	0.303	0.025	0.027	0.982	1.000
θ_{12} DZ	0.225	0.225	0.028	0.030	0.975	1.000
Fit indices	χ^2 rejection rate	RMSEA	CFI	TLI		
Average	0.054	0.003	1.000	1.000		
SD		0.005	0.000	0.000		

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

** Proportions of significant coefficients less than 0.8 for non-zero parameters were bold faced.

Table 23.nalysis of categorized data sets using the alternative model specification with zero γ_{*SI} and $\lambda_1 = 1$.

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.
λ_2	2.429	2.427	0.057	0.059	0.003	0.950
λ_3	3.858	3.849	0.119	0.120	0.014	0.950
λ_4	5.287	5.277	0.199	0.199	0.039	0.939
γ_{AI}	0.505	0.474	0.115	**0.142**	0.014	1.000
γ_{CI}	0.391	0.389	0.118	**0.307**	0.014	0.950
γ_{EI}	0.319	0.317	0.061	0.061	0.004	0.953
γ_{AS}	0.495	0.495	0.030	0.031	0.001	0.953
γ_{CS}	0.383	0.384	0.032	0.033	0.001	0.957
γ_{ES}	0.313	0.314	0.014	0.015	0.000	0.957
α_I	-0.700	-0.702	0.033	0.033	0.493	0.000
α_S	0.700	0.703	0.029	0.029	0.089	0.000
Δ_1	0.816	0.816	0.012	0.012	0.000	0.950
Δ_2	0.506	0.506	0.008	0.008	0.000	0.939
Δ_3	0.347	0.348	0.007	0.007	0.000	0.932
Δ_4	0.261	0.261	0.007	0.007	0.000	0.946
θ_{12} MZ	0.300	0.303	0.025	0.027	0.001	0.982
θ_{12} DZ	0.225	0.225	0.028	0.030	0.001	0.975
Fit indices	χ^2 rejection rate	RMSEA	CFI	TLI		
Average	0.050	0.003	1.000	1.000		
SD		0.005	0.000	0.000		

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

Table 24. Analysis of categorized data with low heritability (A:C:E = 20%:60%:20%) for *I* and *S* factors (ρ_{IS} = 0.4, n = 4000)

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.**
λ_2	2.000	2.000	0.046	0.045	0.972	1.000
λ_3	3.000	3.008	0.091	0.090	0.956	1.000
γ_{AI}	0.410	0.380	0.162	**1.243**	0.932	**0.627**
γ_{ASI}	0.710	0.679	0.080	0.085	0.996	0.996
γ_{CI}	0.410	0.387	0.072	**0.080**	0.980	0.972
γ_{CSI}	0.447	0.453	0.081	0.088	0.960	0.984
γ_{EI}	0.179	0.143	0.156	**0.186**	0.928	**0.016**
γ_{ESI}	0.775	0.768	0.046	0.046	0.952	1.000
γ_{AS}	0.310	0.337	0.081	0.085	0.964	0.996
γ_{CS}	0.447	0.444	0.026	0.028	0.964	1.000
γ_{ES}	0.179	0.193	0.056	**0.064**	0.976	0.932
α_I	0.000	0.000	0.018	0.018	0.960	0.040
α_S	1.000	1.002	0.025	0.025	0.948	1.000
Δ_1	0.816	0.818	0.014	0.013	0.939	1.000
Δ_2	0.550	0.551	0.009	0.009	0.934	1.000
Δ_3	0.375	0.376	0.008	0.008	0.967	1.000
Δ_4	0.278	0.278	0.008	0.008	0.930	1.000
θ_{12} MZ	0.300	0.298	0.025	0.026	0.948	1.000
θ_{12} DZ	0.225	0.226	0.026	0.026	0.960	1.000
θ_1	0.500	0.486				
θ_2	0.500	0.477				
θ_3	0.500	0.488				
θ_4	0.500	0.387				

Fit indices	χ^2 rejection rate	RMSEA	CFI	TLI
Average	0.037	0.005	1.000	1.000
SD		0.006	0.000	0.000

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

** Proportions of significant coefficients less than 0.8 for non-zero parameters were bold faced.

Table 25. Analysis of categorized data with moderate heritability (A:C:E = 50%:30%:20%) for *I* and *S* factors (ρ_{IS} = 0.4, n = 4000)

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.**
λ_2	2.000	2.002	0.052	0.051	0.941	1.000
λ_3	3.000	3.010	0.099	0.101	0.965	1.000
γ_{AI}	0.648	0.611	0.126	**0.145**	0.979	0.906
γ_{ASI}	0.283	0.295	0.121	0.133	0.979	**0.641**
γ_{CI}	0.502	0.471	0.142	**0.441**	0.955	0.805
γ_{CSI}	0.219	0.222	0.129	0.140	0.972	**0.303**
γ_{EI}	0.410	0.396	0.082	**0.115**	0.930	0.920
γ_{ESI}	0.179	0.183	0.070	0.071	0.962	**0.780**
γ_{AS}	0.707	0.707	0.064	0.069	0.969	1.000
γ_{CS}	0.548	0.544	0.068	0.076	0.976	1.000
γ_{ES}	0.447	0.444	0.031	0.031	0.951	1.000
α_I	0.000	0.000	0.019	0.020	0.965	0.035
α_S	1.000	1.000	0.026	0.027	0.965	1.000
Δ_1	0.816	0.818	0.014	0.015	0.943	1.000
Δ_2	0.550	0.551	0.010	0.010	0.933	1.000
Δ_3	0.375	0.375	0.009	0.009	0.951	1.000
Δ_4	0.278	0.278	0.009	0.009	0.951	1.000
θ_{12} MZ	0.300	0.298	0.031	0.028	0.916	1.000
θ_{12} DZ	0.225	0.224	0.031	0.030	0.930	1.000
θ_1	0.500	0.475				
θ_2	0.500	0.528				
θ_3	0.500	0.476				
θ_4	0.500	0.448				

Fit indices	χ^2 rejection rate	CFI	TLI	RMSEA
Average	0.053	1.000	1.000	0.005
SD		0.000	0.000	0.006

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

** Proportions of significant coefficients less than 0.8 for non-zero parameters were bold faced.

Table 26. Analysis of categorized data with high heritability (A:C:E = 70%:20%:10%) for *I* and *S* factors (ρ_{IS} = 0.4, n = 4000)

parameter	Pop. values	Est. Avg.	Est. SD	Avg. SE*	95% coverage	Sig. Coeff.**
λ_2	2.000	2.002	0.051	0.051	0.959	1.000
λ_3	3.000	3.006	0.102	0.101	0.950	1.000
γ_{AI}	0.767	0.732	0.085	**0.108**	1.000	1.000
γ_{ASI}	0.335	0.361	0.089	**0.110**	1.000	0.971
γ_{CI}	0.410	0.401	0.125	**0.279**	0.946	**0.665**
γ_{CSI}	0.179	0.155	0.132	**0.167**	0.963	**0.045**
γ_{EI}	0.290	0.276	0.101	**0.507**	0.930	**0.719**
γ_{ESI}	0.126	0.117	0.078	**0.093**	0.950	**0.120**
γ_{AS}	0.837	0.830	0.050	**0.057**	0.983	1.000
γ_{CS}	0.447	0.452	0.074	**0.090**	0.971	0.988
γ_{ES}	0.316	0.318	0.030	0.035	0.967	1.000
α_I	0.000	-0.001	0.019	0.020	0.955	0.045
α_S	1.000	1.000	0.026	0.028	0.971	1.000
Δ_1	0.816	0.818	0.014	0.015	0.958	1.000
Δ_2	0.550	0.550	0.010	0.010	0.946	1.000
Δ_3	0.375	0.375	0.009	0.009	0.946	1.000
Δ_4	0.278	0.278	0.009	0.009	0.946	1.000
θ_{12} MZ	0.300	0.300	0.026	0.027	0.963	1.000
θ_{12} DZ	0.225	0.222	0.032	0.030	0.926	1.000
θ_1	0.500	0.478				
θ_2	0.500	0.518				
θ_3	0.500	0.465				
θ_4	0.500	0.440				

Fit indices	χ^2 rejection rate	CFI	TLI	RMSEA
Average	0.058	1.000	1.000	0.005
SD		0.000	0.000	0.006

* Average standard errors which deviated from their population values (Est. SD) by more than 10% were bold faced.

** Proportions of significant coefficients less than 0.8 for non-zero parameters were bold faced.

VITA

Seung Bin Cho was born in the Republic of Korea. After completing high school at Gimchon City, he served in the air force. He attended Chunga-Ang University, Seoul at 1997, where he received a Bachelor of Arts degree at 2002, with a major in psychology. After graduating the college, he moved to the Unites States of America, and started graduate study at the University of Missouri, Columbia, Missouri, with a major in quantitative psychology. At the summer of 2007, he received a Master of Arts degree in psychology with a study of multiple group behavior genetic model.