Using a linear mixed-effect model framework to estimate multivariate generalizability theory parameters in R

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Abstract

Multivariate generalizability theory (mG-theory) is an important framework in many behavioral and educational studies, as it describes useful psychometric properties of multidimensional assessments. Nevertheless, the use of mG-theory estimation is limited due to the lack of available software for carrying out the necessary calculations: users rely heavily on independent software programs such as mGENOVA and the BUGS/JAGS suite of programs. Considering the prevalence of R software, this paper presents a solution using the *glmmTMB* package to accomplish the estimation task. Users adopting the proposed method may find it more convenient for conducting both applied investigation and simulation studies without the need to switch between different software programs.

Keywords Generalizability · Multivariate · R · lme4 · glmmTMB · Mixed-model

Introduction

Since its introduction by Cronbach and colleagues in the 1960s, generalizability theory (G-theory) has played a critical role in research on behavioral and educational assessments (Cronbach, Gleser, & Rajaratnam, 1963; Cronbach, Gleser, Nanda, & Rajaratnam, 1972; Gleser, Cronbach, & Rajaratnam, 1965). G-Theory extends classical test theory by using ANOVA procedures to estimate the magnitude of multiple sources of measurement errors. For example, in a writing test, G-theory allows one to separate observed test score variance into multiple facets, so that one can determine the relative contributions of various sources such as items, raters, or occasions (Brennan, 2001a; Shavelson & Webb, 1981). This is particularly important given the complex nature of the assessments used in educational and psychological settings. With the information produced by G-theory, a

researcher can understand the quality of an assessment and make decisions accordingly (e.g., increasing the number of items or decreasing the number of raters). Multivariate G-theory (mG-theory), as its name suggests, expands the univariate conception of measurement procedures into multivariate scenarios (Joe & Woodward, 1976; Marcoulides, 1995; Woodward & Joe, 1973), which tend to be more practically useful in many research contexts. For example, mG-theory allows researchers to study measurement designs for which more than a single dimension or subtest is of interest. Such analyses incorporate covariance components and/or correlations across multiple dimensions into a single overall analysis.

The information provided by mG-theory can be useful when studying complex measurement designs to help determine when to combine two or more scores into a single score, to identify halo errors (Lance, LaPointe, & Stewart, 1994) and other types of correlated errors, and to evaluate the consistency of different sources of errors across the multiple test scores of interest. Furthermore, ignoring the correlations of the dimensions could be detrimental, because it typically results in biased estimates (Rao & Mudholkar, 1967). Applications of mG-theory can be found in various areas. For instance, Nußbaum (1984) adopted mG-theory to study students' watercolor painting skills in multiple dimensions, while Wu and Tzou (2015) analyzed standard setting data over multiple content areas and levels of proficiency. Clauser, Harik, and Margolis (2006) studied multiple sources of errors on a performance test where physicians interacted with several

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standardized patients and were evaluated on multiple skill domains (e.g., physical exam and communication), and Raymond and Jiang used mG-theory to evaluate the quality of subscores on multiple-choice tests (Jiang & Raymond, 2018; Raymond & Jiang, 2019). Brennan (2001a) provides more comprehensive examples of measurement problems that require mG-theory for scientific decision-making procedures.

Software for estimation

Estimates of variance-covariance components for random- and fixed-effect measurement designs are required by mG-theory. The variance-covariance components provide the foundation for consistency of the measurement(s), where in a testing scenario, reliability is one of form of such consistency. One of the simplest designs, using writing test score as an example, is where examinees respond to test items, and test items are nested within multiple content categories (i.e., dimensions). Examinees and items are random effects, while the content categories are fixed. Brennan (2001a) refers to this as the table of specifications design. However, the designs quickly become more complex as additional factors are added (e.g., raters and occasions). At present, mG-theory relies primarily on two software programs for estimating variance-covariance components: mGENOVA (Brennan, 2001b) and the BUGS/JAGS suite of programs. As a frequentist product, mGENOVA is an ANSI C program powered by mean square error calculations, which are typically seen in traditional repeated-measures ANOVA estimations. These ANOVA approaches can also be realized in a structural equation modeling framework (Jiang, Walker, Shi, & Cao, 2018; Marcoulides, 1996; Raykov & Marcoulides, 2006). On the other hand, BUGS/JAGS refers to three variants sharing highly similar algorithmic functionalities: WinBUGS (Lunn, Thomas, Best, & Spiegelhalter 2000; Spiegelhalter, Thomas, Best, & Lunn 2003), OpenBUGS (Thomas, O'Hara, Ligges, & Sturtz 2006), and JAGS (Plummer 2003, 2010). These programs manage the estimation from a Bayesian perspective, which enables features such as the incorporation of prior distributions, missing data imputation, and posterior distributions for variance/covariance estimates (LoPilato, Carter, & Wang, 2015).

Because of the algorithmic differences, mGENOVA is computationally faster than BUGS/JAGS, and can process a large number of observations (Brennan, 2001b). However, mGENOVA is limited with respect to handling unbalanced designs and sparse or missing data, and produces negative variance estimates under certain conditions. In contrast, BUGS/JAGS uses a Monte Carlo simulation paradigm—random sampling strategy—that almost always consumes more processing time than frequentist approaches, for which the updating steps and directions are deterministic (Jiang & Skorupski, 2018).

Despite the fact that the two software programs process data in different ways, they do share a common feature: both are independent, stand-alone software programs that are not compatible with R software (R Development Core Team, 2019). The R environment has become the preferred choice in statistical analysis across numerous disciplines (Chen, Dios, Mili, Wu, & Wang, 2005). The prevalence of R software in behavioral and educational research has led to the creation of many packages/functions for specific inquiries (Li & Baron, 2011, p. 5). For example, the *Rethomics* package (Geissmann, Rodriguez, Beckwith, & Gilestro, 2019) provides a framework for analyzing high-throughput behavioral data, and the *catR* package (Magis & Barrada, 2017) is designed to manage computer-adaptive testing. The present paper describes and illustrates how the *glmmTMB* package (Brooks et al., 2017) can be adapted to estimate the variance-covariance components required for mG-theory. The primary advantage of this approach is that processing and analysis of data can all be performed in the R computing environment (R Development Core Team, 2019).

Linear mixed-effect model and multivariate generalizability theory

Moore (2016) adopted the *lme4* package (Bates, Mächler, Bolker, & Walker, 2015) to create the *gtheory* package to handle G-theory estimation in a linear mixed-effect model (LMM) framework. Jiang and Skorupski (2018) extended the *lme4* approach (Bates et al., 2015) to additional G-theory designs; similar works can be found in Huebner and Lucht (2019). This paper follows Jiang and Skorupski's approach (2018) and demonstrates procedures for gearing LMM analysis towards mG-theory estimation. Prior to introducing the R steps, the concepts of LMM are reviewed.

Linear mixed-effect models, also known as hierarchical linear models or multilevel models, comprise a class of statistical models specified for analyzing complex designs with clustering or nested structures (Raudenbush & Bryk, 2002). To illustrate, if multiple high schools with multiple students are recruited into a research program, the students from the same high schools will have more in common with each other than with those from different high schools. Because students are nested within high schools, an LMM should be considered. As a special form, a cross-classified LMM is used when non-exclusive groups/structures exist: students from the same high school do not necessarily come from the same middle school, and vice versa. Therefore, the relation between the high schools and the middle schools is called a cross-classification (Goodman, 1985). For each nesting structure (e.g., high schools), variance can be estimated in the LMM to determine the significance of the difference among the entities. That said, if the between-school variance is not

statistically significant, the hypothesis of no between-school difference cannot be rejected. In this instance, the higher-level entities, or schools, are treated as “random effects.” In an educational testing setting, if examinees take all items, which are further scored by all raters, the cross-classified structure describes the relation between the item (random) effect and the rater (random) effect.

Mathematically, a typical two-level LMM with three predictors can be found in Eq. 1: Y is the dependent variable; β_0 is the intercept; β_1 , β_2 , and β_3 are the slopes of predictors X_1 , X_2 , and X_3 ; γ_{00} , γ_{10} , γ_{20} , and γ_{30} are the means of β_0 , β_1 , β_2 , and β_3 , respectively, while u_0 , u_1 , u_2 , and u_3 are the level-2 residuals; and finally, r represents the level-1 residual:

$$\begin{aligned} Y &= \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + r, \\ \beta_0 &= \gamma_{00} + u_0, \\ \beta_1 &= \gamma_{10} + u_1, \\ \beta_2 &= \gamma_{20} + u_2, \\ \beta_3 &= \gamma_{30} + u_3. \end{aligned} \quad (1)$$

Conventionally, r is assumed to follow a univariate normal distribution $r \sim N(0, \epsilon)$. On the other hand, u_0 , u_1 , u_2 , and u_3 can be framed with more complex structures. Let $\mathbf{u} = [u_0, u_1, u_2, u_3]^T$; $\mathbf{u}$ is assumed to follow a multivariate normal distribution $\mathbf{u} \sim MN(\mathbf{0}, \Sigma)$, where Σ is a 4×4 matrix whose shape can be customized accordingly. Figure 1 shows typical specifications of Σ : panels 1 to 4 are *diagonal*, *unstructured*, *compound symmetric*, and *first-order autoregressive* covariance matrices, respectively. These structures are adopted according to theoretical assumptions or operational guidelines, while the results of fitting different structures can also be compared from an empirical perspective.

To illustrate how mG-theory can be converted to an LMM, two typical mG-theory designs are introduced: $p \times i^0$ and $p \times i \bullet$. The notations and symbols follow Brennan’s delineation (2001a) for labeling of random effects: p is the person effect and i is the item effect, where $p \times i^0$ indicates that different sets of items are nested within each dimension, and $p \times i \bullet$ indicates that items nested within all dimensions are identical. Examples in Jiang and Skorupski (2018) are reproduced to assist in explaining. As seen in Fig. 2, 200 examinees take a test that consists of 30 items in total. Items $i1$ to $i10$ are nested within the first dimension $v1$, items $i11$ to $i20$ belong to the second dimension $v2$, and the rest of the items measure the last

dimension $v3$. Each examinee responds to each test item only once. The design can be expressed as:

$$\begin{pmatrix} X_{1pi} \\ X_{2pi} \\ X_{3pi} \end{pmatrix} = \begin{pmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \end{pmatrix} + \begin{pmatrix} \theta_{1p} \\ \theta_{2p} \\ \theta_{3p} \end{pmatrix} + \begin{pmatrix} \theta_{1i} \\ \theta_{2i} \\ \theta_{3i} \end{pmatrix} + \begin{pmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \end{pmatrix}. \quad (2)$$

X represents the actual responses, and the subscripts 1 to 3 indicate dimension v , where p and i define the examinee and the item, respectively. Equation 2 shows that a response for an item i on dimension v can be broken down into the grand mean μ , the examinee’s contribution θ_p , the item effect θ_i , and the error term ϵ . It is assumed that all θ and ϵ follow multivariate normal distributions whose mean vectors are $\mathbf{0}$ in mG-theory. Correspondingly, the variance-covariance matrices from Eq. 2 can be written as three blocks:

$$\begin{bmatrix} \sigma_{1X_{pi}}^2 & \sigma_{12X_{pi}}^2 & \sigma_{13X_{pi}}^2 \\ \sigma_{12X_{pi}}^2 & \sigma_{2X_{pi}}^2 & \sigma_{23X_{pi}}^2 \\ \sigma_{13X_{pi}}^2 & \sigma_{23X_{pi}}^2 & \sigma_{3X_{pi}}^2 \end{bmatrix} = \begin{bmatrix} \sigma_{1p}^2 & \sigma_{1p2p}^2 & \sigma_{1p3p}^2 \\ \sigma_{1p2p}^2 & \sigma_{2p}^2 & \sigma_{2p3p}^2 \\ \sigma_{1p3p}^2 & \sigma_{2p3p}^2 & \sigma_{3p}^2 \end{bmatrix} + \begin{bmatrix} \sigma_{1i}^2 & 0 & 0 \\ 0 & \sigma_{2i}^2 & 0 \\ 0 & 0 & \sigma_{3i}^2 \end{bmatrix} + \begin{bmatrix} \sigma_{1e}^2 & 0 & 0 \\ 0 & \sigma_{2e}^2 & 0 \\ 0 & 0 & \sigma_{3e}^2 \end{bmatrix}. \quad (3)$$

Now consider the $p \times i \bullet$ design, which also follows Eq. 2 but with different variance-covariance structures. Figure 3 shows a typical example of the design: 200 examinees take a 10-item test. These items measure three dimensions and therefore are scored three times. This situation would arise, for example, in a writing test where students’ essay responses are graded on grammar, style, and content. The variance-covariance structure can be formulated as:

$$\begin{bmatrix} \sigma_{1X_{pi}}^2 & \sigma_{12X_{pi}}^2 & \sigma_{13X_{pi}}^2 \\ \sigma_{12X_{pi}}^2 & \sigma_{2X_{pi}}^2 & \sigma_{23X_{pi}}^2 \\ \sigma_{13X_{pi}}^2 & \sigma_{23X_{pi}}^2 & \sigma_{3X_{pi}}^2 \end{bmatrix} = \begin{bmatrix} \sigma_{1p}^2 & \sigma_{1p2p}^2 & \sigma_{1p3p}^2 \\ \sigma_{1p2p}^2 & \sigma_{2p}^2 & \sigma_{2p3p}^2 \\ \sigma_{1p3p}^2 & \sigma_{2p3p}^2 & \sigma_{3p}^2 \end{bmatrix} + \begin{bmatrix} \sigma_{1i}^2 & \sigma_{1i2i}^2 & \sigma_{1i3i}^2 \\ \sigma_{1i2i}^2 & \sigma_{2i}^2 & \sigma_{2i3i}^2 \\ \sigma_{1i3i}^2 & \sigma_{2i3i}^2 & \sigma_{3i}^2 \end{bmatrix} + \begin{bmatrix} \sigma_{1e}^2 & \sigma_{1e2e}^2 & \sigma_{1e3e}^2 \\ \sigma_{1e2e}^2 & \sigma_{2e}^2 & \sigma_{2e3e}^2 \\ \sigma_{1e3e}^2 & \sigma_{2e3e}^2 & \sigma_{3e}^2 \end{bmatrix} \quad (4)$$

One can see that the examinee effect in the $p \times i^0$ design is distributed in the *unstructured* shape, while others follow the *diagonal* structure. In contrast, the $p \times i \bullet$ design adopts the *unstructured* structure for all variance and covariance components. These structures are specified according to both theory and actual design. For instance, in the $p \times i^0$ design, the given items nested in each dimension come from different item sets, and thus the variance-covariance matrix should be of a *diagonal* structure instead of *unstructured*. On the other hand, since examinees nested in the dimensions are from the same group of respondents, the covariance components (i.e., the correlations) cannot be ignored.

$$\begin{aligned} \text{1} \quad \Sigma &= \begin{bmatrix} \sigma_1^2 & 0 & 0 & 0 \\ 0 & \sigma_2^2 & 0 & 0 \\ 0 & 0 & \sigma_3^2 & 0 \\ 0 & 0 & 0 & \sigma_4^2 \end{bmatrix} & \text{2} \quad \Sigma &= \begin{bmatrix} \sigma_1^2 & \sigma_{12} & \sigma_{13} & \sigma_{14} \\ \sigma_{12} & \sigma_2^2 & \sigma_{23} & \sigma_{24} \\ \sigma_{13} & \sigma_{23} & \sigma_3^2 & \sigma_{34} \\ \sigma_{14} & \sigma_{24} & \sigma_{34} & \sigma_4^2 \end{bmatrix} \\ \text{3} \quad \Sigma &= \begin{bmatrix} 1 & p & p & p \\ p & 1 & p & p \\ p & p & 1 & p \\ p & p & p & 1 \end{bmatrix} & \text{4} \quad \Sigma &= \begin{bmatrix} 1 & p & p^2 & p^3 \\ p & 1 & p & p^2 \\ p^2 & p & 1 & p \\ p^3 & p^2 & p & 1 \end{bmatrix} \end{aligned}$$

Fig. 1 Covariance structure examples

p	v1				v2				v3			
	i1	i2	...	i10	i11	i2	...	i20	i21	i22	...	i30
1	x	x	...	x	x	x	...	x	x	x	...	x
2	x	x	...	x	x	x	...	x	x	x	...	x
...	...	...	...	...	...	...	...	...	...	...	...	...
200	x	x	...	x	x	x	...	x	x	x	...	x

Fig. 2 A typical example of $p \times i^0$ design

One can rewrite $\mu_1 = \mu + \Delta\mu_1$, $\mu_2 = \mu + \Delta\mu_2$, and $\mu_3 = \mu + \Delta\mu_3$ from Eq. 2. Therefore, referring Eq. 2 to Eq. 1, μ can be regarded as β_0 (i.e., γ_{00}) and u_0 can be removed. At first glance, it appears that no predictors are used in the aforementioned mG-theory designs. However, dummy variables can serve as predictors to indicate the dimension of a response. That said, a response labeled with $[X_1, X_2, X_3] = [1, 0, 0]$ origins from dimension v1, and $[0, 1, 0]$ and $[0, 0, 1]$ from dimensions v2 and v3, respectively. As seen above, if $\mu_1 = \beta_0 + \Delta\mu_1$, $\Delta\mu_1$ can be treated as γ_{10} for a response in dimension v1. The same idea applies to dimensions v2 and v3. Now, what remains in level 2 of Eq. 1 is u . Unsurprisingly, since $u \sim MN(0, \Sigma)$, all mG-theory variance and covariance components can be wired to u . Recall the examples illustrated in Figs. 2 and 3: responses are nested within examinees and items. Taking the examinee block, for example, $[u_1,$

$u_2, u_3]^T$ is distributed with $\begin{bmatrix} \sigma_{1p}^2 & \sigma_{1p2p}^2 & \sigma_{1p3p}^2 \\ \sigma_{1p2p}^2 & \sigma_{2p}^2 & \sigma_{2p3p}^2 \\ \sigma_{1p3p}^2 & \sigma_{2p3p}^2 & \sigma_{3p}^2 \end{bmatrix}$, where the

number of the level-2 clusters is P (i.e., the total number of the examinees). Given that a cross-classified relation can be built in the LMM, other blocks can then be formulated with the same flow. Therefore, $[u_1, u_2, u_3]^T$ can be further extended to $[u_{1p}, u_{2p}, u_{3p}]^T$, $[u_{1i}, u_{2i}, u_{3i}]^T$, and $[u_{1e}, u_{2e}, u_{3e}]^T$ to synthesize all three variance and covariance blocks in Eqs. 3 and 4. Last but not least, since mG-theory does not assume a univariate normal distribution, the r term in the LMM needs to be fixed to 0. This step is critical, as $[u_{1e}, u_{2e}, u_{3e}]^T$ should already include the residual components; specifying the r term can result in a redundant residual specification, which violates the assumption of unique residuals for each dimension in mG-theory (Webb, Shavelson, & Haertel, 2006). To be clear, if the r term in the LMM were permissible, the final estimates would be “parameters in Eq. 4

plus a new r .” At this point, the connection between LMMs and mG-theory should be perceptible.

The *glmmTMB* package

The *glmmTMB* package (Brooks et al., 2017) offers comprehensive solutions to fit generalized linear mixed models and their extensions. Similar to the famous *lme4* package (Bates et al., 2015), the *glmmTMB* package (Brooks et al., 2017) allows users to create a model with (1) different response types such as Gaussian, Poisson, and beta distributions; (2) link functions such as log, logit, identity, and complementary log-log; and (3) single or multiple random effects and fixed effects, and others. Jiang (2018) claimed that, due to the prohibition of correlated residuals, the *lme4* approach (and therefore the *gtheory* package) could not be extended to mG-theory designs. To be clear, the *lme4* package (Bates et al., 2015) does not provide the capacity to specify different covariance structures for random effects: if a design contains two dimensions, all covariance structures are identical except the *diagonal* one; however, if the number of dimensions is larger than two, an *unstructured* covariance, which the *lme4* package (Bates et al., 2015) cannot afford, is needed to model the unique correlations between each pair of dimensions. In addition, for crossed designs, such as $p \times i$, the ability to obtain correlations for the residual components is required, and the *lme4* package (Bates et al., 2015) is not capable of providing such a feature. The *glmmTMB* package (Brooks et al., 2017) possesses higher flexibility than the *lme4* package (Bates et al., 2015) for specifying variance and covariance structures. In accordance with the connection between LMMs and mG-theory, the challenging estimation becomes achievable in R software.

p	v1				v2				v3			
	i1	i2	...	i10	i1	i2	...	i10	i1	i2	...	i10
1	x	x	...	x	x	x	...	x	x	x	...	x
2	x	x	...	x	x	x	...	x	x	x	...	x
...	...	...	...	...	...	...	...	...	...	...	...	...
200	x	x	...	x	x	x	...	x	x	x	...	x

Fig. 3 A typical example of $p \times i \times$ design

To increase speed and flexibility, the *glmmTMB* estimation is achieved using Template Model Builder, and its interface is designed to be similar to the *lme4* package (Bates et al., 2015); therefore, the *lme4* means of specifying models and marking notations is inherent in the *glmmTMB* package (Brooks et al., 2017). Readers interested in seeing detailed syntax are referred to Bates (2005) and to Doran, Bates, Bliese, and Dowling (2007).

Prior to the analysis, datasets should be converted to a long format. As Table 1 illustrates, in a long format, each row of the dataset should be one response, where the columns contain the identity. For example, in the fourth row (i.e., ID = 4), the response, 46, is from examinee #4 in item #1 and belongs to the first dimension. Therefore, *d1* is 1, whereas *d2* and *d3* are 0, as they are the dummy coding variables for the dimension. Note that in a long format, statistically one will not encounter missingness, as NA (i.e., not available) responses need not be present in the dataset. The process of reshaping a wide format into a long format can be found in Lander (2014, p. 149). The example demonstrated in Fig. 2 can be modeled via the *glmmTMB* package (Brooks et al., 2017) as shown below.

```
mGtheory<-glmmTMB(
  Response~d1+d2+d3+us(0+d1+d2+d3|Examinee)+diag(0+d1+d2+d3|Item)+
    diag(0+d1+d2+d3|ID),
  data=dataset,
  dispformula=~0,
  control = glmmTMBControl(optCtrl=list(iter.max=1e3,eval.max=1e3))
)
```

The names of the variables used in the R syntax follow the convention shown in Table 1. The notation “~” bridges the linear relationship between “Response” and the dummy-coded “Dimension.” By default, the *glmmTMB* package (Brooks et al., 2017) generates an intercept, which is β_0 in an LMM context. The coefficients of “Dimension”—“d1” to “d3”—are the estimates of $\Delta\mu_1$ to $\Delta\mu_3$, respectively. As addressed above, the example in Fig. 2 contains three random-effect blocks. The “us” and “diag” correspond to the *unstructured* and the *diagonal* structures, respectively. One can see that this specification aligns with Eqs. 1 and 2. Note that “0” should be included in all blocks to ensure that the intercept component is not automatically included in the blocks’ formulas. The “data” navigates the name of the dataset, and the

Table 1 The dataset used in the analysis in a long format

ID	Examinee	Item	Dimension	d1	d2	d3	Response
1	1	1	1	1	0	0	47
2	2	1	1	1	0	0	42
3	3	1	1	1	0	0	42
4	4	1	1	1	0	0	46
...	...	...	...	...	...	...	...
3001	1	11	2	0	1	0	52
3002	2	11	2	0	1	0	53
...	...	...	...	...	...	...	...
5998	198	30	3	0	0	1	61
5999	199	30	3	0	0	1	63
6000	200	30	3	0	0	1	64

“dispformula” defines the shape of the residuals. To reiterate, the *r* term in LMMs will be fixed to 0 to estimate mG-theory. Therefore, “=~0” is entered to force the constraint. Finally, the “control” is simply a batch of commands for algorithmic configurations, such as the number of iterations and other stopping criteria. Alternatively, if the attribute of the dimension variable in the dataset (i.e., “Dimension” in Table 1) is converted to *factor*, the modeling specification part in the *glmmTMB* syntax can be rewritten as: Response~Dimension+us(0+ Dimension |Examinee)+diag(0+ Dimension |Item)+ diag(0+ Dimension |ID). To adjust the *glmmTMB* syntax to $p \times i$ design, the “diag” should be replaced with the “us” to update variance structures appropriately.

Data analysis example

In this section, the *glmmTMB* R code for the $p \times i^0$ design is used to analyze a simulated dataset. This is conducted for the purpose of providing a tutorial, not for performing a large-scale simulation study with numerous replications. That said, parameter recovery is not part of the present study. The dataset generation and true value specifications follow the practice by Jiang and Skorupski (2018). That is, a one-facet fully crossed design is employed where the number of dimensions is three. Mathematically, the design can be expressed as Eq. 2. The true values for μ are [3, 4, 5], where the variance components are specified as below in Eq. 5:

$$\begin{bmatrix} \sigma_{1X_{pi}}^2 & \sigma_{12X_{pi}}^2 & \sigma_{13X_{pi}}^2 \\ \sigma_{12X_{pi}}^2 & \sigma_{2X_{pi}}^2 & \sigma_{23X_{pi}}^2 \\ \sigma_{13X_{pi}}^2 & \sigma_{23X_{pi}}^2 & \sigma_{3X_{pi}}^2 \end{bmatrix} = \begin{bmatrix} 4 & 3 & 2 \\ 3 & 5 & 1 \\ 2 & 1 & 4.5 \end{bmatrix} \quad (5)$$

$$+ \begin{bmatrix} 6.5 & 0 & 0 \\ 0 & 8.5 & 0 \\ 0 & 0 & 4.5 \end{bmatrix} + \begin{bmatrix} 4.1 & 0 & 0 \\ 0 & 5.1 & 0 \\ 0 & 0 & 2.3 \end{bmatrix}.$$

After the variance and covariance components are estimated, the generalizability coefficient, known as the G-coefficient, in mG-theory can also be calculated. The G-coefficient in mG-theory is defined as:

$$\rho_{\delta}^2 = \frac{\mathbf{a}'\Sigma_p\mathbf{a}}{\mathbf{a}'\Sigma_p\mathbf{a} + \mathbf{a}'\Sigma_{\delta}\mathbf{a}/n_i}. \quad (6)$$

Σ_p is the examinee effect covariance matrix, while Σ_{δ} is the error covariance matrix, and n_i is the number of items. The $\mathbf{a}$ vector is a weighting scheme defining the relative importance of each dimension (see Wang & Stanley, 1970 for an overview). Although there are different ways to specify $\mathbf{a}$ (Brennan, 2001a; Marcoulides, 1994; Srinivasan & Shocker, 1973), to simplify the illustration, an equal weight scheme is adopted and therefore results in the true $\rho_{\delta}^2 = 0.98$. In addition to adopting equal weight scheme or other nominal specifications, effective weight and data-driven weight schemes are developed to offer different perspectives (see Appendix for the calculation). Specifically, nominal weights express the researcher's judgment regarding the relative importance of the various levels of a facet, where effective weights indicate the relative statistical contributions, and data-driven weighting schemes use iterative approaches to optimize generalizability (Marcoulides, 1994). Weight schemes have a great impact on decision-making in evaluating measurement instruments. Therefore, defining weights should be supported with evidence and thorough literature reviews. In the present scheme, the number of persons and the number of items is 200 and 30, respectively, while

Table 3. The estimates yielded by the *gltmmTMB* package

Random-effects (co)variances:			
Conditional model:			
Groups	Name	Std. Dev.	Corr
Examinee	d1	1.8204895	
	d2	2.0899889	0.83
	d3	1.9196811	0.58 0.42
Item	d1	2.8143787	
	d2	2.7247539	0.00
	d3	1.4266613	0.00 0.00
ID	d1	2.0428350	
	d2	2.2564543	0.00
	d3	1.5667994	0.00 0.00
Residual	0.0001221		
Number of obs: 6000 / Conditional model: Examinee, 200; Item, 30; ID, 6000			
Fixed Effects:			
Conditional model:			
(Intercept)	d1	d2	d3
44.45	5.75	14.85	25.85

each dimension comprises 10 items. The preview of the dataset in a long format is listed in Table 1; in total, there are 6000 responses. The computer used is a Lenovo IdeaPad with 8 GB RAM and a 2.6 GHz i7 6th Gen 4-core Intel processor. To compare the estimations, the dataset was fed into mGENOVA (Brennan, 2001b), and the estimates of interest are presented in Table 2.

Table 2 The estimates yielded by mGENOVA

INFORMATION ABOUT VARIABLE 1:		First	
Grand mean:		50.20154	
INFORMATION ABOUT VARIABLE 2:		Second	
Grand mean:		59.30468	
INFORMATION ABOUT VARIABLE 3:		Third	
Grand mean:		70.30240	
ESTIMATED G STUDY VARIANCE AND COVARIANCE COMPONENTS			
Note.		Lower diagonal elements are covariances.	
		Upper diagonal elements are correlations.	
Effect	First	Second	Third
p	3.28212	0.83023	0.57758
	3.17494	4.45575	0.40256
	2.00298	1.62659	3.66417
i	8.76900	8.17218	2.25605
pi	4.09697	5.01437	2.33697

The results produced by the *glmmTMB* package (Brooks et al., 2017) are presented in Table 3. Note that the estimates are the standard deviations and the correlations, instead of the variance and the covariance. As one can see, the results returned by mGENOVA (Brennan, 2001b) and the *glmmTMB* package (Brooks et al., 2017) are similar, meaning that the proposed approach indeed works and can be substituted for mGENOVA (Brennan, 2001b) when one prefers to analyze data using R software. While they are not substantial, the discrepancies reflect the functional differences in the selected algorithms: the *glmmTMB* package (Brooks et al., 2017) is powered by automatic differentiation to estimate model gradients and the Laplace approximation for handling random effects, whereas mGENOVA (Brennan, 2001b) is engineered by an ANOVA-based algorithm targeting expected mean squares. It is unsurprising that different algorithms, or different settings within the same algorithm, can produce different results, given the same dataset. Similarly, packages such as the *lme4* (Bates et al., 2015) and the *glmmTMB* are known to have a certain likelihood of producing inconsistent mixed-model estimates (Bolker, 2017).

Further, even though the dispersion was constrained to be zero, the residual estimate is not exactly zero in Table 3, as the algorithm is approximation-based. The grand means (i.e., the intercepts) can be calculated by $44.45 + 5.75$, $44.45 + 14.85$, and $44.45 + 25.85$ for the μ estimate. The $\hat{\rho}_\delta^2$ can be obtained via Eq. 7 as 0.96, which is slightly lower than the true value. The correlation terms are all zeros for the “Item” and the “ID” blocks in Table 3, as they were specified to follow the *diagonal* structure, in alignment with the present design. As a one-time simulation, these differences are expected, but they also warrant caution: since mG-theory is essentially an LMM variant, the random effects require a large number of observations and/or clusters to ensure that they are capable of both (1) representing the properties of the population and (2) recovering the model parameters (Stegmüller, 2013). In the data analysis example, however, the numbers of fixed-effect levels are not sufficiently large (e.g., 10 levels of the item facet per dimension), so both the generated dataset and its analysis tend to deviate from the true values.

Discussion

This paper presents a new approach for estimating the variance and covariance components of mG-theory. Compared with G-theory, mG-theory offers researchers perspectives concerning the relations between dimensions, which are critical to measurement instrument developers interested in studying subtests and their variance

differences. Therefore, the estimates in each dimension indicate how much variance a certain facet can contribute to the corresponding dimension. For instance, in the analysis example, the item variance estimates for the first two dimensions are larger than that of the last dimension; this finding may encourage researchers to further investigate the sources of variance in the uneven distribution across dimensions.

With the flexibility of the *glmmTMB* package (Brooks et al., 2017), users can tune LMMs to mG-theory such that the analysis can all be conducted in R software. The proposed method was also proven to yield results similar to mGENOVA (Brennan, 2001b) and therefore can serve as an alternative. Given that the *glmmTMB* package (Brooks et al., 2017) requires the dataset to be in a long format, estimations can still be made despite missing values, although biases can occur if the missingness is attributable to two patterns: missing at random and missing not at random. On the other hand, mGENOVA (Brennan, 2001b) does not allow the dataset to contain missing cells.

Like any other method, the proposed approach has limitations. The computational speed of the *glmmTMB* package (Brooks et al., 2017) can be significantly lower than mGENOVA (Brennan, 2001b) when a large dataset is used. In the previous section, the *glmmTMB* package (Brooks et al., 2017) required more than five seconds to converge, while mGENOVA (Brennan, 2001b) produced results immediately. As mGENOVA (Brennan, 2001b) algorithms are not matrix-based (Brennan, 2001a, p. 388), matrix operations deployed in the *glmmTMB* package (Brooks et al., 2017) can be avoided in mGENOVA (Brennan, 2001b), so the computation tends to be faster with the latter software. In addition to computational speed, a lack of intrinsic G-theory features in the software makes the proposed approach less appealing if comprehensive mG-theory results are preferred. For instance, sequential research addressing the practical application of a measurement procedure, called a decision (D) study, is incorporated in mGENOVA (Brennan, 2001b). A D study can help users design a measurement procedure that reduces errors at selected facets. To illustrate, a D study for writing test scores can inform users of the degree of impact on the G-coefficient by changing the number of raters within a budget limit. As non-mG-theory-specific software, the *glmmTMB* package (Brooks et al., 2017) can achieve the same functionality only by constructing a separate model for the decisional references. Thus, further research directions could include constructing a comprehensive mG-theory R package on top of the *glmmTMB* package (Brooks et al., 2017); for instance, users could deploy the package directly to produce a generalizability index for $\mathcal{G}$ score profiles or to specify different designs with a simple parameter change.

Appendix

```

##Read Sample Data
mGtheory<-
read.table("https://alabama.box.com/shared/static/9omab5aadtp2ofvkmcqamtv1c2vw8sqq.txt",
          header = FALSE, sep = "", dec = ";")

##Convert Data to Long Format
mGtheory_long<-NULL
for (iter in 1:ncol(mGtheory)){
  mGtheory_long<-c(mGtheory_long,as.numeric(as.character(mGtheory[,iter])))
}
Item<-NULL
num_i=30
num_p=200
num_e=num_p*num_i
num_v=3
for (iter_i in 1:num_i){
  Item<-c(Item,rep(iter_i, nrow(mGtheory)))
}
Examinee<-rep(1:num_p,num_i)
Dimension<-rep(1:num_v,each=num_p*(num_i/num_v))
d1<-rep(0,length(mGtheory_long))
d2<-rep(0,length(mGtheory_long))
d3<-rep(0,length(mGtheory_long))
for(iter in 1:length(mGtheory_long)){
  if(Dimension[iter]==1){d1[iter]<-1}
  if(Dimension[iter]==2){d2[iter]<-1}
  if(Dimension[iter]==3){d3[iter]<-1}
}
ID<-1:length(mGtheory_long)
mGtheoryLong<-as.data.frame(ID)
mGtheoryLong$Examinee<-Examinee
mGtheoryLong$Item<-Item
mGtheoryLong$Dimension<-Dimension
mGtheoryLong$d1<-d1
mGtheoryLong$d2<-d2
mGtheoryLong$d3<-d3
mGtheoryLong$Response<-round(mGtheory_long,0)

##Calculate phi-coefficient
numerator<-(((1/3)^2)*4+((1/3)^2)*5+((1/3)^2)*4.5+
            2*(1/3)*(1/3)*3 +2*(1/3)*(1/3)*2 +2*(1/3)*(1/3)*1
demoninator<-numerator+((((1/3)^2)*4.1+
                        ((1/3)^2)*5.1+
                        ((1/3)^2)*2.3))/30
phi<-numerator/demoninator

```



```
##Use glmmTMB to estimate p_dot*i_circle mG-theory
library(glmmTMB)
glmmTMB(Response~d1+d2+d3+us(0+d1+d2+d3|Examinee)+diag(0+d1+d2+d3|Item)+diag(0+
d1+d2+d3| ID),
  data=mGtheoryLong,
  dispformula=~0,
  control = glmmTMBControl(optCtrl=list(iter.max=1e4,eval.max=1e4)))
```

```
##Alternative way to execute glmmTMB for p_dot*i_circle mG-theory
mGtheoryLong$Dimension<-as.factor(mGtheoryLong$Dimension)
glmmTMB(Response~Dimension+us(Dimension|Examinee)+diag(Dimension|Item)+diag(Dime
nsion| ID),
  data=mGtheoryLong,
  dispformula=~0,
  control = glmmTMBControl(optCtrl=list(iter.max=1e4,eval.max=1e4)))
```

```
##Use glmmTMB to estimate p_dot*i_dot mG-theory
glmmTMB(Response~Dimension+us(Dimension|Examinee)+us(Dimension|Item)+us(Dimensio
n| ID),
  data=mGtheoryLong,
  dispformula=~0,
  control = glmmTMBControl(optCtrl=list(iter.max=1e4,eval.max=1e4)))
```

```
##Use glmmTMB to estimate p_dot*i_dot*h_dot example in Jiang & Skorupski (2018)
mGtheory2<-
read.table("https://alabama.box.com/shared/static/fs02xjabzinwf85jt37wsp3rvbzpzt7.txt",
  header = FALSE, sep = "", dec = ";")
mGtheory2_long<-NULL
for (iter in 1:ncol(mGtheory2)){
  mGtheory2_long<-c(mGtheory2_long,as.numeric(as.character(mGtheory2[,iter])))
}
num_i<-4
num_h<-3
num_v<-2
num_p<-100
Item<-rep(rep(c(1:num_i),each=num_p),num_v*num_h)
Rater<-rep(rep(c(1:num_h),each=num_p*num_i),num_v)
Dimension<-rep(1:num_v,each=length(mGtheory2_long)/num_v)
Examinee<-rep(c(1:num_p),length(mGtheory2_long)/num_p)
ID<-1:length(mGtheory2_long)
mGtheoryLong2<-as.data.frame(ID)
mGtheoryLong2$Examinee<-Examinee
mGtheoryLong2$Item<-Item
mGtheoryLong2$Dimension<-as.factor(Dimension)
mGtheoryLong2$Rater<-Rater
mGtheoryLong2$Response<-round(mGtheory2_long,0)
glmmTMB(Response~Dimension+us(Dimension|Examinee)+us(Dimension|Item)+us(Dimensio
n|Rater)+
  us(Dimension|Examinee:Item)+us(Dimension|Item:Rater)+us(Dimension|Examinee:Rater)+
  us(Dimension|ID),
  data=mGtheoryLong2,
  dispformula=~0,
  control = glmmTMBControl(optCtrl=list(iter.max=1e4,eval.max=1e4)))
```

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