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ESTIMATION OF A RAMSAY-CURVE ITEM RESPONSE THEORY MODEL BY THE METROPOLIS-HASTINGS ROBBINS-MONRO ALGORITHM

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Abstract

In Ramsay curve item response theory (RC-IRT, Woods & Thissen, 2006) modeling, the shape of the latent trait distribution is estimated simultaneously with the item parameters. In its original implementation, RC-IRT is estimated via Bock and Aitkin's (1981) EM algorithm, which yields maximum marginal likelihood estimates. This method, however, does not produce the parameter covariance matrix as an automatic byproduct upon convergence. In turn, researchers are limited in when they can employ RC-IRT, as the covariance matrix is needed for many statistical inference procedures. The present research remedies this problem by estimating the RC-IRT model parameters by the Metropolis-Hastings Robbins-Monro (MH-RM, Cai, 2010) algorithm. An attractive feature of MH-RM is that the structure of the algorithm makes estimation of the covariance matrix convenient. Additionally, MH-RM is ideally suited for multidimensional IRT, whereas EM is limited by the "curse of dimensionality." Based on the current research, when RC-IRT or similar semi-nonparametric IRT models are eventually generalized to include multiple latent dimensions, MH-RM would appear to be the logical choice for estimation.

Introduction

In unidimensional item response theory (IRT), two typical assumptions are that the item response functions (IRFs) are parametric (e.g., based on the logistic cumulative distribution function) and that the latent trait distribution $g(\theta)$ is Gaussian. These assumptions are supported by decades of success in empirical research in educational and psychological measurement. However, only one of these assumptions is necessary, because many different IRF-$g(\theta)$ combinations can produce the same joint distribution of item responses (Duncan & MacEachern, 2008). In some of these combinations, nonparametric IRFs may be employed while retaining certain parametric assumptions on the latent trait distribution and in others, the latent trait distribution may be characterized empirically without invoking the normality assumption.

There are major advantages associated with retaining the logistic form for IRFs. Doing so retains the interpretability of the item parameters and their estimates. In addition, a large part of existing assessment design, assembly, delivery, and reporting infrastructure based on standard IRT models requires no modifications, in contrast to the case of using non-parametric IRFs. At the same time, abandoning the normality assumption is attractive because it is easy to imagine scenarios where assuming normality of g(θ) is likely resulting in model misspecification (see e.g., Woods & Thissen, 2006). For example, sampling of participants in psychological or educational studies may suggest the correct latent trait distribution should be a mixture of normals, or that the distribution of proficiency latent variables may be expected to be non-normally distributed in certain sub-populations of interest (e.g. English learners), or perhaps the underlying latent variable represents the severity of a psychiatric disorder (e.g., depression) whose distribution should be non-normal in the general adult population. Consequently, researchers have developed several methods to characterize the shape of the latent trait distribution. These methods include empirical histograms (Bock & Aitkin, 1981), normal mixtures (Mislevy, 1984), Ramsay Curves (RC; Woods & Thissen, 2006; Woods, 2006), Davidian Curves (Woods & Lin, 2008), among alternatives.

Despite the availability of the new techniques, most IRT analyses in practice fall back on the traditional assumption of normality. One reason for this incongruence is that the methods need further development and generalization. As a primary example, as well as a motivation for this research, standard errors for the item parameters are not currently available when using Ramsay Curve IRT (RC-IRT). Without standard errors or, more generally, the observed data information matrix, researchers are limited in when they can use RC-IRT. For instance, standard errors are routinely used in test assembly as part of the item selection process. Also, the observed information matrix is needed for some limited-information goodness-of-fit testing (see, e.g., Cai, Maydeu-Olivares, Coffman, & Thissen, 2006) and differential item functioning analyses (Langer, 2008; Lord, 1980).

All model parameters of RC-IRT, in its original implementation, are estimated using Bock and Aitkin’s (1981) EM algorithm. Decades after its development, the method still enjoys extensive use because of its stability and, often, its speed. However, the EM algorithm does not yield the observed information matrix upon convergence. Consequently, standard errors for RC-IRT item parameters are not currently available. There are methods designed to address this deficiency within the framework of EM (see, e.g., Cai, 2008; Louis, 1982). However, an alternative strategy, adopted here, is to choose another estimation method that is more amenable to estimation of standard errors.

This research uses the Metropolis-Hastings Robbins-Monro algorithm (MH-RM, Cai, 2010) to perform maximum marginal likelihood (MML) estimation for RC-IRT, and to obtain the observed information matrix upon convergence. As noted above, Bock and Aitkin’s (1981) EM does not preclude approximation of the observed information matrix. Nevertheless, MH-RM is preferred here because it is better-suited to accommodate further generalizations of RC-IRT.

More specifically, when future research generalizes RC-IRT (or a similar methodology) to multidimensional latent traits, MH-RM would seem to be a logical and attractive choice for estimation. This is because the MH-RM algorithm is, in some sense, designed to address the "curse of dimensionality" that limits the feasibility of numerical quadrature based Bock-Aitkin EM in multidimensional IRT. This is also one of the first applications of the MH-RM algorithm to non-normal latent variable models, significantly expanding the boundaries of feasibility of MH-RM as a general estimation approach for maximum marginal likelihood IRT modeling.

As an aside, we are not advocates of RC-IRT, specifically. Rather, we view latent trait density estimation, generally, as theoretically appealing and practically useful. The characterization of the density, however, may be accomplished by numerous methods, all serving the same purpose. We focus on RC-IRT because it is one of the most elegant and well-studied semi-nonparametric density estimation approaches for IRT.

The remainder of this paper is organized as follows. The section labeled *A Graded Response Model for IRT* presents Samejima's (1969) graded response model. This is followed by a review of Ramsay curves and RC-IRT in *Ramsay Curve Item Response Theory*. The next 3 sections (*Two Approaches to Estimation for RC-IRT*; *Bock-Aitkin EM for RC-IRT*; *A Review of the Metropolis-Hastings Robbins-Monro Algorithm*) review and compare Bock and Aitkin (1981) EM and MH-RM (Cai, 2010) algorithms. In *An MH-RM Approach to RC-IRT*, the details of RC-IRT implementation for MH-RM are provided. Then, *Simulation Study* presents a simulation study examining the accuracy of point estimates and standard error estimates. *Empirical Data Analysis* contains an empirical study. Finally, the paper concludes in the *Discussion and Conclusion* section with directions for future research.

A Graded Response Model for IRT

This section introduces notation for a logistic IRT model for graded responses following Samejima (1969). In principle, other IRT models (e.g., rating scale or partial credit models) may also be used, but due to space constraints we do not go into their details.

Some Notation

Let there be i = 1, 2,..., N respondents, and j = 1, 2,..., n items. Let K_j be the number of response categories for item j. And, let U_{ij} be a random variable denoting the item response from person i to item j, with its realization denoted as $u_{ij} \in \{0, 1, ..., K_j - 1\}$. Then, $\mathbf{u}_i$ is an $n \times 1$ vector of observed item responses from person i, and $\mathbf{U}$ is an $N \times n$ matrix of observed response patterns, whose ith row is $\mathbf{u}'_i$.

For the *j*th item, let a_j be the item slope. Let $\mathbf{c}_j = (\mathbf{c}_{j1},\ldots,\mathbf{c}_{j(K_j-1)})'$, be a $(K_j - 1) \times 1$ vector of intercepts for item *j*. Parameters for item *j* are collected in the $K_j \times 1$ vector $\boldsymbol{\beta}_j = (a_j, \mathbf{c}_j)$. Collecting all of the item parameters, $\boldsymbol{\beta} = (\boldsymbol{\beta}'_1, \boldsymbol{\beta}'_2,\ldots, \boldsymbol{\beta}'_n)'$ is a $(\Sigma_{j=1}^{n} K_j) \times 1$ vector. For the *i*th person, let θ_i be the latent trait score, and let $\boldsymbol{\theta}$ be the $N \times 1$ vector of latent traits scores for all respondents.

Often, the θ_i's are assumed to follow a normal distribution. However, in RC-IRT, they are assumed to follow a Ramsay curve density having $\boldsymbol{\eta}$ as a vector of parameters. The size of $\boldsymbol{\eta}$ is v = *degree* + number of *knots* − 1. The terms *degree* and *knots* will be discussed in *A Review of Ramsay Curves*. As with density estimation procedures in general, the support of the Ramsay Curve density can be numerically represented over a set of points $\{x_q; q = 1,\ldots, Q\}$ along the real number line. In the current research, the points are equally spaced every 0.1, and the range can be determined by the analyst (e.g., choosing a range from −6 to 6 results in 121 points). Assuming a standardized latent trait, this choice of support ensures that the vast majority of the response pattern probabilities are captured.

Observed and Complete Data Likelihood

Conditional on an individual's latent trait score, θ_i, and the item parameters, $\boldsymbol{\beta}_j$, the conditional probability for response $U_{ij} = k$ is given by

$$\begin{aligned}\pi_{ij}(k) &= P(U_{ij} = k|\boldsymbol{\beta}_j, \theta_i) = \frac{1}{1+\exp(-a_j\theta_i - c_{jk})} - \frac{1}{1+\exp(-a_j\theta_i - c_{j(k+1)})} \\ &= T_{ij}(k) - T_{ij}(k+1),\end{aligned} \quad (1)$$

where T_{ij} (*k*) is the (cumulative) conditional response probability for categories *k* and higher. The following response probabilities are defined for the boundary categories: $T_{ij}(0) = 1$ and $T_{ij}(K_j) = 0$. Based on Equation (1), the conditional distribution of U_{ij} is a multinomial with K_j cells and cell probabilities $\pi_{ij}(k)$:

$$f(u_{ij}|\boldsymbol{\beta}_j, \theta_i) = P(U_{ij} = u_{ij}|\boldsymbol{\beta}_j, \theta_i) = \prod_{k=0}^{K_j-1} [\pi_{ij}(k)]^{\chi_k(u_{ij})}, \quad (2)$$

where $\chi_k(u)$ is an indicator function defined as

$$\chi_k(u) = \begin{cases} 1, & \text{if } u = k \\ 0, & \text{otherwise} \end{cases}. \quad (3)$$

Assuming conditional independence (Lord & Novick, 1968), the conditional response pattern probability is

$$f(\mathbf{u}_i|\boldsymbol{\beta},\theta_i) = \prod_{j=1}^{n} f(u_{ij}|\boldsymbol{\beta}_j,\theta_i). \tag{4}$$

Again, for RC-IRT, the shape of the latent distribution depends on the RC parameters, $\boldsymbol{\eta}$. Therefore, the density for any θ_i depends on $\boldsymbol{\eta}$, and will hereafter be expressed as $g(\theta_i\,|\boldsymbol{\eta})$. Also, let $\boldsymbol{\omega} = (\boldsymbol{\beta}, \boldsymbol{\eta})$ be the vector of all model parameters with length $d = \left(\sum_{j=1}^{n} K_j\right) + v$. Thus, for a person sampled from this potentially non-normal distribution, the marginal probability of $\mathbf{u}_i$ is:

$$f(\mathbf{u}_i|\boldsymbol{\omega}) = \int \prod_{j=1}^{n} f(u_{ij}|\boldsymbol{\beta}_j,\theta) g(\theta|\boldsymbol{\eta}) d\theta. \tag{5}$$

Treating response patterns as fixed once observed, the observed data likelihood is

$$L(\boldsymbol{\omega}|\mathbf{U}) = \prod_{i=1}^{N} \left[\int \prod_{j=1}^{n} f(u_{ij}|\boldsymbol{\beta}_j,\theta) g(\theta|\boldsymbol{\eta}) d\theta \right]. \tag{6}$$

If we treat the individual latent traits $\boldsymbol{\theta} = (\theta_1,..., \theta_N)'$ as missing data, then the complete data can be expressed as $(\mathbf{U}, \boldsymbol{\theta})$. Due to conditional independence of item responses and independence of respondents, the complete data likelihood has a completely factored form (see, e.g., Cai, 2010),

$$L(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta}) = \prod_{i=1}^{N} \left[g(\theta_i|\boldsymbol{\eta}) \prod_{j=1}^{n} f(u_{ij}|\boldsymbol{\beta}_j,\theta_i) \right] = \left[\prod_{i=1}^{N} g(\theta_i|\boldsymbol{\eta}) \right] \left[\prod_{i=1}^{N}\prod_{j=1}^{n} f(u_{ij}|\boldsymbol{\beta}_j,\theta_i) \right]. \tag{7}$$

Taking natural logarithm of the right-hand side of Equation (7), the complete data log-likelihood can be expressed as

$$\log L(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta}) = \log L(\boldsymbol{\eta}|\boldsymbol{\theta}) + \log L(\boldsymbol{\beta}|\mathbf{U},\boldsymbol{\theta}). \tag{8}$$

Equation (8) reveals that the complete data log-likelihood can be understood as the sum of two independent parts: a log-likelihood component for the RC parameters, $\boldsymbol{\eta}$, and a log-likelihood component for the item parameters, $\boldsymbol{\beta}$. Moreover, the latter part corresponds to n ordinal logistic regressions, one for each item. This structure implies that during estimation, each of these sets of parameters can be updated separately, resulting in additional computational savings.

Ramsay Curve Item Response Theory

Given the structure of Equation (8), we seek a model that describes the form of the latent trait density given values of $\boldsymbol{\theta}$. Equation (8) also makes it clear that such a model does not depend on item parameters or responses. Our model uses Ramsay Curves.

A Review of Ramsay Curves

What follows is a brief and general overview of Ramsay Curves. The mathematical details are beyond the scope of this research, but interested readers should consult Ramsay (2000) and de Boor (2001) for a thorough treatment. Also, Woods and Thissen (2006) provide an introduction to Ramsay Curves from a psychometric perspective.

The shape of the RC density is found by connecting a set of curves known as B-splines. The range and potential flexibility of the RC is determined by the analyst, through three choices: the *range*, the *degree,* and the number of *knots*. First, the range defines the support of the density $g(\theta|\boldsymbol{\eta})$. As mentioned earlier, a typical range for standardized latent traits is from −6 to 6. Second, the degree refers to the degree of the polynomial for each B-spline. Higher degrees can accommodate sharper curves. Third, the knots are where the B-splines connect to one another. Typically, the knots are evenly spaced across the range of support. A greater number of knots also allows more flexibility in the RC. The second and third choices (i.e., degree and number of knots) determine the number of elements in $\boldsymbol{\eta}$, the vector of RC parameters. As mentioned above, the length of $\boldsymbol{\eta}$ is v = *degree* + number of *knots* − 1.

Together, the three choices determine the structure of the $\mathbf{B}^*$ matrix (see Equation 11 in Woods & Thissen, 2006). Assuming that $\mathbf{B}^*$ can be obtained, the height of the RC at θ is given by

$$g(\theta|\boldsymbol{\eta}) = \frac{\exp\left[\mathbf{B}^*(\theta)\boldsymbol{\eta}\right]}{C}, \tag{9}$$

where

$$C = \sum_{q=1}^{Q} \exp\left[\mathbf{B}^*(x_q)\boldsymbol{\eta}\right] \tag{10}$$

is the normalization constant that ensures $g(\theta|\boldsymbol{\eta})$ integrates to 1 and is a proper density. As defined in Equation (8), the log-likelihood for the RC part of the model is

$$\log L(\boldsymbol{\eta}|\boldsymbol{\theta}) = \sum_{i=1}^{N} \log g(\theta_i|\boldsymbol{\eta}). \tag{11}$$

Given $\boldsymbol{\theta}$, the RC parameters in $\boldsymbol{\eta}$ can be obtained by maximization of log $L(\boldsymbol{\eta}|\boldsymbol{\theta})$. Once estimates of $\boldsymbol{\eta}$ are obtained, they can be used in Equation (9) to find $g(\theta_i|\boldsymbol{\eta})$ for a particular respondent or to construct the entire RC density.

In practice, there may be some regions of the latent trait scale over which little or no information about the RC parameters is available. As a result, the corresponding spline coefficients may become empirically under-identified. And due to the dependencies among the

RC parameters, this may cause a failure in estimation for all elements of $\boldsymbol{\eta}$. To guard against this possibility, Woods and Thissen (2006) imposed a diffuse v-variate normal prior on $\boldsymbol{\eta}$, and used Bayesian maximum *a posteriori* estimates in lieu of maximum likelihood estimates for the RC part of the model. The prior mean vector $\boldsymbol{\mu}$ is chosen such that the values match RC coefficients that would reproduce a normal density for θ. The covariance matrix of the prior is a $v \times v$ scaled identity matrix $\varsigma\mathbf{I}_v$, implying that the marginal univariate priors on the components of $\boldsymbol{\eta}$ are independent and share common prior dispersion ς. Since the main purpose of the prior is to stabilize estimation, ς should be as large as possible while still allowing successful estimation. In other words, the actual objective function to be maximized is equal to log $L(\boldsymbol{\eta}|\boldsymbol{\theta})$ + log $\varphi(\boldsymbol{\eta}|\boldsymbol{\mu}, \varsigma\mathbf{I}_v)$, where $\varphi(\cdot)$ is the density of a v-variate normal random variable.

Two Approaches to Estimation for RC-IRT

In this research we compare two alternatives for RC-IRT estimation: Bock and Aitkin's (1981) EM (BA-EM) and MH-RM (Cai, 2010). Both approaches have been applied to standard unidimensional and multidimensional IRT models and are implemented in available software (e.g., IRTPRO; Cai, Thissen, & du Toit, 2011). Further, BA-EM has been used extensively for RC-IRT (Woods, 2007, 2008; Woods & Thissen, 2006).

Both EM and MH-RM exploit relationships between the observed data log-likelihood, $l(\boldsymbol{\omega}|\mathbf{U})$ = log $L(\boldsymbol{\omega}|\mathbf{U})$, and complete data log-likelihood $l(\boldsymbol{\omega}|\mathbf{U}, \boldsymbol{\theta})$ = log $L(\boldsymbol{\omega}|\mathbf{U}, \boldsymbol{\theta})$, but do so in different ways. In EM, the MLE is found by iteratively maximizing the conditional expectation of $l(\boldsymbol{\omega}|\mathbf{U}, \boldsymbol{\theta})$ over $\Pi(\boldsymbol{\theta}|\mathbf{U}, \boldsymbol{\omega})$, where $\Pi(\boldsymbol{\theta}|\mathbf{U}, \boldsymbol{\omega})$ is the posterior predictive distribution of missing data (the latent traits). Convergence results (Wu, 1983) show that the successive EM iterations will result in a (local) maximizer of $l(\boldsymbol{\omega}|\mathbf{U})$.

MH-RM, on the other hand, is at its core a root-finding algorithm. Let $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$ denote the gradient vector of the observed data log-likelihood. Solving the likelihood equations

$$\dot{l}(\boldsymbol{\omega}|\mathbf{U}) = \frac{\partial l(\boldsymbol{\omega}|\mathbf{U})}{\partial \boldsymbol{\omega}} = \mathbf{0}, \tag{12}$$

yields a potential maximizer of $l(\boldsymbol{\omega}|\mathbf{U})$. Due to Fisher 's identity (Fisher, 1925), the conditional expectation of the complete data log-likelihood's gradient vector $\dot{l}(\boldsymbol{\omega}|\mathbf{U}, \boldsymbol{\theta})$ is equal to the observed data log-likelihood's gradient vector $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$, i.e.,

$$\dot{l}(\boldsymbol{\omega}|\mathbf{U}) = \int \dot{l}(\boldsymbol{\omega}|\mathbf{U}, \boldsymbol{\theta})\Pi(\boldsymbol{\theta}|\mathbf{U}, \boldsymbol{\omega})d\boldsymbol{\theta}. \tag{13}$$

Finding the root of the right-hand side of Equation (13) results in a (local) maximizer of $l(\boldsymbol{\omega}|\mathbf{U})$. MH-RM obtains the solution iteratively by drawing imputations from the posterior predictive distribution $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$ and stabilizes the noise introduced by the random draws with the Robbins-Monro (Robbins & Monro, 1951) method.

Bock-Aitkin EM for RC-IRT

Woods and Thissen (2006), in the original RC-IRT implementation, embedded estimation of the Ramsay curve within Bock and Aitkin (1981) EM. This section provides a brief overview of the algorithm, and the modifications needed to accommodate estimation of the Ramsay curve.

A Review of the Bock and Aitkin (1981) EM Algorithm

Notably, Bock and Aitkin (1981) EM (BA-EM) is quadrature-based. This feature dictates how values are computed, and requires equations slightly different in form than those presented in (5) through (8). The primary distinction is that while MH-RM takes a summation over examinees, BA-EM takes a summation over quadrature points. As an aside, this latter summation is what can limit the practicality of BA-EM in multidimensional IRT. The number of quadrature points grows exponentially with the dimensionality of the latent trait, regardless of sample size. In the literature, this phenomenon is sometimes called the “curse of dimensionality.”

Very generally, the EM algorithm (Dempster, Laird, & Rubin, 1977) iteratively maximizes the expectation of $l(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})$ over $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$, where $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$ is the posterior predictive distribution of missing data. The procedure alternates between E-steps (for expectation) and M-steps (for maximization) until convergence. For BA-EM, the steps take the following forms.

For the E-step, given observed data and current parameter estimates, the conditional expectation of the missing data, $\boldsymbol{\theta}$, is found. For each item, this conditional expectation is collected in the so-called E-step tables. For the M-step, for each item, the E-step tables are treated as observed data and logit analysis is performed. The resulting item parameter estimates are used in the next E-step.

Modifications to BA-EM estimation for RC-IRT

Provided the infrastructure for constructing the RC is in place (as discussed in *Ramsay Curve Item Response Theory*), the modifications needed to use BA-EM for RC-IRT are quite minimal. First, revise the E-step by using the current characterization of $g(\theta|\boldsymbol{\eta})$ to find the conditional expectation of $\boldsymbol{\theta}$. As before, fill in the E-step tables for each item. Second, estimate the proportion of respondents at each quadrature point, denoted $N(x_q)$, by summing across all E-step tables. Following Woods and Thissen (2006), at this point, the scale is identified by standardizing $N(x_q)$ to have a mean of 0 and variance of 1.

Finally, in the M-step, update the RC parameters. Given the structure of Equation (8), this update occurs independently of the item parameter updates. Since the set of $N(x_q)$ is akin to a collection of “observed” latent trait scores, the RC methodology in *A Review of Ramsay Curves* can be used to find updated estimates of $\boldsymbol{\eta}$. The updated RC is used in the next E-step. The algorithm is terminated when the iterations convergence.

A Review of the Metropolis-Hastings Robbins-Monro Algorithm

What follows is a broad outline of the MH-RM algorithm. For full details, see Cai (2010). As its name suggests, the MH-RM algorithm couples stochastic imputation via a Metropolis Hastings sampler (Hastings, 1970; Metropolis, Rosenbluth, Rosenbluth, Teller, & Teller, 1953) with a Robbins-Monro (Robbins & Monro, 1951) root-finding algorithm for noise-corrupted functions. Pieced together appropriately, these two methods complement one another to facilitate maximum likelihood estimation.

Recall Fisher ’s identity in Equation (13), which motivates the MH-RM algorithm. If we can find the expectation of $\dot{l}(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})$ over $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$, then we know the value of $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$, the gradient of the observed data log likelihood. And, if we can sample from $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$, we can find the requisite expectation by Monte Carlo approximation. Fortunately, $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$ is proportional to $L(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})$, which allows us to construct an MH sampler. This is the MH part of MH-RM.

By the law of large numbers, we can approximate $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$ with arbitrary precision by increasing the number of MH imputations. However, such a brute force approach may be misguided. From one cycle to the next, the approximation to $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$ is only used to find the direction of the update for $\boldsymbol{\omega}$. For the sake of efficiency, a more sensible approach is to use a small number of imputations. Of course, this renders the sequence of approximations noisy. The RM method, though, was designed for such situations. Despite the noise, the RM method allows us to find the root of $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$, that is, the MLE. This is the RM part of MH-RM.

An MH-RM Approach to RC-IRT

Having sketched an outline of the MH-RM algorithm, more details are needed to understand the implementation for RC-IRT. Some of these details are specific to the RC-IRT model (e.g., derivatives, selection of a sampler), while others are provided for context. The subsections that follow detail choices and results for derivatives, gain constants, starting values, parameter updates, and standard errors.

Complete Log Likelihood Derivatives

As mentioned above, $\dot{l}(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})$ is used to approximate $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$. Thus, first derivatives of the complete log likelihood are clearly needed. In addition, second derivatives are used in MH-RM for two purposes. Following the convention established earlier, let $\ddot{l} = \partial^2 l/(\partial\boldsymbol{\omega}\partial\boldsymbol{\omega}')$ denote the matrix of second derivatives of the log-likelihood function. In MH-RM, $\ddot{l}(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})$ is used to compute a scaling factor for the parameter update which ideally speeds convergence. Also, it is used to approximate the observed information matrix and, by extension, estimates of standard errors. How this is accomplished is discussed below. The derivatives for the graded response model are standard results (see, e.g., Baker & Kim, 2004, p. 213-217). Derivatives for the RC parameters are presented in Appendix A.

Specification of Gain Constants

Let $m = 1, 2,\ldots, \infty$ index the iteration for the MH-RM algorithm. The gain constants γ_m, for $m \geq 1$, scale the updates and serve to slowly average out the noise in the approximations to $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$. For this to occur, the γ_m need to slowly decrease to zero, which is ensured by the following conditions,

$$\gamma_m \in (0,1], \quad \sum_{m=1}^{\infty} \gamma_m = \infty, \text{ and } \quad \sum_{m=1}^{\infty} \gamma_m^2 < \infty. \tag{14}$$

If the γ_m decrease too quickly, then the estimates for $\boldsymbol{\omega}$ may stabilize prematurely, before the MLE is reached. Alternatively, if the γ_m decrease too slowly, the estimates for $\boldsymbol{\omega}$ may never stabilize. One satisfactory option, noted by Cai (2010), is to take γ_m as $1/m$. The rate of the decrease can be further fine-tuned by taking γ_k as $1/m^r$, with $1/2 < r \leq 1$ (Polyak & Juditsky, 1992).

Computing Updates

What follows is an adaptation of Equations (16) through (18) from Cai (2010). There is nothing particular to RC-IRT that needs to be addressed here. Nevertheless, the material is included because it is essential to understanding other aspects of the RC-IRT implementation.

Recall that MH-RM seeks to find the root of $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$ by iteratively estimating the expectation of $\dot{l}(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})$ over $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$, and updating $\boldsymbol{\omega}$ accordingly. Provided appropriate gain constants are specified, and samples from $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$ can be obtained, the parameters are updated in the following manner. Let $d=\left(\sum_{j=1}^{n} c_j\right) + v$ be the number of parameters in the model. Then, let $(\boldsymbol{\omega}^{(0)}, \boldsymbol{\Gamma}_0)$ be initial values, where $\boldsymbol{\Gamma}_0$ is a $d\times d$ symmetric positive definite matrix. Let $\boldsymbol{\omega}^{(m)}$ be the parameter estimate at the end of iteration k. The $(m + 1)$th iteration consists of *stochastic imputation*, *stochastic approximation*, and an *RM update*.

For *stochastic imputation*, we draw S_m sets of missing data $\{\boldsymbol{\theta}_s^{(m+1)}; s = 1, 2,\ldots, S_m\}$ from $\Pi(\boldsymbol{\theta}|\mathbf{U},\boldsymbol{\omega})$, to form S_m complete data sets $\{(\mathbf{U}, \boldsymbol{\theta}_s^{(m+1)}); s = 1, 2,\ldots, S_m\}$. A large S_m is usually unnecessary for MH-RM.

For *stochastic approximation*, using Fisher's (1925) identity, we approximate the observed data gradient, $\dot{l}(\boldsymbol{\omega}|\mathbf{U})$, by the sample average of complete data gradients,

$$\mathbf{g}_{m+1} = \frac{1}{S_m} \sum_{s=1}^{S_m} \dot{l}(\boldsymbol{\omega}^{(m)} | \mathbf{U}, \boldsymbol{\theta}_s^{(m+1)}). \tag{15}$$

Also, to speed convergence, we use curvature information by recursively approximating the conditional expectation of the complete data information matrix,

$$\boldsymbol{\Gamma}_{m+1} = \boldsymbol{\Gamma}_m + \gamma_m \left\{ -\frac{1}{S_m} \sum_{s=1}^{S_m} \ddot{l}(\boldsymbol{\omega}^{(m)} | \mathbf{U}, \boldsymbol{\theta}_s^{(m+1)}) - \boldsymbol{\Gamma}_m \right\}. \tag{16}$$

Finally, in the *RM update*, we set the new parameter estimate to

$$\boldsymbol{\omega}_{m+1} = \boldsymbol{\omega}_m + \gamma_m (\boldsymbol{\Gamma}_{m+1}^{-1} \mathbf{g}_{m+1}). \tag{17}$$

Constructing an MH Sampler

As in Patz and Junker (1999) and Cai (2010), a Metropolis-within-Gibbs sampling scheme is used to impute the latent trait scores. Let $q(\theta_i, \theta_i^*)$ be the transition density for moving from θ_i to θ_i^*. Also, define the acceptance factor as

$$\alpha(\theta_i, \theta_i^*) = \min \left[\frac{f(\mathbf{u}_i | \boldsymbol{\beta}, \theta_i^*) g(\theta_i^* | \boldsymbol{\eta}) q(\theta_i^*, \theta_i)}{f(\mathbf{u}_i | \boldsymbol{\beta}, \theta_i) g(\theta_i | \boldsymbol{\eta}) q(\theta_i, \theta_i^*)}, 1 \right]. \tag{18}$$

Equation (18) depends on the RC parameters to calculate $g(\theta_i | \boldsymbol{\eta})$. However, the acceptance probability for each θ_i depends on neither the latent trait scores of other persons, nor their item responses. Thus, all draws can be performed simultaneously with vector operations. Commonly, a symmetric random walk chain with some scalar dispersion parameter is used (Metropolis et al., 1953) for the transition density. In such a case, $q(\theta_i^*, \theta_i) = q(\theta_i, \theta_i^*)$, and the acceptance factor can be further simplified.

However, for RC-IRT, a symmetric random walk chain proves problematic. The minimum and maximum for x_q are user-defined (say, $x_{\min}$ and $x_{\max}$). The RC has no density outside this range. Consequently, for all $\theta_i^* \notin [x_{\min}, x_{\max}]$, the RC density evaluates to zero $g(\theta_i^* | \boldsymbol{\eta}) = 0$, which implies $\alpha(\theta_i, \theta_i^*) = 0$. Clearly, a transition density producing proposal values that are routinely not accepted can become highly inefficient. proposal values that are routinely not accepted can become highly inefficient. To address this issue, the implemented transition density is constructed so that $\alpha(\theta_i, \theta_i^*) \neq 0$ (except very rarely), regardless of the scalar dispersion parameter.

To accomplish this goal, we seek a transition density where $\mathrm{Var}(\boldsymbol{\theta}^*) = 1$. Such a condition will ensure that the imputations only rarely fall outside of the range for x_q. Let δ be the scalar dispersion parameter, let $e_i \sim N(0, 1)$ and let **e** be a vector of normal deviates whose *i*th element is e_i. As a reminder, $\mathrm{Var}(\boldsymbol{\theta}) = 1$ to identify the scale. Then, let $\phi = \mathrm{Var}(\boldsymbol{\theta} + \delta e) = 1 + \delta^2$. Finally, let the proposal draws be generated by θ^* = ($\boldsymbol{\theta}$/$\sqrt{\varphi}$) + (δ/$\sqrt{\varphi}$)**e**. It can be verified that Var($\boldsymbol{\theta}^*$) = 1, which achieves the stated goal.

Written as a density function, the proposal draws are generated from

$$q(\theta_i, \theta_i^*) = \frac{1}{\sqrt{2\pi(\delta^2/\varphi)}} \exp\left\{-\frac{1}{2}\frac{(\theta^* - (\theta/\sqrt{\varphi}))^2}{(\delta^2/\varphi)}\right\}. \tag{19}$$

Examining the exponent of Equation (19), it is clear that $q(\theta_i^*$,$\theta_i) \neq q(\theta_i$,$\theta_i^*)$. Consequently, the ratio of transition densities in Equation (18) cannot be further simplified.

Providing Reasonable Starting Values

Without reasonable starting values, MH-RM estimation may fail, particularly if there is little information to identify some of parameters. This is not surprising as the convergence theory for the algorithm depends on the use of sufficiently good starting values (Borkar, 2008). Fortunately, the flexibility of the method admits a simple solution.

To explain this solution, it helps to consider the algorithm as proceeding through three successive stages: Stage 1, Stage 2, and Stage 3. These will be explained momentarily. Similarly, it is useful to introduce two types of starting values: “crude” and “refined.” Crude starting values are far away from the optimum, whereas refined ones are reasonably close to the solution. Let us assume for a moment that if refined values are available to start Stage 3, then estimation will succeed. The goal, then, is to find refined values to start Stage 3.

This goal is achieved in the following way. First, crude values are provided to start Stage 1. For instance, set all item slopes to 1.0 and item intercepts to values found by inverting cumulative category endorsement proportions on the standard normal cumulative distribution function. These values are crude but they can be obtained cheaply. Next, we set γ_m and S_m equal to unity for all of the iterations in Stage 1. As noted in Cai (2010), the MH-RM algorithm, specified in this way, is a close relative to Diebolt and Ip’s (1996) stochastic EM (SEM) algorithm. Importantly, the SEM-type iterations move ω_m quickly to the neighborhood of the MLE. Stage 1 should run as long as necessary for the analyst to be confident that ω_m has reached this neighborhood. In particular, one may observe a trend that the sequence of negative complete data log-likelihood function values $\{-l(\boldsymbol{\omega}^{(0)}|\mathbf{U}, \boldsymbol{\theta}_s^{(1)})$**,…,** $-l(\boldsymbol{\omega}^{(m)}|\mathbf{U}, \boldsymbol{\theta}_s^{(m+1)})$**,…**$\}$ may exhibit: it would typically start off at a large value, but would quickly move toward a region where it starts to oscillate. This concludes Stage 1.

In Stage 2, the SEM-type iterations continue where Stage 1 left off, but with a different purpose. As a reminder, the goal of this process is to provide refined starting values for Stage 3.

These refined values can be obtained by averaging $\boldsymbol{\omega}_m$ for some number of Stage 2 iterations (e.g., 100). The averaging dampens the Monte Carlo noise in the iterates. Upon obtaining these averages, Stage 2 is complete.

Finally, the refined values are used to start Stage 3. In this last stage, decreasing gain constants are used. In this way, the Monte Carlo noise is filtered out and the estimates converge to the MLE point-wise. This strategy is effective because the mean of the invariant distribution in Stage 2 is close to the MLE.

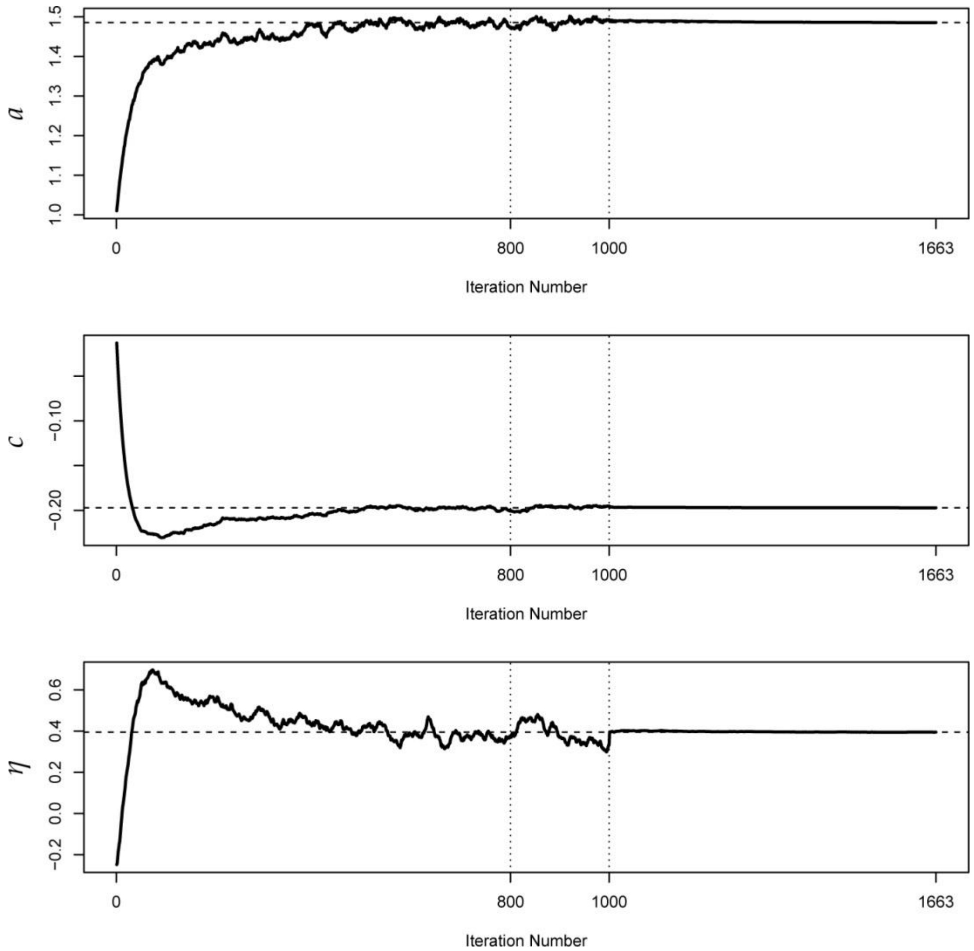

Figure 1. Example of MH-RM for RC-IRT: Sequences of estimates for three parameters. *a* = slope parameter; *c* = intercept parameter; *η* = RC parameter. Horizontal lines (dashed) indicate MLE values. Vertical lines (dotted) demarcate the 3 stages of iterations. Stage 1 consisted of the first 800 iterations. Stage 2 consisted of the next 200 iterations. Stage 3 continued until the convergence criteria was reached at 1,663 iterations.

Figure 1 shows the Stages for three typical sequences of estimates from one replication of the simulation study (presented in *Simulation Study*). From the top, the three panels show the estimates for a slope parameter, an intercept parameter, and an RC parameter. In Stage 1 (SEM-type iterations $1 - 800$), the estimates move (relatively) quickly to reach the neighborhood of the MLE. In Stage 2 (SEM-type iterations $801 - 1000$), sample estimates are collected to compute means with which to start Stage 3. And lastly, in Stage 3 (decreasing γ_m iterations $1, 001 - 1, 663$), the estimates converge to the MLE.

Approximating the Observed Information

Louis (1982) derived a useful equality, linking the observed information to functions of the complete log likelihood. The information matrix of the observed log likelihood is

$$-\ddot{l}(\boldsymbol{\omega}|\mathbf{U}) = E_{\omega}\{-\ddot{l}(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})\} - \mathrm{cov}_{\omega}\{\dot{l}(\boldsymbol{\omega}|\mathbf{U},\boldsymbol{\theta})\}, \tag{20}$$

where the expectation is with respect to $\Pi(\boldsymbol{\theta}|\mathbf{U}, \boldsymbol{\omega})$. Cai (2010) proposed a method that uses Louis's equation, where the elements needed for computation are byproducts of the MH-RM estimation procedure (Cai, 2010, p. 42). This is one of the (two) methods of approximation implemented in IRTPRO (Cai et al., 2011) (Accumulation method) for IRT models with normal latent traits. A benefit of this approach is that the observed information matrix is computed concurrently with parameter estimation.

Another approach, again following Louis (1982), is proposed by Diebolt and Ip (1996). This strategy uses Monte Carlo integration to approximate the mean and covariance in Equation (20). The parameter estimate, $\hat{\boldsymbol{\omega}}$, is fixed at the MLE, and a large number of (say $S = 1, 000$) Monte Carlo samples of $\boldsymbol{\theta}$ are generated from $\Pi(\boldsymbol{\theta}|\mathbf{U}, \hat{\boldsymbol{\omega}})$. These samples are used to approximate the terms on the right-hand side of Equation (20). For some examples of this latter method, see Diebolt and Ip (1996) and Fox (2003). For standard IRT models, this method is available in IRTPRO (Cai et al., 2011) (Monte Carlo method).

One last feature of the complete information matrix should be noted. Due to the conditional independence assumption, the information matrix is block diagonal. Each block of item parameters is $C_j \times C_j$, and the RC block is $v \times v$. Hence, while the entire matrix is $d \times d$, where $d = (\sum_{j=1}^{n} C_j) + v$, utilizing the blocked structure may lead to substantial savings in storage and computation time.

Simulation Study

A Monte Carlo simulation study was conducted to compare the MH-RM and EM algorithms, and to evaluate the accuracy of the MH-RM standard errors. The purpose of comparing MH-RM and EM is to validate the MH-RM implementation as it is the first time the algorithm is used outside of standard IRT models with normal latent variables. As both methods compute MLEs, substantially discrepant results would indicate an improper implementation of MH-RM.

Methods and Design

This section details how the data were generated and how estimation was specified. Generally, true parameters were chosen to be realistic for psychological or educational measurement. There were N = 1000 simulees and n = 25 items. There were three conditions, based on the true shape of the latent trait distribution. Finally, there were 100 replications for each condition.

The true shape of $g(\theta|\boldsymbol{\eta})$ was either normal, skewed, or bimodal. All densities were represented by rectangular quadrature points, ranging from −6 to 6 by 0.1. The RC parameters for these densities were generated by mixing two normals. For the skewed density, the generating parameters were: $\mu_1 = -0.25$, $\mu_2 = 2.19$, $\sigma_1^2 = 0.37$, $\sigma_2^2 = 1.10$, $mp_1 = 0.9$, and $mp_2 = 0.1$. For the bimodal density, the values were: $\mu_1 = -1$, $\mu_2 = 1$, $\sigma_1^2 = 0.49$, $\sigma_2^2 = 0.49$, $mp_1 = 0.48$, and $mp_2 = 0.52$. The mixtures were then standardized to have $\mu = 0$ and $\sigma_2 = 1$. Next, the standardized mixtures were treated as data in RC log-likelihood functions (see Equation 11) with degree=5 and knots=6. Finally, the log-likelihoods were maximized to yield estimates of $\boldsymbol{\eta}$. These estimates were subsequently treated as the true RC parameters. The resulting densities are shown in Figure 2.

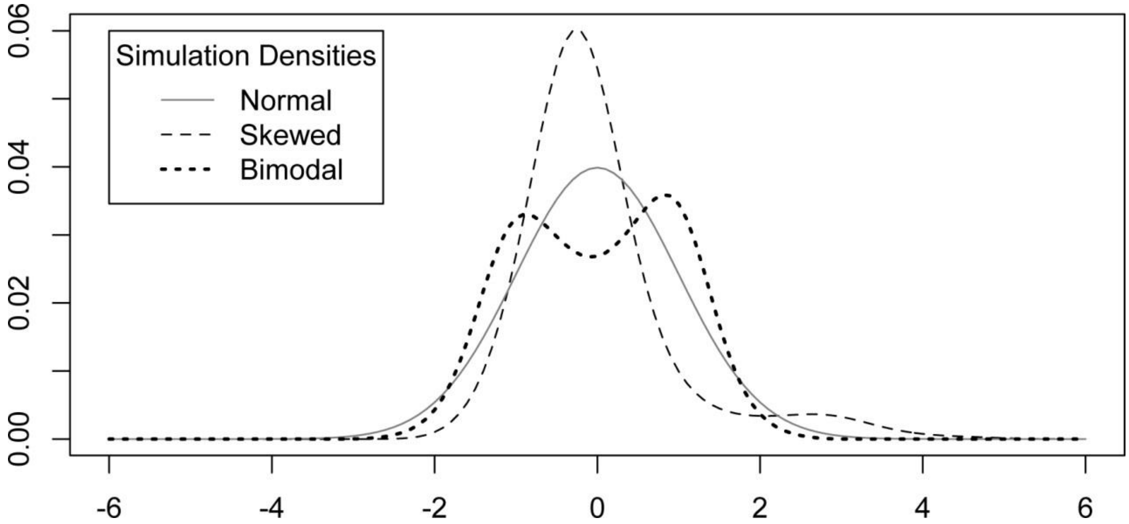

Figure 2. True densities used for the simulation study. True normal curve (gray solid line); true skewed curve (dashed line); true bimodal curve (thick dotted line).

The true item parameters were generated in a manner similar to Woods and Lin (2008). The slope parameters, a, were drawn from a truncated normal distribution with mean = 1.8 and standard deviation = 0.8, and truncation at 0.5 and 4. Difficulty parameters (typically labeled b) were drawn in the following way. The first difficulty parameter (b_1) was drawn from a normal with mean= 1 and *SD*= 0.5. To obtain b_2, a random draw was taken from a normal (mean= 1 and *SD*= 0.2) and *added* to b_1. Both b_3 and b_4 were drawn under the same procedure. Since the graded response model was presented in terms of slopes and intercepts, the latter were calculated as $c = -ab$. The same item parameters were used for all replications across all conditions, and are displayed in Table 1.

Table 1

Simulation study: generating item parameter values

Item	Slope	Intercept 1	Intercept 2	Intercept 3	Intercept 4
1	1.89	1.71	−0.32	−2.59	−4.56
2	1.44	2.37	0.88	−0.66	−1.90
3	1.45	3.71	2.50	1.42	0.24
4	2.18	3.20	0.60	−1.24	−2.97
5	1.56	0.47	−1.66	−3.36	−5.11
6	1.81	3.28	1.42	−0.25	−2.69
7	0.50	1.07	0.58	0.20	−0.27
8	0.89	0.37	−0.48	−1.56	−2.66
9	0.94	1.00	−0.22	−1.24	−2.37
10	1.30	1.09	−0.32	−1.30	−2.60
11	1.56	2.05	0.20	−1.17	−3.17
12	1.37	2.28	0.51	−1.05	−1.82
13	3.18	5.04	2.11	−2.37	−5.47
14	2.02	3.15	1.05	−1.16	−2.65
15	2.34	3.93	1.97	0.44	−1.23
16	3.87	2.94	−1.16	−5.59	−10.14
17	1.63	1.03	−1.06	−2.70	−4.46
18	1.41	1.39	−0.31	−1.33	−2.93
19	0.75	0.62	−0.19	−1.13	−2.22
20	1.99	1.35	−0.37	−2.31	−3.90
21	1.99	−0.48	−2.54	−4.23	−6.34

Item	Slope	Intercept 1	Intercept 2	Intercept 3	Intercept 4
22	1.98	0.04	−1.79	−3.29	−5.88
23	1.85	1.67	−0.52	−2.60	−4.14
24	1.57	0.35	−1.02	−2.23	−4.22
25	1.96	1.06	−0.86	−2.99	−5.14

For each replication, $\boldsymbol{\theta}$ was drawn from the true $g(\theta|\boldsymbol{\eta})$ using rejection sampling (von Neumann, 1951). Then, probabilities of $u_{ij} = 1$ (i.e., correct item responses) were simulated according to the graded model. These probabilities were compared to random uniform (0, 1) variables. Item responses were determined in proportion to the model-implied probabilities.

The graded model was fitted to the data in each replication, using both EM and MH-RM algorithms. The starting values for all a's were equal to 1. For all $\mathbf{c}_j$, the starting values were (1, 1/3, −1/3, −1). The starting values for $\boldsymbol{\eta}$ were those that would reproduce a normal density. The density, $g(\theta|\boldsymbol{\eta})$, was represented using 121 support points, evenly spaced from −6 to 6. Finally, the correct RC was estimated (5-degree with 6 knots). Thus, for both the item responses and RC, the fitted and data generating models were the same.

As mentioned earlier, the forms of the RC likelihood functions for EM and MH-RM take different forms and imply different scales. Thus, different values for ς (the variance for each marginal of the multivariate normal prior) are appropriate depending on the method of estimation. Based on trial and error, ς was set to 1 for MH-RM. For EM, ς was set to 1000.

For MH-RM, the simulation size S_m was set to 1 for all iterations. As in the example in *Providing Reasonable Starting Values*, Stage 1 consisted of 800 iterations, followed by Stage 2 with 200 iterations. For Stage 3, the decreasing gain constants were set to $\gamma_m = 1/m^r$ with $r = 0.75$. For convergence criteria, the iterations were examined across a window of 3 iterations. Once the maximum absolute change across the window dropped below 1.0×10^{-4}, the iterations were deemed converged. For EM, the iterations were considered converged once the maximum absolute between-iteration change in parameter estimates dropped below 1.0×10^{-4}.

Outcome Measurements

Overall model fit was assessed using log-likelihood values. Greater values indicate better fit. To evaluate the accuracy of item parameter recovery, estimated bias and root mean square error (RMSE) are used. Let M be the number of Monte Carlo replications and ω denote the true value of an arbitrary element of the parameter vector $\boldsymbol{\omega}$. Then, estimated bias is defined as

$M^{-1}\sum_{m=1}^{M}(\widehat{\omega}_m - \omega)$ where $\widehat{\omega}_m$ is the MLE for *ω* in replication *m*. RMSE is defined as $\sqrt{M^{-1}\sum_{m=1}^{M}(\widehat{\omega}_m - \omega)^2}$.

Since the scales of the true RC parameters are both unfamiliar and quite variable, estimated bias and RMSE are less appropriate measures of recovery accuracy. Instead, the integrated square error (ISE),

$$ISE(\hat{g}) = \int \{g(\theta|\hat{\boldsymbol{\eta}}) - g(\theta|\boldsymbol{\eta})\}^2 d\theta, \tag{21}$$

is used to measure the similarity between the true and estimated RCs, as in Woods and Lin (2008). The ISE was multiplied by 1,000 to facilitate comparison. Also, when aggregated ISE statistic is reported, the median instead of the mean was used due to skewness and kurtosis.

To assess the accuracy of the estimated standard errors, let $se(\widehat{\omega})_m$ be the estimated standard error for *ω* in replication *m*. Then, $\overline{se}(\widehat{\omega})$ = $M^{-1}\sum_{m=1}^{M}$ $se(\widehat{\omega})_m$ and the Monte Carlo standard deviation is defined as $sd(\widehat{\omega})$ = $\sqrt{(M-1)^{-1}\sum_{m=1}^{M}(\widehat{\omega}_m - \overline{\omega})^2}$, where $\overline{\omega}$ is the mean of the estimates across replications. If the standard errors are estimated accurately, the averages, $\overline{se}(\widehat{\omega})$, should closely correspond to the observed standard deviations, $sd(\widehat{\omega})$ of the sampling distribution.

Results: Points Estimates from MH-RM and EM

All replications converged for both the MH-RM and BA-EM algorithms. For both algorithms, the log-likelihood (plus 30,000), ISE (multiplied by 1,000), and estimated bias and RMSE of item parameters are displayed in Table 2. Generally, the comparability of EM and MH-RM is established by comparing means of outcome measurements across replications, as well as inspecting plots of these measurements by replication.

Table 2

Simulation Results for MH-RM and BA-EM Estimations of RC-IRT

Estimation	LogL	RMSE: *a*	Bias: *a*	RMSE: *c*	Bias: *c*	ISE
ISE Normal $g(\theta\|\boldsymbol{\eta})$						
MH-RM	−500.10	0.10	0.01	0.14	−0.01	0.04
BA-EM	−500.11	0.10	0.01	0.14	0.02	0.04
Skewed g(θ|η)						
MH-RM	−393.75	0.12	0.01	0.13	0.00	0.09
BA-EM	−393.07	0.12	0.01	0.13	0.00	0.09
Bimodal g(θ|η)						
MH-RM	−381.78	0.10	0.01	0.14	−0.00	0.13
BA-EM	−381.77	0.09	−0.00	0.14	0.01	0.14

Note. LogL = log-likelihood (plus 30,000); RMSE = root mean square error; Bias = Monte Carlo average estimate minus the true parameter value; *a* = slope parameter; *c* = intercept parameter; ISE = median of the integrated square error multiplied by 1,000.

For each true $g(\theta|\boldsymbol{\eta})$ shape, the average log-likelihoods for MH-RM and EM are virtually identical. In addition to the average log-likelihoods, the values at each replication are extremely similar. In Figure 3, all of the points are very close to the 45° reference line, regardless of $g(\theta|\boldsymbol{\eta})$. Thus, in terms of global model fit, there is no appreciable difference between the MH-RM and EM results.

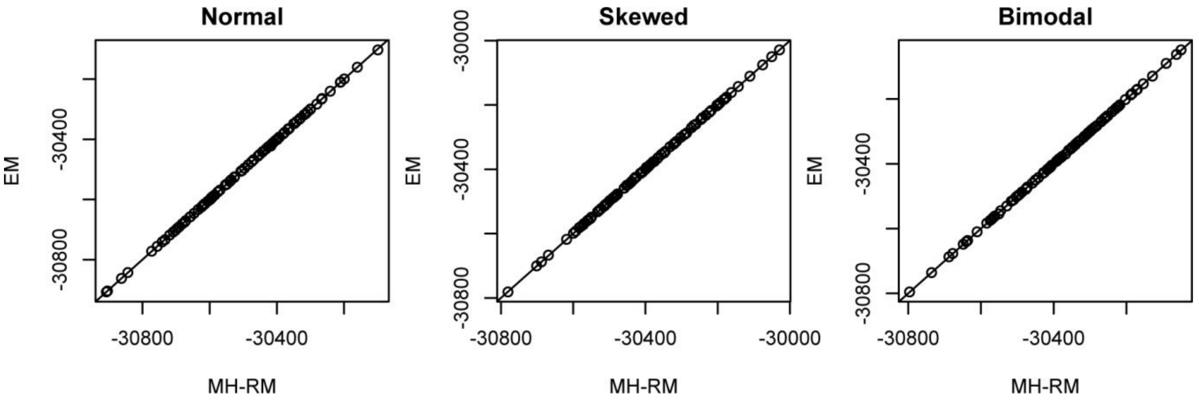

Figure 3. Log-likelihood Values for MH-RM (*x*-axis) and EM (*y*-axis) Algorithms.

Again consulting Table 2, the average RMSE and estimated bias for the item parameters are nearly indistinguishable under MH-RM and EM. Assessing item parameter recovery from another perspective, Figure 4 compares the average RMSE for all item parameters, by replication, for MH-RM and EM. Again, the vast majority of points are close to the 45° reference line, indicating that within each replication MH-RM and EM are producing generally comparable results.

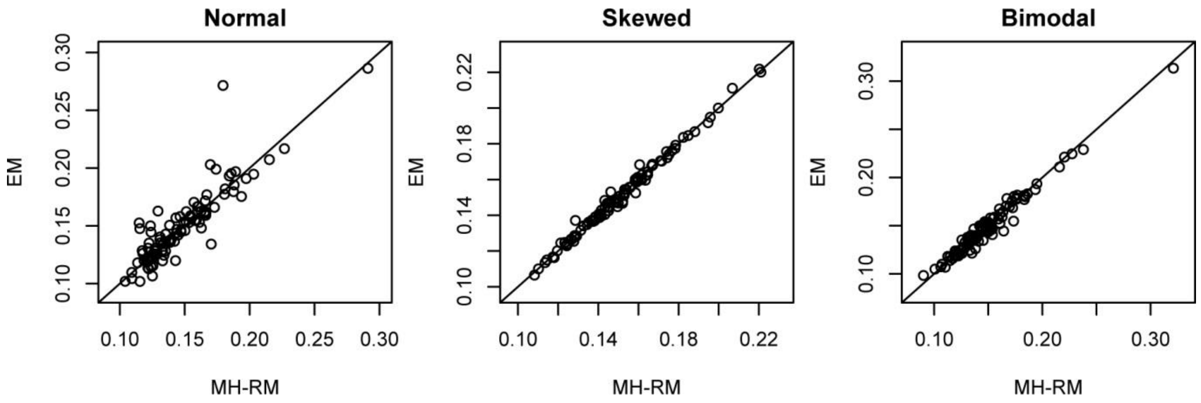

Figure 4. Average RMSE for Item Parameters within a Replication for MH-RM (x-axis) and EM (y-axis) Algorithms.

Results for the accuracy of the estimated RCs is also presented in Table 2 via the ISE statistic. As should be expected, the ISE values for the normal $g(\theta|\boldsymbol{\eta})$ are the lowest among the three distributions. While Table 2 presents the median ISE values, Figure 5 compares the MH-RM and EM ISE values for each distribution by replication. The proximity of the points to the 45$_{\circ}$ reference line implies that the two methods are yielding comparable density estimates.

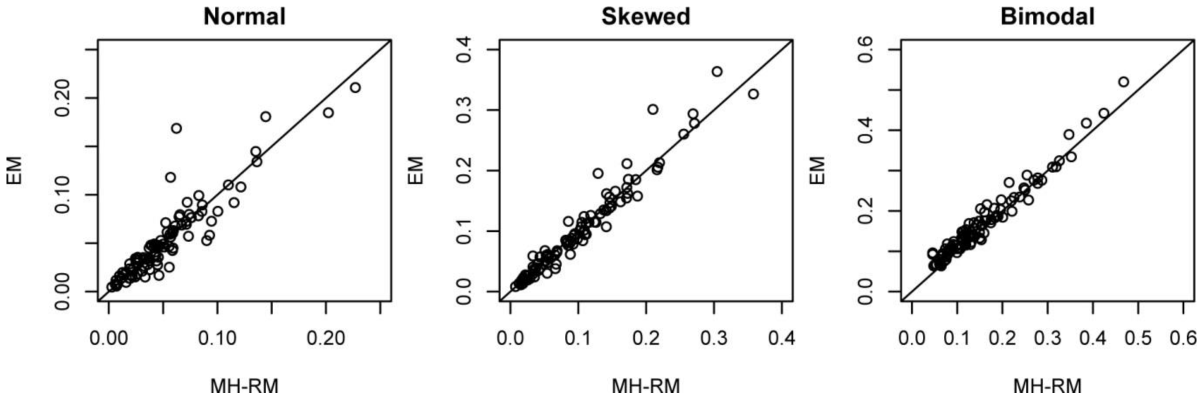

Figure 5. ISE for MH-RM (x-axis) and EM (y-axis) Algorithms.

Given all of the evidence above, it is clear that MH-RM and EM produce very similar point estimates for RC-IRT. Additionally, for MH-RM, Figure 6 shows the average approximated RC for each condition (left column) and the 95% confidence intervals (right column). For the normal and skewed distributions, the differences between true and average approximated RC are nearly indistinguishable. Also, the 95% confidence intervals for the normal and skewed distributions clearly capture the true curves. For the bimodal distribution, the approximated RCs are less accurate. While the approximated curves are largely bimodal distributions, they fail to capture the full extent of the local extrema.

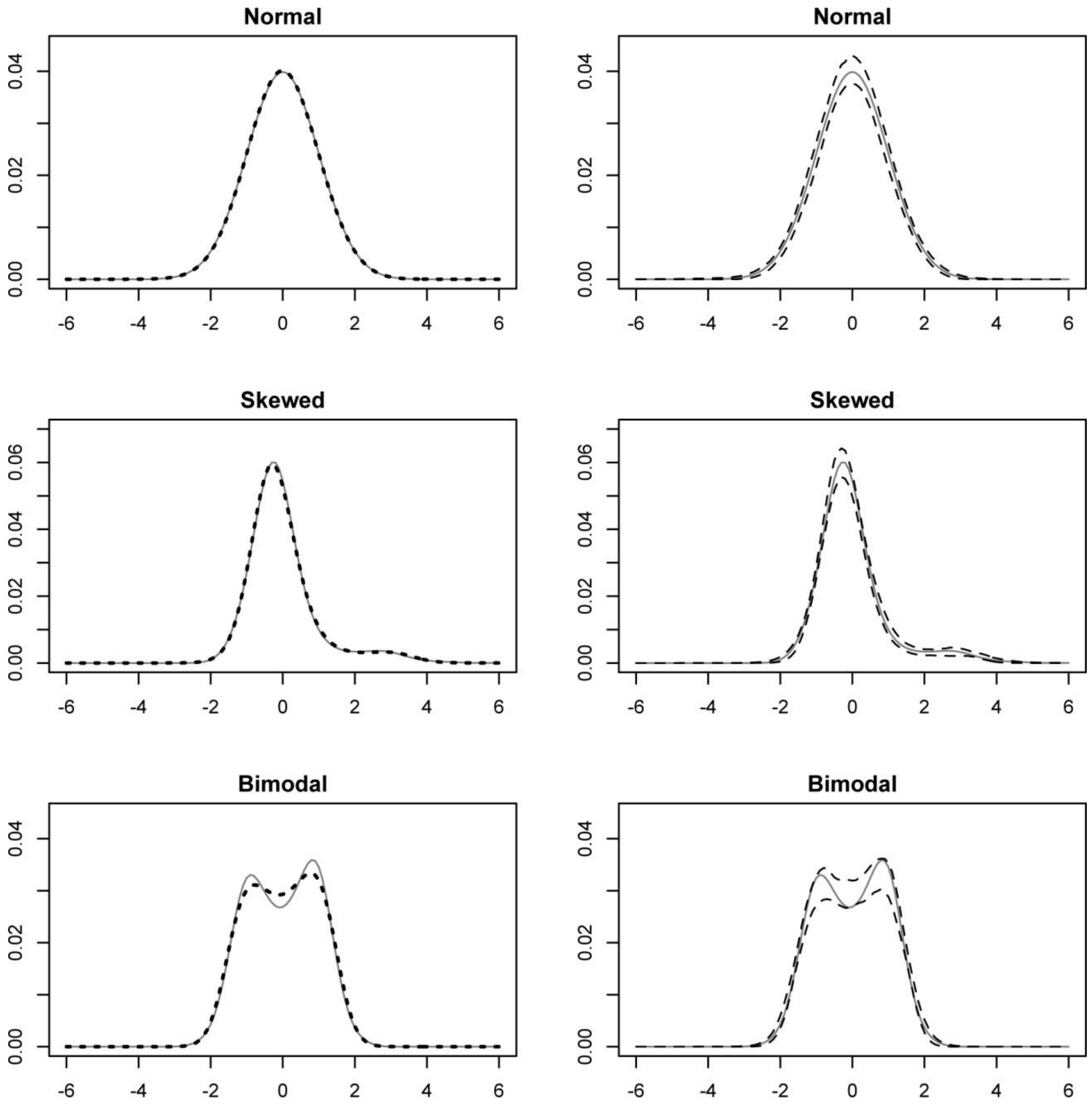

Figure 6. True densities (gray solid lines) used for the simulations, average RC-IRT estimates (dotted lines), and 95% confidence intervals (dashed lines). RC-IRT = Ramsay-curve item response theory. Left column: True curves (gray solid lines) and average RC-IRT estimate (dotted line). Right column: True curves (gray solid lines) and 95% confidence interval (dashed lines) for RC-IRT estimate.

Results: Standard Errors from MH-RM

Table 3 presents the average standard error and Monte Carlo standard deviation (in parentheses) for all slope parameters across the three distributions. As can be seen, overall, the values are very close to one another. Figure 7 presents the same statistics, but for all item parameters. From the plots, it is clear that the Monte Carlo standard deviations tend to be slightly larger than the average standard errors.

Table 3

Average Standard Errors and Monte Carlo Standard Deviations for Slope Parameters

Item	Normal	Skewed	Bimodal
1	0.09 (0.10)	0.10 (0.11)	0.09 (0.10)
2	0.08 (0.08)	0.09 (0.12)	0.08 (0.08)
3	0.09 (0.09)	0.12 (0.13)	0.09 (0.10)
4	0.10 (0.12)	0.12 (0.13)	0.10 (0.09)
5	0.09 (0.10)	0.09 (0.11)	0.09 (0.10)
6	0.09 (0.09)	0.10 (0.11)	0.09 (0.10)
7	0.06 (0.06)	0.07 (0.07)	0.06 (0.06)
8	0.07 (0.07)	0.07 (0.07)	0.07 (0.07)
9	0.07 (0.07)	0.07 (0.07)	0.07 (0.06)
10	0.08 (0.09)	0.08 (0.10)	0.07 (0.08)
11	0.08 (0.09)	0.09 (0.10)	0.08 (0.07)
12	0.08 (0.08)	0.09 (0.09)	0.08 (0.07)
13	0.15 (0.18)	0.17 (0.20)	0.15 (0.14)
14	0.10 (0.10)	0.11 (0.12)	0.09 (0.09)
15	0.11 (0.12)	0.13 (0.14)	0.11 (0.13)
16	0.20 (0.23)	0.21 (0.23)	0.20 (0.20)
17	0.09 (0.09)	0.09 (0.12)	0.09 (0.09)
18	0.08 (0.08)	0.08 (0.11)	0.08 (0.07)
19	0.07 (0.07)	0.07 (0.07)	0.06 (0.06)
20	0.10 (0.12)	0.10 (0.12)	0.10 (0.10)
21	0.11 (0.13)	0.11 (0.14)	0.11 (0.11)
22	0.11 (0.12)	0.11 (0.13)	0.10 (0.10)
23	0.09 (0.10)	0.10 (0.13)	0.09 (0.08)
24	0.09 (0.09)	0.09 (0.11)	0.09 (0.10)
25	0.10 (0.11)	0.10 (0.12)	0.10 (0.11)

Note. Entries are the Monte Carlo averages of estimated standard errors and the Monte Carlo standard deviations (in parentheses) of the estimated parameters.

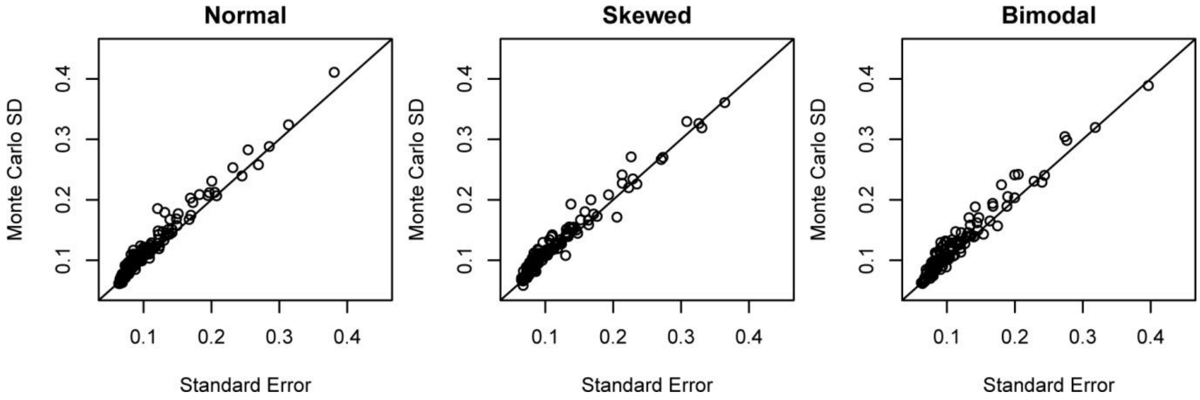

Figure 7. Average Standard Errors and Monte Carlo Standard Deviations for Item Parameters.

Empirical Data Analysis

Data used to illustrate estimation of RC-IRT model via the MH-RM algorithm come from the Drug Abuse Treatment Outcome Studies (DATOS). DATOS is a national evaluation of treatment effectiveness funded by the National Institute on Drug Abuse. The available sample was quite large, and N = 2,500 respondents were randomly selected for the analysis. 11 Likert-type items measuring mental health and emotional distress were analyzed using RC-IRT. As an example, one item asked, “How troubled or distressed (bothered) are you now by emotional or psychological problems?” Respondents could answer with one of the following: *not at all* (0), *somewhat* (1), or *very troubled* (2). Accordingly, higher latent trait scores correspond with greater emotional distress.

To verify that a unidimensional analysis was appropriate, and to provide a comparison for RC-IRT, a standard IRT analysis was carried out using Bock and Aitkin’s (1981) EM algorithm in flexMIRT® (Cai, 2012). All items were fitted using the graded response model. The resulting RMSEA value was 0.04, suggesting that a unidimensional model fits the data reasonably well. Further results from the standard IRT analysis will be discussed below.

RC-IRT was carried out with maximums of *degree* = 5 and *number of knots* = 6 (see A *Review of Ramsay Curves*). Model selection was based on the Hannan-Quinn information criteria (HQIC), as recommended by Woods (2007, 2008). The MH-RM specifications were identical to those used for the simulation study (see *Simulation Study*).

Empirical Analysis Results

For RC-IRT, the 1-3 model (i.e., *degree* = 1 and *knots* = 3) yielded the lowest HQIC, and was thus selected. Table 4 displays different comparison criteria for both the RC-IRT and standard IRT models. For all criteria, the 1-3 RC-IRT model has the lower values, indicating better fit. Point estimates and standard error estimates for both RC-IRT and standard IRT models are displayed in Figure 8. Notably, some standard errors obtained for the 1-3 RC-IRT model are appreciably larger than the corresponding values obtained via traditional analysis.

Table 4

Model Comparison Criteria for 11 DATOS Items ($N = 2,500$)

Model	Parameters	-2LogL	AIC	BIC	HQIC
1-3 RC	46	8685.07	8777.07	9044.97	8874.33
Normal	43	8750.19	8836.19	9086.63	8927.11

Note. 1-3 RC = RC-IRT Model with *degree* = 1 and *knots* = 3; Normal = IRT estimation assuming a normal distribution for $g(\theta)$; AIC = Akaike information criteria; BIC= Bayesian information criteria; HQIC = Hannan-Quinn information criteria. All values are less 30,000 to facilitate comparison.

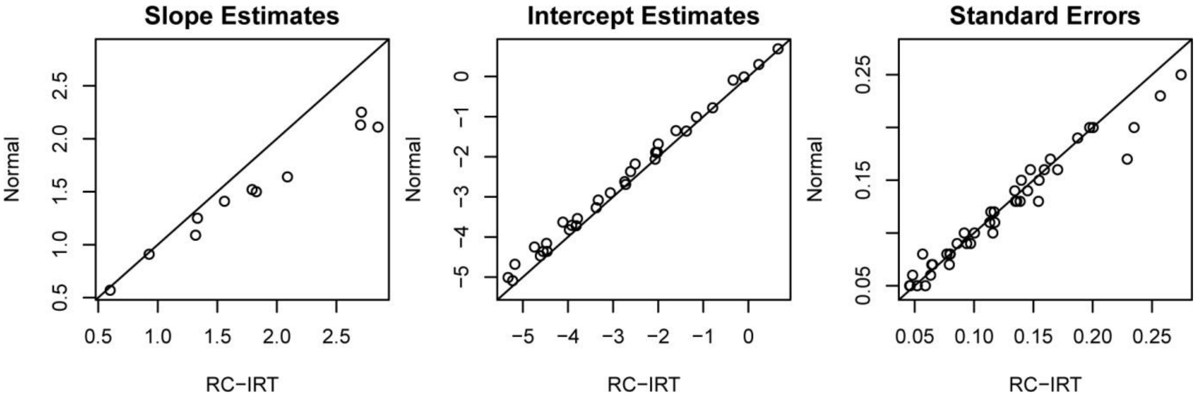

Figure 8. Estimates of Item Parameter Standard Errors for 11 DATOS Items. RC-IRT = Ramsay curve IRT; Normal = Standard IRT with Assumption of Normal Density.

Figure 9 shows the estimated RC associated with this scale. Interestingly, the distribution is skewed left. In comparison to the normal density, the estimated RC indicates a greater number of the respondents are characterized by a lack of emotional distress. The difference in the two sets of results also manifests itself in the test information curves, shown in Figure 10. Of note, neither curve dominates. This implies that the conditional standard error of measurement is not uniformly higher for either analysis. That being said, the most obvious difference in the curves occurs at moderately positive values for the latent trait, where the RC-IRT analysis reveals more information.

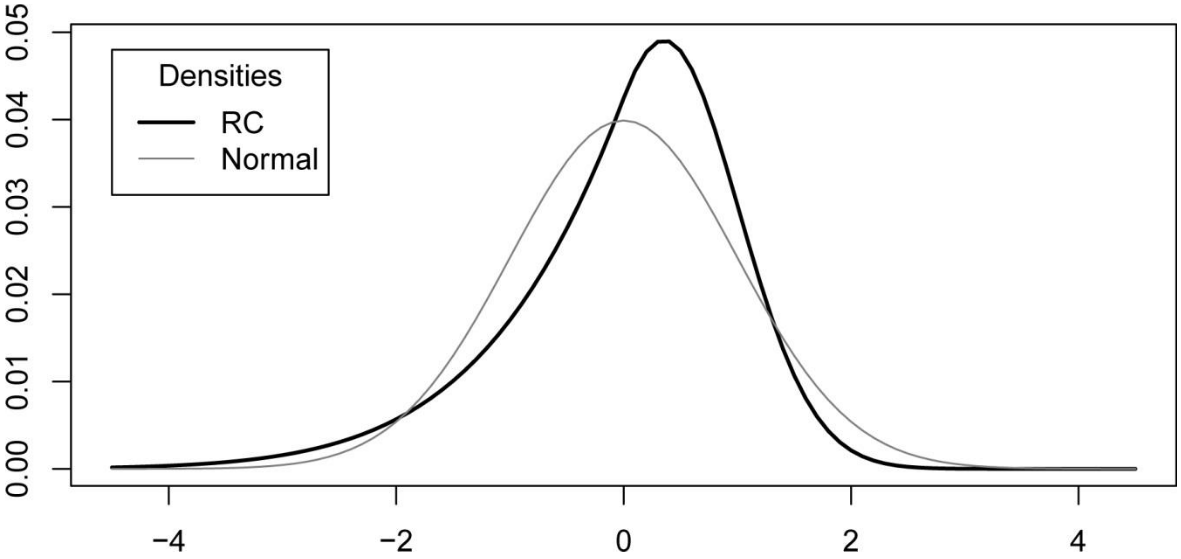

Figure 9. Estimated RC-IRT Curve for 11 DATOS Items ($N = 2,500$).

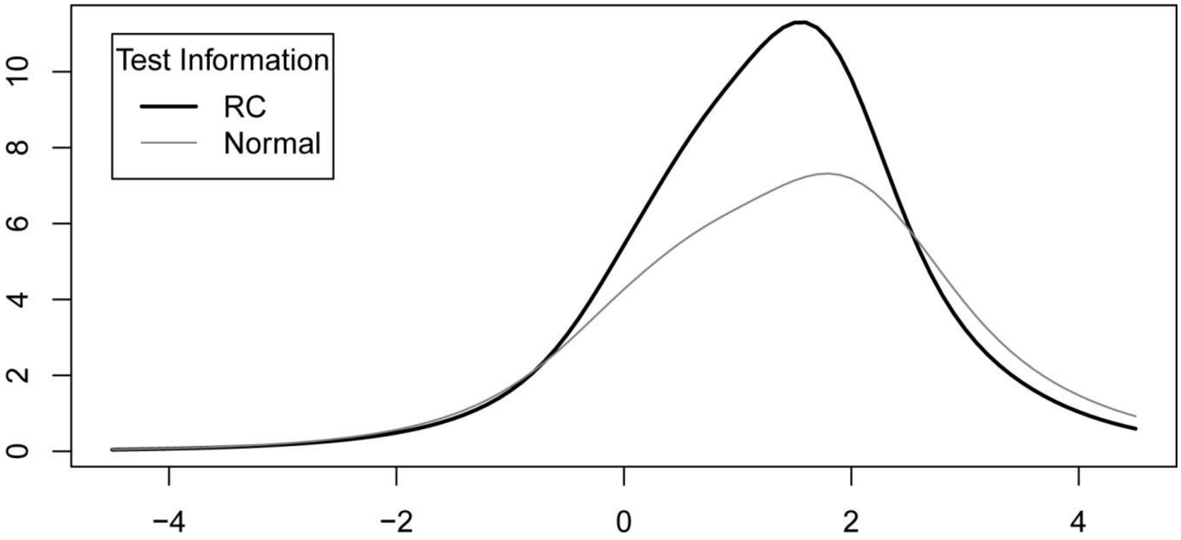

Figure 10. Estimated Test Information Curve for 11 DATOS Items ($N = 2,500$).

Discussion and Conclusion

The empirical example provides a nice context for discussing some of the advantages of RC-IRT, as well as remaining challenges. First, conventional model selection criteria indices (e.g., BIC, HQIC) ensure that the Ramsay curve may be parsimoniously modeled. In the empirical example, the Ramsay curve was a function of just three parameters. Nevertheless, its shape was clearly non-normal. Furthermore, the RC-IRT model fit better than the corresponding standard IRT model, as measured by conventional criteria. And, if the criteria reveal that the data do not support non-normality, we can always use the standard model. Thus, from the standpoint of improving model fit, there is little to be lost by using RC-IRT or at least starting off the analysis with RC-IRT.

On the other hand, by not using RC-IRT, the potential misspecification may lead to other undesirable results. As shown in Figure 10, the test information curves from the RC-IRT and standard analyses are clearly different. This discrepancy can have a practical impact on test assembly and item selection, where obtaining a certain test information or conditional standard error of measurement (SEM) curve may be the ultimate goal. Another practical implication involves computerized adaptive testing (CAT), where stopping criteria may be based on the conditional SEM. To the extent that RC-IRT models result in smaller conditional SEM values, CAT efficiency may be improved.

In empirical applications, the form of the latent trait distribution is unknown. Thus, treating it as such and estimating its shape from the data is a compelling argument. This theoretical argument, along with the practical advantages mentioned above, make a strong case for RC-IRT. Nevertheless, researchers need and prefer methods that do not limit their lines of inquiry. The unavailability of item parameter standard errors is clearly one such limitation. This research has provided the means to remedy this situation.

Still, other limitations exist. A notable example is that a multidimensional generalization of RC-IRT has not yet been developed. When such a development does occur, MH-RM will be a logical choice for estimation. Unlike EM, MH-RM does not impose artificial ceilings on the dimensionality of a model. To the contrary, the method is, in a sense, designed to address “the curse of dimensionality.” While other methods for implementing standard errors for unidimensional RC-IRT exist, choosing MH-RM lends itself to future generalizations. Hopefully, when this occurs, the problems identified and the pitfalls overcome by the current research can serve as a better starting point for future investigations involving multidimensional models with non-normal latent variables.

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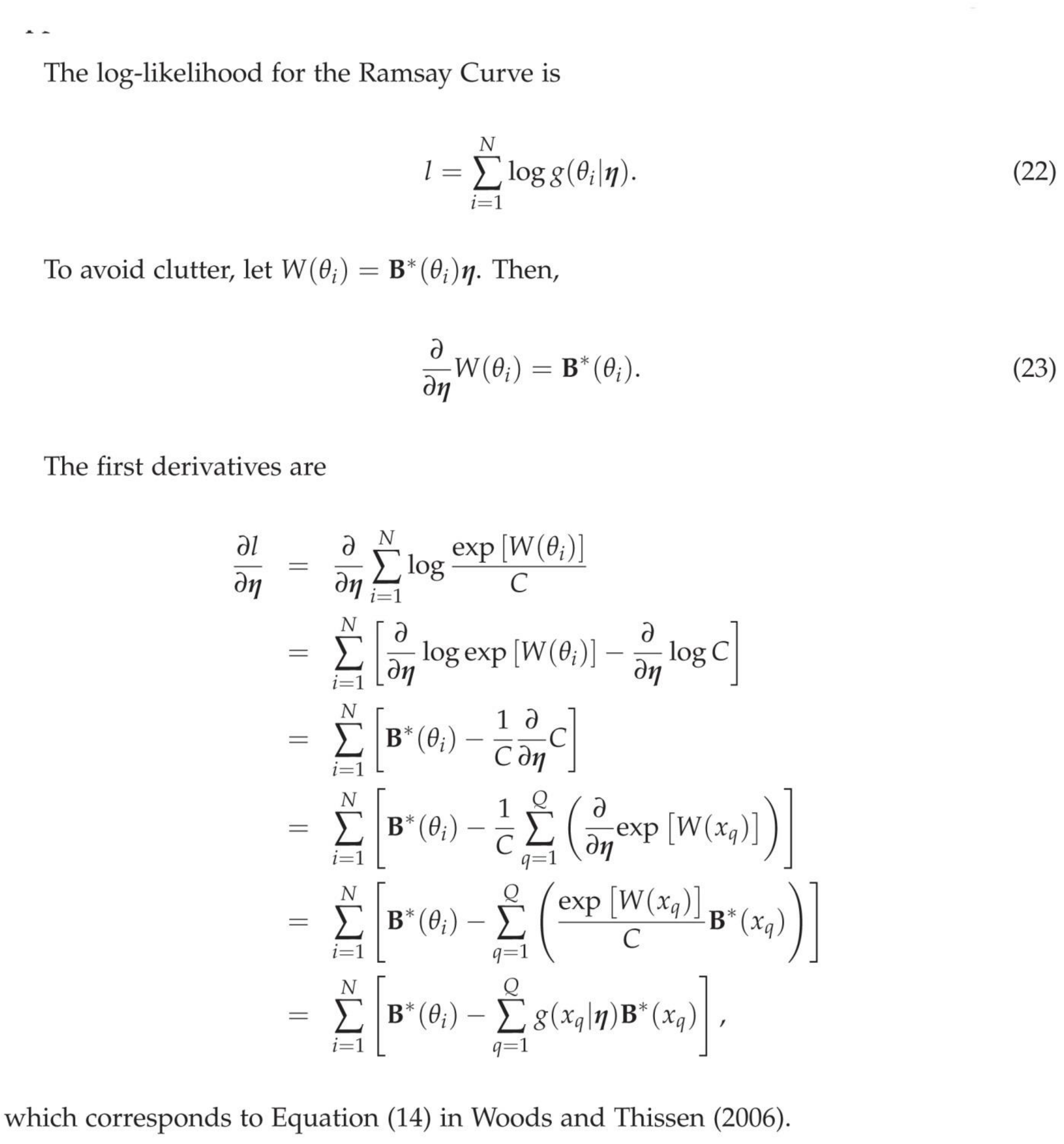
Appendix A

Complete Data Log-Likelihood and Derivatives for the Ramsay Curve



The log-likelihood for the Ramsay Curve is

$$l = \sum_{i=1}^{N} \log g(\theta_i|\boldsymbol{\eta}). \tag{22}$$

To avoid clutter, let $W(\theta_i) = \mathbf{B}^*(\theta_i)\boldsymbol{\eta}$. Then,

$$\frac{\partial}{\partial \boldsymbol{\eta}} W(\theta_i) = \mathbf{B}^*(\theta_i). \tag{23}$$

The first derivatives are

$$\begin{aligned}
\frac{\partial l}{\partial \boldsymbol{\eta}} &= \frac{\partial}{\partial \boldsymbol{\eta}} \sum_{i=1}^{N} \log \frac{\exp\left[W(\theta_i)\right]}{C} \\
&= \sum_{i=1}^{N} \left[\frac{\partial}{\partial \boldsymbol{\eta}} \log \exp\left[W(\theta_i)\right] - \frac{\partial}{\partial \boldsymbol{\eta}} \log C \right] \\
&= \sum_{i=1}^{N} \left[\mathbf{B}^*(\theta_i) - \frac{1}{C} \frac{\partial}{\partial \boldsymbol{\eta}} C \right] \\
&= \sum_{i=1}^{N} \left[\mathbf{B}^*(\theta_i) - \frac{1}{C} \sum_{q=1}^{Q} \left(\frac{\partial}{\partial \boldsymbol{\eta}} \exp\left[W(x_q)\right] \right) \right] \\
&= \sum_{i=1}^{N} \left[\mathbf{B}^*(\theta_i) - \sum_{q=1}^{Q} \left(\frac{\exp\left[W(x_q)\right]}{C} \mathbf{B}^*(x_q) \right) \right] \\
&= \sum_{i=1}^{N} \left[\mathbf{B}^*(\theta_i) - \sum_{q=1}^{Q} g(x_q|\boldsymbol{\eta}) \mathbf{B}^*(x_q) \right],
\end{aligned}$$

which corresponds to Equation (14) in Woods and Thissen (2006).

The second derivatives involve $\frac{\partial}{\partial \eta} g(x_q|\boldsymbol{\eta})$, which is:

$$\begin{aligned}
\frac{\partial}{\partial \boldsymbol{\eta}} g(x_q|\boldsymbol{\eta}) &= \frac{\partial}{\partial \boldsymbol{\eta}} \frac{\exp\left[W(x_q)\right]}{C} \\
&= \frac{C\left(\frac{\partial}{\partial \eta} \exp\left[W(x_q)\right]\right) - \left(\frac{\partial}{\partial \eta} C\right) \exp\left[W(x_q)\right]}{C^2} \\
&= \frac{C(\exp\left[W(x_q)\right])\mathbf{B}^*(x_q) - \left(\sum_{q=1}^{Q} \exp\left[W(x_q)\right] \mathbf{B}^*(x_q)\right) \exp\left[W(x_q)\right]}{C^2}
\end{aligned}$$

which, should be noted, does not involve any subscript i. That is, the term is constant across persons.

Finally, the second derivatives are:

$$\begin{aligned}
\frac{\partial^2 l}{\partial \boldsymbol{\eta} \partial \boldsymbol{\eta}'} &= \frac{\partial}{\partial \boldsymbol{\eta}'} \sum_{i=1}^{N} \left[\mathbf{B}^*(\theta_i) - \sum_{q=1}^{Q} g(x_q|\boldsymbol{\eta}) \mathbf{B}^*(x_q)\right] \\
&= \sum_{i=1}^{N} \left[0 - \sum_{q=1}^{Q} \left(\frac{\partial}{\partial \boldsymbol{\eta}} g(x_q|\boldsymbol{\eta}) \mathbf{B}^*(x_q)\right)\right] \\
&= -N \sum_{q=1}^{Q} \left[\left(\frac{\partial}{\partial \boldsymbol{\eta}} g(x_q|\boldsymbol{\eta})\right) \mathbf{B}^*(x_q)' + g(x_q|\boldsymbol{\eta}) \left(\frac{\partial}{\partial \boldsymbol{\eta}} \mathbf{B}^*(x_q)\right)\right] \\
&= -N \sum_{q=1}^{Q} \left[\left(\frac{\partial}{\partial \boldsymbol{\eta}} g(x_q|\boldsymbol{\eta})\right) \mathbf{B}^*(x_q)'\right]
\end{aligned}$$

where $\frac{\partial}{\partial \eta} g(x_q|\boldsymbol{\eta})$ is the $v \times 1$ vector given above.