SRMR in Mplus

Tihomir Asparouhov and Bengt Muthén

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1 Introduction

In this note we describe the Mplus implementation of the SRMR (standardized root mean squared residual) fit index for the models where the index is computed. Starting with Mplus 8.1, changes have been implemented to improve the quality of the fit index and to prevent failures. The index is now computed for more models including SEM models with categorical data estimated with the weighted least squares family of estimators: wls/wlsm/wlsmv/ulsmv. We also discuss how the Mplus SRMR fit index should be used in practice.

The definition of SRMR varies slightly across publications and software implementations. In addition, the early definitions of SRMR do not apply to all SEM models. For example, the definition in Hu and Bentler (1999) does not apply to growth models that include mean structure modeling and are a part of the general SEM framework. If one is to use the Hu and Bentler (1999) SRMR definition with a growth model, one can easily make the erroneous conclusion of approximate fit, simply because that definition does not include terms comparing the model estimated and the sample means. Another important example relates to the inclusion of covariates in the SEM model. The definition used in Hu and Bentler (1999) is intended for models that have all observed variables modeled as dependent variables. The Mplus SEM framework however enables us to separate the variables into two groups: endogenous/dependent variables, usually denoted by Y, and exogenous/independent variables, usually denoted by X. The goal of the SEM model is then to fit the conditional distribution of $[Y|X]$ while not attempting to model the distribution of X. This is an important modeling technique as it allows us to focus on the more parsimonious model for $[Y|X]$ which has

fewer modeling assumptions, because no modeling assumptions are made regarding X but only for $[Y|X]$. For such a SEM model, the definition of Hu and Bentler (1999) is also inappropriate because it can easily be manipulated: any SEM model can be made "approximately well fitting" simply by adding a sufficient number of arbitrary covariates. Starting with Mplus 8.1, the SRMR definition has been updated to reflect the growing number of SEM models and features while preserving the nature of the SRMR index. In this note we describe the SRMR computations implemented in Mplus 8.1.

SRMR is an approximate fit index. It can be used to establish approximate fit for a particular SEM model when that model is rejected using the formal chi-square test of model fit. It should be noted that both SRMR and the chi-square test of fit are designed to compare the same two models: the SEM model (referred to as the H0 model) and the multivariate model of unrestricted mean and variance covariance matrix (referred to as the H1 model). The SRMR index is not intended to substitute the chi-square test or to compete with it. Instead it is intended to complement it. It is well known that if the sample size is sufficiently large, the chi-square test can reject the null hypothesis (the SEM model) due to discrepancies that are of very small size, i.e. have no substantive significance, even though they are of statistical significance. In such situations the chi-square conclusion, i.e., that the model does not fit well, is quite impractical. Using approximate fit indices such as SRMR, we can then establish approximate fit, as long as the approximate fit indices fall in a pre-established range. The acceptable range for the SRMR index is between 0 and 0.08, see Hu and Bentler (1999). Since most of the terms in the SRMR definition are simply MSE of estimated and observed correlations, the value of 0.08 can be interpreted as follows. If all correlations are equally misfitted, the model is approximately well fitting if the estimated and the observed correlations are less than 0.08 apart.

The SRMR as implemented in Mplus is not a test. It is simply a quantity that represents the direct distance between the H0 and the H1 models. It is a MSE of observed and estimated correlations, standardized means and variances. Thus it has the following advantage over other approximate fit indices such as CFI and TLI. SRMR is easy to interpret and can be used to locate the sources of misfit when the model is not fitting well. In the Mplus residual output one can find all the information that is needed to reconstruct the computation of SRMR, and thus locate the source of misfit as the largest residual values, where the residuals are the observed minus the estimated quantities. Note also that a proper use of the SRMR index

mandates that the residuals are evaluated not only as a part of the SRMR index but also individually. An approximately well fitting model is a model with SRMR$<$ 0.08 but also a model that does not include any large residual values. Large residual values indicate that model modifications are needed. SRMR values smaller than 0.08 should not be used as a justification to ignore major model misfits. Large residual values indicate major discrepancy between the model and the data and it would be inaccurate to call such models approximately well fitting models. Because SRMR is averaging the error terms, it is important to make sure that there is no large errors hidden in that average. Therefore proper use of SRMR to establish approximate fit should include an inspection of the Mplus residual output to verify that the residuals are many small values and there are no large residual values at all.

The chi-square test of fit and the SRMR index should be used as follows. The chi-square test of fit should be used first. This test is sometimes referred to as the test of "exact" fit. If the exact fit does not hold, then the SRMR index should be used to establish approximate fit. The three possible outcomes of this stepwise procedure are as follows.

- Exact Fit
  If the model fits well according to the chi-square test, there is in principle no need to consider the SRMR index. Exact fit trumps approximate fit. There is no situation when exact fit holds but approximate fit doesn't hold. Nevertheless, one can look at the SRMR index simply as a distance tool which shows how different the H0 and the H1 models are. The SRMR index and the residual output can also be used to discover large standardized residuals. It is not uncommon that a chi-square test of fit does not reject the null model while another test for a specific part of the model can reject the null model. This is because the test of fit is an omnibus test that has less power than tests that are more targeted. Even if a null model is not rejected, i.e., there is no significant evidence that the model is incorrect, inspecting SRMR and the largest residual values can often lead to discovering statistically significant incremental model improvements. Furthermore, large residuals maybe of interest even if they are not statistically significant.

  It is also not uncommon that the chi-square test of fit does not reject the model but the SRMR value is larger than 0.08. The interpretation in this case is that the information in this sample is not sufficient to reject the null model even though it appears that the H1 and the H0 model are

not very close. These larger SRMR values can occur quite often when the sample size is 200 or less, however, this is not a reason to doubt the null model and the exact fit conclusion holds. In small samples there is less certainty in the sample and the estimated correlations and there is natural sampling variation that contributes to the larger SRMR values. Regardless, when the exact fit holds, even if SRMR$>$ 0.08, the model should be considered well fitting.

- Approximate Fit
  If the chi-square test rejects the model but SRMR$\leq$ 0.08 and all standardized residuals are small (i.e. there are no large residuals) then we can claim that the model is approximately well fitting. We can argue that substantively insignificant but statistically significant differences between the H0 and the H1 model are responsible for the chi-square rejection.

  It should be noted that the usability of SRMR with small samples is very limited. This is because in small sample sizes correlation residuals that are statistically significant must be large, because the standard errors are large. Thus for samples smaller than 200 it is difficult to argue that the concept of approximate fit even exist. For small samples, if the fit is not an exact fit, then the differences between the H0 and the H1 model must be large so there is limited possibility for establishing approximate fit in such circumstances. The approximate fit concept should primarily be used for samples larger than 200 and is most useful for samples greater than 500.

- Poorly Fitting model
  If the chi-square test rejects the model and SRMR$>$ 0.08, the model is poorly fitting and has to be modified. Modification indices or the residual output can be used to guide the modifications.

We summarize this decision making process in Table 1. This also clarifies the definition of "Approximate fit". Approximate fit is not defined as the cases where $SRMR \leq 0.08$, rather it is defined as the cases where $SRMR \leq 0.08$ and the chi-square test rejects the model.

The above discussion applies exclusively to the Mplus implementation of SRMR. The main purpose of the above procedure is to provide a tool for dealing with substantively insignificant but statistically significant model

Table 1: Using chi-square and SRMR to determine model fit

	$SRMR \leq 0.08$	$SRMR > 0.08$
chi-square does not rejects	Exact Fit	Exact Fit
chi-square rejects	Approximate fit	Poor fit

misfits that tend to appear in large samples. Different definitions of SRMR and intended purpose can be found in the literature. For example, in Maydeu-Olivares (2017) and Maydeu-Olivares et al. (2018), an alternative definition of SRMR is given and it is treated as a test of close fit with the goal of providing a p-value for SRMR to fall within a certain range. This approach is similar to the Mplus PPPP value implemented with the Bayes estimation, see Hoijtink and van de Schoot (2017) and Asparouhov and Muthén (2017). The main target of interest in Maydeu-Olivares (2017) and Maydeu-Olivares et al. (2018) is the distribution of SRMR for smaller samples, which is in contrast to the Mplus treatment of SRMR with intended use for larger samples, i.e., the SRMR in Maydeu-Olivares (2017) is defined differently and its intended purpose is also different.

2 SRMR definition

In this section we provide the SRMR computational details for the various Mplus models.

2.1 The general SEM model with continuous dependent variables

Let p be the number of variables in the model. Let s_{jk} and σ_{jk} be the sample and the model-estimated covariance between the $j-$th and $k-$th variables. Let m_j and μ_j be the sample and the model-estimated mean of the $j-$th variable. The SRMR fit index is defined as follows

$$SRMR = \sqrt{\frac{S}{p(p+1)/2+p}}, \tag{1}$$

where S is

$$S = \sum_{j=1}^{p} \sum_{k=1}^{j-1} \left(\frac{s_{jk}}{\sqrt{s_{jj} s_{kk}}} - \frac{\sigma_{jk}}{\sqrt{\sigma_{jj} \sigma_{kk}}} \right)^2 + \tag{2}$$

$$\sum_{j=1}^{p} \left(\frac{m_j}{\sqrt{s_{jj}}} - \frac{\mu_j}{\sqrt{\sigma_{jj}}} \right)^2 + \sum_{j=1}^{p} \left(\frac{s_{jj} - \sigma_{jj}}{s_{jj}} \right)^2. \tag{3}$$

This definition is simply the MSE (mean squared error) distance between the H0 and the H1 models, for all standardized variance covariances and means residuals. The denominator $p(p+1)/2 + p$ is the total number of residuals used in S. Note that the correlation residuals in equation (2) are simply the difference between two correlations and have a maximum of 2. The mean and the variance residuals, however, seen in equation (3), despite the fact that they are standardized, are not limited by any number and can produce very large SRMR values. This expanded SRMR definition has the advantage over the definition in Hu and Bentler (1999) as it accounts for the model estimated means and not just the model estimated variance covariance matrix. Structural mean modeling occurs in many popular structural equation models, including growth modeling and multiple group scalar CFA, and for such models it is essential to use formula (1) instead of the the SRMR defined in Hu and Bentler (1999). Note also that any SEM model estimated with data that has missing values automatically becomes a structural mean model. That is because with missing data the variance covariance parameter estimation is intertwined with the mean parameter estimation and the SEM model may not have zero mean residuals even if all the dependent variable means are free parameters. This further illustrates the need to include standardized mean residuals in SRMR.

2.2 EFA models

EFA models by definition fit only the correlation matrix, i.e., by definition these model have zero residuals for the means and for the diagonal of the variance covariance matrix. Thus the proper definition of SRMR is as follows

$$SRMR = \sqrt{\frac{S}{p(p-1)/2}}, \tag{4}$$

where S is

$$S = \sum_{j=1}^{p} \sum_{k=1}^{j-1} \left(\frac{s_{jk}}{\sqrt{s_{jj} s_{kk}}} - \frac{\sigma_{jk}}{\sqrt{\sigma_{jj} \sigma_{kk}}} \right)^2. \tag{5}$$

2.3 SEM models with covariates

Suppose that q of the p variables in the model are exogenous variables. The distribution of these variables is not modeled, i.e., the distribution of the exogenous variables is the unrestricted mean and variance covariance matrix. Thus $q(q+1)/2 + q$ of the residual terms in S are by default zero. These terms therefore should not be counted in the denominator in formula (1). Thus we compute SRMR in this case as

$$SRMR = \sqrt{\frac{S}{p(p+1)/2 + p - q(q+1)/2 - q}} \tag{6}$$

while formula (2) remains the same (the zero residuals do not contribute anything to the definition of S). If this adjustment is not made, the SRMR converges to zero if we add large number of irrelevant covariates and so it will not correctly portray the quality of the SEM model regarding $[Y|X]$. Note also that if a model has relatively few number of dependent variables but a large number of covariates, this adjustment becomes very important. That is because the number of true residuals involving the correlations between the dependent variables and the covariates is a linear function of the number of covariates, while the number of fake/zero residuals involving correlations between the covariates is a quadratic function of the number of covariates, meaning that it will grow much faster. In such situations the adjustment becomes extremely important.

2.4 SEM models with NOMEANSTRUCTURE

When the MODEL=NOMEANSTRUCTURE is used in Mplus the means are not modeled at all. Equivalently we can assume that the model mean estimates are equal to the sample means. In this case the formula (1) is adjust to reflect the fact that p of the residuals are zero by default. Thus in this case

$$SRMR = \sqrt{\frac{S}{p(p+1)/2}}. \tag{7}$$

In certain situations, for example a simple CFA model, in the case of no missing data, the means are also guaranteed to have zero residuals by default. Mplus will not however make this adjustment unless the MODEL=NOMEANSTRUCTURE option is specified.

2.5 Using Information=expected

In this case Mplus uses a slight modification of the SRMR formula

$$SRMR = \sqrt{\frac{S}{p(p+1)/2+p}}, \tag{8}$$

where S is defined as follows

$$S = \sum_{j=1}^{p}\sum_{k=1}^{j}\left(\frac{s_{jk}}{\sqrt{s_{jj}s_{kk}}} - \frac{\sigma_{jk}}{\sqrt{s_{jj}s_{kk}}}\right)^2 + \tag{9}$$

$$\sum_{j=1}^{p}\left(\frac{m_j}{\sqrt{s_{jj}}} - \frac{\mu_j}{\sqrt{s_{jj}}}\right)^2. \tag{10}$$

This definition is identical to the one given in equation (1) when the sample variances and the estimated variances are equal. This is often the case in SEM models because the residual variances are often estimated as free parameters and thus the diagonal elements of the variance covariance matrix can be match exactly. The above definition also becomes identical to the Hu and Bentler (1999) definition when used in combination with MODEL=NOMEANSTRUCTURE.

2.6 Multiple groups

In multiple group modeling the SRMR_g is computed for each group $g = 1, ..., G$ where G is the total number of groups. The SRMR for the full model is computed as follows

$$SRMR = \sum_{g=1}^{G}\frac{n_g}{n}SRMR_g \tag{11}$$

where n_g is the sample size for group g and n is the total sample size $n = \sum_{g=1}^{G} n_g$.

2.7 WLS family of estimators

The WLS/WLSM/WLSMV/ULSMV estimators are used to estimate SEM models with continuous dependent variables, categorical dependent variables as well as covariates. Let Y be the total vector of variables of size p, let Y^* be the vector of underlying continuous variables, that is, the Y^* is identical for the continuous dependent variables and the covariates but for the categorical variables it is the continuous underlying variable that is cut to obtain the observed categorical values as in a standard probit model. Denote by p_1 the number of categorical dependent variables, p_2 the number of continuous dependent variables and p_3 the number of covariates and let's assume that they appear in the Y vector in that order. Suppose that the H0 model estimated variance covariance matrix is Σ and that the corresponding H1 model variance covariance matrix is S. Suppose again that the H0 model estimated mean vector is μ and that H1 model mean vector is m. We are not including means for the categorical variables, instead we will consider the corresponding values on the probability scale, which is very similar to the correlation scale where the compared quantities are smaller than 1. Thus we can assume that the first p_1 values in μ and m are zero. Denote by p_{ij} the H0 model estimated probability of a categorical variable Y_i being in the $j-$th category $p_{ij} = P(Y_i = j|H_0)$, for $i = 1, ..., p_1$ and $j = 1, ..., l_i$ where l_i is the number of categories the variable Y_i can take. Similarly denote by q_{ij} the H1 model estimated quantity $q_{ij} = P(Y_i = j|H_1)$. The SRMR can now be defined as follows

$$SRMR = \sqrt{\frac{S}{d}}, \tag{12}$$

where S is

$$S = \sum_{j=1}^{p}\sum_{k=1}^{j-1}\left(\frac{s_{jk}}{\sqrt{s_{jj}s_{kk}}} - \frac{\sigma_{jk}}{\sqrt{\sigma_{jj}\sigma_{kk}}}\right)^2 + \tag{13}$$

$$\sum_{j=1}^{p}\left(\frac{m_j}{\sqrt{s_{jj}}} - \frac{\mu_j}{\sqrt{\sigma_{jj}}}\right)^2 + \tag{14}$$

$$\sum_{j=1}^{p}\left(\frac{s_{jj} - \sigma_{jj}}{s_{jj}}\right)^2 + \tag{15}$$

$$\sum_{i=1}^{p_1}\sum_{j=1}^{l_i}(p_{ij} - q_{ij})^2 \tag{16}$$

and d is the number of residuals in the above sum that are not zero by default, that is, d is the total number of residuals $p(p+3)/2 + \sum_{i=1}^{p_1} l_i$ minus those that are zero by default. In equation (13) the covariates correlation residuals are zero by default. For that part of the equation we subtract $p_3(p_3-1)/2$ from d. For equation (14) we subtract p_1+p_3 as only the continuous variables have standardized means that can have non-zero residuals. For equation (15) we subtract p_3 as the covariates have zero variance residuals by default. In addition, however, if there are no covariates in the model we subtract p_1 elements for equation (15) as all categorical variables have 1 on the diagonal of the variance covariance matrix under both the H1 and the H0 model. In total if there are covariates in the model

$$d = p(p+3)/2 + \sum_{i=1}^{p_1} l_i - p_1 - p_3(p_3+3)/2 \tag{17}$$

and if there are no covariates

$$d = p(p+3)/2 + \sum_{i=1}^{p_1} l_i - 2p_1. \tag{18}$$

In the above SRMR definition all residuals are standardized and can be considered to be on a unit/comparable scale. As previously noted the residuals in (14) and (15) can be larger than 1 even though they are standardized. The residuals in (13) are always less than 2 and the residuals in (16) are always less than 1. Just as in the continuous SEM, the SRMR is dominated by the residuals for the correlation matrix as the number of correlations is a quadratic function of the number of variables while the means are a linear function of the number of variables. However, mean structure is accounted for, meaning that, model misfit in the means will contribute to the SRMR value. This applies to both the continuous and the categorical variables. When a categorical variable Y_i is binary both $P(Y_i = 1)$ and $P(Y_i = 2)$ are included in the SRMR even though the residual for the two categories are the same. This is done for consistency with respect to non-binary categorical variables where such a residual relationship is more complex.

With the WLS family of estimators a conditional model for $[Y|X]$ is estimated. Let $Y = (Y_0, X)$ where Y_0 represents the vector all dependent variables and X represents all covariates. Under both the H0 and the H1 model the following linear regression model is estimated for the underlying continuous variables Y_0^*

$$Y_0^* = \alpha + \beta X + \varepsilon \tag{19}$$

where $\theta = Var(\varepsilon)$. The quantities α, β and θ can be found in the Mplus residual output for the H0 model and in the sample statistics output for the H1 model. The differences between these quantities can be found in the Mplus residual output as well. Under the H0 model usually there is a structure on α, β and θ imposed by the estimated SEM model. Under the H1 model α, β and θ are estimated as unrestricted parameters.

The computation of both Σ and S is based on the above equation. Using the sample covariance for the covariates S_x the total variance covariance matrix for the entire vector Y is computed as

$$V = \begin{pmatrix} \theta + \beta S_x \beta^T & S_x \beta^T \\ \beta S_x & S_x \end{pmatrix} \tag{20}$$

and from here the correlations in equation (13) are computed. These correlations and the corresponding residuals can be found in Mplus residual output.

The probabilities p_{ij} and q_{ij} are computed similarly. Denote the threshold parameters for a categorical variable Y_i by τ_{ij}. The probability

$$P(Y_i = j) = \Phi\Big(\frac{\tau_{ij} - \beta_i \mu_x}{\sqrt{V_{ii}}}\Big) - \Phi\Big(\frac{\tau_{i,j-1} - \beta_i \mu_x}{\sqrt{V_{ii}}}\Big) \tag{21}$$

where μ_x is the sample mean of the covariates, β_i is the $i-$th row of β and V_{ii} is the $i-$th diagonal element of V computed in (20). This method of computing $P(Y_i = j)$ is slightly different from the more elaborate method used in the Mplus residual output, where $P(Y_i = j)$ is computed for each observation in the data (i.e. for each observed set of covariates) and averaged across observations. As usual, the first threshold $\tau_{i,0}$ in equation (21) is assumed to be $-\infty$ and the last threshold τ_{i,l_i} is assumed to be $+\infty$.

In Mplus 8.1 for the WLS family of estimators this SRMR fit index replaces the WRMR fit index which has been shown to perform poorly for situations with extremely large sample sizes, see DiStefano et al. (2018).

2.8 Multilevel models

Two-level models in Mplus are based on the fundamental decomposition of each variable into a within level component and a between level component

$$Y = Y_w + Y_b, \tag{22}$$

where $Y_w \sim N(\mu_w, \Sigma_w)$ and $Y_b \sim N(\mu_b, \Sigma_b)$. For identification purpose the mean parameter exist only on one of the levels and for each variable this is determined as the highest level the variable is present on. That is, variables that are declared as within-only variables (on the within list) have a mean parameter in the within-level mean vector μ_w, while variables that are between-only variables (on the between list) or variables that are within-between (not on either the within or the between list) have their mean parameter in the μ_b vector. In addition, within-only variable have zeros in the corresponding Σ_b rows and columns while between-only variables have zeros in the corresponding Σ_w rows and columns. The H1 model estimates unrestricted μ_w, Σ_w, μ_b, and Σ_b parameters while the H0 model estimates structured μ_w, Σ_w, μ_b, and Σ_b. These quantities are the basis for forming the residuals that are used for the construction of SRMR for multi-level models. Once the quantities are estimated under both the H0 and the H1 model the SRMR is computed separately for the two-levels using the same approach as for single level models, such as for example equations (1) and (2). In equation (1) the denominator is always adjusted so that it represents the number of residuals used in the definition of the SRMR on that level that are not zero by default. For example, means are counted only for the level where the mean residual is present, i.e., only on one of the two levels. If a variable is a between only variable, it will not contribute to the SRMR definition on the within level both in the numerator and the denominator in equation (1). Similarly within-only variables do not contribute to the SRMR on the between level. In three level models similar approach is implemented and the SRMR is computed on each level separately. In multilevel models it is not unusual that the between level variance for a particular variable is very small. To avoid division by near-zero in equation (3) variances smaller than 0.01 are replaced by 0.01. In addition, the standardization of the mean parameters for multilevel models uses the variance from both levels rather than the variance on the level that the mean is present. That is, the contribution of the mean residuals to the SRMR in equation (3), in two-level models is replaced by

$$\sum_{j=1}^{p} \left(\frac{m_j}{\sqrt{s_{w,jj} + s_{b,jj}}} - \frac{\mu_j}{\sqrt{\sigma_{w,jj} + \sigma_{b,jj}}} \right)^2 . \tag{23}$$

where $s_{w,jj}$ and $s_{b,jj}$ are the H1 estimated within and between variance parameters for the $j-$th variables and $\sigma_{w,jj}$ and $\sigma_{b,jj}$ are the corresponding H0 estimated quantities. This is important because standardizing with between

level variances only (which can be very small) would produce improperly standardized means.

An additional complexity arises in multilevel models for SRMR on the between level. Because the sample size on the between level is the number of clusters in the sample, it is not unusual to have samples with fewer than 200 clusters. That implies that the 0.08 cut-off value is too strict for such situations. Well fitting models can exceed that value simply because of the small number of clusters on the between level. In such situations chi-square testing is needed that can test the within level model separately or the between level model separately to verify that the model on the between or the within level is fitting well. Such chi-square can be constructed as follows. The H0 model consists of an H0 model for the within level and an H0 model for the between level. Consider the model M1 that preserves the H0 model for the between level while estimating unrestricted variance covariance on the within level. Estimating M1 and testing that model against the H1 model will allow us to essentially test only the H0 model for the between level using the standard chi-square test. Thus in those situations where the SRMR on the between level is above the 0.08 level and the number of clusters is small we can check whether or not the large SRMR value indicates a statistically significant rejection of the H0 between level model or not. Similarly we can construct a model M2 which has unrestricted between level model and H0 within level model to separately evaluate the fit on the within level through the regular chi-square test. Using the models M1 and M2 we can therefore establish exact or approximate fit for each of the two-levels.

Note also that the H0 model SRMR on the between level may be slightly different between the M1 and the H0 models. That is because the estimations on the within and the between levels are not independent of each other. In principle, however, the differences should be small. If larger differences are observed a sever model misspecification is likely, such as for example, a variable declared as within-only when a substantial cluster level contribution exist.

2.9 Combinations

In the above sections we listed the various feature that affect the definition of the SRMR model. Such features can of course appear in combination. For example, multiple group multilevel models, or multilevel models with covariates, or multilevel models with categorical and continuous variables. To

construct the SRMR in such situations the considerations for the combined features apply. For example, consider a within-only covariate in multilevel models. The within-only covariate does not provide non-zero mean and variance residuals either on the within or the between level. Thus such residuals are not counted towards the denominator in equation (1) the same way that this is done in equation (6). That covariate will contribute to the within level SRMR in terms of correlation residuals between the covariate and all dependent variables with the exception of between-only dependent variables.

Similarly, in two-level models with categorical variables, when the mean structure is computed for categorical variables, i.e. when the probabilities for the separate categories are computed, the threshold parameters in equation (21) are standardized using the sum of the within-level and the between-level variance

$$P(Y_i = j) = \Phi\Big(\frac{\tau_{ij} - \beta_i \mu_x}{\sqrt{V_{w,ii} + V_{b,ii}}}\Big) - \Phi\Big(\frac{\tau_{i,j-1} - \beta_i \mu_x}{\sqrt{V_{w,ii} + V_{b,ii}}}\Big) \tag{24}$$

as this was done in equation (23) for the means of the continuous variables.

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