We need to change how we compute RMSEA for nested model comparisons in structural
equation modeling

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Abstract

Comparison of nested models is common in applications of structural equation modeling (SEM). When two models are nested, model comparison can be done via a chi-square difference test or by comparing indices of approximate fit. The advantage of fit indices is that they permit some amount of misspecification in the additional constraints imposed on the model, which is a more realistic scenario. The most popular index of approximate fit is the root mean square error of approximation (RMSEA). In this article, we argue that the dominant way of comparing RMSEA values for two nested models, which is simply taking their difference, is problematic and will often mask misfit, particularly in model comparisons with large initial degrees of freedom. We instead advocate computing the RMSEA associated with the chi-square difference test, which we call $RMSEA_D$. We are not the first to propose this index, and we review numerous methodological articles that have suggested it. Nonetheless, these articles appear to have had little impact on actual practice. The modification of current practice that we call for may be particularly needed in the context of measurement invariance assessment. We illustrate the difference between the current approach and our advocated approach on three examples, where two involve multiple-group and longitudinal measurement invariance assessment and the third involves comparisons of models with different numbers of factors. We conclude with a discussion of recommendations and future research directions.

Introduction

In applications of structural equation modeling (SEM), comparison of nested models is very popular. Two models are *parameter nested* (Bentler & Bonett, 1980) if the parameters of the more restricted model (Model B) include some but not all of the parameters of the less restricted model (Model A). For example, Model B may differ from Model A because it constrains some parameters in Model A to zero or to equality. Less obviously, two models can also be *covariance matrix nested* (Bentler & Bonett, 1980) if the set of all possible covariance matrices implied by Model B is a subset of the set of all possible covariance matrices implied by Model A. For example, a 1-factor model is nested within a 2-factor model, and a hierarchical factor model is nested within the bifactor model (Yung, Thissen, & McLeod, 1999). While parameter nesting is easier to recognize, there is no difference between the two types of nesting when it comes to implications for how the models can be compared; all nested models can be compared via chi-square difference tests. Because whether two models are nested is not always obvious, an empirical procedure exists to evaluate whether nesting holds (Bentler & Satorra, 2010). In R (R Core Team, 2021), this tool is available via the *net* function in the *semTools* package (Jorgensen, Pornprasertmanit, Schoemann, & Rosseel, 2021), which integrates with *lavaan* (Rosseel, 2012).

In some applications, such as in studies of *measurement invariance* (MI), there is a pre-determined sequence of nested models that is evaluated sequentially once the initial model has been found to fit the data. MI can be assessed across independent samples (via a multiple groups model) or longitudinally. The less restricted model is typically the configural invariance model, wherein the same factor model is fit to each group or at each timepoint, without any constraints. The researcher then proceeds by imposing between-group or across-time equality constraints on

factor loadings, followed by constraints on indicator intercepts, and, if of further interest, on residual variances and/or factor variances and/or factor covariances (Meredith, 1993; Millsap & Everson, 1991; Millsap & Hartog, 1988; Millsap, 2011; Millsap & Cham, 2012; Vandenberg & Lance, 2000).

The statistical comparison of nested models can be done by evaluating the deterioration in fit created by Model B relative to the fit of Model A, using either the exact or the approximate fit approach. Under *the exact fit* approach, a researcher computes a chi-square difference test, which tests the null hypothesis that, assuming that Model A is correct, the additional restrictions imposed by Model B are also correct. When it comes to the evaluation of the overall model fit (e.g., assessing the fit of Model A), the exact fit approach has fallen out of favor because it will reject even trivial deviations from the null hypothesis in large samples. However, when it comes to nested model comparisons, chi-square difference tests are still used by some researchers, usually to show the superiority of their preferred model relative to some more constrained model (Crede & Harms, 2019). For example, a researcher may argue that a multi-factor model is appropriate by demonstrating that it fits the data better than the 1-factor model by the chi-square difference test (Ronkko & Cho, 2020). Because of their focus on the exact fit of the added constraints, chi-square difference tests will tend to be significant if the sample size is sufficiently large, rejecting the simpler model.

Under *the approximate fit* approach, a researcher assesses the fit of Models A and B using fit indices. The most popular fit indices are the root mean square error of approximation (RMSEA; Steiger & Lind, 1980) and the comparative fit index (CFI; Bentler & Bonett, 1980). It is common to simply report these indices for both models (or for all models in a nested sequence). However, the approach of formally calculating the change in fit indices between

Models A and B, ΔRMSEA and ΔCFI , has gained popularity in recent years. This approach originated in the context of studies of measurement invariance (Cheung & Rensvold, 2002). In this context, retaining additional constraints (i.e., concluding that some types of invariance hold) is usually the desired outcome, and chi-square difference tests have been all but replaced by fit index differences (Putnick & Bornstein, 2016). Chen (2007) proposed tentative cutoffs for ΔRMSEA and ΔCFI . Others have followed with more nuanced recommendations (e.g., Meade, Johnson, & Braddy, 2008). The popularity of this approach is evidenced by the thousands of citations that these articles have gathered.¹

This bifurcation of practice, whereby chi-square difference tests continue to be used when the researcher wants to retain the more complex model, whereas fit index differences are used when constraints are desirable, is problematic. From the point of view of statistical theory, there should be no difference in the fit assessment strategy depending on the type of nested model comparison. The divergence of norms pertaining to how to conduct nested model comparison in different areas of application may be partially driven by researchers' motivations to reach the desired conclusions (Yuan & Bentler, 2004). Chi-square difference tests tend to be statistically significant in the vast majority of applications, supporting the more complex Model A. On the other hand, fit index differences, as we will argue here, tend to provide a very weak test of the constraints in Model B, particularly when the degrees of freedom for Model A are already large. As a result, they frequently support the more constrained Model B.

In this article, we propose to unify the practice of fit assessment for nested models by advocating that researchers primarily rely on the RMSEA associated with the chi-square

¹ As of January 7, 2022, Cheung & Rensvold (2002) has been cited 12,468 times, and Chen (2007) has been cited 6,032 times, according to Google Scholar.

difference test. This index, which we call RMSEA_D , is obtained by substituting the chi-square difference test statistic D and its degrees of freedom df_D into the usual RMSEA equation (see next section). Because it is completely parallel to the overall model RMSEA, this index is on the same metric and can be referred to the same cutoffs; further, an analytic CI for it is also readily available. RMSEA_D zeroes in on the constraints imposed by Model B and evaluates only their contribution to misfit relative to the introduced degrees of freedom. Particularly when the df associated with the initial Model A are already large, RMSEA_D will tend to be more sensitive than ΔRMSEA . On the other hand, because it is an approximate fit index, RMSEA_D will approach a stable population value as the sample size increases and will not become increasingly sensitive to misspecification. Thus, this index overcomes the disadvantages of both ΔRMSEA and chi-square difference tests, and does not make the outcome of model comparison a foregone conclusion.

This index is quite old. It was first proposed by Browne and Du Toit (1992), and extended by Dudgeon (2004) to multiple-group models. Unfortunately, after these initial developments, the use of RMSEA_D was discouraged by a team of methodologists, including one of the authors who invented it (MacCallum, Browne, & Cai, 2006). However, the idea behind it is so intuitive that it has been reinvented multiple times in different modeling contexts (e.g., Crede & Harms, 2019; McDonald & Ho, 2002; Williams & O’Boyle, 2011; Yuan and Chan, 2016), usually without reference to original sources. Our proposal therefore echoes many others that have advocated this index.

The remainder of this article is organized as follows. First, we discuss the theoretical relationship between ΔRMSEA and RMSEA_D for single-group and multiple-group (MG) models. Next, we review the existing methodological literature that has proposed the use of

RMSEA_D in some context. We then illustrate the use of RMSEA_D on three examples, reanalyzing data from published articles. We conclude with recommendations, limitations, and areas of future research.

RMSEA Definitions

Table 1 provides definitions of the normal theory maximum likelihood (ML) fit function, the model chi-square test statistic, and the overall model RMSEA for single-group and MG models. Because it is central to this article, the general equation for the RMSEA for single group models is repeated here:

$$RMSEA = \sqrt{\frac{T - df}{df(N - 1)}}, \quad (1)$$

where T is the chi-square test statistic, df is the degrees of freedom, and N is sample size. In the rare case when $T < df$, RMSEA is set to zero. The RMSEA is among the most popular SEM fit indices (McDonald & Ho, 2002), and it captures the amount of misfit per degree of freedom (Browne & Cudeck, 1992). The generalization of single-group RMSEA to MG RMSEA in Table 1 is due to Steiger (1998), who noted that in this case the fit function is a weighted average of the fit function values within each group, so that dividing by the average rather than total degrees of freedom provides a better measure of the average amount of misfit per degree of freedom.

While methodologists caution against strict cutoffs, tentative guidelines exist for declaring acceptable overall model fit, such as $RMSEA < .05$, $.06$, $.08$, or $.10$ (e.g., Hu & Bentler, 1999; Browne & Cudeck, 1992), and these are widely used by applied researchers. An analytic confidence interval (CI) is also available (Browne & Cudeck, 1992), permitting statistical tests of the null hypothesis of “close fit” (i.e., $H_0: RMSEA_0 < c$, where $RMSEA_0$

denotes the population value) and of “not close fit” (i.e., $H_0: \text{RMSEA} > c$; MacCallum, Browne, & Sugawara, 1996). We recommend tests of “not close fit”, also known as equivalence tests (Yuan, Chan, Marcoulides, & Bentler, 2016), because they permit the reversal of the null hypothesis testing paradigm back to the more usual situation where the researcher wants to reject an undesirable null hypothesis.

Chi-Square Difference Test

Let df_A and df_B be the degrees of freedom for Model A and Model B, respectively, where Model B is nested within Model A. It follows that $df_A < df_B$. Denote the chi-square test statistics for Model A and Model B by T_A and T_B respectively. The chi-square difference test is computed as

$$D = T_B - T_A.$$

When Model A is true, and when the additional restrictions imposed by Model B are also true, D has an asymptotic central chi-square distribution with $df_D = df_B - df_A$ degrees of freedom. When Model A is true, but when the additional restrictions imposed by Model B are false, D has an asymptotic noncentral chi-square distribution (Steiger, Shapiro, & Browne, 1985).² Additionally, D is asymptotically independent of T_A , whereas T_A and T_B can be quite strongly correlated (Steiger, Shapiro, & Browne, 1985). The property of asymptotic independence means that the outcome of the difference test is independent of the outcome of the test of fit for Model A, as assessed by T_A . The recommended practice is to evaluate T_A , and if found to be nonsignificant,

² In order to derive this result, a technical assumption of “population drift” or “sequence of local alternatives” must be made. We refer the reader to more technical sources (e.g., Chun & Shapiro, 2009). In practical terms, it means the misspecification cannot be too large or else the noncentral chi-square approximation will begin to fail.

to accept Model A; then to evaluate D , and if found to be nonsignificant, to accept the additional constraints imposed by Model B. Sticking to this procedure will avoid inconsistencies in statistical decision making that can arise if T_B is also inspected (for example, T_B may turn out to be significant, even while T_A and D are not, or vice versa).

In reality, Model A almost never fits the data by the chi-square test T_A . Whether the use of difference tests is justified in such a situation is a matter of some controversy. Steiger, Shaprio, and Browne (1985) proved a broader result: When Model A is false, but Model B does not introduce any *additional* misfit (i.e., the noncentrality parameter is the same for Models A and B), D will continue to have an asymptotic central chi-square distribution. This result provides some justification for interpreting D when T_A is statistically significant. However, caution must be exercised because under some types of misspecification in Model A, constraints imposed by Model B may appear false even when they are true in the population, affecting Type I error rates of the difference test.³ Relatively little research has addressed how seriously Model A must be misspecified before the outcome of difference test is seriously affected (but see Yuan & Bentler, 2004; Yuan & Chan, 2016). We return to this point in the discussion.

$\Delta RMSEA$

³ To see why, consider an example where Model A is a 1-factor model and Model B imposes equality constraints on the factor loadings. Suppose the true model is a 1-factor model with equal factor loadings (i.e., the constraints imposed by Model B are true in the population) but also with several residual covariances that were not included in Model A. When Model A is fit to data, the omitted residual covariances will create bias in the estimated loadings, making them appear more unequal (e.g., loadings involving indicators that share a residual covariance in the true model will be estimated at higher values). Then, a chi-square difference test of equality constraints on the loadings will falsely indicate these constraints are not met with a probability greater than .05 (nominal Type I error). The extent of this inflation at the range of sample sizes typically used in psychology will depend on how misspecified Model A is relative to the true model (i.e., on the number and size of the omitted residual covariances). We also note that the converse can in principle occur (false constraints may appear true when Model A is misspecified), affecting the power of the difference test.

When comparing nested models in terms of approximate fit, it is common for researchers to simply report fit indices associated with each model and to eyeball their differences; we call this the “naked eye” approach. It has also become common to take the difference of fit indices, especially in the context of MI assessment (Cheung & Rensvold, 2002). For the RMSEA, the difference index is defined as:

$$\Delta RMSEA = RMSEA_B - RMSEA_A, \quad (2)$$

where $RMSEA_A$ and $RMSEA_B$ are model RMSEAs for Models A and B, respectively. This index has several disadvantages. First, it is not on the same metric as the model RMSEA values (in fact, it is not even guaranteed to be nonnegative), and conventional RMSEA cutoffs do not apply. Limited research exists that has proposed cutoffs specifically for this index. Chen (2007) proposed that $\Delta RMSEA < .01$ or $.015$ (depending on sample size) before constraints in Model B are accepted. Second, an analytic CI for $\Delta RMSEA$ is not yet easily available (but see recent work by Lai, 2020), and researchers relying on cutoffs in small sample sizes could be overinterpreting sampling fluctuations. Third, and most importantly, $\Delta RMSEA$ often lacks sensitivity to detect misfit due to the added constraints for models with large initial degrees of freedom, df_A (MacCallum, Browne, & Cai, 2006). In such models, $RMSEA_A$ and $RMSEA_B$ will often be quite similar to each other, because any change in the fit function will be “diluted” by dividing by the overall df in their computation (see Equation (1)). As a result, given the same change in the chi-square value (D) and in the degrees of freedom (df_D), $\Delta RMSEA$ will be smaller if the initial degrees of freedom, df_A , are large.⁴ The proposed cutoffs for this index do not take

⁴ For example, if $RMSEA_A = .05$, $df_A = 50$, and $df_D = 10$, $\Delta RMSEA = .01$. However, if $df_A = 200$, while all the other values are the same (that is, the amount of misfit per added degree of freedom has not changed), $\Delta RMSEA = 0.003$. One can see another variant of this relationship in Figure 2 of MacCallum, Browne, & Cai (2006), where $\Delta RMSEA$ is held constant while df_A increases, and it is shown that the power of the chi-square difference test increases. That is, $\Delta RMSEA$ is not directly capturing the noncentrality associated with this test. These authors also show (their

this dependency on the size of the initial model into account, and as a result, in larger models this index will tend to accept nearly all constraints. In a later section, we illustrate this behavior on three examples.

RMSEA associated with the difference test

Instead of Equation (2), we propose to compute RMSEA associated with the difference test to compare nested models. This computation is given by (Browne and Du Toit, 1992):

$$RMSEA_D = \sqrt{\frac{D - df_D}{df_D(N-1)}}, \quad (3)$$

which is a direct generalization of Equation (1). When $D < df_D$, $RMSEA_D$ is set to zero. Table 1 provides a parallel definition for multiple group models, due to Dudgeon (2004).

$RMSEA_D$ has the conventional interpretation as the amount of additional misfit introduced by the constraints in Model B per additional degree of freedom gained by Model B. It is on the same metric as any other RMSEA (e.g., it cannot be negative), permitting the use of existing guidelines. Because $RMSEA_D$ is a transformation of the chi-square difference test in the same way the overall model RMSEA is a transformation of the model chi-square test, a simple analytic CI for $RMSEA_D$ can be obtained using existing methodology (Raykov & Penev, 1998; Steiger & Fouladi, 1996). Lastly, this index is the most direct test of the close fit of the proposed constraints; it does not depend on df_A , only on df_D , and therefore it will not lose sensitivity in larger models. We recommend the same sequential testing procedure for the evaluation of close fit using the RMSEA as for the evaluation of the exact model fit; that is, evaluate $RMSEA_A$, and

Figure 4) that $\Delta RMSEA$ does not capture the loss of power in the chi-square difference test when the initial model fits more poorly. In their words, “[The] effect size is determined by the pair of the RMSEA values and not simply by their difference” (p. 25). Actually, it is determined directly by $RMSEA_D$.

if close fit of Model A is accepted, then evaluate $RMSEA_D$. If this procedure is followed, $RMSEA_D$ will inherit the desirable property of asymptotic independence that is enjoyed by the chi-square difference test.

Table 2 gives population-level expressions for $\Delta RMSEA$ and $RMSEA_D$ in terms of $RMSEA_A$ and $RMSEA_B$ in three different scenarios: both models are true, Model A is true while Model B is false, and both models are false. This table illustrates the interpretational advantage of $RMSEA_D$ over $\Delta RMSEA$ at the population level from another angle. When Model A is true but Model B is false, $\Delta RMSEA$ is equal to $RMSEA_B$ in the population, so it is not a test of the specific constraints distinguishing Model B from Model A, and the misfit due to the additional constraints may not be noticeable in the overall value of $\Delta RMSEA$. On the other hand, $RMSEA_D$ undoes this dilution by multiplying by a factor of $\sqrt{df_B / df_D}$, resulting in a more sensitive test of the constraints (see also Brace, 2020).

Prior Literature on $RMSEA_D$

Equation (3) was proposed by Browne and Du Toit (1992), who called it the Root Deterioration per Restriction (RDR).⁵ Following the ideas of Steiger (1998), Dudgeon (2004) extended Equation (3) to MG models (see Table 1). The use of this index has been limited. Only about a dozen substantive articles cite Browne and Du Toit (1992) specifically for the development of Equation (3) and subsequently use it to compare nested models (e.g., del Barrio, Carrasco, & Holgado, 2006; Ehm, Hasselhorn, & Schmiedek, 2019; Ferrando, 2003; Ferrando, Anguiano-Carrasco, & Chico, 2011; Fouladi, McCarthy, & Moller, 2002; Hilderbrandt et. al,

⁵ We opted not to use the abbreviation “RDR” in this article, but to refer to this index as $RMSEA_D$, in order to stress that it can be interpreted as the usual RMSEA.

2011; Hilderbrandt, Wilhelm, & Robitzsch, 2009; Raykov & Marcoulides, 2009; Oort, 2009; Penk & Richter, 2016; Pekrun, et. al, 2019; Wu & Hughes, 2015; Zimprich, Allemand, & Dellenbach, 2009). While some of these applications compute Equation (3) in a multiple-group context, none use the correct extension to multiple groups due to Dudgeon (2004; see Table 1). Only two articles reference Dudgeon (2004) for the MG version of Equation (3); both are assessments of measurement invariance (Koomen et. al., 2012; Huizink et al, 2016).

While it is difficult to say for certain why the development of Browne and Du Toit (1992) has been forgotten, we speculate that there are at least two reasons. First, the unfortunate labeling of it as “RDR” rather than a type of RMSEA may have led methodologists interested in using RMSEA for nested model comparisons to miss these contributions. Second, the original developers of this index may have begun discouraging its use. We found the following reflection in MacCallum, Browne, and Cai (2006): “[E]xperience with RDR has indicated that it is difficult to use or interpret. Michael W. Browne, who initially proposed RDR and is the second author of the current article, has abandoned the RDR index... The RDR can indicate a large difference in fit between two models that both have small RMSEA values and consequently both fit closely.” (p. 23). The interpretational inconsistency that can arise when $RMSEA_A$ and $RMSEA_B$ are similar and small but $RMSEA_D$ indicates lack of fit in the added constraints was therefore seen by these authors as a problem. However, we see the sensitivity of $RMSEA_D$ to the misspecification in the added constraints as a feature and not a bug. It is not desirable that constraints should be tested less stringently when the initial model is larger, but this is the situation when $RMSEA_A$ and $RMSEA_B$ tend to be similar and small. As already noted, the same interpretational inconsistency can arise when examining the overall chi-square values T_A and T_B

versus the difference test D , where the recommended sequence is: T_A , D . We return to this issue in the discussion.

Equation (3) is so intuitive that several methodologists have reinvented it in specific contexts, without appearing to be aware of the earlier developments. Without claiming to be exhaustive, we describe several such contributions. McDonald and Ho (2002), in their classic review of reporting practices in SEM, computed Equation (3) for a set of 14 articles reporting on the fit of an SEM with both a measurement (i.e., relations between latent variables and observed indicators) and a structural component (i.e., relations among latent variables). Model A was the original model, whereas Model B had a saturated structural (“path”) part. McDonald and Ho write: “If we are willing to rest on the established properties of the RMSEA, the results suggest that in all but a few cases the goodness of fit of the composite structural model, with its large number of degrees of freedom, conceals the badness of fit of the path model, with its much smaller number of degrees of freedom” (p. 75). It is notable that these authors cite Browne & du Toit (1992), but not for the development of Equation (3).

Building on McDonald and Ho (2002), Williams and O’Boyle (2011) dubbed Equation (3) RMSEA-P, or “RMSEA, with a focus on the path model” (p. 361). O’Boyle and Williams (2011) computed Equation (3) for 43 studies across applied psychology and organizational behavior journals, finding that it was greater than .08 in 63% of the studies, indicating misfit in the structural part of the model. They describe Equation (3) as “a relatively novel fit index” (p. 1) and do not cite Browne and du Toit (1992).

In an article focusing on best practices in higher-order confirmatory factor analysis research, Crede and Harms (2015) recommended the use of Equation (3) to compare the fit of a higher-order factor model and the model with correlated first-order factors, citing both

McDonald and Ho (2002) and Williams and O’Boyle (2011). In a literature review of 20 published articles from organizational psychology and management journals, Crede and Harms (2015) found that 80% had $RMSEA_D > .08$, suggesting many articles missed significant misfit in the higher-order factor structure.

In the context of MI assessment, Yuan and Chan (2016) advocated that chi-square difference tests be replaced by equivalence tests (i.e., tests of “not close fit”; MacCallum, Browne, & Sugawara, 1996), where the null hypothesis specifies the value of the population RMSEA. They illustrated this approach on the RMSEA associated with the difference test, computed using the generalization of Equation (3) to multiple groups (see Table 1). These authors do not cite any of the earlier literature on Equation (3) and refer to all RMSEA values, whether based on the overall model chi-square or on the difference test, simply as RMSEA.

A Related Development

Li and Bentler (2011) proposed the following RMSEA-like index for comparing nested models, which differs from Equation (3) only in that it uses df_B rather than df_D in the

denominator: $RMSEA_{LB} = \sqrt{\frac{D - df_D}{df_B(N - 1)}}$. This index captures the amount of additional misfit

introduced by the constraints in Model B averaged over the initial *and* the added degrees of freedom ($df_B = df_A + df_D$). This index will always be smaller than $RMSEA_B$ (because $df_B > df_D$), and thus it will be insensitive to the misspecification introduced by the constraints in Model B, particularly for models with large initial degrees of freedom (df_A).

Empirical Examples

The articles reviewed in the previous section provide many examples of the use of $RMSEA_D$. In this section we provide three additional examples that explicitly compare $RMSEA_D$

and ΔRMSEA on data that appeared in published articles. The first two examples focus on MI assessment in multiple groups and over time, respectively. The third example focuses on the comparison of single-group models with different numbers of factors. Our re-analysis is purposely simple, ignoring in some cases the issues of fit of the less restrictive model. It is meant for illustration and not as a re-interpretation of the published results.

Example 1: Measurement Invariance in Multiple Groups

Byrne (2006) illustrated the use of MG SEM on a sample of responses to the 22-item Maslach Burnout Inventory (MBI; Maslach & Jackson, 1986) by elementary ($N_1 = 580$) and secondary ($N_2 = 692$) school teachers. Following Byrne, we fit a modified 3-factor model, containing 2 cross-loadings and 4 residual covariances, as the configural invariance model to the raw data.⁶ This model does not fit by the chi-square test (see Table 3), but produces $\text{RMSEA} = .056$ with $90\% \text{CI} = [.053, .060]$. Following Yuan and Chan (2016), we interpreted this evidence of good approximate fit as permitting further invariance assessment. Table 3 shows the results for a sequence of MI tests that constrain, in turn, factor loadings, intercepts, residual variances, factor variances and covariances, and factor means.

Illustrating the problem described in this article, the overall model RMSEA changes very little across the five models. The large initial degrees of freedom ($df = 400$) make it difficult to evaluate the added misfit coming from the constraints imposed by each model. As a result of little change in the overall RMSEA , ΔRMSEA lacks sensitivity, equaling essentially zero and supporting all constraints. On the other hand, the chi-square difference tests are all statistically significant due to a large sample size. In contrast to both the difference tests and ΔRMSEA , RMSEA_D communicates meaningful differentiating information about the amount of misfit

⁶ R code to reproduce this and all other examples is available on our OSF page: <https://osf.io/2ycd6/>

resulting from each set of constraints. The point estimates indicate that, using existing guidelines for the RMSEA, the constraints associated with metric invariance (i.e., equal loadings) have close fit, and the next three constraints can be described as having either “mediocre” or “fair” fit (MacCallum et al., 1996; Yuan & Chan, 2016).

In order to account for sampling variability, we also performed equivalence tests based on $RMSEA_D$. There is a duality between the outcome of an equivalence test of $H_0: RMSEA_{D,0} > c$ and the 90% CI. An equivalence test is statistically significant at $\alpha = .05$ whenever the corresponding 90% CI lies completely below c . The 90% CIs for $RMSEA_D$ are shown in Table 3.⁷ The value c can be interpreted as the largest acceptable population value, and should ideally be selected prior to seeing the data. For illustration, setting $c = .10$ (values $> .10$ have been described as “poor” fit; Browne & Cudeck, 1993) results in the rejection of the null hypothesis of $H_0: RMSEA_{D,0} > .10$ for loading and intercept constraints (the upper bound of the CI for these tests is just below .10), permitting the researcher to accept these constraints, but the null hypothesis of poor fit for further constraints cannot be rejected. In addition to the results of the equivalence test, researchers should also inspect the CI itself, because its width can communicate whether the test is uninformative due to insufficient sample size (MacCallum et al., 1996). Note that in addition to sample size, the CI for the RMSEA is affected by the df for the corresponding chi-square test, so that for tests based on fewer df, as is the case with the constraints of factor variances and covariances in this example, a larger sample size would be needed to draw informative conclusions based on the RMSEA.

Example 2: Longitudinal Measurement Invariance

⁷ We provide R code for obtaining the exact p-values for the equivalence test at <https://osf.io/2ycd6/>

As part of a larger study of subjective well-being during the COVID-19 pandemic, Zacher and Rudolph (2021) conducted a longitudinal MI assessment (across 4 time points) of a 10-item 2-factor measure of positive and negative affect. The configural model has $RMSEA = .055$ with 90% CI $[.053, .056]$, based on $N = 1,588$. Beyond the configural model, the authors tested three levels of invariance, shown in Table 4. The overall RMSEA again changes very little across the four models, and as a result $\Delta RMSEA$ has little sensitivity. In contrast, $RMSEA_D$ values are more informative. Specifically, the constraints on the loadings are found to have very close fit, whereas subsequent constraints add more substantial misfit. To take sampling fluctuations into account, we performed the equivalence test of the null hypothesis $H_0: RMSEA_{D,0} > .10$ for each set of constraints. The null hypothesis is rejected for all three sets of constraints (the CI falls below .10). If a more stringent value of c was selected (e.g., .08), different conclusions would be reached, accepting the constraints on the loadings but not the additional constraints. Using the terminology of MacCallum et al. (1996), we can conclude that the constraints on the loadings have “fair” fit ($< .08$), but we can only conclude that the remaining constraints have “mediocre” fit ($< .10$).

Example 3: Factor Structure Assessment

Szigeti, Balazs, Bikfalvi, and Urban (2016) fit a series of confirmatory factor analysis models to data collected from $N = 211$ school teachers who filled out the Hungarian version of the Maslach Burnout Inventory (same as in Example 1). Raw data for this example were not available, so we computed $RMSEA_D$ and $\Delta RMSEA$ from the chi-square statistics and degrees of freedom reported in the article. Table 5 shows these values for a subset of models considered by the authors: 4-, 3-, 2-, and 1-factor models, where models with fewer factors are obtained by combining some factors from the previous model into a single factor, resulting in a sequence of

nested models. In this example, the least restricted model is a 4-factor model, which strictly speaking did not have “fair” ($<.08$) approximate fit to the data by the equivalence test, $RMSEA = 0.072$, $90\%CI = [.062, .081]$. However, we will proceed with further constraints for illustration.

Again, the overall RMSEA changes very little across the first three models (4-, 3-, and 2-factor models), and the resulting $\Delta RMSEA$ values are essentially zero. Even when evaluating the additional constraints leading to the 1-factor model, $\Delta RMSEA$ is only .015, which is on the border of a commonly used cutoff (Chen, 2007).⁸ In contrast, all point estimates of $RMSEA_D$ are quite high. Only the value for the 3-factor model constraints is below .10. To take sampling fluctuations into account, we performed equivalence tests of the null hypothesis $H_0: RMSEA_{D,0} > .10$ for each comparison. The null hypothesis is not rejected for any of the three comparisons. However, the CIs for the model constraints are wide, e.g., [.027, .174] for the constraints imposed by the 3-factor model, suggesting that sampling variability is too high. This effect is in part due to the very small df (Kenny, Kaniskan, & McCoach, 2015). Thus, a more appropriate conclusion for this example is that the equivalence tests are severely underpowered, and a larger sample size would be needed. This example illustrates the impact of the combination of small df and small sample size on the width of the CI for $RMSEA_D$. It also illustrates how equivalence tests revert the logic of hypothesis testing in SEM back to the familiar situation where researchers would wish to have a larger sample size rather than worrying about “too much” power, so that the undesirable null hypothesis of poor fit of a more constrained model could be rejected, if false.

⁸ We note that cutoffs for $\Delta RMSEA$ were developed in the context of MI evaluation, and may not be as applicable here.

Discussion

Summary

In nested model comparison of SEMs, a shift has been occurring away from reliance on chi-square difference tests and toward the evaluation of approximate fit. This shift is particularly pronounced in areas of research where researchers view constraints as desirable, such as evaluations of metric or scalar invariance (Putnick & Bornstein, 2016). In these applications, approximate fit of nested models is often evaluated by computing differences in fit indices, such as ΔRMSEA . At the same time, chi-square difference tests are still being used when researchers are interested in showing the superiority of a more complex model (e.g., a model with more latent factors). In this article we have advocated for the use of RMSEA associated with the chi-square difference test (Browne & Du Toit, 1992; Dudgeon, 2004), which we call RMSEA_D , to compare nested models. This fit index is parallel to the overall model RMSEA, which is routinely reported alongside the chi-square test of model fit. Like the overall model RMSEA, RMSEA_D has an advantage over the chi-square difference test in that it focuses on approximate rather than exact fit of constraints. It also has advantages over ΔRMSEA , as summarized below.

First, ΔRMSEA can have little sensitivity to added misspecification, as was illustrated in all three examples in this article. This lack of sensitivity is due to the fact that the initial Model A often has large degrees of freedom (df_A) relative to the degrees of freedom introduced by the constraints in Model B (df_D). When RMSEA_B is computed, the additional misfit introduced by the constraints is spread over the entire degrees of freedom for Model B, $df_B = df_A + df_D$, resulting in very similar values of RMSEA_B and RMSEA_A , and therefore a very small value of ΔRMSEA . In contrast, RMSEA_D assesses the worsening of fit due to the introduced constraints per introduced degree of freedom (df_D). Therefore, it is a more focused measure that does not

involve irrelevant parts of the model already presumed to be mostly correct, and will often have much greater sensitivity to misspecification.

Second, ΔRMSEA is not on the same metric as RMSEA, and its values cannot be interpreted like a traditional RMSEA index. Cutoffs have been developed specifically for this index in the context of multiple-group MI assessment (e.g., Chen, 2007), but this research is limited, and ΔRMSEA is increasingly being used in areas of application outside of MI. These cutoffs also do not account for the dependence of ΔRMSEA on the initial degrees of freedom df_A . In contrast, RMSEA_D is just an RMSEA computed from the chi-square difference test. Its metric and interpretation remain the same: it captures the amount of additional misfit in per introduced degree of freedom. Therefore, new guidelines for how to interpret its values are not necessarily needed, although future research should address under what circumstances tentative cutoffs may need to be adjusted, as we discuss in the next section.

Third, an analytic CI is not easily available for ΔRMSEA . Recently, Lai (2020) developed an analytic approach for CIs for differences in fit indices, but the computations are complex and not easily accessible to applied researchers. In contrast, a simple analytic CI for RMSEA_D can be computed in the same way as for the RMSEA (Browne & Cudeck, 1993; Raykov & Penev, 1998), so that sampling fluctuations can be taken into account when assessing the increase in misfit. The CI also enables researchers to evaluate the hypothesis of “not close fit” using equivalence tests (MacCallum, Browne, & Sugawara, 1996; Yuan, Chan, Marcoulides, & Bentler, 2016). These tests specify a directional null hypothesis that researchers should want to reject (i.e., $H_0: \text{RMSEA}_0 > c$). The hypothesis is rejected when the 90% CI for the RMSEA or RMSEA_D is completely below the specified cutoff value c . The main advantage of these tests is

that they return the logic of hypothesis testing back to where a large sample results in a more informative test because the null hypothesis is no longer trivially true.

Recommendations

Before researchers proceed with nested model comparisons, the least restricted model (Model A) should be established to be well-fitting. We recommend that Model A should be found to be well-fitting by the equivalence test based on $RMSEA_A$, using a cutoff value that is specified ahead of time (commonly used values include .06 and .08). While many researchers follow best practices of reporting the CI for the overall model $RMSEA$, few interpret the results in accordance with the logic of equivalence tests. For example, if researchers say in Methods that they will consider a model to have acceptable approximate fit if $RMSEA < .08$ (i.e., “fair” fit), but then they obtain a point estimate of .072 and a 90% CI = [0.062, 0.081], they fail to reject the null hypothesis that $RMSEA_0 > .08$ in the population, and the model cannot be said to have “fair” fit. Strictly speaking, researchers should then not proceed with nested model comparisons. In addition to the equivalence test based on $RMSEA_A$, the evaluation of Model A should be supplemented by inspecting other fit indices (e.g., CFI, SRMR), model residuals, reasonableness of the estimated parameter values, and so on. The model may also need to be modified in order to achieve good initial fit.

When evaluating constraints imposed by the nested Model B, we recommend that researchers report the chi-square difference test along with its degrees of freedom, and $RMSEA_D$ and its associated 90% CI. These recommendations parallel best practices when reporting on the fit of the overall model (e.g., chi-square test should be reported, even if it is not interpreted; Kline, 2015). We recommend that inference about the fit of constraints imposed by Model B be conducted via the equivalence test based on $RMSEA_D$, along with the inspection of the

associated CI. Adhering to the logic of equivalence tests is even more important for judgements of fit based on $RMSEA_D$, because CIs for the RMSEA are wider when the associated degrees of freedom are small. Because RMSEA is also more sensitive to misspecification when the degrees of freedom are small, a researcher may decide that the cutoff for $RMSEA_D$ should be more relaxed than for $RMSEA_A$ (e.g., .1 rather than .08, as we illustrated in all three examples in this article). Prior knowledge and existing literature should be taken into consideration when determining these values. For example, cutoffs may need to be more relaxed when evaluating MI across different cultural groups when such a comparison has not been done before, but they may be stricter in a replication study. In the next section, we also discuss other “nuisance variables” that may influence the choice of RMSEA cutoffs in a given research situation.

Our recommendations are similar to the approach to nested model comparison followed in Yuan and Chan (2016), who focused on multiple-group MI assessment, but we depart from their approach in two ways. First, these authors evaluated the fit of Model B using both the overall RMSEA for the nested model (i.e., $RMSEA_B$) and $RMSEA_D$, but they did not make clear recommendations for a preferred strategy should this procedure yield conflicting results. Yet conflicting results are possible: For instance, in our Example 1, all model RMSEAs are relatively small, but the RMSEA based on the difference test reveals substantial misfit in some types of constraints (see Table 3). We recommend evaluating the fit of the additional constraints in Model B based on $RMSEA_D$, not based on $RMSEA_B$. We make this recommendation for the same reason we do not recommend $\Delta RMSEA$ to compare nested models: $RMSEA_B$ is highly similar to $RMSEA_A$ for models with large initial degrees of freedom, and $RMSEA_D$ will provide a more sensitive assessment of the constraints. As noted earlier, a similar issue arises with the use of chi-square difference tests, where contradictions between the overall test of fit and the difference test

are also possible; chi-square difference tests are usually recommended because they are asymptotically independent and because they specifically evaluate the additional constraints, rather than the overall model (Steiger, Shapiro, & Browne, 1985).

The second difference between our approach and that Yuan and Chan (2016) is that they develop an alternative way to descriptively label fit based on RMSEA, which involves comparing the upper limit of the corresponding 90% CI to new cutoffs, which are sample-size and df-dependent. These cutoffs intend to approximate what the CI limit would have been if the sample RMSEA had been equal exactly to the pre-specified cutoff value (e.g., .08). We believe, however, that this procedure erases the advantage of equivalence tests because it is roughly equivalent to just comparing sample RMSEA to the specified cutoff without using the CI.⁹ Yuan and Chan (2016) do make an important point that in some situations both the chi-square difference test *and* the equivalence test can be nonsignificant, leaving the researcher in a predicament where they cannot reject either the hypothesis of exact fit or the hypothesis of poor fit. Unfortunately, in some cases the data are simply uninformative about the model at hand, and the best solution is to collect a larger sample.¹⁰ In situations where this is not possible, a simpler alternative to Yuan and Chan's procedure would be to conduct an equivalence test with a more

⁹ Alternatively, this procedure can be understood as permitting the cutoff value for the equivalence test to depend on sample size, so that asymptotically the cutoff values remain unchanged (e.g., .08), but in small samples they are more relaxed. Because specifying a population level hypothesis using information about sample size is non-standard, we recommend the simpler procedure of selecting a more relaxed cutoff for the equivalence test a priori if the researcher wants to test a less stringent hypothesis.

¹⁰ This situation is not unique to SEM. In the context of psychology's replication crisis, much has been written about the drawbacks of null hypothesis significance tests, and the superiority of both Bayes factors and equivalence tests, which often yield similar conclusions (Lakens, McLatchie, Isager, Scheel, & Dienes, 2020). In small samples, it is possible that neither the traditional null hypothesis of zero effect nor the equivalence test null hypothesis of "effect size of interest" can be rejected. Similarly, a Bayes factor may take on values between common cutoffs of 1/3 and 3, which is uninformative and indicates that more data is needed.

relaxed cutoff, specified ahead of time, or to simply report the CI to indicate which levels of misfit *can* be rejected.

When using RMSEA_D, we assume the initial Model A fits the data well, and this assessment is typically done using global indices of approximate fit. However, a major limitation of all global indices of fit is that small values can mask serious local misfit in one part of the model. This criticism has appeared with striking regularity in the methodological literature (e.g., Mulaik, 1989; McDonald & Ho, 2002; McDonald, 2010; Lance, Beck, Fan, & Carter, 2016). Therefore, our broader recommendation is to follow an approach to model testing that is as disaggregated as possible (Anderson & Gerbing, 1988), beginning with a model that is as saturated as possible, and ending with the final model that is obtained from the initial model by imposing a series of constraints.

Limitations and Future Research Directions

Despite its near universal use to assess fit of SEMs, RMSEA has also been criticized on various grounds, and some of these critiques are inherited by RMSEA_D. Despite these limitations, we believe RMSEA is a useful index of fit assessment in SEM, and we frame the discussion of its limitations in terms of open questions for future research.

The first limitation of all indices of approximate fit is their sensitivity to the so-called “nuisance factors,” or variables that some researchers believe they should not be sensitive to. In the case of the RMSEA, the most notable finding is that it is sensitive to the strength of the factor loadings, all else being equal (Browne et al., 2002; Hancock & Mueller, 2011; Miles and Shevlin, 2007; Saris & Satorra, 1992; Savalei, 2012). This finding is not too surprising, given that RMSEA is based on the chi-square test, which is known to lose power when the correlations

among the variables decrease, because the residuals will be low even if the model is very wrong. In fact, Moshagen and Auerwald (2018) showed that the sensitivity of RMSEA to loadings disappears if the size of the model residuals is held constant while the loadings increase. Nonetheless, methodologists have cautioned against “universal cutoffs” that do not take measurement quality into account (Savalei, 2012; McNeish, An, & Hancock, 2018). Future research should address how much of this sensitivity to correlation strength is inherited by the RMSEA_D in different application contexts.

Another “nuisance factor” is the number of variables in the model, or the model’s degrees of freedom (they are often conflated in simulations). Population values of RMSEA have been found to generally decrease with model size, and this effect is most pronounced when correlations among the variables (i.e., loadings in a CFA model) are high (Breivik & Olsson, 2001; Kenny & McCoach, 2003; Savalei, 2012; Shi, Lee, & Maydeu-Olivares, 2019). Future research should investigate whether RMSEA_D inherits this property, and to what extent. Depending on the type of misspecification, one could make the argument that some sensitivity to model size is actually desirable—for example, if a CFA model is misspecified because there are three omitted residual correlations, this is arguably a much smaller misspecification if the number of variables is 20 than if it is 10. Nonetheless, when variables have high correlations and the *df* are relatively small, more lax cutoffs could be considered for the overall model RMSEA and for RMSEA_D (e.g., .10 instead of .06 or .08).¹¹ Future research should also try to disentangle the effects of *df* from the effects of model size (*p*). Note that RMSEA_D can be based on relatively

¹¹ Other fit indices, such as CFI and SRMR, may be less sensitive to model size or sensitive to it in different ways (Shi, Lee, & Maydeu-Olivares, 2019; Shi, DiStefano, Maydeu-Olivares, & Lee, 2021), but they have other shortcomings (Moshagen & Auerwald, 2018). We do not want to create the impression that only RMSEA is sensitive to “nuisance factors”, but our focus is on the RMSEA in this article. Relying on multiple fit indices is recommended when assessing the overall model fit.

small df regardless of the overall model size, as would be the case when comparing models with different numbers of factors. In other contexts, such as assessment of metric or scalar MI, model size and the degrees of freedom for $RMSEA_D$ will be correlated.

A second limitation, which is specific to $RMSEA_D$, is that in order for the chi-square difference test to behave as expected (e.g., to maintain accurate Type I error rates when the constraints imposed by Model B are true), Model A must be true in the population. When this is not the case, conclusions based on the chi-square test, and by extension $RMSEA_D$, may be biased. This is because the limiting values of parameter estimates of interest may be distorted by the misspecification in other parts of the model, so that correct constraints imposed by Model B may appear incorrect or vice versa (see footnote 4 for an example). However, the extent of this bias has been studied very little. The most well-known article alerting researchers to this problem (Yuan & Bentler, 2004) presents some examples of this bias, but they are such that Model A exhibits very poor initial fit to the data, which is not the typical situation in which researchers compare nested models. Yuan and Chan (2016) endorse the practice of interpreting $RMSEA_D$ whenever $RMSEA_A$ is found to be acceptable. Future research should investigate how the type and the degree of misspecification in Model A can bias chi-square difference tests, and therefore $RMSEA_D$, in typical research contexts.

Yet another limitation of the RMSEA is that it tends to have large sampling variability when the degrees of freedom are small (e.g., Kenny, Kanishkan, & McCoach, 2015; Shi, DiStefano, Maydeu-Olivares, & Lee, 2021). This criticism is especially relevant for $RMSEA_D$, as the chi-square difference test is more likely to be based on small df . Example 3 (Table 5) provides an illustration of this phenomenon in the extreme case when $df_D = 1, 2, \text{ or } 3$. Thus, inferences about the RMSEA may require much larger sample sizes when the df are very small.

However, the CIs reflect this uncertainty, and it is important to use this information when interpreting the RMSEA. Simulation studies examining the behavior of the RMSEA with small df have found that while point estimates performed poorly, CIs performed quite well (Kenny, Kanishkan, & McCoach, 2015; Shi, DiStefano, Maydeu-Olivares, & Lee, 2021). We note that this criticism of the RMSEA tends to apply only to the very smallest df; in such contexts, researchers may not need a summary index of misfit and could simply look at the estimated parameters in the less restricted model to gauge the need for constraints (e.g., the CI for the estimated correlation in a 2-factor model can be used to judge whether a 1-factor model is a reasonable approximation). In the context of MI assessment, the most common tests, namely metric and scalar invariance, will tend to have large enough df so that CIs on RMSEA_D will be informative (e.g., see Tables 3 and 4).

Lastly, we note several additional future directions. When data are nonnormal and the robust methodology is used (Satorra & Bentler, 1994), a finite sample adjustment to Equation (1) that preserves the population value but improves small sample performance is given by

$$RMSEA_{ROBUST} = \sqrt{\frac{T - k}{df(N - 1)}}, \text{ where } k \text{ is the scaling correction (Brosseau-Liard, Savalei, \& Li,}$$

2012). The same type of adjustment can be applied to Equation (3), but there are several versions of the scaling correction for robust difference tests (Satorra, 2000; Satorra & Bentler 2001; 2010), and future research should address whether this choice affects the robust version of RMSEA_D.¹² Future research should also investigate the performance of different types of CIs for the robust version of RMSEA_D (Savalei, 2018). Developments for incomplete (and possibly also

¹² All these scaling corrections are available via the *lavaan* function `lavTestLRT` by specifying `method="satorra.bentler.2001"`, `method="satorra.bentler.2010"`, or `method="satorra.2000"`.

nonnormal) data that parallel those for the model RMSEA in Zhang and Savalei (2022) will also be the subject of future research. Lastly, while we advocate reporting RMSEA_D over ΔRMSEA as a relatively simple solution that will dramatically increase power to detect local misspecification, other approaches to local fit evaluation have recently been proposed that should be seriously considered and studied (e.g., Lance, Beck, Fan, & Carter, 2016; Thoemmes, Rosseel, & Textor, 2018; Bollen, 2019). There is emerging consensus in the methodological literature that local fit assessment has to become more central in the evaluation of fit of SEMs.

CFI Comparison for Nested Models

This article focused on the RMSEA for nested model comparisons, but this index is often used in conjunction with other fit indices, most commonly the CFI (Bentler, 1990), computed in the sample as $CFI = 1 - (T - df) / (T_N - df_N)$, where T_N is the chi-square for the baseline model with df_N degrees of freedom.¹³ For this index to make sense, the baseline model must be nested within the proposed model. Typically under the baseline model, covariances are constrained to zero while variances are freely estimated, and in the case of a mean structure, means are constrained to be equal. When constraints on the mean or on the variance parameters are present in the proposed model (e.g., MI constraints on item intercepts and/or on the residual variances), the baseline model should be properly modified to remain nested (Widaman & Thompson, 2003; Lai & Yoon, 2015), although such modifications are not automated in popular software. We recommend that researchers use CFI_A to evaluate the fit of the initial model A, as well as other

¹³ We state this simplified definition for ease of discussion. Technically, the numerator is $\max\{T - df, 0\}$ and the denominator is $\max\{T - df, T_N - df_N, 0\}$, so that CFI remains between 0 and 1.

indices of approximate fit. Recently, a CI has been developed for the CFI index (Lai, 2019), though it is not yet implemented in SEM software.

In nested model comparisons, $\Delta RMSEA$ is often used in conjunction with $\Delta CFI = CFI_B - CFI_A$ (Cheung & Rensvold, 2002; Chen, 2007). A commonly proposed combination of cutoffs to be used to reject the added constraints in larger samples is $\Delta RMSEA > .015$ and $\Delta CFI < -.01$ (Chen, 2007), though other guidelines exist (e.g., Meade et al., 2008, Putnick & Bornstein, 2016). Similar concerns apply to ΔCFI as to $\Delta RMSEA$, namely, that this index is not very sensitive to misspecification in Model B (French & Finch, 2006; 2018), although some authors suggest it may work better than $\Delta RMSEA$ (Chen, 2007). An additional concern is that researchers typically do not adjust the baseline model so that it remains nested when computing CFI for some models, relying on default values produced by software packages. For tests of scalar and further forms of invariance in studies of MI, the CFI value for all models with constraints on the mean structure is incorrectly computed by software, resulting in incorrect values of ΔCFI as well.

Unfortunately, a solution parallel to $RMSEA_D$ to replace ΔCFI does not help very much even when CFI_A and CFI_B are correctly computed so that the baseline model for each is nested within Models A and B. Suppose we make a further modification so that the baseline model used for CFI_A and CFI_B is the same, and it is properly nested within Models A and B. More generally, when comparing a series of nested models, the researcher would pick *one* baseline model that is nested within all. In this case, $\Delta CFI < 0$, and we can define $CFI_D \equiv 1 - \frac{T_D - df_D}{T_N - df_N} = 1 + \Delta CFI$. This index is a trivial transformation of ΔCFI and will not gain greater sensitivity (although existing studies of ΔCFI did not adjust the baseline model). However, it is now on the metric of the CFI,

in that larger values indicate better fit, and it is bound to the [0,1] interval, so it does represent a small improvement over ΔCFI .

A better solution that is possible in some cases is to change the baseline model to result in a more sensitive relevant comparison. In the context where Model A is a measurement model (i.e., the structural part is saturated) and Model B imposes constraints on relationships among the latent variables, one can define a “structural null” model where the latent variables are unrelated to each other, and other comparative fit indices become possible (Williams & O’Boyle, 2011; Lance et al., 2016). However, such a solution is not easily generalizable to other nested model comparisons.¹⁴ Overall, when comparing nested models, an index of comparative fit that compares each model to a baseline model may just not be the right tool in the evaluation of the specific constraints introduced by the more nested model. Because the existing approach of reporting ΔCFI lacks sensitivity, whether researchers report it or not alongside RMSEA_D may not make a material difference.

Conclusion

MacCallum, Browne, and Cai (2006) dismissed the RMSEA associated with the difference test as a useful index of fit, citing evidence that it often indicated misfit when the overall RMSEA for the more constrained model was acceptable. In this article we argue that RMSEA_D ’s greater ability to detect misfit specifically due to the added constraints is a feature and not a bug. Given the widespread criticism that global fit indices are insensitive to

¹⁴ Given that the original conceptualization of the CFI already involves a comparison of nested models (a proposed model and a very restrictive baseline model), a CFI-like index for a nested model comparison of Models A and B can be computed as $(T_A - df_A) / (T_B - df_B)$, which would be close to 1 when the additional constraints introduced by Model B do not introduce much more misfit relative to Model A. But this index is based on the same information as RMSEA_D , capturing the change in fit on a percentage instead of a difference metric, and thus it departs in spirit somewhat from the overall model RMSEA and CFI, which are based on different information. We plan to explore this index in future research.

misspecification in large models, $RMSEA_D$ has been repeatedly re-discovered by different methodologists to help solve this problem. We believe $RMSEA_D$ should be computed in all nested SEM comparisons and reported alongside the chi-square difference test. To take sampling variability into account, it should be reported with a CI, and equivalence tests against a priori defined values are recommended.

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Appendix. The relationship between $RMSEA_A$, $RMSEA_B$, and $RMSEA_D$

For single-group models, the population-level definitions (i.e., assuming N is large enough to be ignored, and applying the definition in Table 1) of the $RMSEA$ for Model A and Model B are:

$$RMSEA_{A,0} = \sqrt{\frac{\hat{F}_A}{df_A}}; \quad RMSEA_{B,0} = \sqrt{\frac{\hat{F}_B}{df_B}}$$

Then, $\hat{F}_B = df_B RMSEA_{B,0}^2$ and $\hat{F}_A = df_A RMSEA_{A,0}^2$, from where it follows that

$$RMSEA_{D,0} = \sqrt{\frac{\hat{F}_B - \hat{F}_A}{df_B - df_A}} = \sqrt{\frac{df_B RMSEA_{B,0}^2 - df_A RMSEA_{A,0}^2}{df_B - df_A}},$$

which leads to

$$df_D RMSEA_{D,0}^2 = df_B RMSEA_{B,0}^2 - df_A RMSEA_{A,0}^2,$$

or equivalently

$$RMSEA_{D,0}^2 = \frac{df_B}{df_D} RMSEA_{B,0}^2 - \frac{df_A}{df_D} RMSEA_{A,0}^2.$$

Taking the square-root will yield the expression for $RMSEA_{D,0}$ given in Table 2. The same

relationship also holds for the sample definitions, as shown below:

$$\begin{aligned} RMSEA_D^2 &= \frac{\hat{F}_B - \hat{F}_A}{df_D} - \frac{1}{N-1} = \left(\frac{\hat{F}_B}{df_B} - \frac{1}{N-1} \right) \frac{df_B}{df_D} - \frac{\hat{F}_A}{df_D} + \frac{1}{N-1} \frac{df_B}{df_D} - \frac{1}{N-1} \\ &= \frac{df_B}{df_D} RMSEA_B^2 - \frac{df_A}{df_D} \left(\frac{\hat{F}_A}{df_A} - \frac{1}{N-1} \right) - \frac{df_A}{df_D} \frac{1}{N-1} + \frac{df_B}{df_D} \frac{1}{N-1} - \frac{1}{N-1} \\ &= \frac{df_B}{df_D} RMSEA_B^2 - \frac{df_A}{df_D} RMSEA_A^2 - \frac{1}{N-1} \left(\frac{df_A - df_B}{df_D} + 1 \right) = \frac{df_B}{df_D} RMSEA_B^2 - \frac{df_A}{df_D} RMSEA_A^2 \end{aligned}$$

The same relationship holds for MG models. In this case, expressions for all RMSEA indices are multiplied by $\sqrt{G}$. In finite samples, the term $1/(N-1)$ is replaced by $1/(N-G)$ in all equations, not affecting the algebra.

Table 1. Definitions of the ML fit function, test statistic, RMSEA for overall model fit, and RMSEA for the difference test in single-group and MG models.

Model	ML Fit Function	Test Statistic	RMSEA	RMSEA _D
Single Group	$F(\mu(\theta), \Sigma(\theta) \bar{x}, S)$ $= \log \Sigma(\theta)S^{-1} + \text{tr}(S\Sigma(\theta)^{-1})$ $+ (\bar{x} - \mu(\theta))' \Sigma(\theta)^{-1} (\bar{x} - \mu(\theta)) - p$	$T = (N - 1)F(\mu(\hat{\theta}), \Sigma(\hat{\theta}) \bar{x}, S)$ $= (N - 1)\hat{F}$	$RMSEA = \sqrt{\frac{T - df}{df(N - 1)}}$ $= \sqrt{\frac{\hat{F}}{df} - \frac{1}{N - 1}}$	$RMSEA_D = \sqrt{\frac{D - df_D}{df_D(N - 1)}}$ $= \sqrt{\frac{\hat{F}_B - \hat{F}_A}{df_D} - \frac{1}{N - 1}}$
Multiple Groups	$F_{MG} = \sum_{g=1}^G \frac{N_j - 1}{N - G} F(\mu_j(\theta), \Sigma_j(\theta) \bar{x}_g, S_g)$	$T = \sum_{g=1}^G (N_j - 1)F(\mu_j(\hat{\theta}), \Sigma_j(\hat{\theta}) \bar{x}_g, S_g)$ $= (N - G)\hat{F}_{MG}$	$RMSEA_{MG} = \sqrt{\frac{T - df}{df(N - G) / G}}$ $= \sqrt{\frac{\hat{F}_{MG}}{df / G} - \frac{G}{N - G}}$	$RMSEA_{D, MG} = \sqrt{\frac{D - df_D}{df_D(N - G) / G}}$ $= \sqrt{\frac{\hat{F}_{MG, B} - \hat{F}_{MG, A}}{df_D / G} - \frac{G}{N - G}}$

Note. For a single group, $\bar{x}$ and S are sample mean vector and covariance matrix, N is the number of observations, p is the number of variables, and $\mu(\theta)$ and $\Sigma(\theta)$ are the model-implied mean vector and covariance matrix under the proposed SEM, where θ contains the model parameters. For multiple-groups, $\bar{x}_g$ and S_g are sample mean vector and covariance matrix in group g , where $g = 1, \dots, G$; N_j is the sample size in group g ; N is the total sample size; and $\mu_g(\theta)$ and $\Sigma_g(\theta)$ are the model-implied mean vector and covariance matrix for group g , where θ is the vector of all model parameters, whether group-specific or common to all groups. When the test statistic value is smaller than df , RMSEA is set to zero. In some computer programs, the default sample size multiplier is N rather than $N - 1$, which is consistently used in all computations such as the test statistic and the RMSEA. This makes little practical difference except in very small samples. For nested models A and B, their fit function minima are denoted by subscripts “A” and “B”, respectively, and $D = T_B - T_A$ and $df_D = df_B - df_A$. In all RMSEA equations, if the numerator in the fraction under the square-root is negative, it is set to zero.

Table 2. Population values of the RMSEA indices under three possible scenarios.

Scenario	$RMSEA_{A,0}$	$RMSEA_{B,0}$	$RMSEA_{D,0}$	$\Delta RMSEA_0$
Model B is true (and therefore Model A is true)	0	0	0	0
Model B is false, Model A is true	0	$RMSEA_{B,0}$	$\sqrt{\frac{df_B}{df_D}} RMSEA_{B,0}$	$RMSEA_{B,0}$
Model A is false (and therefore Model B is false)	$RMSEA_{A,0}$	$RMSEA_{B,0}$	$\sqrt{\frac{df_B}{df_D} RMSEA_{B,0}^2 - \frac{df_A}{df_D} RMSEA_{A,0}^2}$	$RMSEA_{B,0} - RMSEA_{A,0}$

Note. Population values are denoted by subscript “0”. All equations apply to single-group and MG models, and subscripts “MG” are omitted for simplicity. See Appendix for the derivation of the expression in the last row.

Table 3. Example of multiple-group MI assessment with RMSEA_D using data from Byrne (2006)

Invariance Test	Model chi-square	Model df	Model RMSEA	T_D	df_D	ΔRMSEA	RMSEA_D	90% CI for RMSEA_D
configural	1208.4	400	0.056	--	--	--	--	--
loadings	1250.4	421	0.056	42.037	21	-0.0007	0.040	[0.022, 0.057]
intercepts	1352.9	440	0.057	102.527	19	0.0015	0.083	[0.068, 0.099]
residual variances	1482.9	462	0.059	129.966	22	0.0018	0.088	[0.074, 0.103]
factor (co)variances	1508.1	468	0.059	25.189	6	0.0002	0.071	[0.044, 0.101]
factor means	1564.8	471	0.060	56.693	3	0.0013	0.168	[0.131, 0.207]

Note. Our configural invariance model differs slightly from the final configural model obtained via model modification in Byrne (2006). Specifically, in our model, the additional parameters (2 cross-loadings and 4 residual covariances) are freely estimated in both groups, whereas Byrne (2006) constrained one of the cross-loadings and one of the residual covariances to zero in one of the groups. Thus, our configural model has 2 fewer df and fits slightly better.

Table 4. Example of longitudinal MI assessment with RMSEA_D using data from Zacher & Rudolph (2021)

Invariance Test	Model chi-square	Model df	Model RMSEA	T_D	df_D	ΔRMSEA	RMSEA_D	90% CI for RMSEA_D
configural	3743.76	652	0.055	--	--	--	--	--
loadings	3805.91	676	0.054	62.14	24	-0.001	0.032	[0.022, 0.041]
intercepts	4118.49	700	0.055	312.59	24	0.001	0.087	[0.079, 0.096]
factor means	4176.74	706	0.056	58.25	6	0.000	0.074	[0.057, 0.092]

Note. All models include residual covariances among the same items measured at different time points. Uncorrected full information maximum likelihood (FIML) model chi-square and RMSEA are reported. This longitudinal study had high amounts of missing data, so FIML fit indices may underestimate misfit (Zhang & Savalei, 2020).

Table 5. Example of factor structure assessment with RMSEA_D using statistics reported in Szigeti et al. (2016)

Model	Model chi- square	Model df	Model RMSEA	T_D	df_D	ΔRMSEA	RMSEA_D	90% CI for RMSEA_D
4-factor	423	203	0.072	--	--	--	--	--
3-factor	432	206	0.072	9	3	0.000	0.098	[0.027, 0.174]
2-factor	442	208	0.073	10	2	0.001	0.138	[0.062, 0.228]
1-factor	547	209	0.088	105	1	0.015	0.704	[0.594, 0.821]

Note. Model chi-square values were reported rounded to whole values in the original article. Robust statistics based on the FIML estimator were reported, which may underestimate misfit (Brosseau-Liard, Savalei, & Li, 2012).